



wwPDB EM Validation Summary Report ⓘ

Oct 30, 2024 – 09:21 AM EDT

PDB ID : 4V78
EMDB ID : EMD-2475
Title : E. coli 70S-fMetVal-tRNAVal-tRNAfMet complex in intermediate post-translocation state (post3a)
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 : 20.00 Å(reported)
Based on initial models : 2WRI, 2K4C, 3I1O, 2HGP

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

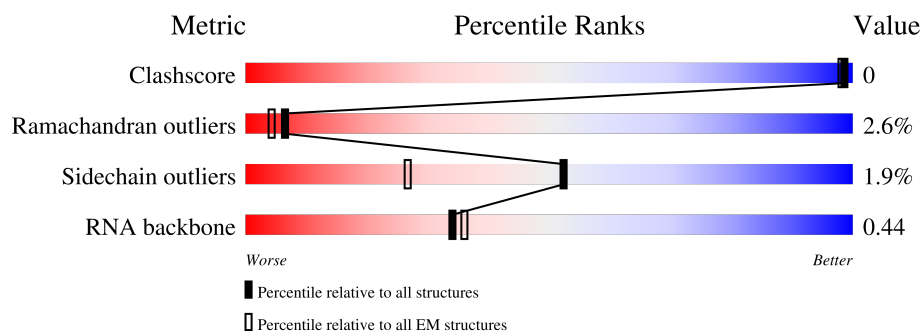
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 20.00 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>35%</div> <div>94%</div> <div>5%</div> </div>
2	AC	208	<div> <div>37%</div> <div>87%</div> <div>12%</div> </div>
3	AD	206	<div> <div>22%</div> <div>86%</div> <div>12%</div> </div>
4	AE	152	<div> <div>23%</div> <div>94%</div> <div>6%</div> </div>
5	AF	101	<div> <div>49%</div> <div>87%</div> <div>13%</div> </div>
6	AG	152	<div> <div>14%</div> <div>88%</div> <div>11%</div> </div>
7	AH	130	<div> <div>8%</div> <div>92%</div> <div>8%</div> </div>

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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	

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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

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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		

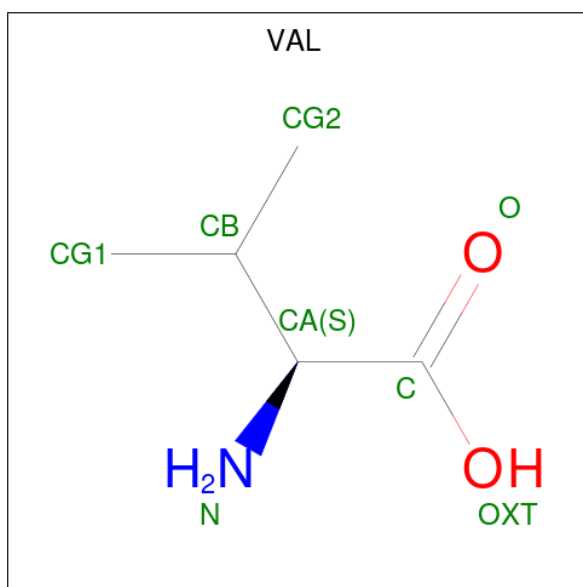
- Molecule 55 is a RNA chain called 5S ribosomal RNA.

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.

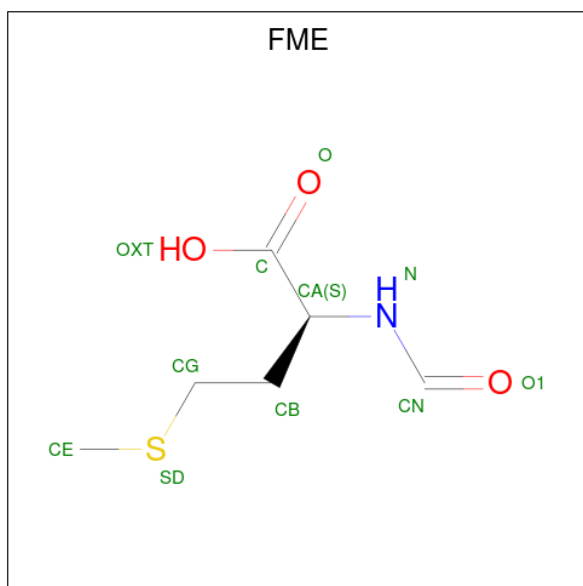
Mol	Chain	Residues	Atoms					AltConf	Trace
56	B5	223	Total	C	N	O	S	0	0
			1658	1038	302	312	6		

- Molecule 57 is VALINE (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).

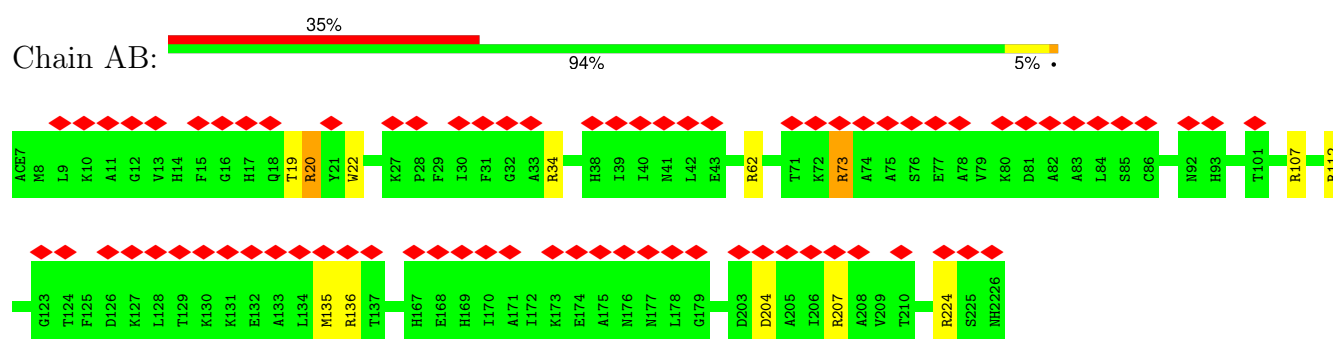


Mol	Chain	Residues	Atoms					AltConf
58	BA	1	Total	C	N	O	S	0
			10	6	1	2	1	

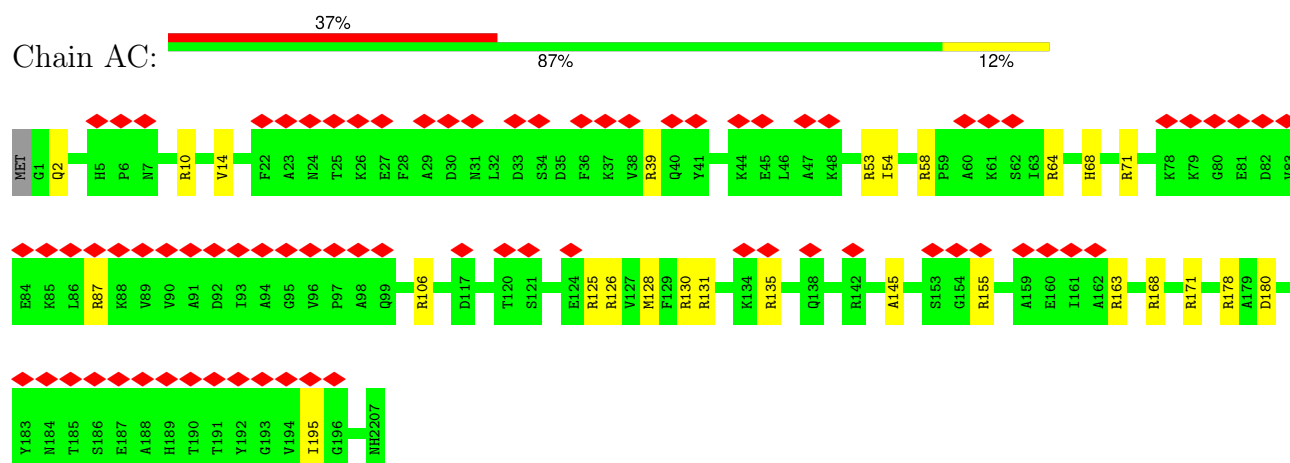
3 Residue-property plots [i](#)

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.

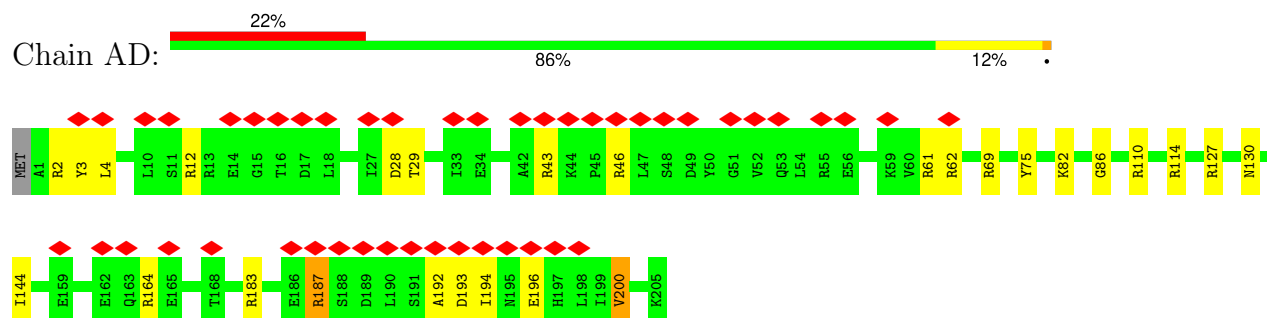
- Molecule 1: 30S ribosomal protein S2



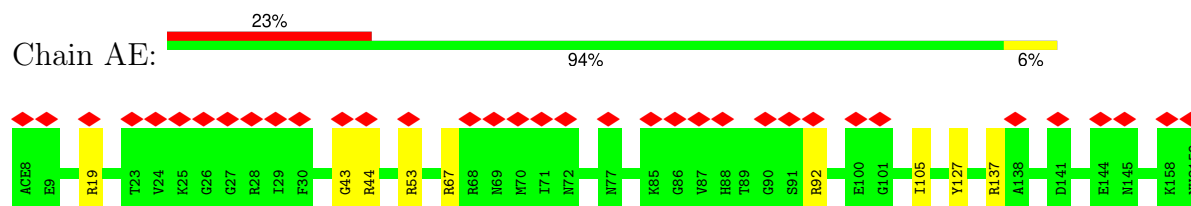
- Molecule 2: 30S ribosomal protein S3



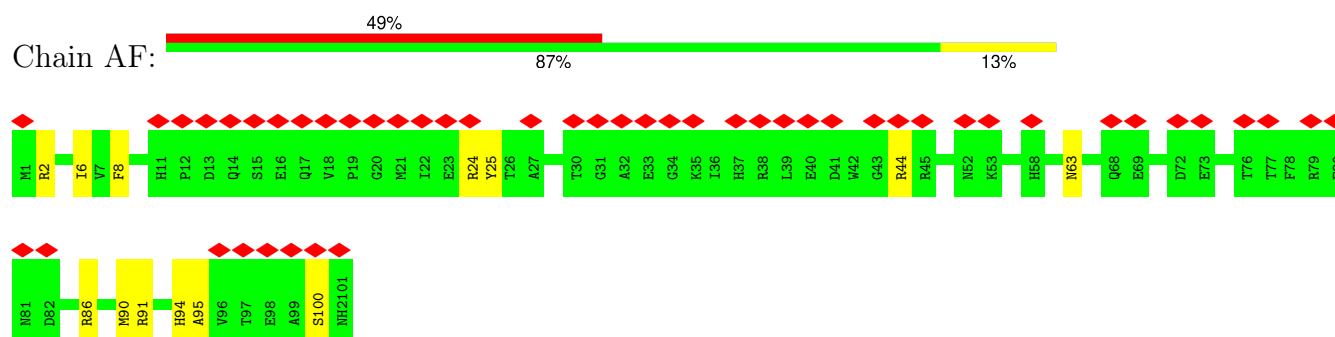
- Molecule 3: 30S ribosomal protein S4



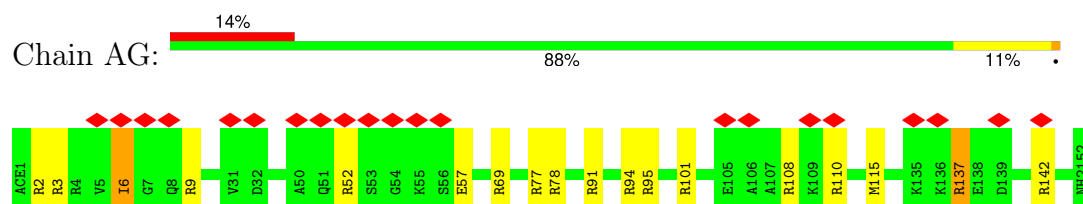
- Molecule 4: 30S ribosomal protein S5



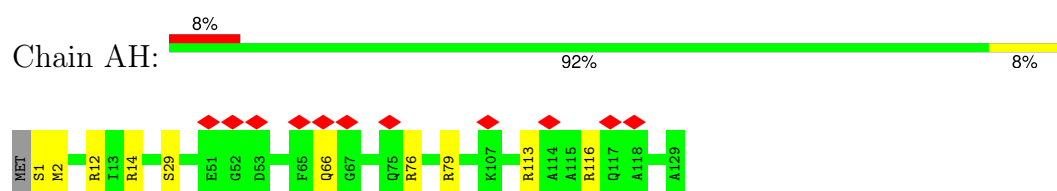
- Molecule 5: 30S ribosomal protein S6



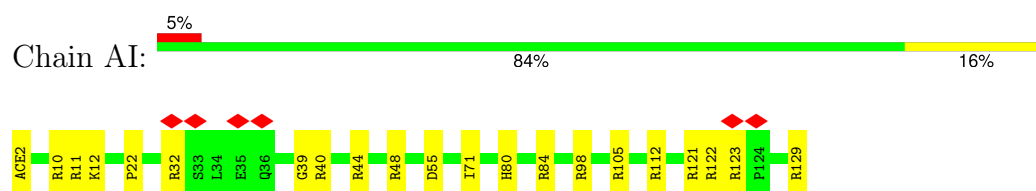
- Molecule 6: 30S ribosomal protein S7



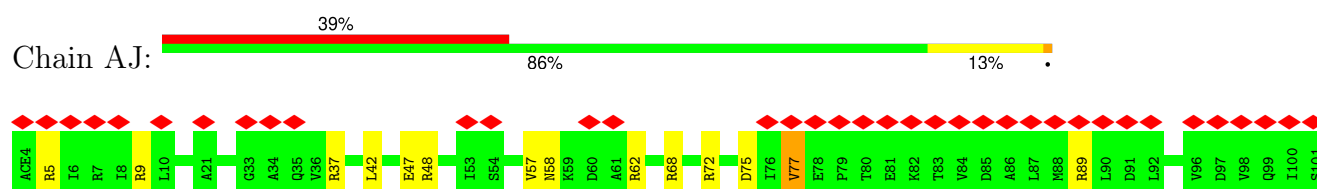
- Molecule 7: 30S ribosomal protein S8



- Molecule 8: 30S ribosomal protein S9

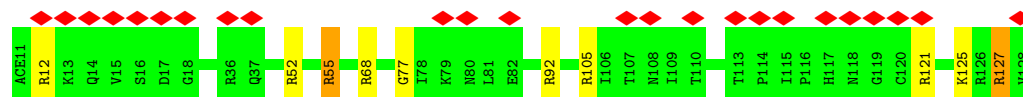


- Molecule 9: 30S ribosomal protein S10

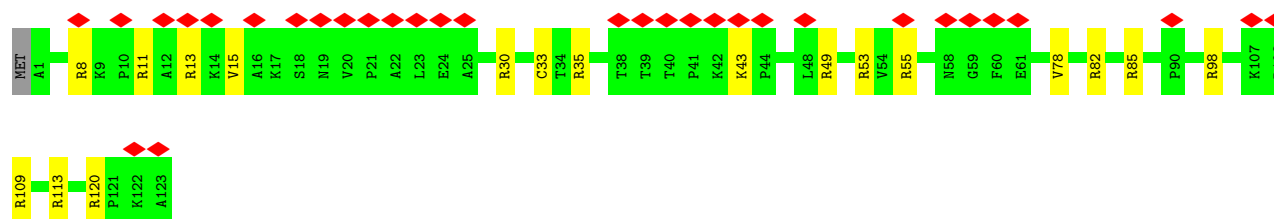
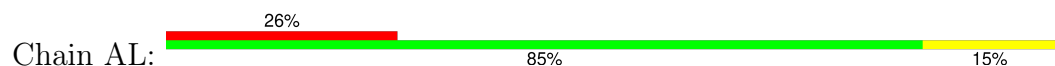




