



wwPDB EM Validation Summary Report ⓘ

Oct 22, 2024 – 06:32 PM EDT

PDB ID : 4V74
EMDB ID : EMD-1720
Title : 70S-fMetVal-tRNAVal-tRNAfMet complex in hybrid pre-translocation state (pre5b)
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 : 17.00 Å (reported)
Based on initial models : 2HGP, 2WRI, 3I1O, 2K4C

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev113
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

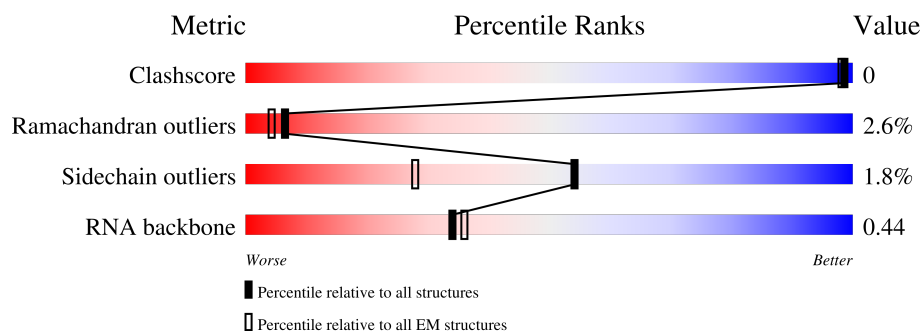
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 17.00 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	AB	220	<div> <div>42%</div> <div>95%</div> <div>5%</div> </div>
2	AC	208	<div> <div>51%</div> <div>89%</div> <div>10%</div> </div>
3	AD	206	<div> <div>41%</div> <div>88%</div> <div>12%</div> </div>
4	AE	152	<div> <div>42%</div> <div>89%</div> <div>11%</div> </div>
5	AF	101	<div> <div>13%</div> <div>90%</div> <div>9%</div> </div>
6	AG	152	<div> <div>23%</div> <div>87%</div> <div>12%</div> </div>
7	AH	130	<div> <div>27%</div> <div>89%</div> <div>10%</div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
8	AI	128	
9	AJ	100	
10	AK	118	
11	AL	124	
12	AM	115	
13	AN	101	
14	AO	89	
15	AP	81	
16	AQ	82	
17	AR	57	
18	AS	81	
19	AT	86	
20	AU	53	
21	AA	1533	
22	A1	76	
23	A2	15	
24	A3	77	
25	BC	273	
26	BD	209	
27	BE	201	
28	BF	179	
29	BG	177	
30	BH	149	
31	BI	142	
32	BJ	142	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
33	BK	123	
34	BL	144	
35	BM	136	
36	BN	121	
37	BO	117	
38	BP	115	
39	BQ	118	
40	BR	103	
41	BS	110	
42	BT	94	
43	BU	104	
44	BV	94	
45	BW	80	
46	BX	79	
47	BY	63	
48	BZ	59	
49	B0	57	
50	B1	52	
51	B2	46	
52	B3	65	
53	B4	38	
54	BA	2903	
55	BB	118	
56	B5	234	

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

Continued on next page...

Continued from previous page...

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*P*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		

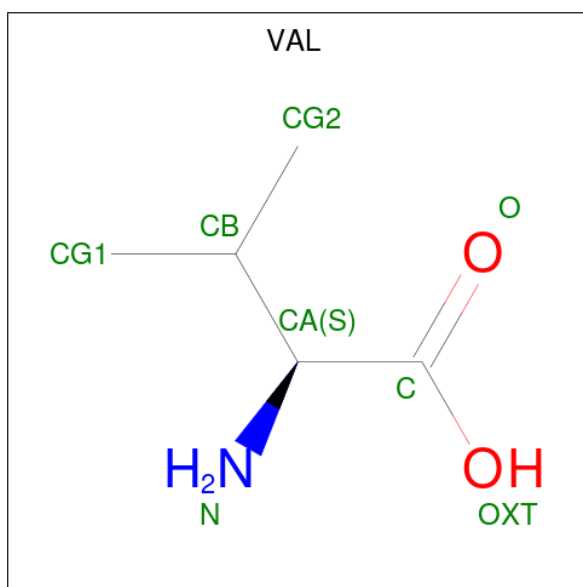
- Molecule 55 is a RNA chain called 5S ribosomal RNA.

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.

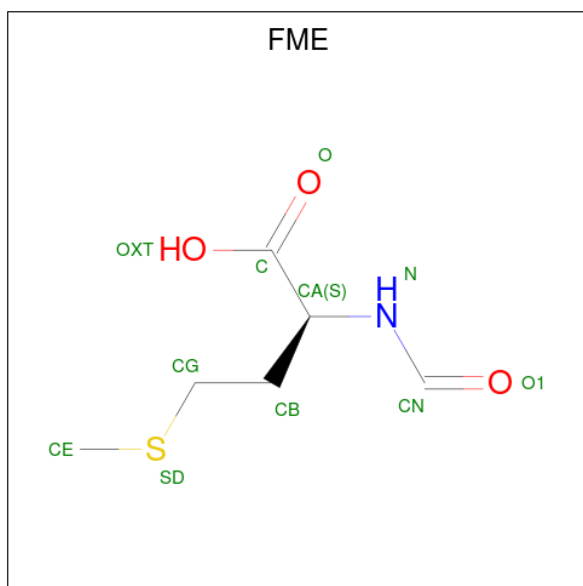
Mol	Chain	Residues	Atoms					AltConf	Trace
56	B5	223	Total	C	N	O	S	0	0
			1658	1038	302	312	6		

- Molecule 57 is VALINE (three-letter code: 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 (three-letter code: FME) (formula: C₆H₁₁NO₃S).

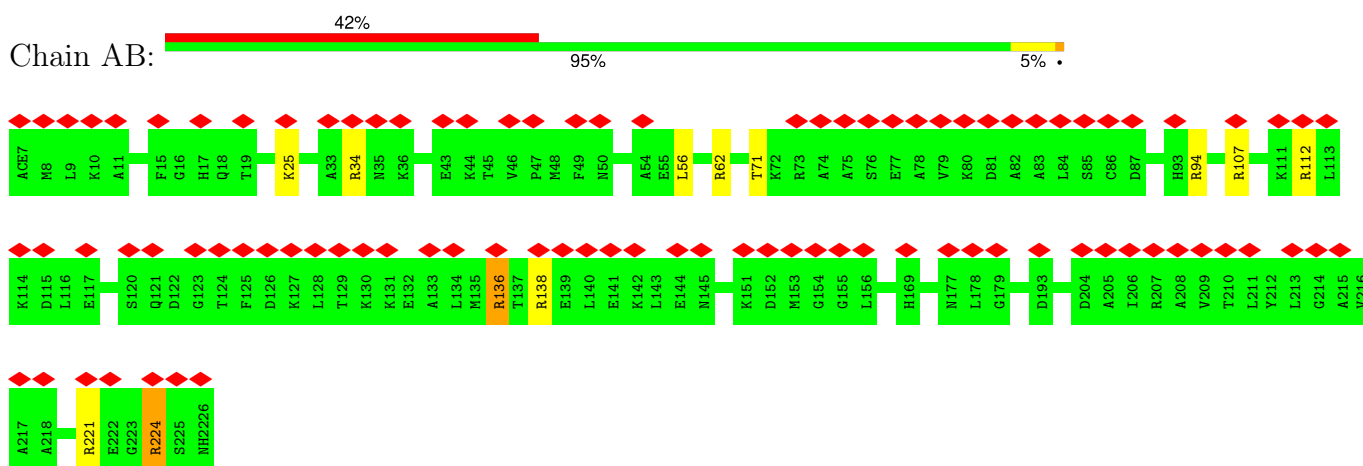


Mol	Chain	Residues	Atoms					AltConf
58	BA	1	Total	C	N	O	S	0
			10	6	1	2	1	

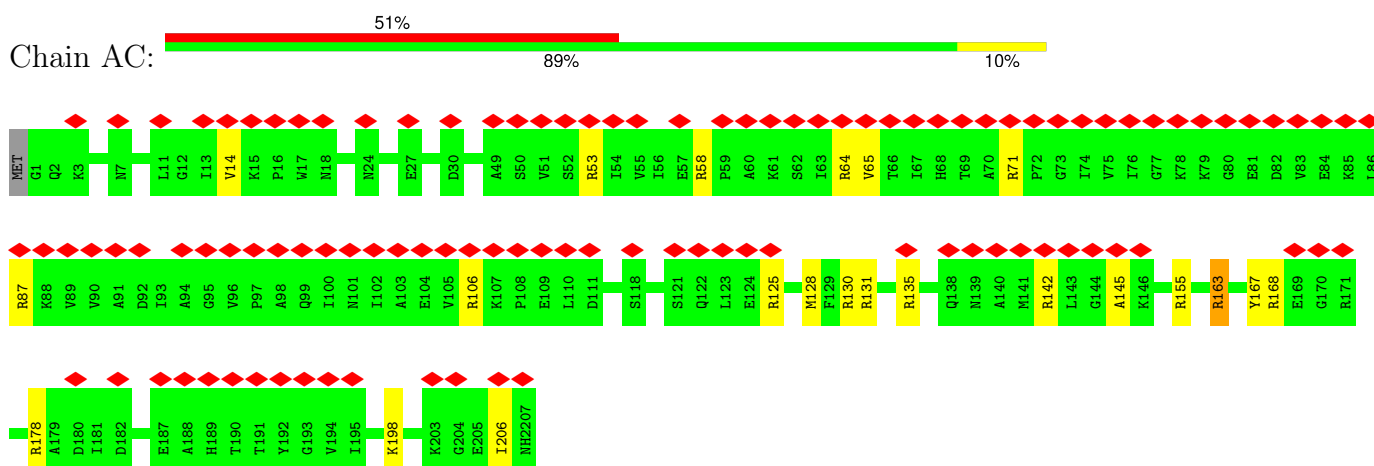
3 Residue-property plots

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.

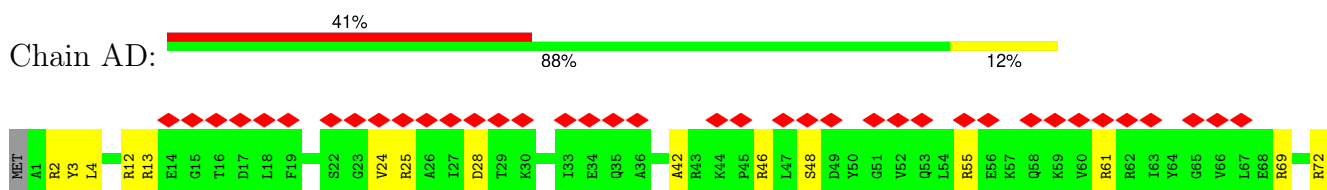
• Molecule 1: 30S ribosomal protein S2

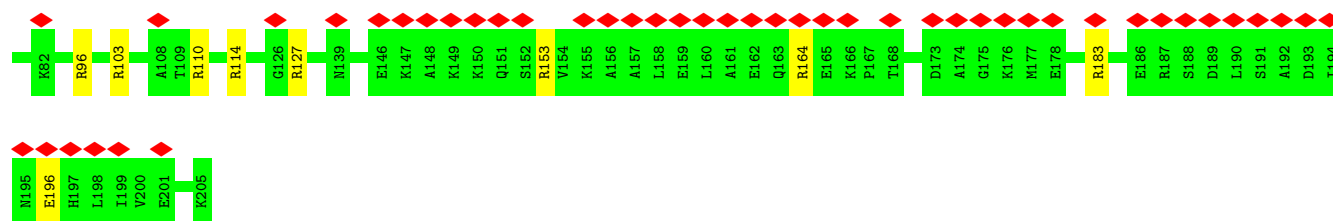


• Molecule 2: 30S ribosomal protein S3

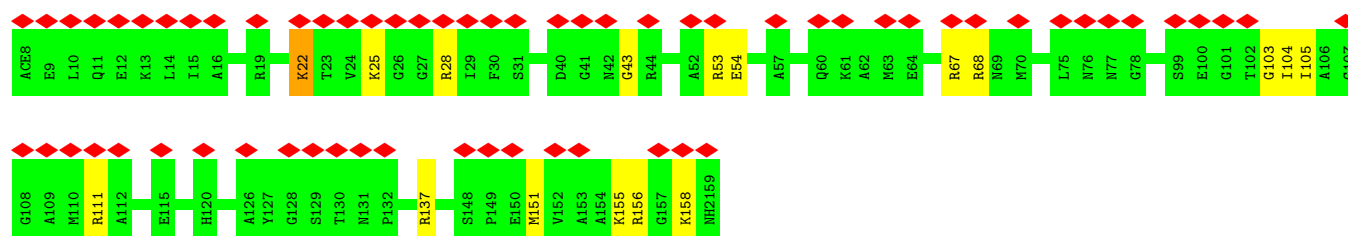
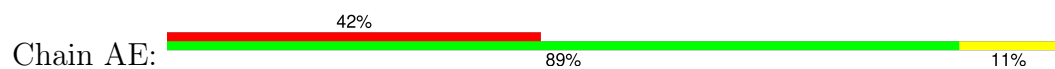


• Molecule 3: 30S ribosomal protein S4

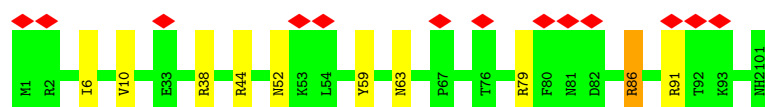
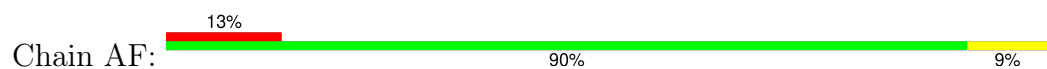




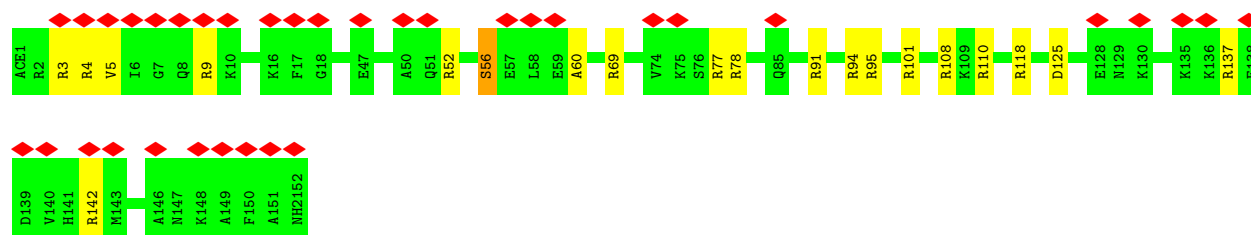
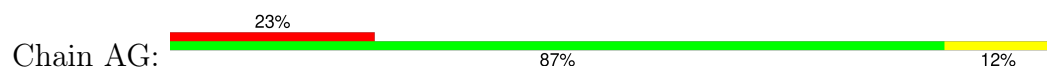
• Molecule 4: 30S ribosomal protein S5



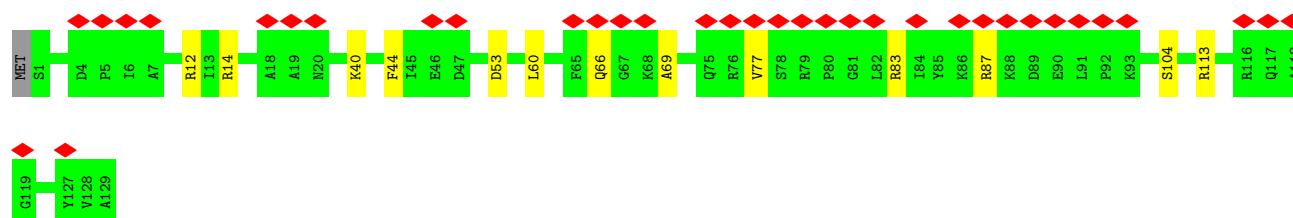
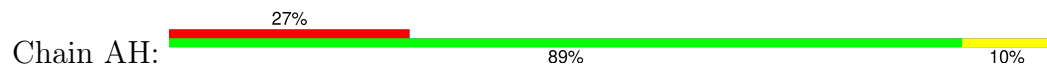
• Molecule 5: 30S ribosomal protein S6



