



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 05:57 AM UTC

PDB ID : 4V65 / pdb_00004v65
EMDB ID : EMD-1055
Title : Structure of the E. coli ribosome in the Pre-accommodation state
Authors : Devkota, B.; Caulfield, T.R.; Tan, R.-Z.; Harvey, S.C.
Deposited on : 2008-08-03
Resolution : 9.00 Å(reported)
Based on initial models : 1EHZ, 2I2P

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

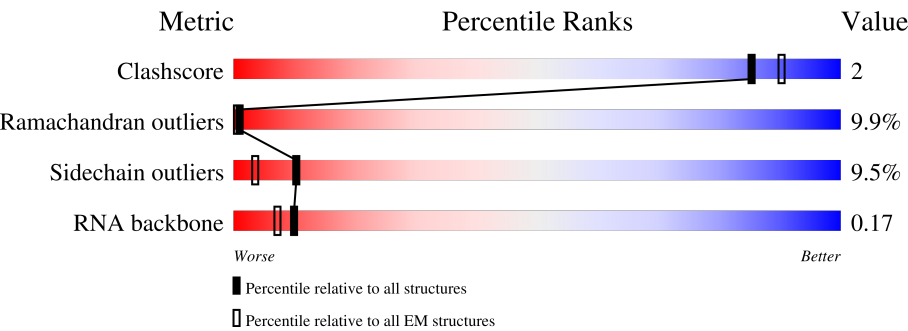
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 9.00 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RNA backbone	8273	3508

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	76	57% 14% 53% 29%
1	AE	76	58% 12% 33% 38% 17%
1	AP	76	50% 30% 42% 24%
2	AM	20	25% 30% 35% 35%
3	A1	1530	65% 6% 25% 40% 29%
4	AB	241	71% 61% 23% 6% 10%
5	AC	129	47% 64% 23% 9%

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Mol	Chain	Length	Quality of chain
6	AD	124	76% 52% 33% 12% ..
7	AF	118	55% 53% 35% 8% ..
8	AG	101	88% 61% 27% 7% 5%
9	AH	89	84% 53% 39% . . .
10	AI	82	100% 49% 39% 12%
11	AJ	84	73% 55% 35% 5% . 5%
12	AK	75	29% 45% 27% . 27%
13	AL	92	82% 43% 33% 9% . 14%
14	AN	87	56% 67% 26% . . .
15	AO	233	31% 60% 24% . 12%
16	AQ	71	39% 41% 23% . . 28%
17	AR	206	62% 63% 30% 6%
18	AS	159	38% 58% 28% 6% . 6%
19	AT	135	55% 46% 23% . . 26%
20	AU	179	35% 50% 28% 5% . 16%
21	AV	130	48% 76% 19% . .
22	AW	130	81% 63% 31% . . .
23	AX	103	73% 46% 42% 8% 5%
24	BA	117	71% 35% 41% 20%
25	BB	2903	52% 6% 26% 41% 27%
26	BC	94	72% 64% 33% .
27	BD	123	48% 47% 40% 10% . .
28	BE	144	67% 51% 36% 10% .
29	BF	136	57% 53% 33% 12% .
30	BG	127	35% 57% 38% . .

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Mol	Chain	Length	Quality of chain
31	BH	117	
32	BI	115	
33	BJ	118	
34	BK	103	
35	BL	110	
36	BM	99	
37	BN	270	
38	BO	103	
39	BP	85	
40	BQ	63	
41	BR	59	
42	BS	70	
43	BT	57	
44	BU	54	
45	BV	46	
46	BW	64	
47	BX	38	
48	BY	209	
49	BZ	213	
50	B1	201	
51	B2	178	
52	B3	177	
53	B4	149	
54	B5	142	
55	B6	140	

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 149248 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 A/T, P and E-site tRNAs.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	75	Total	C	N	O	P	0	0
			1600	715	288	523	74		
1	AP	75	Total	C	N	O	P	0	0
			1600	715	288	523	74		
1	AE	76	Total	C	N	O	P	0	0
			1622	725	293	529	75		

- Molecule 2 is a RNA chain called mRNA model.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AM	20	Total	C	N	O	P	0	0
			397	180	40	158	19		

- Molecule 3 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A1	1530	Total	C	N	O	P	0	0
			32828	14642	6024	10633	1529		

- Molecule 4 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AB	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 5 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AC	117	Total	C	N	O	S	0	0
			876	540	174	159	3		

- Molecule 6 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AD	123	Total	C	N	O	S	0	0
			954	590	196	164	4		

- Molecule 7 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AF	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 8 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AG	96	Total	C	N	O	S	0	0
			773	483	160	127	3		

- Molecule 9 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AH	88	Total	C	N	O	S	0	0
			715	440	146	128	1		

- Molecule 10 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AI	82	Total	C	N	O	S	0	0
			648	406	128	113	1		

- Molecule 11 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AJ	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 12 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	AK	55	Total	C	N	O	0	0
			455	288	86	81		

- Molecule 13 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AL	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 14 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	85	Total	C	N	O	S	0	0
			664	411	137	113	3		

- Molecule 15 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AO	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 16 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AQ	51	Total	C	N	O	S	0	0
			425	265	86	73	1		

- Molecule 17 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AR	205	Total	C	N	O	S	0	0
			1642	1026	315	297	4		

- Molecule 18 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AS	150	Total	C	N	O	S	0	0
			1105	687	211	201	6		

- Molecule 19 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AT	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 20 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AU	150	Total	C	N	O	S	0	0
			1174	730	226	214	4		

- Molecule 21 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AV	129	Total	C	N	O	S	0	0
			978	616	173	183	6		

- Molecule 22 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AW	127	Total	C	N	O	S	0	0
			1021	634	206	178	3		

- Molecule 23 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AX	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 24 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BA	117	Total	C	N	O	P	0	0
			2504	1116	459	813	116		

- Molecule 25 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BB	2903	Total	C	N	O	P	0	0
			62317	27801	11467	20147	2902		

- Molecule 26 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BC	94	Total	C	N	O	S	0	0
			752	479	137	133	3		

- Molecule 27 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BD	121	Total	C	N	O	S	0	0
			930	582	179	164	5		

- Molecule 28 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BE	144	Total	C	N	O	S	0	0
			1052	654	207	189	2		

- Molecule 29 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BF	136	Total	C	N	O	S	0	0
			1073	686	205	176	6		

- Molecule 30 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BG	127	Total	C	N	O	S	0	0
			1007	621	204	177	5		

- Molecule 31 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BH	117	Total	C	N	O	S	0	0
			899	557	179	162	1		

- Molecule 32 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BI	114	Total	C	N	O	S	0	0
			916	574	179	162	1		

- Molecule 33 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	BJ	117	Total	C	N	O	0	0
			946	604	192	150		

- Molecule 34 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BK	103	Total	C	N	O	S	0	0
			815	516	153	144	2		

- Molecule 35 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BL	110	Total	C	N	O	S	0	0
			856	532	166	155	3		

- Molecule 36 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BM	99	Total	C	N	O	S	0	0
			777	491	145	139	2		

- Molecule 37 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BN	267	Total	C	N	O	S	0	0
			2053	1271	416	359	7		

- Molecule 38 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BO	102	Total	C	N	O		0	0
			779	492	146	141			

- Molecule 39 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BP	84	Total	C	N	O	S	0	0
			633	391	129	112	1		

- Molecule 40 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BQ	63	Total	C	N	O	S	0	0
			508	313	99	94	2		

- Molecule 41 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BR	58	Total	C	N	O	S	0	0
			448	281	87	78	2		

- Molecule 42 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BS	70	Total	C	N	O	S	0	0
			548	339	104	99	6		

- Molecule 43 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BT	56	Total	C	N	O	S	0	0
			443	269	94	79	1		

- Molecule 44 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BU	54	Total	C	N	O	S	0	0
			440	284	81	75			

- Molecule 45 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BV	46	Total	C	N	O	S	0	0
			376	228	90	56	2		

- Molecule 46 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BW	64	Total	C	N	O	S	0	0
			503	323	105	73	2		

- Molecule 47 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BX	38	Total	C	N	O	S	0	0
			301	185	65	47	4		

- Molecule 48 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BY	209	Total	C	N	O	S	0	0
			1564	979	288	293	4		

- Molecule 49 is a protein called 50S ribosomal protein L1P.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BZ	213	Total	C	N	O	S	0	0
			1687	1078	300	308	1		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BZ	1	MET	-	insertion	UNP P35024
BZ	?	-	MET	deletion	UNP P35024
BZ	70	SER	PHE	conflict	UNP P35024
BZ	82	LYS	ASN	conflict	UNP P35024
BZ	?	-	MET	deletion	UNP P35024
BZ	?	-	MET	deletion	UNP P35024
BZ	?	-	MET	deletion	UNP P35024

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	B1	201	Total	C	N	O	S	0	0
			1551	974	283	289	5		

- Molecule 51 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	B2	178	Total	C	N	O	S	0	0
			1419	905	251	257	6		

- Molecule 52 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	B3	176	Total	C	N	O	S	0	0
			1322	832	243	245	2		

- Molecule 53 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	B4	149	Total	C	N	O	S	0	0
			1110	699	197	213	1		

- Molecule 54 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	B5	141	Total	C	N	O	S	0	0
			1031	651	179	195	6		

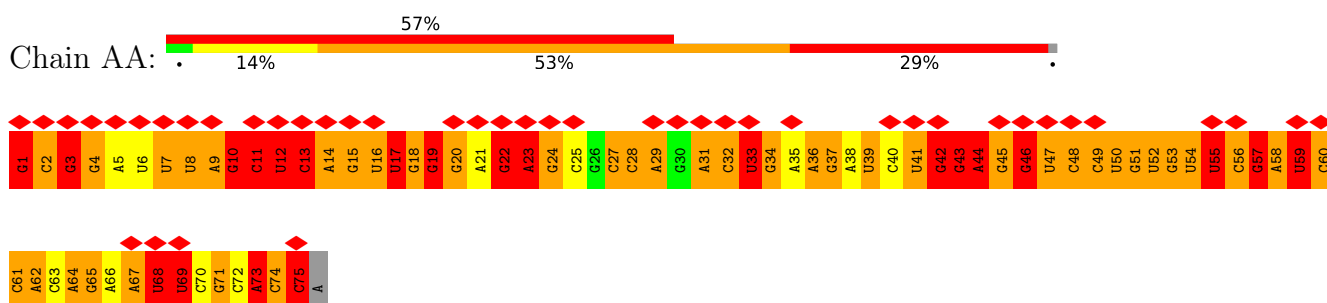
- Molecule 55 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	B6	140	Total	C	N	O	S	0	0
			1112	704	210	194	4		

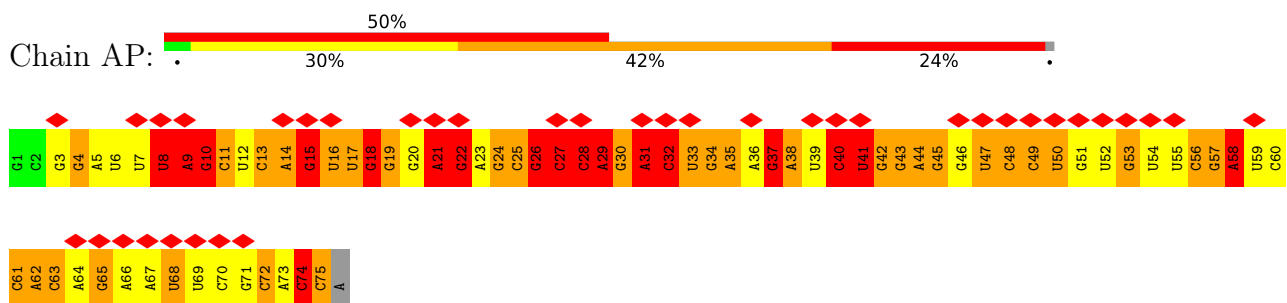
3 Residue-property plots

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.

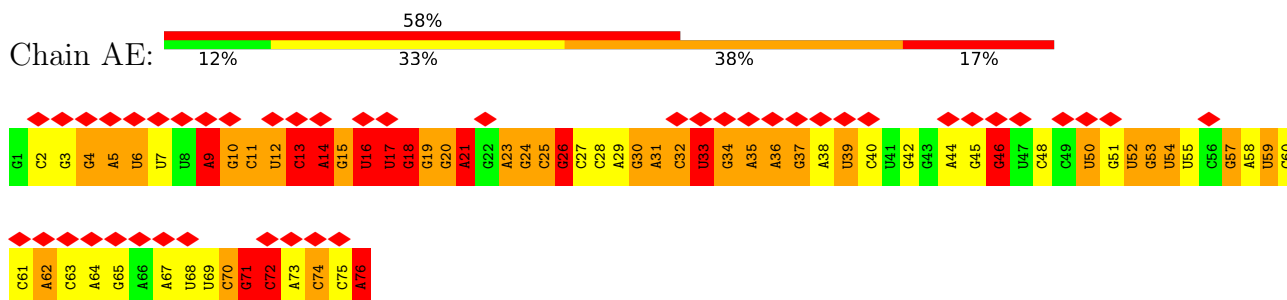
- Molecule 1: A/T, P and E-site tRNAs



- Molecule 1: A/T, P and E-site tRNAs



- Molecule 1: A/T, P and E-site tRNAs



- Molecule 2: mRNA model



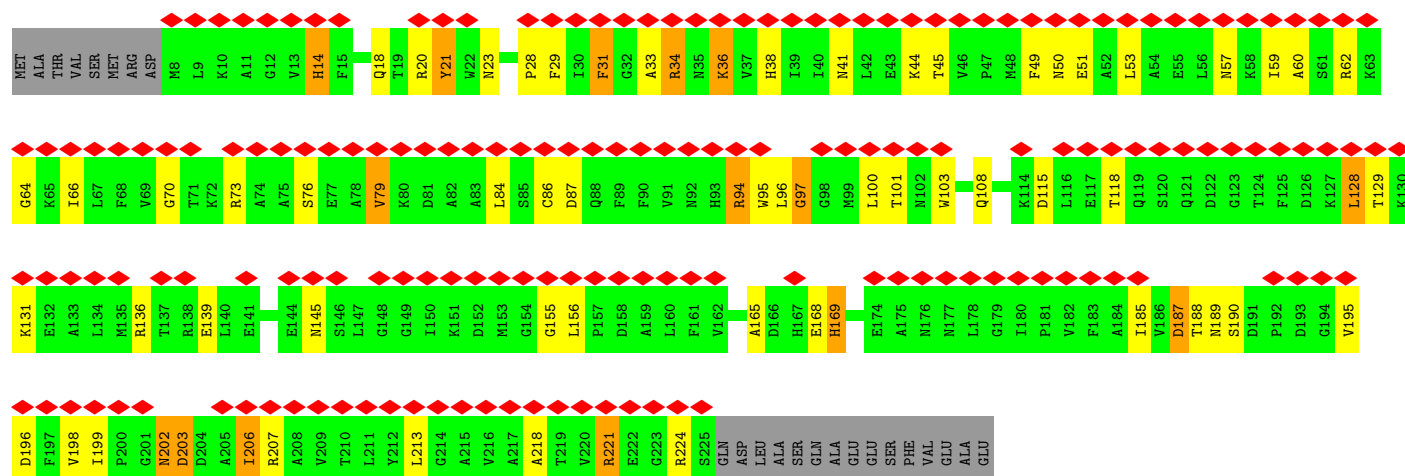
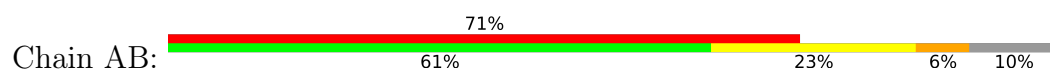
Chain A1: 6% 25% 40% 29%



