



wwPDB EM Validation Summary Report ⓘ

Jun 23, 2026 – 09:09 AM EDT

PDB ID : 4V6Z / pdb_00004v6z
EMDB ID : EMD-2472
Title : E. coli 70S-fMetVal-tRNAVal-tRNA^fMet complex in classic pre-translocation state (pre1b)
Authors : Blau, C.; Bock, L.V.; Schroder, G.F.; Davydov, I.; Fischer, N.; Stark, H.; Rodnina, M.V.; Vaiana, A.C.; Grubmuller, H.
Deposited on : 2013-10-14
Resolution : 12.00 Å (reported)
Based on initial models : 3I1O, 2K4C, 2HGP, 2WRI

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

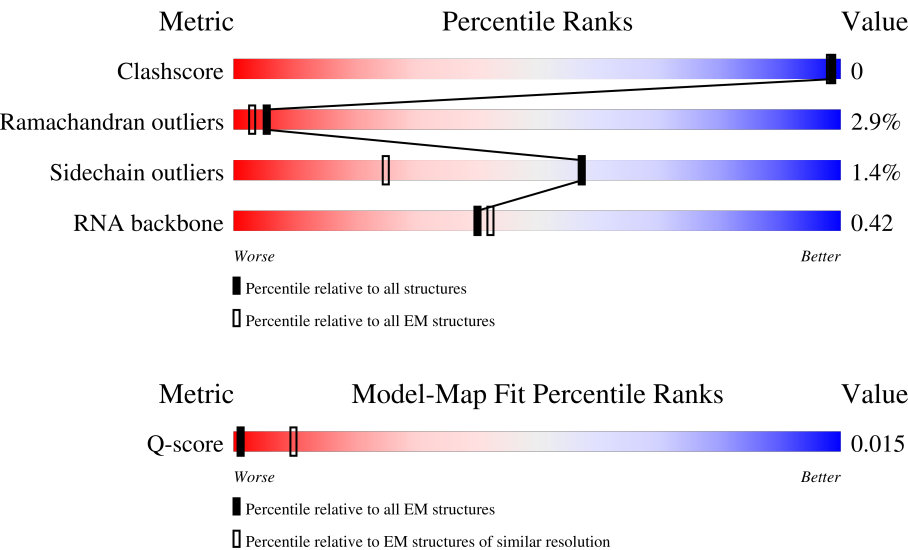
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 i

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

The reported resolution of this entry is 12.00 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	93 (11.50 - 12.50)

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	AB	220	50% 95% 5%
2	AC	208	46% 96% .
3	AD	206	51% 95% 5%

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Mol	Chain	Length	Quality of chain
4	AE	152	45% 91% 8%
5	AF	101	26% 89% 10%
6	AG	152	36% 99%
7	AH	130	43% 97%
8	AI	128	25% 95% 5%
9	AJ	100	54% 90% 8%
10	AK	118	26% 97%
11	AL	124	31% 98%
12	AM	115	31% 94% 5%
13	AN	101	60% 95%
14	AO	89	26% 96%
15	AP	81	54% 95% 5%
16	AQ	82	43% 96%
17	AR	57	39% 95% 5%
18	AS	81	31% 98%
19	AT	86	27% 90% 9%
20	AU	53	34% 79% 21%
21	AA	1533	28% 60% 31% 8%
22	A1	76	41% 62% 30% 8%
23	A2	15	33% 67% 33%
24	A3	77	60% 57% 36% 6%
25	BC	273	53% 90% 10%
26	BD	209	51% 90% 9%
27	BE	201	35% 96%
28	BF	179	37% 94% 6%

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Mol	Chain	Length	Quality of chain
29	BG	177	53% 91% 7% ..
30	BH	149	76% 97% .
31	BI	142	99% 93% 6% .
32	BJ	142	51% 94% 6% .
33	BK	123	51% 93% 5% .
34	BL	144	33% 84% 15% ..
35	BM	136	54% 91% 7% .
36	BN	121	42% 98% .
37	BO	117	11% 95% . ..
38	BP	115	53% 90% 7% ..
39	BQ	118	43% 95% . ..
40	BR	103	31% 92% 8%
41	BS	110	46% 94% 6%
42	BT	94	36% 96% .
43	BU	104	39% 92% 5% ..
44	BV	94	34% 97% .
45	BW	80	39% 86% 11% .
46	BX	79	49% 94% . ..
47	BY	63	40% 98% .
48	BZ	59	51% 92% 7% .
49	B0	57	23% 91% 7% .
50	B1	52	48% 88% 12%
51	B2	46	57% 93% 7%
52	B3	65	51% 92% 5% ..
53	B4	38	45% 92% 8%

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Mol	Chain	Length	Quality of chain
54	BA	2903	35% 60% 32% 7%
55	BB	118	23% 58% 38%
56	B5	234	60% 94% 5%

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 147653 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AB	220	Total	C	N	O	S	0	1
			1708	1083	306	312	7		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AB	7	ACE	-	acetylation	UNP P0A7V0
AB	226	NH2	-	amidation	UNP P0A7V0

- Molecule 2 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AC	207	Total	C	N	O	S	0	1
			1625	1028	306	288	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AC	207	NH2	-	amidation	UNP P0A7V3

- Molecule 3 is a protein called 30S ribosomal protein S4.

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

- Molecule 4 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AE	152	Total	C	N	O	S	0	1
			1109	689	212	202	6		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AE	8	ACE	-	acetylation	UNP P0A7W1
AE	159	NH2	-	amidation	UNP P0A7W1

- Molecule 5 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AF	101	Total	C	N	O	S	0	1
			818	515	149	148	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AF	101	NH2	-	amidation	UNP P02358

- Molecule 6 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AG	152	Total	C	N	O	S	0	1
			1178	732	227	215	4		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AG	1	ACE	-	acetylation	UNP P02359
AG	152	NH2	-	amidation	UNP P02359

- Molecule 7 is a protein called 30S ribosomal protein S8.

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

- Molecule 8 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AI	128	Total	C	N	O	S	0	0
			1025	636	206	180	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AI	2	ACE	-	acetylation	UNP P0A7X3

- Molecule 9 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AJ	100	Total	C	N	O	S	0	1
			790	495	151	143	1		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AJ	4	ACE	-	acetylation	UNP P0A7R5
AJ	103	NH2	-	amidation	UNP P0A7R5

- Molecule 10 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AK	118	Total	C	N	O	S	0	0
			880	542	174	161	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AK	11	ACE	-	acetylation	UNP P0A7R9

- Molecule 11 is a protein called 30S ribosomal protein S12.

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

- Molecule 12 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AM	114	Total	C	N	O	S	0	1
			877	541	178	155	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AM	114	NH2	-	amidation	UNP P0A7S9

- Molecule 13 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AN	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 14 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AO	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 15 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AP	81	Total	C	N	O	S	0	1
			639	400	127	111	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AP	81	NH2	-	amidation	UNP P0A7T3

- Molecule 16 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AQ	82	Total	C	N	O	S	0	1
			652	413	122	114	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AQ	2	ACE	-	acetylation	UNP P0AG63
AQ	83	NH2	-	amidation	UNP P0AG63

- Molecule 17 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AR	57	Total	C	N	O		0	1
			459	290	87	82			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AR	18	ACE	-	acetylation	UNP P0A7T7

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Chain	Residue	Modelled	Actual	Comment	Reference
AR	74	NH2	-	amidation	UNP P0A7T7

- Molecule 18 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AS	81	Total	C	N	O	S	0	1
			641	410	121	108	2		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AS	1	ACE	-	acetylation	UNP P0A7U3
AS	81	NH2	-	amidation	UNP P0A7U3

- Molecule 19 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AT	86	Total	C	N	O	S	0	0
			668	413	137	115	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AT	1	ACE	-	acetylation	UNP P0A7U7

- Molecule 20 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AU	53	Total	C	N	O	S	0	1
			429	267	87	74	1		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AU	2	ACE	-	acetylation	UNP P68679
AU	54	NH2	-	amidation	UNP P68679

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

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

- Molecule 22 is a RNA chain called fMet-Val-tRNA-Val.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	A1	76	Total	C	N	O	P	S	0	0
			1627	728	292	531	75	1		

- Molecule 23 is a RNA chain called 5'-R(*AP*CP*UP*AP*UP*GP*GP*UP*UP*UP*UP*UP*AP*UP*U)-3'.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	A2	15	Total	C	N	O	P	0	0
			309	140	46	109	14		

- Molecule 24 is a RNA chain called tRNA-fMet.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	A3	77	Total	C	N	O	P	S	0	0
			1642	734	297	534	76	1		

- Molecule 25 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BC	272	Total	C	N	O	S	0	1
			2083	1288	424	364	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BC	272	NH2	-	amidation	UNP P60422

- Molecule 26 is a protein called 50S ribosomal protein L3.

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

- Molecule 27 is a protein called 50S ribosomal protein L4.

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

- Molecule 28 is a protein called 50S ribosomal protein L5.

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

- Molecule 29 is a protein called 50S ribosomal protein L6.

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

- Molecule 30 is a protein called 50S ribosomal protein L9.

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

- Molecule 31 is a protein called 50S ribosomal protein L11.

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

- Molecule 32 is a protein called 50S ribosomal protein L13.

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

- Molecule 33 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BK	123	Total	C	N	O	S	0	1
			939	587	181	165	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BK	123	NH2	-	amidation	UNP P0ADY3

- Molecule 34 is a protein called 50S ribosomal protein L15.

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

- Molecule 35 is a protein called 50S ribosomal protein L16.

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

- Molecule 36 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BN	121	Total	C	N	O	S	0	1
			961	593	197	166	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BN	121	NH2	-	amidation	UNP P0AG44

- Molecule 37 is a protein called 50S ribosomal protein L18.

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

- Molecule 38 is a protein called 50S ribosomal protein L19.

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

- Molecule 39 is a protein called 50S ribosomal protein L20.

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

- Molecule 40 is a protein called 50S ribosomal protein L21.

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

- Molecule 41 is a protein called 50S ribosomal protein L22.

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

- Molecule 42 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BT	94	Total	C	N	O	S	0	1
			739	466	140	131	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BT	94	NH2	-	amidation	UNP P0ADZ0

- Molecule 43 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	BU	103	Total	C	N	O	0	1
			780	492	147	141		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BU	103	NH2	-	amidation	UNP P60624

- Molecule 44 is a protein called 50S ribosomal protein L25.

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

- Molecule 45 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BW	80	Total	C	N	O	S	0	0
			599	369	120	109	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BW	5	ACE	-	acetylation	UNP P0A7L8

- Molecule 46 is a protein called 50S ribosomal protein L28.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BX	-1	ACE	-	acetylation	UNP P0A7M2

- Molecule 47 is a protein called 50S ribosomal protein L29.

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

- Molecule 48 is a protein called 50S ribosomal protein L30.

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

- Molecule 49 is a protein called 50S ribosomal protein L32.

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
50	B1	52	Total	C	N	O	0	1
			413	265	76	72		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B1	2	ACE	-	acetylation	UNP P0A7N9
B1	53	NH2	-	amidation	UNP P0A7N9

- Molecule 51 is a protein called 50S ribosomal protein L34.

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

- Molecule 52 is a protein called 50S ribosomal protein L35.

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

- Molecule 53 is a protein called 50S ribosomal protein L36.

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

- Molecule 54 is a RNA chain called 23S ribosomal RNA.

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

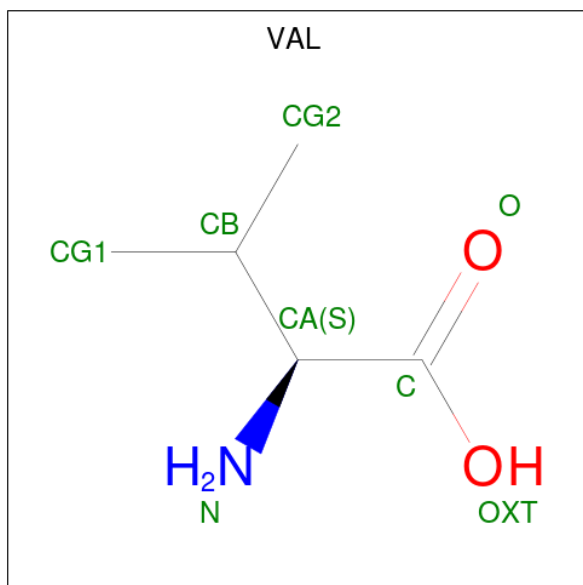
- Molecule 55 is a RNA chain called 5S ribosomal RNA.

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

- Molecule 56 is a protein called 50S ribosomal protein L1.

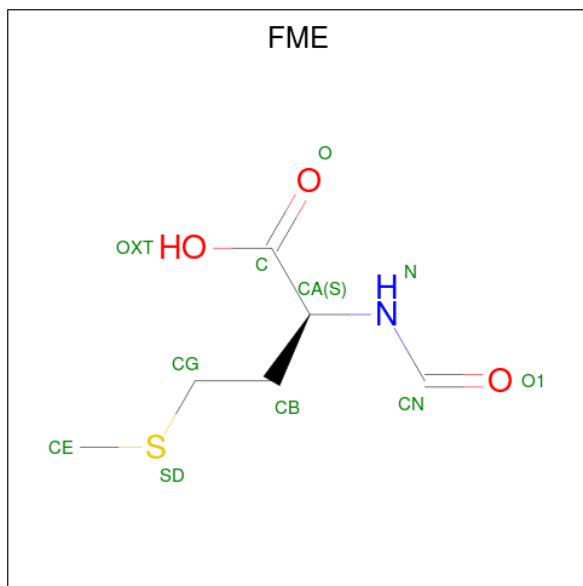
Mol	Chain	Residues	Atoms					AltConf	Trace
56	B5	223	Total	C	N	O	S	0	0
			1658	1038	302	312	6		

- Molecule 57 is VALINE (CCD ID: VAL) (formula: C₅H₁₁NO₂).



Mol	Chain	Residues	Atoms				AltConf
57	A1	1	Total	C	N	O	0
			7	5	1	1	

- Molecule 58 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: C₆H₁₁NO₃S).

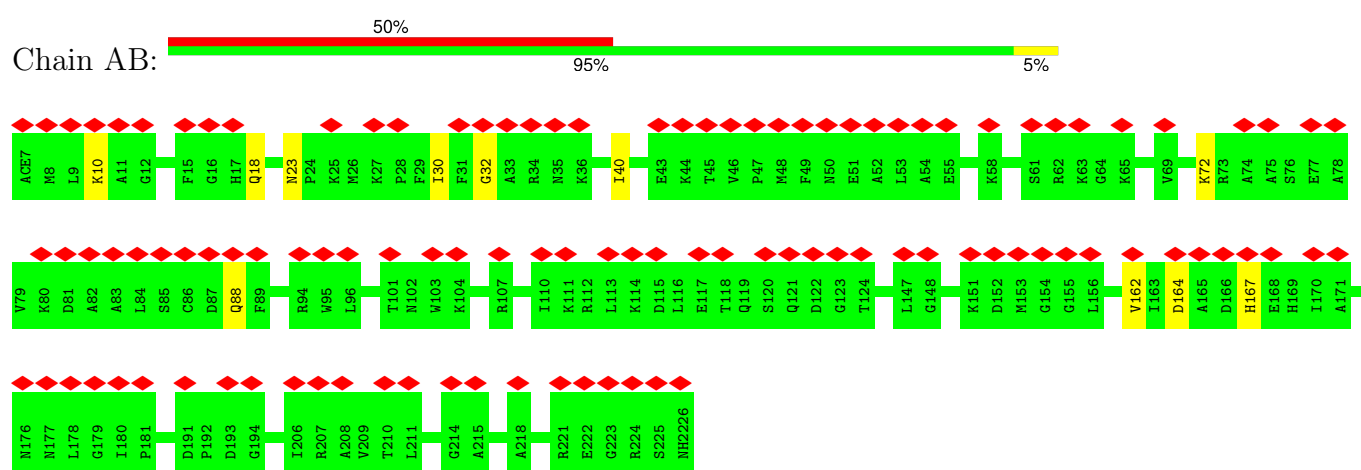


Mol	Chain	Residues	Atoms					AltConf
58	BA	1	Total	C	N	O	S	0
			10	6	1	2	1	

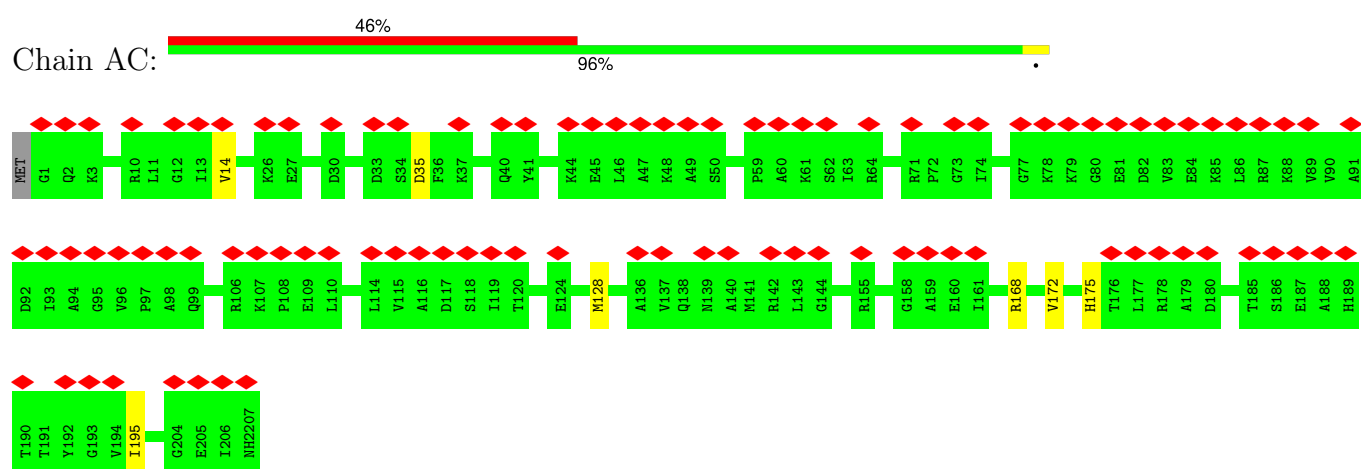
3 Residue-property plots [i](#)