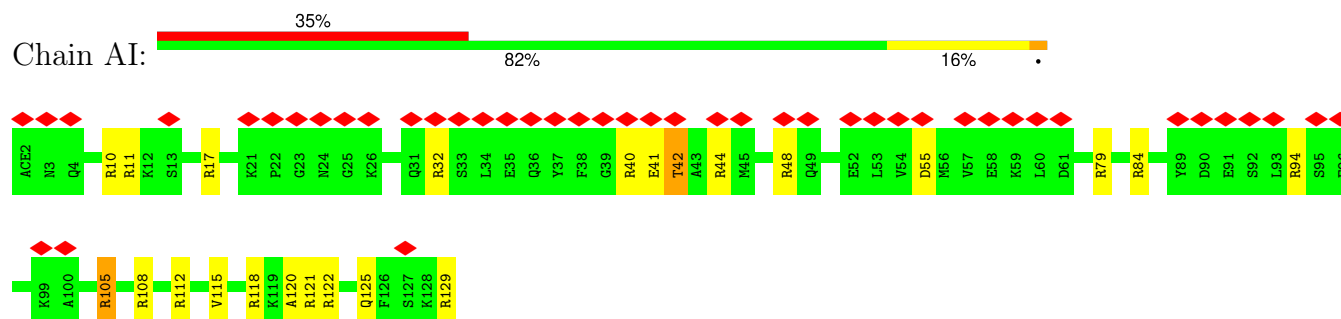
• Molecule 6: 30S ribosomal protein S7



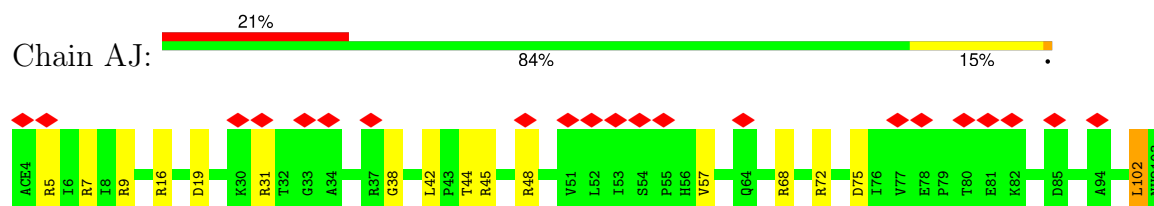
• Molecule 7: 30S ribosomal protein S8



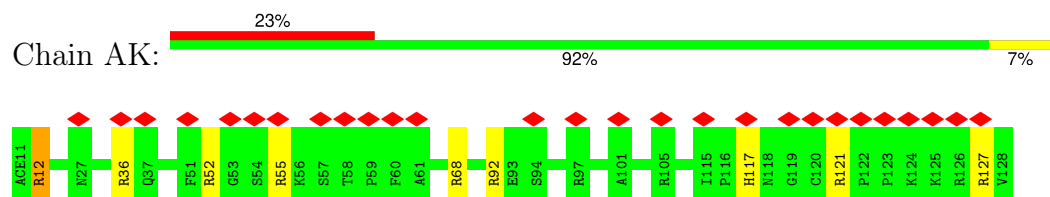
- Molecule 8: 30S ribosomal protein S9



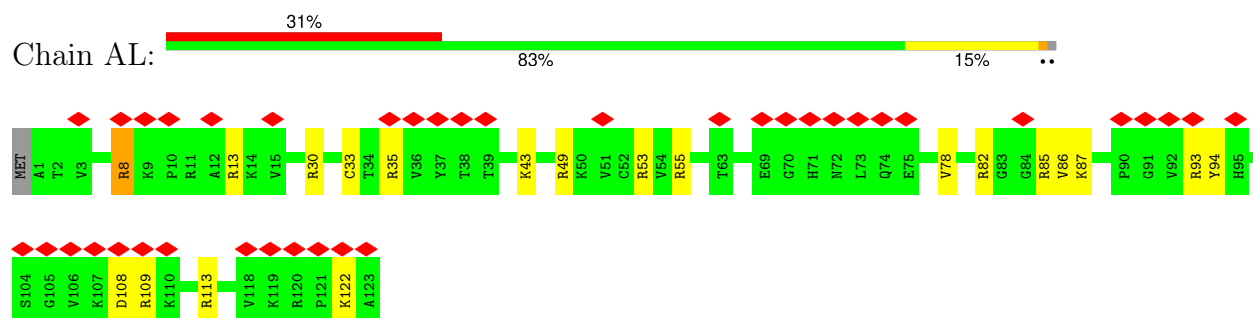
- Molecule 9: 30S ribosomal protein S10



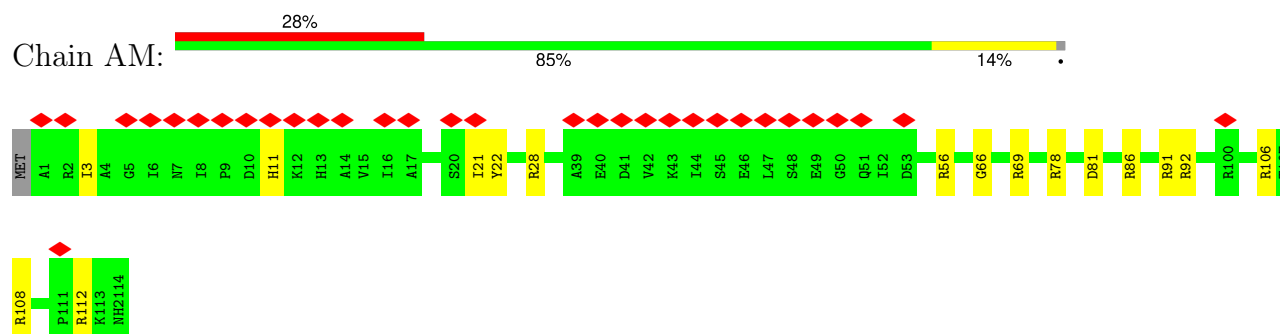
- Molecule 10: 30S ribosomal protein S11



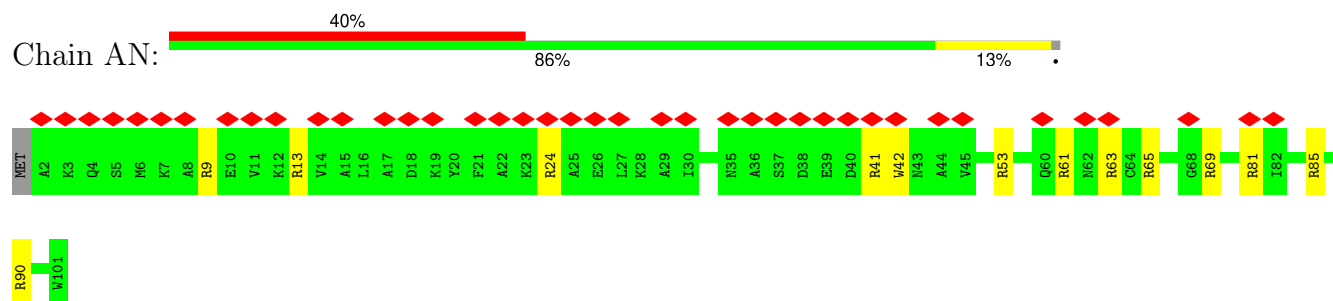
- Molecule 11: 30S ribosomal protein S12



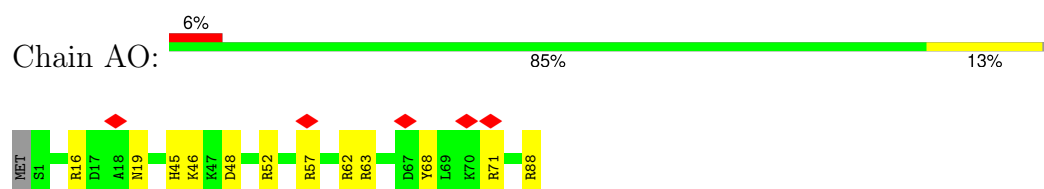
- Molecule 12: 30S ribosomal protein S13



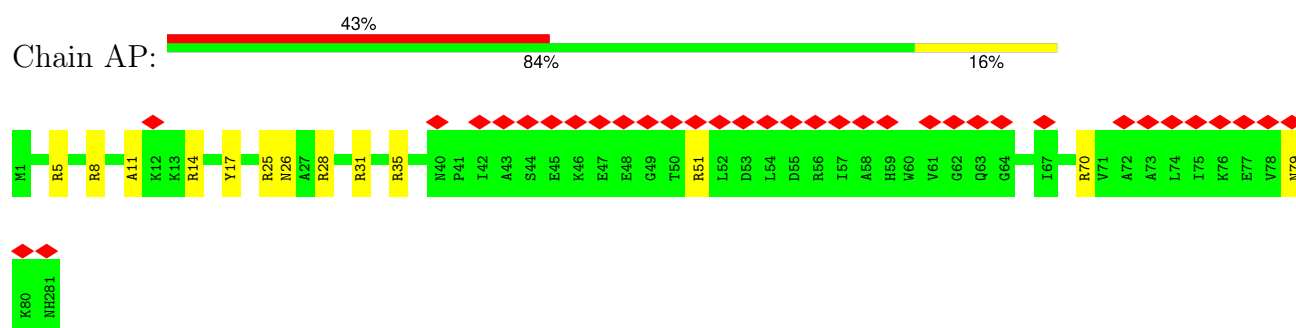
- Molecule 13: 30S ribosomal protein S14



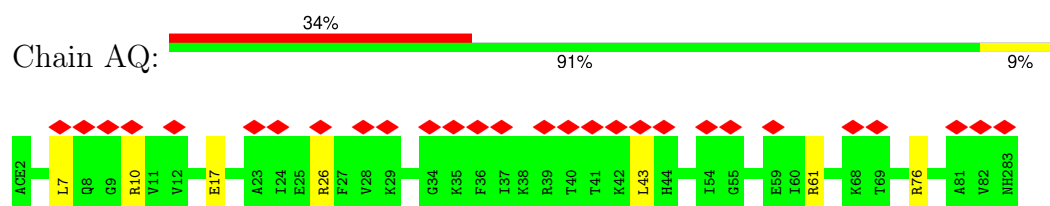
- Molecule 14: 30S ribosomal protein S15



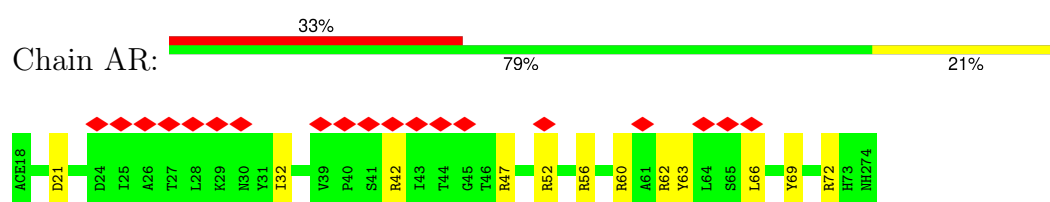
- Molecule 15: 30S ribosomal protein S16



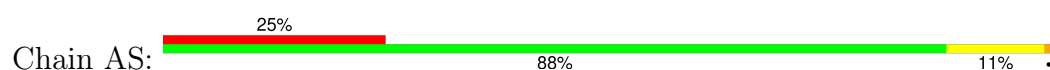
- Molecule 16: 30S ribosomal protein S17

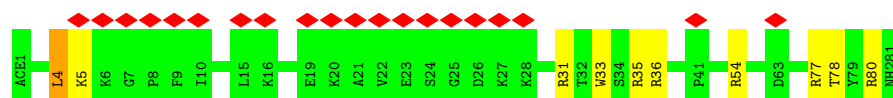


- Molecule 17: 30S ribosomal protein S18

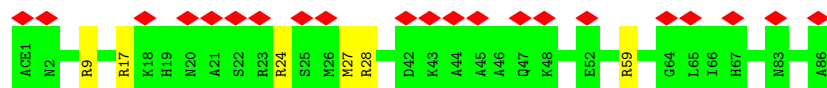


- Molecule 18: 30S ribosomal protein S19

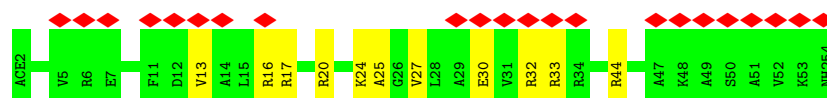
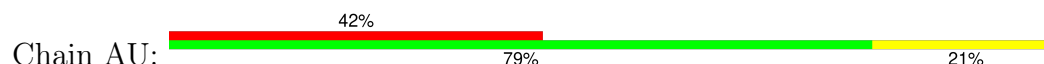




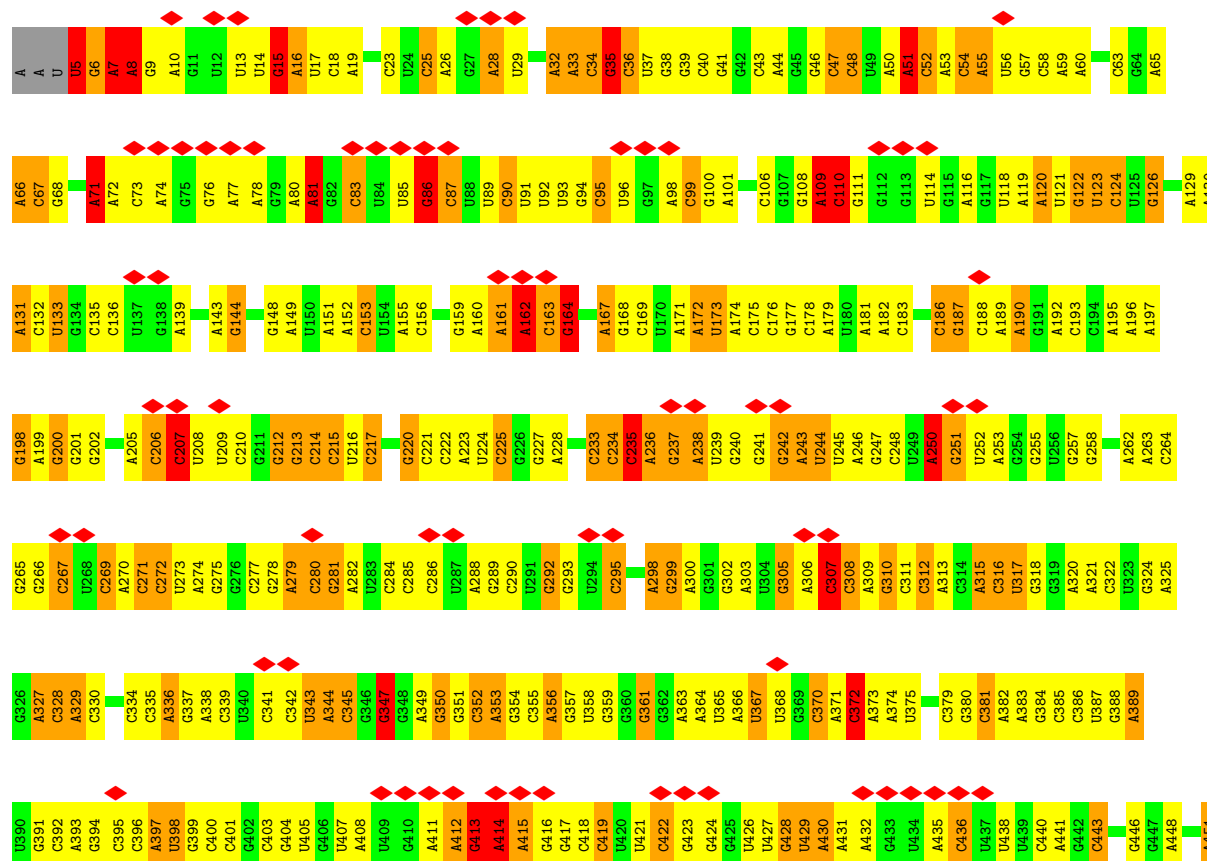
- Molecule 19: 30S ribosomal protein S20



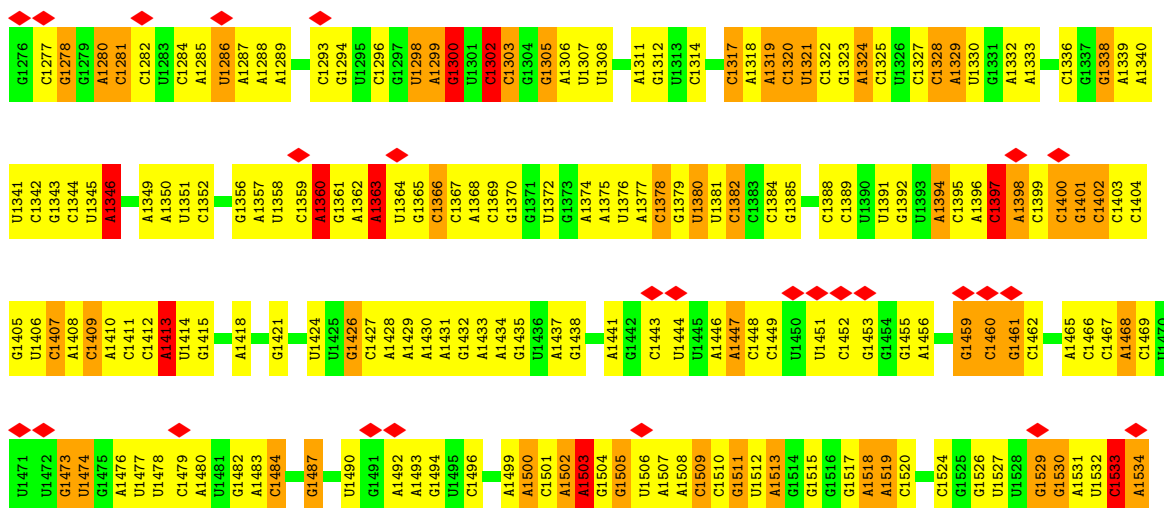
- Molecule 20: 30S ribosomal protein S21