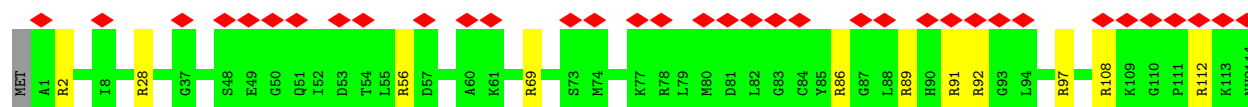
- Molecule 10: 30S ribosomal protein S11



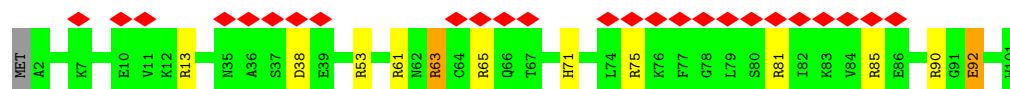
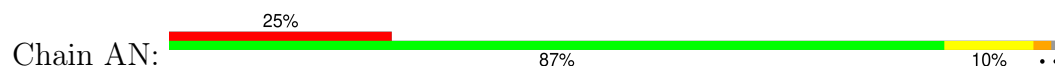
- Molecule 11: 30S ribosomal protein S12



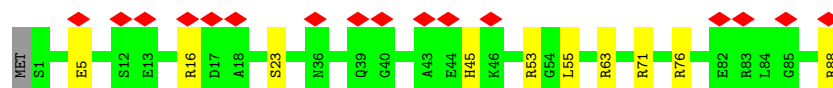
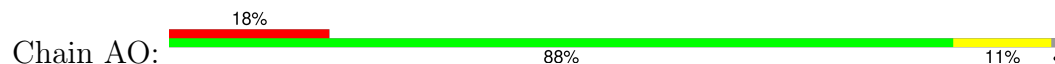
- Molecule 12: 30S ribosomal protein S13



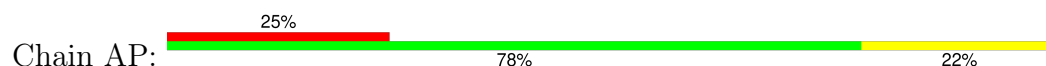
- Molecule 13: 30S ribosomal protein S14

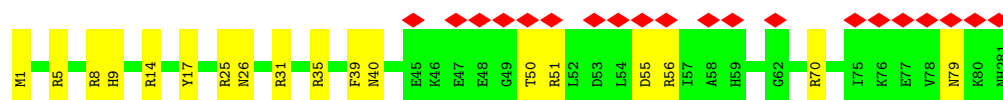


- Molecule 14: 30S ribosomal protein S15

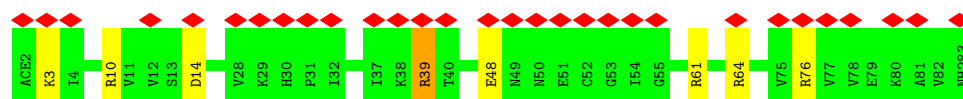
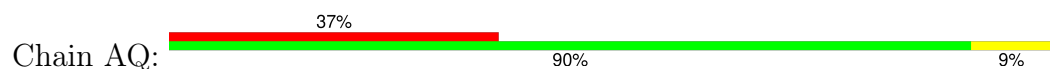


- Molecule 15: 30S ribosomal protein S16

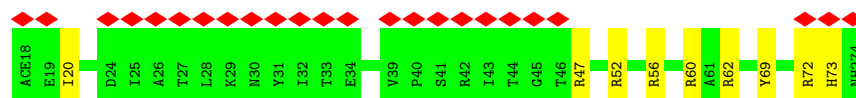
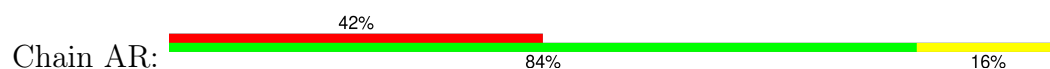




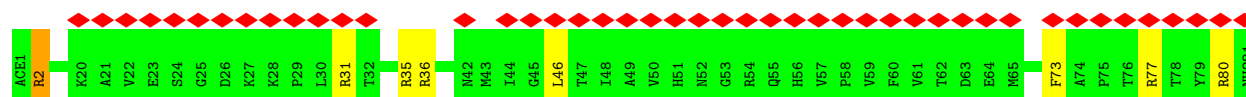
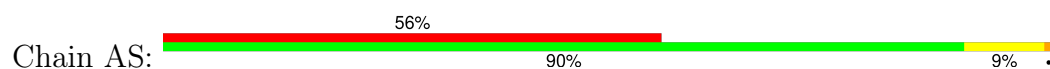
- Molecule 16: 30S ribosomal protein S17



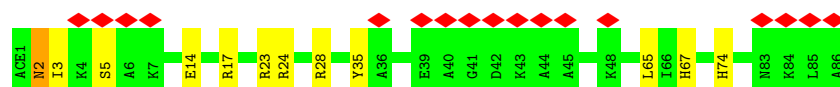
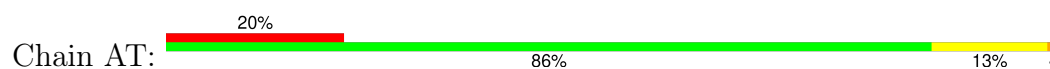
- Molecule 17: 30S ribosomal protein S18



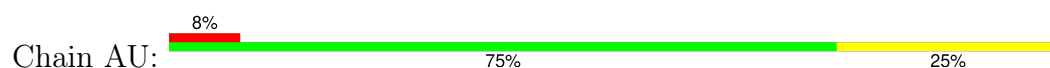
- Molecule 18: 30S ribosomal protein S19



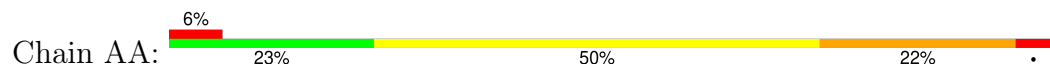
- Molecule 19: 30S ribosomal protein S20

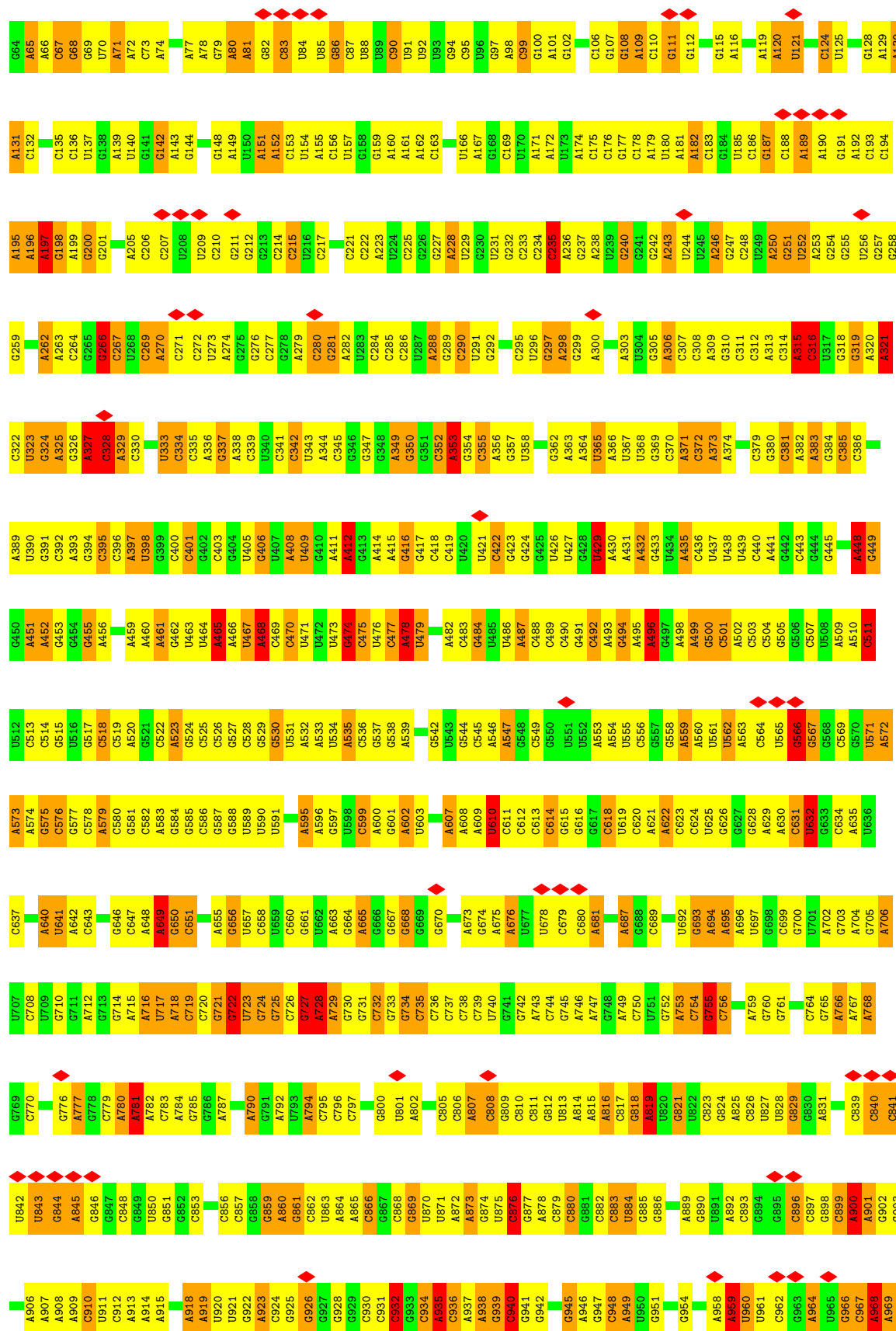


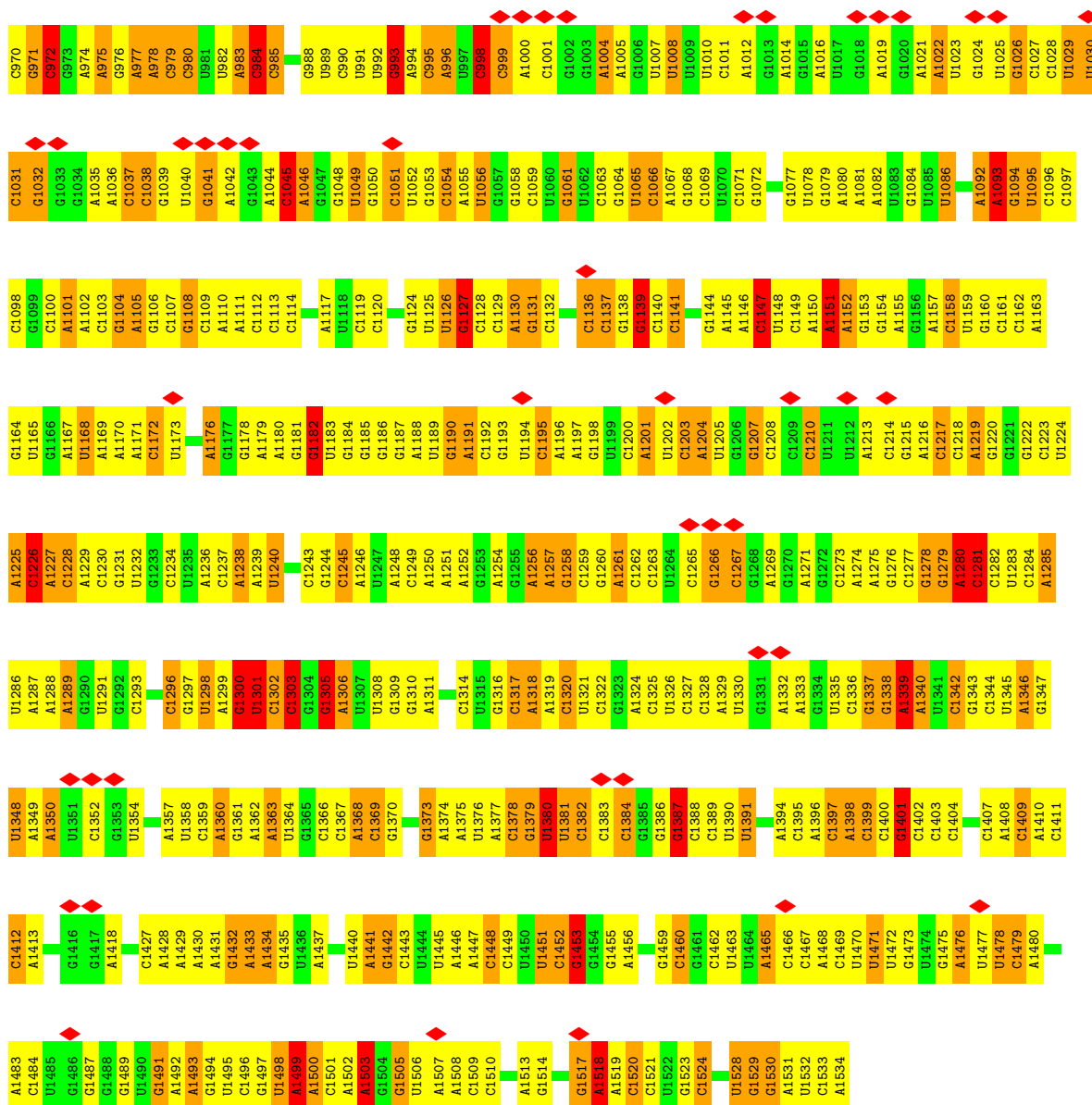
- Molecule 20: 30S ribosomal protein S21