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

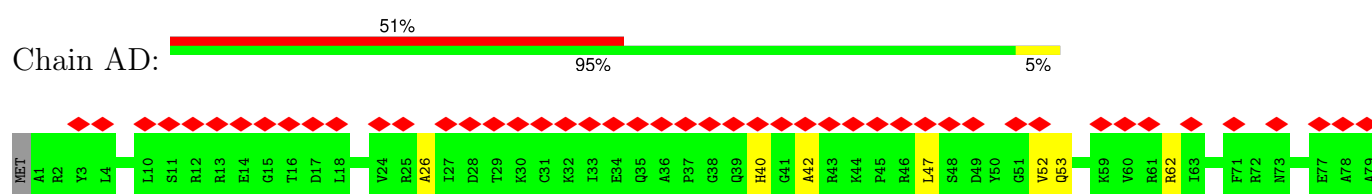
• Molecule 1: 30S ribosomal protein S2

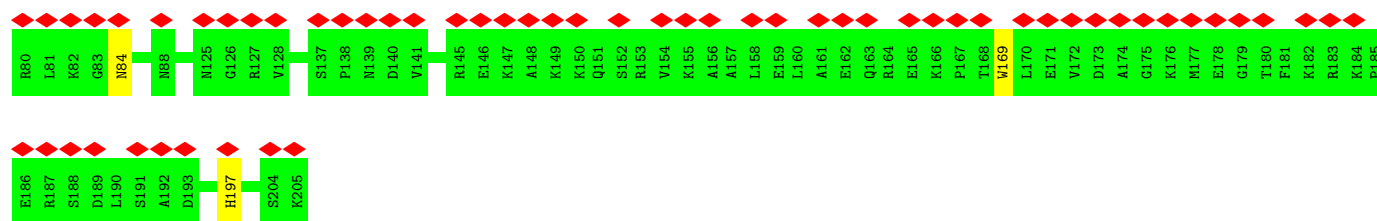


• Molecule 2: 30S ribosomal protein S3

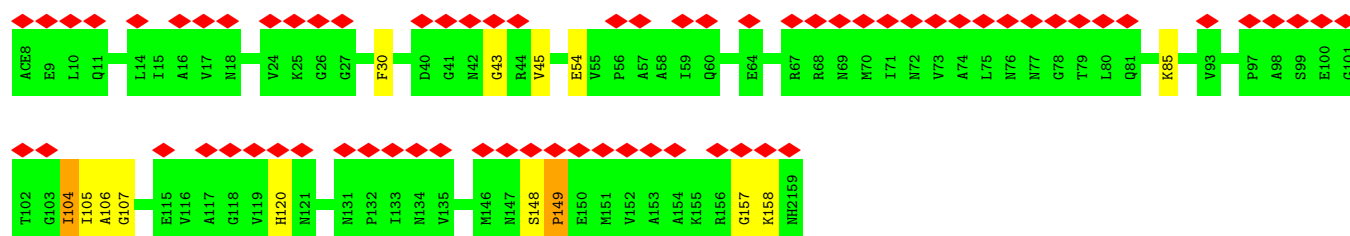


• Molecule 3: 30S ribosomal protein S4

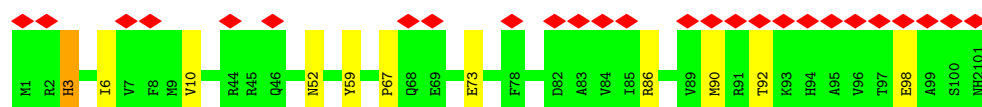
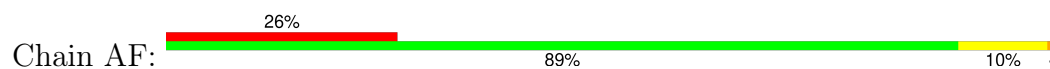




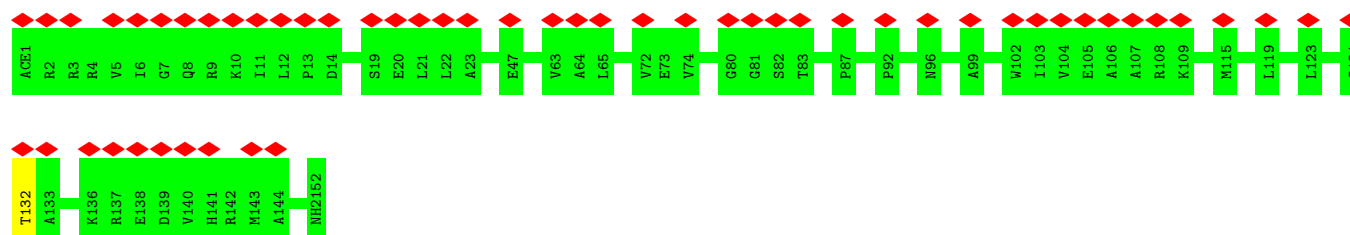
• Molecule 4: 30S ribosomal protein S5



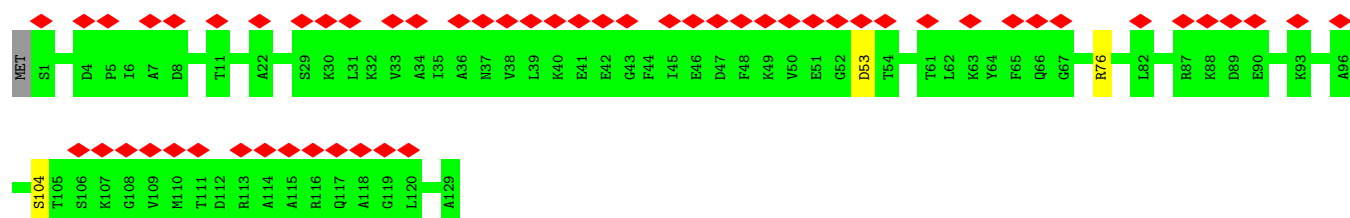
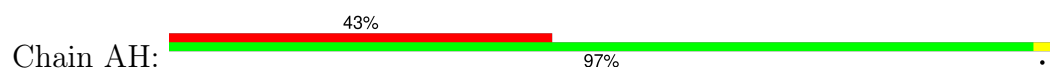
• Molecule 5: 30S ribosomal protein S6



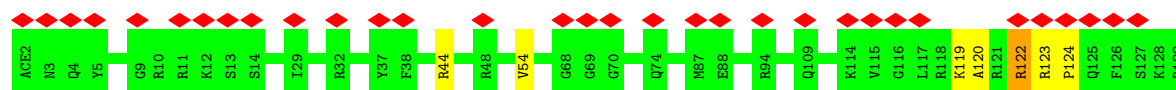
• Molecule 6: 30S ribosomal protein S7



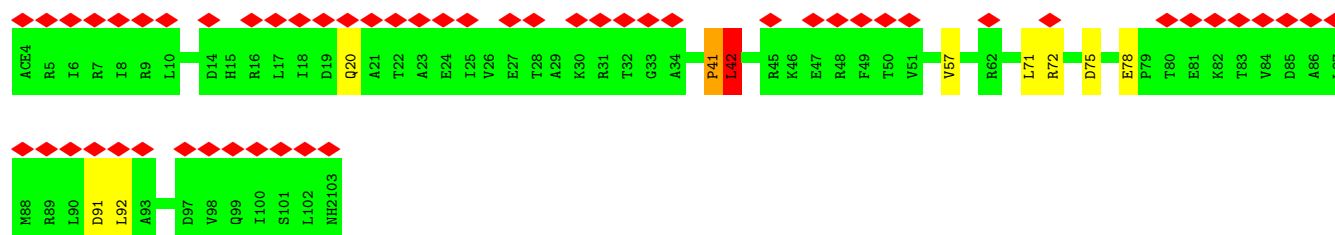
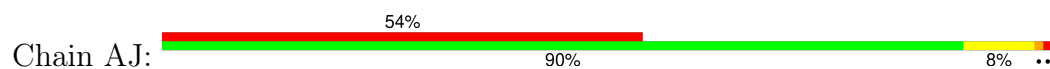
• Molecule 7: 30S ribosomal protein S8



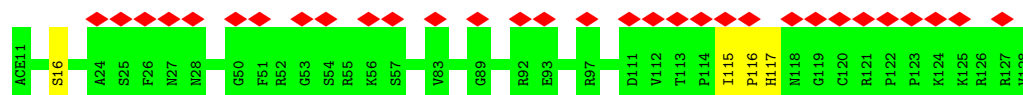
- Molecule 8: 30S ribosomal protein S9



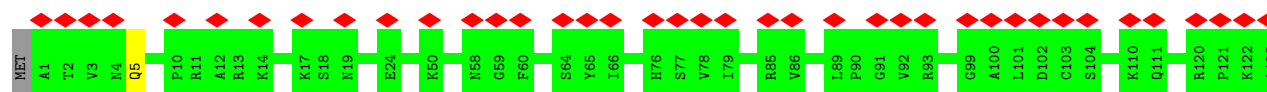
- Molecule 9: 30S ribosomal protein S10



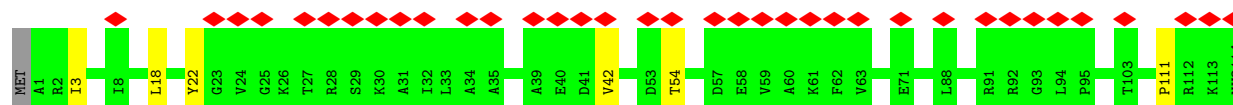
- Molecule 10: 30S ribosomal protein S11



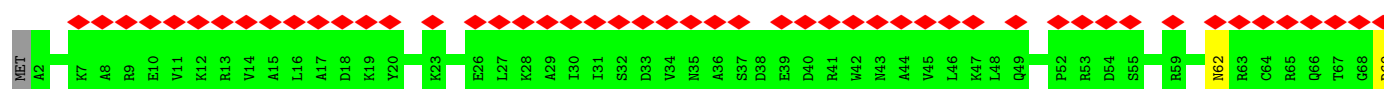
- Molecule 11: 30S ribosomal protein S12

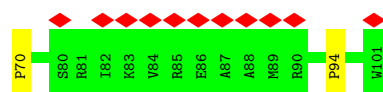


- Molecule 12: 30S ribosomal protein S13

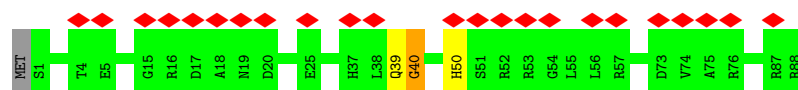


- Molecule 13: 30S ribosomal protein S14

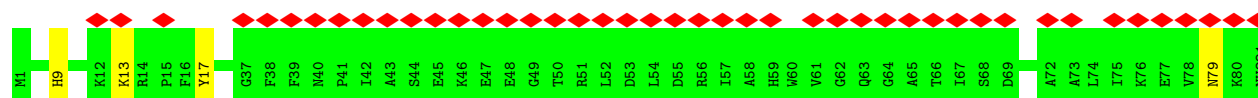




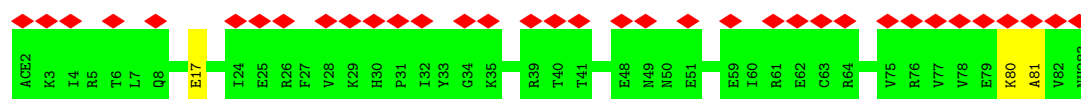
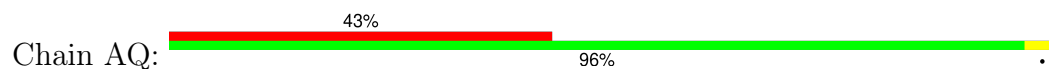
- Molecule 14: 30S ribosomal protein S15



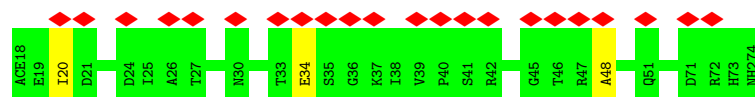
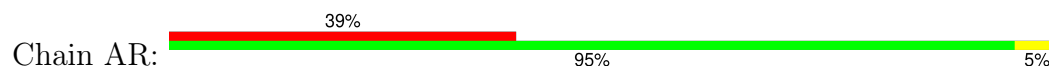
- Molecule 15: 30S ribosomal protein S16



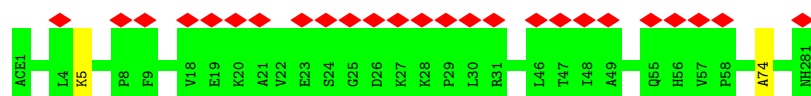
- Molecule 16: 30S ribosomal protein S17



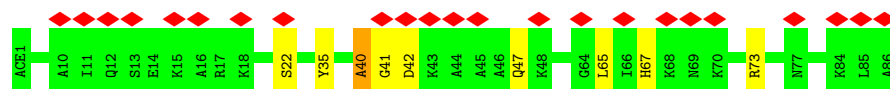
- Molecule 17: 30S ribosomal protein S18



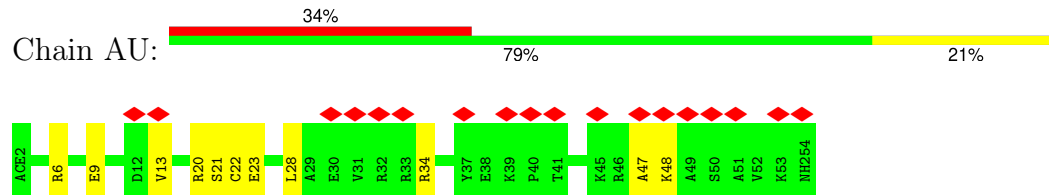
- Molecule 18: 30S ribosomal protein S19



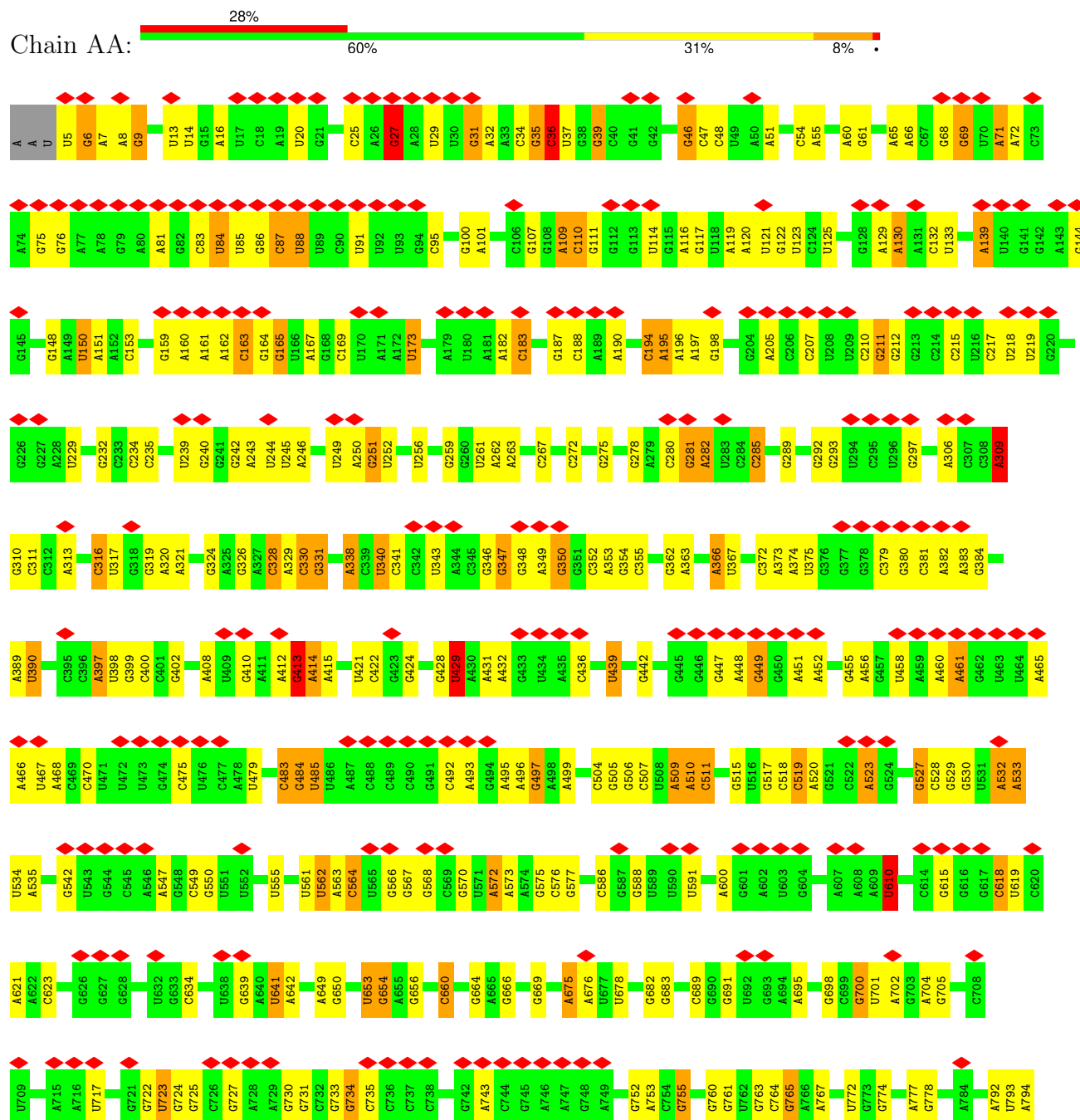
- Molecule 19: 30S ribosomal protein S20