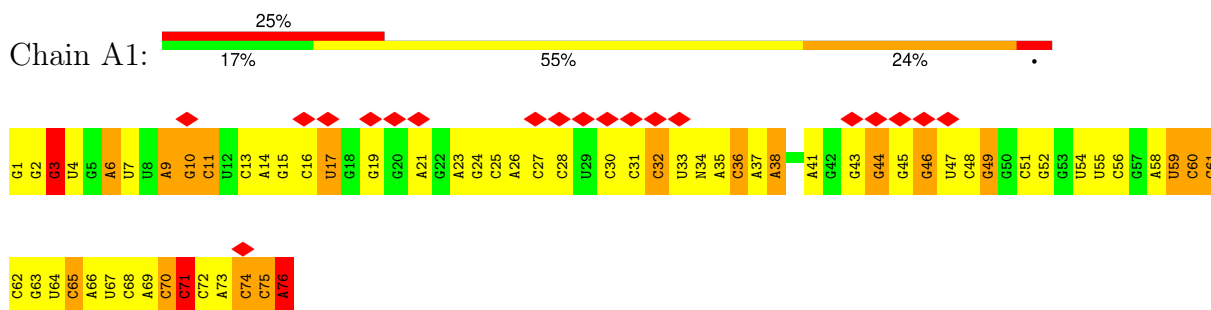
- Molecule 21: 16S ribosomal RNA



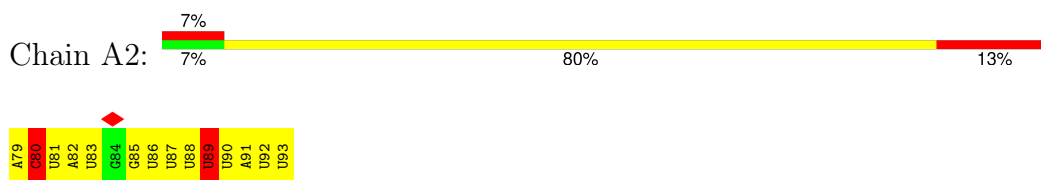
A1216	A1151	U1086	U1023	U960	C897	A831	C764	U701	C637	C576	U512	A452
C1217	A1152	A1092	U1024	U961	C898	G832	G765	A702	A640	G577	C513	G453
A1218	A1153	A1093	U1025	C962	C899	G833	A766	A703	U641	C578	C514	G454
A1219	A1154	A1094	U1026	G963	A900	A767	A768	A704	U642	A579	G515	G455
G1220	A1155	U1095	C1027	A964	A901	G839	G769	G705	A643	C580	U516	A456
G1221	A1156	G965	G1028	G966	G902	C840	C770	A706	C643	G581	G517	G457
G1222	A1157	G966	U1029	C967	U905	C841	G771	C708	G646	C582	C518	U458
C1223	A1158	C967	U1030	C968	A906	U842	A777	G711	C647	A583	C519	A459
C1224	A1159	A969	C1031	U843	A907	U844	G778	A712	C648	A584	A520	A460
A1225	A1160	C970	G1032	G844	A908	G845	C779	A713	A649	G585	G521	A461
C1226	C1161	G971	A1033	A845	A909	G846	A780	G713	A649	C586	G522	G462
A1227	C1162	G972	G1034	G847	C910	G847	A781	G714	C651	C587	A523	U463
C1228	A1163	G973	A1035	C848	U911	C848	A782	A715	U852	G588	G524	A464
A1229	U1164	A974	A1036	U850	C912	C849	C783	U717	U853	U591	C525	A465
C1230	U1165	G975	C1037	U851	A913	G849	A784	A718	G554	G592	C526	A466
G1231	G1166	G976	C1038	G851	A914	U850	A787	C719	A655	U593	C527	U467
G1232	U1167	A978	G1039	G852	U915	G851	A787	C720	G656	U594	C528	A468
C1233	U1168	C979	A1040	G853	U916	G852	A787	C721	C660	A596	G529	C469
C1234	U1169	C980	A1041	C854	U917	G853	A787	G722	C661	G597	G530	U470
U1235	A1170	U981	G1043	C856	A918	C856	A790	G726	U662	C599	A532	U472
A1236	A1171	U982	A1044	C857	A919	C857	G791	C727	U663	A600	A533	U473
C1237	C1172	U983	C1045	G858	U920	C858	A794	G728	A664	G601	U534	G474
A1238	A1173	C984	A1046	G859	U921	G859	C795	A729	G664	U602	A535	C475
A1239	G1176	C985	G1047	A860	G922	G860	C796	A730	G665	U603	C536	U476
U1240	G1177	C986	U1048	A861	A923	A861	C797	G731	G666	G504	G537	C477
G1241	G1178	C987	U1049	C862	C924	C862	U798	G732	G669	G606	A538	U478
G1242	A1179	U997	U1050	U870	G925	U870	U799	G733	G670	U607	C545	U479
C1243	G1180	U998	C1051	U871	G926	U871	G800	G734	A673	A507	A546	U480
G1244	U1181	U999	U1052	A872	G927	A872	A802	C735	G674	A508	A547	G481
C1245	U1182	U999	U1053	C876	C931	C876	C805	C736	A675	A509	G548	A482
A1246	U1183	U999	G1054	G877	C932	G877	C806	C737	A676	U610	C549	C483
U1247	G1187	A994	A1055	A878	G933	A878	C807	C738	U677	C611	G550	G484
A1248	A1188	U994	A1056	C879	G934	C879	A807	C739	U678	U552	U551	U486
C1249	U1189	C995	G1057	C880	C935	C880	C808	C740	C612	C513	U553	A487
A1250	G1190	C996	C1058	C881	A936	C881	C809	G741	C613	C514	A554	C488
A1251	G1191	U997	G1059	C882	A937	C882	G810	G742	G615	G616	U555	C489
A1252	U1192	C998	U1060	C883	A938	C883	G811	G743	G617	G618	C556	G491
G1253	G1193	C999	U1061	C884	A939	C884	G812	G744	U688	C518	G557	C492
G1254	U1194	A1000	C1063	C885	C940	C885	G813	G745	U689	C519	A558	A493
G1255	C1195	C1001	U1065	C886	C941	C886	G814	G746	U690	U619	A560	G494
A1256	A1196	A1004	G1066	C887	G942	C887	A815	A747	U691	A621	U561	A495
A1257	U1197	A1005	A1067	C878	G943	C878	A816	G748	U692	G622	U562	G496
G1258	C1200	G1006	G1068	C889	G944	C889	A817	G749	U693	C623	A563	G497
C1259	A1201	G1007	C1069	C890	G945	C890	A818	G750	U694	C624	A564	A498
A1260	U1202	U1008	U1070	C891	G946	C891	G819	C751	U695	U625	U565	A499
A1261	C1203	U1009	U1071	C892	G947	C892	U820	G752	U696	G626	G566	G500
C1262	A1204	U1010	U1072	C893	C948	C893	U821	G753	U697	G627	G567	C501
C1263	U1205	C1011	U1073	C894	A949	C894	U822	G754	U698	G628	G568	A502
U1264	G1206	A1012	U1074	C895	U950	C895	U823	C755	U699	A629	C569	C503
C1265	G1207	A1013	U1075	C896	U951	C896	G824	G756	U700	A630	U571	C504
G1266	C1208	A1014	G1076	C897	U952	C897	G825	U757	G698	C631	A572	G505
C1267	G1209	A1015	U1077	C898	U953	C898	A826	G758	G699	U632	A573	G506
G1268	C1210	A1016	A1080	C899	G954	C899	U827	G759	C632	G633	A574	C507
A1269	U1211	A1017	A1081	C900	G955	C900	U828	G760	U633	C634	G575	U508
G1270	C1212	A1018	U1082	C901	U956	C901	U829	G761	U634	A635	U509	A509
G1271	U1213	A1019	U1083	C902	U957	C902	G830	U762	U635	U510	C511	C511
G1272	C1214	A1020	G1084	C903	U958	C903	G831	U763	U636	U511	C512	C512
A1273	C1215	A1021	U1085	C904	A959	C904	G832	U764	U637	U512	C513	C513
A1274	A1275	A1022		C905		C905	G833	U765	U638	U513	C514	C514
				C906		C906	G834	U766	U639	U514	C515	C515
				C907		C907	G835	U767	U640	U515	C516	C516
				C908		C908	G836	U768	U641	U516	C517	C517
				C909		C909	G837	U769	U642	U517	C518	C518
				C910		C910	G838	U770	U643	U518	C519	C519
				C911		C911	G839	U771	U644	U519	C520	C520
				C912		C912	G840	U772	U645	U520	C521	C521
				C913		C913	G841	U773	U646	U521	C522	C522
				C914		C914	G842	U774	U647	U522	C523	C523
				C915		C915	G843	U775	U648	U523	C524	C524
				C916		C916	G844	U776	U649	U524	C525	C525
				C917		C917	G845	U777	U650	U525	C526	C526
				C918		C918	G846	U778	U651	U526	C527	C527
				C919		C919	G847	U779	U652	U527	C528	C528
				C920		C920	G848	U780	U653	U528	C529	C529
				C921		C921	G849	U781	U654	U529	C530	C530
				C922		C922	G850	U782	U655	U530	C531	C531
				C923		C923	G851	U783	U656	U531	C532	C532
				C924		C924	G852	U784	U657	U532	C533	C533
				C925		C925	G853	U785	U658	U533	C534	C534
				C926		C926	G854	U786	U659	U534	C535	C535
				C927		C927	G855	U787	U660	U535	C536	C536
				C928		C928	G856	U788	U661	U536	C537	C537
				C929		C929	G857	U789	U662	U537	C538	C538
				C930		C930	G858	U790	U663	U538	C539	C539
				C931		C931	G859	U791	U664	U539	C540	C540
				C932		C932	G860	U792	U665	U540	C541	C541
				C933		C933	G861	U793	U666	U541	C542	C542
				C934		C934	G862	U794	U667	U542	C543	C543
				C935		C935	G863	U795	U668	U543	C544	C544
				C936		C936	G864	U796	U669	U544	C545	C545
				C937		C937	G865	U797	U670	U545	C546	C546
				C938		C938	G866	U798	U671	U546	C547	C547
				C939		C939	G867	U799	U672	U547	C548	C548
				C940		C940	G868	U800	U673	U548	C549	C549
				C941		C941	G869	U801	U674	U549	C550	C550
				C942		C942	G870	U802	U675	U550	C551	C551
				C943		C943	G871	U803	U676	U551	C552	C552
				C944		C944	G872	U804	U677	U552	C553	C553
				C945		C945	G873	U805	U678	U553	C554	C554
				C946		C946	G874	U806	U679	U554	C555	C555
				C947		C947	G875	U807	U680	U555	C556	C556
				C948		C948	G876	U808	U681	U556	C557	C557
				C949		C949	G877	U809	U682	U557	C558	C558
				C950		C950	G878	U810	U683	U558	C559	C559
				C951		C951	G879	U811	U684	U559	C560	C560
				C952		C952	G880	U812	U685	U560	C561	C561
				C953		C953	G881	U813	U686	U561	C562	C562
				C954		C954	G882	U814	U687	U562	C563	C563
				C955		C955	G883	U815	U688	U563	C564	C564
				C956		C956	G884	U816	U689	U564	C565	C565
				C957		C957	G885	U817	U690	U565	C566	C566
				C958		C958	G886	U818	U691	U566	C567	C567
				C959		C959	G887	U819	U692	U567	C568	C568
				C960		C960	G888	U820	U693	U568	C569	C569
				C961		C961	G889	U821	U694	U569	C570	C570
				C962		C962	G890	U822	U695	U570	C571	C571
				C963		C963	G891	U823	U696	U571	C572	C572



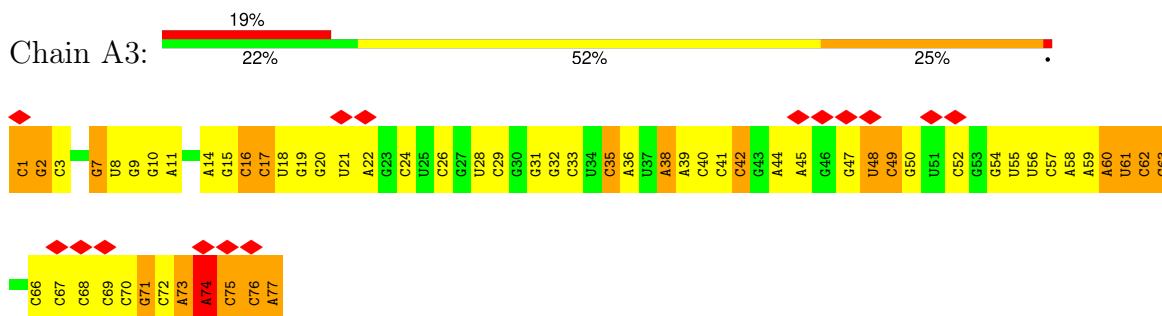
- Molecule 22: fMet-Val-tRNA-Val



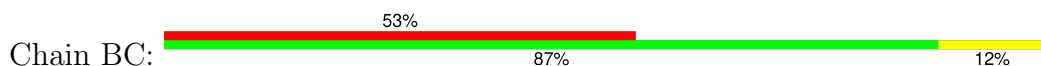
● Molecule 23: 5'-R(*AP*CP*UP*AP*UP*GP*GP*UP*UP*UP*UP*UP*AP*UP*U)-3'

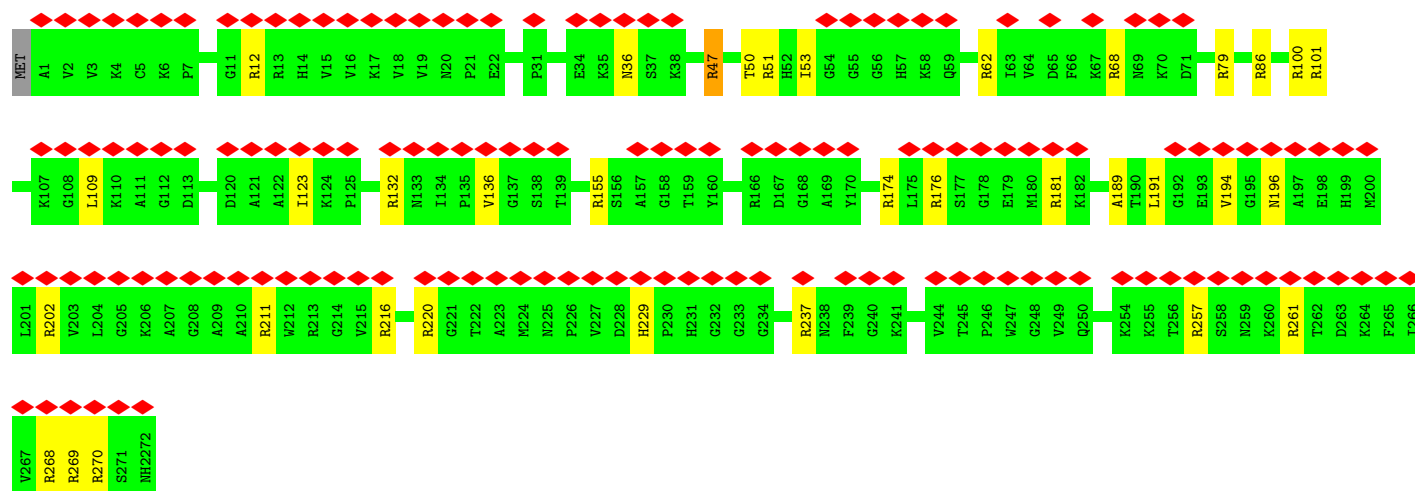


- Molecule 24: tRNA-fMet

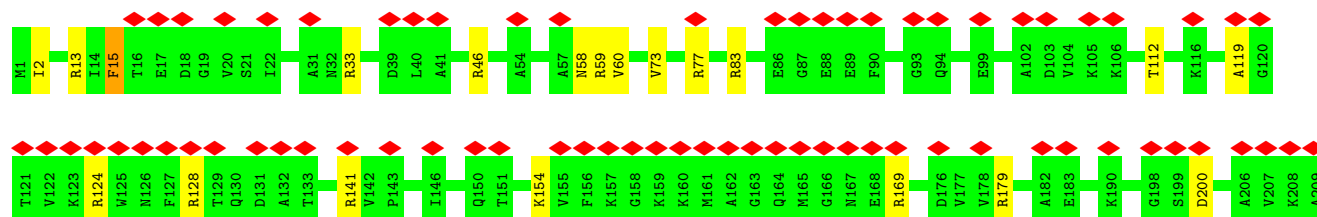


- Molecule 25: 50S ribosomal protein L2

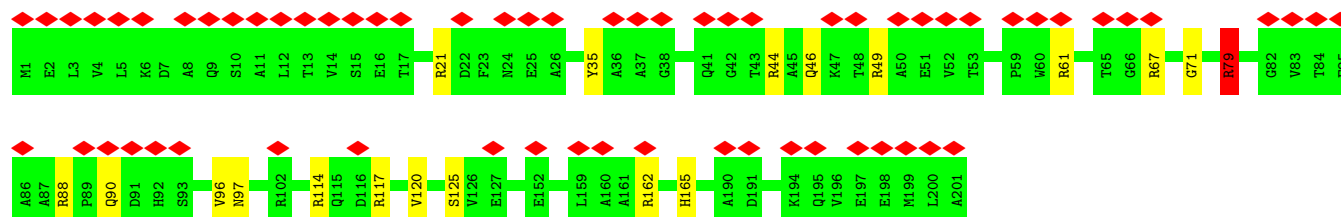




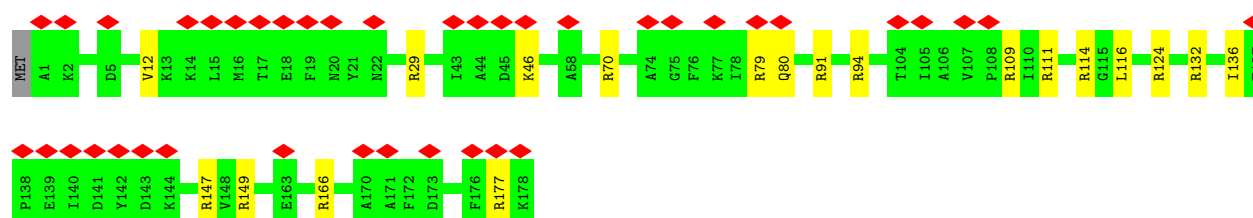
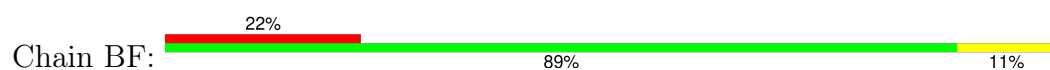
- Molecule 26: 50S ribosomal protein L3




- Molecule 27: 50S ribosomal protein L4

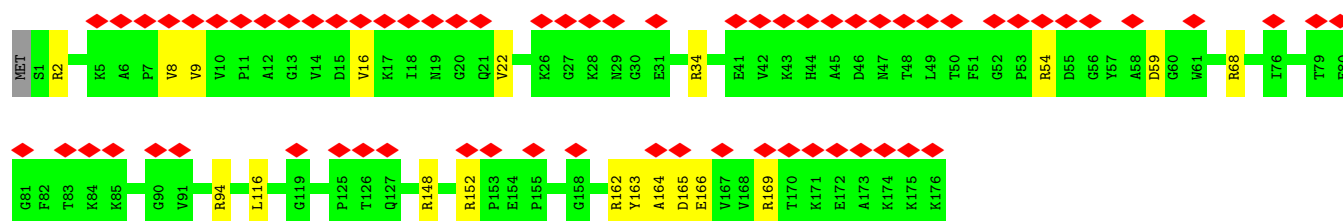


- Molecule 28: 50S ribosomal protein L5

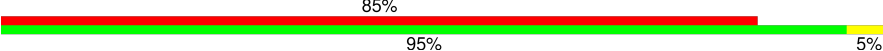


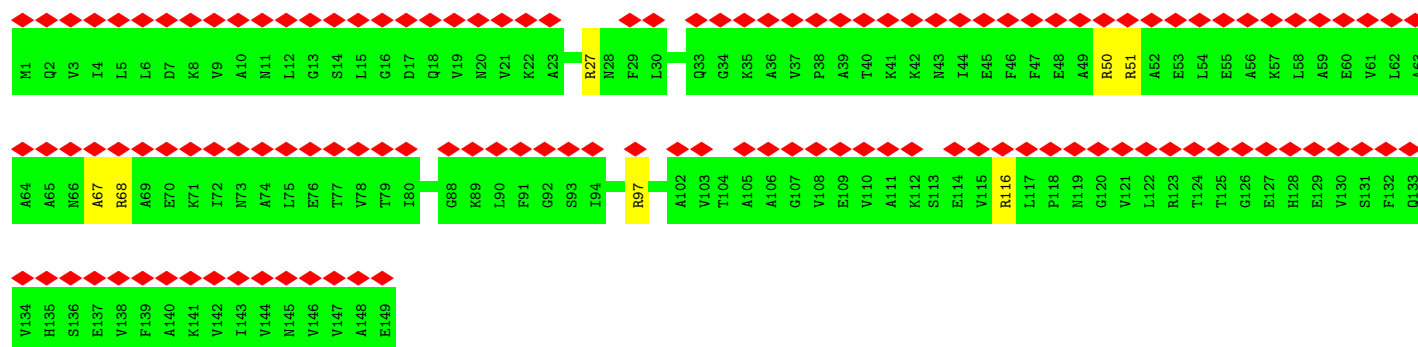
- Molecule 29: 50S ribosomal protein L6

Chain BG: 