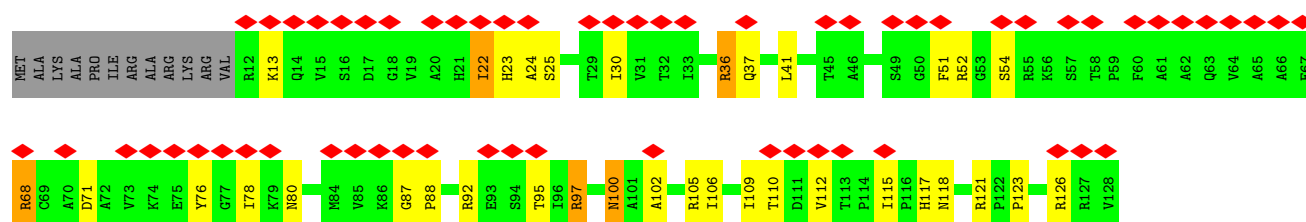




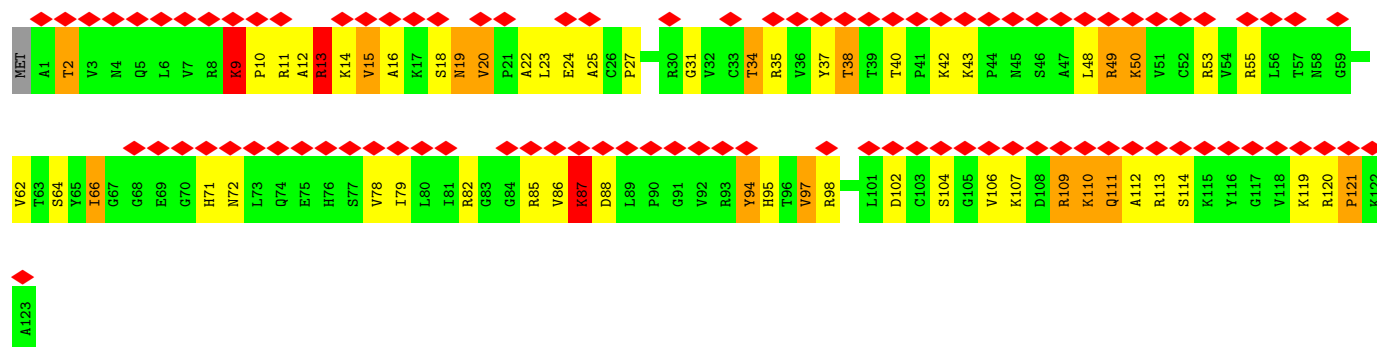
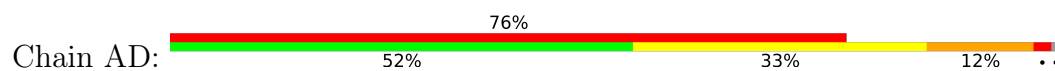
• Molecule 4: 30S ribosomal protein S2



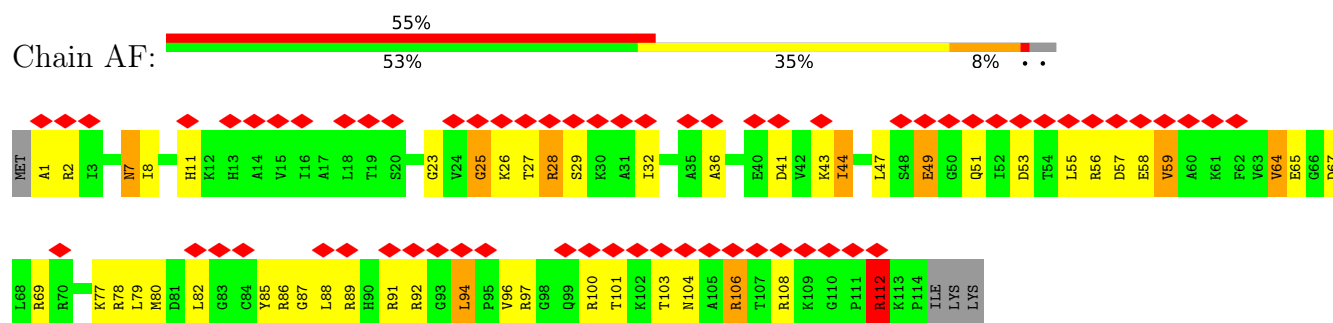
• Molecule 5: 30S ribosomal protein S11



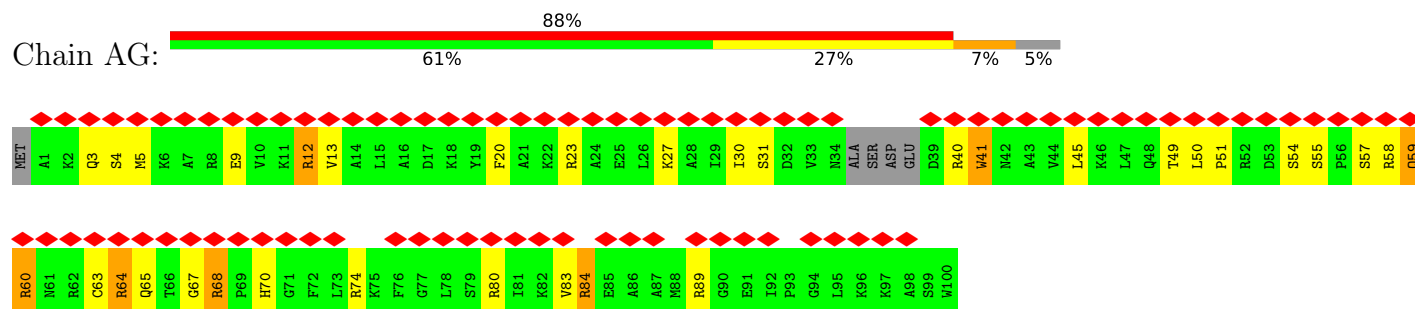
• Molecule 6: 30S ribosomal protein S12



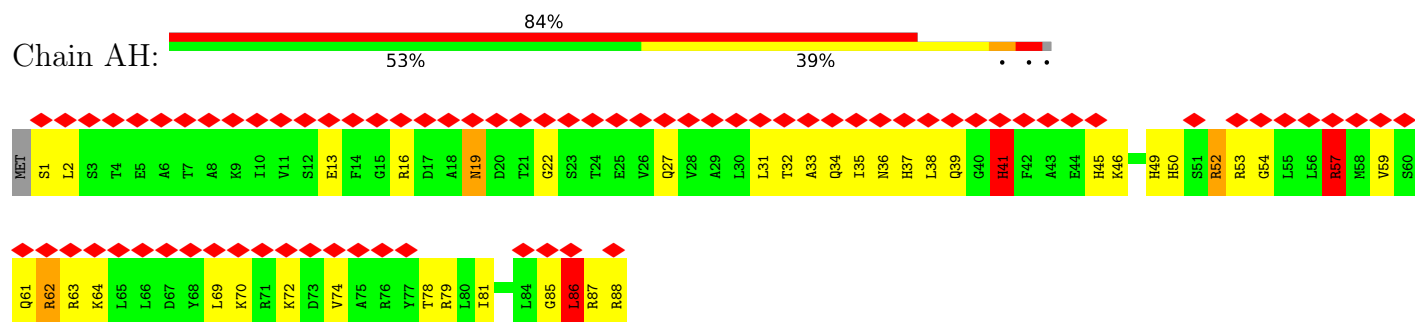
• Molecule 7: 30S ribosomal protein S13



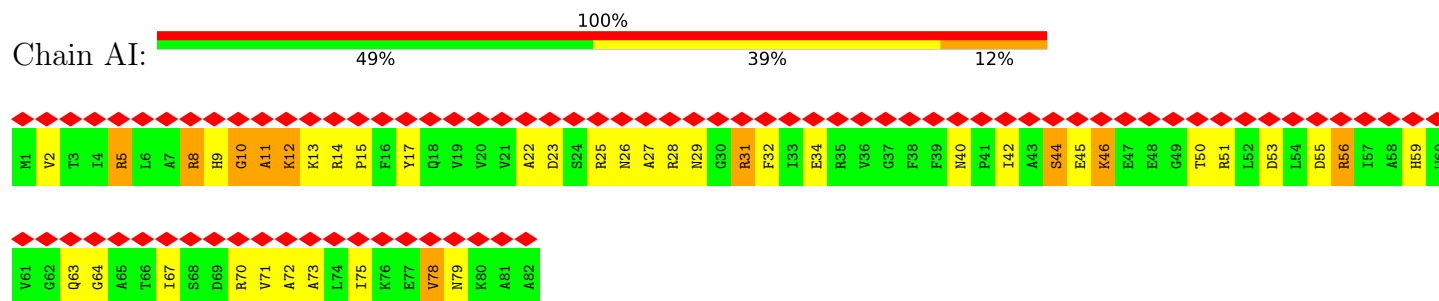
- Molecule 8: 30S ribosomal protein S14



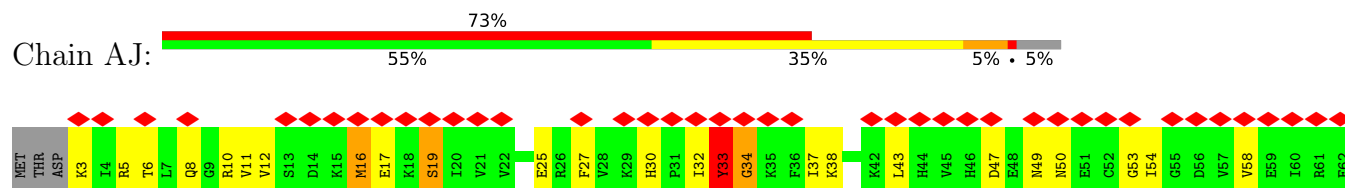
- Molecule 9: 30S ribosomal protein S15



- Molecule 10: 30S ribosomal protein S16

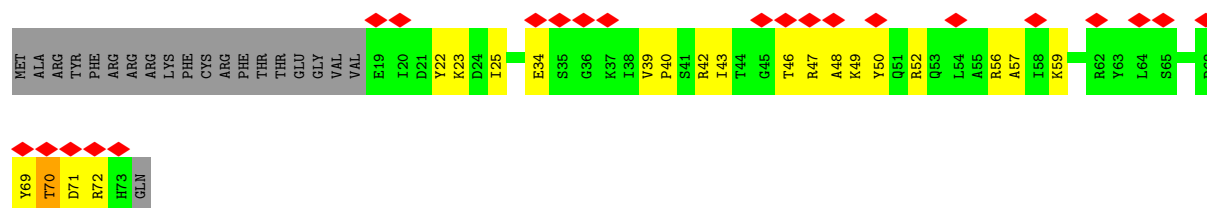


- Molecule 11: 30S ribosomal protein S17

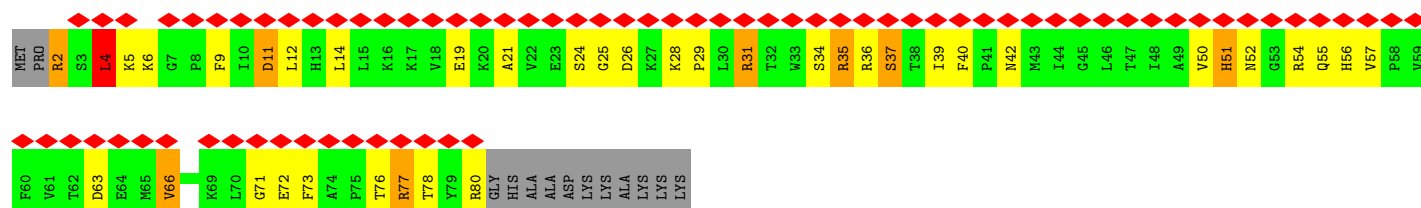
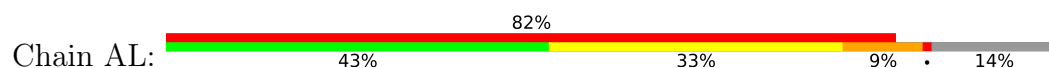




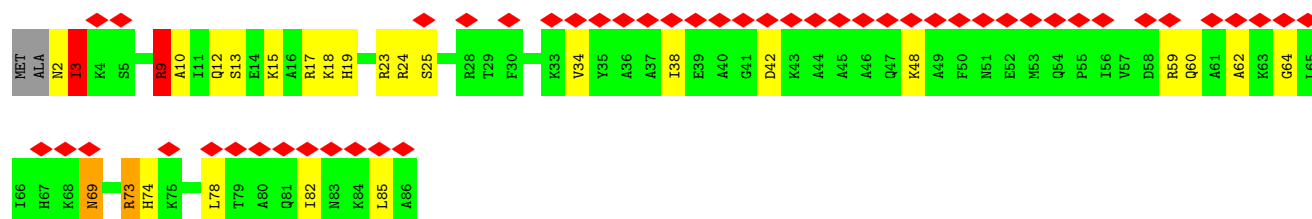
- Molecule 12: 30S ribosomal protein S18



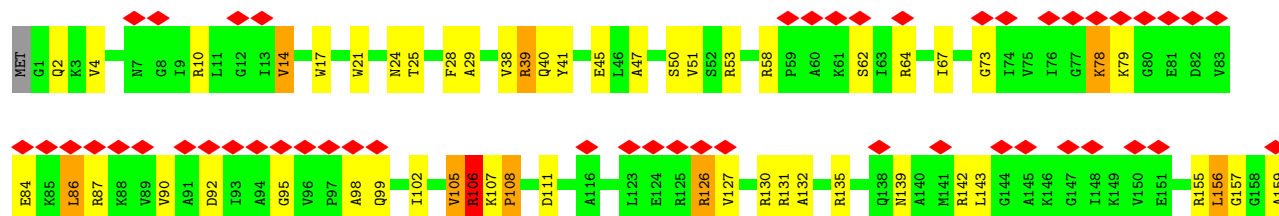
- Molecule 13: 30S ribosomal protein S19

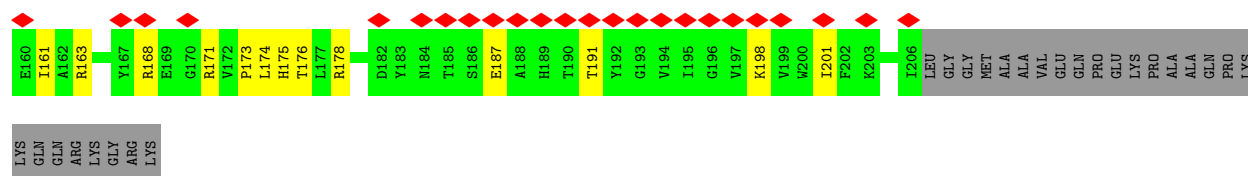


- Molecule 14: 30S ribosomal protein S20

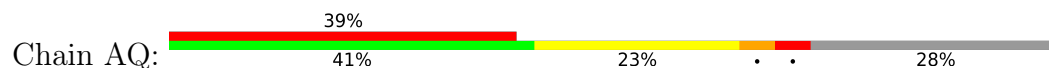


- Molecule 15: 30S ribosomal protein S3

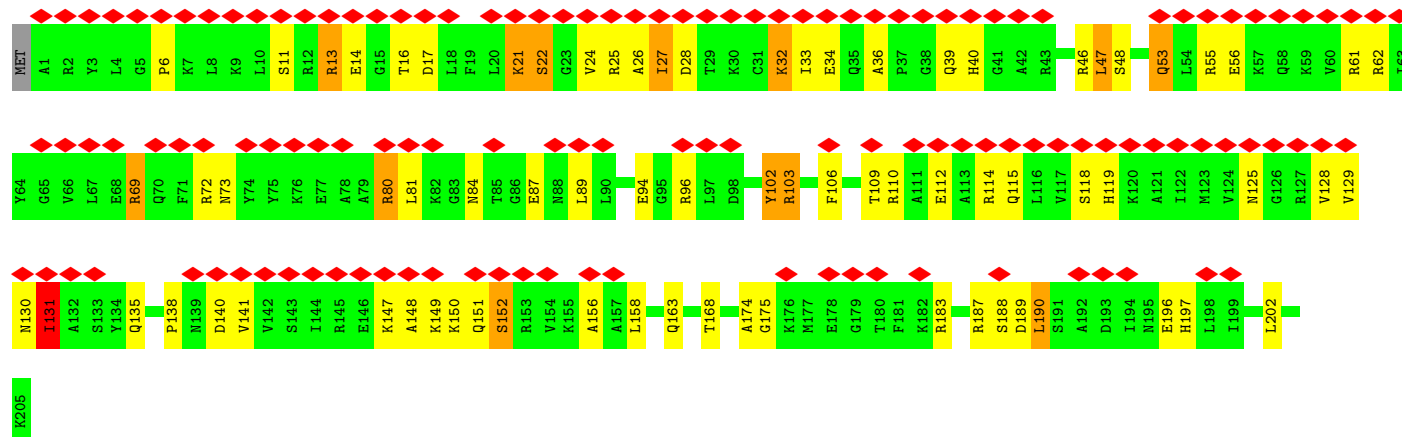




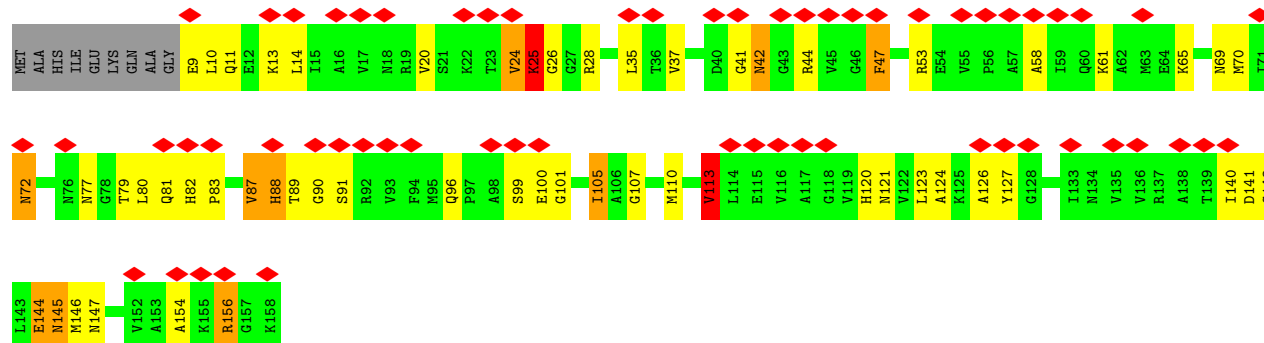
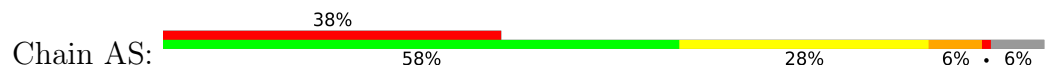
- Molecule 16: 30S ribosomal protein S21