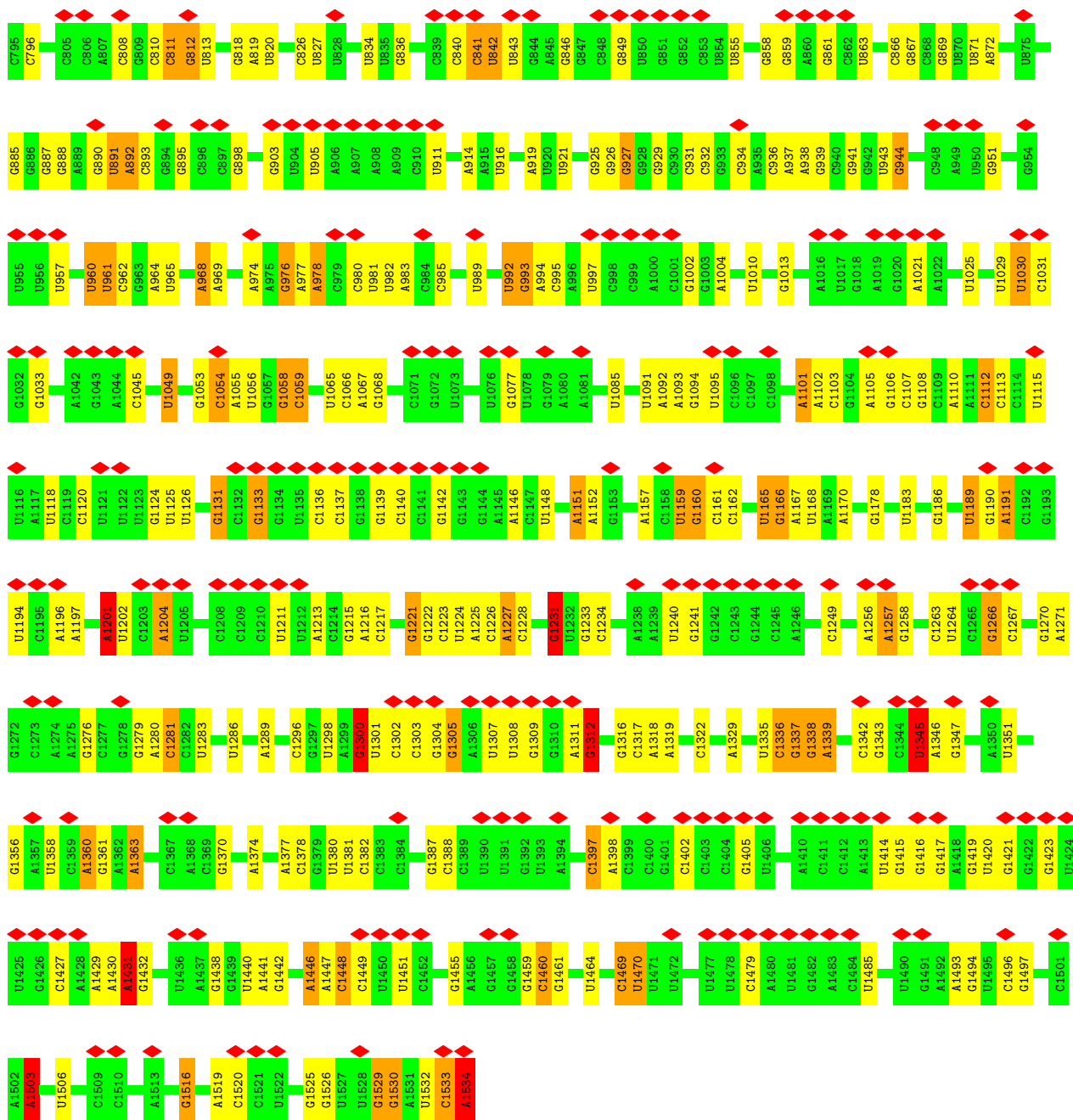


• Molecule 20: 30S ribosomal protein S21

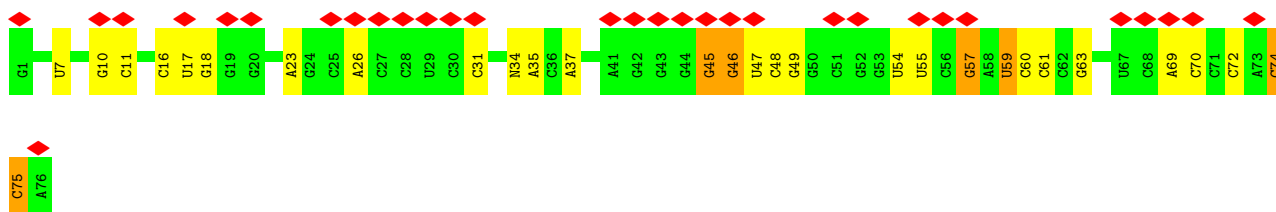
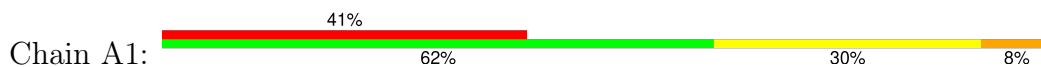


• Molecule 21: 16S ribosomal RNA

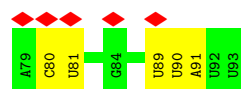




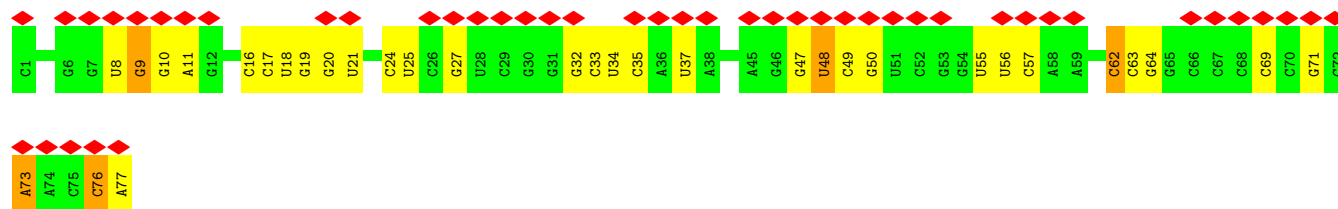
• Molecule 22: fMet-Val-tRNA-Val



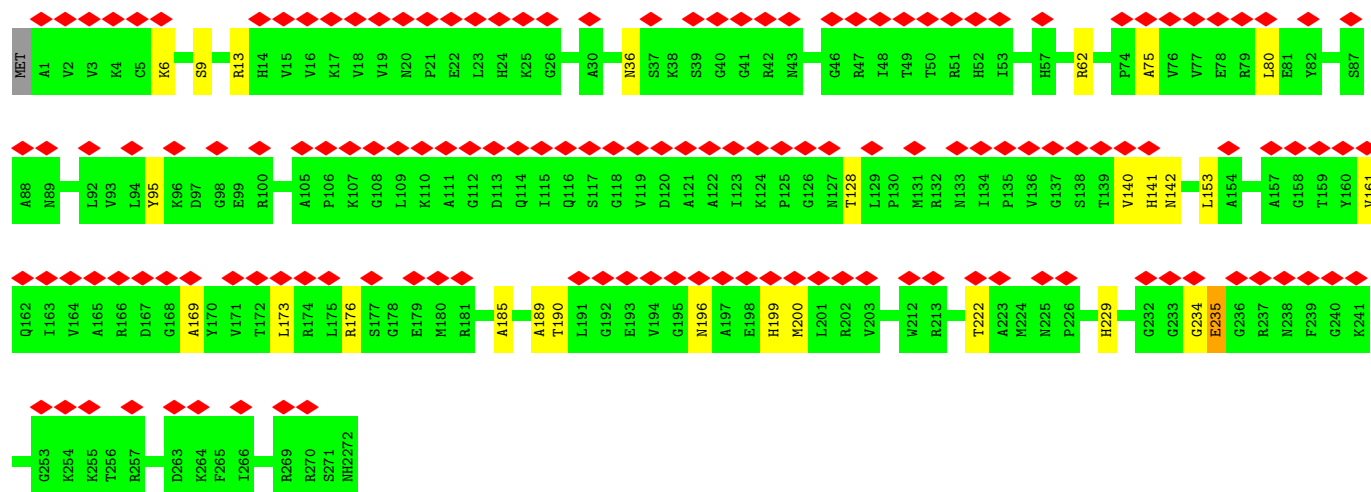
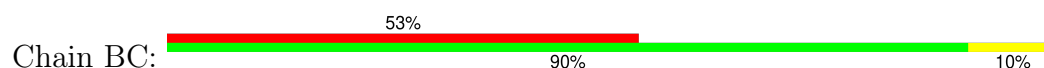
• Molecule 23: 5'-R(*AP*CP*UP*AP*UP*GP*GP*UP*UP*UP*UP*UP*AP*UP*U)-3'



