



wwPDB EM Validation Summary Report ⓘ

Mar 26, 2026 – 09:42 AM UTC

PDB ID : 7LV0 / pdb_00007lv0
EMDB ID : EMD-23528
Title : Pre-translocation rotated ribosome +1-frameshifting(CCC-A) complex (Structure Irot-FS)
Authors : Demo, G.; Loveland, A.B.; Svidritskiy, E.; Gamper, H.B.; Hou, Y.M.; Korostelev, A.A.
Deposited on : 2021-02-23
Resolution : 3.20 Å(reported)
Based on initial models : 6ENJ, 4V9P, 4V7D, 5UYM

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

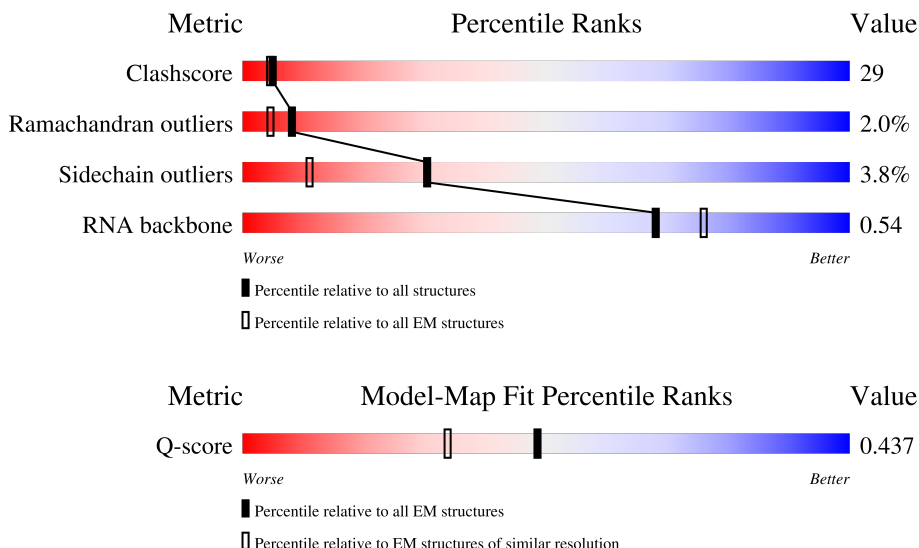
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.20 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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	b	271	
2	c	209	

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Mol	Chain	Length	Quality of chain
3	d	201	
4	e	177	
5	f	176	
6	g	149	
7	h	131	
8	i	141	
9	j	142	
10	k	122	
11	l	143	
12	m	136	
13	n	120	
14	o	116	
15	p	114	
16	q	117	
17	r	103	
18	s	110	
19	t	93	
20	u	102	
21	v	94	
22	w	75	
23	x	77	
24	y	63	
25	z	58	
26	A	66	
27	B	56	

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Mol	Chain	Length	Quality of chain
28	C	50	
29	D	46	
30	E	64	
31	F	38	
32	G	225	
33	H	206	
34	I	205	
35	J	157	
36	K	100	
37	L	151	
38	M	129	
39	N	127	
40	O	98	
41	P	116	
42	Q	123	
43	R	114	
44	S	100	
45	T	88	
46	U	82	
47	V	80	
48	W	65	
49	X	79	
50	Y	85	
51	Z	65	
52	a	223	

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Mol	Chain	Length	Quality of chain
53	3	1539	
54	1	2903	
55	2	120	
56	5	77	
57	6	77	
58	4	18	

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 147330 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 50S ribosomal protein L2.

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

- Molecule 2 is a protein called 50S ribosomal protein L3.

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

- Molecule 3 is a protein called 50S ribosomal protein L4.

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

- Molecule 4 is a protein called 50S ribosomal protein L5.

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

- Molecule 5 is a protein called 50S ribosomal protein L6.

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

- Molecule 6 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	g	57	Total	C	N	O	S	0	0
			440	281	79	79	1		

- Molecule 7 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	h	79	Total	C	N	O	S	0	0
			593	369	109	111	4		

- Molecule 8 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	i	71	Total	C	N	O	S	0	0
			511	313	93	102	3		

- Molecule 9 is a protein called 50S ribosomal protein L13.

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

- Molecule 10 is a protein called 50S ribosomal protein L14.

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

- Molecule 11 is a protein called 50S ribosomal protein L15.

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

- Molecule 12 is a protein called 50S ribosomal protein L16.

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

- Molecule 13 is a protein called 50S ribosomal protein L17.

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

- Molecule 14 is a protein called 50S ribosomal protein L18.

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

- Molecule 15 is a protein called 50S ribosomal protein L19.

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

- Molecule 16 is a protein called 50S ribosomal protein L20.

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

- Molecule 17 is a protein called 50S ribosomal protein L21.

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

- Molecule 18 is a protein called 50S ribosomal protein L22.

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

- Molecule 19 is a protein called 50S ribosomal protein L23.

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

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	u	102	Total	C	N	O		0
			780	492	146	142		0

- Molecule 21 is a protein called 50S ribosomal protein L25.

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

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	w	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 23 is a protein called 50S ribosomal protein L28.

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

- Molecule 24 is a protein called 50S ribosomal protein L29.

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

- Molecule 25 is a protein called 50S ribosomal protein L30.

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

- Molecule 26 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	A	47	Total	C	N	O	S	0	0
			364	227	64	67	6		

- Molecule 27 is a protein called 50S ribosomal protein L32.

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

- Molecule 28 is a protein called 50S ribosomal protein L33.

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

- Molecule 29 is a protein called 50S ribosomal protein L34.

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

- Molecule 30 is a protein called 50S ribosomal protein L35.

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

- Molecule 31 is a protein called 50S ribosomal protein L36.

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

- Molecule 32 is a protein called 30S ribosomal protein S2.

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

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	H	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 34 is a protein called 30S ribosomal protein S4.

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

- Molecule 35 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	J	157	Total	C	N	O	S	0	0
			1157	719	218	214	6		

- Molecule 36 is a protein called 30S ribosomal protein S6.

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

- Molecule 37 is a protein called 30S ribosomal protein S7.

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

- Molecule 38 is a protein called 30S ribosomal protein S8.

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

- Molecule 39 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	N	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	O	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

- Molecule 41 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	P	116	Total	C	N	O	S	0	0
			870	535	173	159	3		

- Molecule 42 is a protein called 30S ribosomal protein S12.

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

- Molecule 43 is a protein called 30S ribosomal protein S13.

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

- Molecule 44 is a protein called 30S ribosomal protein S14.

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

- Molecule 45 is a protein called 30S ribosomal protein S15.

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

- Molecule 46 is a protein called 30S ribosomal protein S16.

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

- Molecule 47 is a protein called 30S ribosomal protein S17.

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

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	W	65	Total	C	N	O	S	0	0
			536	339	100	96	1		

- Molecule 49 is a protein called 30S ribosomal protein S19.

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

- Molecule 50 is a protein called 30S ribosomal protein S20.

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

- Molecule 51 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Z	65	Total	C	N	O	S	0	0
			545	335	117	92	1		

- Molecule 52 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	a	134	Total	C	N	O	S	0	0
			1027	645	186	194	2		

- Molecule 53 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	3	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
54	1	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 802133627

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

Mol	Chain	Residues	Atoms					AltConf	Trace
55	2	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	120	A	-	insertion	GB 1266961702

- Molecule 56 is a RNA chain called tRNAPro.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	5	77	Total	C	N	O	P	0	0
			1647	733	295	542	77		

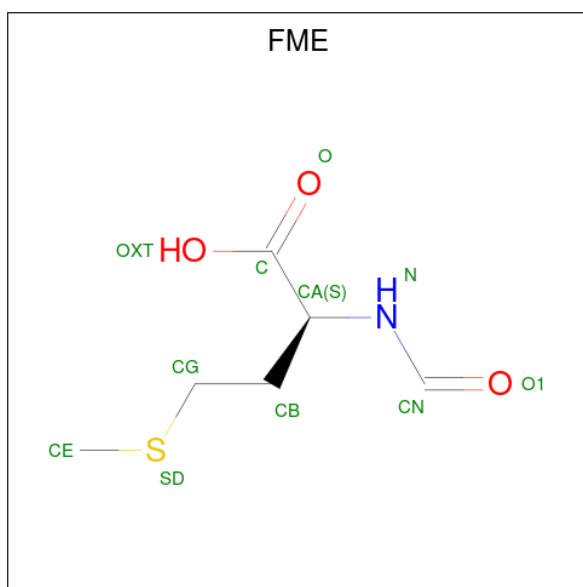
- Molecule 57 is a RNA chain called tRNAfMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	6	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 58 is a RNA chain called mRNA.

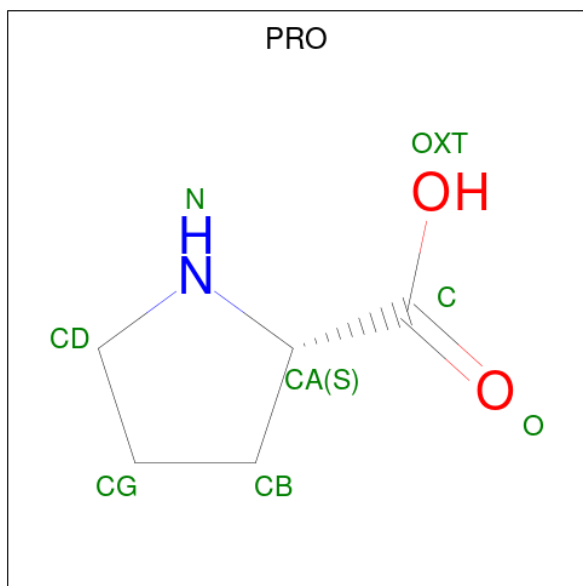
Mol	Chain	Residues	Atoms					AltConf	Trace
58	4	18	Total	C	N	O	P	0	0
			388	175	78	118	17		

- Molecule 59 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: C₆H₁₁NO₃S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
59	1	1	Total	C	N	O	S	0
			10	6	1	2	1	

- Molecule 60 is PROLINE (CCD ID: PRO) (formula: $C_5H_9NO_2$) (labeled as "Ligand of Interest" by depositor).

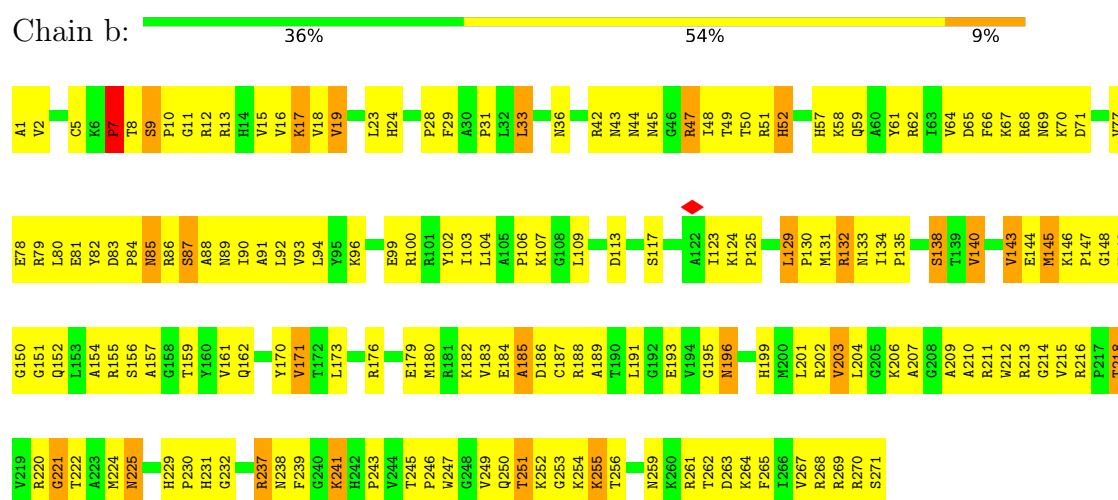


Mol	Chain	Residues	Atoms				AltConf
60	5	1	Total	C	N	O	0
			7	5	1	1	

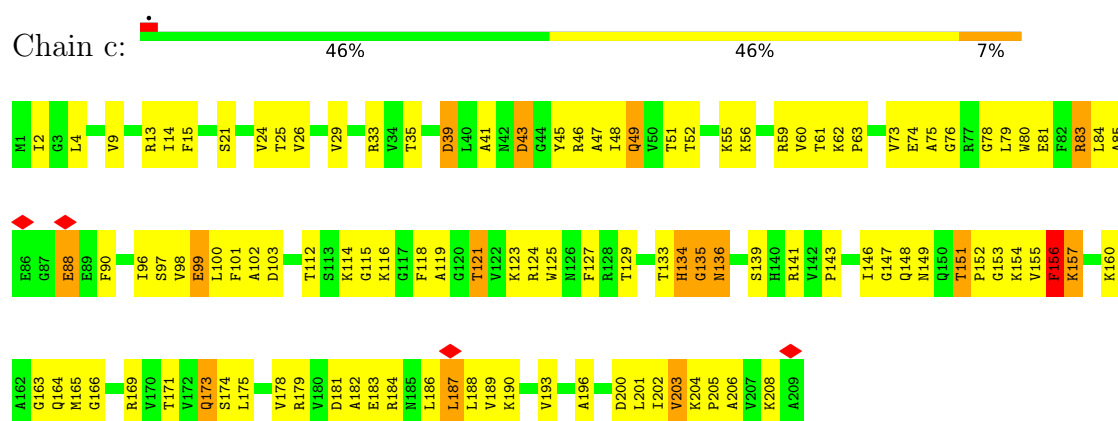
3 Residue-property plots

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.