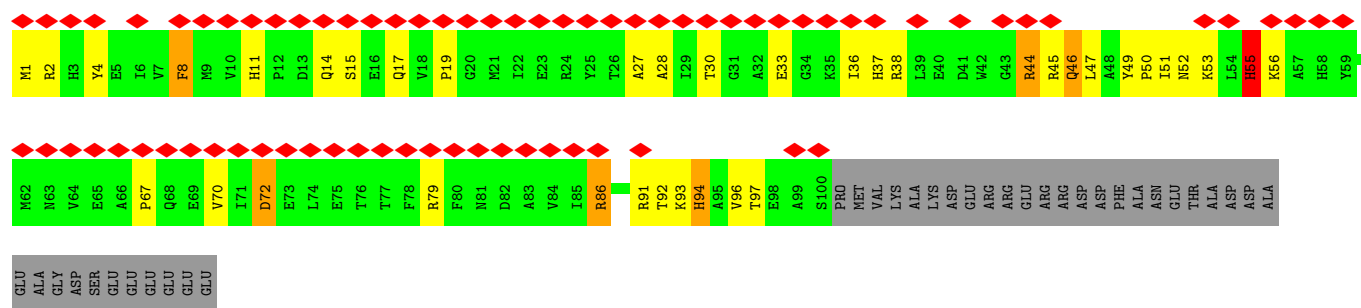
- Molecule 17: 30S ribosomal protein S4

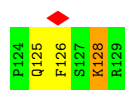


- Molecule 18: 30S ribosomal protein S5

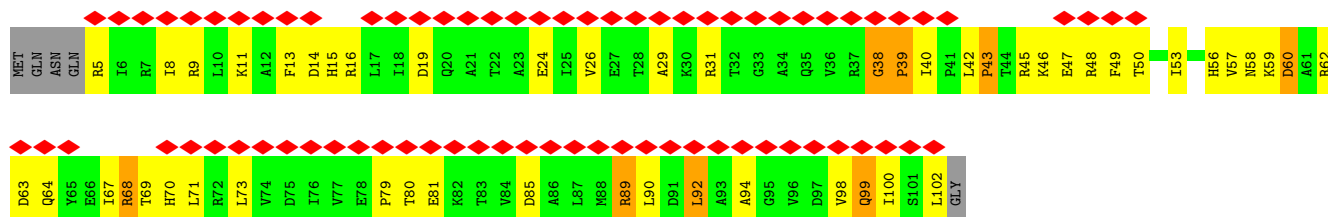
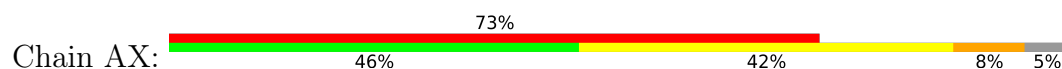


- Molecule 19: 30S ribosomal protein S6

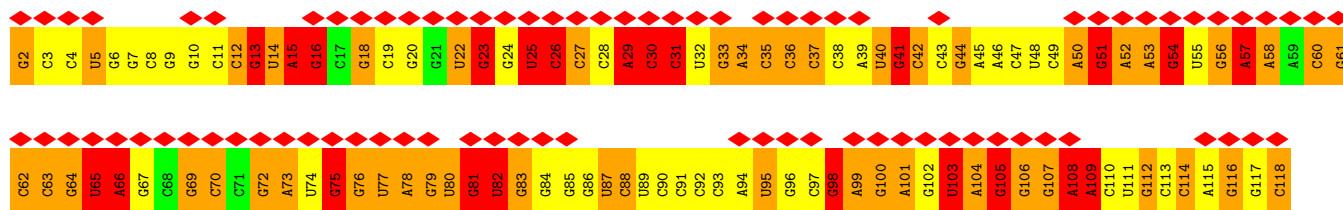
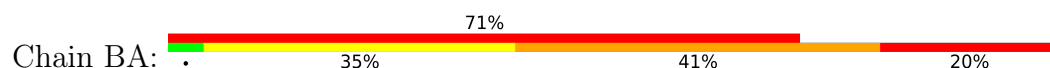




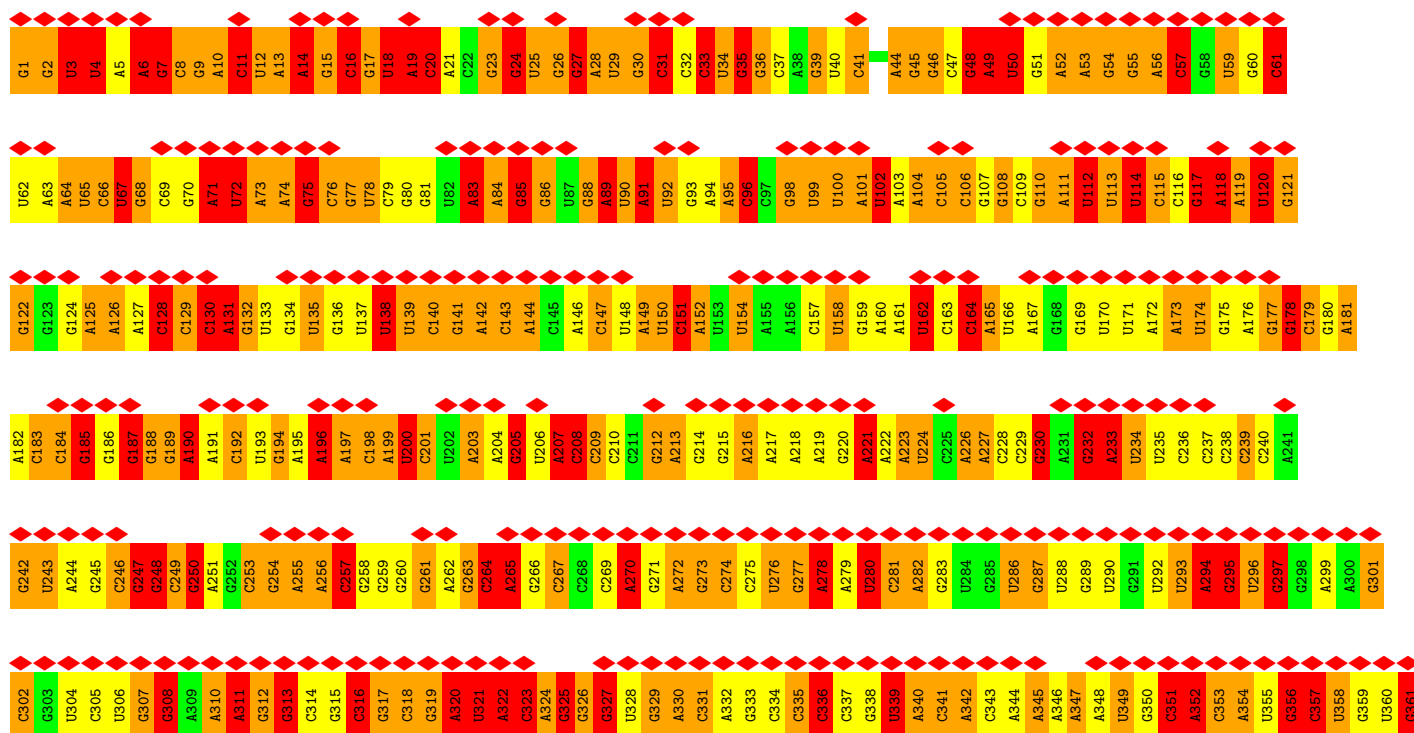
• Molecule 23: 30S ribosomal protein S10



• Molecule 24: 5S rRNA



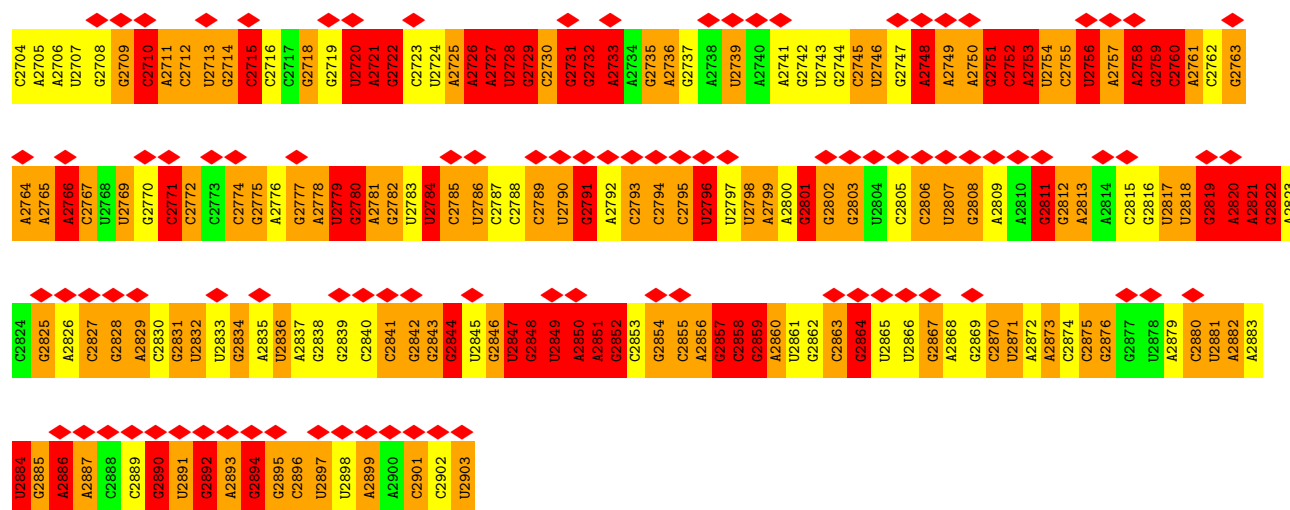
• Molecule 25: 23S rRNA



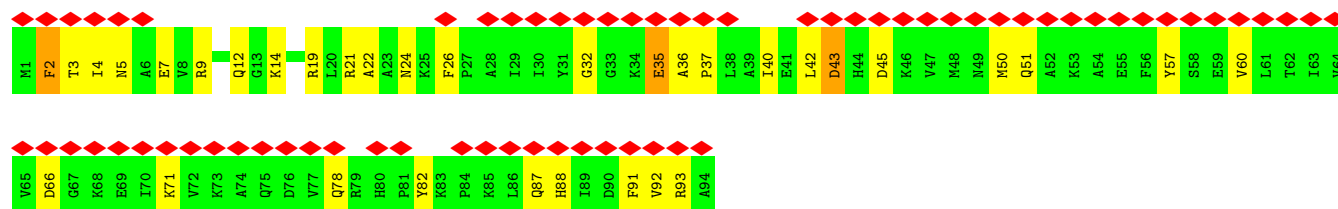
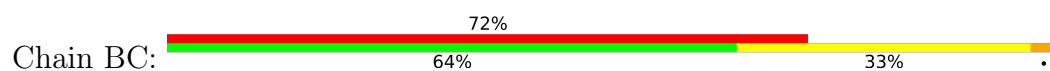


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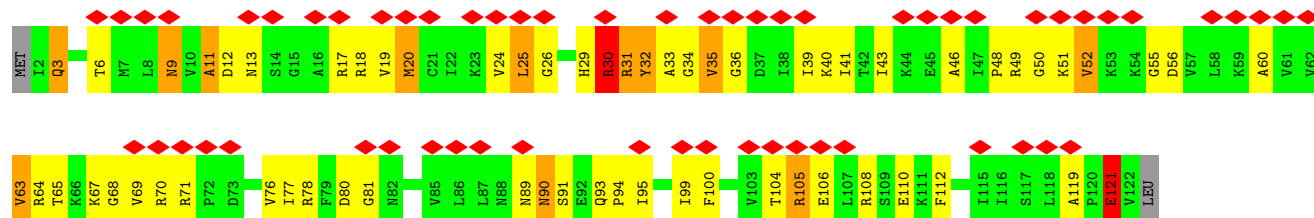
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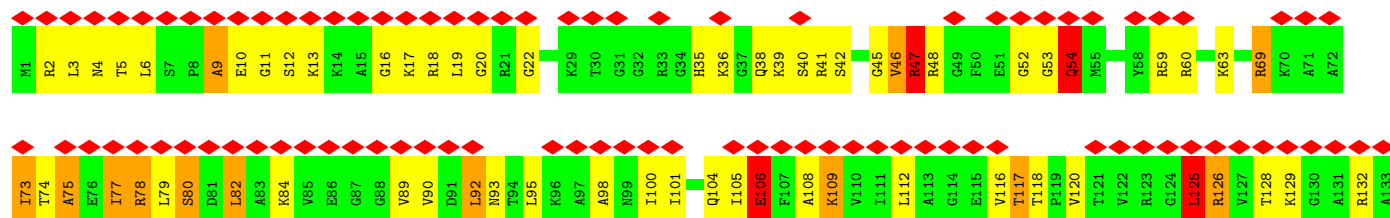
• Molecule 26: 50S ribosomal protein L25

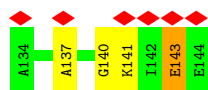


• Molecule 27: 50S ribosomal protein L14

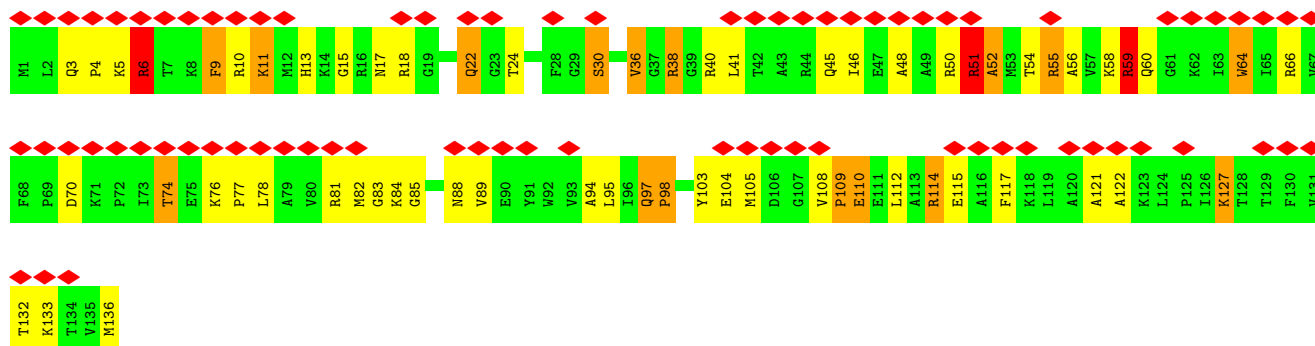


• Molecule 28: 50S ribosomal protein L15

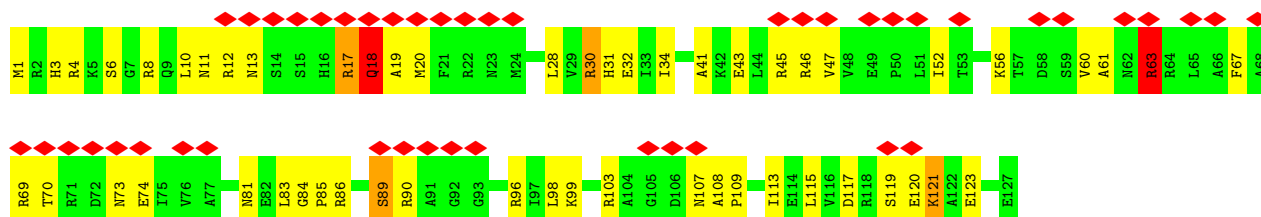




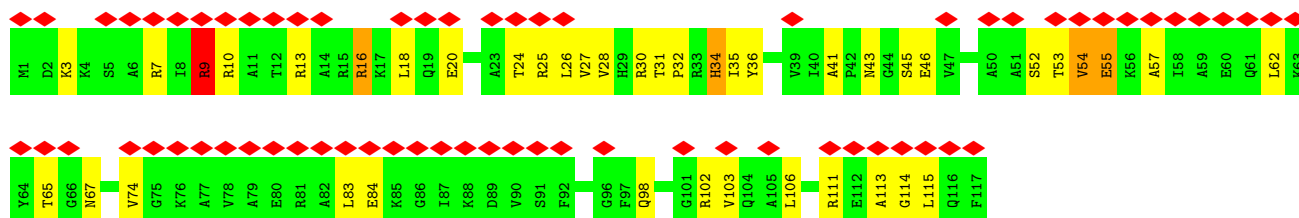
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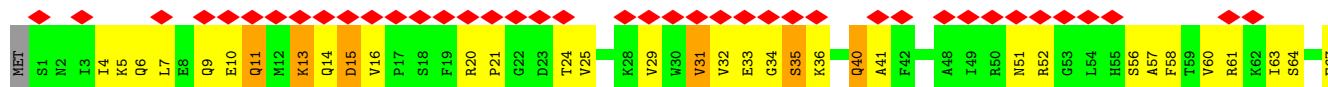
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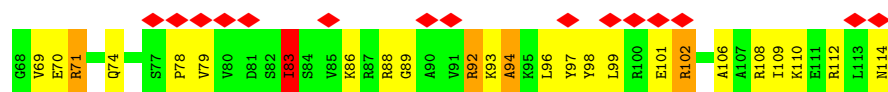