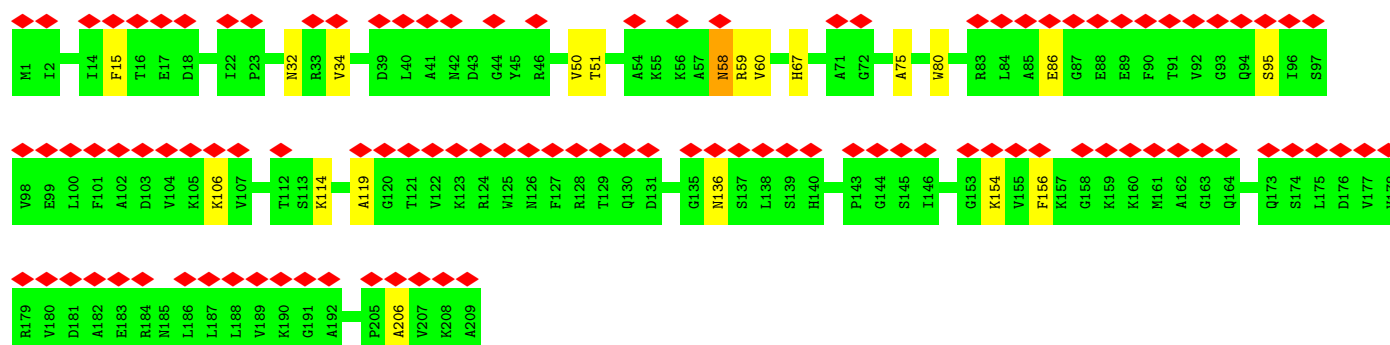
• Molecule 24: tRNA-fMet



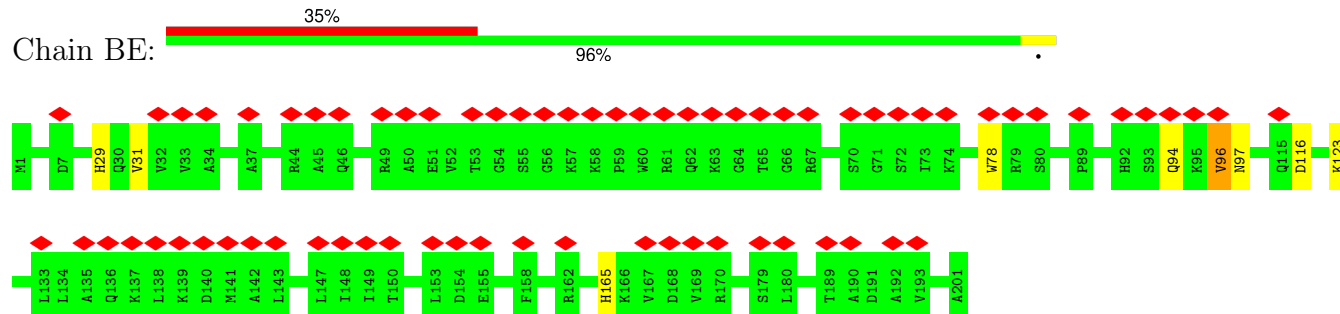
• Molecule 25: 50S ribosomal protein L2



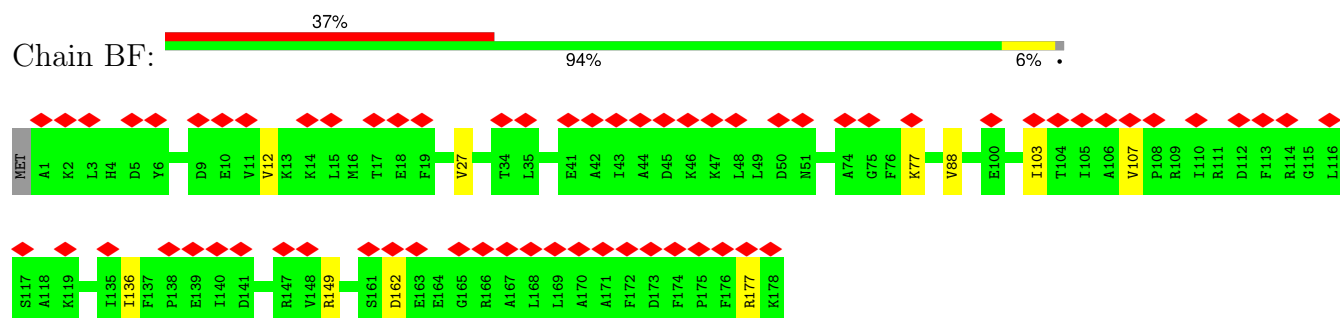
• Molecule 26: 50S ribosomal protein L3



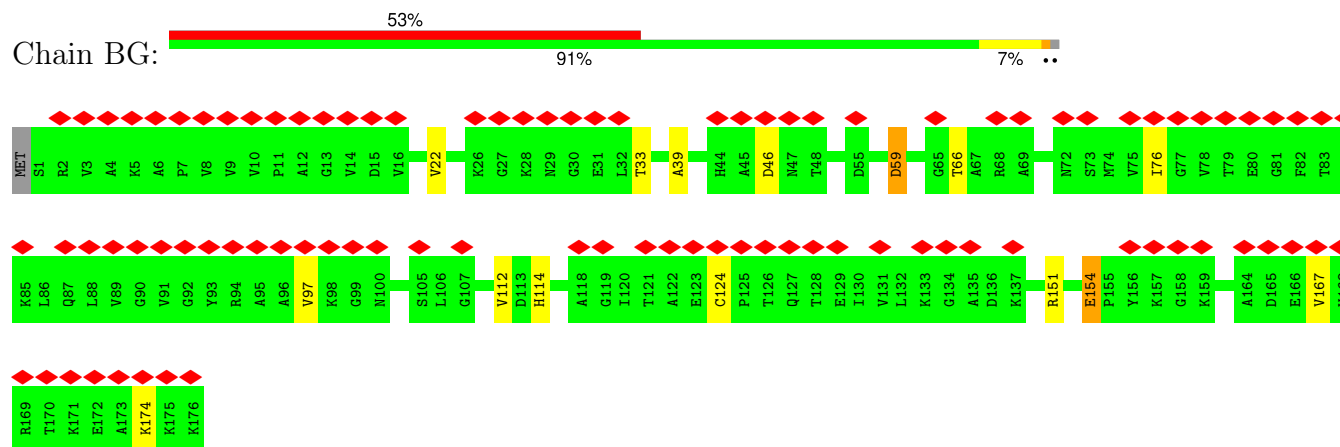
- Molecule 27: 50S ribosomal protein L4



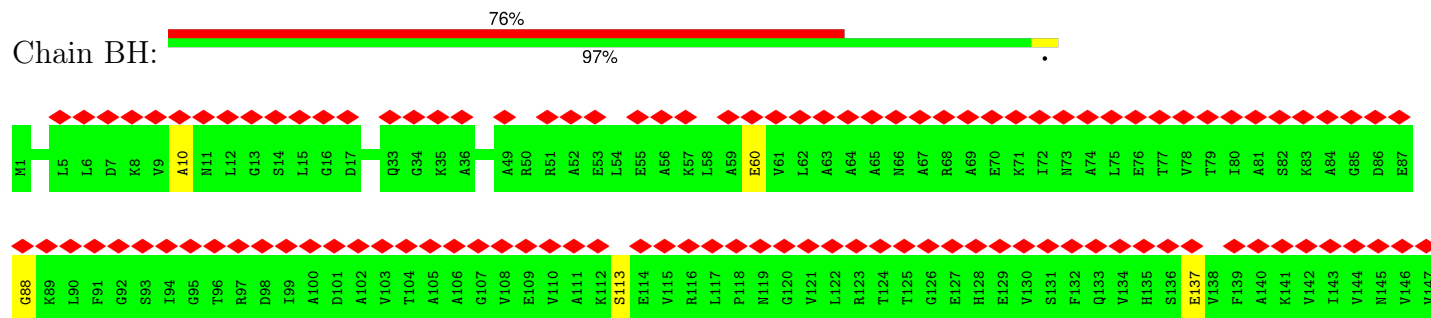
- Molecule 28: 50S ribosomal protein L5



- Molecule 29: 50S ribosomal protein L6

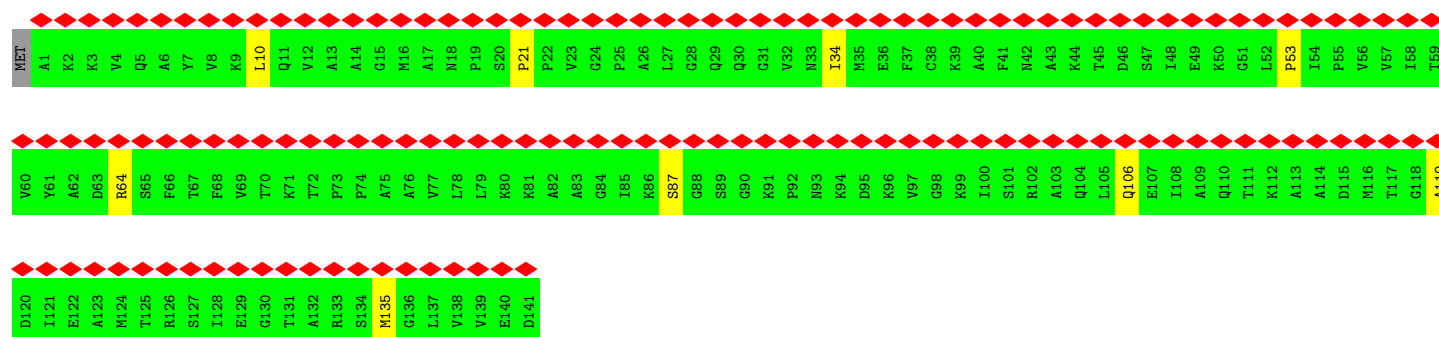


- Molecule 30: 50S ribosomal protein L9

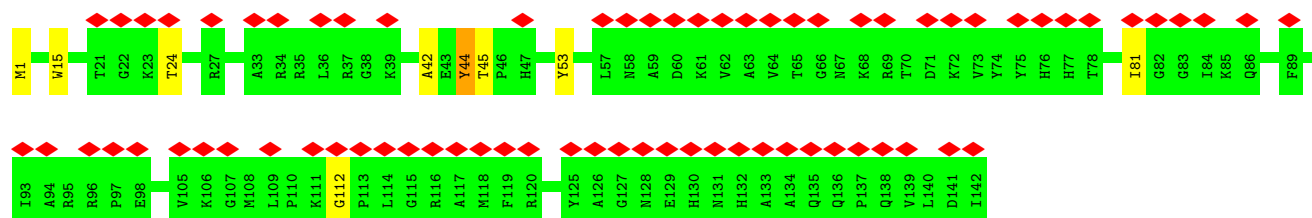




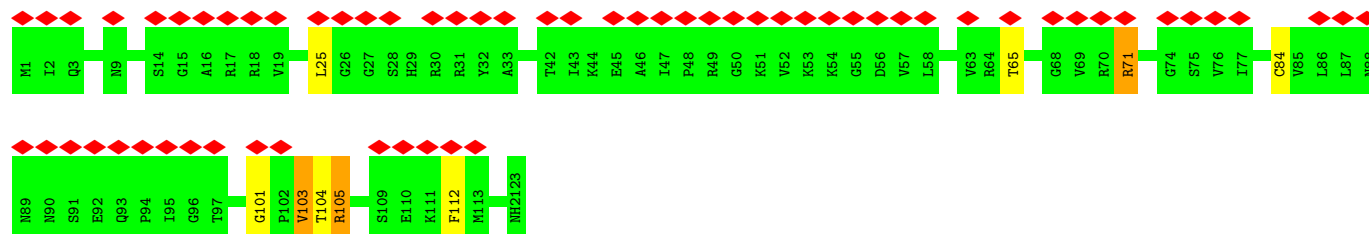
• Molecule 31: 50S ribosomal protein L11



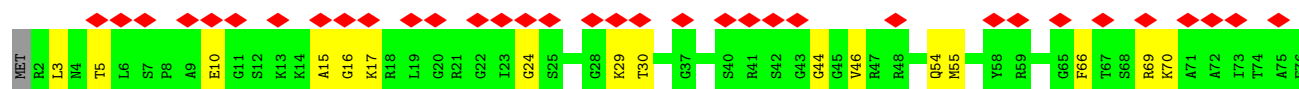
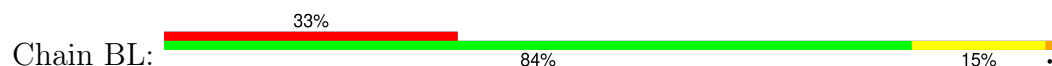
• Molecule 32: 50S ribosomal protein L13

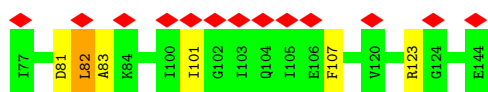


• Molecule 33: 50S ribosomal protein L14

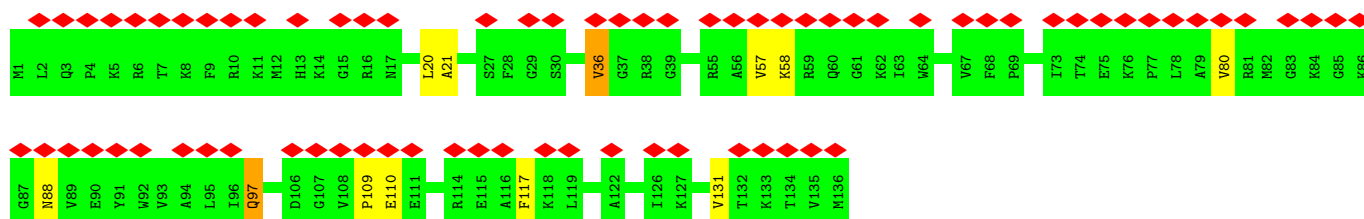


• Molecule 34: 50S ribosomal protein L15

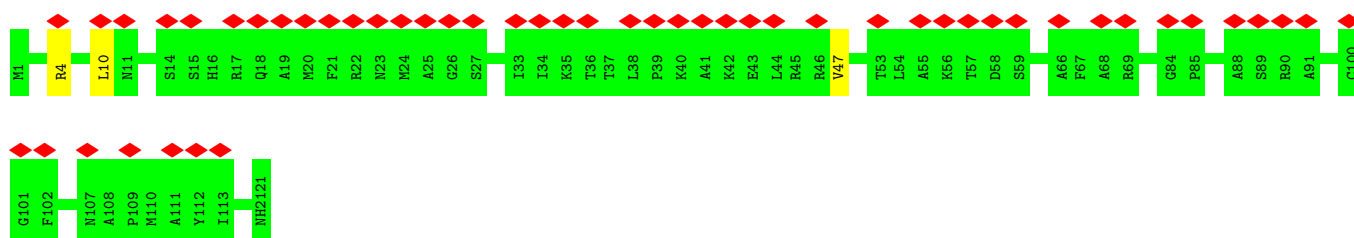
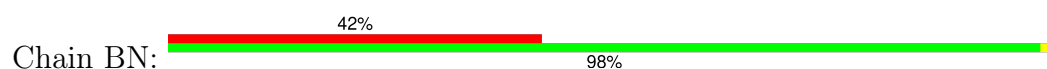




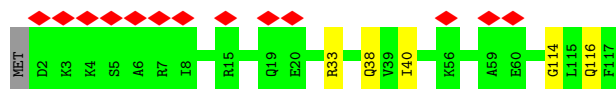
- Molecule 35: 50S ribosomal protein L16



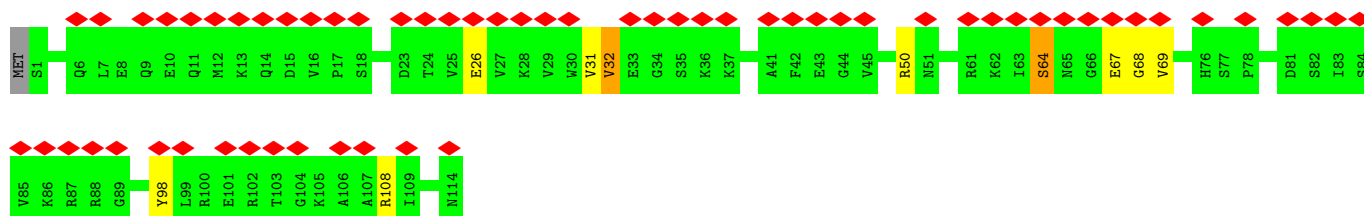
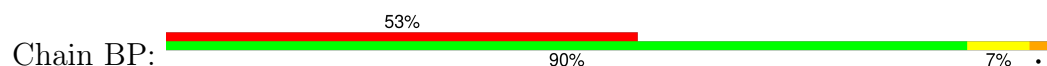
- Molecule 36: 50S ribosomal protein L17



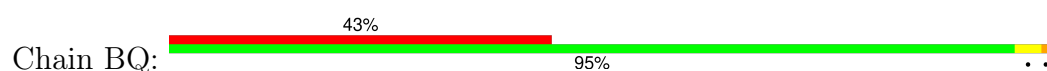
- Molecule 37: 50S ribosomal protein L18

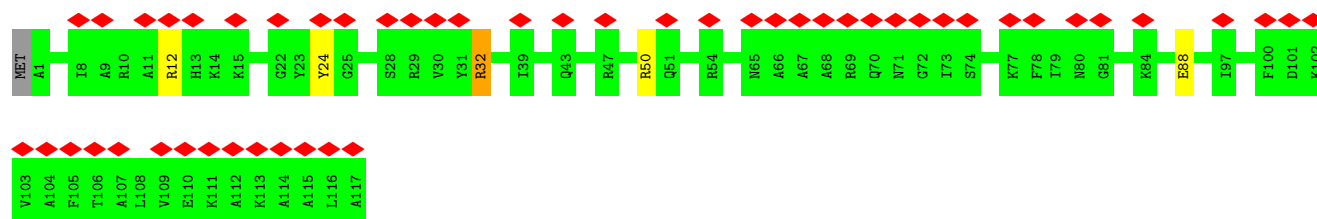


- Molecule 38: 50S ribosomal protein L19

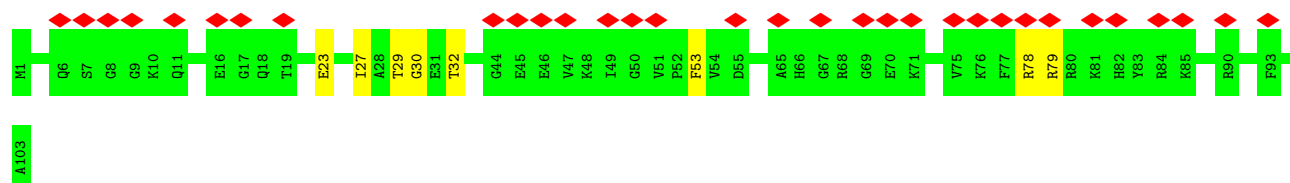


- Molecule 39: 50S ribosomal protein L20

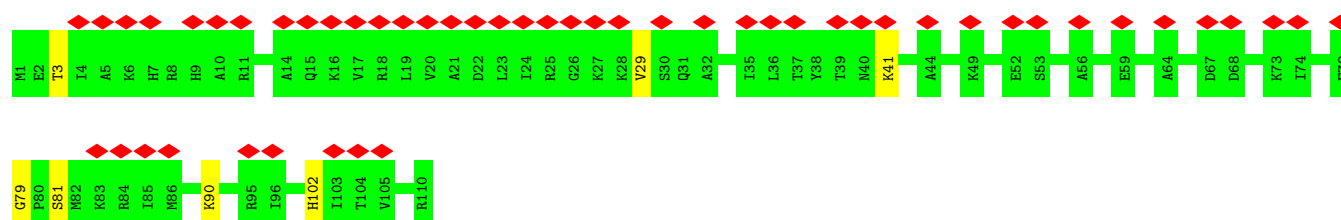




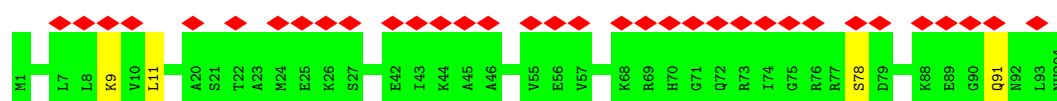
- Molecule 40: 50S ribosomal protein L21



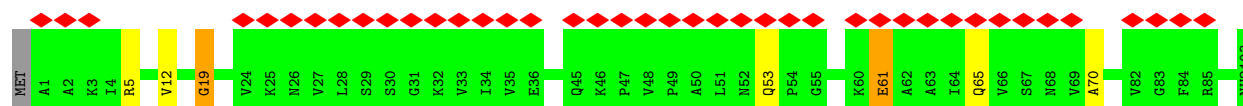
- Molecule 41: 50S ribosomal protein L22



- Molecule 42: 50S ribosomal protein L23

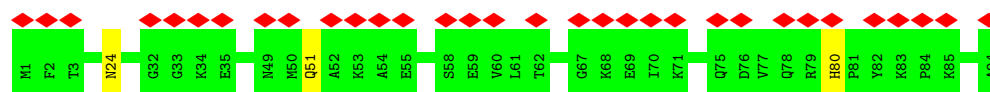


- Molecule 43: 50S ribosomal protein L24

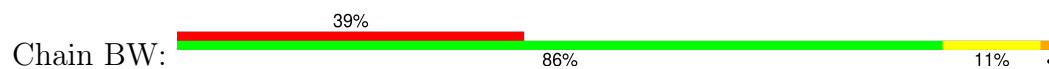


- Molecule 44: 50S ribosomal protein L25

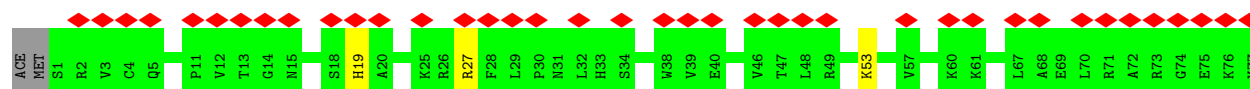




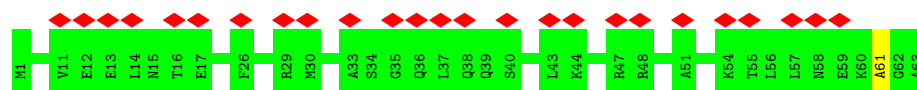
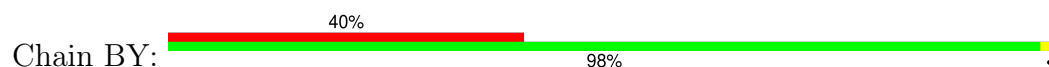
- Molecule 45: 50S ribosomal protein L27



- Molecule 46: 50S ribosomal protein L28



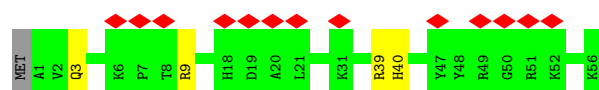
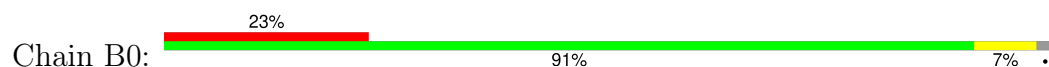
- Molecule 47: 50S ribosomal protein L29



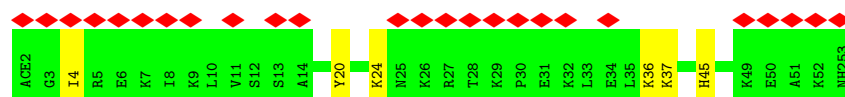
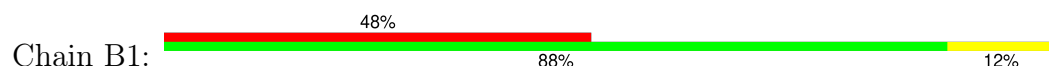
- Molecule 48: 50S ribosomal protein L30



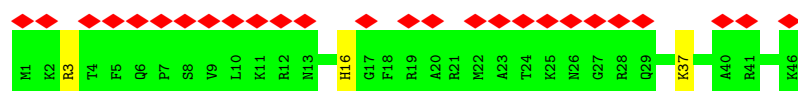
- Molecule 49: 50S ribosomal protein L32



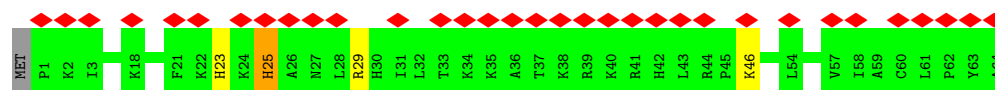
- Molecule 50: 50S ribosomal protein L33



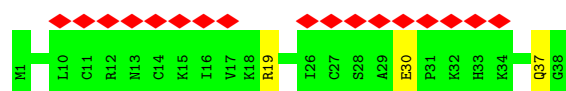
- Molecule 51: 50S ribosomal protein L34