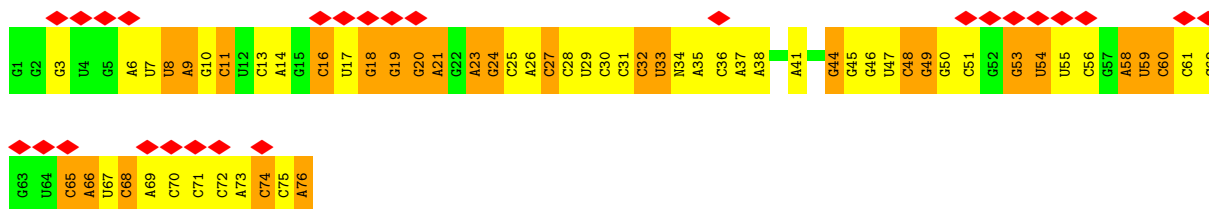
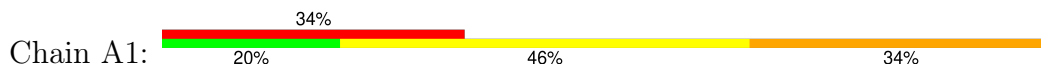
- Molecule 21: 16S ribosomal RNA





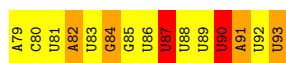


• Molecule 22: fMet-Val-tRNA-Val

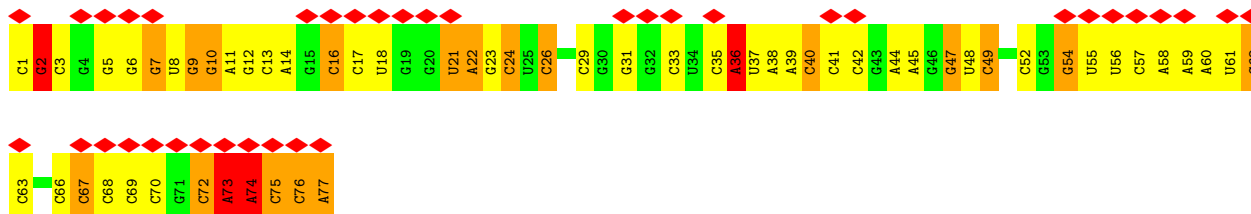


• Molecule 23: 5'-R(*AP*CP*UP*AP*UP*GP*GP*UP*UP*UP*UP*UP*AP*UP*U)-3'

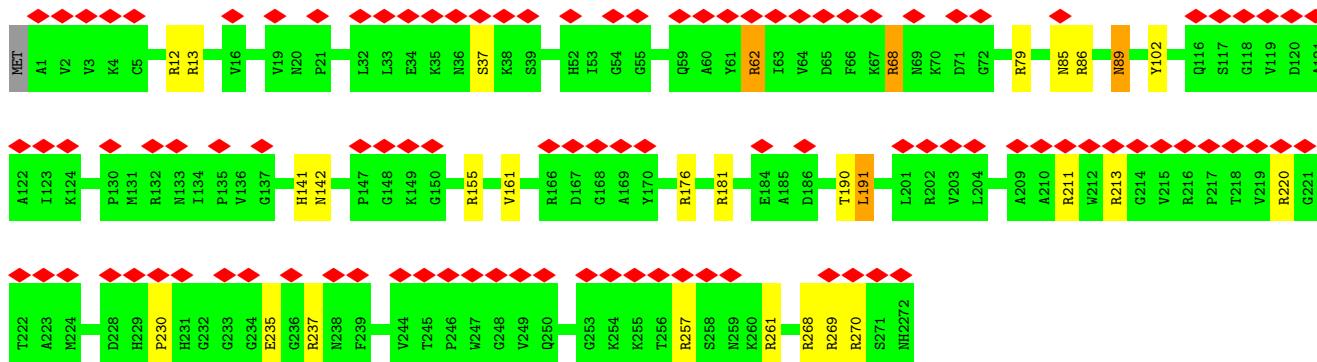
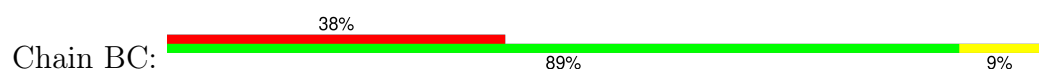




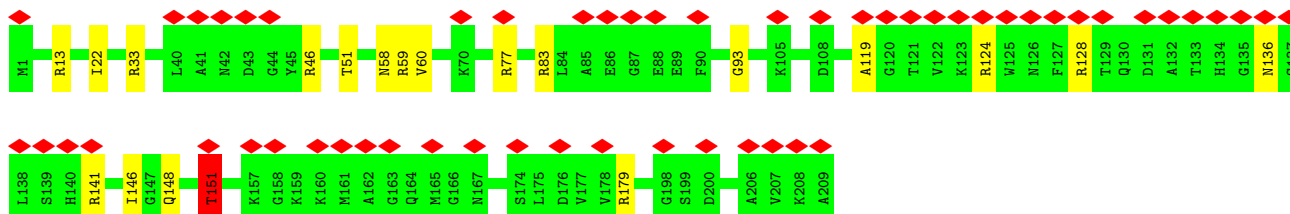
• Molecule 24: tRNA-fMet



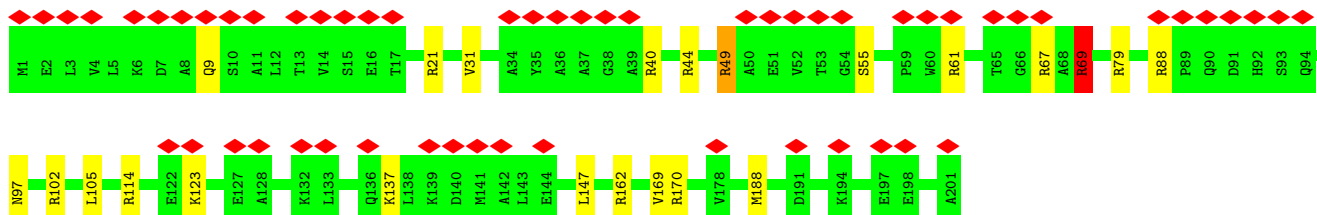
• Molecule 25: 50S ribosomal protein L2



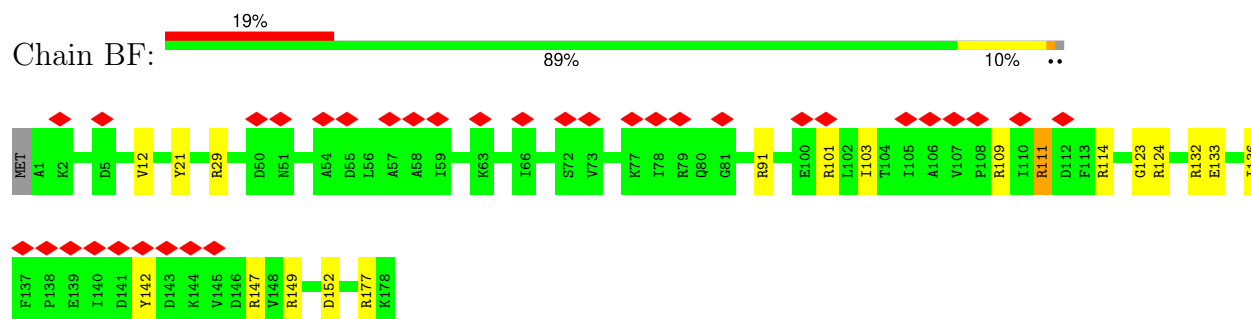
• Molecule 26: 50S ribosomal protein L3



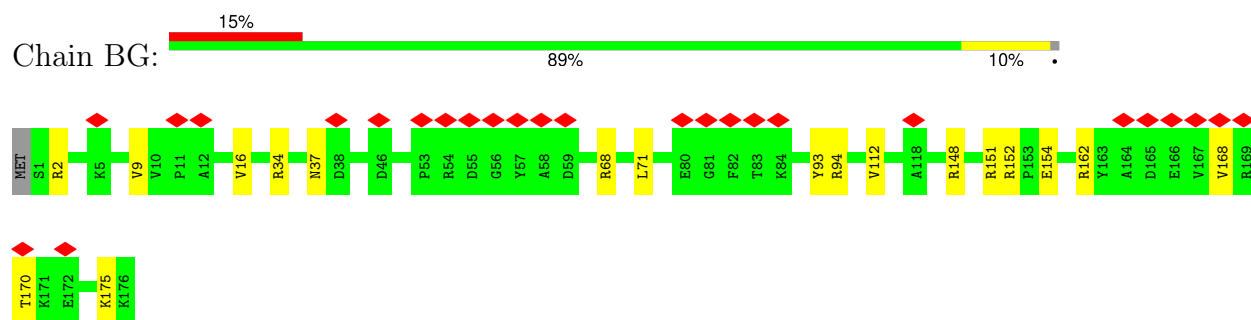
• Molecule 27: 50S ribosomal protein L4



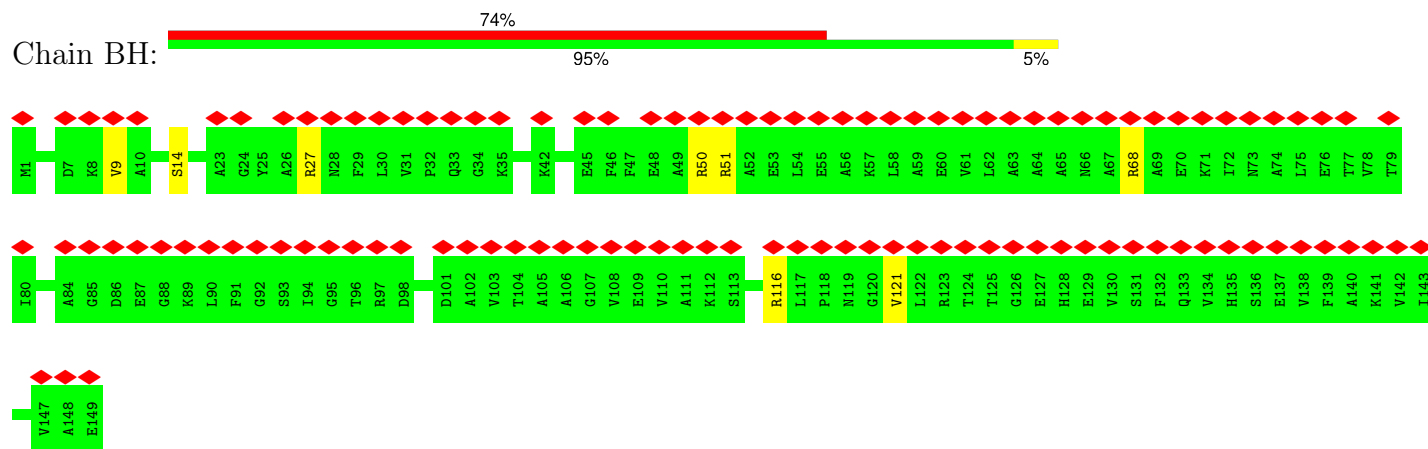
- Molecule 28: 50S ribosomal protein L5



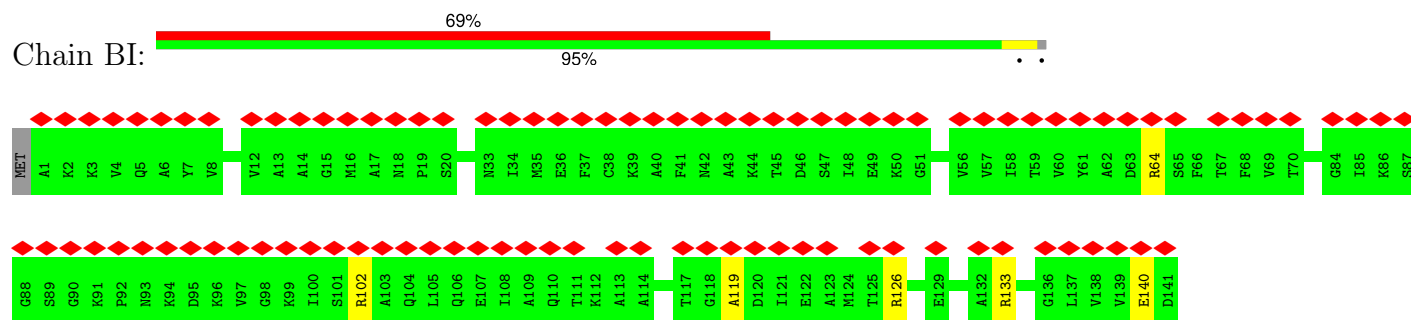
- Molecule 29: 50S ribosomal protein L6



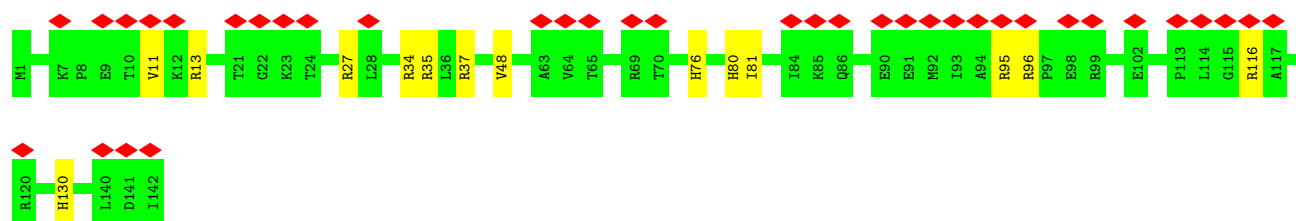
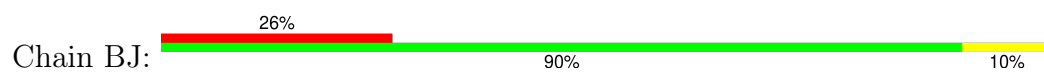
- Molecule 30: 50S ribosomal protein L9



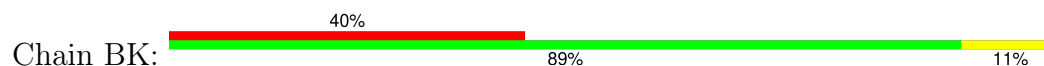
- Molecule 31: 50S ribosomal protein L11



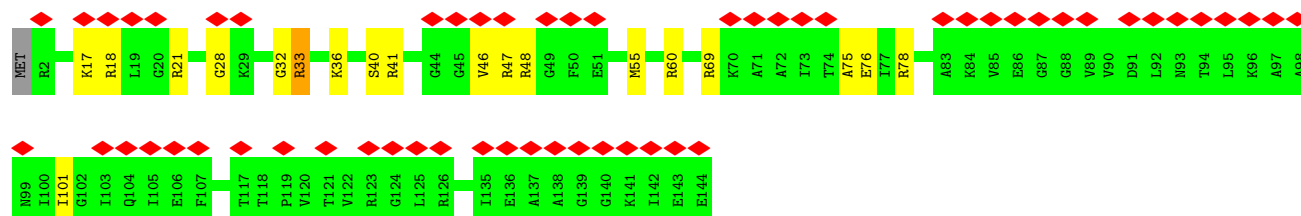
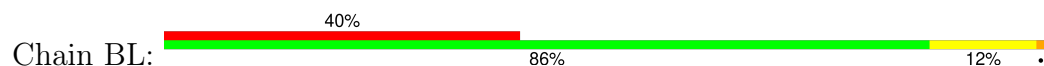
- Molecule 32: 50S ribosomal protein L13