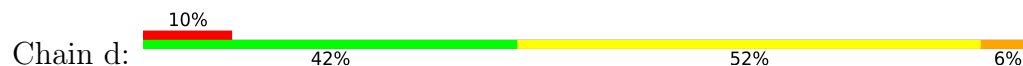
• Molecule 1: 50S ribosomal protein L2

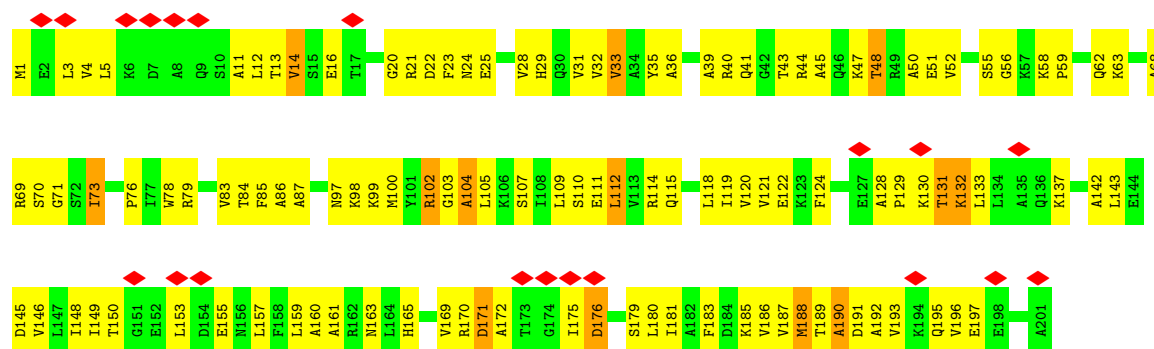


• Molecule 2: 50S ribosomal protein L3

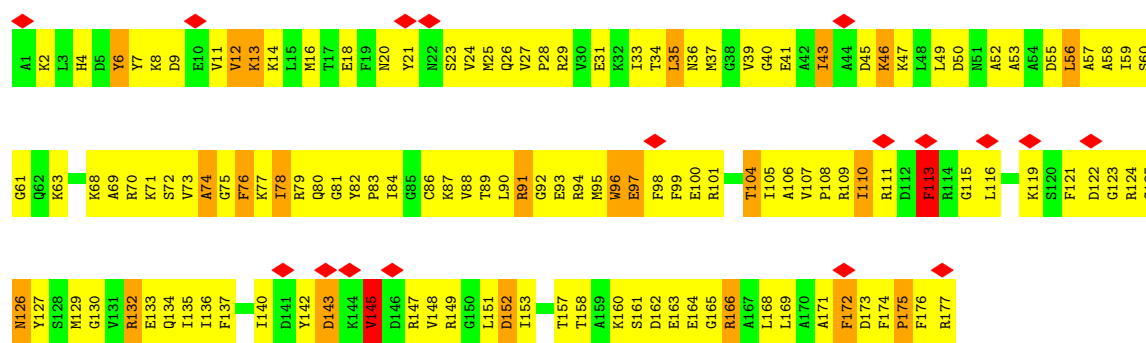


• Molecule 3: 50S ribosomal protein L4

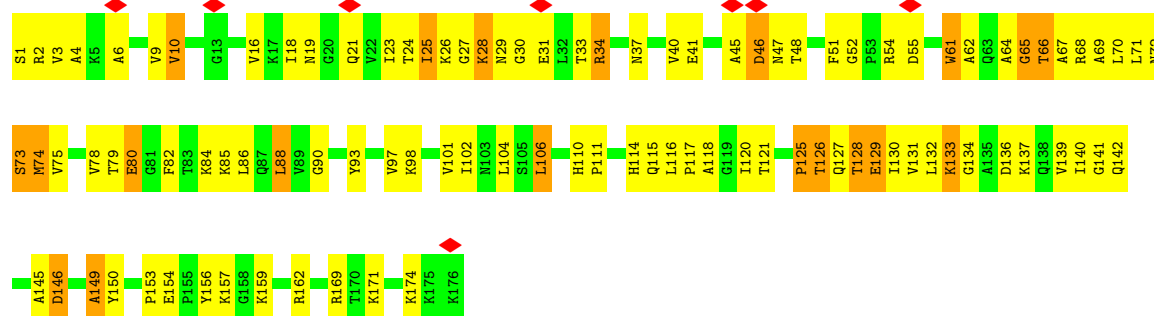
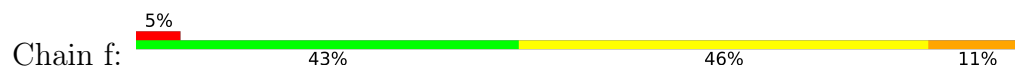




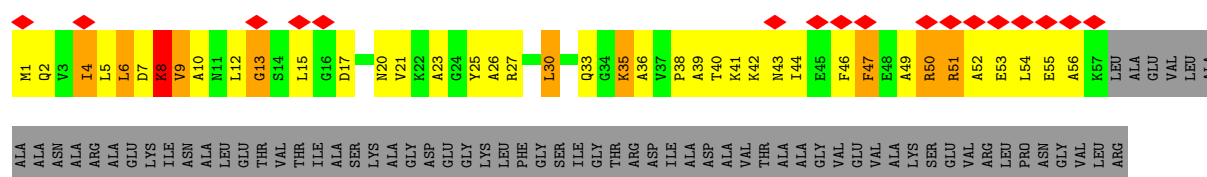
• Molecule 4: 50S ribosomal protein L5



• Molecule 5: 50S ribosomal protein L6



• Molecule 6: 50S ribosomal protein L9



THR THR GLY GLU HIS GLU VAL SER PHE GLN VAL HIS SER GLU VAL PHE ALA LYS VAL ILE VAL ASN VAL VAL ALA GLU

• Molecule 7: 50S ribosomal protein L10

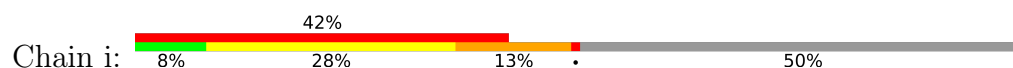


M1 A2 L3 N4 L5 Q6 D7 Q8 A10 I11 V12 A13 E14 V15 S16 E17 V18 A19 R20 G21 A22 L23 S24 A25 V26 V27 A28 D29 S30 A31 R32 V33 T34 V35 D36 K37 K38 T39 F40 L41 R42 K43 A44 C45 R46 E47 A48 G49 V50 Y51 H52 R53 V54 V55 H56 T57 L58 L59 L60

R61 R62 A63 V64 E65 T67 P68 F69 E70 C71 L72 K73 D74 A75 F76 V77 P79 THR LEU ILE ALA TYR MET GLU HIS PRG GLY ALA ARG LEU PHE LYS GLU PHE LYS LYS ALA ASN ALA LYS PHE GLU VAL LYS ALA ALA PHE GLU LEU ILE PRO THR

SER GLN ILE ASP ARG LEU THR PRO THR

• Molecule 8: 50S ribosomal protein L11



ALA LYS VAL GLN TYR VAL LYS LEU GLN VAL ALA ALA GLY MET ALA ASN PRO SER PRO VAL PRO GLY PRO ALA LEU GLY GLN GLY VAL ASN ILE MET GLU PHE CYS LYS PHE ASN ALA LYS THR ASP SER ILE GLU LYS GLY LEU PRO ILE PRO VAL THR VAL

TYR ALA ASP GLN SER PHE THR PHE VAL THR K71 T72 P73 P74 A75 A76 A77 L78 L79 K80 K81 A82 A83 G84 I85 K86 K87 G88 S89 G90 K91 P92 N93 K94 P95 K96 V97 G98 K99 I100 S101 R102 A103 Q104 L105 Q106 E107 I108 Q109 T110 K111 A113 A114 D115 M116 T117 G118 A119 D120

I121 E122 A123 M124 T125 R126 E127 I128 E129 T130 T131 A132 R133 S134 M135 G136 L137 V138 V139 E140 D141

• Molecule 9: 50S ribosomal protein L13



M1 K2 T3 F4 T5 A6 K7 P8 E9 D14 Y15 Y16 V17 A20 T21 G26 R27 L28 A29 T30 E31 L32 A33 R34 R35 L36 R37 G38 K39 H40 K41 P42 A42 E43 Y44 T45 P46 V47 D48 D49 D52 Y53 T54 I55 V56 L57 N58 A59 D60 K61 V64 R69 T70 H76

H77 T78 G79 H80 I81 G82 G83 I84 K85 F89 E90 I93 A94 R95 R96 P97 E98 R99 V100 I101 E102 I103 A104 V105 K106 G107 M108 L109 P110 K111 G112 P113 L114 G115 R116 A117 M118 F119 K120 K121 K122 K123 V124 Y125 I126 G127 N128 E129 H130 M131 A132 A133 Q138 V139 D141 I142

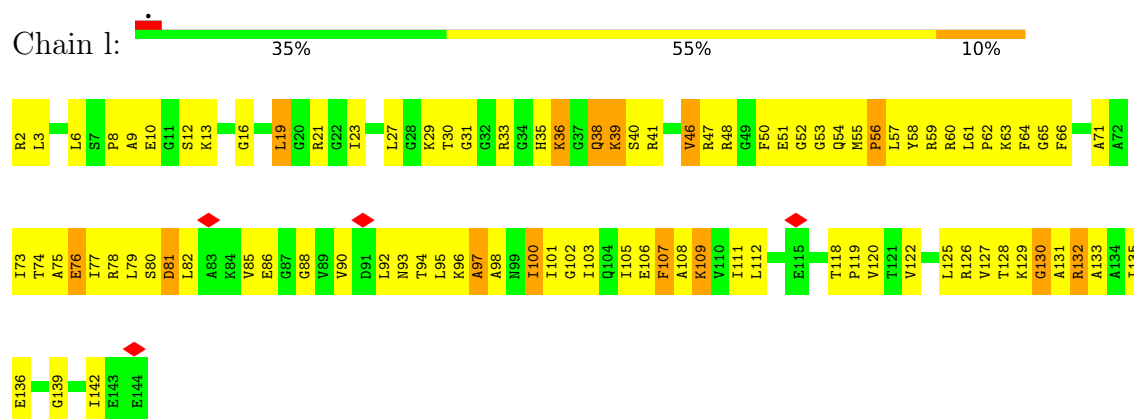
• Molecule 10: 50S ribosomal protein L14



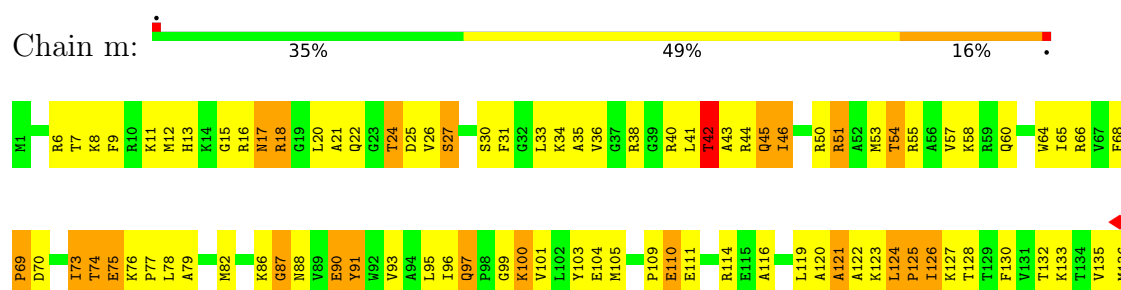
M1 I2 Q3 E4 Q5 T6 M7 L8 V10 A11 D12 M13 S14 G15 A16 R17 R18 V19 M20 C21 T22 K23 V24 L25 S28 H29 R30 R31 Y32 A33 G34 V35 G36 D37 T38 I39 K40 T41 T42 T43 K44 K45 A46 P47 P48 R49 G50 K54 V57 L58 K59 A60 V61 V62 V63 R64

T65 K66 K67 G68 V69 R70 R71 F72 L73 S74 V75 V76 T77 R78 F79 N82 A83 C84 R85 L86 L87 N88 N89 N90 S91 E92 Q93 P94 I95 R98 I99 F100 T104 R105 E106 L107 R108 S109 E110 K111 F112 M113 K114 I115 I116 S117 L118 A119 V122