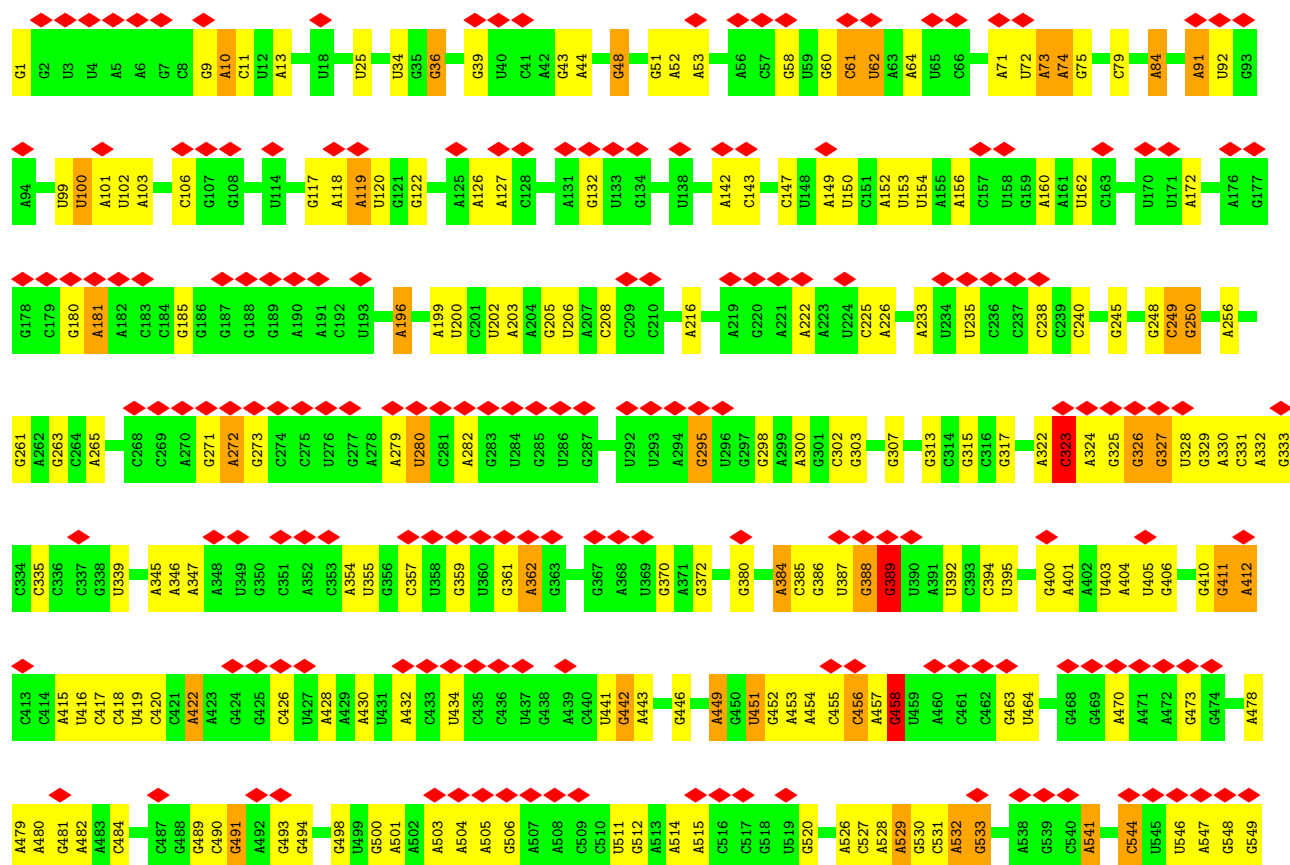
• Molecule 52: 50S ribosomal protein L35

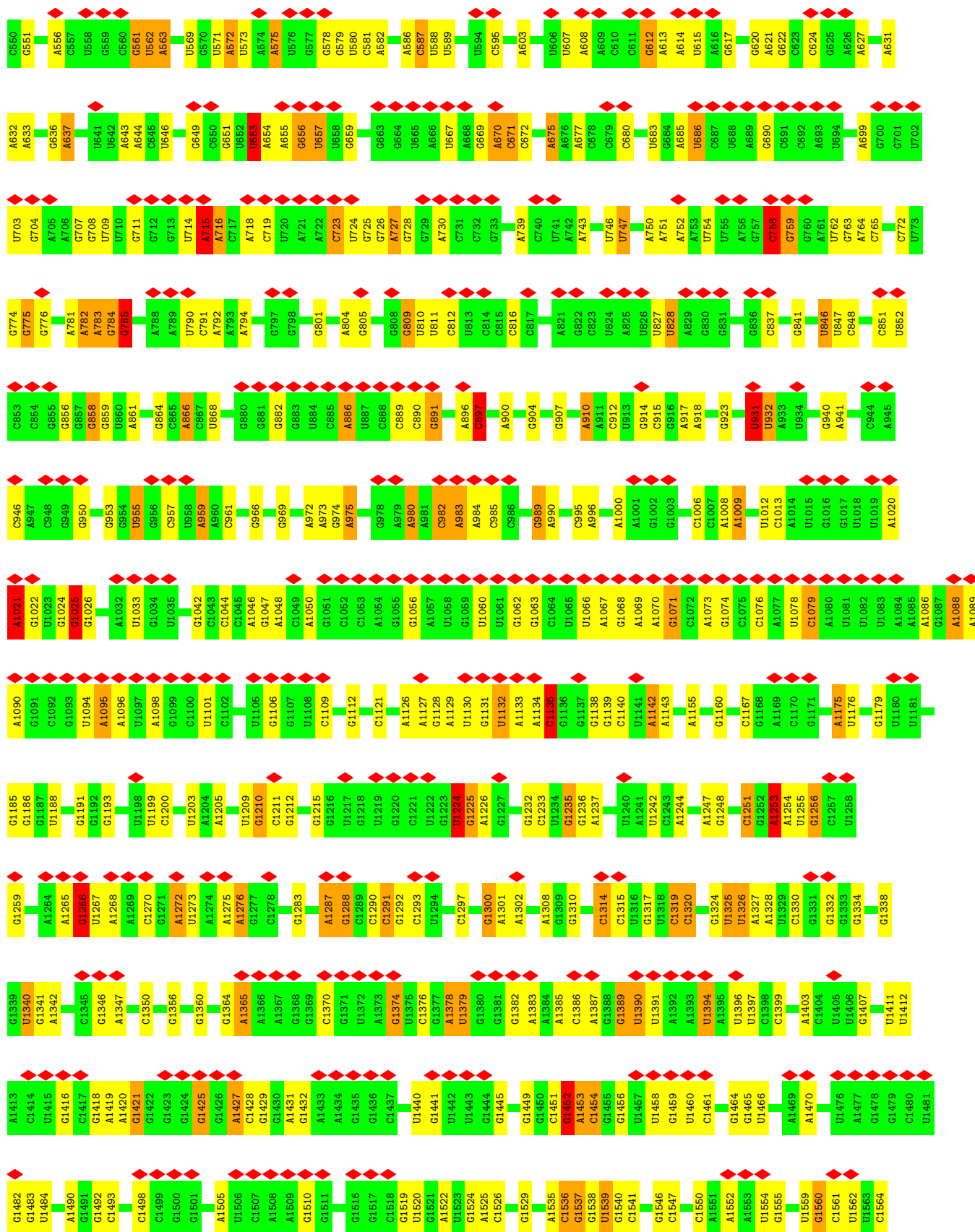


• Molecule 53: 50S ribosomal protein L36

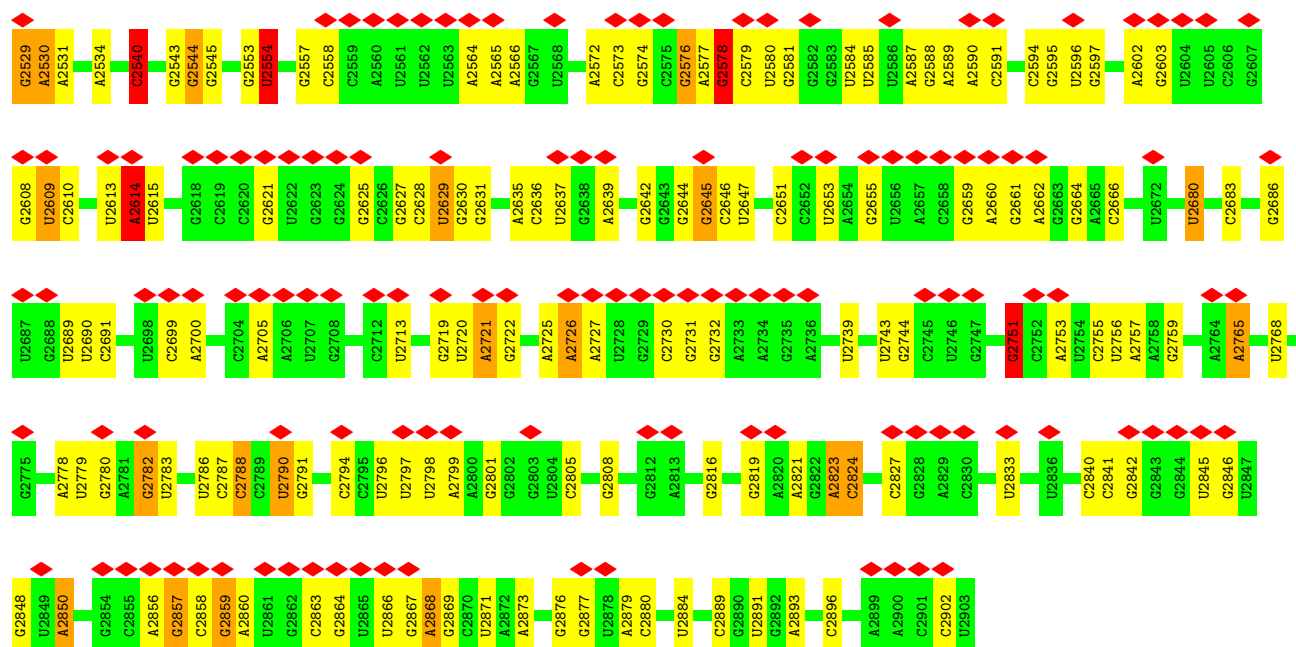


• Molecule 54: 23S ribosomal RNA

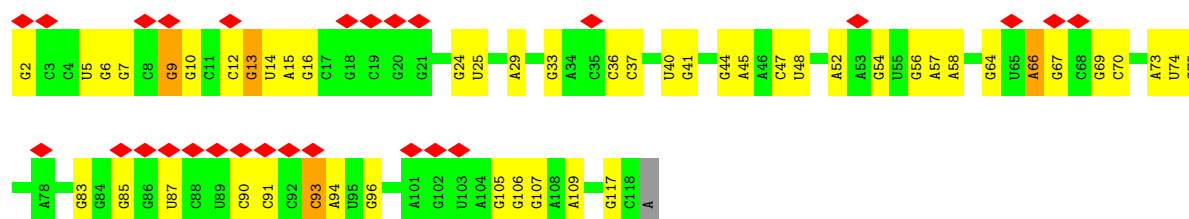




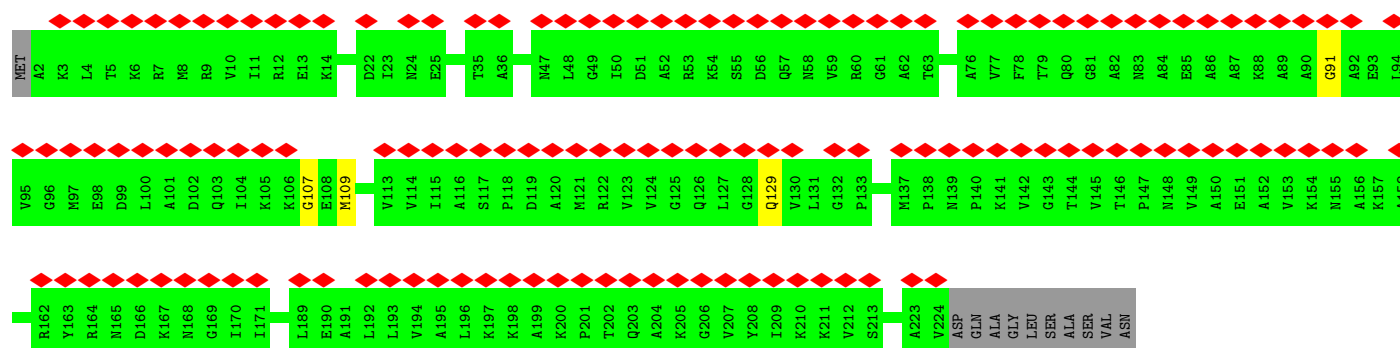
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U2172	A2173	C2174	C2175	C2178	C2179	U2180	U2181	U2182	A2183	A2184	U2185	G2186	U2187	U2188	U2189	G2190	A2191	U2192	G2193	U2194	U2195	C2196	U2197	A2198	G2201	U2202	U2203	G2204	A2205	C2206	C2207	C2208	G2209	U2210	A2211	A2212	U2213	C2214	C2215	G2216	U2220	G2221	C2222	G2223	G2224	A2225	G2226	A2227	G2228	U2229	G2230	U2233	G2234	G2235	U2236
U2099	G2100	C2104	U2105	U2106	A2107	U2109	G2110	U2111	G2112	U2113	A2114	G2115	G2116	U2117	U2118	A2119	G2125	A2126	G2127	G2133	A2134	A2135	G2136	U2137	G2138	U2139	G2140	G2141	A2142	G2143	G2144	C2145	C2146	A2147	C2150	U2151	G2152	C2153	A2154	U2155	G2156	G2157	A2158	U2159	C2160	A2163	C2164	C2165	U2166	U2167	A2168	A2169			
C2021	U2028	G2029	A2030	A2031	G2032	G2035	U2039	G2040	U2041	A2042	C2043	C2044	C2045	G2048	A2051	A2052	A2054	C2055	A2058	A2059	A2060	G2061	A2062	C2063	C2064	C2065	C2066	G2067	U2068	C2069	A2070	U2074	U2075	U2076	A2077	U2079	G2083	C2084	U2085	U2086	C2089	G2093	A2094	A2095	C2096	A2097	U2098								
U1951	A1952	A1953	G1954	U1955	U1956	C1957	A1960	C1961	U1962	U1963	G1964	C1965	A1966	A1969	U1970	U1971	G1972	G1973	C1974	U1975	U1976	A1977	U1978	U1979	G1980	A1981	U1982	G1983	G1984	C1985	C1986	A1987	G1988	G1989	C1990	U1991	G1992	U1993	C1994	U1995	C1996	C1997	G2002	A2003	C2008	G2012	A2013	A2014	A2015	G2018	A2019	A2020			
G1875	A1876	A1877	G1878	C1879	U1883	U1884	A1885	U1886	C1887	G1888	C1895	G1896	G1897	U1898	A1899	A1900	A1901	C1902	G1903	G1906	G1910	A1913	C1914	U1915	A1918	A1919	C1920	C1924	A1928	G1929	U1930	U1931	A1932	G1933	C1934	G1935	A1936	A1937	A1938	U1939	U1940	C1941	U1942	U1943	U1944	U1945	U1946	C1947	G1948	G1949	G1950				
G1797	U1798	G1799	C1800	A1801	A1802	G1807	A1808	G1814	A1815	C1816	G1817	U1818	A1819	U1820	A1821	C1822	G1823	G1824	U1825	G1826	U1827	G1830	G1831	C1832	C1833	U1834	G1835	C1836	C1837	C1838	G1839	C1843	C1844	G1845	G1846	A1847	G1849	G1857	A1858	U1859	G1860	G1863	U1864	U1865	A1866	G1867	C1868	G1869	A1872	G1873	C1874				
C1726	C1727	C1728	U1729	C1730	U1736	G1737	G1738	U1739	G1740	G1743	A1746	U1747	C1748	U1749	G1750	U1751	G1752	G1753	A1754	U1755	G1756	A1757	U1758	C1760	G1761	A1762	G1763	C1764	U1765	G1766	G1767	U1688	G1768	U1769	G1770	A1773	U1775	G1776	U1781	U1782	A1783	A1784	A1787	C1788	U1789	C1790	A1791	G1792	C1793	A1794	C1795	U1796			
U1648	G1649	A1650	G1651	A1652	G1653	A1654	A1655	C1656	U1657	C1658	U1662	G1663	A1664	A1665	G1666	G1667	A1668	A1669	C1670	U1671	A1672	G1673	G1674	C1675	U1679	U1680	G1681	G1682	C1685	C1686	G1687	U1688	A1689	A1690	C1691	U1692	U1693	C1694	A1705	C1706	G1707	G1710	A1711	U1712	A1713	U1714	G1715	U1716	A1717	G1723	G1724	U1725			
C1565	A1566	G1567	G1568	A1569	G1573	C1574	C1575	U1576	C1577	G1581	U1584	C1585	G1588	U1589	A1590	A1591	C1595	A1596	A1597	A1598	U1599	C1600	G1601	U1602	A1603	C1604	C1607	A1608	A1609	A1610	C1611	A1618	G1619	G1620	U1621	G1622	G1623	U1624	C1625	A1626	U1629	A1630	G1631	A1632	C1633	A1634	A1635	U1636	A1641	G1642					



• Molecule 55: 5S ribosomal RNA



• Molecule 56: 50S ribosomal protein L1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	13091	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI/PHILIPS CM200FEG	Depositor
Voltage (kV)	160	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	161000	Depositor
Image detector	GENERIC TVIPS (4k x 4k)	Depositor
Maximum map value	191.487	Depositor
Minimum map value	-133.057	Depositor
Average map value	-0.914	Depositor
Map value standard deviation	20.362	Depositor
Recommended contour level	25	Depositor
Map size ($\text{\AA}$)	358.4, 358.4, 358.4	wwPDB
Map dimensions	128, 128, 128	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	2.8, 2.8, 2.8	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 7MG, CM0, 5MU, 6MZ, NH2, H2U, PSU, ACE, OMC, 4SU, FME