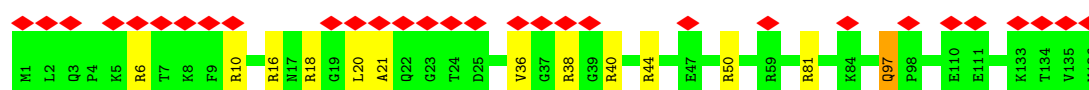
- Molecule 33: 50S ribosomal protein L14



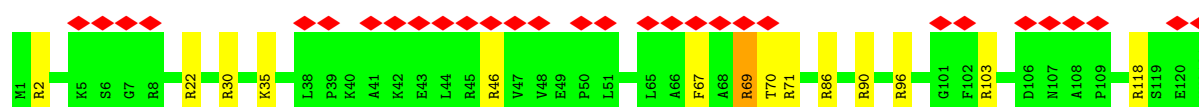
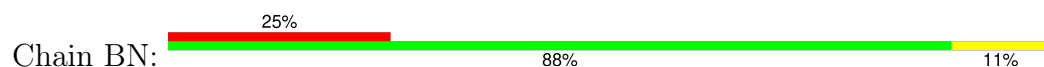
- Molecule 34: 50S ribosomal protein L15




- Molecule 35: 50S ribosomal protein L16

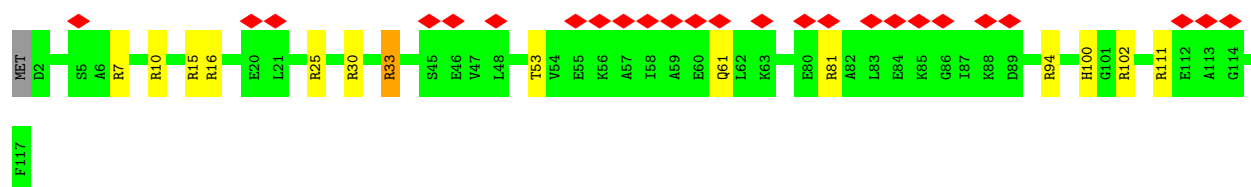


- Molecule 36: 50S ribosomal protein L17




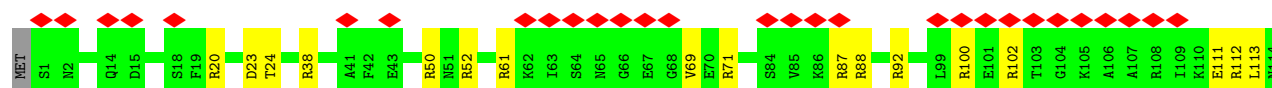
- Molecule 37: 50S ribosomal protein L18

Chain BO: 




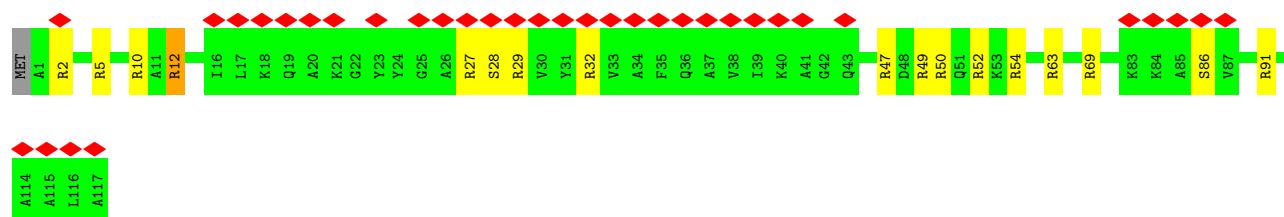
- Molecule 38: 50S ribosomal protein L19

Chain BP: 

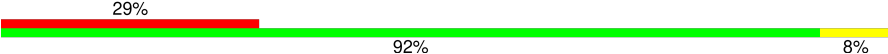


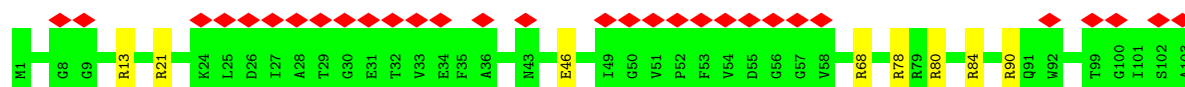
- Molecule 39: 50S ribosomal protein L20

Chain BQ: 



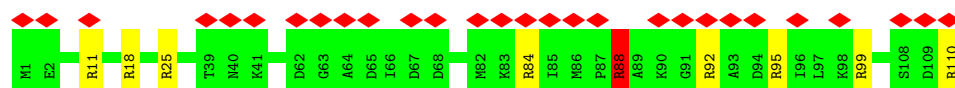
- Molecule 40: 50S ribosomal protein L21

Chain BR: 




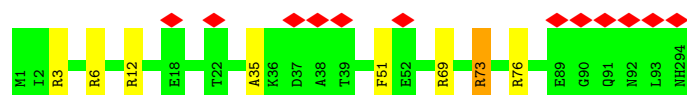
- Molecule 41: 50S ribosomal protein L22

Chain BS: 

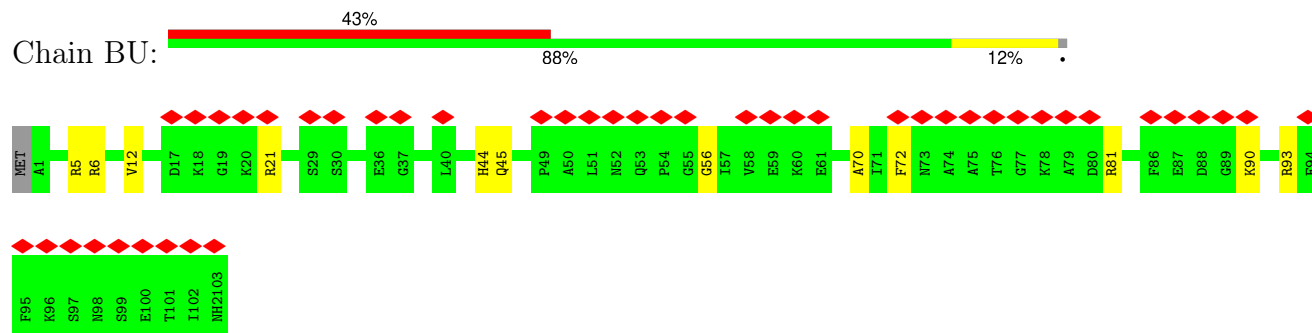


- Molecule 42: 50S ribosomal protein L23

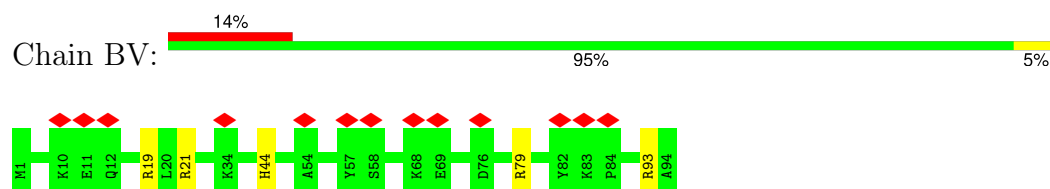
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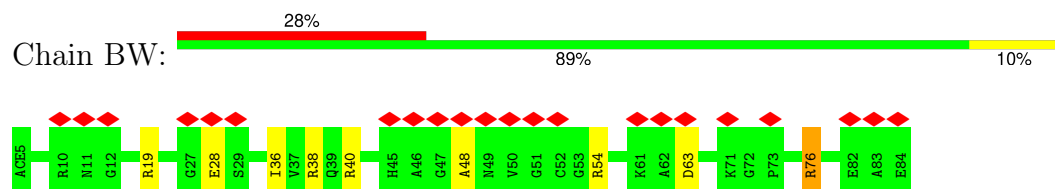
- Molecule 43: 50S ribosomal protein L24



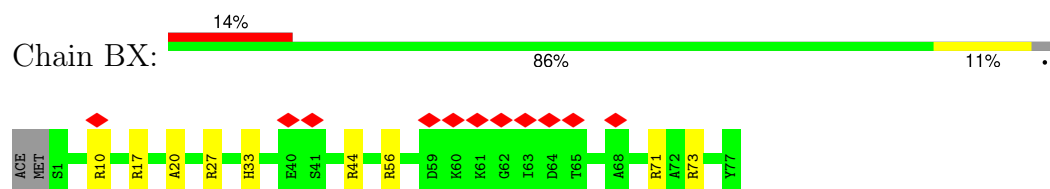
- Molecule 44: 50S ribosomal protein L25



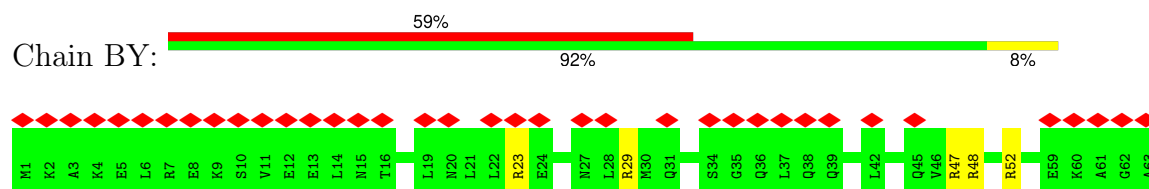
- Molecule 45: 50S ribosomal protein L27



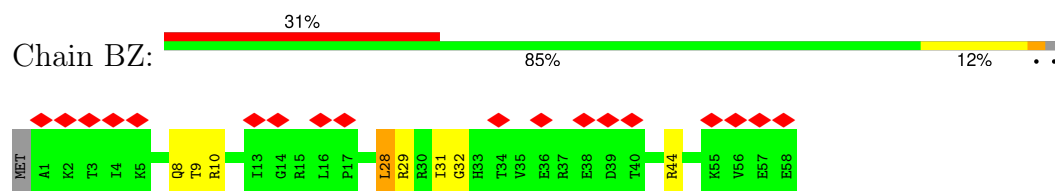
- Molecule 46: 50S ribosomal protein L28



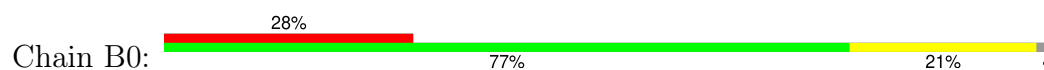
- Molecule 47: 50S ribosomal protein L29



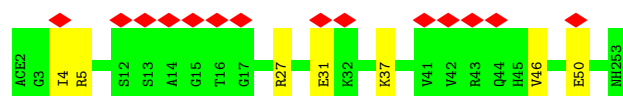
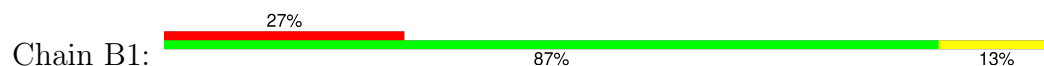
- Molecule 48: 50S ribosomal protein L30



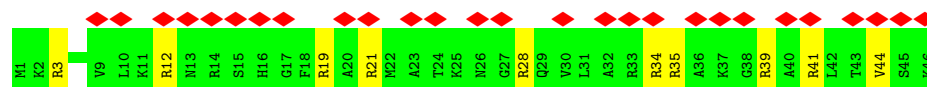
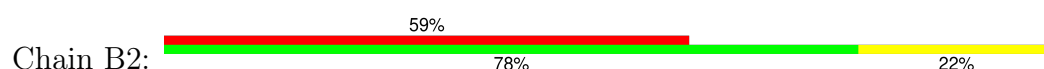
- Molecule 49: 50S ribosomal protein L32



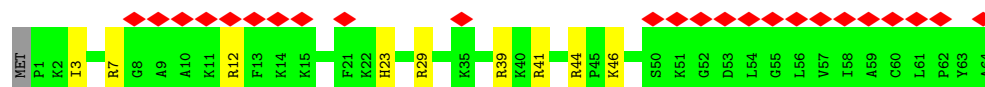
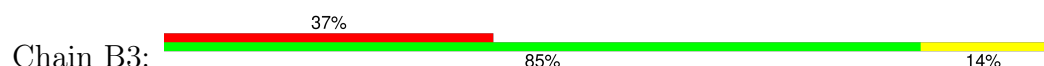
- Molecule 50: 50S ribosomal protein L33



- Molecule 51: 50S ribosomal protein L34



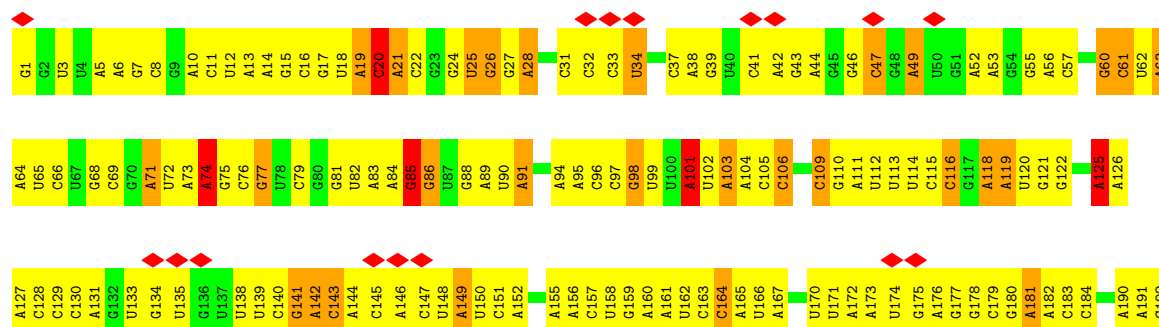
- Molecule 52: 50S ribosomal protein L35