• Molecule 31: 50S ribosomal protein L18

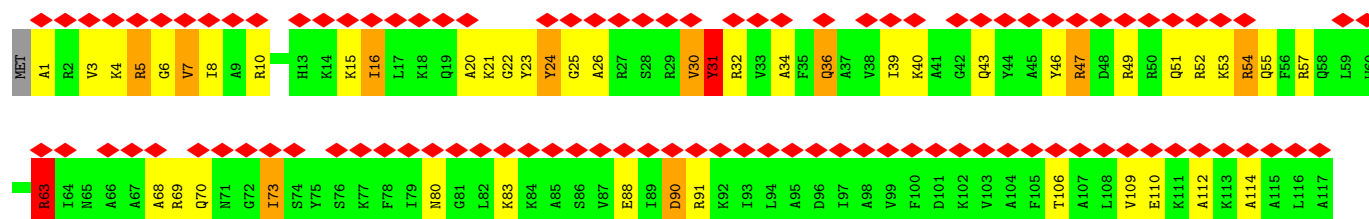
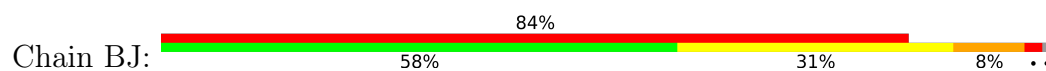


• Molecule 32: 50S ribosomal protein L19

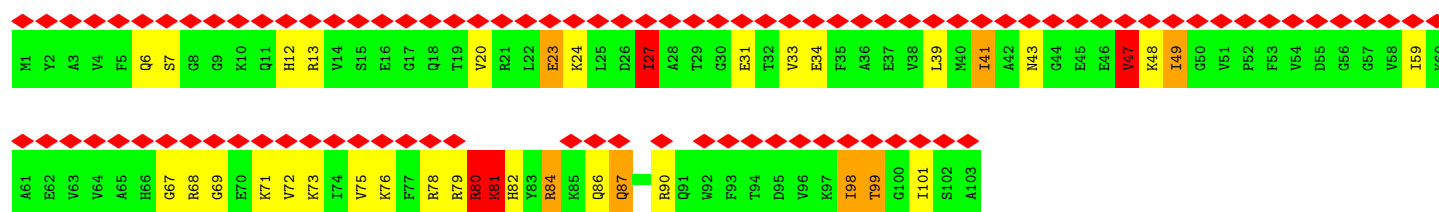




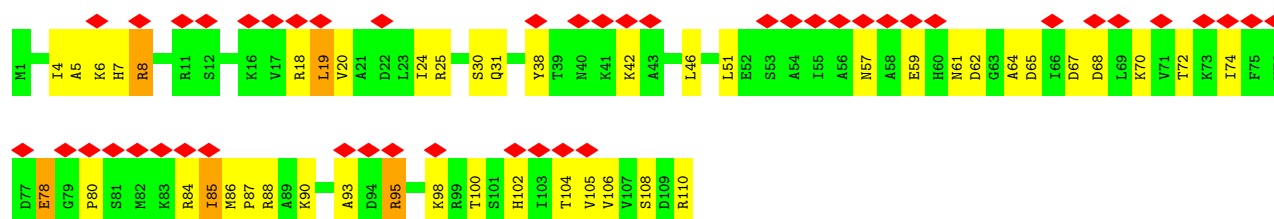
- Molecule 33: 50S ribosomal protein L20



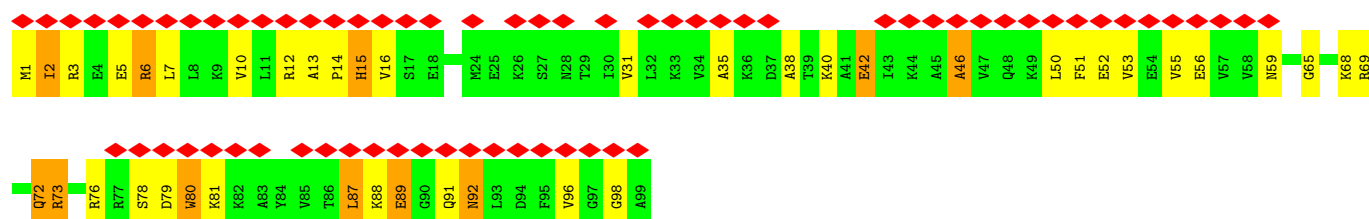
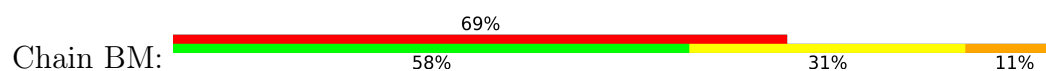
- Molecule 34: 50S ribosomal protein L21



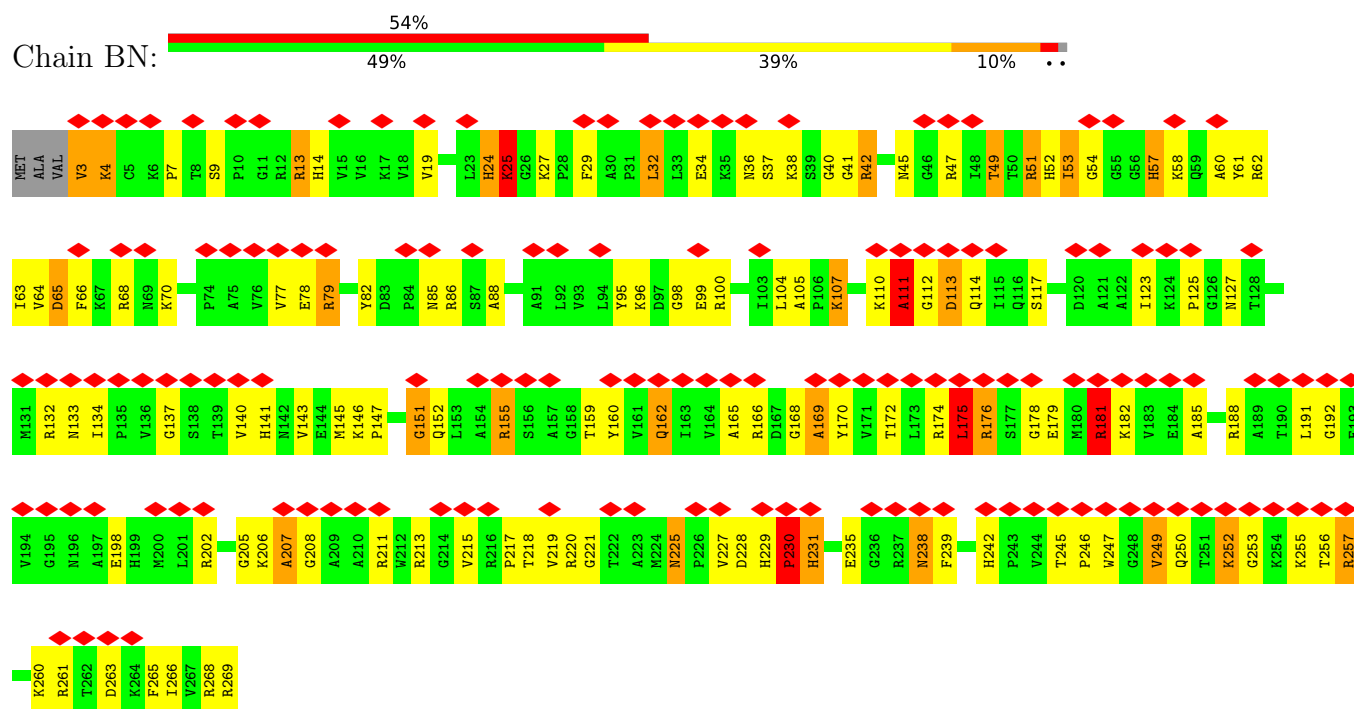
- Molecule 35: 50S ribosomal protein L22



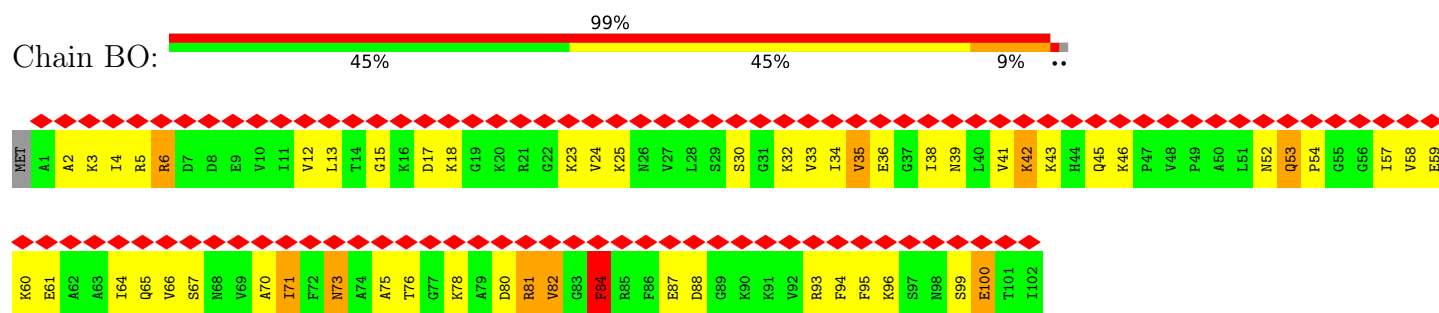
- Molecule 36: 50S ribosomal protein L23



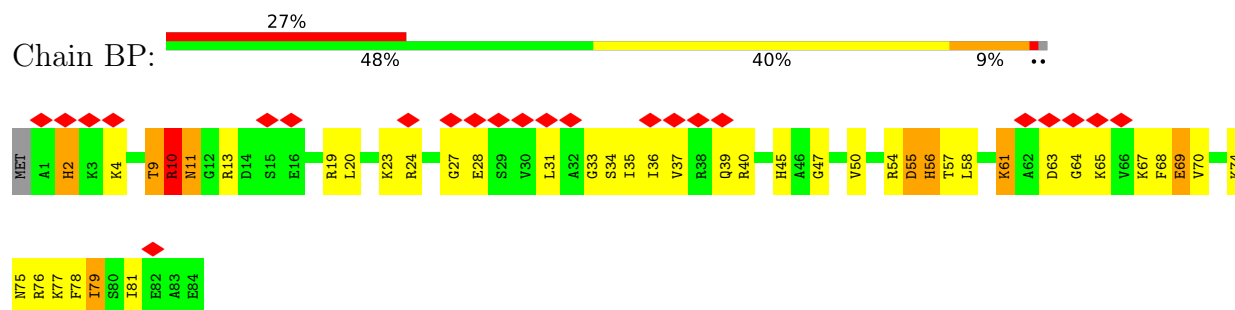
- Molecule 37: 50S ribosomal protein L2



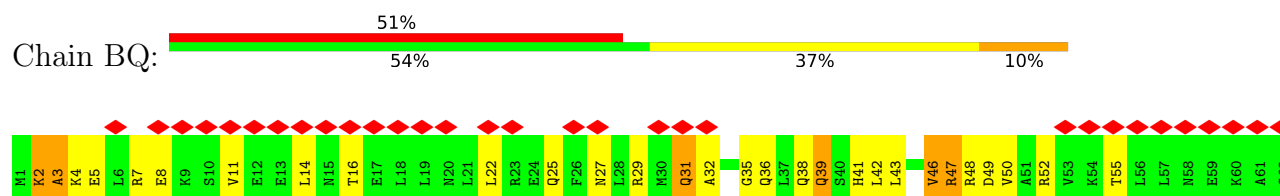
• Molecule 38: 50S ribosomal protein L24



• Molecule 39: 50S ribosomal protein L27

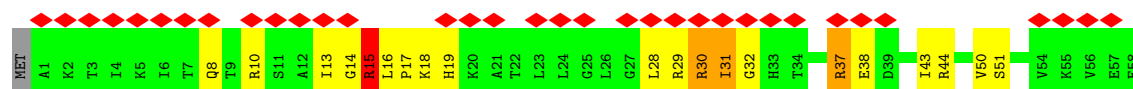


• Molecule 40: 50S ribosomal protein L29

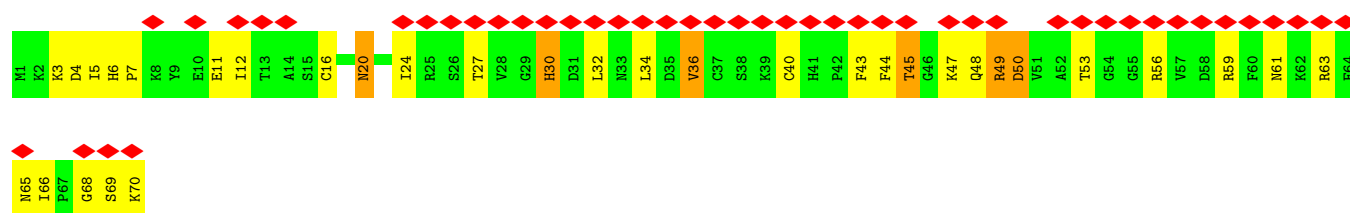




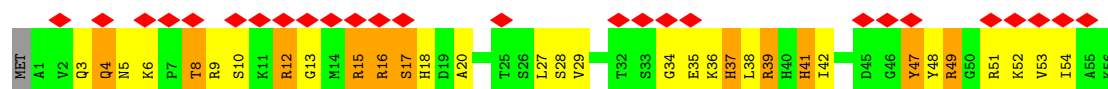
- Molecule 41: 50S ribosomal protein L30



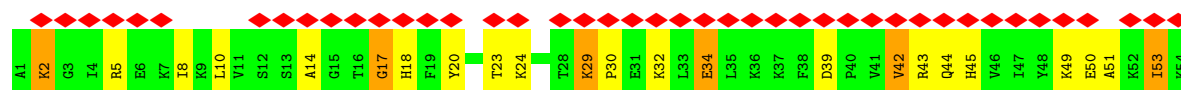
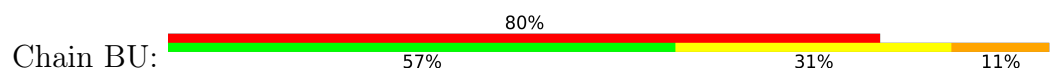
- Molecule 42: 50S ribosomal protein L31



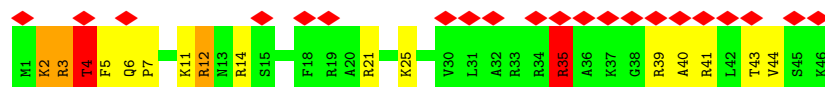
- Molecule 43: 50S ribosomal protein L32