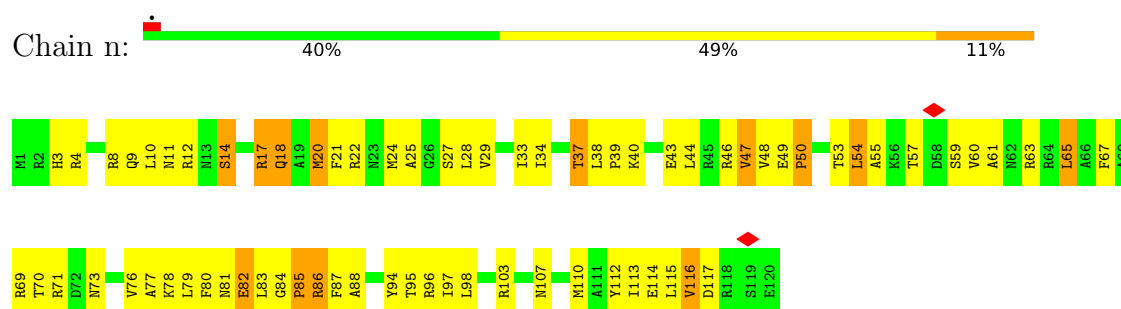
- Molecule 11: 50S ribosomal protein L15



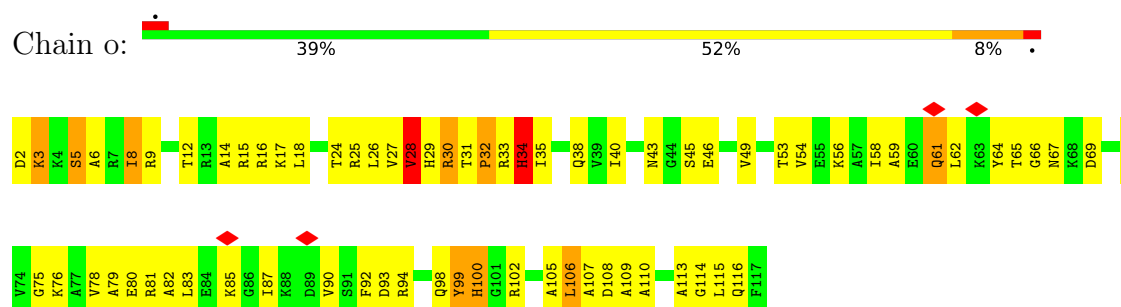
- Molecule 12: 50S ribosomal protein L16



- Molecule 13: 50S ribosomal protein L17



- Molecule 14: 50S ribosomal protein L18

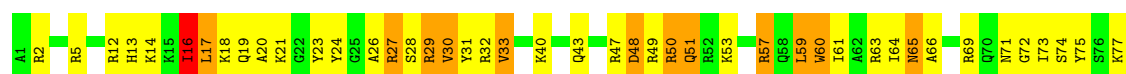


- Molecule 15: 50S ribosomal protein L19

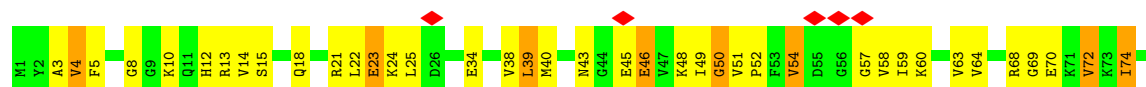




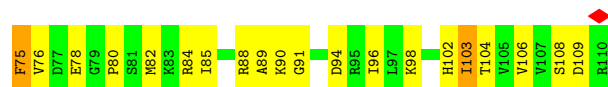
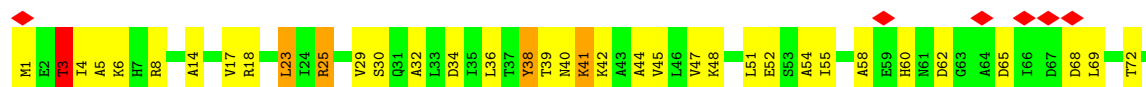
• Molecule 16: 50S ribosomal protein L20



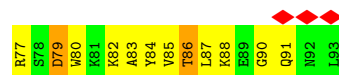
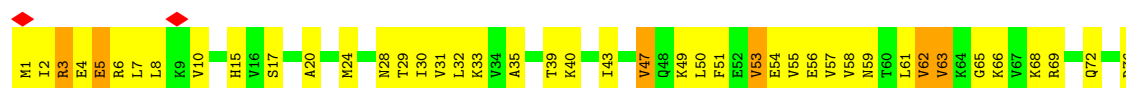
• Molecule 17: 50S ribosomal protein L21



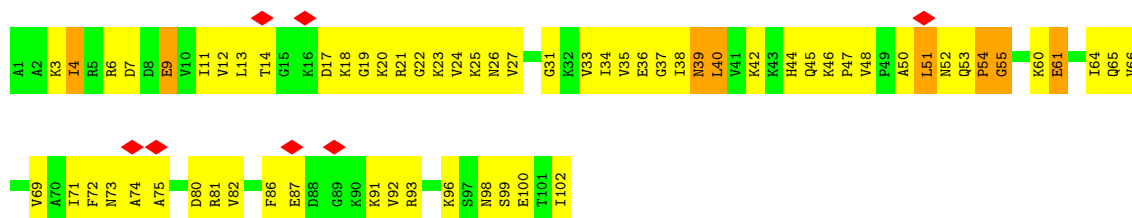
• Molecule 18: 50S ribosomal protein L22



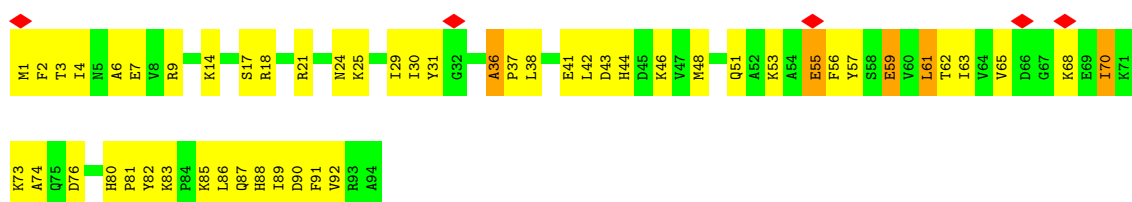
• Molecule 19: 50S ribosomal protein L23



- Molecule 20: 50S ribosomal protein L24



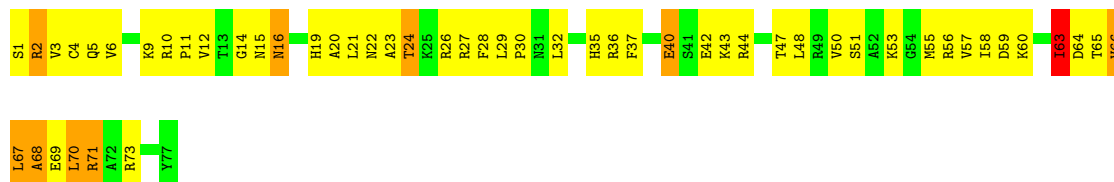
- Molecule 21: 50S ribosomal protein L25



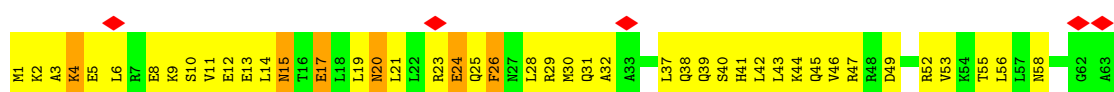
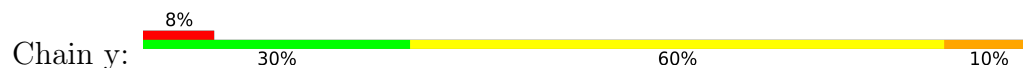
- Molecule 22: 50S ribosomal protein L27



- Molecule 23: 50S ribosomal protein L28



- Molecule 24: 50S ribosomal protein L29

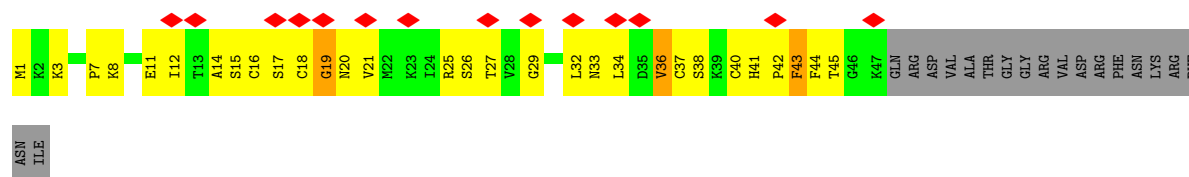


- Molecule 25: 50S ribosomal protein L30





- Molecule 26: 50S ribosomal protein L31



- Molecule 27: 50S ribosomal protein L32



- Molecule 28: 50S ribosomal protein L33



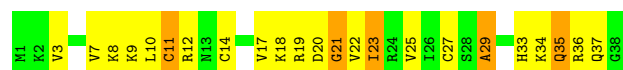
- Molecule 29: 50S ribosomal protein L34



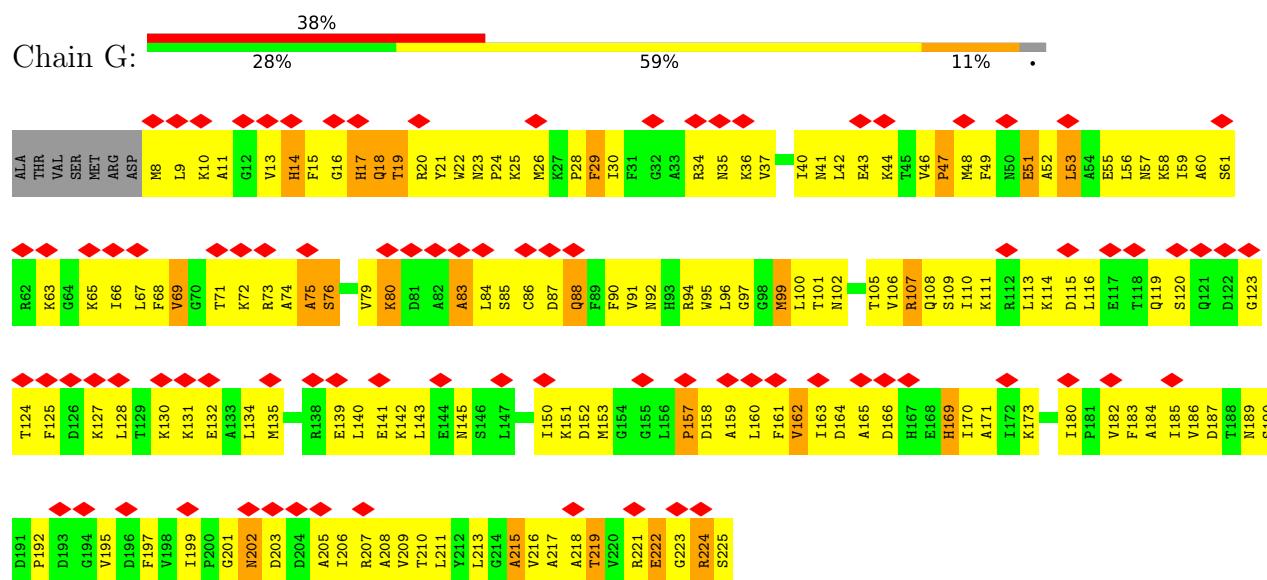
- Molecule 30: 50S ribosomal protein L35



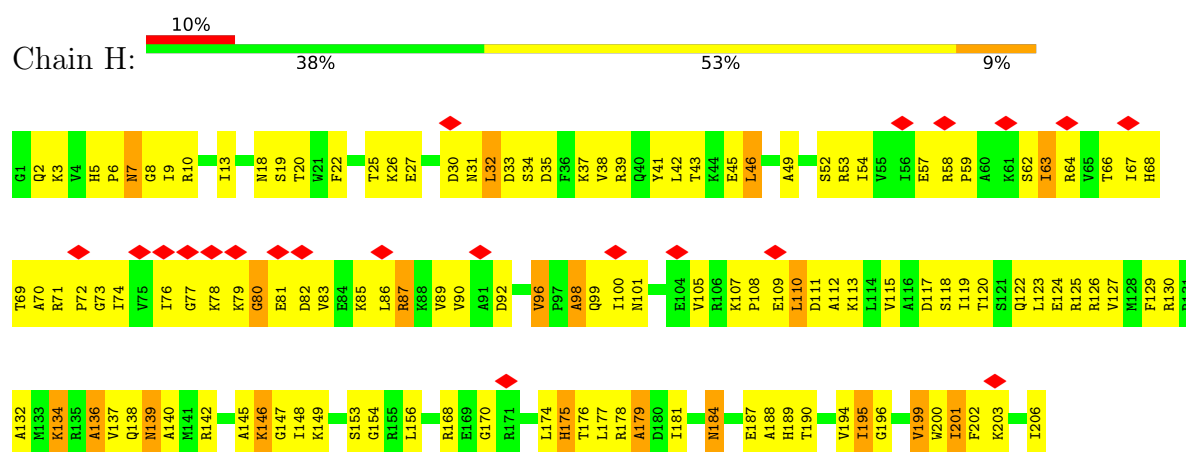
- Molecule 31: 50S ribosomal protein L36