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	AB	0.98	0/1736	1.41	7/2340 (0.3%)
2	AC	1.04	0/1651	1.42	0/2225
3	AD	1.02	0/1665	1.50	12/2227 (0.5%)
4	AE	0.99	0/1119	1.48	18/1506 (1.2%)
5	AF	1.01	0/835	1.48	4/1128 (0.4%)
6	AG	1.01	0/1188	1.39	0/1593
7	AH	1.01	0/989	1.40	2/1326 (0.2%)
8	AI	1.06	0/1035	1.50	7/1377 (0.5%)
9	AJ	1.06	0/797	1.48	8/1079 (0.7%)
10	AK	1.09	0/894	1.44	3/1207 (0.2%)
11	AL	1.06	0/969	1.44	1/1300 (0.1%)
12	AM	1.09	0/884	1.51	2/1181 (0.2%)
13	AN	1.08	1/817 (0.1%)	1.46	3/1088 (0.3%)
14	AO	1.06	0/722	1.50	4/964 (0.4%)
15	AP	1.10	0/648	1.47	0/870
16	AQ	0.98	0/658	1.40	3/883 (0.3%)
17	AR	1.09	0/463	1.44	2/623 (0.3%)
18	AS	1.09	0/653	1.50	2/879 (0.2%)
19	AT	1.07	0/672	1.47	5/890 (0.6%)
20	AU	1.10	0/431	1.66	2/572 (0.3%)
21	AA	1.24	0/36759	1.20	107/57346 (0.2%)
22	A1	1.25	0/1668	1.22	8/2595 (0.3%)
23	A2	1.19	0/343	1.20	1/531 (0.2%)
24	A3	1.26	0/1722	1.20	6/2685 (0.2%)
25	BC	1.05	1/2121 (0.0%)	1.55	7/2852 (0.2%)
26	BD	0.98	0/1586	1.54	4/2134 (0.2%)
27	BE	0.95	0/1571	1.47	1/2113 (0.0%)
28	BF	0.99	0/1444	1.50	5/1937 (0.3%)
29	BG	0.96	0/1343	1.45	5/1816 (0.3%)
30	BH	0.92	0/1122	1.41	3/1515 (0.2%)
31	BI	0.95	1/1046 (0.1%)	1.48	2/1410 (0.1%)
32	BJ	1.00	0/1152	1.51	4/1551 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	BK	1.01	0/947	1.50	5/1268 (0.4%)
34	BL	1.02	0/1054	1.61	11/1403 (0.8%)
35	BM	1.04	0/1093	1.54	9/1460 (0.6%)
36	BN	1.08	0/973	1.49	0/1301
37	BO	1.08	0/902	1.57	7/1209 (0.6%)
38	BP	1.04	0/929	1.57	3/1242 (0.2%)
39	BQ	1.03	0/960	1.48	6/1278 (0.5%)
40	BR	1.00	0/829	1.48	3/1107 (0.3%)
41	BS	0.99	0/864	1.53	6/1156 (0.5%)
42	BT	0.98	0/744	1.52	1/994 (0.1%)
43	BU	0.96	0/787	1.54	4/1051 (0.4%)
44	BV	0.97	0/766	1.48	1/1025 (0.1%)
45	BW	1.00	0/604	1.59	3/799 (0.4%)
46	BX	1.05	0/635	1.55	1/848 (0.1%)
47	BY	0.96	0/510	1.51	0/677
48	BZ	1.10	0/453	1.63	1/605 (0.2%)
49	B0	1.06	0/450	1.60	2/599 (0.3%)
50	B1	0.94	0/417	1.45	0/556
51	B2	1.14	0/380	1.61	2/498 (0.4%)
52	B3	0.99	0/513	1.56	3/676 (0.4%)
53	B4	1.04	0/303	1.51	3/397 (0.8%)
54	BA	1.13	0/69796	1.19	193/108888 (0.2%)
55	BB	1.13	0/2800	1.21	5/4367 (0.1%)
56	B5	0.95	0/1673	1.43	0/2255
All	All	1.13	3/160085 (0.0%)	1.28	507/239402 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	AC	0	2
8	AI	0	1
10	AK	0	1
21	AA	0	365
22	A1	0	10
23	A2	0	1
24	A3	0	14
25	BC	0	2
33	BK	0	1
34	BL	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
54	BA	0	666
55	BB	0	30
All	All	0	1094

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	BI	53	PRO	CA-CB	-5.55	1.49	1.53
13	AN	69	ARG	CZ-NH2	-5.45	1.26	1.33
25	BC	176	ARG	CZ-NH2	-5.02	1.26	1.33

The worst 5 of 507 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	AE	149	PRO	CA-N-CD	-8.80	99.68	112.00
26	BD	58	ASN	CA-C-N	8.62	137.21	121.70
26	BD	58	ASN	C-N-CA	8.62	137.21	121.70
25	BC	140	VAL	N-CA-C	8.45	118.29	111.62
54	BA	411	G	C2'-C3'-O3'	7.99	121.49	109.50

There are no chirality outliers.

5 of 1094 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
21	AA	6	G	Sidechain
2	AC	168	ARG	Sidechain
2	AC	172	VAL	Peptide
8	AI	124	PRO	Peptide
10	AK	115	ILE	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	AB	1708	0	1736	2	0
2	AC	1625	0	1699	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	AD	1643	0	1710	0	0
4	AE	1109	0	1152	0	0
5	AF	818	0	808	0	0
6	AG	1178	0	1234	0	0
7	AH	979	0	1034	0	0
8	AI	1025	0	1074	0	0
9	AJ	790	0	832	2	0
10	AK	880	0	891	0	0
11	AL	955	0	1019	0	0
12	AM	877	0	937	0	0
13	AN	805	0	844	0	0
14	AO	714	0	737	0	0
15	AP	639	0	656	0	0
16	AQ	652	0	695	0	0
17	AR	459	0	482	0	0
18	AS	641	0	669	1	0
19	AT	668	0	718	2	0
20	AU	429	0	453	0	0
21	AA	32828	0	15886	9	0
22	A1	1627	0	798	0	0
23	A2	309	0	156	0	0
24	A3	1642	0	801	1	0
25	BC	2083	0	2157	2	0
26	BD	1565	0	1616	3	0
27	BE	1552	0	1619	1	0
28	BF	1420	0	1460	0	0
29	BG	1323	0	1374	1	0
30	BH	1111	0	1148	0	0
31	BI	1032	0	1088	0	0
32	BJ	1129	0	1162	0	0
33	BK	939	0	1012	2	0
34	BL	1045	0	1117	1	0
35	BM	1074	0	1157	0	0
36	BN	961	0	1000	0	0
37	BO	892	0	923	1	0
38	BP	917	0	965	0	0
39	BQ	947	0	1022	0	0
40	BR	816	0	839	1	0
41	BS	857	0	922	0	0
42	BT	739	0	807	0	0
43	BU	780	0	834	1	0
44	BV	753	0	780	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
45	BW	599	0	614	2	0
46	BX	625	0	655	0	0
47	BY	509	0	543	0	0
48	BZ	449	0	491	1	0
49	B0	444	0	461	0	0
50	B1	413	0	444	1	0
51	B2	377	0	418	1	0
52	B3	504	0	574	0	0
53	B4	302	0	343	0	0
54	BA	62317	0	30186	21	0
55	BB	2504	0	1181	0	0
56	B5	1658	0	1751	0	0
57	A1	7	0	8	0	0
58	BA	10	0	10	0	0
All	All	147653	0	97702	50	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 0.

The worst 5 of 50 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)
19:AT:40:ALA:HB1	19:AT:41:GLY:HA2	1.81	0.62
48:BZ:28:LEU:H	48:BZ:28:LEU:HD23	1.76	0.51
26:BD:154:LYS:HE3	26:BD:156:PHE:CE1	2.46	0.51
54:BA:931:U:C5	54:BA:1167:C:H1'	2.46	0.50
21:AA:5:U:H4'	21:AA:6:G:C6	2.46	0.50

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AB	218/220 (99%)	195 (89%)	22 (10%)	1 (0%)	24	63
2	AC	205/208 (99%)	191 (93%)	12 (6%)	2 (1%)	12	49
3	AD	203/206 (98%)	185 (91%)	15 (7%)	3 (2%)	8	40
4	AE	150/152 (99%)	134 (89%)	9 (6%)	7 (5%)	2	16
5	AF	99/101 (98%)	86 (87%)	6 (6%)	7 (7%)	1	11
6	AG	150/152 (99%)	143 (95%)	7 (5%)	0	100	100
7	AH	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
8	AI	126/128 (98%)	110 (87%)	12 (10%)	4 (3%)	3	21
9	AJ	98/100 (98%)	88 (90%)	5 (5%)	5 (5%)	1	15
10	AK	116/118 (98%)	110 (95%)	5 (4%)	1 (1%)	14	51
11	AL	121/124 (98%)	111 (92%)	10 (8%)	0	100	100
12	AM	112/115 (97%)	98 (88%)	12 (11%)	2 (2%)	6	34
13	AN	98/101 (97%)	90 (92%)	7 (7%)	1 (1%)	12	49
14	AO	86/89 (97%)	78 (91%)	7 (8%)	1 (1%)	10	44
15	AP	79/81 (98%)	68 (86%)	7 (9%)	4 (5%)	1	15
16	AQ	80/82 (98%)	71 (89%)	7 (9%)	2 (2%)	4	26
17	AR	55/57 (96%)	52 (94%)	2 (4%)	1 (2%)	6	34
18	AS	79/81 (98%)	73 (92%)	6 (8%)	0	100	100
19	AT	84/86 (98%)	74 (88%)	8 (10%)	2 (2%)	4	27
20	AU	51/53 (96%)	27 (53%)	14 (28%)	10 (20%)	0	2
25	BC	270/273 (99%)	238 (88%)	21 (8%)	11 (4%)	2	18
26	BD	207/209 (99%)	178 (86%)	18 (9%)	11 (5%)	1	15
27	BE	199/201 (99%)	177 (89%)	17 (8%)	5 (2%)	4	26
28	BF	176/179 (98%)	151 (86%)	21 (12%)	4 (2%)	5	28
29	BG	174/177 (98%)	152 (87%)	13 (8%)	9 (5%)	1	15
30	BH	147/149 (99%)	132 (90%)	13 (9%)	2 (1%)	9	40
31	BI	139/142 (98%)	125 (90%)	10 (7%)	4 (3%)	3	23
32	BJ	140/142 (99%)	125 (89%)	8 (6%)	7 (5%)	1	16
33	BK	121/123 (98%)	106 (88%)	12 (10%)	3 (2%)	4	26
34	BL	141/144 (98%)	117 (83%)	12 (8%)	12 (8%)	0	9
35	BM	134/136 (98%)	117 (87%)	12 (9%)	5 (4%)	2	20
36	BN	119/121 (98%)	107 (90%)	10 (8%)	2 (2%)	7	36

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	BO	114/117 (97%)	111 (97%)	3 (3%)	0	100	100
38	BP	112/115 (97%)	91 (81%)	15 (13%)	6 (5%)	1	15
39	BQ	115/118 (98%)	100 (87%)	15 (13%)	0	100	100
40	BR	101/103 (98%)	94 (93%)	3 (3%)	4 (4%)	2	18
41	BS	108/110 (98%)	100 (93%)	6 (6%)	2 (2%)	6	32
42	BT	92/94 (98%)	78 (85%)	11 (12%)	3 (3%)	3	21
43	BU	101/104 (97%)	85 (84%)	12 (12%)	4 (4%)	2	18
44	BV	92/94 (98%)	88 (96%)	4 (4%)	0	100	100
45	BW	78/80 (98%)	65 (83%)	6 (8%)	7 (9%)	0	8
46	BX	75/79 (95%)	70 (93%)	3 (4%)	2 (3%)	4	25
47	BY	61/63 (97%)	56 (92%)	4 (7%)	1 (2%)	7	38
48	BZ	56/59 (95%)	50 (89%)	4 (7%)	2 (4%)	2	20
49	B0	54/57 (95%)	48 (89%)	5 (9%)	1 (2%)	6	32
50	B1	50/52 (96%)	43 (86%)	3 (6%)	4 (8%)	1	9
51	B2	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
52	B3	62/65 (95%)	58 (94%)	2 (3%)	2 (3%)	3	21
53	B4	36/38 (95%)	34 (94%)	2 (6%)	0	100	100
56	B5	221/234 (94%)	210 (95%)	8 (4%)	3 (1%)	9	40
All	All	5876/6008 (98%)	5249 (89%)	458 (8%)	169 (3%)	5	23

5 of 169 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	AE	149	PRO
8	AI	44	ARG
16	AQ	80	LYS
20	AU	6	ARG
20	AU	9	GLU

5.3.2 Protein sidechains ⓘ

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

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AB	180/180 (100%)	178 (99%)	2 (1%)	65	76
2	AC	170/171 (99%)	167 (98%)	3 (2%)	51	68
3	AD	172/173 (99%)	171 (99%)	1 (1%)	78	83
4	AE	113/113 (100%)	112 (99%)	1 (1%)	70	79
5	AF	87/87 (100%)	85 (98%)	2 (2%)	44	64
6	AG	123/123 (100%)	122 (99%)	1 (1%)	73	80
7	AH	104/105 (99%)	102 (98%)	2 (2%)	50	67
8	AI	105/105 (100%)	105 (100%)	0	100	100
9	AJ	86/86 (100%)	85 (99%)	1 (1%)	63	75
10	AK	90/90 (100%)	90 (100%)	0	100	100
11	AL	103/104 (99%)	103 (100%)	0	100	100
12	AM	91/92 (99%)	88 (97%)	3 (3%)	33	55
13	AN	83/84 (99%)	82 (99%)	1 (1%)	63	75
14	AO	76/77 (99%)	76 (100%)	0	100	100
15	AP	65/65 (100%)	65 (100%)	0	100	100
16	AQ	74/74 (100%)	74 (100%)	0	100	100
17	AR	48/48 (100%)	47 (98%)	1 (2%)	47	65
18	AS	70/70 (100%)	70 (100%)	0	100	100
19	AT	65/65 (100%)	62 (95%)	3 (5%)	24	45
20	AU	44/44 (100%)	44 (100%)	0	100	100
25	BC	216/217 (100%)	210 (97%)	6 (3%)	38	60
26	BD	164/164 (100%)	163 (99%)	1 (1%)	78	83
27	BE	165/165 (100%)	162 (98%)	3 (2%)	51	68
28	BF	149/150 (99%)	146 (98%)	3 (2%)	48	66
29	BG	137/138 (99%)	133 (97%)	4 (3%)	37	58
30	BH	114/114 (100%)	113 (99%)	1 (1%)	70	79
31	BI	109/110 (99%)	107 (98%)	2 (2%)	51	68
32	BJ	116/116 (100%)	115 (99%)	1 (1%)	70	79
33	BK	103/103 (100%)	100 (97%)	3 (3%)	37	58
34	BL	102/103 (99%)	100 (98%)	2 (2%)	48	66
35	BM	109/109 (100%)	105 (96%)	4 (4%)	30	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	BN	100/100 (100%)	99 (99%)	1 (1%)	68	78
37	BO	86/87 (99%)	86 (100%)	0	100	100
38	BP	99/100 (99%)	95 (96%)	4 (4%)	28	49
39	BQ	89/90 (99%)	88 (99%)	1 (1%)	65	76
40	BR	84/84 (100%)	83 (99%)	1 (1%)	63	75
41	BS	93/93 (100%)	92 (99%)	1 (1%)	65	76
42	BT	80/80 (100%)	80 (100%)	0	100	100
43	BU	83/84 (99%)	82 (99%)	1 (1%)	63	75
44	BV	78/78 (100%)	76 (97%)	2 (3%)	40	62
45	BW	59/59 (100%)	58 (98%)	1 (2%)	53	69
46	BX	67/68 (98%)	67 (100%)	0	100	100
47	BY	55/55 (100%)	55 (100%)	0	100	100
48	BZ	48/49 (98%)	48 (100%)	0	100	100
49	B0	47/48 (98%)	46 (98%)	1 (2%)	47	65
50	B1	45/45 (100%)	45 (100%)	0	100	100
51	B2	38/38 (100%)	38 (100%)	0	100	100
52	B3	51/52 (98%)	50 (98%)	1 (2%)	48	66
53	B4	34/34 (100%)	33 (97%)	1 (3%)	37	58
56	B5	173/181 (96%)	172 (99%)	1 (1%)	78	83
All	All	4842/4870 (99%)	4775 (99%)	67 (1%)	57	72

5 of 67 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
40	BR	32	THR
43	BU	61	GLU
53	B4	19	ARG
25	BC	190	THR
25	BC	173	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 54 such sidechains are listed below:

Mol	Chain	Res	Type
27	BE	62	GLN

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Mol	Chain	Res	Type
30	BH	28	ASN
45	BW	11	ASN
28	BF	26	GLN
29	BG	63	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
21	AA	1529/1533 (99%)	270 (17%)	72 (4%)
22	A1	75/76 (98%)	10 (13%)	6 (8%)
23	A2	14/15 (93%)	3 (21%)	1 (7%)
24	A3	76/77 (98%)	12 (15%)	6 (7%)
54	BA	2902/2903 (99%)	493 (16%)	132 (4%)
55	BB	116/118 (98%)	18 (15%)	3 (2%)
All	All	4712/4722 (99%)	806 (17%)	220 (4%)

5 of 806 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
21	AA	7	A
21	AA	8	A
21	AA	9	G
21	AA	13	U
21	AA	14	U

5 of 220 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
54	BA	651	G
54	BA	1300	G
55	BB	57	A
54	BA	2494	G
54	BA	675	A