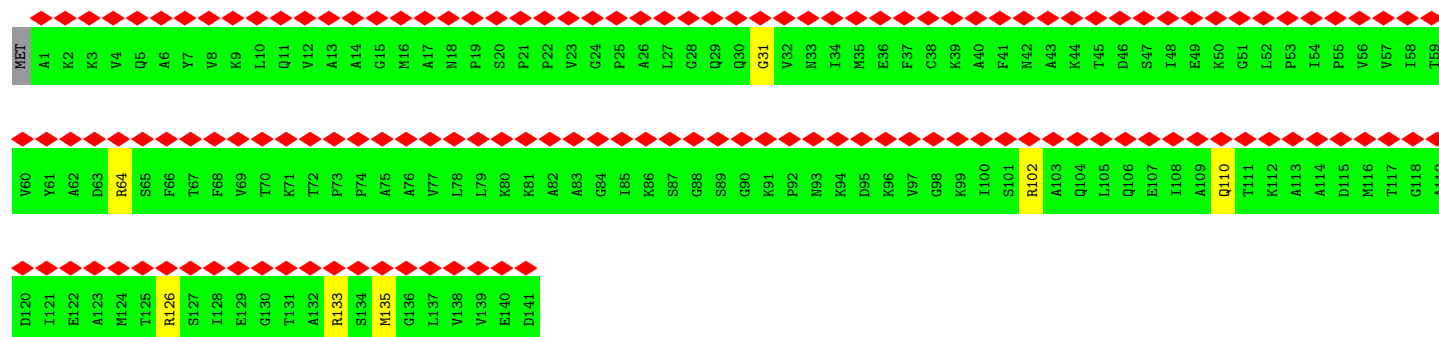
• Molecule 30: 50S ribosomal protein L9

Chain BH: 




• Molecule 31: 50S ribosomal protein L11

Chain BI: 



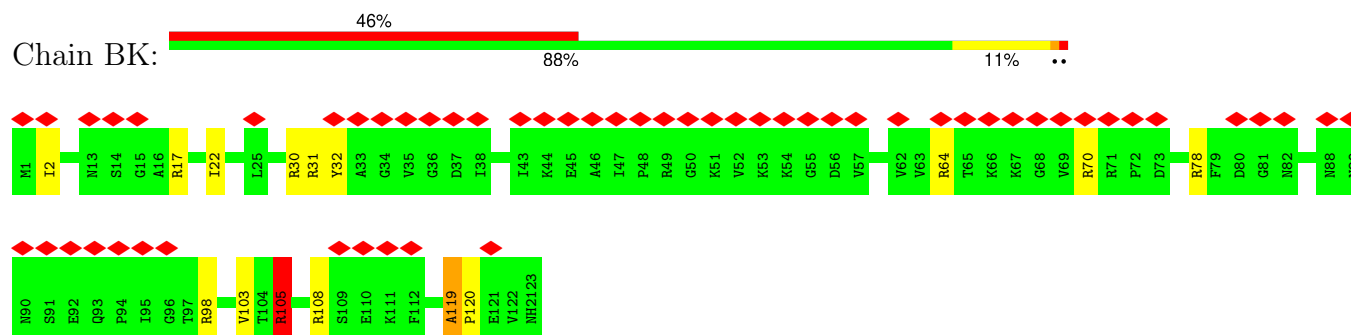
• Molecule 32: 50S ribosomal protein L13

Chain BJ: 



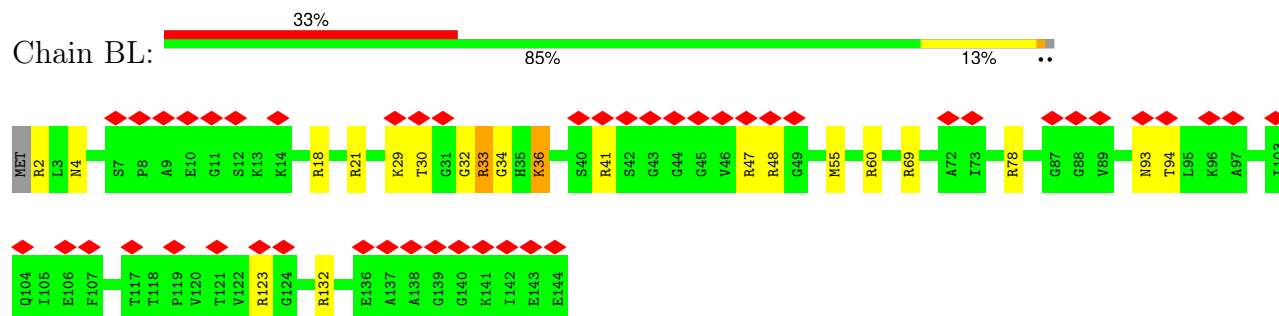
- Molecule 33: 50S ribosomal protein L14

Chain BK:



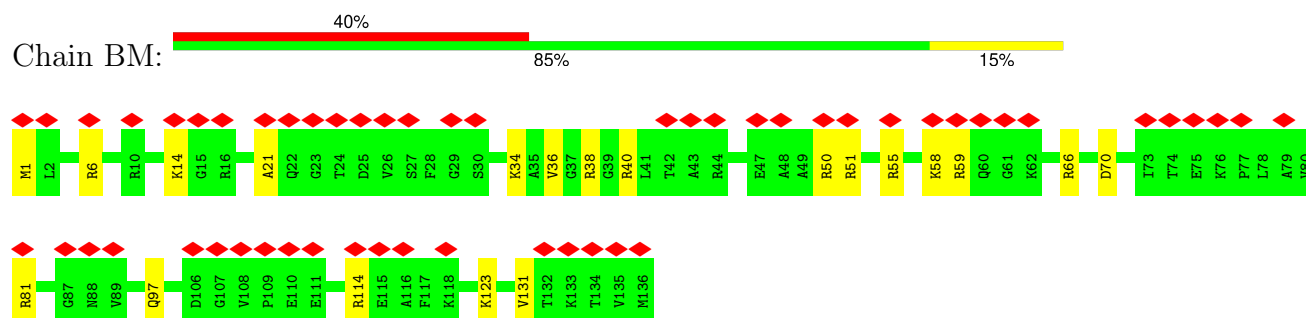
- Molecule 34: 50S ribosomal protein L15

Chain BL:



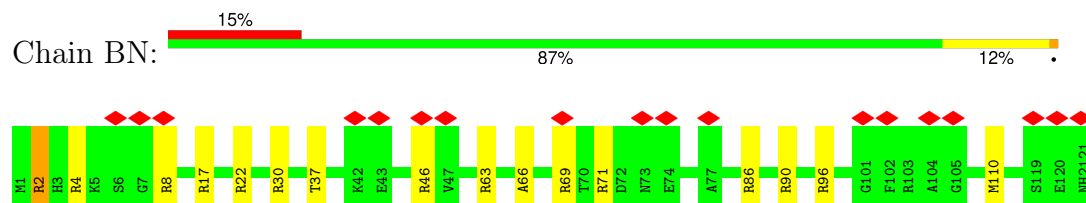
- Molecule 35: 50S ribosomal protein L16

Chain BM:



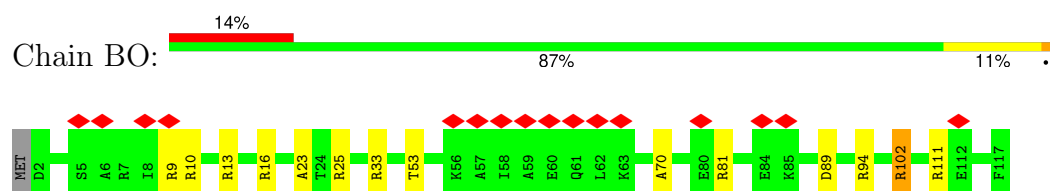
- Molecule 36: 50S ribosomal protein L17

Chain BN:

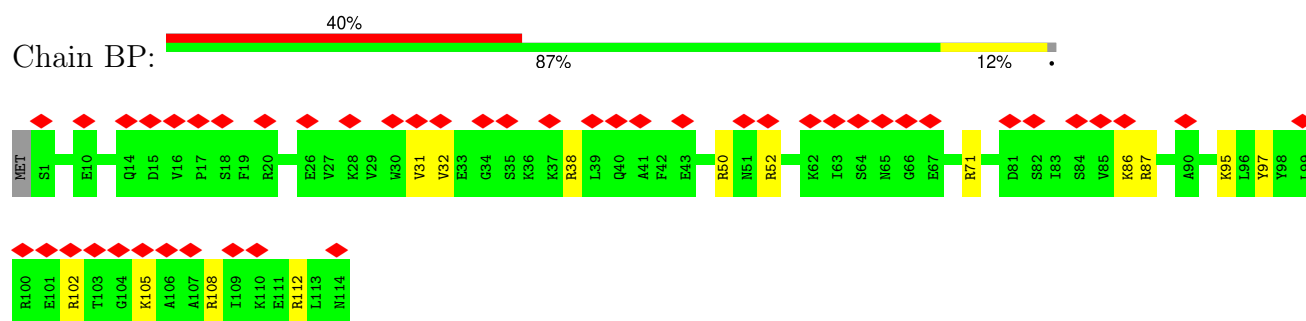


- Molecule 37: 50S ribosomal protein L18

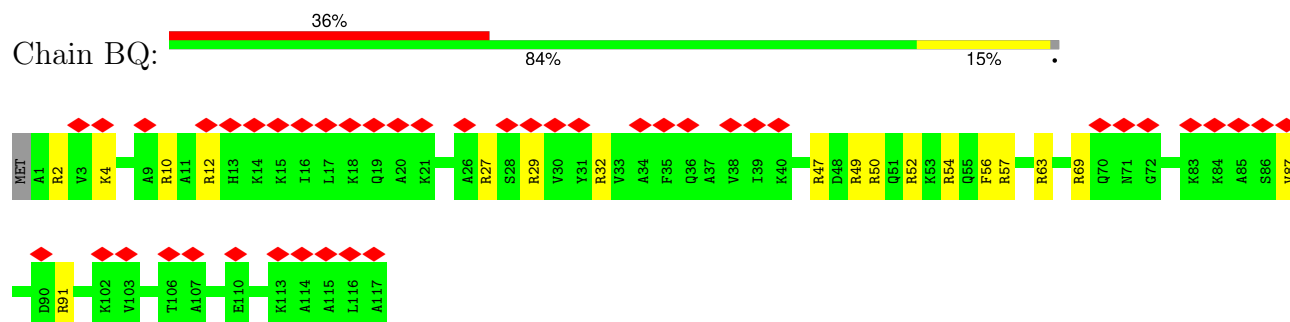
Chain BO:



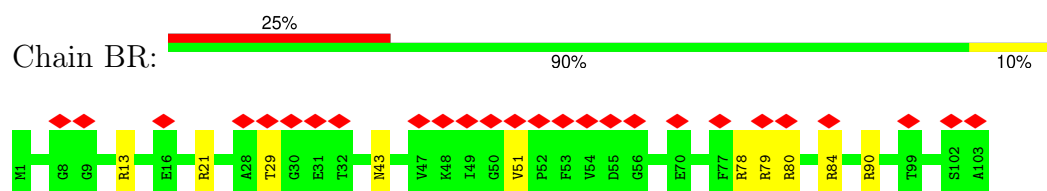
- Molecule 38: 50S ribosomal protein L19



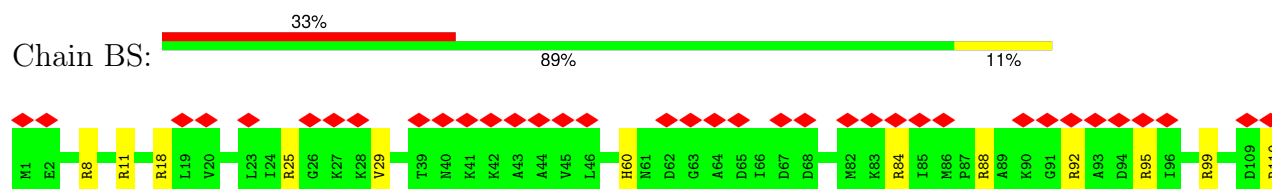
- Molecule 39: 50S ribosomal protein L20



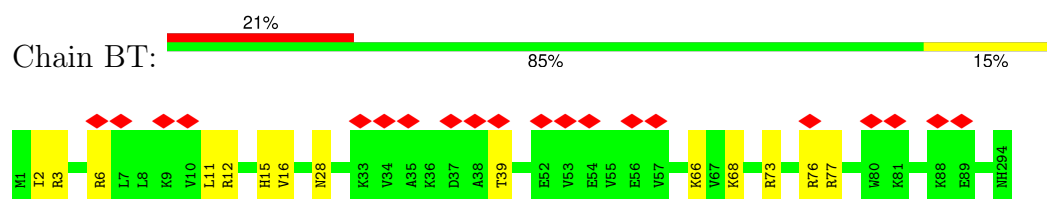
- Molecule 40: 50S ribosomal protein L21



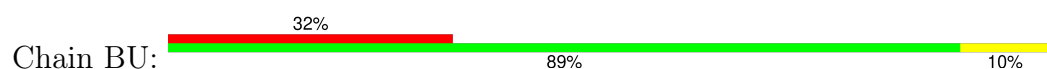
- Molecule 41: 50S ribosomal protein L22

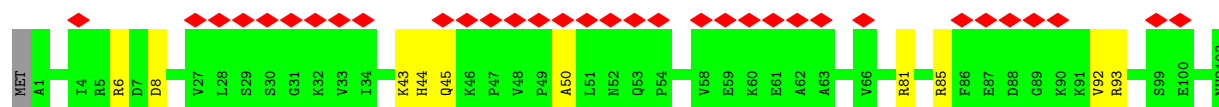


- Molecule 42: 50S ribosomal protein L23

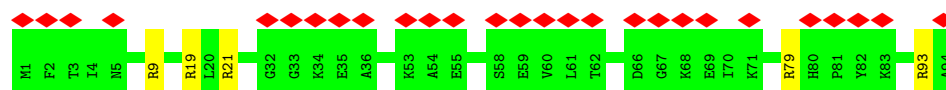


- Molecule 43: 50S ribosomal protein L24

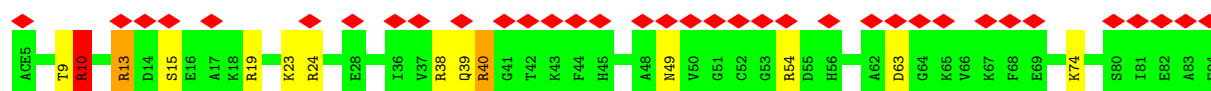
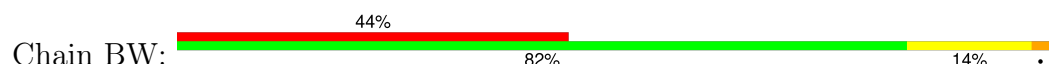




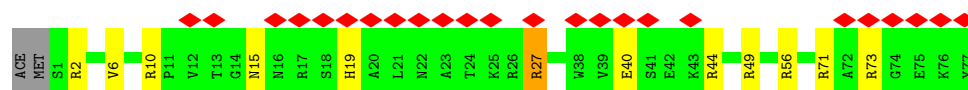
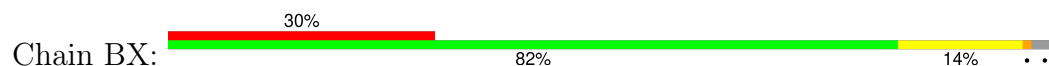
- Molecule 44: 50S ribosomal protein L25



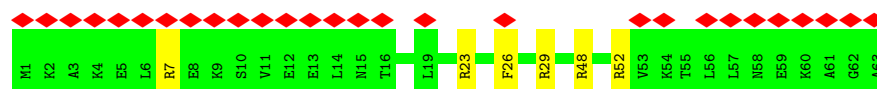
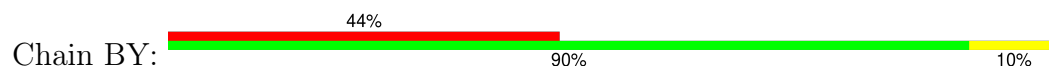
- Molecule 45: 50S ribosomal protein L27



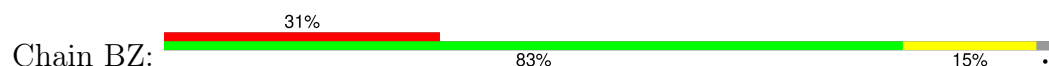
- Molecule 46: 50S ribosomal protein L28



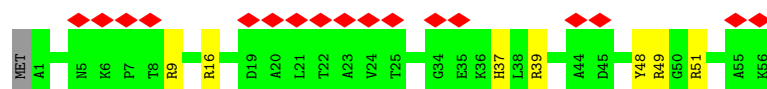
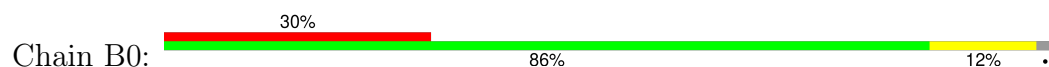
- Molecule 47: 50S ribosomal protein L29



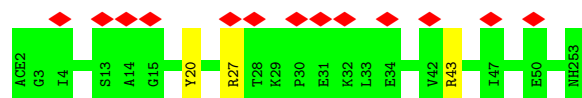
- Molecule 48: 50S ribosomal protein L30



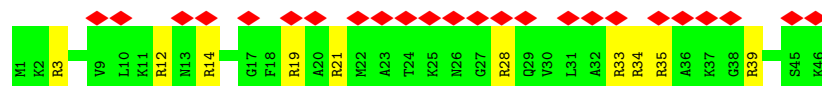
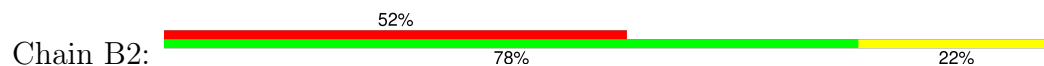
- Molecule 49: 50S ribosomal protein L32



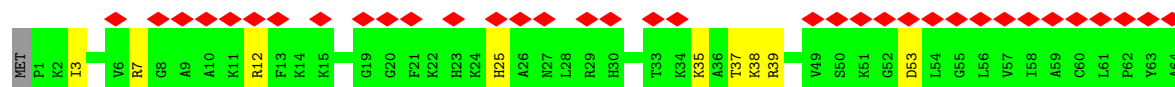
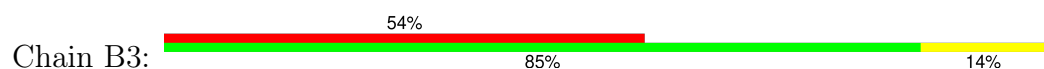
- Molecule 50: 50S ribosomal protein L33