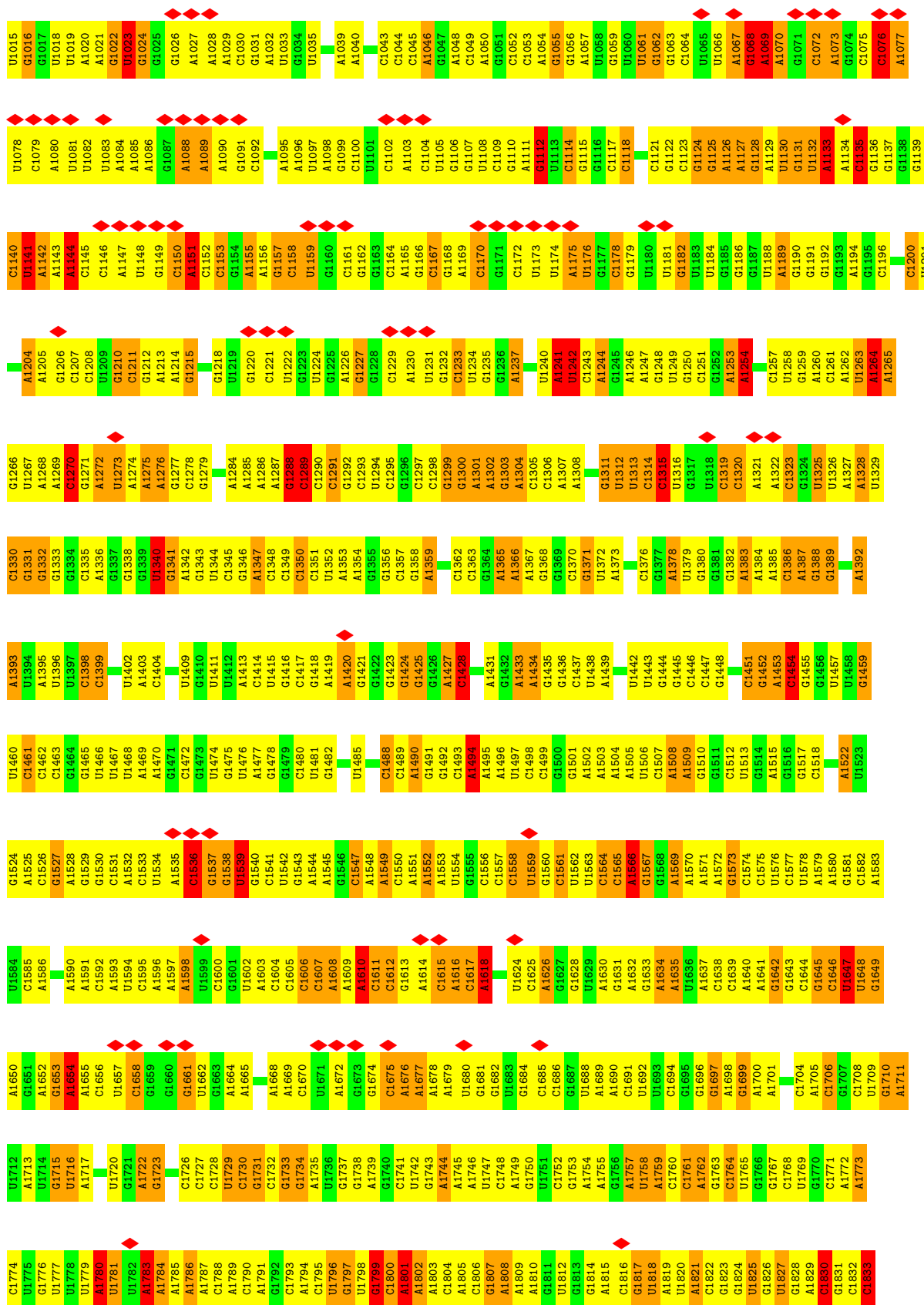
- Molecule 53: 50S ribosomal protein L36



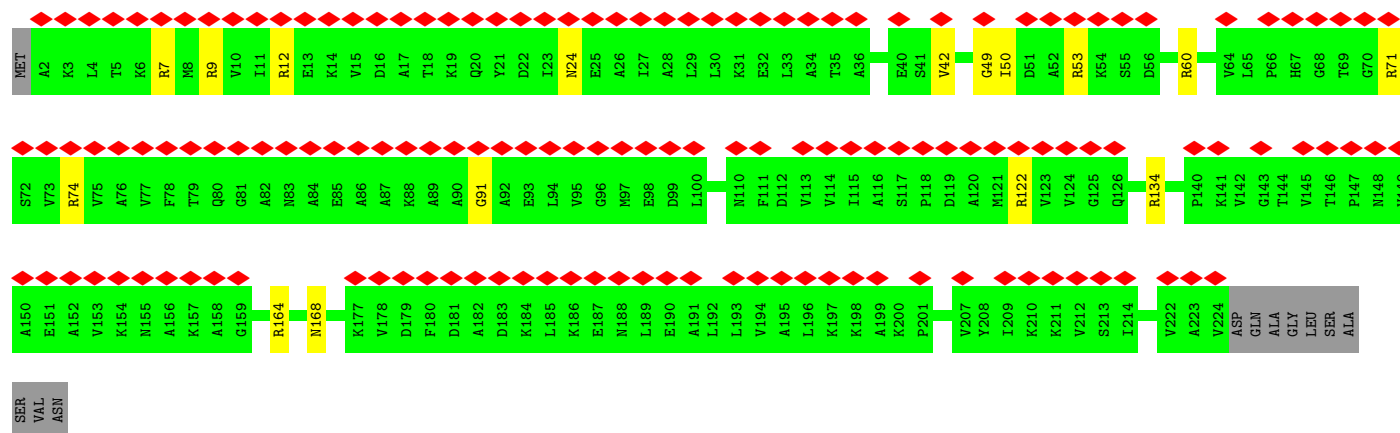
- Molecule 54: 23S ribosomal RNA







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G2594	G2595	G2527	G2342	G2280	G2255	U2402	G2343	G2281	U2213	U2151	U2085	G2025	U1899	A1900	C1836	
G2596	G2597	G2528	G2344	G2282	G2256	U2403	G2345	G2283	U2214	G2152	G2086	U2026	U1963	A1901	C1837	
G2598	G2599	G2529	U2346	G2284	G2257	U2404	G2347	G2285	G2215	C2153	G2087	U2027	U1964	A1902	C1838	
G2600	G2601	G2530	G2348	G2286	G2258	G2405	G2349	G2287	G2216	C2154	G2088	G2028	U1965	A1903	G1839	
G2602	G2603	G2531	G2350	G2288	G2259	G2406	G2351	G2289	U2220	U2155	A2090	G2029	U1966	G1904	G1840	
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G2606	G2607	G2533	G2354	U2292	G2261	U2408	G2355	G2291	G2222	G2157	U2092	G2032	C1968	C1905	G1843	
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G2642	G2643	G2551	G2390	G2313	G2279	G2426	G2391	G2313	G2238	G2175	A2114	C2050	C1990	U1928	U1864	
G2644	G2645	G2552	G2392	G2314	G2280	G2427	G2393	G2314	G2239	G2176	U2115	A2051	G1991	G1929	U1865	
G2646	G2647	G2553	G2394	G2315	G2281	G2428	G2395	G2315	G2240	G2177	G2116	A2052	U1992	G1930	U1866	
G2648	G2649	G2554	G2396	G2316	G2282	G2429	G2397	G2316	G2241	G2178	G2117	G2053	U1993	U1931	U1867	
G2650	G2651	G2555	G2398	G2317	G2283	G2430	G2399	G2317	G2242	G2179	U2118	C2054	U1994	G1870	G1868	
G2652	G2653	G2556	G2400	G2318	G2284	G2431	G2401	G2318	G2243	G2180	A2119	C2055	U1995	C1934	C1871	
G2654	G2655	G2557	G2402	G2319	G2285	G2432	G2403	G2319	G2244	U2181	G2120	G2056	U1996	G1872	A1871	
G2656	G2657	G2558	G2404	G2320	G2286	G2433	G2405	G2320	G2245	U2182	G2121	G2057	U1997	G1873	A1872	
G2658	G2659	G2559	G2406	G2321	G2287	G2434	G2407	G2321	G2246	U2183	G2122	G2058	U1998	G1874	C1874	
G2660	G2661	G2560	G2408	G2322	G2288	G2435	G2409	G2322	G2247	U2184	U2122	G2059	U1999	G1875	G1875	
G2662	G2663	G2561	G2410	G2323	G2289	G2436	G2411	G2323	G2248	U2185	A2126	A2060	C1997	A1876	A1876	
G2664	G2665	G2562	G2412	G2324	G2290	G2437	G2413	G2324	G2249	U2186	G2127	A2061	C1998	G1877	G1877	
G2666	G2667	G2563	G2414	G2325	G2291	G2438	G2415	G2325	G2250	U2187	G2128	A2062	C1999	G1878	G1878	
G2668	G2669	G2564	G2416	G2326	G2292	G2439	G2417	G2326	G2251	U2188	G2129	C2063	C2000	U1938	G1879	
G2670	G2671	G2565	G2418	G2327	G2293	G2440	G2419	G2327	G2252	U2189	U2130	C2064	C2001	U1939	C1879	
G2672	G2673	G2566	G2420	G2328	G2294	G2441	G2421	G2328	G2253	U2190	U2131	C2065	G2002	U1940	G1876	
G2674	G2675	G2567	G2422	G2329	G2295	G2442	G2423	G2329	G2254	G2191	U2132	C2066	A2003	C1941	A1877	
G2676	G2677	G2568	G2424	G2330	G2296	G2443	G2425	G2330	G2255	G2192	U2133	G2067	G2004	C1942	G1878	
G2678	G2679	G2569	G2426	G2331	G2297	G2444	G2427	G2331	G2256	U2193	A2134	U2068	A2005	U1943	G1879	
G2680	G2681	G2570	G2428	G2332	G2298	G2445	G2429	G2332	G2257	G2194	A2135	G2069	C2006	U1944	U1880	
G2682	G2683	G2571	G2430	G2333	G2299	G2446	G2431	G2333	G2258	U2195	G2136	A2070	U2007	G1945	U1881	
G2684	G2685	G2572	G2432	G2334	G2300	G2447	G2433	G2334	G2259	U2196	U2137	A2071	C2008	U1946	G1884	
G2686	G2687	G2573	G2434	G2335	G2301	G2448	G2435	G2335	G2260	U2197	G2138	C2072	A2009	C1947	U1885	
G2688	G2689	G2574	G2436	G2336	G2302	G2449	G2437	G2336	G2261	U2198	U2139	C2073	G1948	G1948	A1886	
G2690	G2691	G2575	G2438	G2337	G2303	G2450	G2439	G2337	G2262	U2199	G2140	U2074	A2013	G1949	U1887	
G2692	G2693	G2576	G2440	G2338	G2304	G2451	G2441	G2338	G2263	A2200	G2141	U2075	A2014	U1950	U1888	
G2694	G2695	G2577	G2442	G2339	G2305	G2452	G2443	G2339	G2264	G2200	G2142	U2076	A2015	U1951	G1889	
G2696	G2697	G2578	G2444	G2340	G2306	G2453	G2445	G2340	G2265	U2201	A2143	U2077	A2016	A1952	A1889	
G2698	G2699	G2579	G2446	G2341	G2307	G2454	G2447	G2341	G2266	U2202	A2144	U2078	U2017	A1953	A1890	
G2700	G2701	G2580	G2448	G2342	G2308	G2455	G2449	G2342	G2267	U2203	G2145	U2079	A2018	G1954	G1891	
G2702	G2703	G2581	G2450	G2343	G2309	G2456	G2451	G2343	G2268	G2204	G2146	U2080	A2019	U1955	C1892	
G2704	G2705	G2582	G2452	G2344	G2310	G2457	G2453	G2344	G2269	G2205	G2147	A2081	A2020	U1956	C1893	
G2706	G2707	G2583	G2454	G2345	G2311	G2458	G2455	G2345	G2270	G2206	G2148	U2082	A2021	C1957	C1894	
G2708	G2709	G2584	G2456	G2346	G2312	G2459	G2457	G2346	G2271	G2207	G2149	A2082	C2021	U1958	C1895	
G2710	G2711	G2585	G2458	G2347	G2313	G2460	G2459	G2347	U2272	C2208	A2147		U2022	G1959		
G2712	G2713	G2586	G2460	G2348	G2314		G2460	G2348	G2273							
G2714	G2715	G2587		G2349	G2315			G2349	G2274							
G2716	G2717	G2588		G2350	G2316			G2350	G2275							
G2718	G2719	G2589		G2351	G2317			G2351	G2276							
G2720	G2721	G2590		G2352	G2318			G2352								
G2722	G2723	G2591		G2353	G2319			G2353								
G2724	G2725	G2592		G2354	G2320			G2354								
G2726	G2727	G2593		G2355	G2321			G2355								
G2728	G2729	G2594		G2356	G2322			G2356								
G2730	G2731	G2595		G2357	G2323			G2357								
G2732	G2733	G2596		G2358	G2324			G2358								
G2734	G2735	G2597		G2359	G2325			G2359								
G2736	G2737	G2598		G2360	G2326			G2360								
G2738	G2739	G2599		G2361	G2327			G2361								
G2740	G2741	G2600		G2362	G2328			G2362								
G2742	G2743	G2601		G2363	G2329			G2363								
G2744	G2745	G2602		G2364	G2330			G2364								
G2746	G2747	G2603		G2365	G2331			G2365								
G2748	G2749	G2604		G2366	G2332			G2366								
G2750	G2751	G2605		G2367	G2333			G2367								
G2752	G2753	G2606		G2368	G2334			G2368								
G2754	G2755	G2607		G2369	G2335			G2369								
G2756	G2757	G2608		G2370	G2336			G2370								
G2758	G2759	G2609		G2371	G2337			G2371								
G2760	G2761	G2610		G2372	G2338			G2372								
G2762	G2763	G2611		G2373	G2339			G2373								
G2764	G2765	G2612		G2374	G2340			G2374								
G2766	G2767	G2613		G2375	G2341			G2375								
G2768	G2769	G2614		G2376	G2342			G2376								
G2770	G2771	G2615		G2377	G2343			G2377								
G2772</																



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	5371	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	222.167	Depositor
Minimum map value	-162.027	Depositor
Average map value	0.002	Depositor
Map value standard deviation	24.233	Depositor
Recommended contour level	25	Depositor
Map size (\AA)	359.04, 359.04, 359.04	wwPDB
Map dimensions	96, 96, 96	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	3.74, 3.74, 3.74	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.67	0/1736	1.06	12/2340 (0.5%)
2	AC	0.70	0/1651	1.18	18/2225 (0.8%)
3	AD	0.74	0/1665	1.20	17/2227 (0.8%)
4	AE	0.66	0/1119	1.03	7/1506 (0.5%)
5	AF	0.71	0/835	1.12	7/1128 (0.6%)
6	AG	0.72	0/1188	1.27	17/1593 (1.1%)
7	AH	0.69	0/989	1.07	8/1326 (0.6%)
8	AI	0.77	0/1035	1.21	13/1377 (0.9%)
9	AJ	0.71	0/797	1.16	9/1079 (0.8%)
10	AK	0.73	0/894	1.10	8/1207 (0.7%)
11	AL	0.73	0/969	1.29	17/1300 (1.3%)
12	AM	0.72	0/884	1.36	14/1181 (1.2%)
13	AN	0.75	0/817	1.18	10/1088 (0.9%)
14	AO	0.70	0/722	1.18	7/964 (0.7%)
15	AP	0.74	0/648	1.27	11/870 (1.3%)
16	AQ	0.66	0/658	1.17	7/883 (0.8%)
17	AR	0.76	0/463	1.17	6/623 (1.0%)
18	AS	0.72	0/653	1.19	7/879 (0.8%)
19	AT	0.67	0/672	1.13	6/890 (0.7%)
20	AU	0.83	0/431	1.48	7/572 (1.2%)
21	AA	1.61	27/36759 (0.1%)	2.23	2065/57346 (3.6%)
22	A1	1.63	0/1668	2.16	80/2595 (3.1%)
23	A2	1.49	0/343	2.31	18/531 (3.4%)
24	A3	1.64	0/1722	2.26	102/2685 (3.8%)
25	BC	0.73	0/2121	1.28	21/2852 (0.7%)
26	BD	0.65	0/1586	1.19	14/2134 (0.7%)
27	BE	0.66	0/1571	1.22	14/2113 (0.7%)
28	BF	0.72	0/1444	1.18	12/1937 (0.6%)
29	BG	0.65	0/1343	1.14	9/1816 (0.5%)
30	BH	0.62	0/1122	1.08	5/1515 (0.3%)
31	BI	0.63	0/1046	1.03	4/1410 (0.3%)
32	BJ	0.71	0/1152	1.22	10/1551 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	BK	0.70	0/947	1.23	10/1268 (0.8%)
34	BL	0.72	0/1054	1.29	10/1403 (0.7%)
35	BM	0.71	0/1093	1.19	9/1460 (0.6%)
36	BN	0.75	0/973	1.34	12/1301 (0.9%)
37	BO	0.71	0/902	1.27	13/1209 (1.1%)
38	BP	0.70	0/929	1.22	11/1242 (0.9%)
39	BQ	0.76	0/960	1.30	16/1278 (1.3%)
40	BR	0.68	0/829	1.18	8/1107 (0.7%)
41	BS	0.63	0/864	1.22	10/1156 (0.9%)
42	BT	0.62	0/744	1.19	7/994 (0.7%)
43	BU	0.65	0/787	1.21	6/1051 (0.6%)
44	BV	0.66	0/766	1.06	4/1025 (0.4%)
45	BW	0.71	0/604	1.26	7/799 (0.9%)
46	BX	0.72	0/635	1.28	7/848 (0.8%)
47	BY	0.65	0/510	1.24	5/677 (0.7%)
48	BZ	0.67	0/453	1.23	5/605 (0.8%)
49	B0	0.72	0/450	1.30	7/599 (1.2%)
50	B1	0.68	0/417	1.10	2/556 (0.4%)
51	B2	0.79	0/380	1.49	9/498 (1.8%)
52	B3	0.70	0/513	1.23	6/676 (0.9%)
53	B4	0.69	0/303	1.35	5/397 (1.3%)
54	BA	1.48	61/69796 (0.1%)	2.23	4183/108888 (3.8%)
55	BB	1.48	1/2800 (0.0%)	2.19	150/4367 (3.4%)
56	B5	0.62	0/1673	1.09	11/2255 (0.5%)
All	All	1.34	89/160085 (0.1%)	2.01	7075/239402 (3.0%)