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

11 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	4SU	A1	7	22	18,21,22	1.58	2 (11%)	25,30,33	1.13	2 (8%)
24	OMC	A3	33	24	19,22,23	0.95	0	25,31,34	1.18	2 (8%)
22	7MG	A1	46	22	23,26,27	4.17	2 (8%)	27,39,42	1.59	3 (11%)
22	5MU	A1	54	22	19,22,23	0.80	0	27,32,35	1.62	6 (22%)
24	5MU	A3	55	24	19,22,23	0.91	0	27,32,35	1.55	4 (14%)
24	4SU	A3	8	24	18,21,22	1.70	3 (16%)	25,30,33	0.84	1 (4%)
24	PSU	A3	56	24	18,21,22	1.05	1 (5%)	21,30,33	1.67	4 (19%)
22	CM0	A1	34	23,22	21,26,27	1.49	2 (9%)	26,37,40	1.36	3 (11%)
22	PSU	A1	55	22	18,21,22	1.01	1 (5%)	21,30,33	1.39	2 (9%)
24	H2U	A3	21	24	18,21,22	1.40	2 (11%)	19,30,33	1.14	3 (15%)
22	6MZ	A1	37	22	22,25,26	0.69	0	29,36,39	1.25	1 (3%)

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	4SU	A1	7	22	-	0/7/25/26	0/2/2/2
24	OMC	A3	33	24	-	0/9/27/28	0/2/2/2
22	7MG	A1	46	22	-	1/7/37/38	0/3/3/3
22	5MU	A1	54	22	-	0/7/25/26	0/2/2/2
24	5MU	A3	55	24	-	0/7/25/26	0/2/2/2
24	4SU	A3	8	24	-	0/7/25/26	0/2/2/2
24	PSU	A3	56	24	-	2/7/25/26	0/2/2/2
22	CM0	A1	34	23,22	-	2/12/30/31	0/2/2/2
22	PSU	A1	55	22	-	0/7/25/26	0/2/2/2
24	H2U	A3	21	24	-	0/7/38/39	0/2/2/2
22	6MZ	A1	37	22	-	0/9/27/28	0/3/3/3

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	A1	46	7MG	C8-N9	-19.48	1.33	1.45
24	A3	8	4SU	C5-C4	-5.69	1.35	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	A1	34	CM0	O5-C5	-5.14	1.24	1.36
22	A1	7	4SU	C5-C4	-5.08	1.36	1.42
24	A3	21	H2U	C2-N3	-3.66	1.31	1.38

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	A1	46	7MG	N9-C8-N7	6.40	112.43	103.37
22	A1	37	6MZ	C9-N6-C6	5.01	127.49	122.85
22	A1	55	PSU	C6-C5-C4	4.17	120.99	118.17
22	A1	34	CM0	C7-O5-C5	4.14	122.76	117.48
22	A1	54	5MU	C5M-C5-C6	-4.12	117.27	122.85

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
24	A3	56	PSU	O4'-C1'-C5-C4
24	A3	56	PSU	O4'-C1'-C5-C6
22	A1	34	CM0	O5-C7-C8-O8
22	A1	34	CM0	O5-C7-C8-O9
22	A1	46	7MG	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
58	FME	BA	3001	57	8,9,10	0.74	0	8,9,11	1.05	0
57	VAL	A1	101	58,22	4,6,7	0.80	0	6,7,9	1.10	1 (16%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
58	FME	BA	3001	57	-	1/7/9/11	-
57	VAL	A1	101	58,22	-	0/5/6/8	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	A1	101	VAL	O-C-CA	-2.67	117.91	124.77

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
58	BA	3001	FME	O1-CN-N-CA

There are no ring outliers.

No monomer is involved in short contacts.

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.

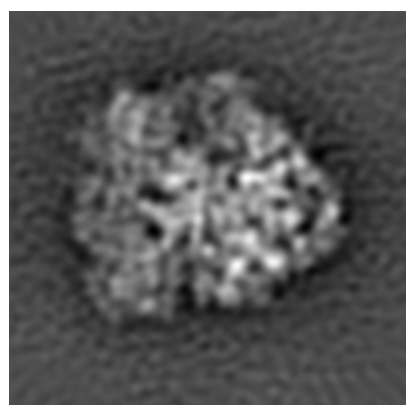
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2472. These allow visual inspection of the internal detail of the map and identification of artifacts.

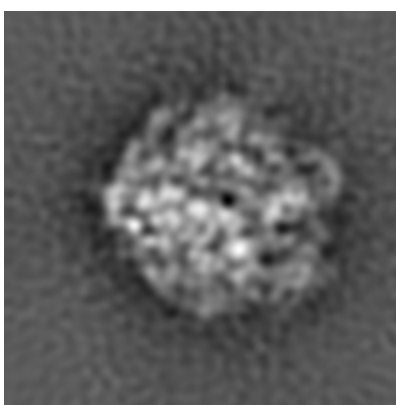
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

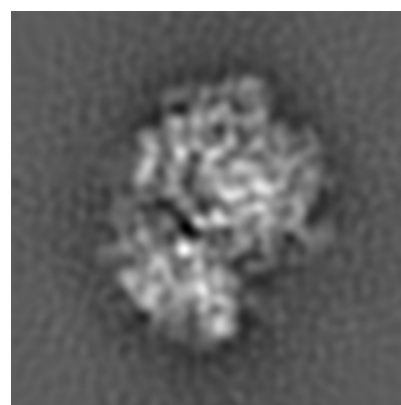
6.1.1 Primary map



X



Y

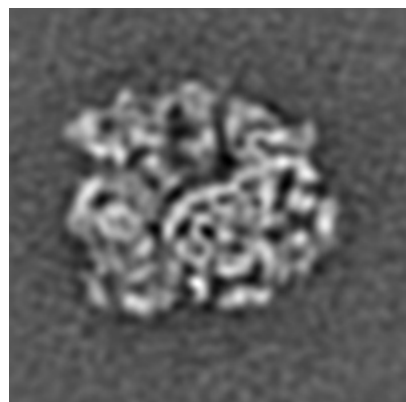


Z

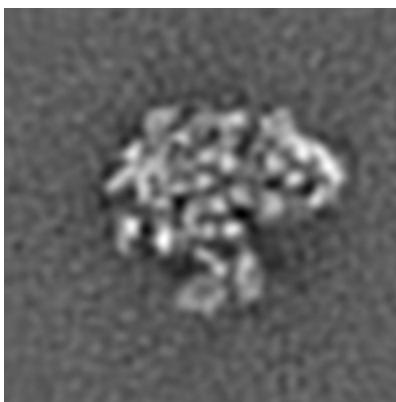
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

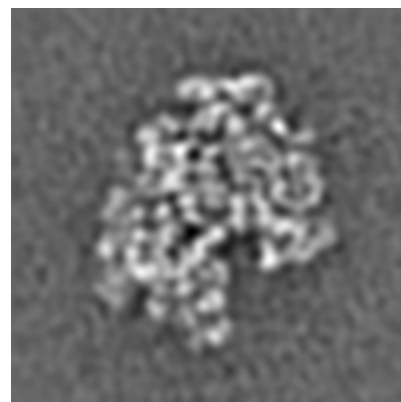
6.2.1 Primary map



X Index: 64



Y Index: 64

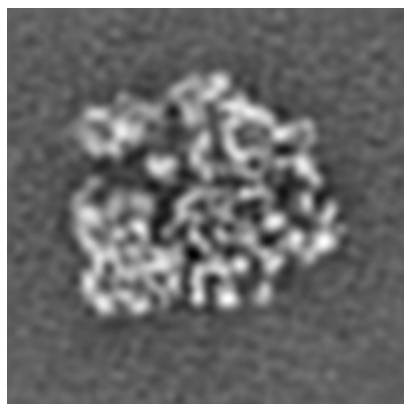


Z Index: 64

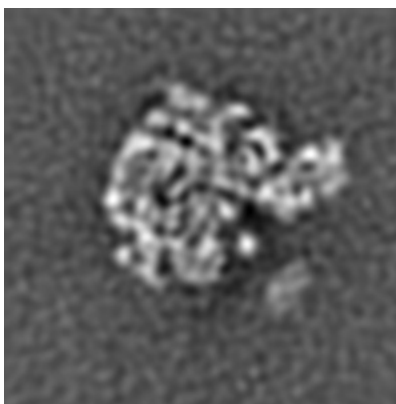
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

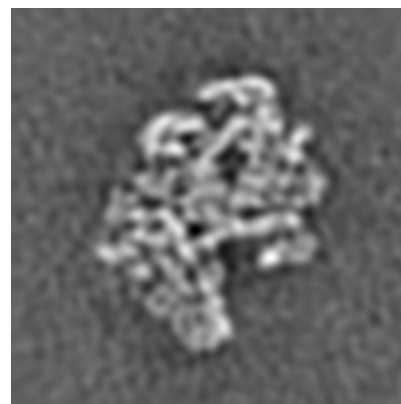
6.3.1 Primary map



X Index: 67



Y Index: 71

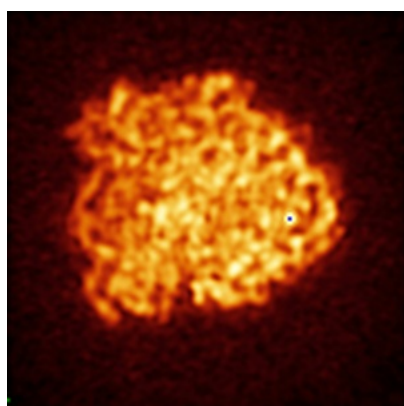


Z Index: 61

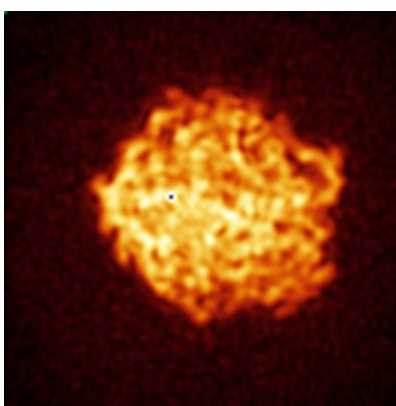
The images above show the largest variance slices of the map in three orthogonal directions.

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

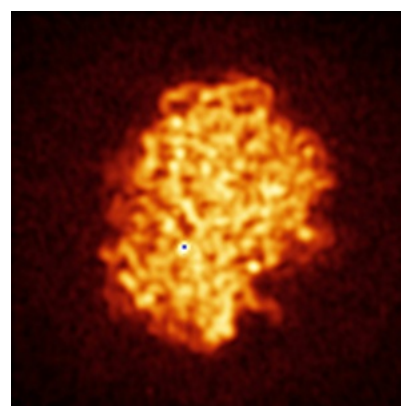
6.4.1 Primary map



X



Y

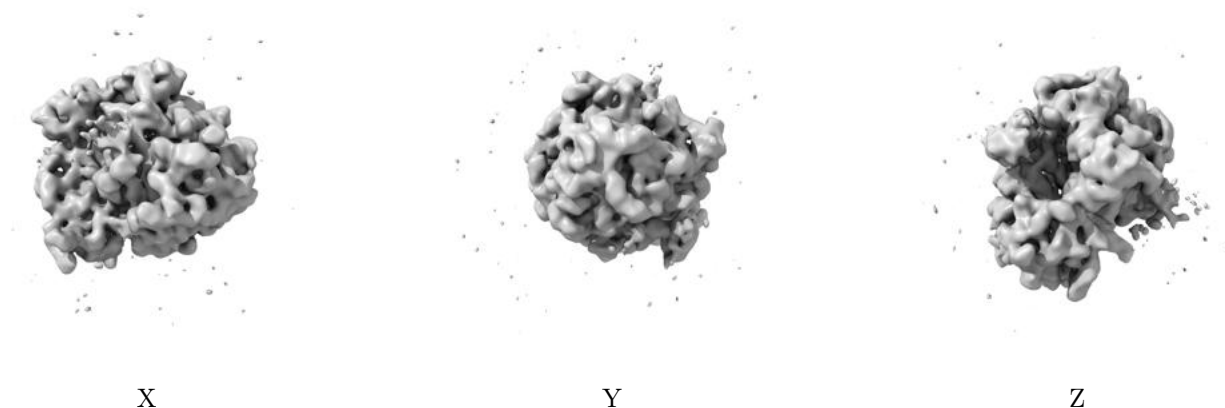


Z

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



The images above show the 3D surface view of the map at the recommended contour level 25.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

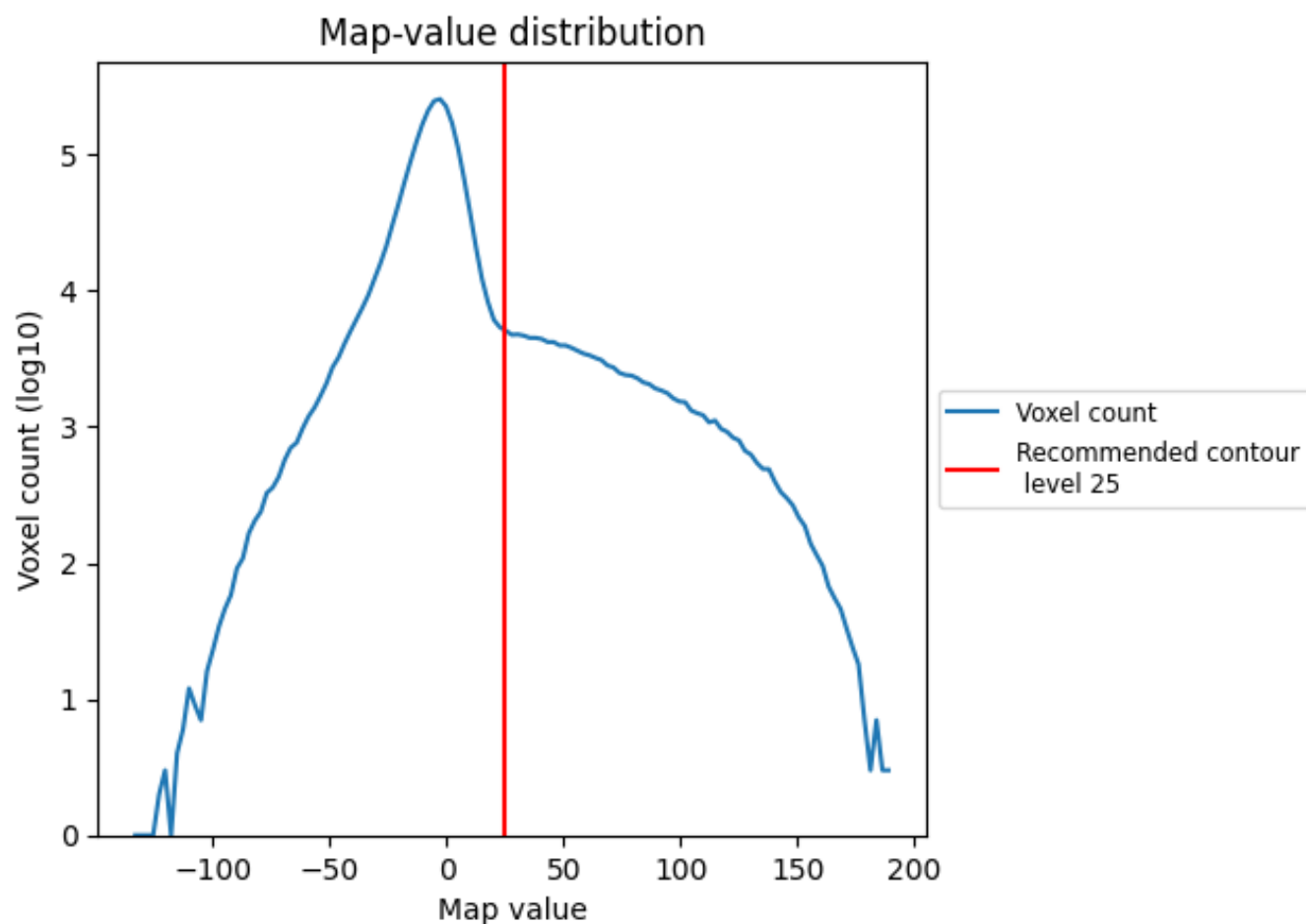
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