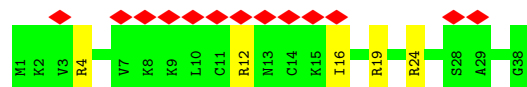
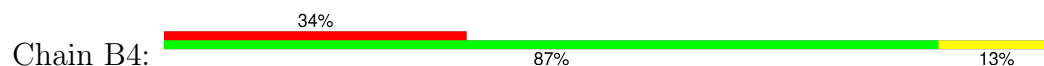
- Molecule 51: 50S ribosomal protein L34



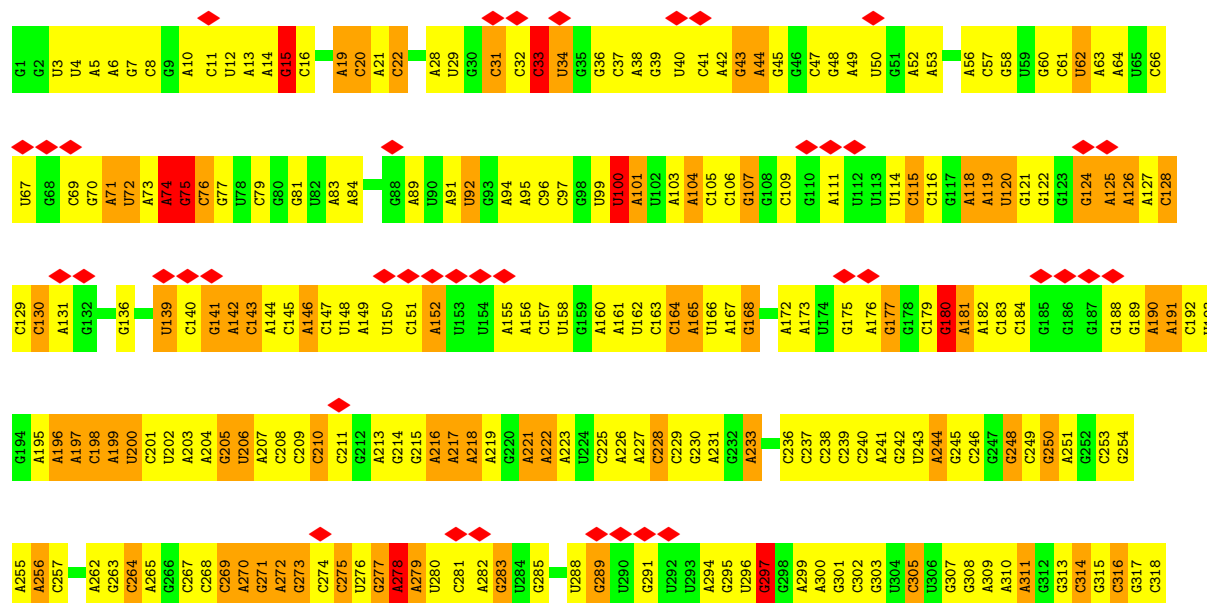
- Molecule 52: 50S ribosomal protein L35

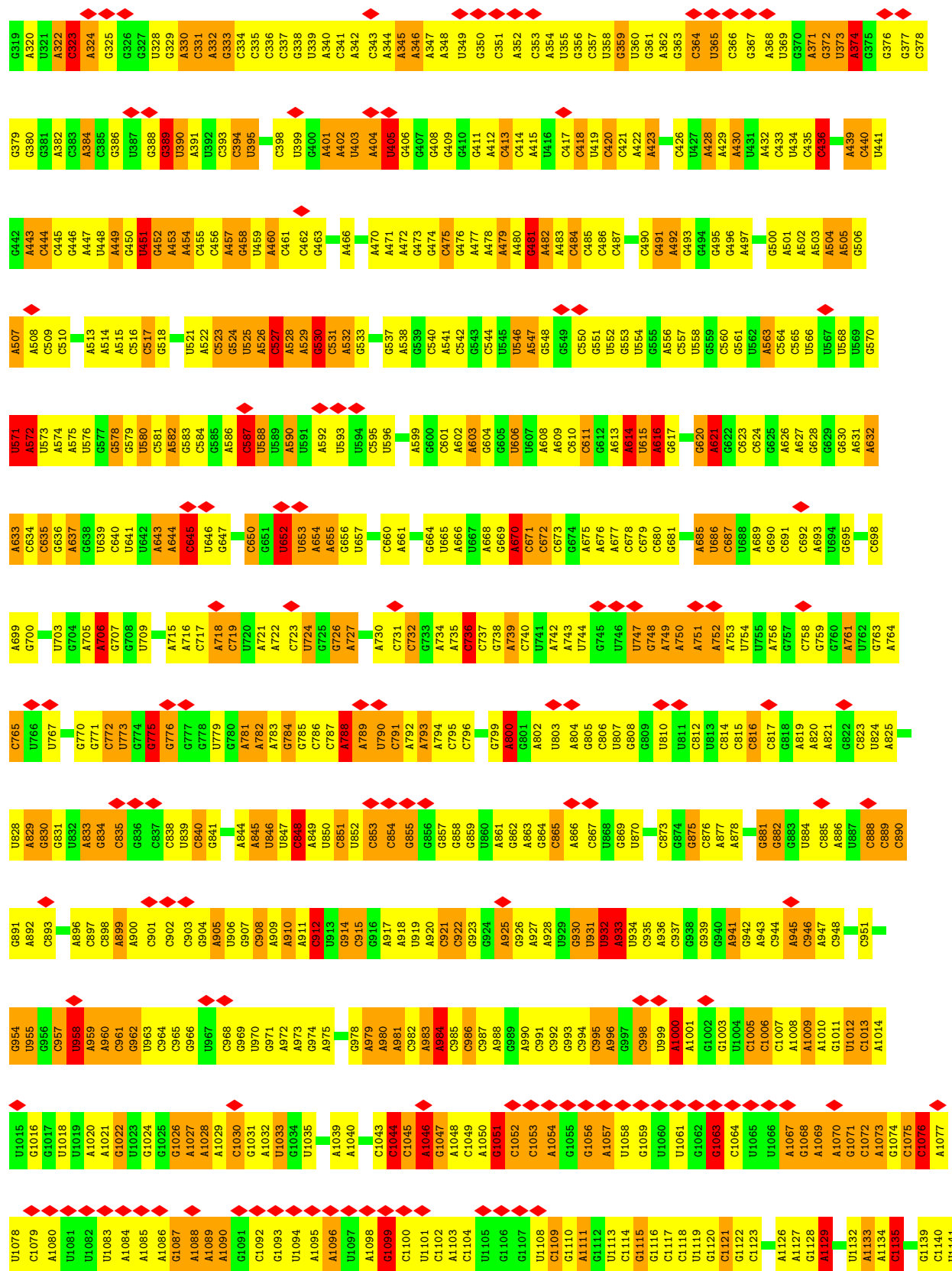


- Molecule 53: 50S ribosomal protein L36



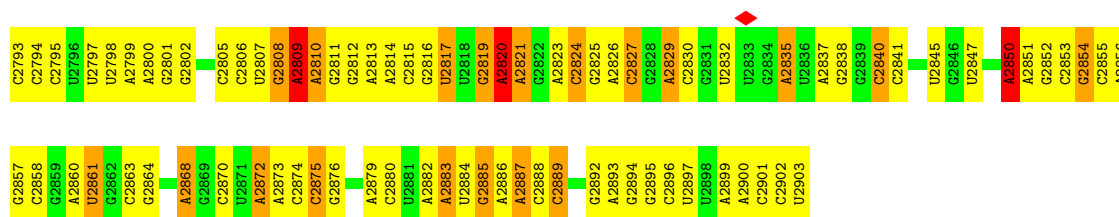
- Molecule 54: 23S ribosomal RNA



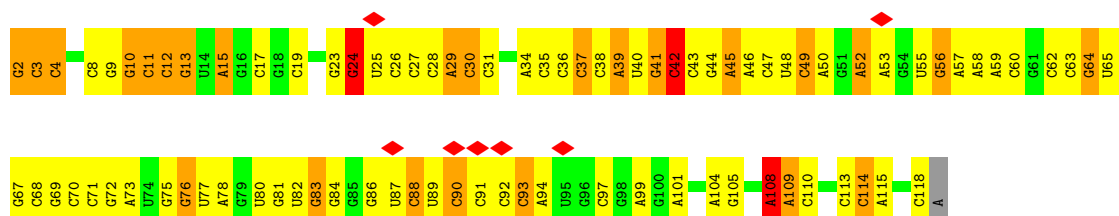


A1899	A1900	A1901	C1902	C1905	C1906	C1907	C1908	C1909	C1910	C1911	C1912	C1913	C1914	C1915	C1916	C1917	C1918	C1919	C1920	C1921	C1922	C1923	C1924	C1925	C1926	C1927	C1928	C1929	C1930	C1931	C1932	C1933	C1934	C1935	C1936	C1937	C1938	C1939	C1940	C1941	C1942	C1943	C1944	C1945	C1946	C1947	C1948	C1949	C1950	C1951	C1952	C1953	C1954	C1955	C1956	C1957	C1958	C1959																
C1837	C1838	C1839	C1840	C1841	C1842	C1843	C1844	C1845	C1846	C1847	C1848	C1849	C1850	C1851	C1852	C1853	C1854	C1855	C1856	C1857	C1858	C1859	C1860	C1861	C1862	C1863	C1864	C1865	C1866	C1867	C1868	C1869	C1870	C1871	C1872	C1873	C1874	C1875	C1876	C1877	C1878	C1879	C1880	C1881	C1882	C1883	C1884	C1885	C1886	C1887	C1888	C1889	C1890	C1891	C1892	C1893	C1894	C1895	C1896	C1897	C1898	C1899												
C1774	C1775	C1780	C1781	C1782	C1783	C1784	C1785	C1786	C1787	C1788	C1789	C1790	C1791	C1792	C1793	C1794	C1795	C1796	C1797	C1798	C1799	C1800	C1801	C1802	C1803	C1804	C1805	C1806	C1807	C1808	C1809	C1810	C1811	C1812	C1813	C1814	C1815	C1816	C1817	C1818	C1819	C1820	C1821	C1822	C1823	C1824	C1825	C1826	C1827	C1828	C1829	C1830	C1831	C1832	C1833	C1834	C1835	C1836																
U1713	U1714	U1715	U1716	U1717	U1718	U1719	U1720	U1721	U1722	U1723	U1724	U1725	U1726	U1727	U1728	U1729	U1730	U1731	U1732	U1733	U1734	U1735	U1736	U1737	U1738	U1739	U1740	U1741	U1742	U1743	U1744	U1745	U1746	U1747	U1748	U1749	U1750	U1751	U1752	U1753	U1754	U1755	U1756	U1757	U1758	U1759	U1760	U1761	U1762	U1763	U1764	U1765	U1766	U1767	U1768	U1769	U1770	U1771	U1772	U1773														
U1648	U1649	U1650	U1651	U1652	U1653	U1654	U1655	U1656	U1657	U1658	U1659	U1660	U1661	U1662	U1663	U1664	U1665	U1666	U1667	U1668	U1669	U1670	U1671	U1672	U1673	U1674	U1675	U1676	U1677	U1678	U1679	U1680	U1681	U1682	U1683	U1684	U1685	U1686	U1687	U1688	U1689	U1690	U1691	U1692	U1693	U1694	U1695	U1696	U1697	U1698	U1699	U1700	U1701	U1702	U1703	U1704	U1705	U1706	U1707	U1708	U1709	U1710	U1711	U1712										
A1586	A1587	A1590	A1591	A1592	A1593	A1594	A1595	A1596	A1597	A1598	A1599	C1600	C1601	C1602	C1603	C1604	C1605	C1606	C1607	C1608	C1609	C1610	C1611	C1612	C1613	C1614	C1615	C1616	C1617	C1618	C1619	C1620	C1621	C1622	C1623	C1624	C1625	C1626	C1627	C1628	U1629	C1630	C1631	C1632	C1633	C1634	C1635	U1636	C1637	C1638	C1639	C1640	C1641	C1642	C1643	C1644	C1645	C1646	U1647															
A1526	A1527	A1528	C1529	C1530	C1531	A1532	C1533	C1534	C1535	A1536	C1537	C1538	C1539	C1540	C1541	C1542	C1543	C1544	C1545	C1546	C1547	C1548	C1549	C1550	C1551	C1552	C1553	C1554	C1555	C1556	C1557	C1558	U1559	C1560	C1561	C1562	C1563	C1564	C1565	C1566	C1567	U1568	C1569	C1570	C1571	C1572	C1573	C1574	C1575	C1576	C1577	C1578	C1579	C1580	C1581	C1582	C1583	C1584	C1585															
C1461	C1462	C1463	C1464	C1465	C1466	C1469	C1470	C1471	C1472	C1473	U1474	U1475	U1476	U1477	U1478	U1479	C1480	C1481	C1482	C1483	C1484	C1487	C1488	C1489	C1490	C1491	C1492	C1493	C1494	C1495	C1496	C1497	C1498	C1499	C1500	C1501	C1502	C1503	C1504	C1505	C1506	C1507	C1508	C1509	C1510	C1511	C1512	C1513	C1514	C1515	C1516	C1517	C1518	C1519	C1520	C1521	C1522	C1523	C1524															
A1392	A1393	U1394	U1395	U1396	U1397	C1398	C1399	A1400	C1404	C1407	U1408	U1409	U1410	U1411	U1412	U1413	C1414	U1415	C1416	C1417	U1418	U1419	C1420	C1421	C1422	C1423	C1424	C1425	C1426	C1427	C1428	C1429	C1430	C1431	C1432	C1433	C1434	C1435	C1436	C1437	U1438	U1439	C1440	C1441	U1442	C1443	C1444	C1445	C1446	C1447	C1448	C1449	C1450	C1451	C1452	C1453	C1454	C1455	C1456	C1457	U1458	C1459	C1460											
A1328	C1329	C1330	C1331	C1332	C1333	C1334	C1335	C1336	C1337	C1338	C1339	C1340	C1341	C1342	C1345	C1346	C1347	C1348	C1349	C1350	C1351	C1352	C1353	C1354	C1355	C1356	C1357	C1358	C1359	C1360	C1361	C1362	C1363	C1364	C1365	C1366	C1367	C1368	C1369	C1370	C1371	C1372	C1373	C1376	C1377	C1378	C1379	C1382	C1383	C1384	C1385	C1386	C1387	C1388	C1389	C1390	C1391																	
G1266	G1267	G1268	G1269	G1270	G1271	G1272	C1273	C1274	C1275	C1276	C1277	C1278	G1281	U1282	G1283	C1284	C1285	C1286	C1287	C1288	C1289	C1290	C1291	C1292	C1293	C1294	C1295	C1296	C1297	C1298	C1299	G1300	C1301	C1302	C1303	C1304	C1305	C1306	C1307	C1308	C1309	C1310	C1311	C1312	C1313	C1314	C1315	C1316	C1317	C1318	C1319	C1320	C1321	C1322	C1323	C1324	C1325	C1326	C1327	C1328	C1329	C1330	C1331	C1332	C1333	C1334	C1335	C1336	C1337	C1338	C1339	C1340	C1341	C1342
G1202	U1203	C1204	C1205	C1206	C1207	C1208	C1209	C1210	C1211	C1212	C1213	C1214	U1217	U1218	U1219	C1220	C1221	C1222	C1223	U1226	C1227	C1228	C1229	C1230	C1231	C1232	C1233	G1236	C1237	C1238	C1239	C1240	C1241	C1242	C1243	C1244	C1245	C1246	C1247	C1248	C1251	C1252	C1253	C1254	C1255	C1256	C1257	C1258	C1259	C1260	C1261	C1262	C1263	C1264	C1265																			
A1142	A1143	A1144	C1145	C1146	C1147	C1148	C1149	C1150	C1151	C1152	C1153	C1154	A1155	A1156	C1157	C1158	U1159	C1160	C1161	C1162	C1163	C1164	C1165	C1166	C1167	C1168	C1169	C1170	C1171	C1172	C1173	C1174	C1175	C1176	C1177	C1178	C1179	C1180	C1181	C1182	C1183	C1184	C1185	C1186	C1187	C1188	C1189	C1190	C1191	C1192	C1193	C1194	C1195	C1196	C1197	C1198	C1199	C1200	C1201															