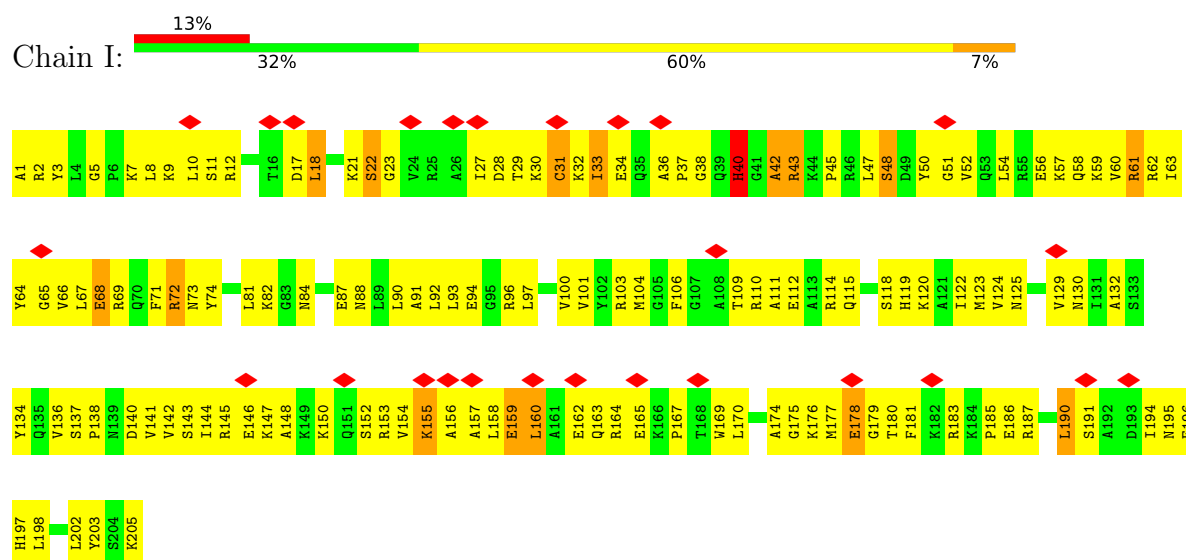
• Molecule 32: 30S ribosomal protein S2



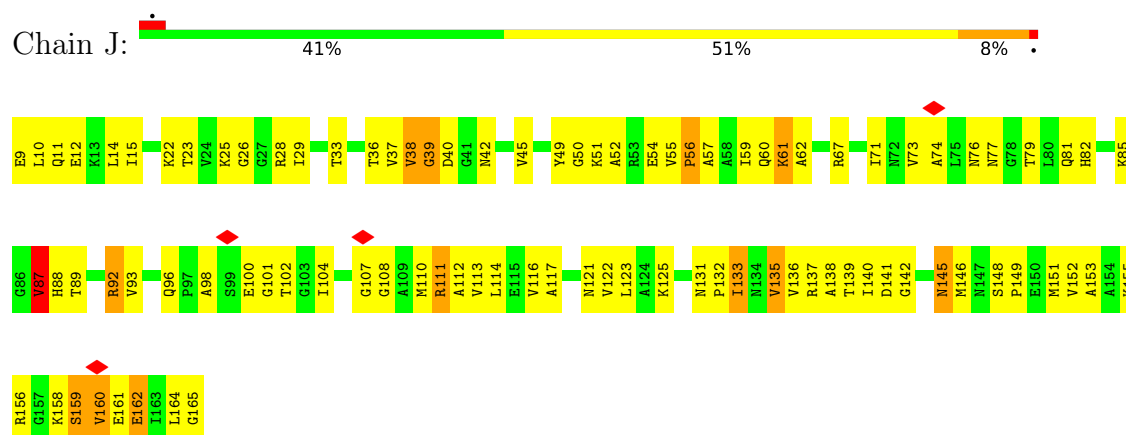
• Molecule 33: 30S ribosomal protein S3



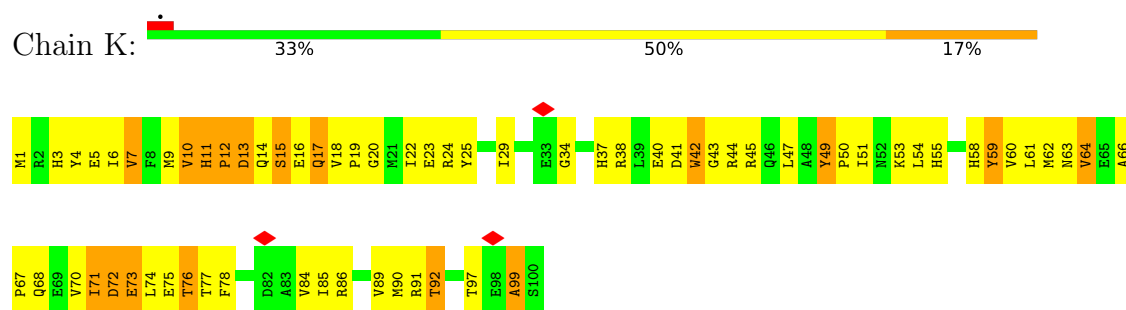
• Molecule 34: 30S ribosomal protein S4



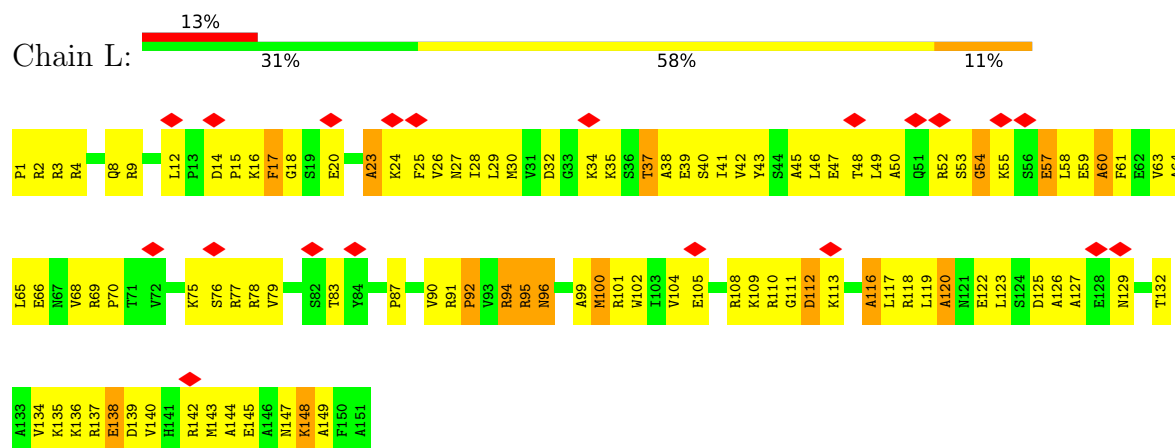
- Molecule 35: 30S ribosomal protein S5



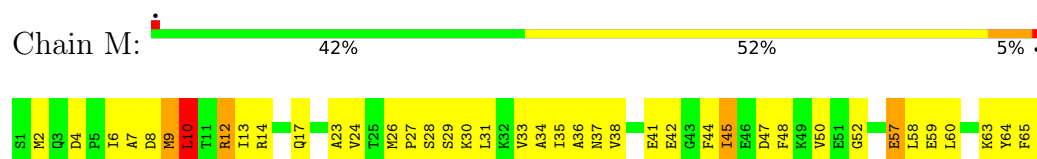
- Molecule 36: 30S ribosomal protein S6



- Molecule 37: 30S ribosomal protein S7

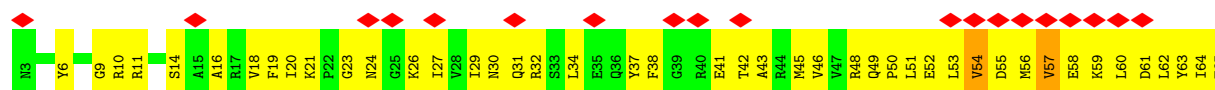


- Molecule 38: 30S ribosomal protein S8

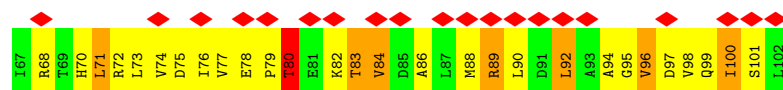




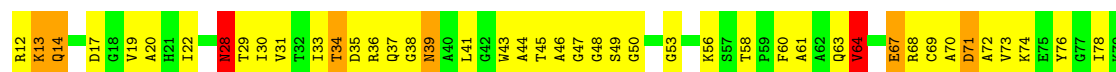
• Molecule 39: 30S ribosomal protein S9



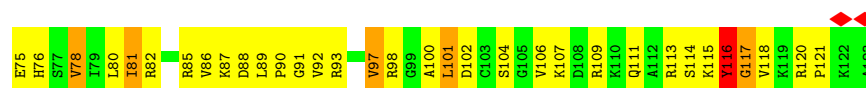
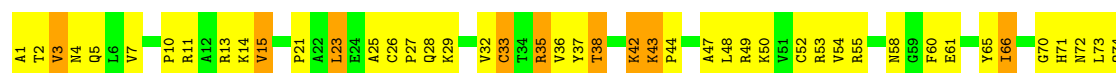
• Molecule 40: 30S ribosomal protein S10



• Molecule 41: 30S ribosomal protein S11

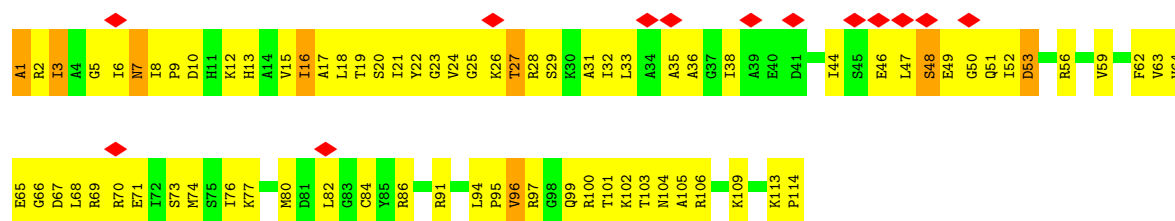


• Molecule 42: 30S ribosomal protein S12

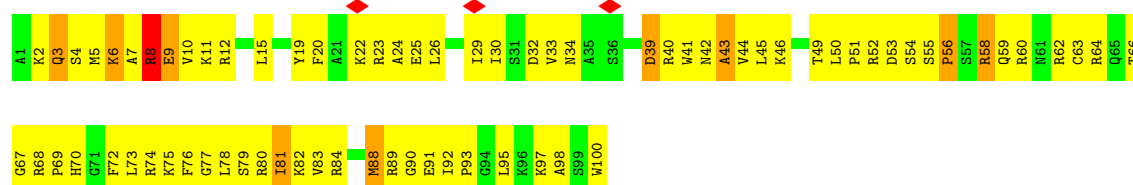


• Molecule 43: 30S ribosomal protein S13

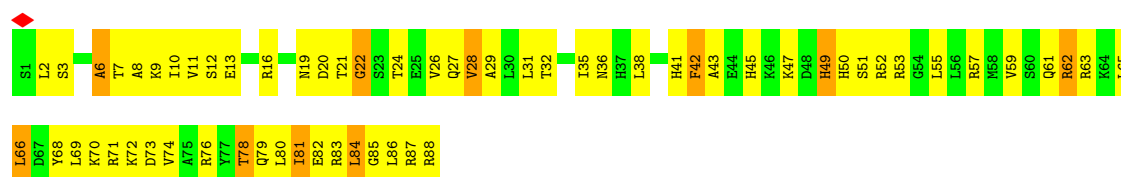




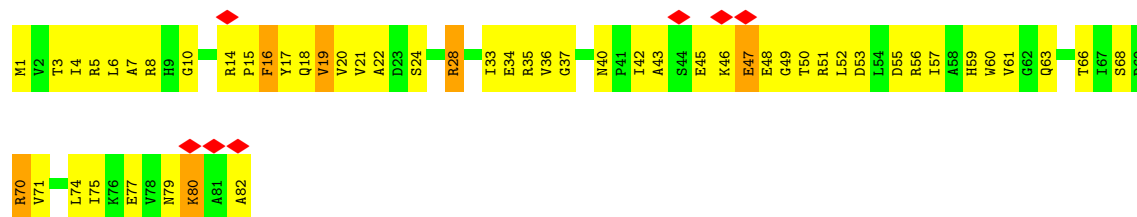
• Molecule 44: 30S ribosomal protein S14



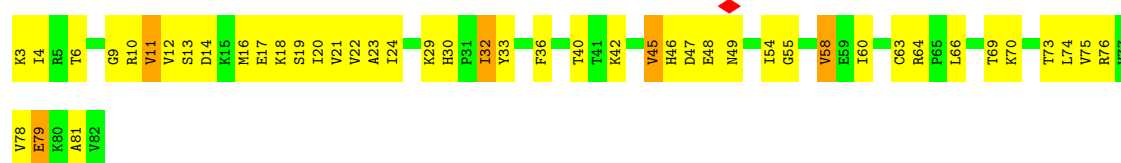
• Molecule 45: 30S ribosomal protein S15