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
3	AD	0	1
10	AK	0	1
21	AA	0	374
22	A1	0	20
23	A2	0	5
24	A3	0	13
25	BC	0	1
26	BD	0	1
31	BI	0	1
35	BM	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
36	BN	0	1
54	BA	0	623
55	BB	0	30
All	All	0	1072

The worst 5 of 89 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	BA	2507	C	C4-N4	-5.63	1.28	1.33
21	AA	742	G	C2-N2	-5.58	1.28	1.34
21	AA	756	C	C4-N4	-5.57	1.28	1.33
54	BA	2164	C	C4-N4	-5.44	1.29	1.33
21	AA	984	C	C4-N4	-5.43	1.29	1.33

The worst 5 of 7075 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	BA	1617	C	N3-C2-O2	-16.02	110.69	121.90
54	BA	640	C	N3-C2-O2	-15.80	110.84	121.90
24	A3	73	A	N1-C6-N6	-13.57	110.46	118.60
54	BA	1847	A	N1-C6-N6	-13.18	110.69	118.60
54	BA	323	C	O4'-C1'-N1	12.86	118.49	108.20

There are no chirality outliers.

5 of 1072 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
21	AA	25	C	Sidechain
21	AA	26	A	Sidechain
21	AA	5	U	Sidechain
3	AD	75	TYR	Sidechain
10	AK	127	ARG	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AB	1708	0	1736	0	0
2	AC	1625	0	1699	1	0
3	AD	1643	0	1710	1	0
4	AE	1109	0	1152	0	0
5	AF	818	0	808	1	0
6	AG	1178	0	1234	0	0
7	AH	979	0	1034	0	0
8	AI	1025	0	1074	1	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	1	0
19	AT	668	0	718	0	0
20	AU	429	0	453	0	0
21	AA	32828	0	16457	2	0
22	A1	1627	0	832	1	0
23	A2	309	0	158	0	0
24	A3	1642	0	839	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	0	0
34	BL	1045	0	1117	0	0
35	BM	1074	0	1157	0	0
36	BN	961	0	1000	0	0
37	BO	892	0	923	0	0
38	BP	917	0	965	0	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	0	0
43	BU	780	0	834	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	BV	753	0	780	0	0
45	BW	599	0	614	0	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	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	31205	8	0
55	BB	2504	0	1269	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	99454	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)
54:BA:1068:G:H1'	54:BA:1069:A:C6	2.45	0.51
54:BA:1131:G:C5	54:BA:2025:C:H4'	2.50	0.46
22:A1:53:G:C8	22:A1:54:5MU:H72	2.50	0.46
18:AS:46:LEU:H	18:AS:46:LEU:HD23	1.81	0.46
3:AD:86:GLY:H	3:AD:200:VAL:HG23	1.81	0.45

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%)	15 (7%)	3 (1%)	9	41
2	AC	205/208 (99%)	188 (92%)	12 (6%)	5 (2%)	5	27
3	AD	203/206 (98%)	190 (94%)	7 (3%)	6 (3%)	3	23
4	AE	150/152 (99%)	136 (91%)	11 (7%)	3 (2%)	6	32
5	AF	99/101 (98%)	83 (84%)	12 (12%)	4 (4%)	2	18
6	AG	150/152 (99%)	133 (89%)	14 (9%)	3 (2%)	6	32
7	AH	127/130 (98%)	116 (91%)	11 (9%)	0	100	100
8	AI	126/128 (98%)	117 (93%)	6 (5%)	3 (2%)	5	27
9	AJ	98/100 (98%)	87 (89%)	6 (6%)	5 (5%)	1	15
10	AK	116/118 (98%)	109 (94%)	5 (4%)	2 (2%)	7	37
11	AL	121/124 (98%)	109 (90%)	8 (7%)	4 (3%)	3	21
12	AM	112/115 (97%)	100 (89%)	12 (11%)	0	100	100
13	AN	98/101 (97%)	86 (88%)	9 (9%)	3 (3%)	3	22
14	AO	86/89 (97%)	79 (92%)	5 (6%)	2 (2%)	5	28
15	AP	79/81 (98%)	64 (81%)	9 (11%)	6 (8%)	1	10
16	AQ	80/82 (98%)	73 (91%)	6 (8%)	1 (1%)	10	43
17	AR	55/57 (96%)	51 (93%)	3 (6%)	1 (2%)	7	35
18	AS	79/81 (98%)	71 (90%)	7 (9%)	1 (1%)	10	43
19	AT	84/86 (98%)	75 (89%)	5 (6%)	4 (5%)	2	16
20	AU	51/53 (96%)	34 (67%)	13 (26%)	4 (8%)	1	10
25	BC	270/273 (99%)	241 (89%)	21 (8%)	8 (3%)	3	23
26	BD	207/209 (99%)	181 (87%)	18 (9%)	8 (4%)	2	19
27	BE	199/201 (99%)	172 (86%)	18 (9%)	9 (4%)	2	17
28	BF	176/179 (98%)	151 (86%)	20 (11%)	5 (3%)	4	24
29	BG	174/177 (98%)	151 (87%)	16 (9%)	7 (4%)	2	18
30	BH	147/149 (99%)	133 (90%)	12 (8%)	2 (1%)	9	41
31	BI	139/142 (98%)	128 (92%)	10 (7%)	1 (1%)	19	57
32	BJ	140/142 (99%)	123 (88%)	14 (10%)	3 (2%)	5	30
33	BK	121/123 (98%)	104 (86%)	13 (11%)	4 (3%)	3	21
34	BL	141/144 (98%)	110 (78%)	23 (16%)	8 (6%)	1	14
35	BM	134/136 (98%)	124 (92%)	7 (5%)	3 (2%)	5	29
36	BN	119/121 (98%)	102 (86%)	16 (13%)	1 (1%)	16	55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	BO	114/117 (97%)	110 (96%)	4 (4%)	0	100	100
38	BP	112/115 (97%)	96 (86%)	12 (11%)	4 (4%)	3	20
39	BQ	115/118 (98%)	105 (91%)	9 (8%)	1 (1%)	14	52
40	BR	101/103 (98%)	95 (94%)	6 (6%)	0	100	100
41	BS	108/110 (98%)	95 (88%)	12 (11%)	1 (1%)	14	52
42	BT	92/94 (98%)	80 (87%)	10 (11%)	2 (2%)	5	29
43	BU	101/104 (97%)	83 (82%)	13 (13%)	5 (5%)	1	16
44	BV	92/94 (98%)	88 (96%)	4 (4%)	0	100	100
45	BW	78/80 (98%)	63 (81%)	11 (14%)	4 (5%)	1	15
46	BX	75/79 (95%)	68 (91%)	5 (7%)	2 (3%)	4	25
47	BY	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
48	BZ	56/59 (95%)	50 (89%)	3 (5%)	3 (5%)	1	15
49	B0	54/57 (95%)	48 (89%)	4 (7%)	2 (4%)	2	20
50	B1	50/52 (96%)	42 (84%)	4 (8%)	4 (8%)	1	9
51	B2	44/46 (96%)	41 (93%)	2 (4%)	1 (2%)	5	28
52	B3	62/65 (95%)	56 (90%)	4 (6%)	2 (3%)	3	21
53	B4	36/38 (95%)	27 (75%)	8 (22%)	1 (3%)	4	24
56	B5	221/234 (94%)	207 (94%)	11 (5%)	3 (1%)	9	41
All	All	5876/6008 (98%)	5232 (89%)	490 (8%)	154 (3%)	6	26

5 of 154 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AB	73	ARG
2	AC	14	VAL
3	AD	82	LYS
9	AJ	77	VAL
15	AP	79	ASN

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%)	70	80
2	AC	170/171 (99%)	169 (99%)	1 (1%)	84	88
3	AD	172/173 (99%)	167 (97%)	5 (3%)	37	56
4	AE	113/113 (100%)	113 (100%)	0	100	100
5	AF	87/87 (100%)	86 (99%)	1 (1%)	70	80
6	AG	123/123 (100%)	121 (98%)	2 (2%)	58	73
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%)	84 (98%)	2 (2%)	45	64
10	AK	90/90 (100%)	89 (99%)	1 (1%)	70	80
11	AL	103/104 (99%)	103 (100%)	0	100	100
12	AM	91/92 (99%)	91 (100%)	0	100	100
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%)	62 (95%)	3 (5%)	23	44
16	AQ	74/74 (100%)	72 (97%)	2 (3%)	40	58
17	AR	48/48 (100%)	46 (96%)	2 (4%)	25	46
18	AS	70/70 (100%)	69 (99%)	1 (1%)	62	75
19	AT	65/65 (100%)	62 (95%)	3 (5%)	23	44
20	AU	44/44 (100%)	42 (96%)	2 (4%)	23	45
25	BC	216/217 (100%)	211 (98%)	5 (2%)	45	64
26	BD	164/164 (100%)	162 (99%)	2 (1%)	67	78
27	BE	165/165 (100%)	160 (97%)	5 (3%)	36	55
28	BF	149/150 (99%)	146 (98%)	3 (2%)	50	68
29	BG	137/138 (99%)	134 (98%)	3 (2%)	47	65
30	BH	114/114 (100%)	113 (99%)	1 (1%)	75	83
31	BI	109/110 (99%)	109 (100%)	0	100	100
32	BJ	116/116 (100%)	113 (97%)	3 (3%)	41	59
33	BK	103/103 (100%)	103 (100%)	0	100	100
34	BL	102/103 (99%)	100 (98%)	2 (2%)	50	68
35	BM	109/109 (100%)	108 (99%)	1 (1%)	75	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	BN	100/100 (100%)	97 (97%)	3 (3%)	36	55
37	BO	86/87 (99%)	82 (95%)	4 (5%)	22	44
38	BP	99/100 (99%)	95 (96%)	4 (4%)	27	47
39	BQ	89/90 (99%)	87 (98%)	2 (2%)	47	65
40	BR	84/84 (100%)	83 (99%)	1 (1%)	67	78
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%)	77 (99%)	1 (1%)	65	77
45	BW	59/59 (100%)	58 (98%)	1 (2%)	56	72
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%)	46 (96%)	2 (4%)	25	46
49	B0	47/48 (98%)	43 (92%)	4 (8%)	8	27
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%)	50 (98%)	1 (2%)	50	68
53	B4	34/34 (100%)	34 (100%)	0	100	100
56	B5	173/181 (96%)	171 (99%)	2 (1%)	67	78
All	All	4842/4870 (99%)	4750 (98%)	92 (2%)	52	69

5 of 92 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	BJ	76	HIS
38	BP	50	ARG
32	BJ	130	HIS
36	BN	69	ARG
39	BQ	28	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
2	AC	184	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
21	AA	1529/1533 (99%)	254 (16%)	77 (5%)
22	A1	73/76 (96%)	10 (13%)	3 (4%)
23	A2	14/15 (93%)	8 (57%)	5 (35%)
24	A3	76/77 (98%)	15 (19%)	5 (6%)
54	BA	2902/2903 (99%)	474 (16%)	117 (4%)
55	BB	116/118 (98%)	18 (15%)	2 (1%)
All	All	4710/4722 (99%)	779 (16%)	209 (4%)

5 of 779 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
21	AA	7	A
21	AA	8	A
21	AA	15	G
21	AA	16	A
21	AA	22	G

5 of 209 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
54	BA	670	A
54	BA	1288	G
54	BA	2602	A
54	BA	804	A
54	BA	1076	C

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	$\# Z > 2$
24	OMC	A3	33	24	19,22,23	0.77	0	25,31,34	1.00	1 (4%)

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	1.41	2 (11%)	25,30,33	0.89	1 (4%)
24	H2U	A3	21	24	18,21,22	1.31	2 (11%)	19,30,33	1.12	2 (10%)
22	CM0	A1	34	22	21,26,27	1.25	1 (4%)	26,37,40	1.39	2 (7%)
22	7MG	A1	46	22	23,26,27	4.24	2 (8%)	27,39,42	1.49	1 (3%)
24	PSU	A3	56	24	18,21,22	0.89	0	21,30,33	1.35	3 (14%)
24	4SU	A3	8	24	18,21,22	1.50	1 (5%)	25,30,33	0.76	1 (4%)
22	6MZ	A1	37	22	17,25,26	1.10	2 (11%)	15,36,39	1.55	3 (20%)
24	5MU	A3	55	24	19,22,23	0.67	0	27,32,35	1.30	4 (14%)
22	PSU	A1	55	22	18,21,22	0.80	0	21,30,33	1.19	2 (9%)
22	5MU	A1	54	22	19,22,23	0.78	0	27,32,35	1.35	4 (14%)

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

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	A1	46	7MG	C8-N9	-19.96	1.32	1.45
24	A3	8	4SU	C5-C4	-5.36	1.36	1.42
22	A1	7	4SU	C5-C4	-4.93	1.36	1.42
22	A1	34	CM0	O5-C5	-4.42	1.26	1.36
24	A3	21	H2U	C2-N3	-3.53	1.31	1.38

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	A1	46	7MG	N9-C8-N7	5.91	111.74	103.37
22	A1	34	CM0	C7-O5-C5	5.20	124.11	117.48
22	A1	37	6MZ	C9-N6-C6	4.08	126.64	122.85
22	A1	54	5MU	C5M-C5-C6	-3.30	118.39	122.85
24	A3	33	OMC	O2-C2-N3	-3.17	117.34	122.33

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	55	PSU	O4'-C1'-C5-C4

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
22	A1	54	5MU	1	0

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	0.63	0	6,7,9	1.41	1 (16%)
58	FME	BA	3001	57	8,9,10	0.56	0	8,9,11	1.26	1 (12%)

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	-	2/7/9/11	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	A1	101	VAL	O-C-CA	-3.38	116.07	124.77
58	BA	3001	FME	C-CA-N	2.53	114.38	109.50

There are no chirality outliers.

All (2) torsion outliers are listed below:

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

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.