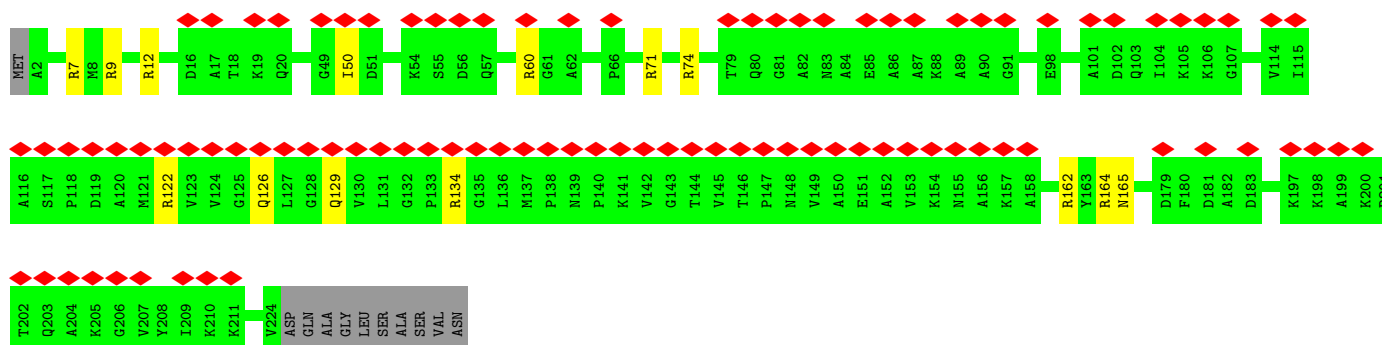
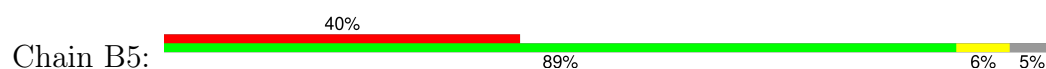
G2732	A2665	C2538	A2471	G2405	G2341	G2277	G2152	C2023	A1960
A2733	C2666	C2539	G2472	A2406	C2342	A2718	C2153	G2024	C1961
G2735	C2667	A2540	U2473	A2407	U2343	G2279	A2154	C2025	C1962
A2736	G2668	A2541	U2474	U2408	G2344	G2280	U2155		U1963
G2737	C2669	A2542	C2475	A2411	G2345	G2281	G2156	G2026	G1964
A2738	A2670		A2476	A2412	C2347	G2282	A2158	A2030	C1965
U2739	A2675	U2546	U2477		C2350	A2284	G2159	A2031	A1966
A2740	C2676	A2547	U2478	C2416	C2351	C2285	C2160	G2032	A1967
G2741	G2677	U2548	U2479	A2417	G2352	G2286	A2161	U2034	G1968
A2742	C2678	G2549	C2480	A2418	A2352	A2287	G2162	G2035	G1969
	A2679	C2551	G2481	U2419	G2353	A2288	C2096	C2036	A1970
C2745	U2680	U2552	C2482	C2420	C2354	A2289	A2097		U1971
U2746	A2681	U2555	C2483	G2421	G2355	G2290	U2098	A2037	G1972
G2747	U2682	C2556		C2422	U2356	U2291	U2099	U2038	G1973
A2748	C2683	C2557	U2491	U2423	A2358	C2295	G2100	G2040	C1974
U2749	U2684	G2557	U2492	C2424	C2359	U2296	A2101	U2041	G1975
G2751	C2685	C2558	U2493	A2425	G2360	A2297	G2102	A2042	U1976
U2752	G2686	U2559	G2495	A2426	C2361	U2298	C2103	C2044	A1977
A2753	G2687	A2560	C2496	G2428	C2362	U2299	C2104	C2045	A1978
U2754	U2689	U2561	A2497	A2429	G2363	U2300	U2105		
G2755	U2690	G2562	C2498	A2430	C2364	C2301	A2108	G2046	
U2756	C2691	U2562	C2499	U2431	G2365	U2302		C2047	A1981
A2757	U2695	U2563	U2500	A2432	A2366		U2111		U1982
U2758	U2696	A2564	U2491	A2433	G2367	U2305	G2112	C2050	G1983
G2759	G2697	A2565	U2492	A2434	C2368	C2306	U2113	A2051	G1984
U2760	U2698	A2566	G2502	A2435	A2369	G2307	A2114	A2062	C1985
A2761	G2699	G2567	G2503		C2370	G2242	G2115	G2063	C1986
C2762	U2700	U2568	U2504	A2439	G2371	U2244	G2116	A2054	A1987
U2763	C2703	G2569	G2505	C2440	G2372	C2310	A2117	C2055	G1988
A2764	A2764	U2571	U2506	U2441	G2373	A2311	U2118	G2056	G1989
U2765	C2704	A2572	C2510	C2442	C2374	G2312	U2119	G2057	C1990
G2766	A2765	C2573	U2511	C2443	G2375	C2313	A2120	A2058	U1991
C2767	U2766	G2574	C2512	G2444	A2376	C2314	G2121	A2059	G1992
U2768	A2767	C2575	U2513	G2445	A2377		U2122	A2060	
U2769	U2769	G2576	A2514	G2446	A2378	G2317	G2061		C1994
G2770	C2770	A2577	U2515	G2447	G2379	G2318	A2126	A2062	U1995
A2771	U2710	G2578	C2516	A2448	C2380	U2319	C2129	C2063	C1996
C2772	C2711	C2579	U2517	U2449	A2381	U2320	U2130	C2064	C1997
U2773	U2712	U2580	A2518	A2450	G2382	U2321	U2131	A2065	A1998
G2774	C2713	G2581	C2519	A2451	G2383	A2322	U2132	C2066	C1999
U2775	A2714	A2582	U2519	C2452	U2384	G2323	G2133	G2067	C2000
C2776	C2715	G2583	G2520	A2453	C2385	U2324	A2134	U2068	C2001
A2777	U2716	U2584	U2521		A2386	G2325	G2135	G2069	U2002
G2778	C2717	U2585	G2522	C2456	U2387	A2326	A2136	A2070	A2003
U2779	U2718	U2586	G2523	U2457	A2388	A2327	A2137	A2071	G2004
G2780	A2719	A2587	G2524	G2458	G2389	A2328	U2138	C2072	A2005
A2781	C2720	C2588	G2525	A2459	U2390	U2329	G2139	C2073	C2006
U2782	U2721	U2589	U2526	U2460	G2391	G2330	U2142	U2074	U2007
G2783	C2722	G2590	U2527	A2461	A2392	C2331	C2200	U2075	C2008
U2784	U2723	C2591	G2528	C2462	U2393	C2332	G2201	U2076	A2009
C2785	A2724	A2592	U2529	C2463	C2394	A2333	U2202	U2077	A2013
U2786	U2725	G2593	G2530	G2464	C2395	U2334	U2203	A2078	A2014
A2787	A2726	A2594	U2531	U2465	U2396	A2335	C2204	U2079	A2015
G2788	U2727	C2595	G2532	C2466	U2397	A2336	C2205	A2080	U2016
U2789	C2728	U2596	U2533	C2467	U2402	G2337	C2206	U2081	U2017
G2790	U2729	G2597	A2534	C2468	C2403	C2338	U2207	A2082	G2018
A2791	C2730	A2598	G2535	A2469	U2404	C2339	C2208	G2083	A2019
U2792	U2731	U2599	G2536	G2470		A2340	C2209	C2084	A2020
		A2600	U2537				U2210	U2085	C2021
							A2211		U2022



- 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	3052	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	local	Depositor
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	162740	Depositor
Image detector	GENERIC TVIPS (4k x 4k)	Depositor
Maximum map value	162.319	Depositor
Minimum map value	-108.564	Depositor
Average map value	-1.515	Depositor
Map value standard deviation	18.464	Depositor
Recommended contour level	20	Depositor
Map size (\AA)	358.4, 358.4, 358.4	wwPDB
Map dimensions	128, 128, 128	wwPDB
Map angles ($^\circ$)	90, 90, 90	wwPDB
Pixel spacing (\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: 6MZ, PSU, H2U, ACE, 7MG, OMC, CM0, FME, NH2, 4SU, 5MU

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	0.70	0/1736	1.07	11/2340 (0.5%)
2	AC	0.72	0/1651	1.16	16/2225 (0.7%)
3	AD	0.77	0/1665	1.23	24/2227 (1.1%)
4	AE	0.70	0/1119	1.06	10/1506 (0.7%)
5	AF	0.74	0/835	1.17	6/1128 (0.5%)
6	AG	0.74	0/1188	1.21	19/1593 (1.2%)
7	AH	0.70	0/989	1.08	5/1326 (0.4%)
8	AI	0.81	0/1035	1.34	20/1377 (1.5%)
9	AJ	0.69	0/797	1.23	13/1079 (1.2%)
10	AK	0.74	0/894	1.15	10/1207 (0.8%)
11	AL	0.76	0/969	1.23	15/1300 (1.2%)
12	AM	0.75	0/884	1.32	11/1181 (0.9%)
13	AN	0.77	0/817	1.26	12/1088 (1.1%)
14	AO	0.74	0/722	1.16	8/964 (0.8%)
15	AP	0.76	0/648	1.27	11/870 (1.3%)
16	AQ	0.70	0/658	1.06	4/883 (0.5%)
17	AR	0.81	0/463	1.29	10/623 (1.6%)
18	AS	0.76	0/653	1.13	7/879 (0.8%)
19	AT	0.68	0/672	1.05	5/890 (0.6%)
20	AU	0.83	0/431	1.44	8/572 (1.4%)
21	AA	1.53	1/36759 (0.0%)	2.22	1991/57346 (3.5%)
22	A1	1.53	0/1668	2.20	85/2595 (3.3%)
23	A2	1.47	0/343	2.25	15/531 (2.8%)
24	A3	1.53	0/1722	2.18	81/2685 (3.0%)
25	BC	0.74	0/2121	1.30	26/2852 (0.9%)
26	BD	0.68	0/1586	1.20	14/2134 (0.7%)
27	BE	0.67	0/1571	1.15	11/2113 (0.5%)
28	BF	0.74	0/1444	1.18	14/1937 (0.7%)
29	BG	0.69	0/1343	1.12	8/1816 (0.4%)
30	BH	0.65	0/1122	1.10	6/1515 (0.4%)
31	BI	0.65	0/1046	1.06	4/1410 (0.3%)
32	BJ	0.73	0/1152	1.16	8/1551 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	BK	0.70	0/947	1.21	10/1268 (0.8%)
34	BL	0.73	0/1054	1.36	17/1403 (1.2%)
35	BM	0.74	0/1093	1.21	11/1460 (0.8%)
36	BN	0.77	0/973	1.36	15/1301 (1.2%)
37	BO	0.72	0/902	1.25	11/1209 (0.9%)
38	BP	0.75	0/929	1.27	8/1242 (0.6%)
39	BQ	0.80	0/960	1.32	15/1278 (1.2%)
40	BR	0.70	0/829	1.22	7/1107 (0.6%)
41	BS	0.64	0/864	1.19	10/1156 (0.9%)
42	BT	0.65	0/744	1.19	7/994 (0.7%)
43	BU	0.68	0/787	1.10	4/1051 (0.4%)
44	BV	0.71	0/766	1.16	5/1025 (0.5%)
45	BW	0.77	0/604	1.36	9/799 (1.1%)
46	BX	0.75	0/635	1.28	10/848 (1.2%)
47	BY	0.65	0/510	1.17	5/677 (0.7%)
48	BZ	0.69	0/453	1.24	6/605 (1.0%)
49	B0	0.72	0/450	1.23	5/599 (0.8%)
50	B1	0.73	0/417	1.05	2/556 (0.4%)
51	B2	0.81	0/380	1.49	11/498 (2.2%)
52	B3	0.72	0/513	1.23	5/676 (0.7%)
53	B4	0.68	0/303	1.24	4/397 (1.0%)
54	BA	1.41	2/69796 (0.0%)	2.21	4018/108888 (3.7%)
55	BB	1.42	0/2800	2.17	151/4367 (3.5%)
56	B5	0.64	0/1673	1.08	9/2255 (0.4%)
All	All	1.28	3/160085 (0.0%)	2.00	6843/239402 (2.9%)

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	AB	0	1
4	AE	0	1
14	AO	0	2
21	AA	0	368
22	A1	0	21
23	A2	0	4
24	A3	0	16
43	BU	0	1
49	B0	0	1
54	BA	0	707

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
55	BB	0	25
All	All	0	1147

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	AA	6	G	C2-N2	-5.63	1.28	1.34
54	BA	1568	G	C2-N2	-5.08	1.29	1.34
54	BA	2627	G	C2-N2	-5.01	1.29	1.34

The worst 5 of 6843 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	BA	1301	A	O4'-C1'-N9	17.59	122.27	108.20
54	BA	2126	A	O4'-C1'-N9	13.48	118.98	108.20
21	AA	547	A	N1-C6-N6	-12.92	110.85	118.60
54	BA	323	C	O4'-C1'-N1	12.84	118.47	108.20
54	BA	2199	A	N1-C6-N6	-12.76	110.94	118.60

There are no chirality outliers.

5 of 1147 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
21	AA	5	U	Sidechain
1	AB	224	ARG	Sidechain
4	AE	22	LYS	Peptide
14	AO	48	ASP	Peptide
14	AO	68	TYR	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	AB	1708	0	1736	0	0
2	AC	1625	0	1699	0	0
3	AD	1643	0	1710	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	AE	1109	0	1152	1	0
5	AF	818	0	808	0	0
6	AG	1178	0	1234	0	0
7	AH	979	0	1034	2	0
8	AI	1025	0	1074	0	0
9	AJ	790	0	832	0	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	0	0
19	AT	668	0	718	0	0
20	AU	429	0	453	0	0
21	AA	32828	0	16520	3	0
22	A1	1627	0	832	0	0
23	A2	309	0	158	1	0
24	A3	1642	0	843	0	0
25	BC	2083	0	2157	0	0
26	BD	1565	0	1616	0	0
27	BE	1552	0	1619	0	0
28	BF	1420	0	1460	0	0
29	BG	1323	0	1374	0	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	3	0
34	BL	1045	0	1117	1	0
35	BM	1074	0	1157	2	0
36	BN	961	0	1000	0	0
37	BO	892	0	923	1	0
38	BP	917	0	965	1	0
39	BQ	947	0	1022	0	0
40	BR	816	0	839	0	0
41	BS	857	0	922	0	0
42	BT	739	0	807	1	0
43	BU	780	0	834	0	0
44	BV	753	0	780	0	0
45	BW	599	0	614	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
46	BX	625	0	655	0	0
47	BY	509	0	543	0	0
48	BZ	449	0	491	0	0
49	B0	444	0	461	0	0
50	B1	413	0	444	0	0
51	B2	377	0	418	0	0
52	B3	504	0	574	0	0
53	B4	302	0	343	0	0
54	BA	62317	0	31341	4	0
55	BB	2504	0	1271	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	99659	17	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 17 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)
34:BL:30:THR:HG21	34:BL:36:LYS:H	1.72	0.54
54:BA:388:G:H2'	54:BA:389:G:H3'	1.91	0.52
42:BT:15:HIS:CG	42:BT:16:VAL:H	2.29	0.50
21:AA:1054:C:C6	23:A2:89:U:H1'	2.48	0.48
37:BO:53:THR:HG21	37:BO:70:ALA:HB1	1.98	0.46

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%)	200 (92%)	17 (8%)	1 (0%)	25	64
2	AC	205/208 (99%)	184 (90%)	15 (7%)	6 (3%)	3	23
3	AD	203/206 (98%)	185 (91%)	14 (7%)	4 (2%)	6	32
4	AE	150/152 (99%)	134 (89%)	10 (7%)	6 (4%)	2	18
5	AF	99/101 (98%)	80 (81%)	13 (13%)	6 (6%)	1	13
6	AG	150/152 (99%)	136 (91%)	10 (7%)	4 (3%)	4	25
7	AH	127/130 (98%)	116 (91%)	8 (6%)	3 (2%)	5	27
8	AI	126/128 (98%)	107 (85%)	15 (12%)	4 (3%)	3	21
9	AJ	98/100 (98%)	88 (90%)	5 (5%)	5 (5%)	1	15
10	AK	116/118 (98%)	107 (92%)	7 (6%)	2 (2%)	7	37
11	AL	121/124 (98%)	107 (88%)	8 (7%)	6 (5%)	1	16
12	AM	112/115 (97%)	94 (84%)	13 (12%)	5 (4%)	2	17
13	AN	98/101 (97%)	87 (89%)	11 (11%)	0	100	100
14	AO	86/89 (97%)	81 (94%)	4 (5%)	1 (1%)	11	44
15	AP	79/81 (98%)	71 (90%)	5 (6%)	3 (4%)	2	19
16	AQ	80/82 (98%)	75 (94%)	5 (6%)	0	100	100
17	AR	55/57 (96%)	50 (91%)	4 (7%)	1 (2%)	7	35
18	AS	79/81 (98%)	71 (90%)	5 (6%)	3 (4%)	2	19
19	AT	84/86 (98%)	76 (90%)	8 (10%)	0	100	100
20	AU	51/53 (96%)	32 (63%)	15 (29%)	4 (8%)	1	10
25	BC	270/273 (99%)	238 (88%)	25 (9%)	7 (3%)	4	26
26	BD	207/209 (99%)	185 (89%)	17 (8%)	5 (2%)	5	27
27	BE	199/201 (99%)	171 (86%)	20 (10%)	8 (4%)	2	18
28	BF	176/179 (98%)	155 (88%)	17 (10%)	4 (2%)	5	28
29	BG	174/177 (98%)	155 (89%)	12 (7%)	7 (4%)	2	18
30	BH	147/149 (99%)	137 (93%)	9 (6%)	1 (1%)	19	57
31	BI	139/142 (98%)	125 (90%)	12 (9%)	2 (1%)	9	41
32	BJ	140/142 (99%)	126 (90%)	11 (8%)	3 (2%)	5	30
33	BK	121/123 (98%)	107 (88%)	10 (8%)	4 (3%)	3	21
34	BL	141/144 (98%)	124 (88%)	11 (8%)	6 (4%)	2	17
35	BM	134/136 (98%)	115 (86%)	14 (10%)	5 (4%)	2	20
36	BN	119/121 (98%)	105 (88%)	11 (9%)	3 (2%)	4	26

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	BO	114/117 (97%)	108 (95%)	3 (3%)	3 (3%)	4	26
38	BP	112/115 (97%)	92 (82%)	17 (15%)	3 (3%)	4	25
39	BQ	115/118 (98%)	108 (94%)	5 (4%)	2 (2%)	7	37
40	BR	101/103 (98%)	91 (90%)	7 (7%)	3 (3%)	3	23
41	BS	108/110 (98%)	105 (97%)	2 (2%)	1 (1%)	14	52
42	BT	92/94 (98%)	80 (87%)	6 (6%)	6 (6%)	1	12
43	BU	101/104 (97%)	83 (82%)	14 (14%)	4 (4%)	2	18
44	BV	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
45	BW	78/80 (98%)	59 (76%)	17 (22%)	2 (3%)	4	26
46	BX	75/79 (95%)	68 (91%)	3 (4%)	4 (5%)	1	15
47	BY	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
48	BZ	56/59 (95%)	49 (88%)	4 (7%)	3 (5%)	1	15
49	B0	54/57 (95%)	48 (89%)	6 (11%)	0	100	100
50	B1	50/52 (96%)	46 (92%)	4 (8%)	0	100	100
51	B2	44/46 (96%)	40 (91%)	4 (9%)	0	100	100
52	B3	62/65 (95%)	54 (87%)	5 (8%)	3 (5%)	2	16
53	B4	36/38 (95%)	33 (92%)	2 (6%)	1 (3%)	4	24
56	B5	221/234 (94%)	211 (96%)	9 (4%)	1 (0%)	25	64
All	All	5876/6008 (98%)	5245 (89%)	476 (8%)	155 (3%)	6	26

5 of 155 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AB	224	ARG
2	AC	14	VAL
5	AF	86	ARG
15	AP	11	ALA
15	AP	17	TYR