• Molecule 46: 30S ribosomal protein S16

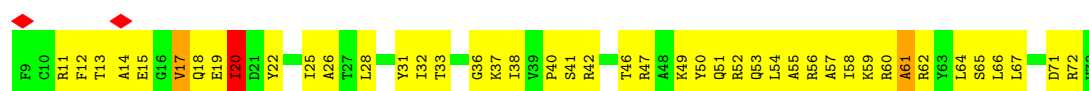


• Molecule 47: 30S ribosomal protein S17



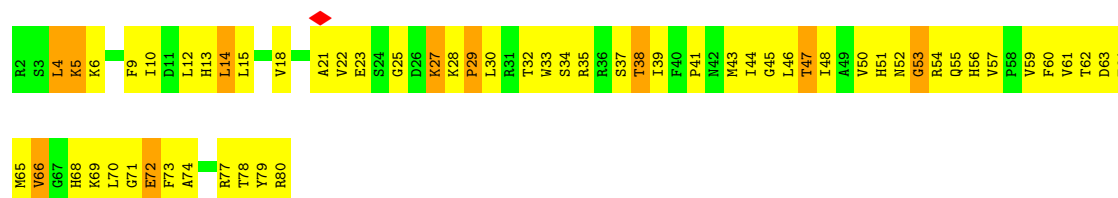
• Molecule 48: 30S ribosomal protein S18

Chain W:  32% 63%



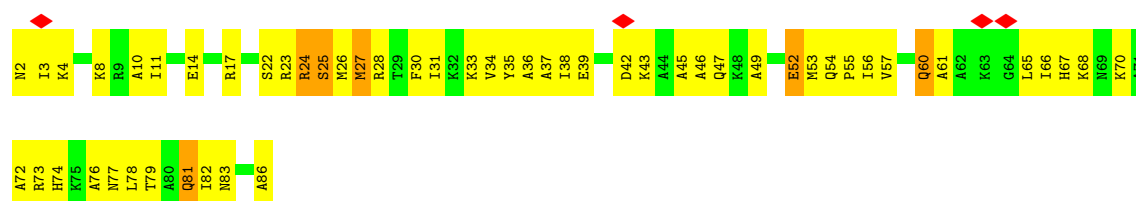
- Molecule 49: 30S ribosomal protein S19

Chain X:  25% 62% 13%

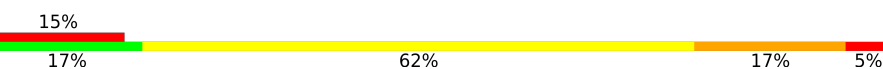


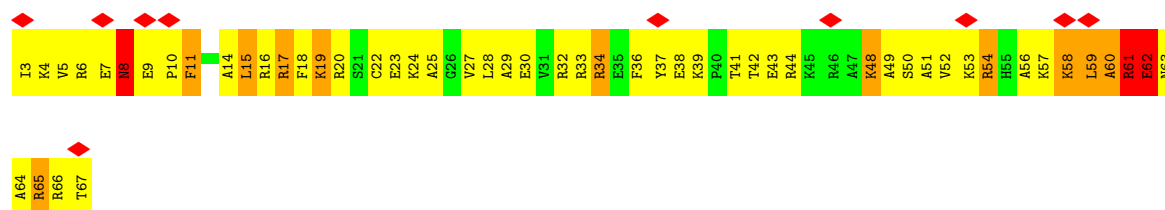
- Molecule 50: 30S ribosomal protein S20

Chain Y:  5% 36% 56% 7%

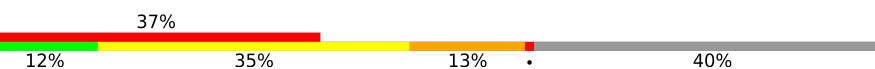


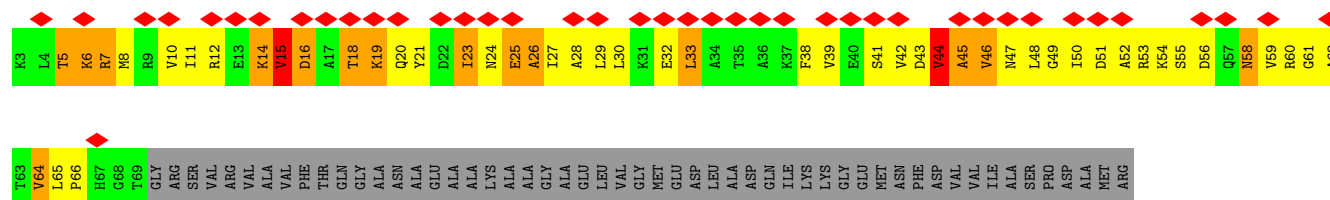
- Molecule 51: 30S ribosomal protein S21