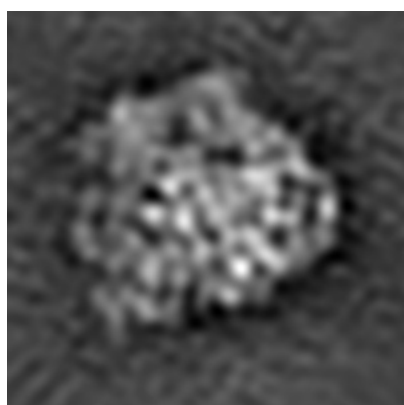
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2475. These allow visual inspection of the internal detail of the map and identification of artifacts.

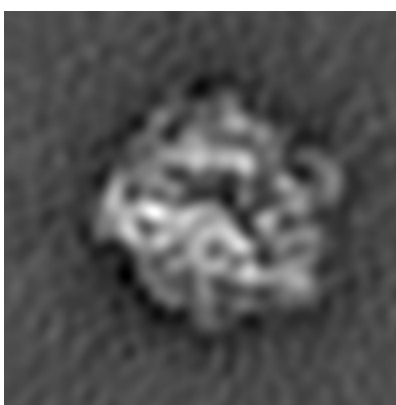
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

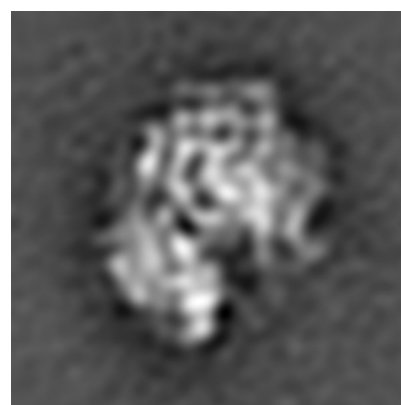
6.1.1 Primary map



X



Y



Z

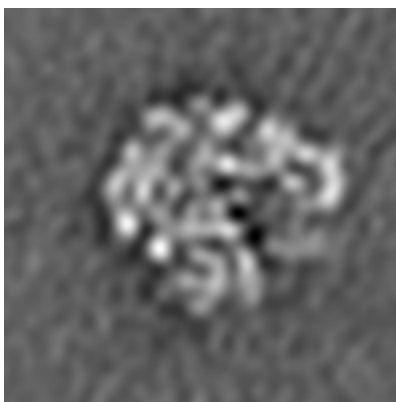
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 48



Y Index: 48

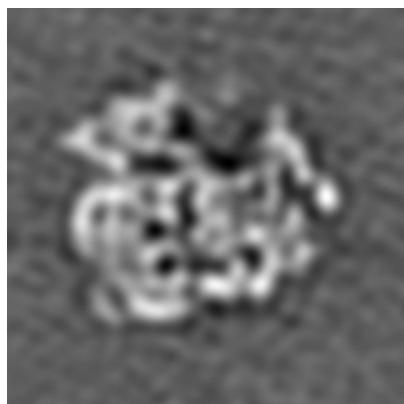


Z Index: 48

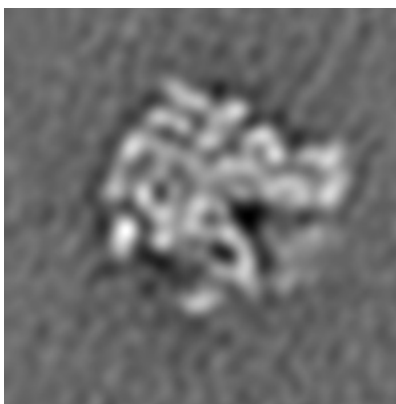
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

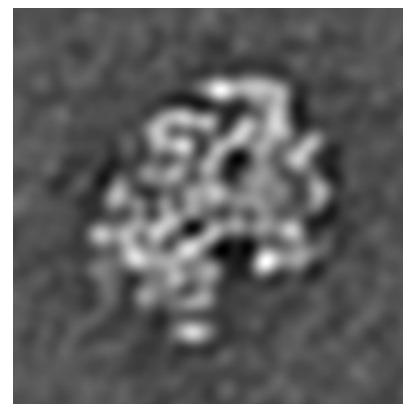
6.3.1 Primary map



X Index: 43



Y Index: 51

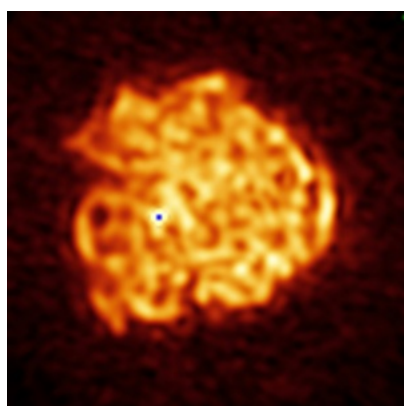


Z Index: 46

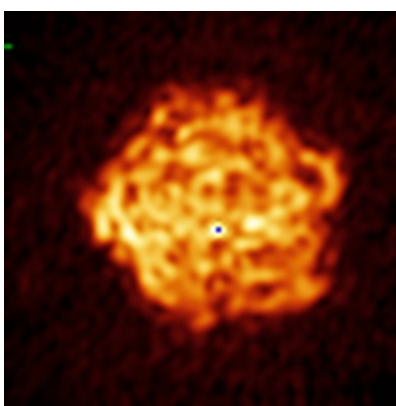
The images above show the largest variance slices of the map in three orthogonal directions.

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

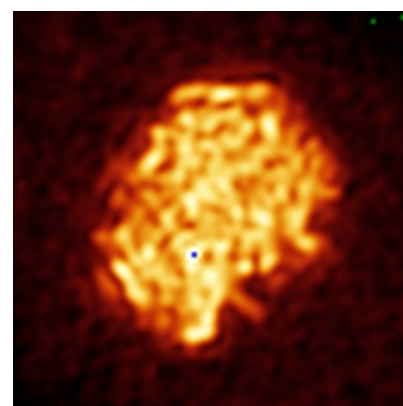
6.4.1 Primary map



X



Y

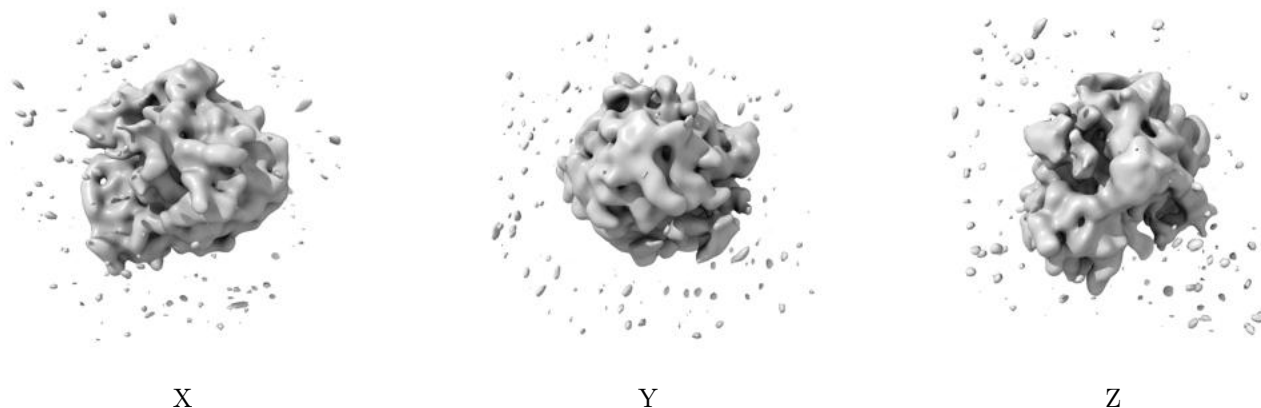


Z

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.

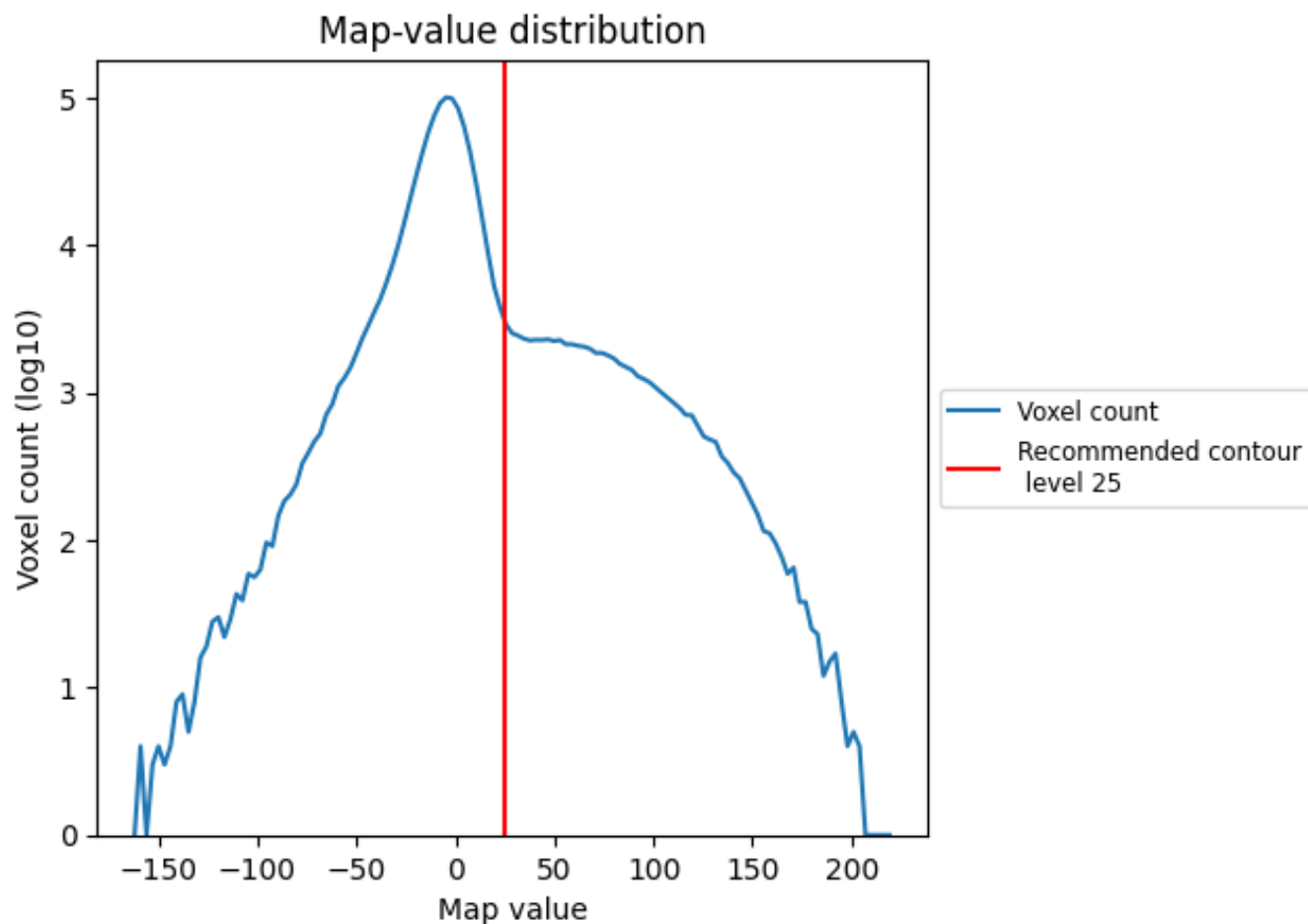
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

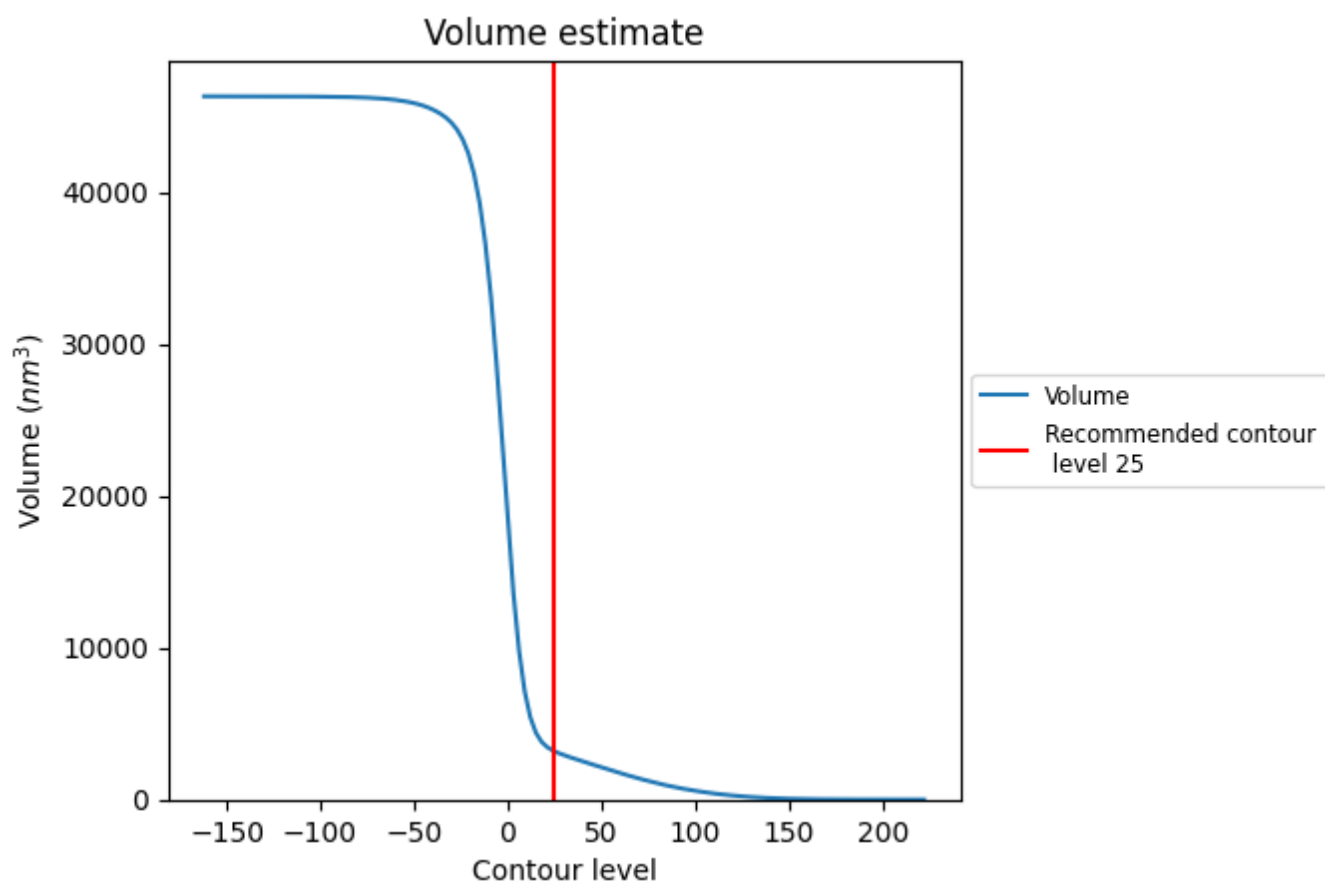
This section contains the results of statistical analysis of the map.

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.