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%)	177 (98%)	3 (2%)	56	72
2	AC	170/171 (99%)	168 (99%)	2 (1%)	67	78
3	AD	172/173 (99%)	171 (99%)	1 (1%)	84	88
4	AE	113/113 (100%)	112 (99%)	1 (1%)	75	83
5	AF	87/87 (100%)	87 (100%)	0	100	100
6	AG	123/123 (100%)	122 (99%)	1 (1%)	79	85
7	AH	104/105 (99%)	101 (97%)	3 (3%)	37	56
8	AI	105/105 (100%)	101 (96%)	4 (4%)	28	49
9	AJ	86/86 (100%)	83 (96%)	3 (4%)	31	51
10	AK	90/90 (100%)	90 (100%)	0	100	100
11	AL	103/104 (99%)	102 (99%)	1 (1%)	73	82
12	AM	91/92 (99%)	90 (99%)	1 (1%)	70	80
13	AN	83/84 (99%)	81 (98%)	2 (2%)	44	62
14	AO	76/77 (99%)	74 (97%)	2 (3%)	41	59
15	AP	65/65 (100%)	65 (100%)	0	100	100
16	AQ	74/74 (100%)	71 (96%)	3 (4%)	26	47
17	AR	48/48 (100%)	45 (94%)	3 (6%)	15	36
18	AS	70/70 (100%)	69 (99%)	1 (1%)	62	75
19	AT	65/65 (100%)	64 (98%)	1 (2%)	60	75
20	AU	44/44 (100%)	44 (100%)	0	100	100
25	BC	216/217 (100%)	210 (97%)	6 (3%)	38	57
26	BD	164/164 (100%)	160 (98%)	4 (2%)	44	62
27	BE	165/165 (100%)	162 (98%)	3 (2%)	54	71
28	BF	149/150 (99%)	147 (99%)	2 (1%)	65	77
29	BG	137/138 (99%)	133 (97%)	4 (3%)	37	56
30	BH	114/114 (100%)	114 (100%)	0	100	100
31	BI	109/110 (99%)	108 (99%)	1 (1%)	75	83
32	BJ	116/116 (100%)	113 (97%)	3 (3%)	41	59
33	BK	103/103 (100%)	102 (99%)	1 (1%)	73	82
34	BL	102/103 (99%)	100 (98%)	2 (2%)	50	68
35	BM	109/109 (100%)	107 (98%)	2 (2%)	54	71

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	BN	100/100 (100%)	99 (99%)	1 (1%)	73	82
37	BO	86/87 (99%)	86 (100%)	0	100	100
38	BP	99/100 (99%)	97 (98%)	2 (2%)	50	68
39	BQ	89/90 (99%)	87 (98%)	2 (2%)	47	65
40	BR	84/84 (100%)	84 (100%)	0	100	100
41	BS	93/93 (100%)	92 (99%)	1 (1%)	70	80
42	BT	80/80 (100%)	80 (100%)	0	100	100
43	BU	83/84 (99%)	81 (98%)	2 (2%)	44	62
44	BV	78/78 (100%)	78 (100%)	0	100	100
45	BW	59/59 (100%)	53 (90%)	6 (10%)	6	20
46	BX	67/68 (98%)	66 (98%)	1 (2%)	60	75
47	BY	55/55 (100%)	54 (98%)	1 (2%)	54	71
48	BZ	48/49 (98%)	48 (100%)	0	100	100
49	B0	47/48 (98%)	46 (98%)	1 (2%)	48	66
50	B1	45/45 (100%)	44 (98%)	1 (2%)	47	65
51	B2	38/38 (100%)	38 (100%)	0	100	100
52	B3	51/52 (98%)	48 (94%)	3 (6%)	16	37
53	B4	34/34 (100%)	34 (100%)	0	100	100
56	B5	173/181 (96%)	169 (98%)	4 (2%)	45	64
All	All	4842/4870 (99%)	4757 (98%)	85 (2%)	54	71

5 of 85 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
34	BL	93	ASN
45	BW	40	ARG
35	BM	97	GLN
41	BS	60	HIS
47	BY	26	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
12	AM	104	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
44	BV	88	HIS
46	BX	15	ASN
49	B0	41	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
21	AA	1530/1533 (99%)	248 (16%)	86 (5%)
22	A1	73/76 (96%)	15 (20%)	7 (9%)
23	A2	14/15 (93%)	5 (35%)	3 (21%)
24	A3	76/77 (98%)	13 (17%)	5 (6%)
54	BA	2902/2903 (99%)	464 (15%)	110 (3%)
55	BB	117/118 (99%)	15 (12%)	4 (3%)
All	All	4712/4722 (99%)	760 (16%)	215 (4%)

5 of 760 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
21	AA	6	G
21	AA	7	A
21	AA	8	A
21	AA	9	G
21	AA	16	A

5 of 215 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
54	BA	389	G
54	BA	1087	G
54	BA	2430	A
54	BA	529	A
54	BA	670	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	CM0	A1	34	21,22	21,26,27	1.37	2 (9%)	26,37,40	1.05	0
24	H2U	A3	21	24	18,21,22	1.39	2 (11%)	19,30,33	1.12	1 (5%)
24	5MU	A3	55	24	19,22,23	0.72	0	27,32,35	1.48	4 (14%)
24	PSU	A3	56	24	18,21,22	0.93	0	21,30,33	1.21	2 (9%)
24	4SU	A3	8	24	18,21,22	1.47	2 (11%)	25,30,33	0.82	1 (4%)
22	PSU	A1	55	22	18,21,22	0.81	0	21,30,33	1.23	2 (9%)
22	6MZ	A1	37	22	17,25,26	1.14	3 (17%)	15,36,39	1.66	3 (20%)
22	5MU	A1	54	22	19,22,23	0.78	0	27,32,35	1.52	5 (18%)
24	OMC	A3	33	24	19,22,23	0.79	0	25,31,34	1.19	2 (8%)
22	4SU	A1	7	22	18,21,22	1.55	2 (11%)	25,30,33	1.08	2 (8%)
22	7MG	A1	46	22	23,26,27	4.00	2 (8%)	27,39,42	1.47	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	CM0	A1	34	21,22	-	4/12/30/31	0/2/2/2
24	H2U	A3	21	24	-	0/7/38/39	0/2/2/2
24	5MU	A3	55	24	-	0/7/25/26	0/2/2/2
24	PSU	A3	56	24	-	0/7/25/26	0/2/2/2
24	4SU	A3	8	24	-	0/7/25/26	0/2/2/2
22	PSU	A1	55	22	-	0/7/25/26	0/2/2/2
22	6MZ	A1	37	22	-	0/5/27/28	0/3/3/3
22	5MU	A1	54	22	-	0/7/25/26	0/2/2/2
24	OMC	A3	33	24	-	0/9/27/28	0/2/2/2
22	4SU	A1	7	22	-	0/7/25/26	0/2/2/2
22	7MG	A1	46	22	-	1/7/37/38	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	-18.81	1.33	1.45
22	A1	7	4SU	C5-C4	-5.33	1.36	1.42
24	A3	8	4SU	C5-C4	-5.09	1.36	1.42

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	A1	34	CM0	O5-C5	-5.02	1.25	1.36
24	A3	21	H2U	C2-N3	-3.58	1.31	1.38

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	A1	46	7MG	N9-C8-N7	5.91	111.75	103.37
22	A1	37	6MZ	C9-N6-C6	4.61	127.12	122.85
22	A1	54	5MU	C5M-C5-C6	-4.06	117.36	122.85
24	A3	55	5MU	C5M-C5-C6	-3.71	117.83	122.85
22	A1	54	5MU	C6-C5-C4	3.45	120.86	118.02

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
22	A1	46	7MG	C4'-C5'-O5'-P
22	A1	34	CM0	O5-C7-C8-O8
22	A1	34	CM0	O5-C7-C8-O9
22	A1	34	CM0	C6-C5-O5-C7
22	A1	34	CM0	C4-C5-O5-C7

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
57	VAL	A1	101	22,58	4,6,7	0.80	0	6,7,9	1.55	1 (16%)
58	FME	BA	3001	57	8,9,10	0.59	0	8,9,11	1.06	0

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
57	VAL	A1	101	22,58	-	0/5/6/8	-
58	FME	BA	3001	57	-	1/7/9/11	-

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	-3.73	115.18	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.

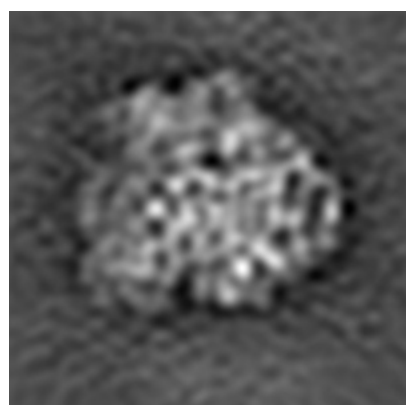
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1720. These allow visual inspection of the internal detail of the map and identification of artifacts.

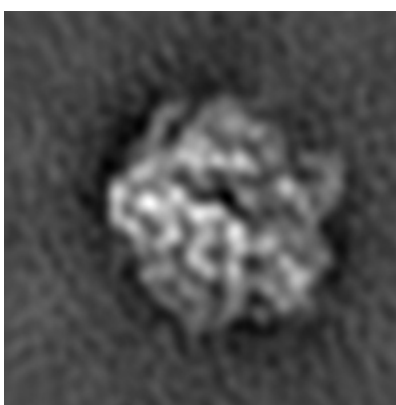
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

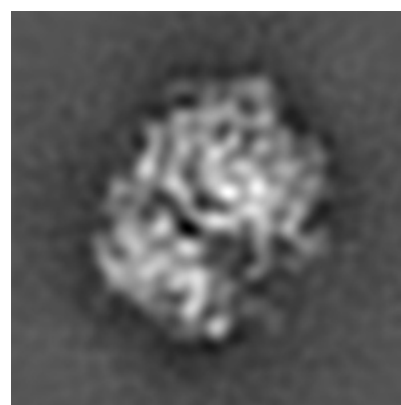
6.1.1 Primary map



X



Y



Z

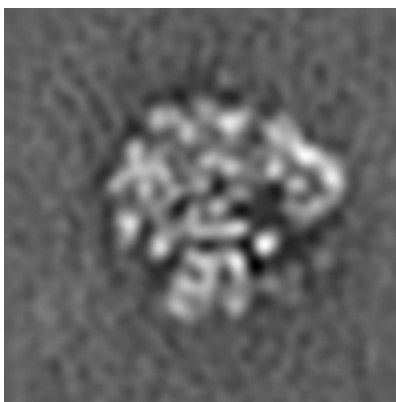
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

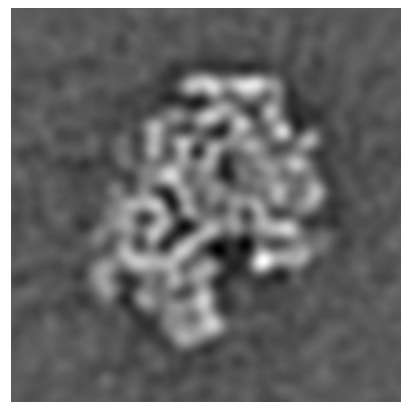
6.2.1 Primary map



X Index: 64



Y Index: 64



Z Index: 64

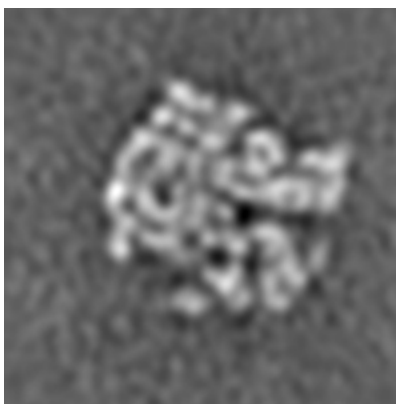
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

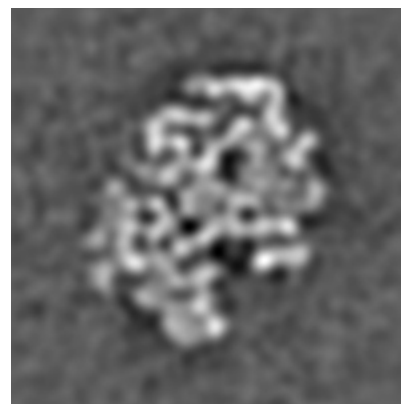
6.3.1 Primary map



X Index: 65



Y Index: 70

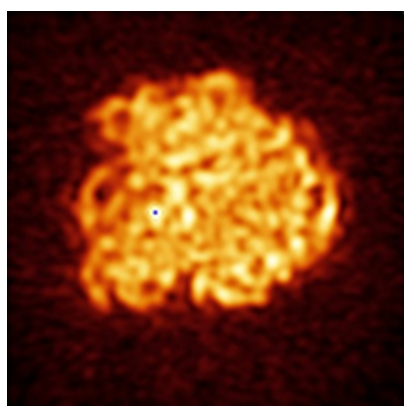


Z Index: 62

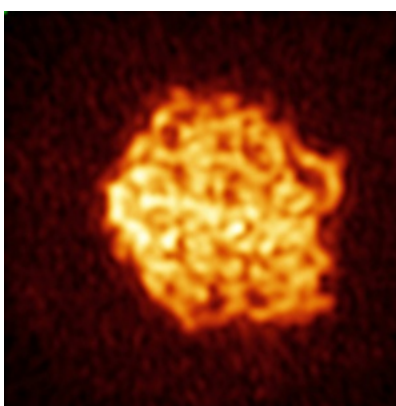
The images above show the largest variance slices of the map in three orthogonal directions.

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

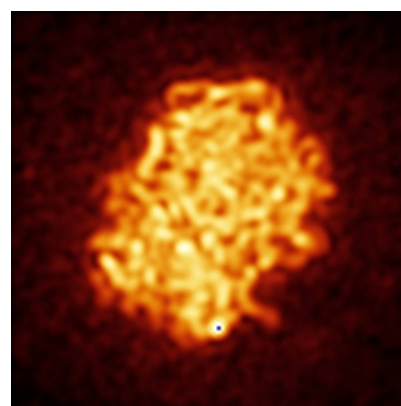
6.4.1 Primary map



X



Y

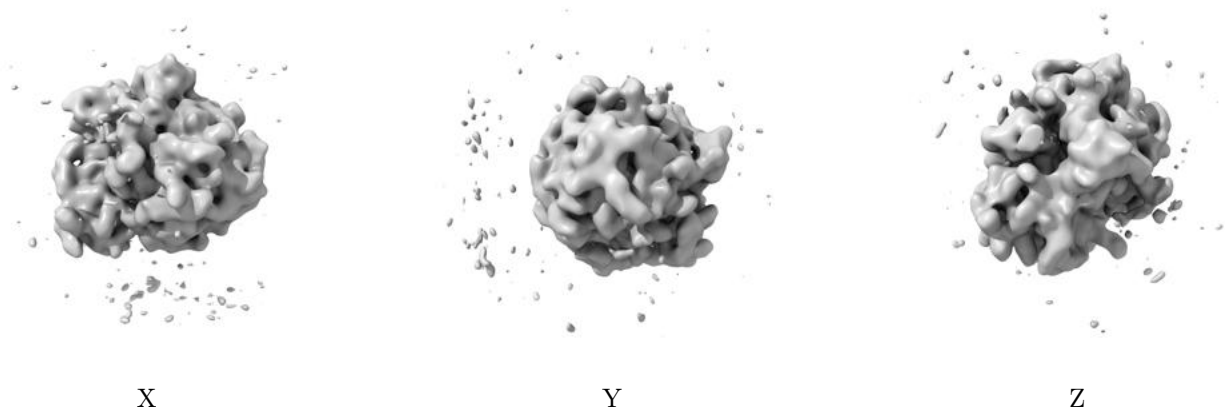


Z

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 20.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

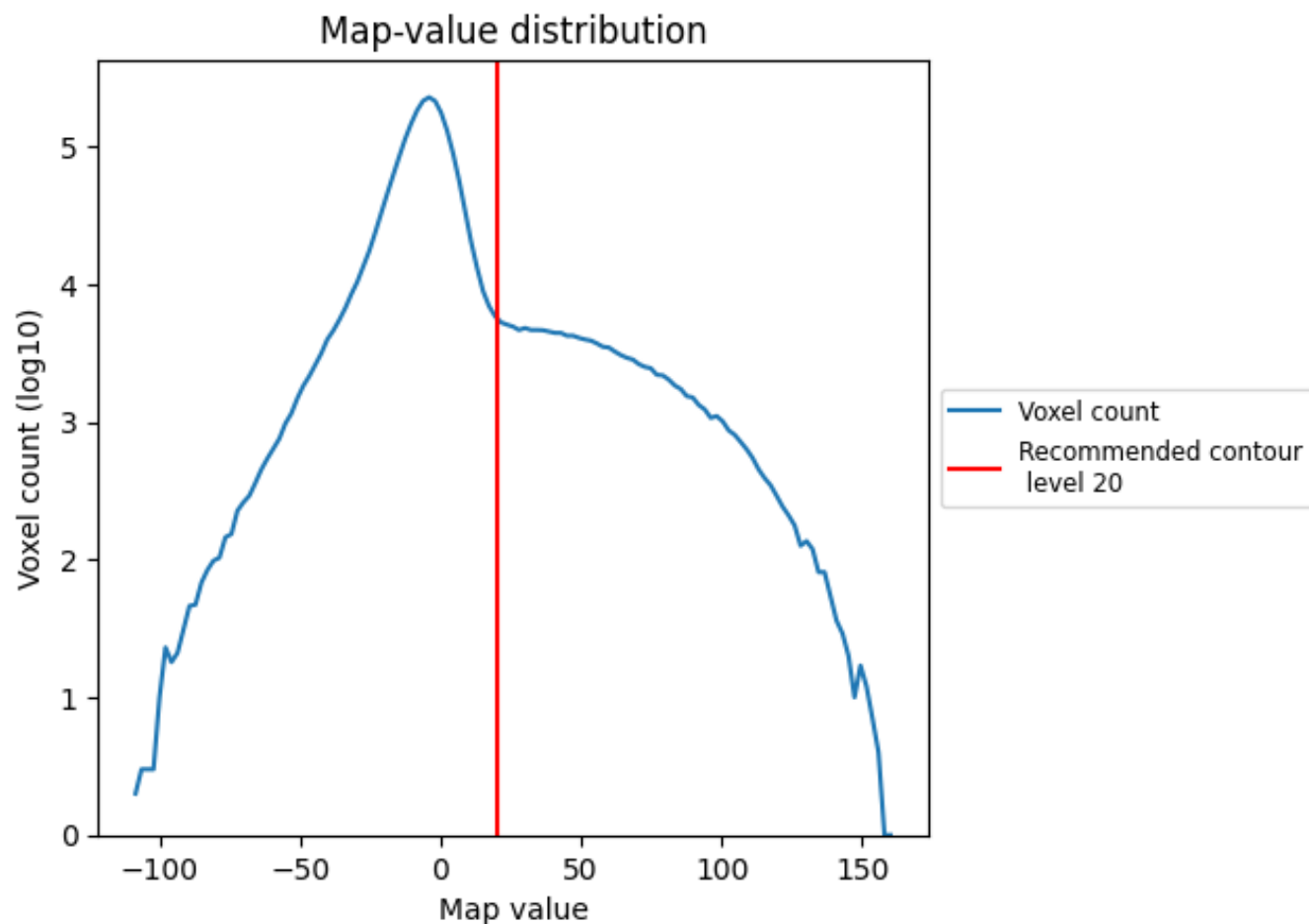
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