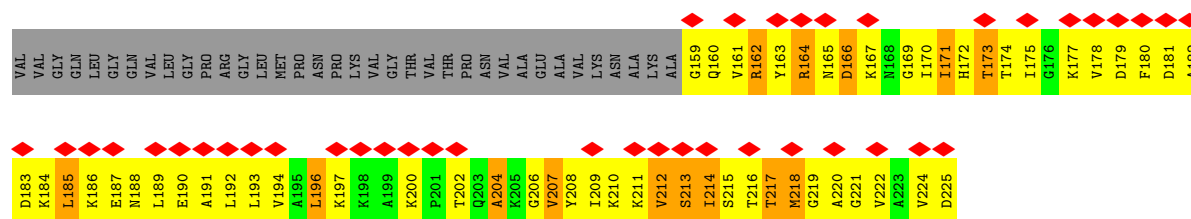
Chain Z:  15% 17% 62% 17% 5%



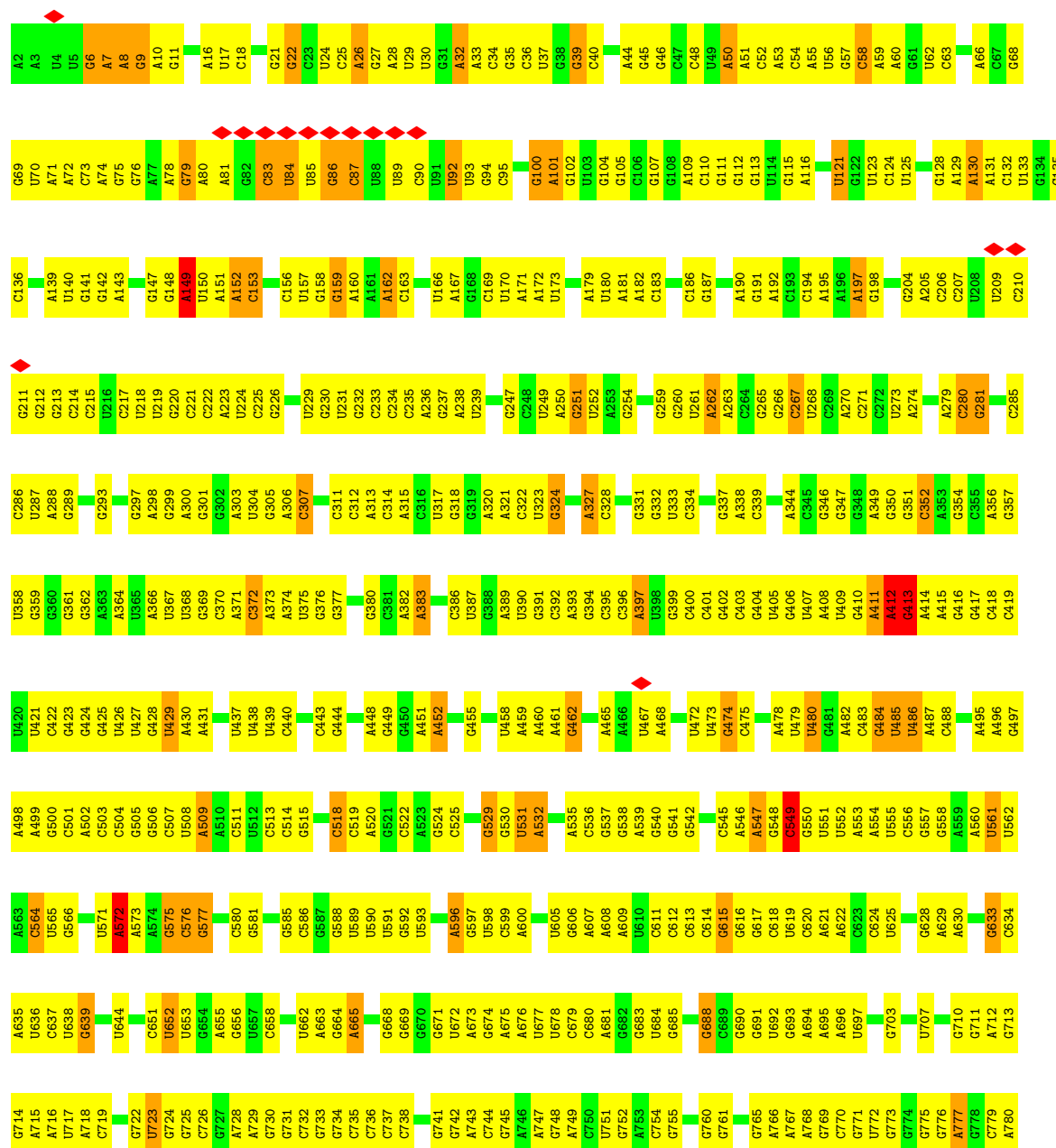
- Molecule 52: 50S ribosomal protein L1

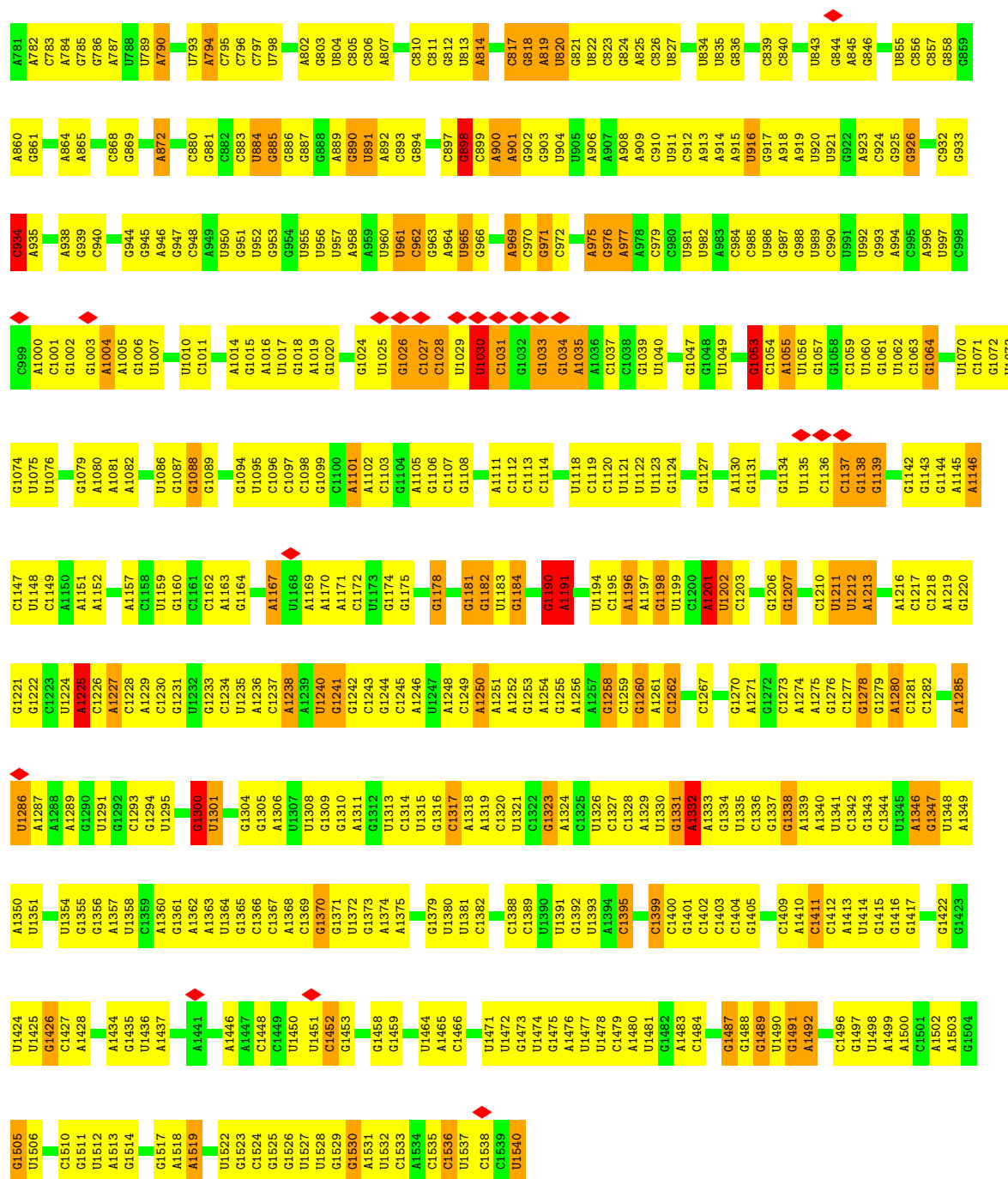
Chain a:  12% 37% 35% 13% 40%





• Molecule 53: 16S ribosomal RNA

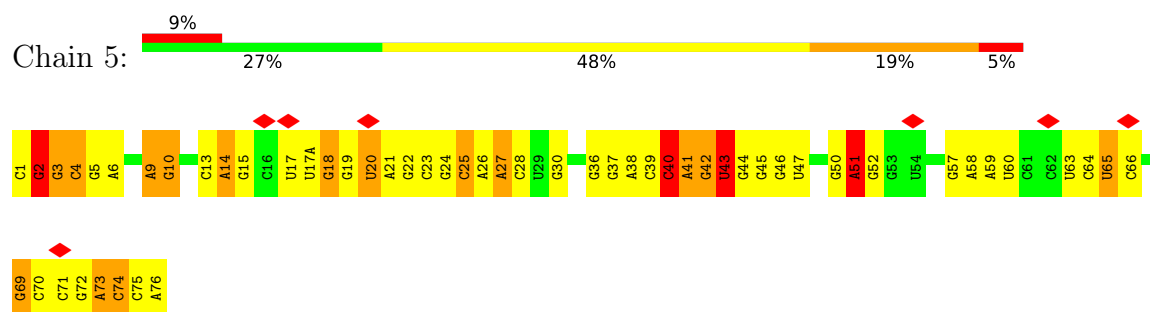




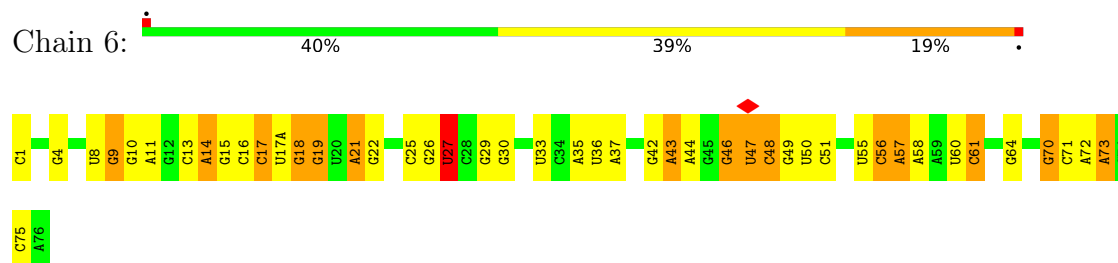
A1103	C1104	U1105	G1106	C1107	U1108	G1109	C1110	A1111	G1112	U1113	C1114	G1115	G1120	G1121	G1122	C1123	U1124	U1130	U1131	U1132	A1133	G1135	G1136	G1137	G1138	G1139	C1140	U1141	A1142	A1143	A1144	G1149	C1150	A1151	C1152	C1153	G1154	A1155	A1156	G1157	C1158	A1084	A1085	A1086	G1087	A1088	A1089	A1090	G1091	C1092	G1093	U1094	A1095	A1096	U1097	A1098	G1099	C1100	U1101	C1102
G1038	A1039	G966	U967	C968	G969	U970	G971	A972	G973	G974	A975	A980	A983	A984	A988	G989	A990	G991	C992	G993	C994	C995	A996	G997	C998	U999	A1000	A1001	A1002	G1003	C1005	C1006	C1007	A1010	G1011	U1012	C1013	A1014	U1015	G1016	U1019	A1020	G1021	G1022	U1023	G1024	G1025	U1026	A1027	A1028	A1029	C1030	U1033	A896	A897	C897				
A830	G831	U832	A833	G834	C840	G841	U842	G843	A844	U845	U846	U847	A848	A849	U850	C851	U852	C853	G857	G858	A863	C865	U868	U871	U872	C873	G876	A877	A878	G882	A883	G884	G885	C876	A877	A878	G879	G880	G881	G882	U883	A884	C885	A886	U887	C888	C889	C890	G891	A892	C893	U894	U895	C896	A899	G900	C901	U902		
U769	G770	G771	C772	U773	G774	G775	G776	G777	G778	U779	A780	A781	A782	U783	G784	C785	G786	G787	A788	A789	U790	C791	G792	A793	A794	G797	G798	G799	A800	G801	A802	U803	A804	C806	U807	G808	G809	U810	U811	C812	U813	C814	C815	U816	U817	A818	A819	A820	G821	G822	U823	A824	A825	U826	U827	U828	A829			
G704	A705	A706	U710	U711	G713	U714	A715	A716	C717	U718	C719	U720	C584	A721	A722	A723	U724	G725	G726	A727	G728	G729	A730	C731	A734	A735	A736	C737	G738	A739	A740	U741	A742	A743	U744	G745	U746	C747	G748	A752	A753	U754	U755	U756	A757	C758	G759	U760	A761	U762	G763	A764	G765	U766	U767	G768				
A637	G638	U639	C640	U641	C645	U646	U647	G648	G649	C650	A654	A655	G656	U657	U658	A661	G662	G663	A664	U665	A666	A667	A668	G669	A670	C671	C672	C673	A674	A675	A676	A677	C678	C679	C680	G681	G682	U683	G684	A685	U686	C687	U688	A689	G690	C691	C692	A693	U694	G695	A699	G700	C655	U666	G701	U702	U703			
U569	G570	U571	A572	U573	A574	A575	U576	U577	G578	U579	U580	C581	A582	G583	C584	U585	A586	C587	U588	U589	A590	A591	A592	U593	U594	C595	G596	G597	A598	A599	G600	A603	U607	A608	A609	C610	G611	G612	A613	A614	A621	G622	C623	G624	G625	A626	A627	G628	U629	G630	A631	A632	A633	C634	U635	U636				
C509	C510	U511	G512	A513	A514	A515	C516	C517	G518	U519	A449	G450	U451	A522	C523	G524	U525	A526	C527	A528	G530	A531	A532	G533	U534	G535	G536	G537	A538	A539	A540	A541	C542	G543	C544	U545	U546	A547	G548	G549	C550	G551	U552	G553	U554	G555	A556	C557	U558	G559	C560	U561	U562	A563	C564	C565	U566	U567	U568	
U569	G570	U571	A572	U573	A574	A575	U576	U577	G578	U579	U580	C581	A582	G583	C584	U585	A586	C587	U588	U589	A590	A591	A592	U593	U594	C595	G596	G597	A598	A599	G600	A603	U607	A608	A609	C610	G611	G612	A613	A614	A621	G622	C623	G624	G625	A626	A627	G628	U629	G630	A631	A632	A633	C634	U635	U636				
A637	G638	U639	C640	U641	C645	U646	U647	G648	G649	C650	A654	A655	G656	U657	U658	A661	G662	G663	A664	U665	A666	A667	A668	G669	A670	C671	C672	C673	A674	A675	A676	A677	C678	C679	C680	G681	G682	U683	G684	A685	U686	C687	U688	A689	G690	C691	C692	A693	U694	G695	A699	G700	C655	U666	G701	U702	U703			







- Molecule 57: tRNAfMet



- Molecule 58: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	3658	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.2	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	20.138	Depositor
Minimum map value	-7.423	Depositor
Average map value	0.007	Depositor
Map value standard deviation	1.205	Depositor
Recommended contour level	3.5	Depositor
Map size (Å)	424.96, 424.96, 424.96	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: FME

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	b	0.97	11/2122 (0.5%)	1.21	11/2852 (0.4%)
2	c	1.01	7/1586 (0.4%)	1.17	8/2134 (0.4%)
3	d	1.16	16/1571 (1.0%)	1.25	5/2113 (0.2%)
4	e	1.32	21/1435 (1.5%)	1.34	24/1926 (1.2%)
5	f	1.14	13/1343 (1.0%)	1.30	18/1816 (1.0%)
6	g	1.29	7/445 (1.6%)	1.49	10/597 (1.7%)
7	h	1.85	17/597 (2.8%)	1.70	21/803 (2.6%)
8	i	2.07	19/513 (3.7%)	1.83	22/684 (3.2%)
9	j	0.90	6/1152 (0.5%)	1.14	12/1551 (0.8%)
10	k	1.05	5/948 (0.5%)	1.45	18/1268 (1.4%)
11	l	0.94	5/1054 (0.5%)	1.26	10/1403 (0.7%)
12	m	1.22	16/1093 (1.5%)	1.33	14/1460 (1.0%)
13	n	0.98	7/974 (0.7%)	1.16	10/1301 (0.8%)
14	o	1.23	9/902 (1.0%)	1.27	15/1209 (1.2%)
15	p	0.75	0/929	1.06	2/1242 (0.2%)
16	q	1.07	7/960 (0.7%)	1.33	14/1278 (1.1%)
17	r	0.84	3/829 (0.4%)	1.10	3/1107 (0.3%)
18	s	1.02	4/864 (0.5%)	1.25	11/1156 (1.0%)
19	t	0.97	6/745 (0.8%)	1.19	10/994 (1.0%)
20	u	0.79	1/788 (0.1%)	1.11	5/1051 (0.5%)
21	v	0.94	4/766 (0.5%)	1.18	2/1025 (0.2%)
22	w	0.80	1/582 (0.2%)	1.04	0/769
23	x	1.13	8/635 (1.3%)	1.24	4/848 (0.5%)
24	y	0.99	4/510 (0.8%)	1.17	1/677 (0.1%)
25	z	0.85	1/453 (0.2%)	1.11	1/605 (0.2%)
26	A	0.98	2/371 (0.5%)	1.17	3/496 (0.6%)
27	B	0.78	0/450	1.03	3/599 (0.5%)
28	C	0.83	1/417 (0.2%)	0.92	0/554
29	D	0.95	1/380 (0.3%)	1.16	4/498 (0.8%)
30	E	0.96	3/513 (0.6%)	1.23	4/676 (0.6%)
31	F	1.07	2/303 (0.7%)	1.35	6/397 (1.5%)
32	G	1.19	25/1736 (1.4%)	1.31	22/2338 (0.9%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	H	1.21	17/1652 (1.0%)	1.27	20/2225 (0.9%)
34	I	1.00	11/1665 (0.7%)	1.23	13/2227 (0.6%)
35	J	1.10	7/1170 (0.6%)	1.32	17/1573 (1.1%)
36	K	1.49	12/836 (1.4%)	1.47	20/1128 (1.8%)
37	L	1.21	9/1196 (0.8%)	1.44	23/1602 (1.4%)
38	M	1.01	5/989 (0.5%)	1.24	10/1326 (0.8%)
39	N	0.86	4/1034 (0.4%)	1.02	3/1375 (0.2%)
40	O	1.20	7/797 (0.9%)	1.34	10/1077 (0.9%)
41	P	1.00	7/886 (0.8%)	1.27	8/1195 (0.7%)
42	Q	1.06	4/969 (0.4%)	1.19	6/1300 (0.5%)
43	R	1.25	10/893 (1.1%)	1.31	7/1193 (0.6%)
44	S	1.05	6/817 (0.7%)	1.14	5/1088 (0.5%)
45	T	1.08	6/722 (0.8%)	1.37	13/964 (1.3%)
46	U	0.87	2/659 (0.3%)	1.03	0/884
47	V	0.80	2/658 (0.3%)	1.06	1/881 (0.1%)
48	W	0.90	2/545 (0.4%)	1.17	4/731 (0.5%)
49	X	0.94	2/653 (0.3%)	1.19	7/877 (0.8%)
50	Y	1.12	7/671 (1.0%)	1.23	0/888
51	Z	1.13	4/551 (0.7%)	1.57	16/728 (2.2%)
52	a	1.58	23/1034 (2.2%)	1.56	27/1387 (1.9%)
53	3	0.64	0/36963	0.63	14/57662 (0.0%)
54	1	0.65	0/69796	0.65	47/108888 (0.0%)
55	2	0.57	0/2872	0.63	0/4479
56	5	0.63	0/1840	0.70	5/2868 (0.2%)
57	6	0.53	0/1832	0.63	0/2855
58	4	0.62	0/436	0.63	1/679 (0.1%)
All	All	0.80	379/160102 (0.2%)	0.85	570/239507 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
3	d	0	1
35	J	0	1
42	Q	0	1
53	3	0	42
54	1	0	113
55	2	0	4
56	5	0	4
57	6	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
58	4	0	1
All	All	0	169

The worst 5 of 379 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	e	73	VAL	C-O	19.62	1.46	1.23
36	K	13	ASP	C-O	18.27	1.45	1.24
7	h	44	ALA	C-O	15.30	1.44	1.24
3	d	150	THR	C-O	14.99	1.38	1.24
14	o	58	ILE	C-O	14.69	1.41	1.24

The worst 5 of 570 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	d	73	ILE	N-CA-C	-12.36	101.97	113.71
10	k	112	PHE	CA-C-N	-11.75	103.22	120.38
10	k	112	PHE	C-N-CA	-11.75	103.22	120.38
41	P	126	ARG	N-CA-C	11.11	123.90	110.91
36	K	13	ASP	CA-C-O	10.97	132.34	120.82

There are no chirality outliers.