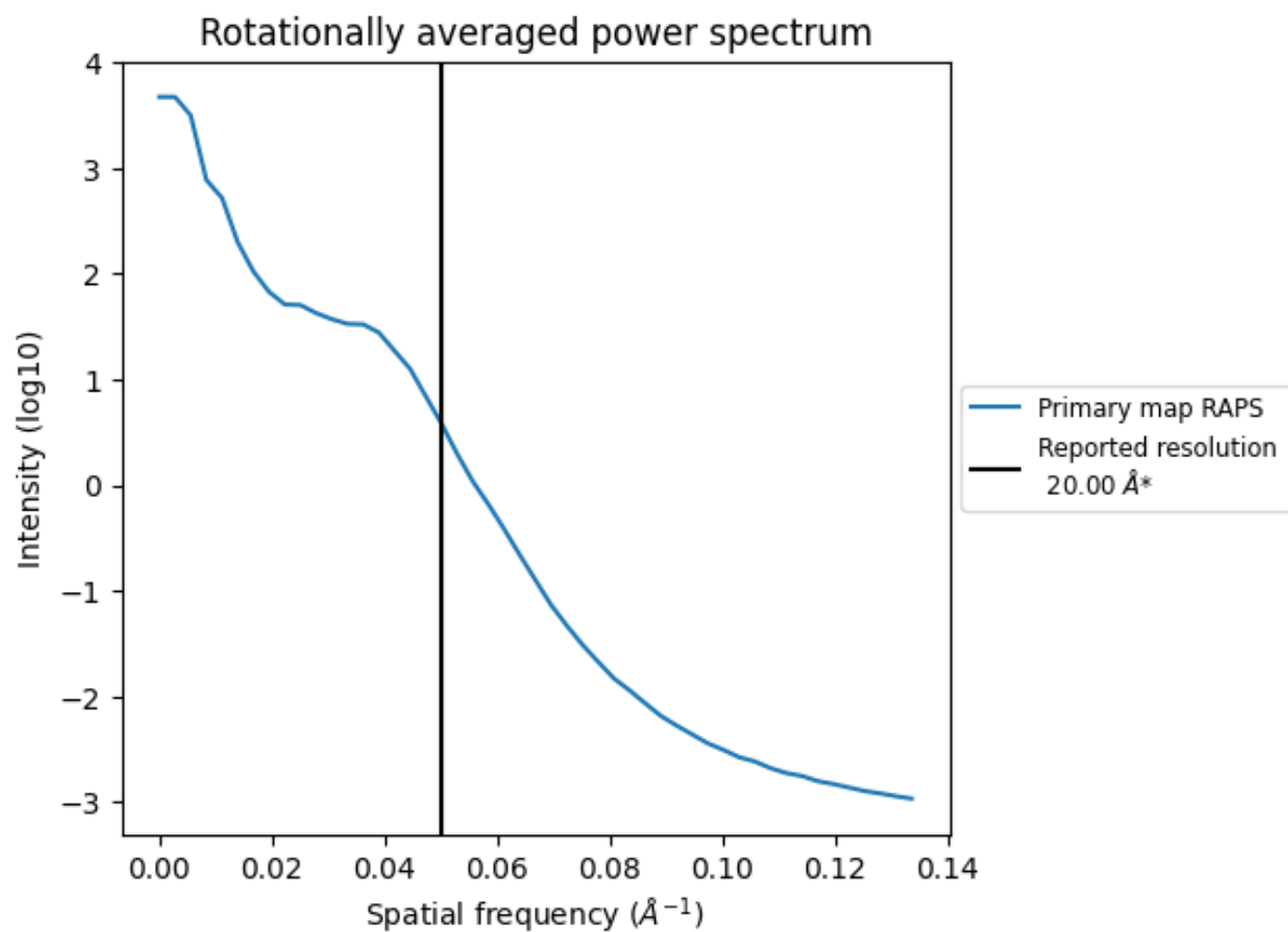
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3179 nm³; this corresponds to an approximate mass of 2872 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 0.050 \AA^{-1}

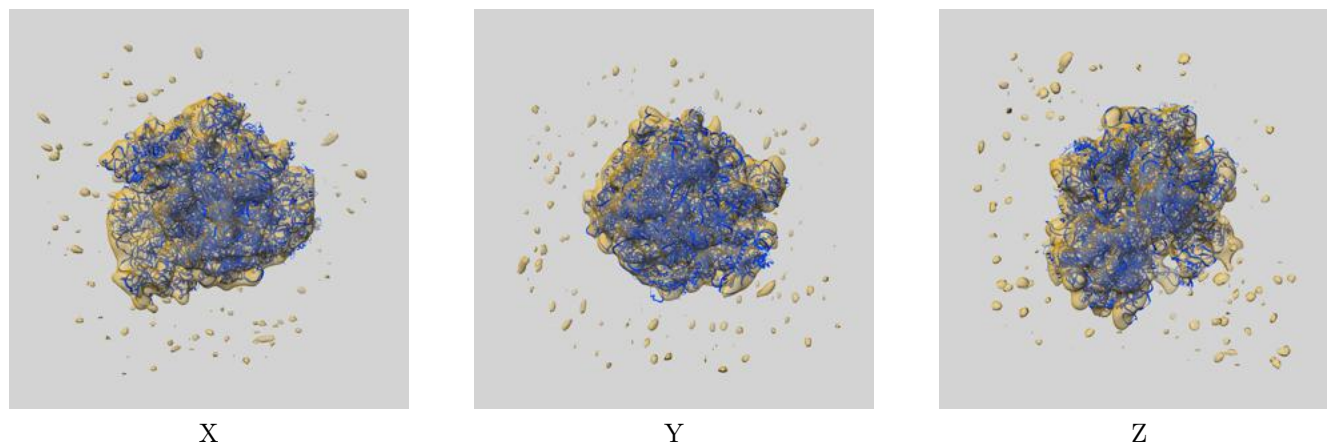
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

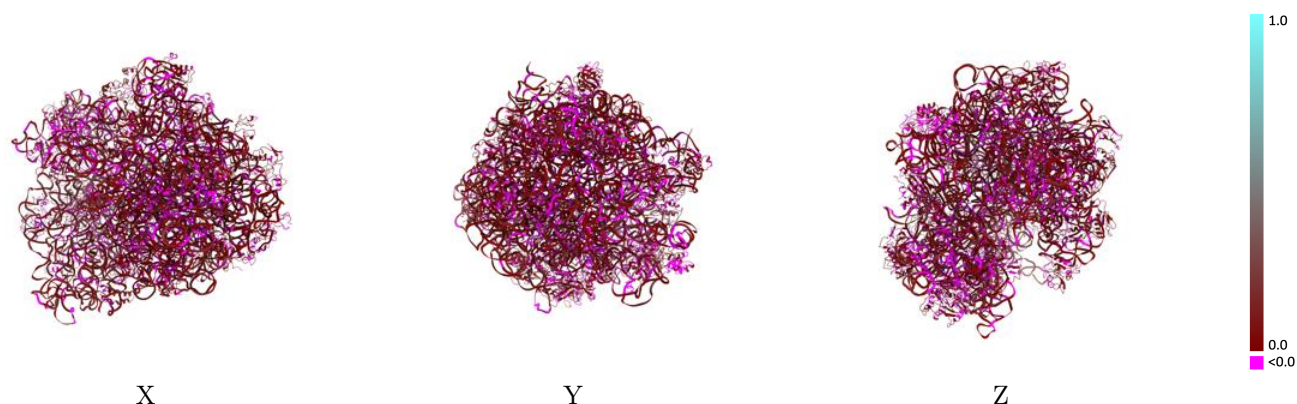
This section contains information regarding the fit between EMDB map EMD-2475 and PDB model 4V78. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

9.1 Map-model overlay [i](#)



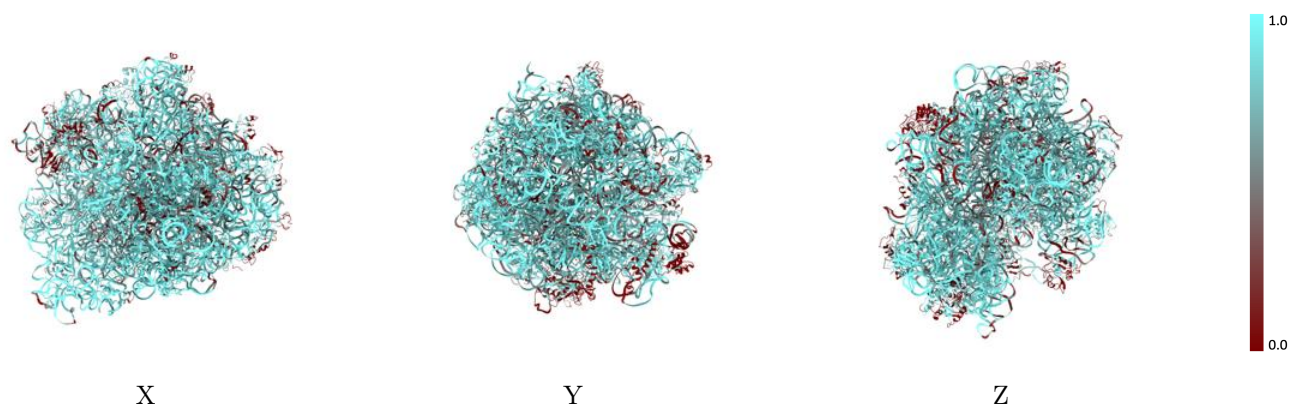
The images above show the 3D surface view of the map at the recommended contour level 25.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



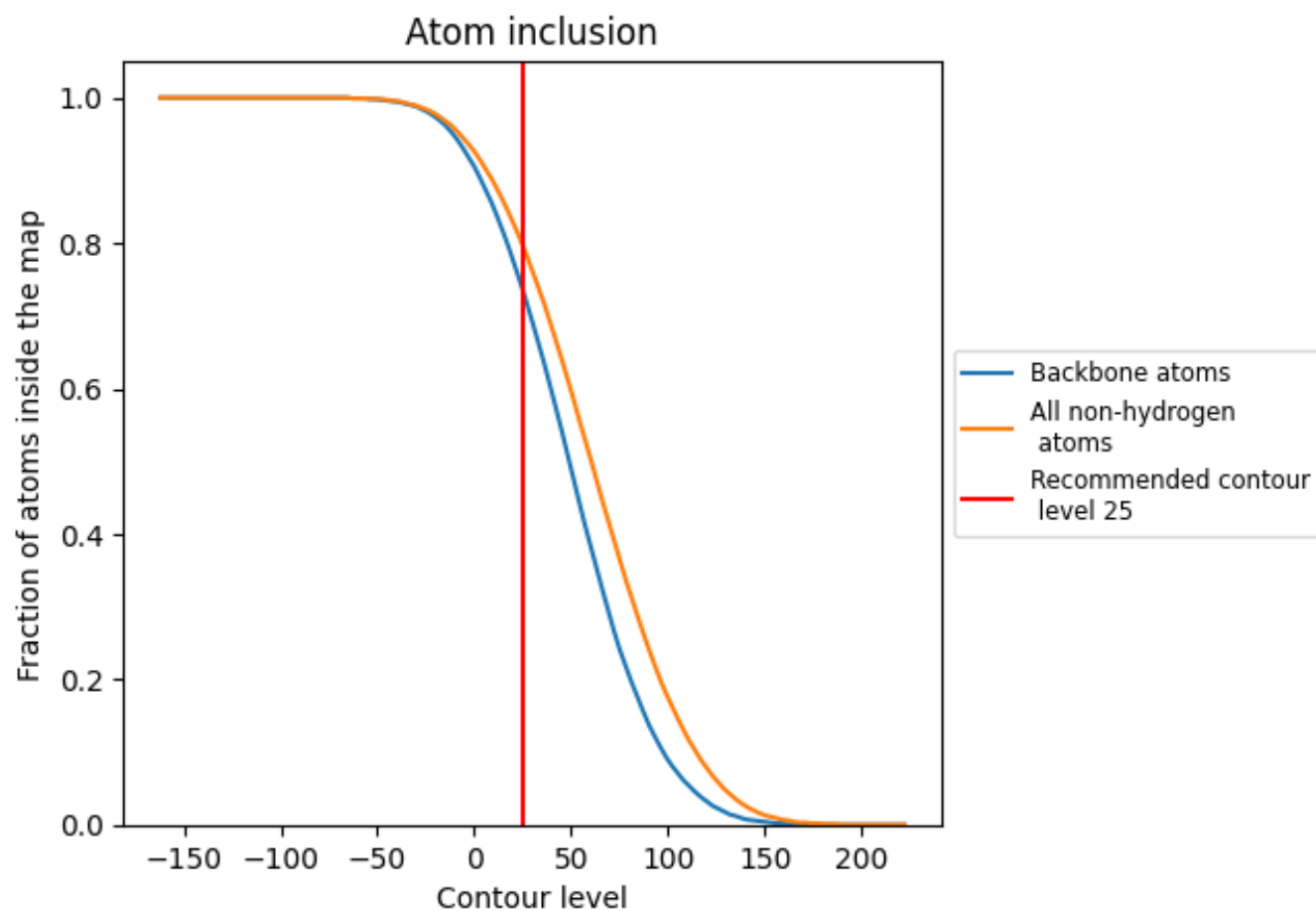
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



At the recommended contour level, 74% of all backbone atoms, 80% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ













































The table lists the average atom inclusion at the recommended contour level (25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7970	 0.0510
A1	 0.5150	 0.0490
A2	 0.9190	 0.0520
A3	 0.4760	 0.0280
AA	 0.8870	 0.0630
AB	 0.6060	 0.0440
AC	 0.6050	 0.0260
AD	 0.7230	 0.0170
AE	 0.7390	 0.0430
AF	 0.4910	 0.0440
AG	 0.8320	 0.0380
AH	 0.8600	 0.0550
AI	 0.9170	 0.0200
AJ	 0.6260	 -0.0080
AK	 0.7710	 0.0520
AL	 0.6990	 0.0160
AM	 0.6720	 0.0430
AN	 0.7460	 0.0050
AO	 0.7930	 0.0410
AP	 0.7390	 0.0280
AQ	 0.5730	 0.0190
AR	 0.5600	 0.0150
AS	 0.4380	 0.0090
AT	 0.8020	 0.0310
AU	 0.8870	 0.0510
B0	 0.6730	 0.0180
B1	 0.6730	 0.0320
B2	 0.3920	 -0.0410
B3	 0.6150	 -0.0450
B4	 0.7980	 -0.0020
B5	 0.3090	 0.0100
BA	 0.8620	 0.0640
BB	 0.8970	 0.0650
BC	 0.5720	 -0.0060
BD	 0.6980	 0.0200



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Chain	Atom inclusion	Q-score
BE	 0.6720	 0.0260
BF	 0.7650	 0.0330
BG	 0.7910	 0.0360
BH	 0.2170	 0.0310
BI	 0.2720	 0.0380
BJ	 0.6930	 0.0220
BK	 0.5480	 0.0350
BL	 0.5630	 0.0080
BM	 0.7380	 0.0230
BN	 0.7270	 -0.0020
BO	 0.7510	 0.0270
BP	 0.7470	 0.0400
BQ	 0.6880	 -0.0030
BR	 0.6830	 0.0520
BS	 0.6760	 0.0060
BT	 0.8510	 0.0140
BU	 0.5420	 0.0130
BV	 0.8290	 0.0630
BW	 0.7110	 0.0170
BX	 0.8000	 0.0480
BY	 0.3840	 -0.0030
BZ	 0.6180	 0.0340