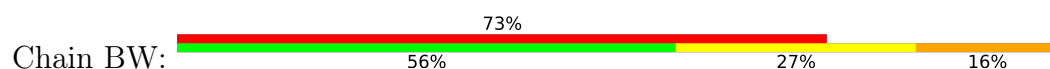
- Molecule 44: 50S ribosomal protein L33

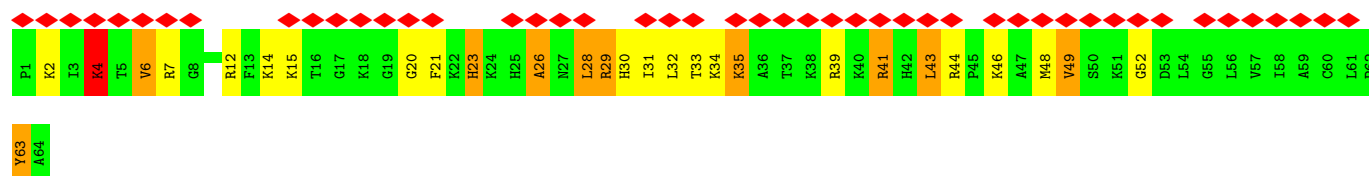


- Molecule 45: 50S ribosomal protein L34

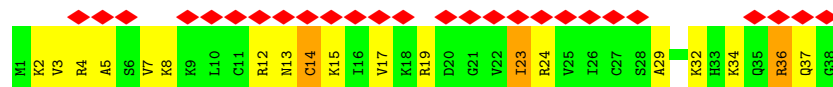


- Molecule 46: 50S ribosomal protein L35

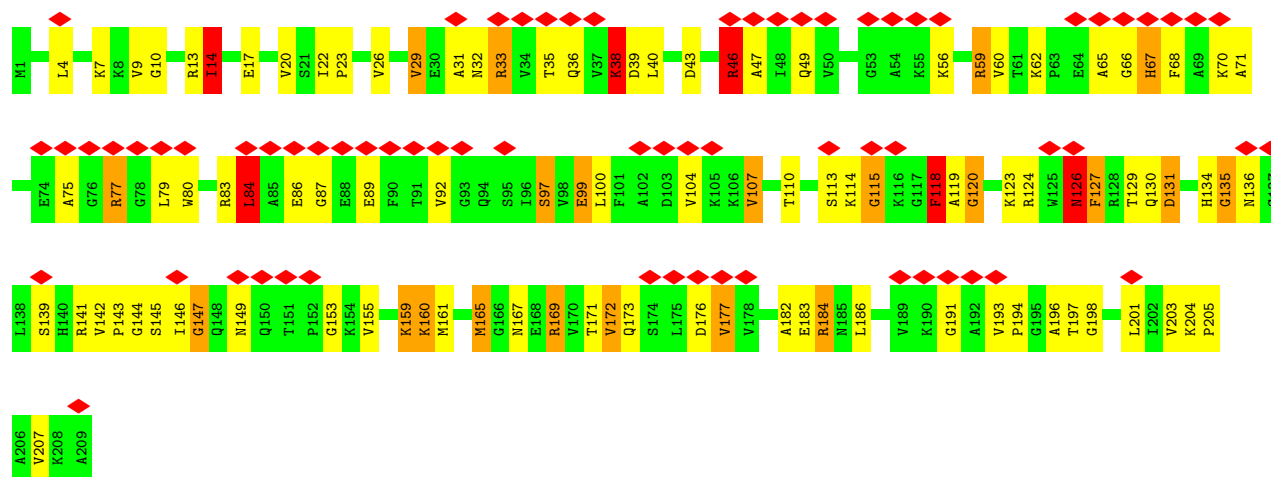




- Molecule 47: 50S ribosomal protein L36



- Molecule 48: 50S ribosomal protein L3

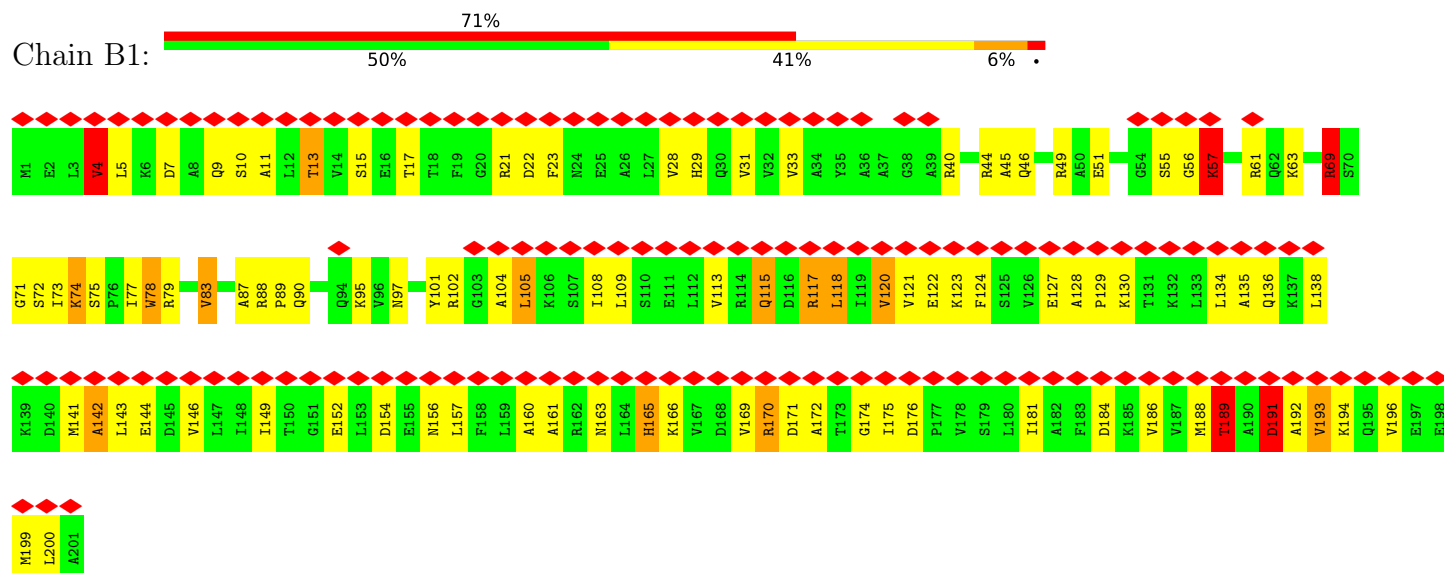


- Molecule 49: 50S ribosomal protein L1P



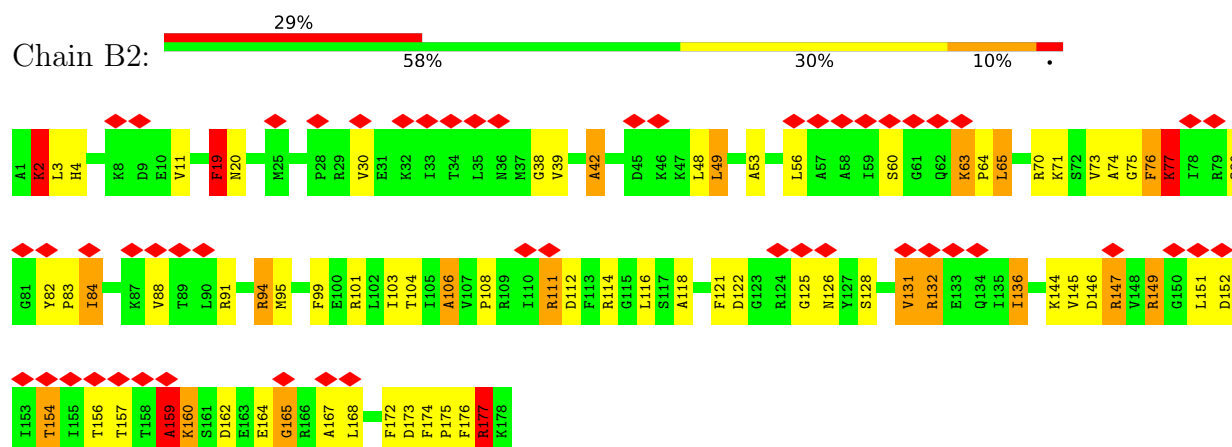
- Molecule 50: 50S ribosomal protein L4

Chain B1:



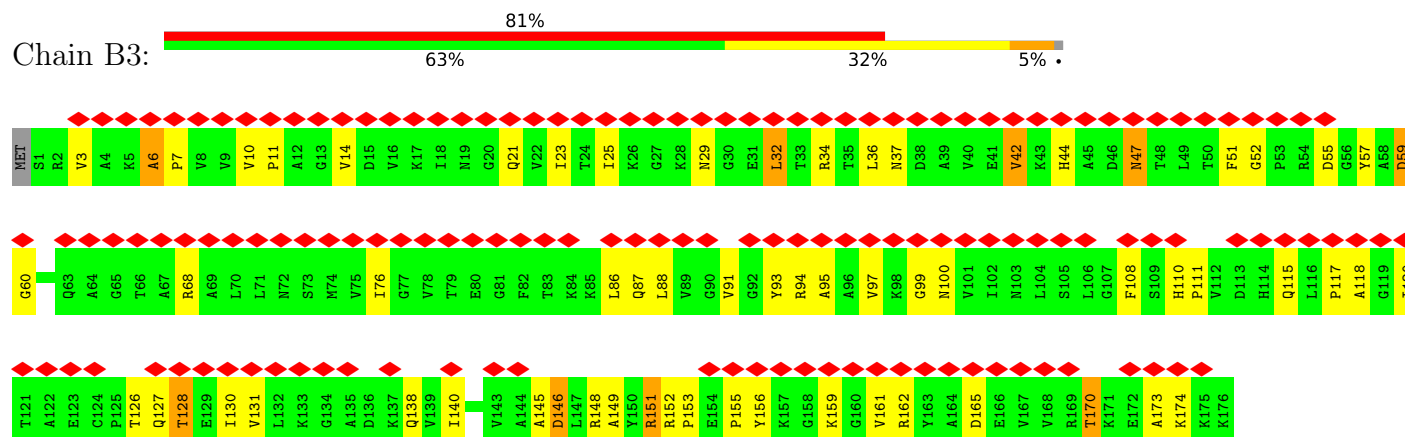
- Molecule 51: 50S ribosomal protein L5

Chain B2:

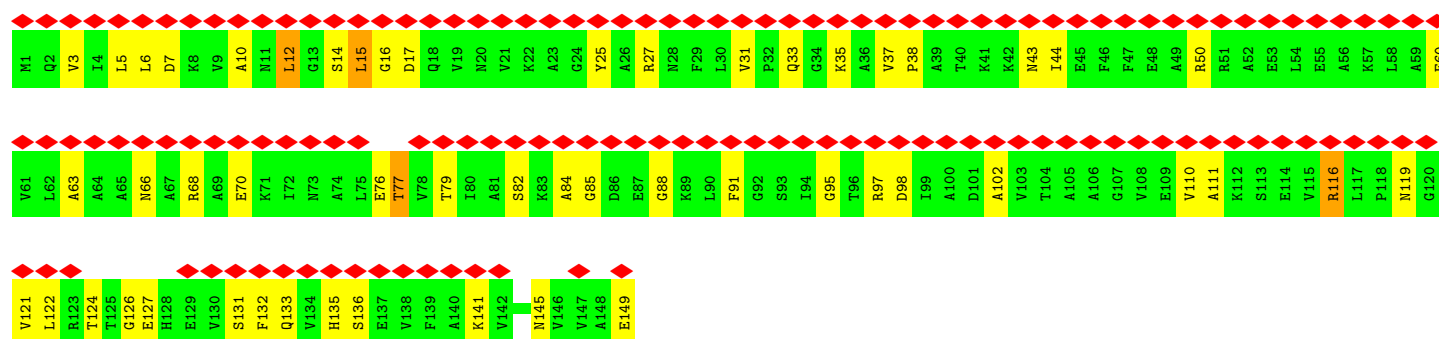
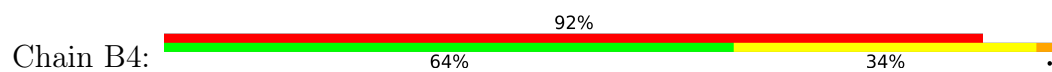


- Molecule 52: 50S ribosomal protein L6

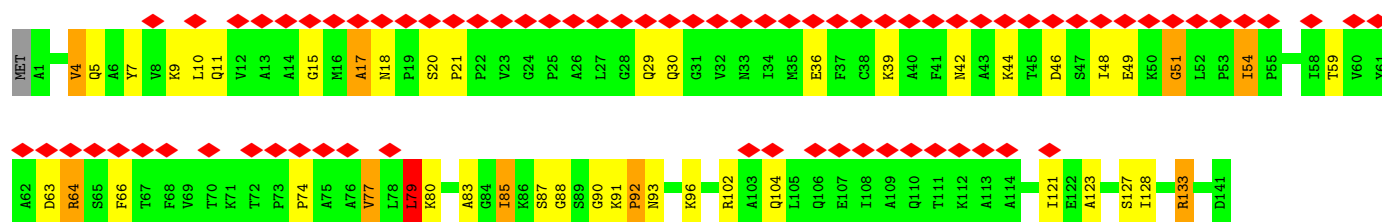
Chain B3:



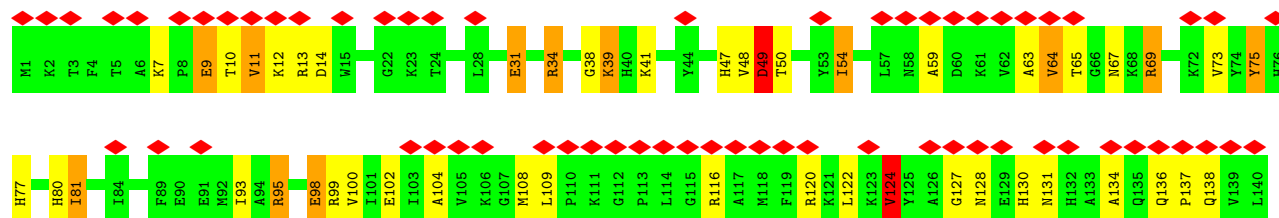
- Molecule 53: 50S ribosomal protein L9



• Molecule 54: 50S ribosomal protein L11



• Molecule 55: 50S ribosomal protein L13



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	75996	Depositor
Resolution determination method	Not provided	
CTF correction method	Not provided	
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	15	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	50000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	250.984	Depositor
Minimum map value	-85.859	Depositor
Average map value	4.444	Depositor
Map value standard deviation	25.344	Depositor
Recommended contour level	57.2	Depositor
Map size ($\text{\AA}$)	366.6, 366.6, 366.6	wwPDB
Map dimensions	130, 130, 130	wwPDB
Map angles ($^\circ$)	90, 90, 90	wwPDB
Pixel spacing ($\text{\AA}$)	2.82, 2.82, 2.82	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	AA	1.53	4/1789 (0.2%)	2.26	134/2788 (4.8%)
1	AE	1.35	4/1814 (0.2%)	1.98	96/2827 (3.4%)
1	AP	2.20	16/1789 (0.9%)	2.49	92/2788 (3.3%)
2	AM	1.64	2/436 (0.5%)	2.34	42/672 (6.2%)
3	A1	1.51	105/36759 (0.3%)	2.00	1869/57346 (3.3%)
4	AB	1.30	4/1735 (0.2%)	2.22	74/2338 (3.2%)
5	AC	1.37	5/892 (0.6%)	2.16	26/1205 (2.2%)
6	AD	1.47	3/968 (0.3%)	2.38	59/1300 (4.5%)
7	AF	1.46	9/892 (1.0%)	2.47	65/1193 (5.4%)
8	AG	1.44	3/785 (0.4%)	2.36	38/1046 (3.6%)
9	AH	1.53	5/723 (0.7%)	2.53	56/966 (5.8%)
10	AI	1.46	4/658 (0.6%)	2.33	38/884 (4.3%)
11	AJ	1.37	0/657	2.30	33/881 (3.7%)
12	AK	1.44	4/462 (0.9%)	2.29	24/621 (3.9%)
13	AL	1.40	5/652 (0.8%)	2.37	35/877 (4.0%)
14	AN	1.39	4/670 (0.6%)	2.15	26/888 (2.9%)
15	AO	1.41	6/1651 (0.4%)	2.19	55/2225 (2.5%)
16	AQ	1.48	2/430 (0.5%)	2.35	22/570 (3.9%)
17	AR	1.34	6/1664 (0.4%)	2.22	65/2227 (2.9%)
18	AS	1.34	0/1118	2.16	45/1504 (3.0%)
19	AT	1.36	1/835 (0.1%)	2.19	41/1128 (3.6%)
20	AU	1.38	8/1187 (0.7%)	2.26	57/1591 (3.6%)
21	AV	1.22	0/988	2.12	31/1326 (2.3%)
22	AW	1.41	4/1033 (0.4%)	2.26	47/1375 (3.4%)
23	AX	1.36	3/796 (0.4%)	2.49	62/1077 (5.8%)
24	BA	1.34	3/2800 (0.1%)	1.94	137/4367 (3.1%)
25	BB	1.35	138/69795 (0.2%)	1.95	3212/108884 (2.9%)
26	BC	1.29	0/765	2.20	29/1025 (2.8%)
27	BD	1.47	4/939 (0.4%)	2.54	66/1258 (5.2%)
28	BE	1.47	6/1061 (0.6%)	2.34	57/1413 (4.0%)
29	BF	1.40	4/1092 (0.4%)	2.38	63/1460 (4.3%)
30	BG	1.44	5/1020 (0.5%)	2.30	50/1364 (3.7%)
31	BH	1.43	3/909 (0.3%)	2.30	42/1219 (3.4%)
32	BI	1.43	3/928 (0.3%)	2.32	56/1242 (4.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	BJ	1.40	3/959 (0.3%)	2.22	47/1278 (3.7%)
34	BK	1.34	1/828 (0.1%)	2.29	38/1107 (3.4%)
35	BL	1.37	3/863 (0.3%)	2.21	39/1156 (3.4%)
36	BM	1.29	2/784 (0.3%)	2.19	42/1048 (4.0%)
37	BN	1.44	15/2092 (0.7%)	2.35	114/2813 (4.1%)
38	BO	1.35	2/787 (0.3%)	2.49	64/1051 (6.1%)
39	BP	1.39	2/641 (0.3%)	2.46	44/848 (5.2%)
40	BQ	1.39	1/509 (0.2%)	2.27	20/677 (3.0%)
41	BR	1.33	2/452 (0.4%)	2.19	16/605 (2.6%)
42	BS	1.39	1/558 (0.2%)	2.31	31/745 (4.2%)
43	BT	1.50	2/449 (0.4%)	2.39	27/599 (4.5%)
44	BU	1.46	1/447 (0.2%)	2.27	17/594 (2.9%)
45	BV	1.45	0/379	2.32	22/498 (4.4%)
46	BW	1.39	0/512	2.15	27/676 (4.0%)
47	BX	1.45	2/302 (0.7%)	2.61	20/397 (5.0%)
48	BY	1.32	2/1585 (0.1%)	2.37	98/2134 (4.6%)
49	BZ	1.28	5/1711 (0.3%)	2.09	65/2305 (2.8%)
50	B1	1.33	3/1570 (0.2%)	2.28	86/2113 (4.1%)
51	B2	1.36	3/1443 (0.2%)	2.22	73/1937 (3.8%)
52	B3	1.36	2/1342 (0.1%)	2.26	66/1816 (3.6%)
53	B4	1.35	2/1121 (0.2%)	2.21	42/1515 (2.8%)
54	B5	1.32	2/1045 (0.2%)	2.24	50/1410 (3.5%)
55	B6	1.37	2/1135 (0.2%)	2.17	42/1529 (2.7%)
All	All	1.41	431/162206 (0.3%)	2.06	7934/242726 (3.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AA	0	55
1	AE	0	49
1	AP	2	50
2	AM	0	9
3	A1	4	945
4	AB	0	3
5	AC	0	3
6	AD	0	7
7	AF	0	5
8	AG	0	4
9	AH	0	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
10	AI	0	3
11	AJ	0	4
13	AL	0	8
14	AN	1	1
15	AO	0	3
16	AQ	0	4
17	AR	0	7
18	AS	0	3
19	AT	0	4
20	AU	0	4
21	AV	0	2
22	AW	0	4
23	AX	0	4
24	BA	0	66
25	BB	3	1717
26	BC	0	3
27	BD	0	6
28	BE	0	6
29	BF	0	4
30	BG	0	4
31	BH	0	1
32	BI	0	4
33	BJ	0	4
34	BK	0	5
35	BL	0	5
36	BM	0	1
37	BN	0	12
38	BO	0	4
39	BP	0	3
40	BQ	0	3
41	BR	0	3
42	BS	0	3
43	BT	0	2
44	BU	0	5
45	BV	0	2
46	BW	0	4
47	BX	0	2
48	BY	0	9
49	BZ	0	2
50	B1	0	9
51	B2	0	6
52	B3	0	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
53	B4	0	4
54	B5	0	3
55	B6	0	8
All	All	10	3101

The worst 5 of 431 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A1	1429	A	P-O5'	89.08	3.38	1.59
3	A1	1340	A	C3'-O3'	70.07	2.82	1.42
1	AP	74	C	O3'-P	-34.97	1.08	1.61
25	BB	1687	G	O4'-C1'	30.64	1.87	1.41
1	AP	31	A	C4'-C3'	29.64	2.11	1.52

The worst 5 of 7934 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AP	74	C	P-O3'-C3'	-63.20	25.40	120.20
1	AP	74	C	O3'-P-O5'	-50.70	27.95	104.00
3	A1	1340	A	P-O3'-C3'	16.53	145.00	120.20
27	BD	108	ARG	NE-CZ-NH2	14.80	132.52	119.20
13	AL	55	GLN	OE1-CD-NE2	-13.56	109.04	122.60

5 of 10 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	AP	31	A	C1',C2'
3	A1	13	U	C1',C2'
3	A1	1198	G	C4'
3	A1	1483	A	C2'
14	AN	13	SER	CA

5 of 3101 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	1	G	Sidechain
1	AA	3	G	Sidechain
1	AA	4	G	Sidechain
1	AA	5	A	Sidechain
1	AA	6	U	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	1600	0	760	11	0
1	AE	1622	0	769	7	0
1	AP	1600	0	755	42	0
2	AM	397	0	202	6	0
3	A1	32828	0	15511	162	0
4	AB	1704	0	1732	9	0
5	AC	876	0	887	3	0
6	AD	954	0	1019	4	0
7	AF	883	0	944	1	0
8	AG	773	0	825	2	0
9	AH	715	0	742	2	0
10	AI	648	0	666	6	0
11	AJ	648	0	691	3	0
12	AK	455	0	478	0	0
13	AL	637	0	665	0	0
14	AN	664	0	714	4	0
15	AO	1624	0	1699	5	0
16	AQ	425	0	449	2	0
17	AR	1642	0	1710	9	0
18	AS	1105	0	1148	4	0
19	AT	817	0	808	2	0
20	AU	1174	0	1230	3	0
21	AV	978	0	1034	0	0
22	AW	1021	0	1070	1	0
23	AX	786	0	828	4	0
24	BA	2504	0	1208	11	0
25	BB	62317	0	29633	225	0
26	BC	752	0	780	4	0
27	BD	930	0	1000	5	0
28	BE	1052	0	1129	10	0
29	BF	1073	0	1157	8	0
30	BG	1007	0	1045	4	0
31	BH	899	0	935	2	0
32	BI	916	0	965	6	0
33	BJ	946	0	1022	8	0
34	BK	815	0	839	4	0
35	BL	856	0	922	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	BM	777	0	840	2	0
37	BN	2053	0	2122	9	0
38	BO	779	0	834	2	0
39	BP	633	0	656	1	0
40	BQ	508	0	543	3	0
41	BR	448	0	491	2	0
42	BS	548	0	552	2	0
43	BT	443	0	461	2	0
44	BU	440	0	485	2	0
45	BV	376	0	418	2	0
46	BW	503	0	574	7	0
47	BX	301	0	343	1	0
48	BY	1564	0	1616	7	0
49	BZ	1687	0	1814	4	0
50	B1	1551	0	1619	7	0
51	B2	1419	0	1460	8	0
52	B3	1322	0	1374	3	0
53	B4	1110	0	1148	2	0
54	B5	1031	0	1088	4	0
55	B6	1112	0	1147	2	0
All	All	149248	0	97556	537	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 2.

The worst 5 of 537 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)
25:BB:1687:G:C2'	25:BB:1687:G:C3'	1.91	1.47
25:BB:1687:G:C2'	25:BB:1687:G:C1'	1.93	1.45
1:AP:31:A:C2'	3:A1:1340:A:H3'	1.45	1.44
25:BB:1687:G:C3'	25:BB:1687:G:C4'	1.96	1.43
1:AP:31:A:C2'	1:AP:31:A:C3'	2.01	1.39

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	
4	AB	216/241 (90%)	178 (82%)	33 (15%)	5 (2%)	5	28
5	AC	115/129 (89%)	91 (79%)	17 (15%)	7 (6%)	1	13
6	AD	121/124 (98%)	78 (64%)	28 (23%)	15 (12%)	0	4
7	AF	112/118 (95%)	80 (71%)	24 (21%)	8 (7%)	1	11
8	AG	94/101 (93%)	69 (73%)	20 (21%)	5 (5%)	1	15
9	AH	86/89 (97%)	73 (85%)	11 (13%)	2 (2%)	5	28
10	AI	80/82 (98%)	55 (69%)	15 (19%)	10 (12%)	0	4
11	AJ	78/84 (93%)	52 (67%)	18 (23%)	8 (10%)	0	6
12	AK	53/75 (71%)	44 (83%)	7 (13%)	2 (4%)	2	19
13	AL	77/92 (84%)	51 (66%)	19 (25%)	7 (9%)	0	8
14	AN	83/87 (95%)	66 (80%)	13 (16%)	4 (5%)	2	16
15	AO	204/233 (88%)	151 (74%)	38 (19%)	15 (7%)	1	10
16	AQ	49/71 (69%)	35 (71%)	8 (16%)	6 (12%)	0	4
17	AR	203/206 (98%)	161 (79%)	29 (14%)	13 (6%)	1	12
18	AS	148/159 (93%)	114 (77%)	20 (14%)	14 (10%)	0	8
19	AT	98/135 (73%)	80 (82%)	13 (13%)	5 (5%)	1	15
20	AU	148/179 (83%)	118 (80%)	19 (13%)	11 (7%)	1	10
21	AV	127/130 (98%)	103 (81%)	19 (15%)	5 (4%)	2	19
22	AW	125/130 (96%)	95 (76%)	23 (18%)	7 (6%)	1	14
23	AX	96/103 (93%)	78 (81%)	9 (9%)	9 (9%)	0	8
26	BC	92/94 (98%)	74 (80%)	14 (15%)	4 (4%)	2	17
27	BD	119/123 (97%)	90 (76%)	16 (13%)	13 (11%)	0	6
28	BE	142/144 (99%)	91 (64%)	30 (21%)	21 (15%)	0	3
29	BF	134/136 (98%)	73 (54%)	40 (30%)	21 (16%)	0	3
30	BG	125/127 (98%)	84 (67%)	32 (26%)	9 (7%)	1	11

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	BH	115/117 (98%)	72 (63%)	32 (28%)	11 (10%)	0	7
32	BI	112/115 (97%)	63 (56%)	32 (29%)	17 (15%)	0	3
33	BJ	115/118 (98%)	77 (67%)	27 (24%)	11 (10%)	0	7
34	BK	101/103 (98%)	59 (58%)	33 (33%)	9 (9%)	0	8
35	BL	108/110 (98%)	72 (67%)	27 (25%)	9 (8%)	0	9
36	BM	97/99 (98%)	69 (71%)	18 (19%)	10 (10%)	0	6
37	BN	265/270 (98%)	165 (62%)	61 (23%)	39 (15%)	0	3
38	BO	100/103 (97%)	60 (60%)	22 (22%)	18 (18%)	0	2
39	BP	82/85 (96%)	44 (54%)	21 (26%)	17 (21%)	0	2
40	BQ	61/63 (97%)	42 (69%)	14 (23%)	5 (8%)	0	9
41	BR	56/59 (95%)	38 (68%)	13 (23%)	5 (9%)	0	8
42	BS	68/70 (97%)	38 (56%)	22 (32%)	8 (12%)	0	4
43	BT	54/57 (95%)	32 (59%)	11 (20%)	11 (20%)	0	2
44	BU	52/54 (96%)	33 (64%)	14 (27%)	5 (10%)	0	7
45	BV	44/46 (96%)	33 (75%)	6 (14%)	5 (11%)	0	5
46	BW	62/64 (97%)	35 (56%)	20 (32%)	7 (11%)	0	5
47	BX	36/38 (95%)	23 (64%)	8 (22%)	5 (14%)	0	3
48	BY	207/209 (99%)	113 (55%)	54 (26%)	40 (19%)	0	2
49	BZ	211/213 (99%)	163 (77%)	33 (16%)	15 (7%)	1	11
50	B1	199/201 (99%)	111 (56%)	53 (27%)	35 (18%)	0	2
51	B2	176/178 (99%)	123 (70%)	26 (15%)	27 (15%)	0	3
52	B3	174/177 (98%)	149 (86%)	20 (12%)	5 (3%)	3	23
53	B4	147/149 (99%)	103 (70%)	33 (22%)	11 (8%)	1	10
54	B5	139/142 (98%)	113 (81%)	17 (12%)	9 (6%)	1	12
55	B6	138/140 (99%)	79 (57%)	41 (30%)	18 (13%)	0	4
All	All	5844/6172 (95%)	4093 (70%)	1173 (20%)	578 (10%)	1	7

5 of 578 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	AB	36	LYS
4	AB	97	GLY
4	AB	169	HIS

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Mol	Chain	Res	Type
6	AD	9	LYS
6	AD	15	VAL

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	
4	AB	180/199 (90%)	165 (92%)	15 (8%)	10	30
5	AC	90/99 (91%)	82 (91%)	8 (9%)	9	28
6	AD	103/104 (99%)	86 (84%)	17 (16%)	2	10
7	AF	92/96 (96%)	84 (91%)	8 (9%)	9	29
8	AG	79/84 (94%)	77 (98%)	2 (2%)	42	63
9	AH	76/77 (99%)	72 (95%)	4 (5%)	20	41
10	AI	65/65 (100%)	62 (95%)	3 (5%)	24	45
11	AJ	74/78 (95%)	70 (95%)	4 (5%)	20	41
12	AK	48/66 (73%)	45 (94%)	3 (6%)	16	37
13	AL	70/79 (89%)	60 (86%)	10 (14%)	3	13
14	AN	65/66 (98%)	58 (89%)	7 (11%)	6	21
15	AO	170/190 (90%)	157 (92%)	13 (8%)	12	33
16	AQ	44/61 (72%)	42 (96%)	2 (4%)	24	46
17	AR	172/173 (99%)	157 (91%)	15 (9%)	9	29
18	AS	113/119 (95%)	95 (84%)	18 (16%)	2	11
19	AT	87/116 (75%)	78 (90%)	9 (10%)	7	23
20	AU	123/147 (84%)	110 (89%)	13 (11%)	6	21
21	AV	104/105 (99%)	97 (93%)	7 (7%)	15	36
22	AW	105/107 (98%)	97 (92%)	8 (8%)	12	33
23	AX	86/90 (96%)	80 (93%)	6 (7%)	14	35
26	BC	78/78 (100%)	74 (95%)	4 (5%)	21	42
27	BD	102/104 (98%)	95 (93%)	7 (7%)	14	36

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	BE	103/103 (100%)	88 (85%)	15 (15%)	3	13
29	BF	109/109 (100%)	96 (88%)	13 (12%)	5	18
30	BG	103/103 (100%)	91 (88%)	12 (12%)	5	18
31	BH	87/87 (100%)	82 (94%)	5 (6%)	18	40
32	BI	99/100 (99%)	95 (96%)	4 (4%)	28	49
33	BJ	89/90 (99%)	79 (89%)	10 (11%)	6	19
34	BK	84/84 (100%)	73 (87%)	11 (13%)	4	15
35	BL	93/93 (100%)	83 (89%)	10 (11%)	6	21
36	BM	83/83 (100%)	71 (86%)	12 (14%)	3	13
37	BN	213/215 (99%)	187 (88%)	26 (12%)	5	17
38	BO	83/84 (99%)	77 (93%)	6 (7%)	13	35
39	BP	62/63 (98%)	57 (92%)	5 (8%)	11	31
40	BQ	55/55 (100%)	45 (82%)	10 (18%)	2	9
41	BR	48/49 (98%)	45 (94%)	3 (6%)	16	37
42	BS	62/62 (100%)	57 (92%)	5 (8%)	11	31
43	BT	47/48 (98%)	37 (79%)	10 (21%)	1	6
44	BU	48/48 (100%)	46 (96%)	2 (4%)	26	48
45	BV	38/38 (100%)	34 (90%)	4 (10%)	6	21
46	BW	51/51 (100%)	44 (86%)	7 (14%)	3	14
47	BX	34/34 (100%)	31 (91%)	3 (9%)	9	28
48	BY	164/164 (100%)	146 (89%)	18 (11%)	6	20
49	BZ	187/187 (100%)	174 (93%)	13 (7%)	14	35
50	B1	165/165 (100%)	146 (88%)	19 (12%)	5	18
51	B2	149/149 (100%)	132 (89%)	17 (11%)	5	18
52	B3	137/138 (99%)	124 (90%)	13 (10%)	8	25
53	B4	114/114 (100%)	105 (92%)	9 (8%)	11	32
54	B5	109/110 (99%)	102 (94%)	7 (6%)	16	37
55	B6	114/114 (100%)	105 (92%)	9 (8%)	11	32
All	All	4856/5043 (96%)	4395 (90%)	461 (10%)	10	25