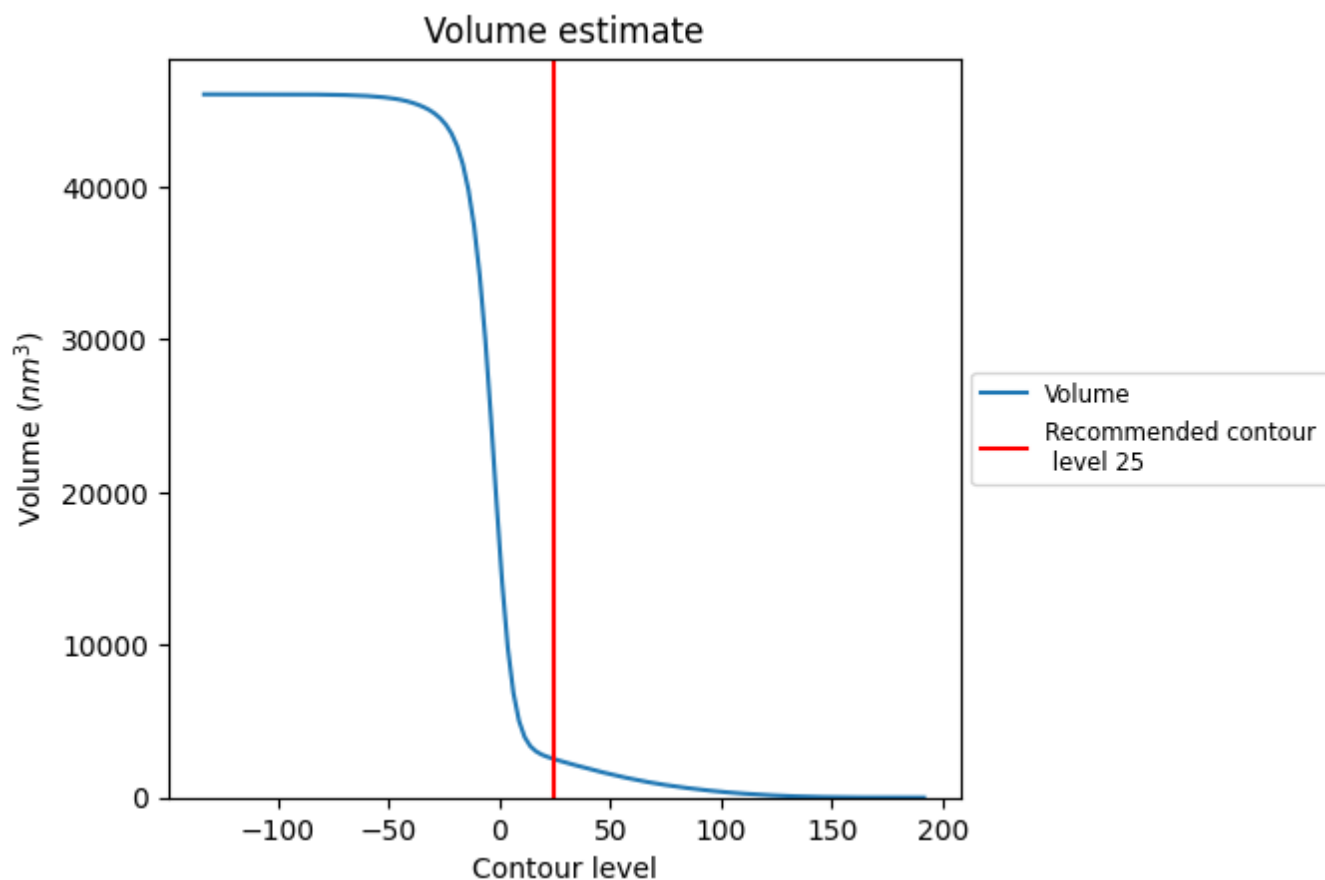
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

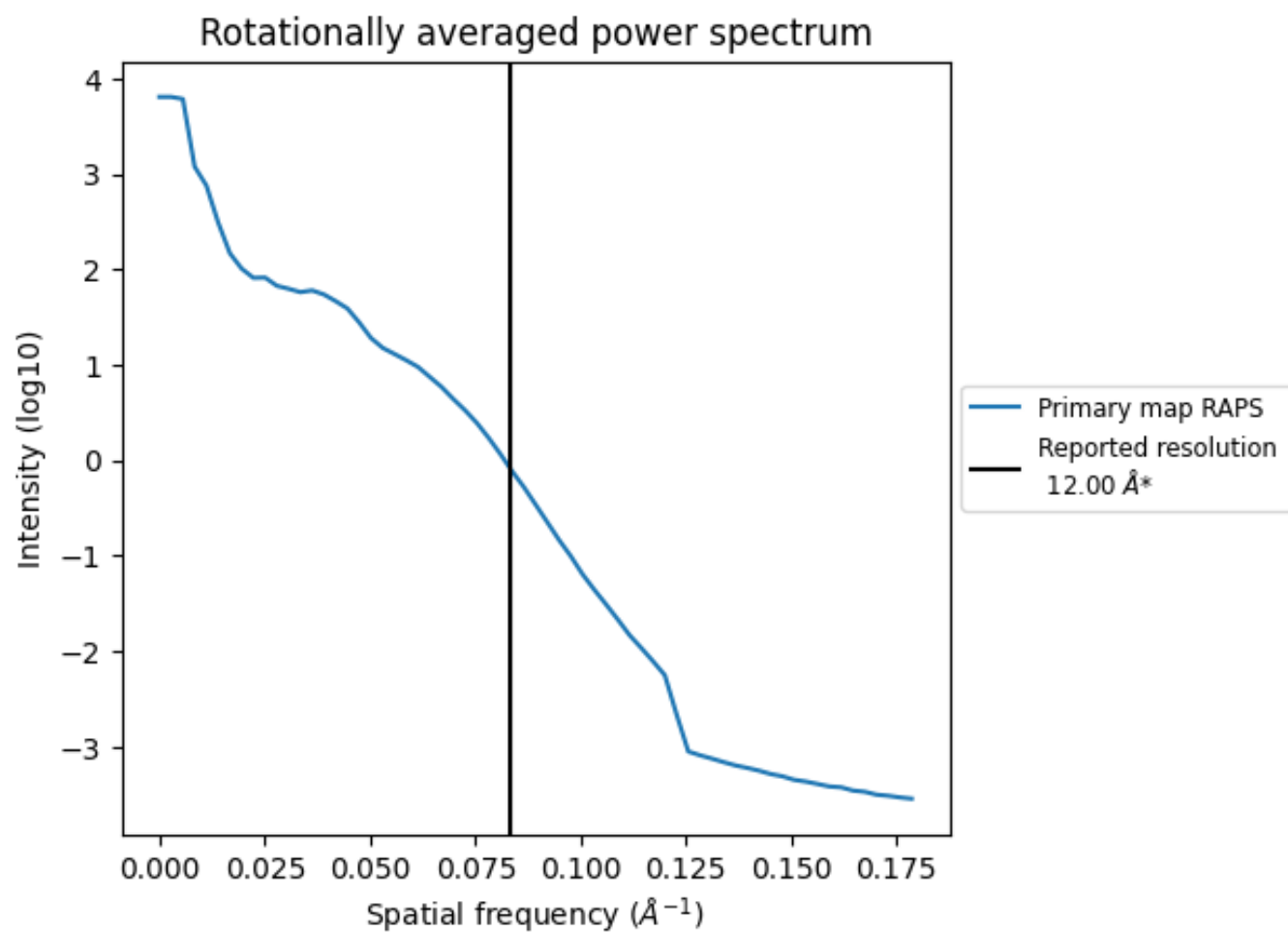
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2507 nm³; this corresponds to an approximate mass of 2264 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 0.083 Å⁻¹

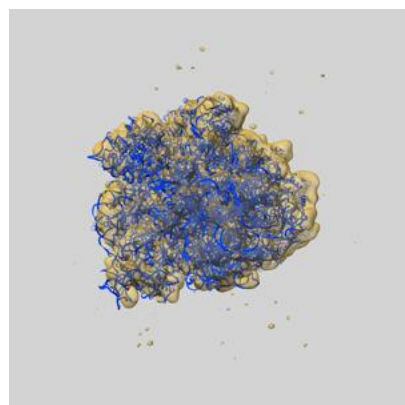
8 Fourier-Shell correlation

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

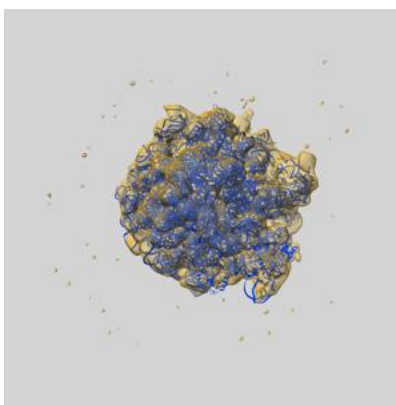
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-2472 and PDB model 4V6Z. Per-residue inclusion information can be found in [section 3](#) on [page 18](#).

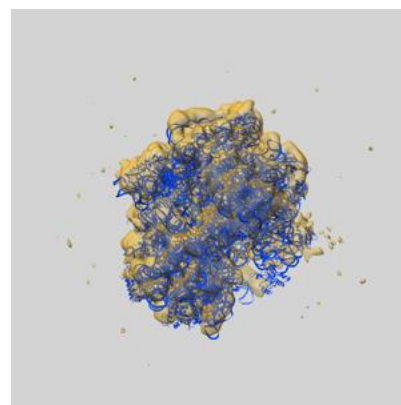
9.1 Map-model overlay [i](#)



X



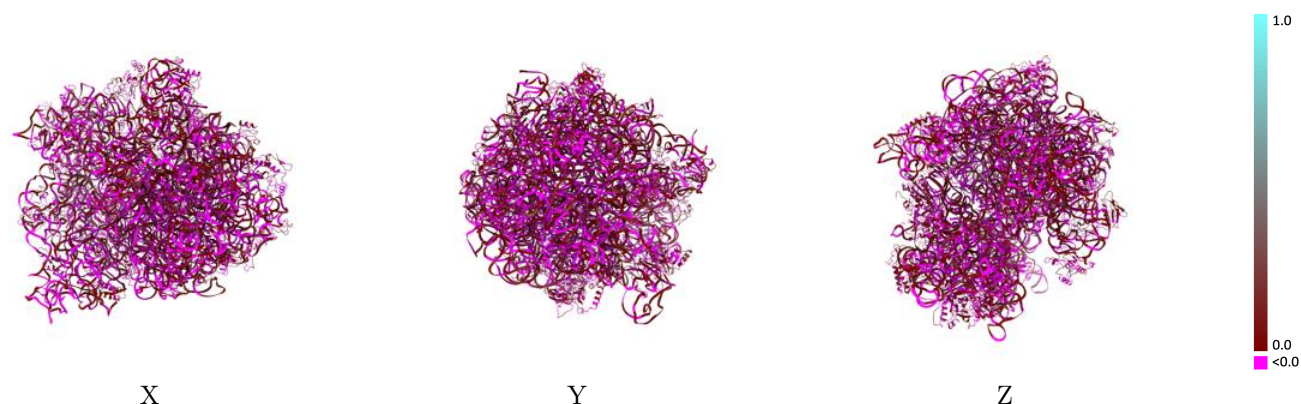
Y



Z

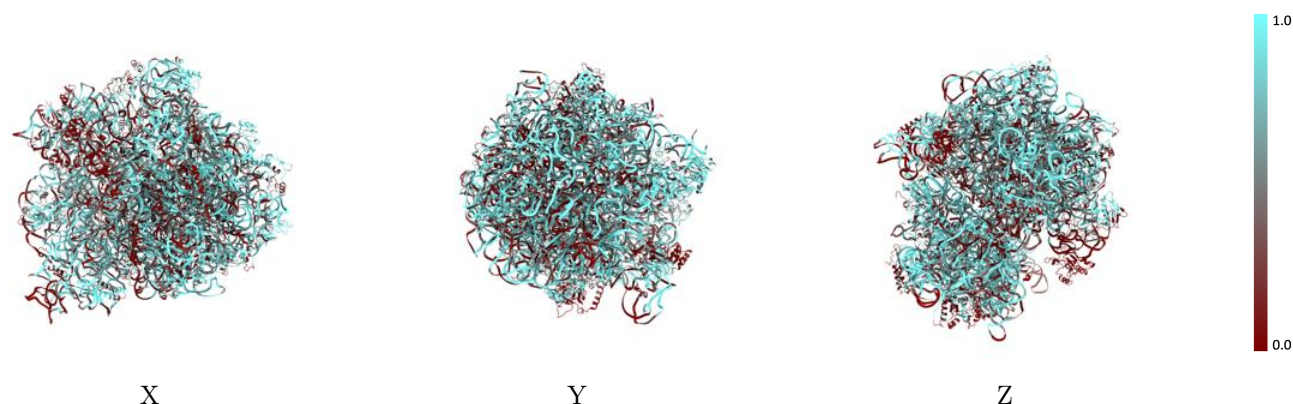
The images above show the 3D surface view of the map at the recommended contour level 25.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



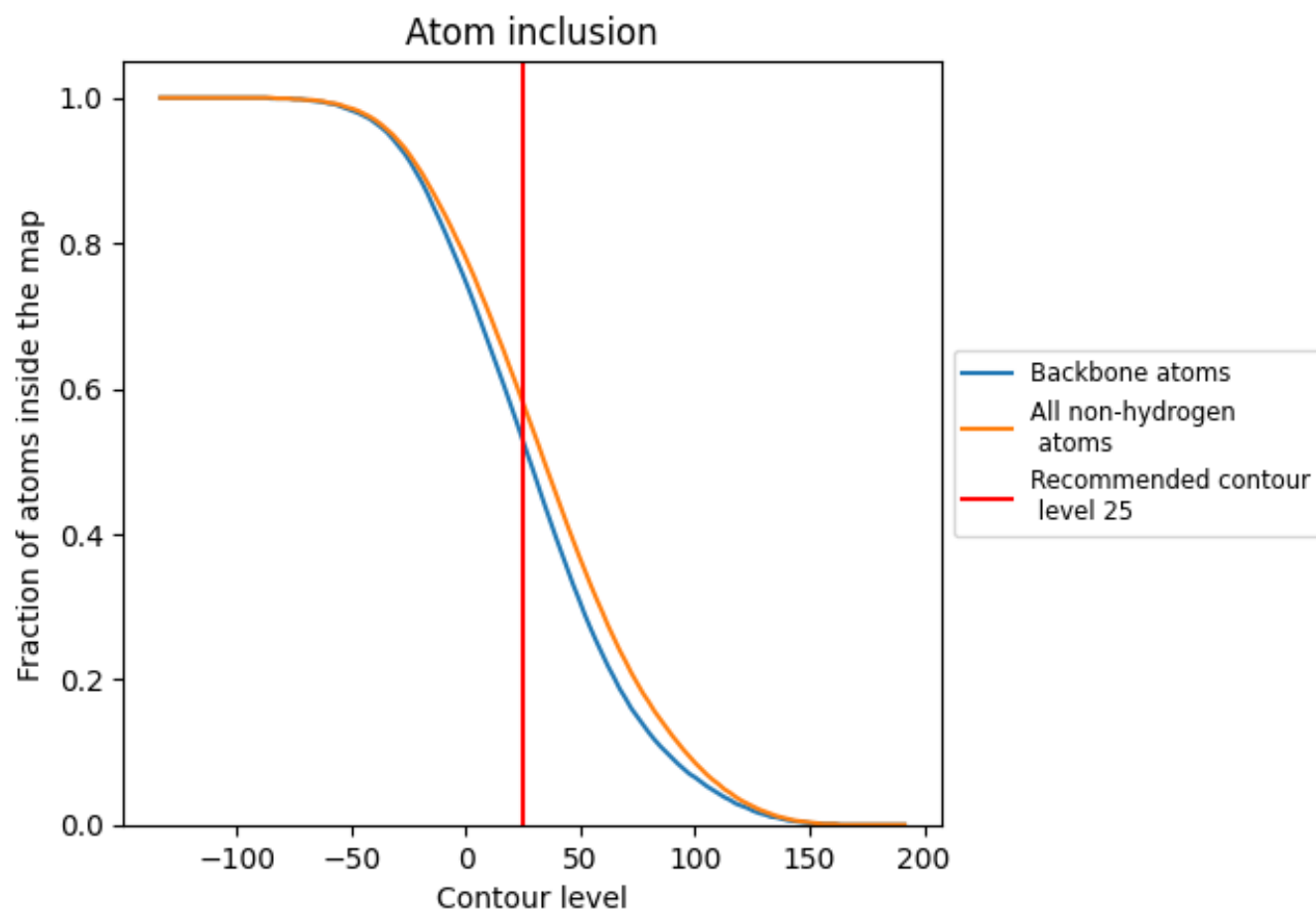
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (25).

9.4 Atom inclusion [i](#)



At the recommended contour level, 53% of all backbone atoms, 58% 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 (25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5810	 0.0150
A1	 0.5160	 0.0210
A2	 0.4760	 -0.0030
A3	 0.3830	 -0.0050
AA	 0.6610	 0.0230
AB	 0.4760	 0.0520
AC	 0.5210	 0.0080
AD	 0.4340	 0.0110
AE	 0.5200	 0.0300
AF	 0.7140	 0.0380
AG	 0.5950	 0.0120
AH	 0.5110	 0.0070
AI	 0.7070	 0.0030
AJ	 0.4240	 0.0020
AK	 0.6720	 0.0330
AL	 0.6300	 0.0140
AM	 0.6530	 0.0320
AN	 0.3420	 -0.0380
AO	 0.7130	 0.0190
AP	 0.4340	 0.0050
AQ	 0.5450	 0.0230
AR	 0.5810	 0.0020
AS	 0.6650	 0.0190
AT	 0.7030	 0.0010
AU	 0.5820	 0.0460
B0	 0.7100	 0.0380
B1	 0.5120	 0.0350
B2	 0.4170	 -0.0450
B3	 0.4130	 -0.0030
B4	 0.5100	 -0.0030
B5	 0.3460	 -0.0020
BA	 0.5880	 0.0150
BB	 0.7180	 0.0320
BC	 0.4310	 -0.0150
BD	 0.4710	 0.0100



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Chain	Atom inclusion	Q-score
BE	 0.5910	 -0.0060
BF	 0.5840	 0.0210
BG	 0.4590	 0.0220
BH	 0.2250	 0.0250
BI	 0.0000	 -0.0030
BJ	 0.4790	 -0.0040
BK	 0.4540	 0.0030
BL	 0.6080	 -0.0140
BM	 0.4260	 0.0170
BN	 0.5740	 -0.0180
BO	 0.8410	 0.0280
BP	 0.4290	 -0.0060
BQ	 0.5300	 -0.0060
BR	 0.6140	 -0.0070
BS	 0.4800	 0.0010
BT	 0.6280	 -0.0100
BU	 0.5690	 0.0050
BV	 0.6310	 0.0560
BW	 0.6220	 0.0220
BX	 0.4460	 -0.0480
BY	 0.5490	 0.0070
BZ	 0.4460	 0.0020