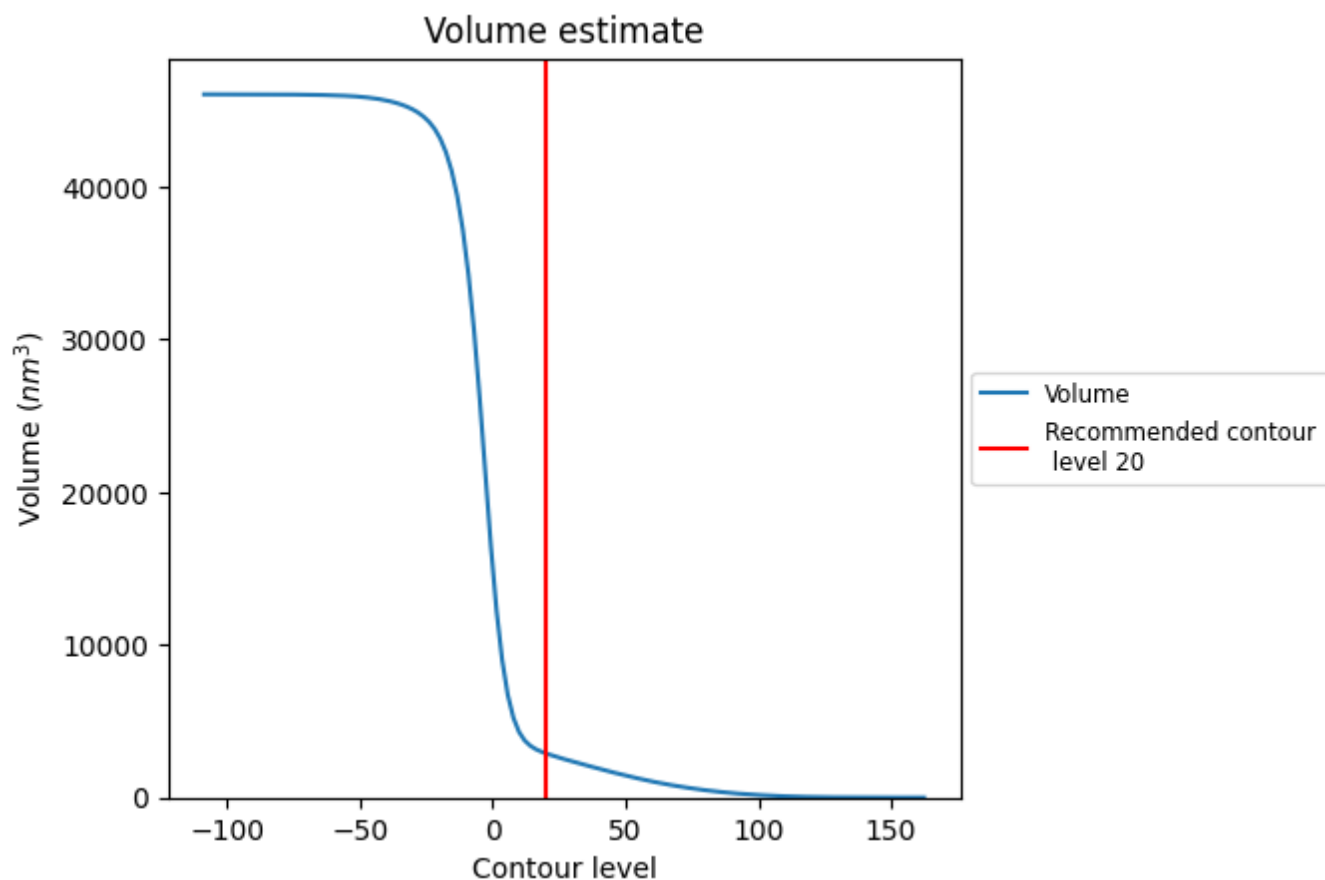
This section contains the results of statistical analysis of the map.

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.

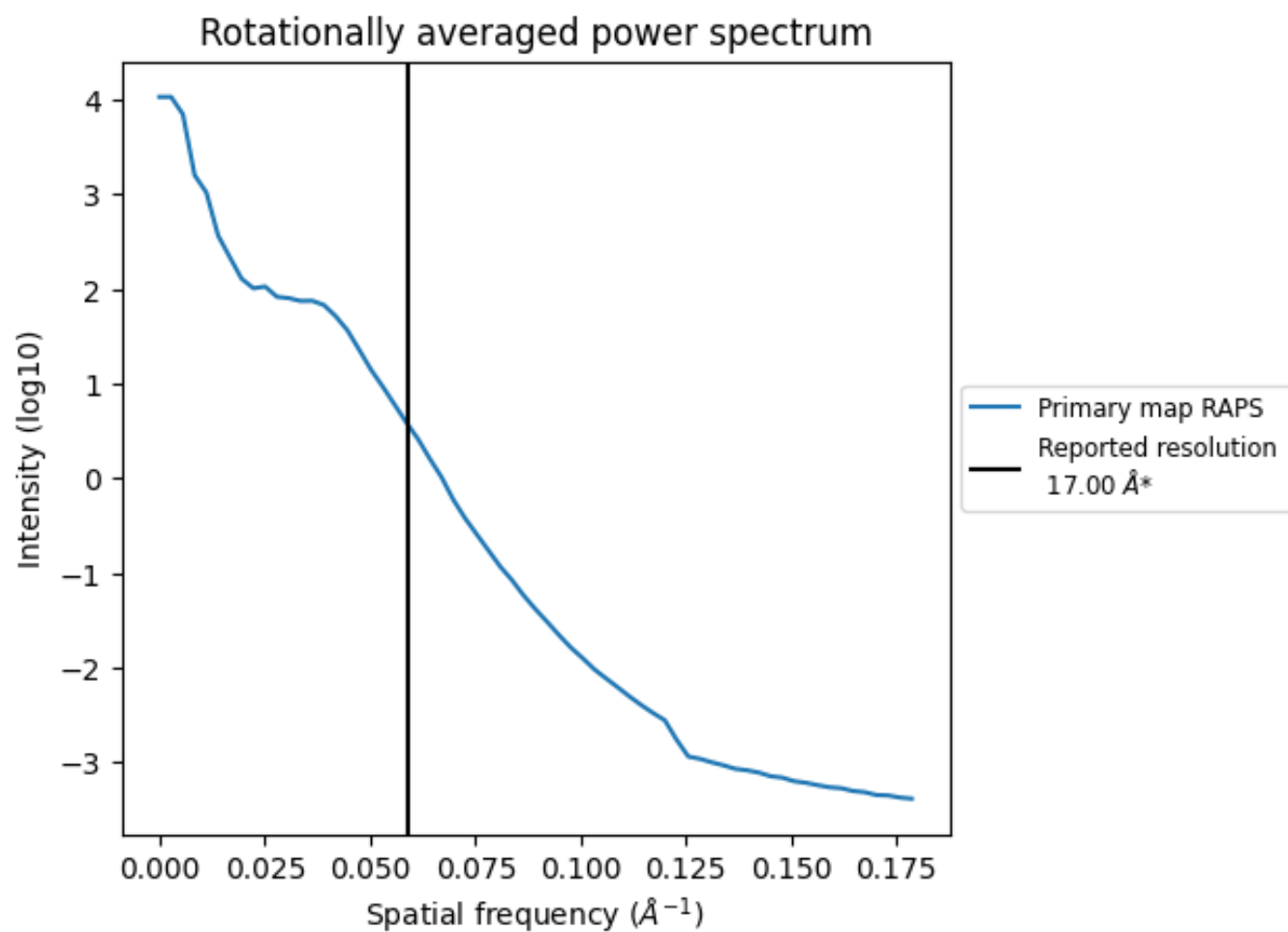
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2895 nm³; this corresponds to an approximate mass of 2615 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 0.059 Å⁻¹

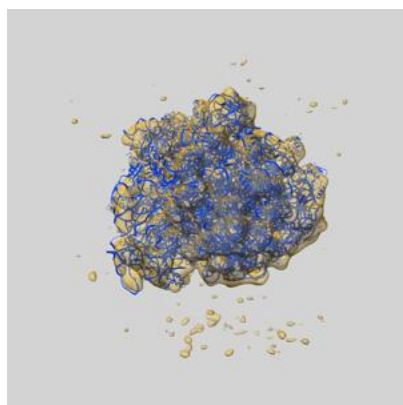
8 Fourier-Shell correlation

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

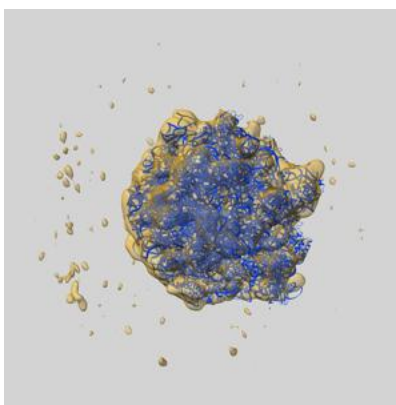
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-1720 and PDB model 4V74. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

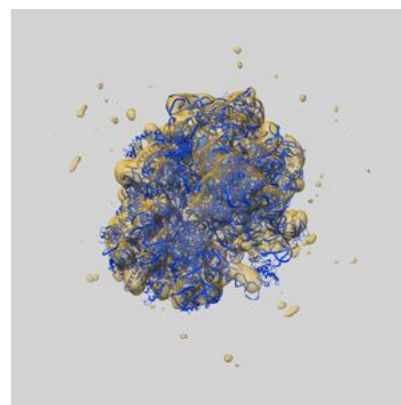
9.1 Map-model overlay [i](#)



X



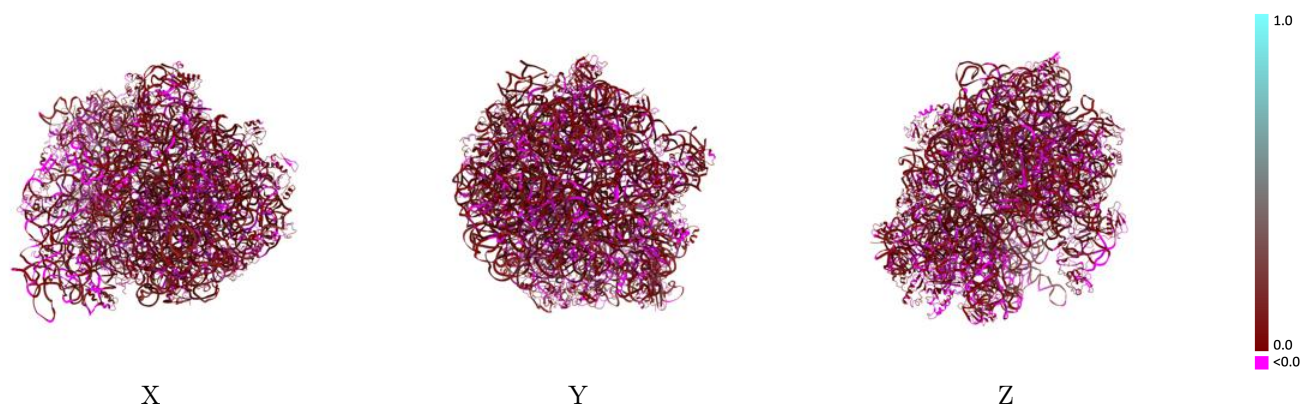
Y



Z

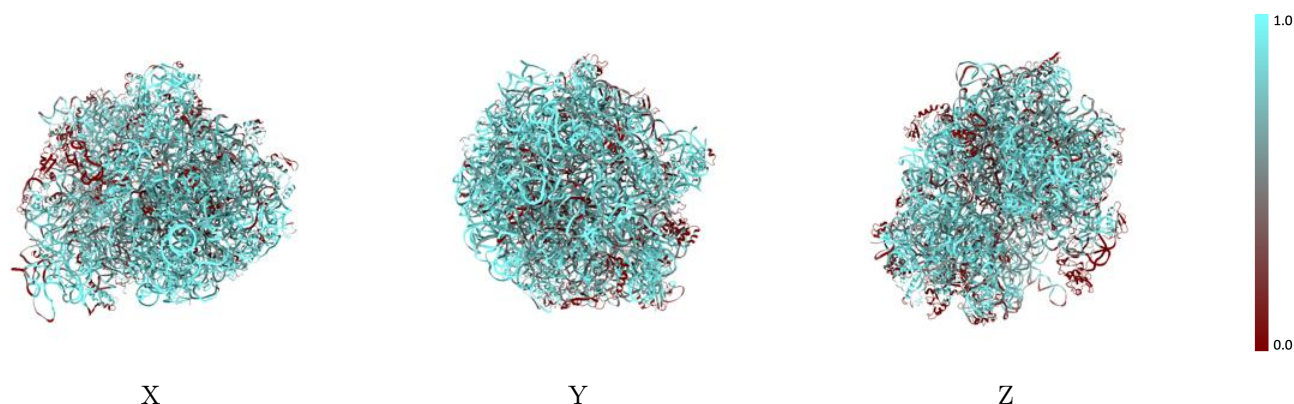
The images above show the 3D surface view of the map at the recommended contour level 20.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



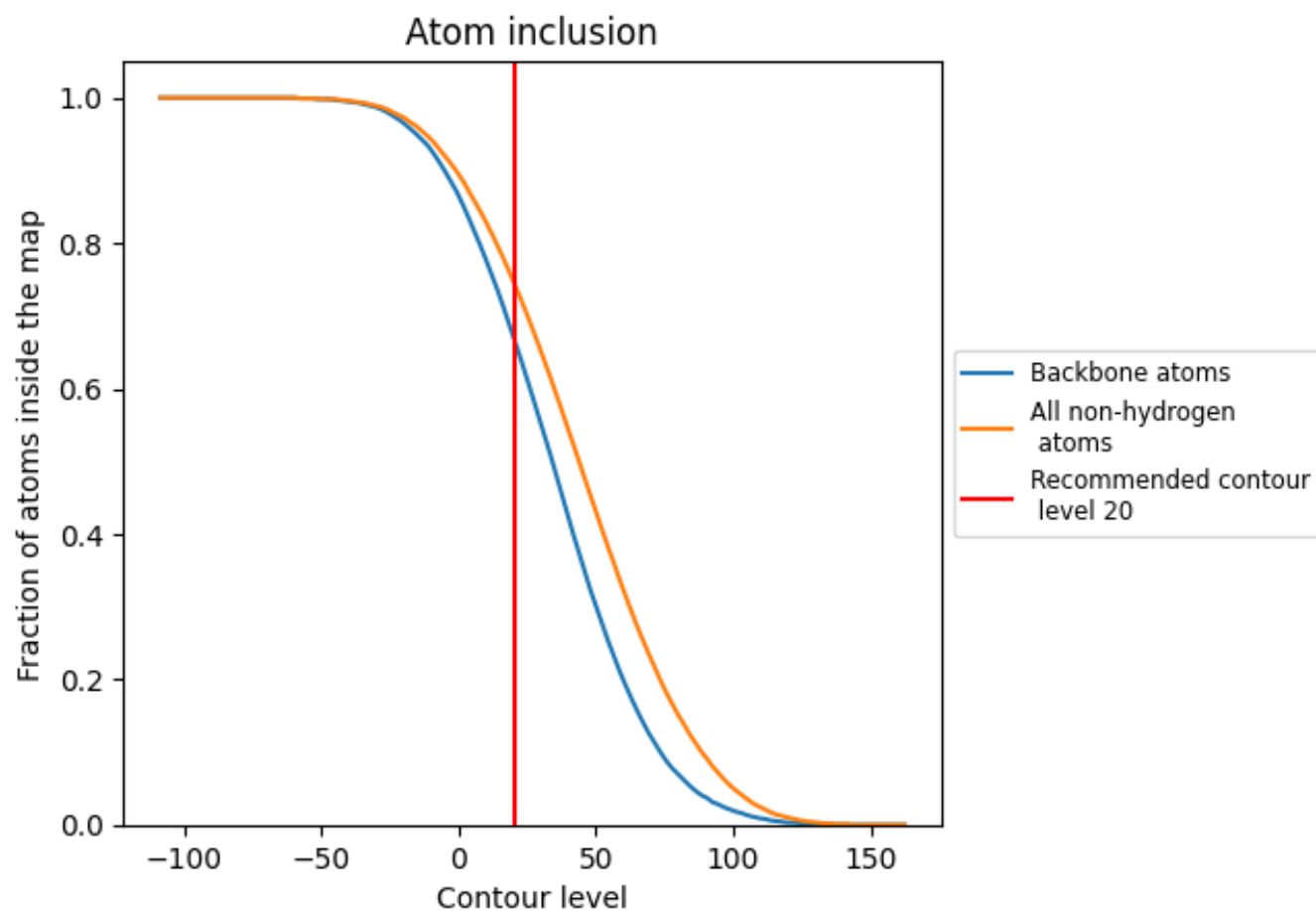
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (20).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 67% of all backbone atoms, 75% 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 (20) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7470	 0.0520
A1	 0.6960	 0.0570
A2	 0.7730	 0.0820
A3	 0.7100	 0.0620
AA	 0.8140	 0.0590
AB	 0.5490	 0.0480
AC	 0.4720	 0.0200
AD	 0.5570	 0.0210
AE	 0.5530	 0.0290
AF	 0.8130	 0.0430
AG	 0.7020	 0.0390
AH	 0.6570	 0.0280
AI	 0.6240	 0.0300
AJ	 0.7700	 0.0250
AK	 0.7090	 0.0460
AL	 0.6170	 0.0240
AM	 0.6730	 0.0350
AN	 0.5580	 0.0250
AO	 0.9090	 0.0320
AP	 0.5250	 -0.0030
AQ	 0.6470	 0.0240
AR	 0.6610	 0.0150
AS	 0.7280	 0.0360
AT	 0.7130	 -0.0010
AU	 0.5550	 0.0350
B0	 0.6820	 0.0130
B1	 0.7010	 0.0550
B2	 0.4680	 0.0060
B3	 0.4520	 -0.0330
B4	 0.6470	 0.0220
B5	 0.5700	 0.0360
BA	 0.8150	 0.0680
BB	 0.8850	 0.0740
BC	 0.4540	 -0.0050
BD	 0.6380	 0.0320



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
BE	 0.6180	 0.0150
BF	 0.7330	 0.0500
BG	 0.5780	 0.0360
BH	 0.1410	 0.0060
BI	 0.0000	 -0.0000
BJ	 0.6790	 0.0210
BK	 0.5450	 0.0280
BL	 0.6460	 0.0230
BM	 0.5870	 0.0190
BN	 0.8300	 0.0250
BO	 0.8390	 0.0260
BP	 0.5480	 0.0270
BQ	 0.5740	 -0.0130
BR	 0.7060	 0.0470
BS	 0.6320	 0.0290
BT	 0.7110	 0.0300
BU	 0.6640	 0.0110
BV	 0.6710	 0.0320
BW	 0.5340	 -0.0070
BX	 0.6340	 0.0030
BY	 0.5250	 0.0260
BZ	 0.6380	 0.0530