5 of 461 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	BI	109	ILE
53	B4	79	THR
37	BN	66	PHE
53	B4	17	ASP
50	B1	138	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 89 such sidechains are listed below:

Mol	Chain	Res	Type
37	BN	36	ASN
48	BY	36	GLN
37	BN	133	ASN
43	BT	37	HIS
48	BY	185	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	75/76 (98%)	24 (32%)	8 (10%)
1	AE	75/76 (98%)	11 (14%)	1 (1%)
1	AP	74/76 (97%)	17 (22%)	6 (8%)
2	AM	20/20 (100%)	9 (45%)	7 (35%)
24	BA	116/117 (99%)	44 (37%)	11 (9%)
25	BB	2902/2903 (99%)	1565 (53%)	511 (17%)
3	A1	1529/1530 (99%)	772 (50%)	280 (18%)
All	All	4791/4798 (99%)	2442 (50%)	824 (17%)

5 of 2442 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	2	C
1	AA	3	G
1	AA	10	G
1	AA	13	C
1	AA	17	U

5 of 824 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
25	BB	914	G
25	BB	1567	G

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Mol	Chain	Res	Type
25	BB	2711	A
25	BB	974	G
25	BB	908	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
25	BB	1
1	AP	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BB	1959:G	O3'	1960:A	P	3.50
1	AP	74:C	O3'	75:C	P	1.08

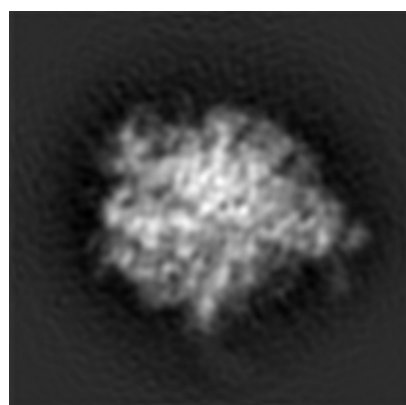
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1055. These allow visual inspection of the internal detail of the map and identification of artifacts.

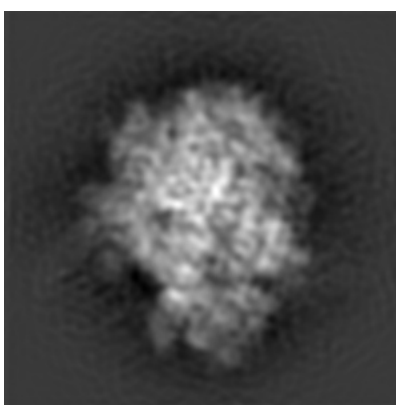
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

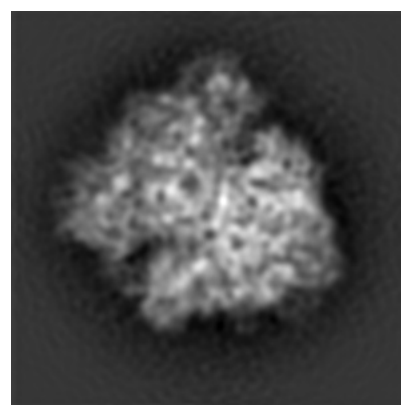
6.1.1 Primary map



X



Y

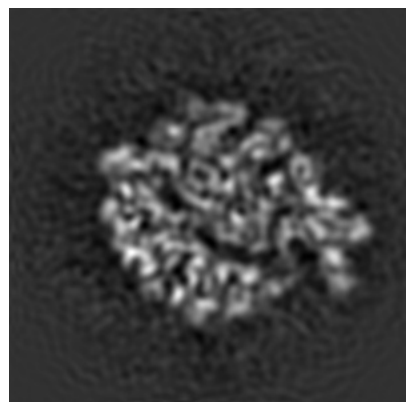


Z

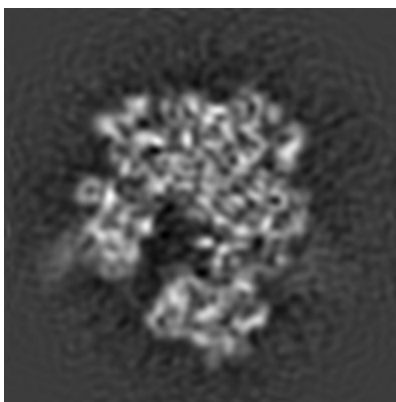
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

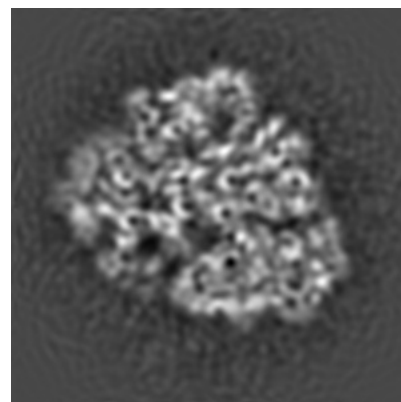
6.2.1 Primary map



X Index: 65



Y Index: 65

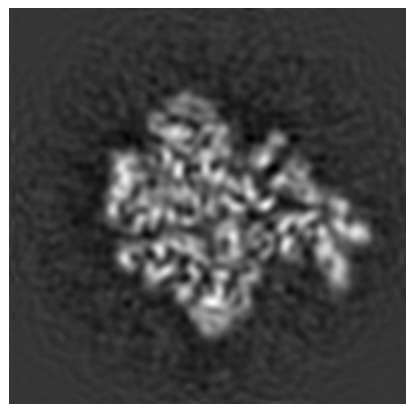


Z Index: 65

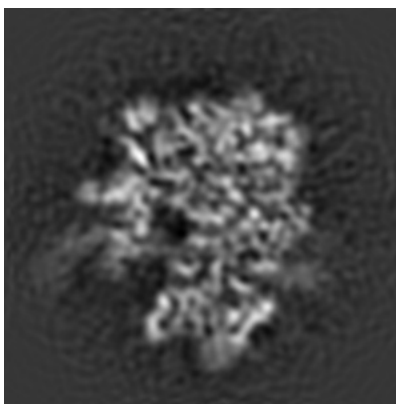
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

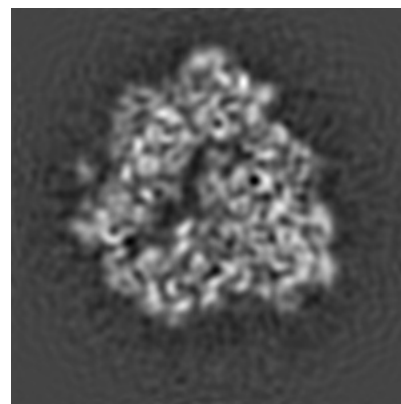
6.3.1 Primary map



X Index: 68



Y Index: 68

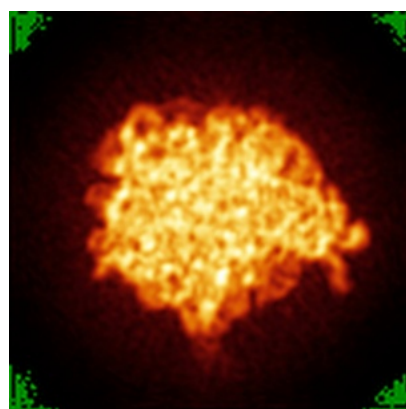


Z Index: 59

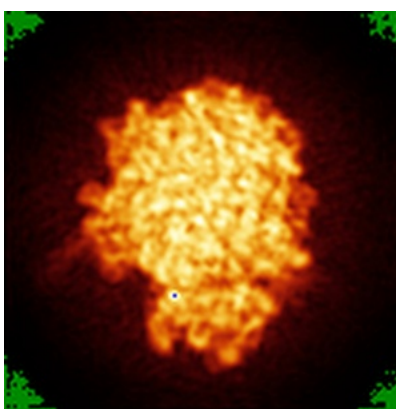
The images above show the largest variance slices of the map in three orthogonal directions.

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

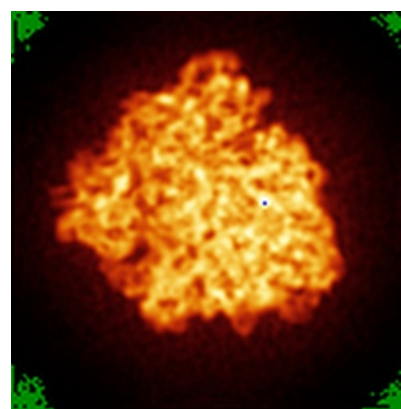
6.4.1 Primary map



X



Y

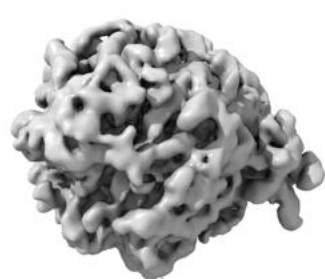


Z

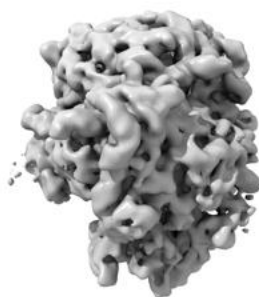
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

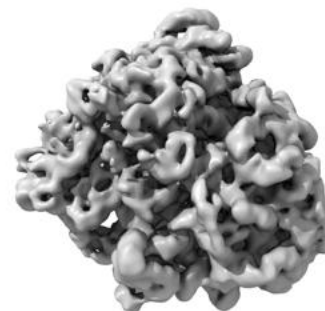
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 57.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

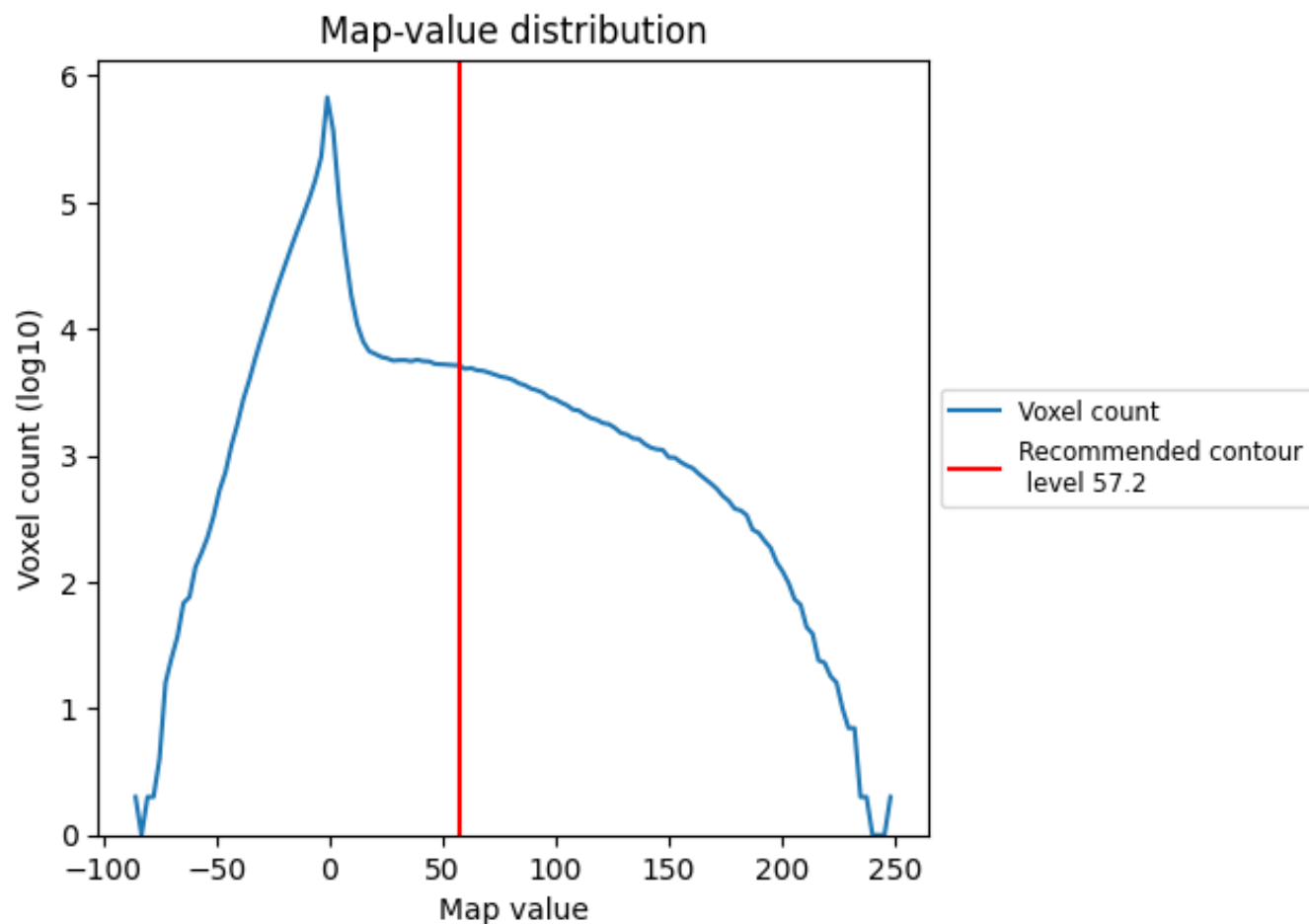
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

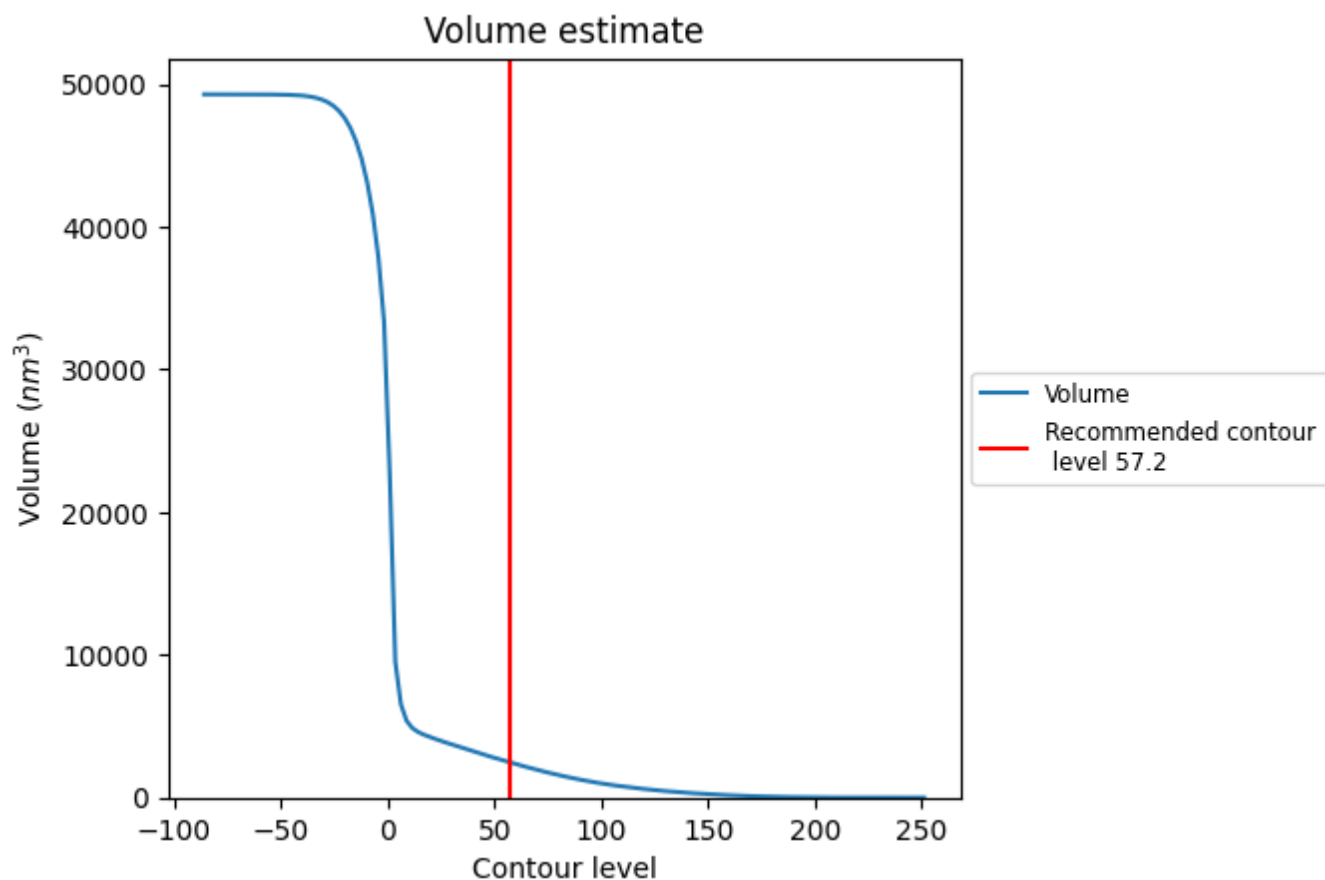
This section contains the results of statistical analysis of the map.