5 of 169 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
53	3	26	A	Sidechain
53	3	58	C	Sidechain
35	J	92	ARG	Mainchain
42	Q	14	LYS	Peptide
3	d	102	ARG	Mainchain

5.2 Too-close contacts [i](#)

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	b	2083	0	2157	196	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	c	1565	0	1616	138	0
3	d	1552	0	1619	120	0
4	e	1411	0	1447	170	0
5	f	1323	0	1374	102	0
6	g	440	0	464	32	0
7	h	593	0	623	66	0
8	i	511	0	544	64	0
9	j	1129	0	1162	78	0
10	k	939	0	1012	138	0
11	l	1045	0	1117	126	0
12	m	1074	0	1157	110	0
13	n	961	0	1000	74	0
14	o	892	0	923	81	0
15	p	917	0	965	99	0
16	q	947	0	1022	91	0
17	r	816	0	839	71	0
18	s	857	0	922	49	0
19	t	739	0	807	55	0
20	u	780	0	834	69	0
21	v	753	0	780	56	0
22	w	575	0	592	46	0
23	x	625	0	655	61	0
24	y	509	0	543	62	0
25	z	449	0	491	29	0
26	A	364	0	366	32	0
27	B	444	0	461	32	0
28	C	410	0	440	25	0
29	D	377	0	418	40	0
30	E	504	0	574	49	0
31	F	302	0	343	25	0
32	G	1705	0	1732	163	0
33	H	1625	0	1699	140	0
34	I	1643	0	1710	161	0
35	J	1157	0	1199	100	0
36	K	818	0	808	78	0
37	L	1182	0	1240	136	0
38	M	979	0	1034	76	0
39	N	1022	0	1070	107	0
40	O	787	0	828	86	0
41	P	870	0	878	72	0
42	Q	955	0	1019	99	0
43	R	884	0	944	70	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	S	805	0	847	92	0
45	T	714	0	737	48	0
46	U	649	0	666	72	0
47	V	649	0	691	58	0
48	W	536	0	552	56	0
49	X	638	0	665	82	0
50	Y	665	0	714	67	0
51	Z	545	0	579	71	0
52	a	1027	0	1092	136	0
53	3	33012	0	16618	1111	0
54	1	62317	0	31346	2241	0
55	2	2568	0	1303	78	0
56	5	1647	0	831	57	0
57	6	1640	0	837	45	0
58	4	388	0	198	8	0
59	1	10	0	10	2	0
60	5	7	0	7	2	0
All	All	147330	0	99121	7238	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 29.

The worst 5 of 7238 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)
12:m:18:ARG:HB3	12:m:18:ARG:HH21	1.07	1.18
52:a:46:VAL:HG22	52:a:213:SER:H	1.10	1.15
42:Q:113:ARG:HB2	42:Q:118:VAL:HB	1.24	1.14
56:5:26:A:N6	56:5:44:G:H1	1.47	1.12
54:1:770:G:H2'	54:1:771:G:H5''	1.23	1.11

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	b	269/271 (99%)	216 (80%)	50 (19%)	3 (1%)	11	43
2	c	207/209 (99%)	160 (77%)	43 (21%)	4 (2%)	6	33
3	d	199/201 (99%)	154 (77%)	43 (22%)	2 (1%)	12	45
4	e	175/177 (99%)	143 (82%)	29 (17%)	3 (2%)	7	35
5	f	174/176 (99%)	139 (80%)	30 (17%)	5 (3%)	3	24
6	g	55/149 (37%)	40 (73%)	11 (20%)	4 (7%)	1	6
7	h	77/131 (59%)	49 (64%)	26 (34%)	2 (3%)	4	26
8	i	69/141 (49%)	59 (86%)	9 (13%)	1 (1%)	9	39
9	j	140/142 (99%)	114 (81%)	24 (17%)	2 (1%)	9	39
10	k	120/122 (98%)	88 (73%)	28 (23%)	4 (3%)	3	21
11	l	141/143 (99%)	99 (70%)	37 (26%)	5 (4%)	3	20
12	m	134/136 (98%)	113 (84%)	17 (13%)	4 (3%)	3	23
13	n	118/120 (98%)	97 (82%)	20 (17%)	1 (1%)	16	50
14	o	114/116 (98%)	94 (82%)	18 (16%)	2 (2%)	6	34
15	p	112/114 (98%)	88 (79%)	23 (20%)	1 (1%)	14	47
16	q	115/117 (98%)	99 (86%)	14 (12%)	2 (2%)	7	35
17	r	101/103 (98%)	78 (77%)	22 (22%)	1 (1%)	12	45
18	s	108/110 (98%)	93 (86%)	14 (13%)	1 (1%)	14	47
19	t	91/93 (98%)	77 (85%)	12 (13%)	2 (2%)	5	29
20	u	100/102 (98%)	76 (76%)	21 (21%)	3 (3%)	3	23
21	v	92/94 (98%)	82 (89%)	10 (11%)	0	100	100
22	w	73/75 (97%)	59 (81%)	12 (16%)	2 (3%)	4	25
23	x	75/77 (97%)	64 (85%)	10 (13%)	1 (1%)	9	40
24	y	61/63 (97%)	53 (87%)	7 (12%)	1 (2%)	7	36
25	z	56/58 (97%)	50 (89%)	5 (9%)	1 (2%)	6	34
26	A	45/66 (68%)	32 (71%)	12 (27%)	1 (2%)	5	29
27	B	54/56 (96%)	38 (70%)	14 (26%)	2 (4%)	2	18
28	C	48/50 (96%)	41 (85%)	7 (15%)	0	100	100
29	D	44/46 (96%)	35 (80%)	9 (20%)	0	100	100
30	E	62/64 (97%)	49 (79%)	12 (19%)	1 (2%)	7	36

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	F	36/38 (95%)	26 (72%)	9 (25%)	1 (3%)	4	25
32	G	216/225 (96%)	170 (79%)	43 (20%)	3 (1%)	9	39
33	H	204/206 (99%)	172 (84%)	32 (16%)	0	100	100
34	I	203/205 (99%)	154 (76%)	48 (24%)	1 (0%)	24	59
35	J	155/157 (99%)	117 (76%)	36 (23%)	2 (1%)	9	40
36	K	98/100 (98%)	73 (74%)	24 (24%)	1 (1%)	12	45
37	L	149/151 (99%)	117 (78%)	30 (20%)	2 (1%)	9	40
38	M	127/129 (98%)	114 (90%)	10 (8%)	3 (2%)	4	28
39	N	125/127 (98%)	88 (70%)	34 (27%)	3 (2%)	4	28
40	O	96/98 (98%)	75 (78%)	17 (18%)	4 (4%)	2	16
41	P	114/116 (98%)	86 (75%)	23 (20%)	5 (4%)	2	15
42	Q	121/123 (98%)	85 (70%)	31 (26%)	5 (4%)	2	17
43	R	112/114 (98%)	96 (86%)	15 (13%)	1 (1%)	14	47
44	S	98/100 (98%)	74 (76%)	22 (22%)	2 (2%)	6	31
45	T	86/88 (98%)	75 (87%)	11 (13%)	0	100	100
46	U	80/82 (98%)	61 (76%)	16 (20%)	3 (4%)	2	18
47	V	78/80 (98%)	59 (76%)	19 (24%)	0	100	100
48	W	63/65 (97%)	48 (76%)	12 (19%)	3 (5%)	2	14
49	X	77/79 (98%)	61 (79%)	15 (20%)	1 (1%)	9	40
50	Y	83/85 (98%)	73 (88%)	10 (12%)	0	100	100
51	Z	63/65 (97%)	36 (57%)	20 (32%)	7 (11%)	0	2
52	a	130/223 (58%)	100 (77%)	26 (20%)	4 (3%)	3	22
All	All	5743/6178 (93%)	4539 (79%)	1092 (19%)	112 (2%)	8	31

5 of 112 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	h	72	LEU
10	k	92	GLU
10	k	105	ARG
11	l	38	GLN
11	l	39	LYS

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	b	216/216 (100%)	199 (92%)	17 (8%)	11	40
2	c	164/164 (100%)	154 (94%)	10 (6%)	17	49
3	d	165/165 (100%)	162 (98%)	3 (2%)	51	74
4	e	148/148 (100%)	145 (98%)	3 (2%)	48	72
5	f	137/137 (100%)	135 (98%)	2 (2%)	57	76
6	g	45/114 (40%)	44 (98%)	1 (2%)	45	71
7	h	62/100 (62%)	60 (97%)	2 (3%)	34	65
8	i	53/109 (49%)	50 (94%)	3 (6%)	18	51
9	j	116/116 (100%)	111 (96%)	5 (4%)	26	59
10	k	103/103 (100%)	93 (90%)	10 (10%)	8	32
11	l	102/102 (100%)	99 (97%)	3 (3%)	37	67
12	m	109/109 (100%)	99 (91%)	10 (9%)	8	33
13	n	100/100 (100%)	95 (95%)	5 (5%)	22	55
14	o	86/86 (100%)	84 (98%)	2 (2%)	44	70
15	p	99/99 (100%)	92 (93%)	7 (7%)	13	44
16	q	89/89 (100%)	83 (93%)	6 (7%)	15	47
17	r	84/84 (100%)	83 (99%)	1 (1%)	63	79
18	s	93/93 (100%)	89 (96%)	4 (4%)	26	59
19	t	80/80 (100%)	80 (100%)	0	100	100
20	u	83/83 (100%)	80 (96%)	3 (4%)	31	63
21	v	78/78 (100%)	75 (96%)	3 (4%)	29	62
22	w	57/57 (100%)	54 (95%)	3 (5%)	20	53
23	x	67/67 (100%)	64 (96%)	3 (4%)	24	58
24	y	55/55 (100%)	55 (100%)	0	100	100
25	z	48/48 (100%)	46 (96%)	2 (4%)	26	60
26	A	43/59 (73%)	42 (98%)	1 (2%)	44	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	B	47/47 (100%)	47 (100%)	0	100	100
28	C	45/45 (100%)	44 (98%)	1 (2%)	45	71
29	D	38/38 (100%)	38 (100%)	0	100	100
30	E	51/51 (100%)	47 (92%)	4 (8%)	11	41
31	F	34/34 (100%)	33 (97%)	1 (3%)	37	67
32	G	180/186 (97%)	179 (99%)	1 (1%)	78	84
33	H	170/170 (100%)	168 (99%)	2 (1%)	63	79
34	I	172/172 (100%)	165 (96%)	7 (4%)	27	60
35	J	119/119 (100%)	115 (97%)	4 (3%)	32	64
36	K	87/87 (100%)	83 (95%)	4 (5%)	24	58
37	L	124/124 (100%)	123 (99%)	1 (1%)	73	82
38	M	104/104 (100%)	100 (96%)	4 (4%)	29	62
39	N	105/105 (100%)	104 (99%)	1 (1%)	68	80
40	O	86/86 (100%)	81 (94%)	5 (6%)	18	51
41	P	89/89 (100%)	87 (98%)	2 (2%)	45	71
42	Q	103/103 (100%)	97 (94%)	6 (6%)	18	51
43	R	92/92 (100%)	91 (99%)	1 (1%)	65	79
44	S	83/83 (100%)	78 (94%)	5 (6%)	17	50
45	T	76/76 (100%)	71 (93%)	5 (7%)	15	47
46	U	65/65 (100%)	61 (94%)	4 (6%)	16	49
47	V	74/74 (100%)	70 (95%)	4 (5%)	20	53
48	W	56/56 (100%)	56 (100%)	0	100	100
49	X	70/70 (100%)	66 (94%)	4 (6%)	18	51
50	Y	65/65 (100%)	64 (98%)	1 (2%)	57	76
51	Z	55/55 (100%)	53 (96%)	2 (4%)	31	63
52	a	110/174 (63%)	104 (94%)	6 (6%)	19	52
All	All	4782/5031 (95%)	4598 (96%)	184 (4%)	30	62

5 of 184 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	G	29	PHE
40	O	100	ILE

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Mol	Chain	Res	Type
34	I	22	SER
36	K	49	TYR
42	Q	81	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 78 such sidechains are listed below:

Mol	Chain	Res	Type
36	K	17	GLN
48	W	51	GLN
39	N	31	GLN
45	T	61	GLN
51	Z	8	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
53	3	1538/1539 (99%)	207 (13%)	10 (0%)
54	1	2902/2903 (99%)	465 (16%)	27 (0%)
55	2	119/120 (99%)	14 (11%)	1 (0%)
56	5	76/77 (98%)	20 (26%)	2 (2%)
57	6	76/77 (98%)	20 (26%)	0
58	4	17/18 (94%)	4 (23%)	0
All	All	4728/4734 (99%)	730 (15%)	40 (0%)

5 of 730 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
53	3	6	G
53	3	7	A
53	3	8	A
53	3	9	G
53	3	22	G

5 of 40 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
54	1	2238	G
54	1	2790	U
54	1	2277	G
54	1	2326	C

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Mol	Chain	Res	Type
55	2	88	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	$\# Z > 2$
59	FME	1	3001	60	8,9,10	0.57	0	8,9,11	0.86	0
60	PRO	5	101	56,59	6,7,8	0.51	0	7,8,10	1.30	1 (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
59	FME	1	3001	60	-	2/7/9/11	-
60	PRO	5	101	56,59	-	0/0/9/11	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	5	101	PRO	O-C-CA	-2.68	117.89	124.77

There are no chirality outliers.