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.

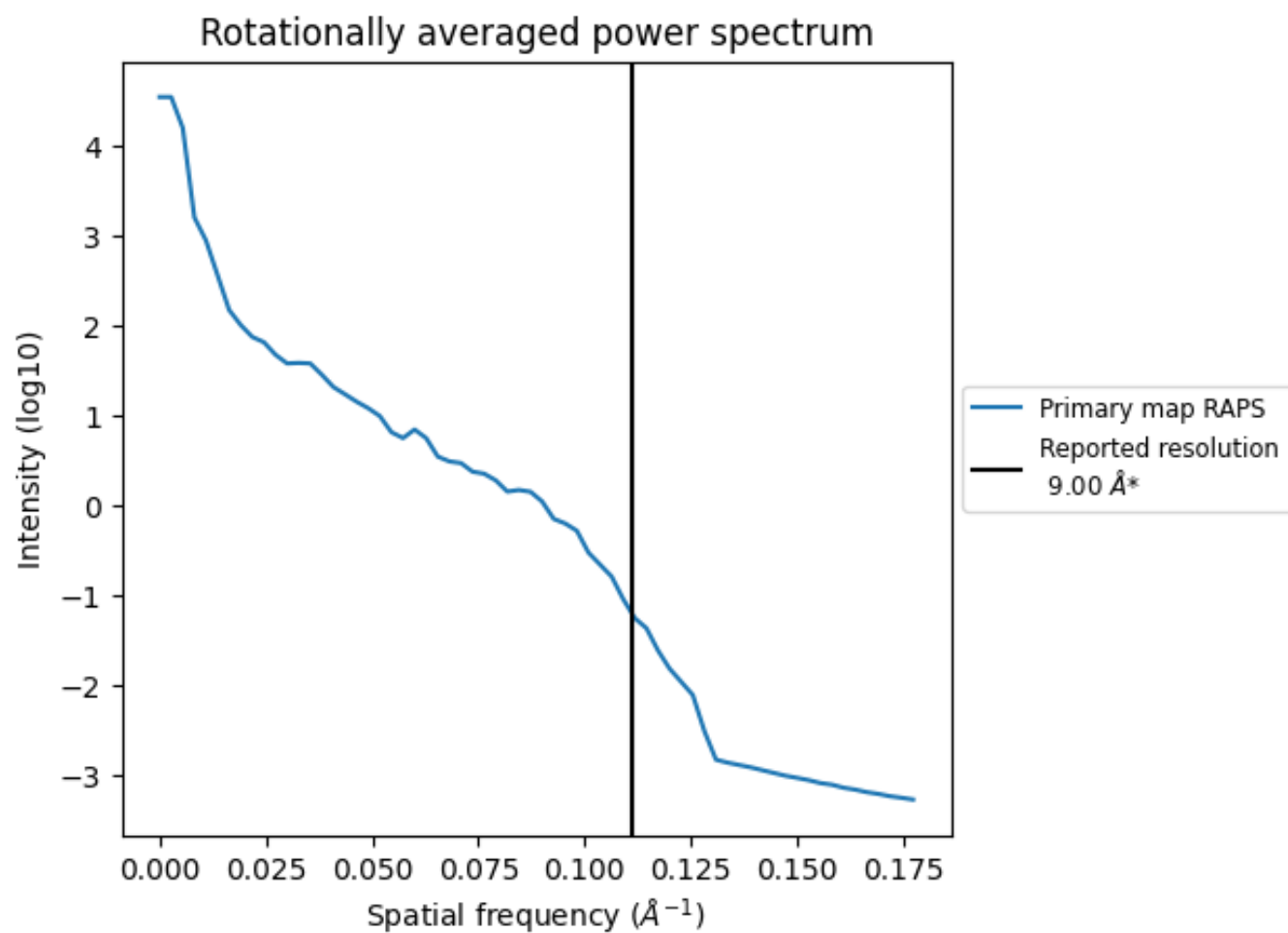
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2467 nm³; this corresponds to an approximate mass of 2228 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 0.111 Å⁻¹

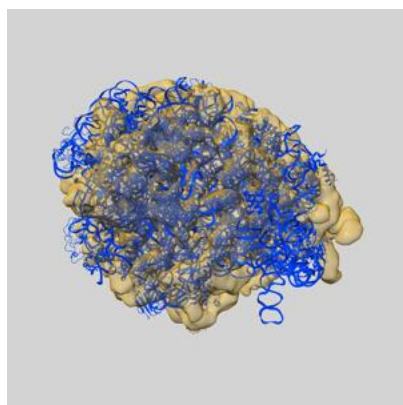
8 Fourier-Shell correlation

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

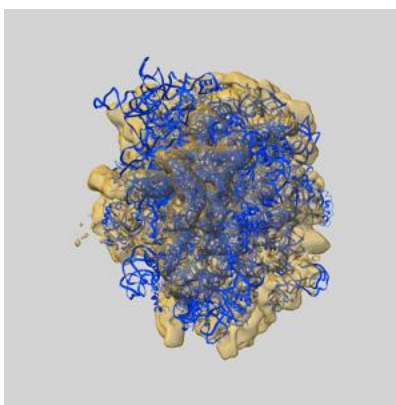
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-1055 and PDB model 4V65. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

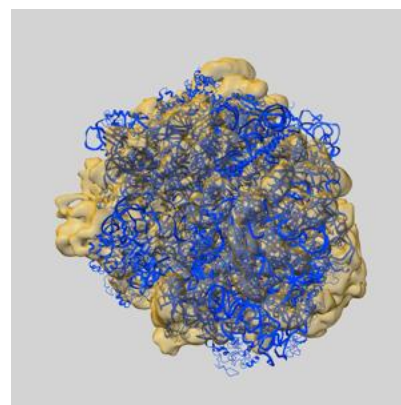
9.1 Map-model overlay [i](#)



X



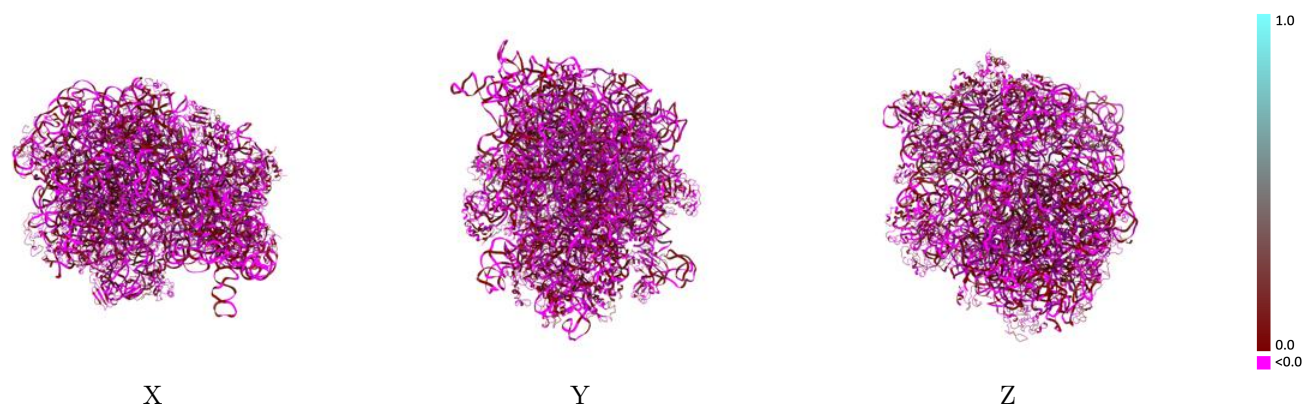
Y



Z

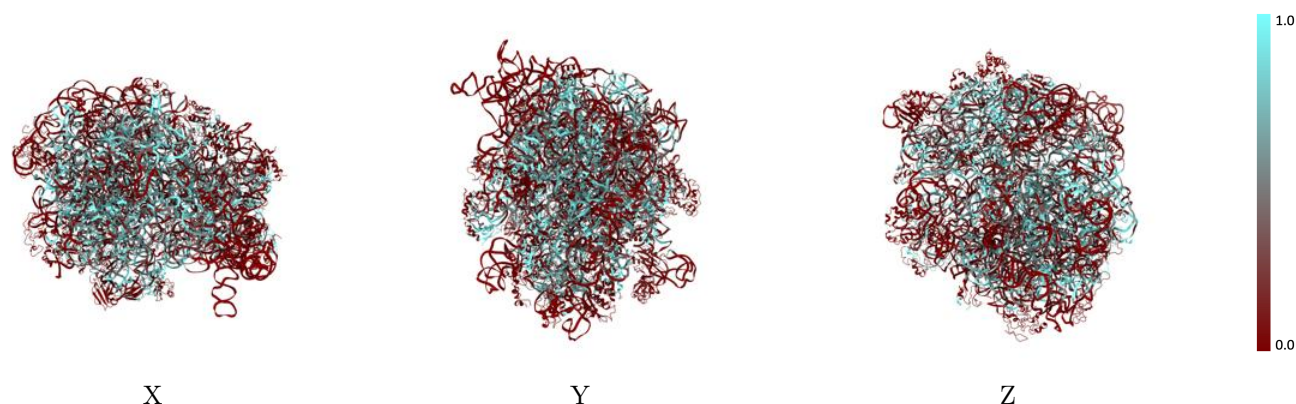
The images above show the 3D surface view of the map at the recommended contour level 57.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



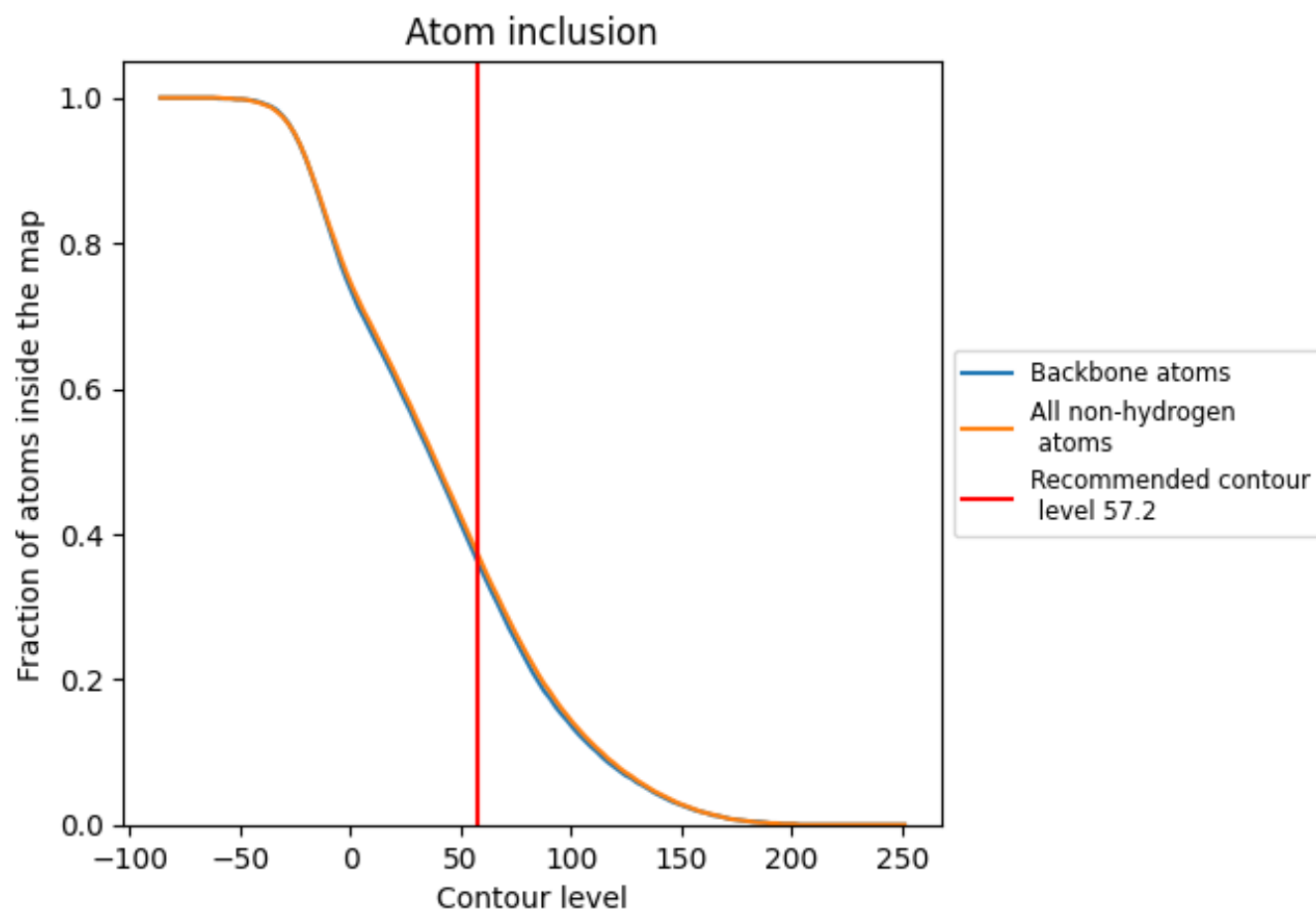
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (57.2).

9.4 Atom inclusion ⓘ



At the recommended contour level, 37% of all backbone atoms, 38% 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 (57.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.3760	-0.0070
A1	0.3220	-0.0130
AA	0.3780	-0.0130
AB	0.2190	-0.0010
AC	0.4260	-0.0050
AD	0.2170	-0.0200
AE	0.4110	-0.0070
AF	0.4210	-0.0010
AG	0.0860	-0.0290
AH	0.1550	-0.0100
AI	0.0000	-0.0440
AJ	0.2480	-0.0170
AK	0.5960	0.0120
AL	0.0340	-0.0240
AM	0.6420	0.0200
AN	0.4280	0.0120
AO	0.6140	0.0210
AP	0.4060	-0.0080
AQ	0.3970	-0.0520
AR	0.3640	-0.0030
AS	0.5510	-0.0110
AT	0.2370	-0.0150
AU	0.5410	0.0030
AV	0.4380	0.0190
AW	0.1440	0.0260
AX	0.2300	0.0050
B1	0.2650	0.0020
B2	0.6520	0.0280
B3	0.1800	-0.0280
B4	0.0720	-0.0250
B5	0.4570	-0.0390
B6	0.5180	0.0080
BA	0.2920	-0.0240
BB	0.4270	-0.0050
BC	0.2500	-0.0150



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Chain	Atom inclusion	Q-score
BD	 0.4830	 0.0040
BE	 0.3080	 -0.0030
BF	 0.3510	 -0.0060
BG	 0.5990	 -0.0100
BH	 0.3760	 -0.0030
BI	 0.4390	 -0.0430
BJ	 0.1550	 -0.0360
BK	 0.0730	 -0.0250
BL	 0.5110	 0.0130
BM	 0.2860	 -0.0330
BN	 0.4240	 -0.0100
BO	 0.0000	 -0.0070
BP	 0.6370	 0.0410
BQ	 0.4540	 0.0330
BR	 0.4200	 -0.0110
BS	 0.3110	 -0.0130
BT	 0.4940	 -0.0230
BU	 0.1760	 -0.0250
BV	 0.5110	 0.0300
BW	 0.2590	 -0.0140
BX	 0.3060	 -0.0010
BY	 0.5940	 0.0050
BZ	 0.0400	 0.0080