All (2) torsion outliers are listed below:

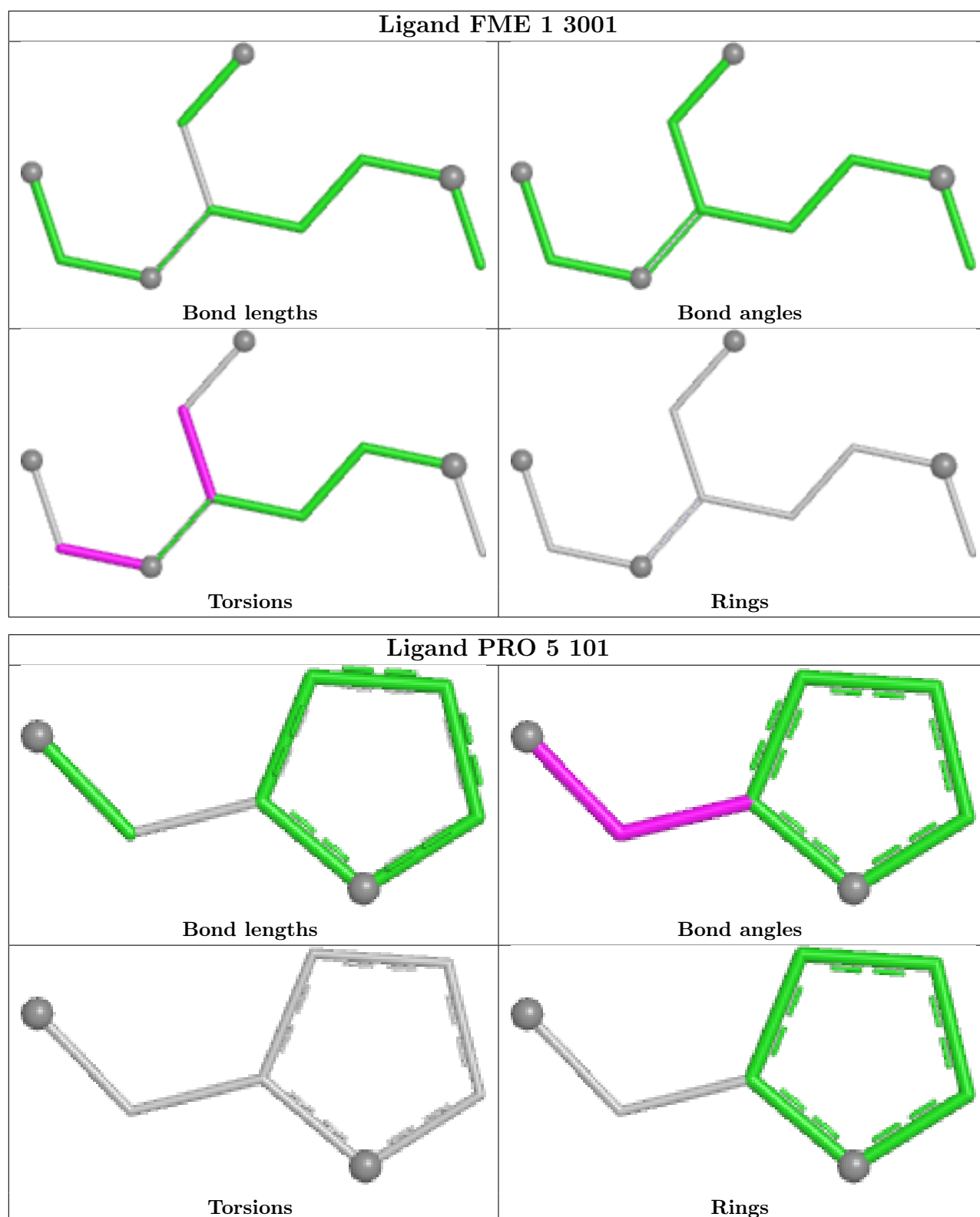
Mol	Chain	Res	Type	Atoms
59	1	3001	FME	O1-CN-N-CA
59	1	3001	FME	O-C-CA-CB

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	1	3001	FME	2	0
60	5	101	PRO	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

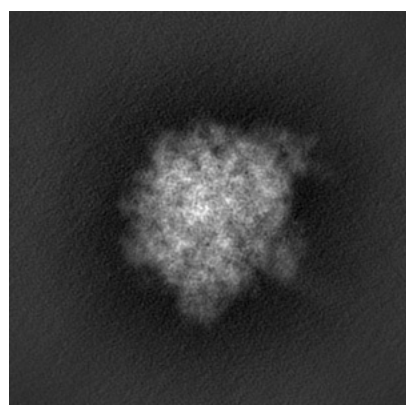
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23528. These allow visual inspection of the internal detail of the map and identification of artifacts.

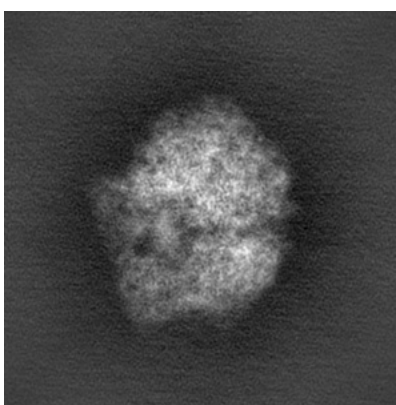
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

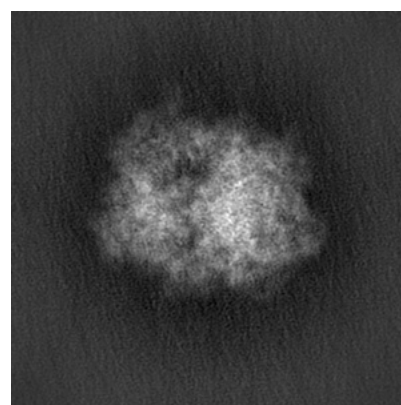
6.1.1 Primary map



X



Y

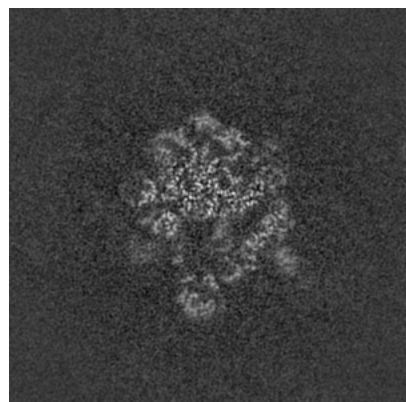


Z

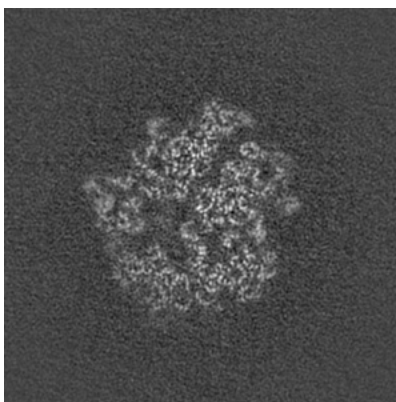
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

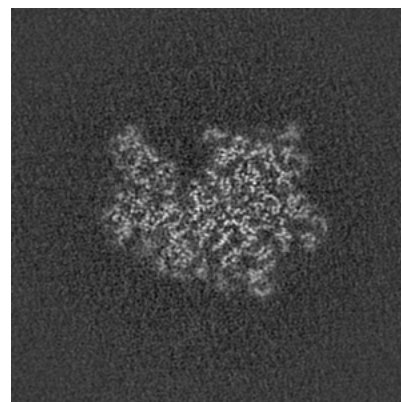
6.2.1 Primary map



X Index: 256



Y Index: 256

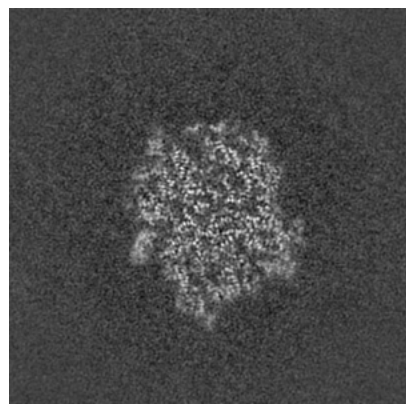


Z Index: 256

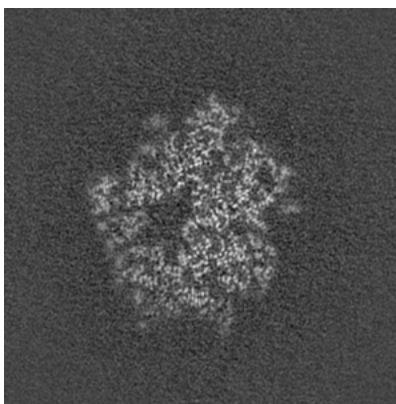
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

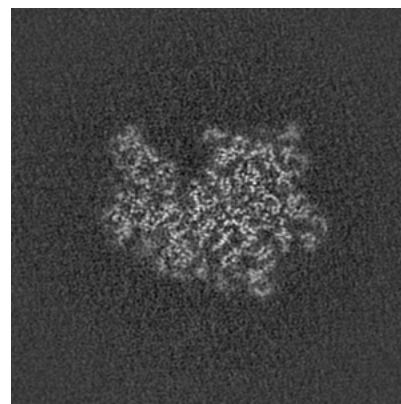
6.3.1 Primary map



X Index: 284



Y Index: 247

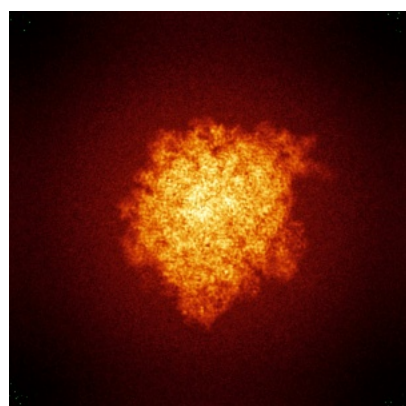


Z Index: 256

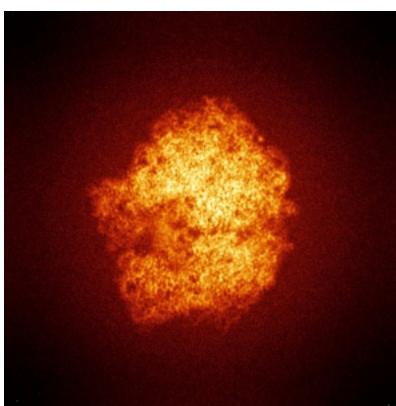
The images above show the largest variance slices of the map in three orthogonal directions.

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

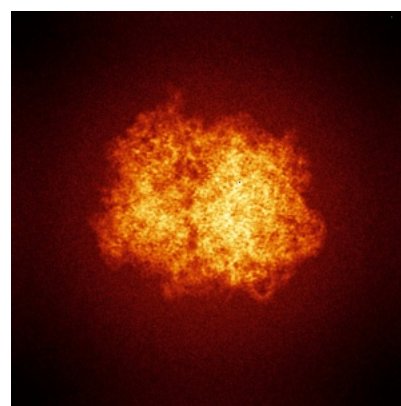
6.4.1 Primary map



X



Y

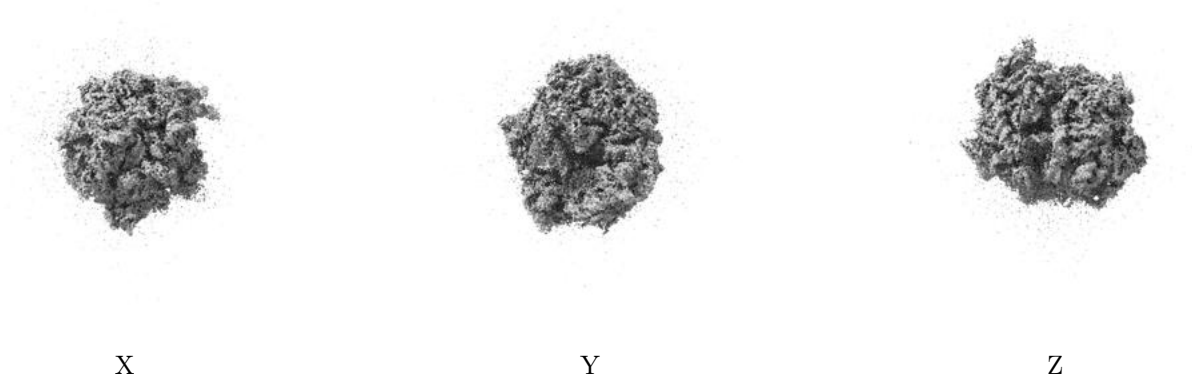


Z

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

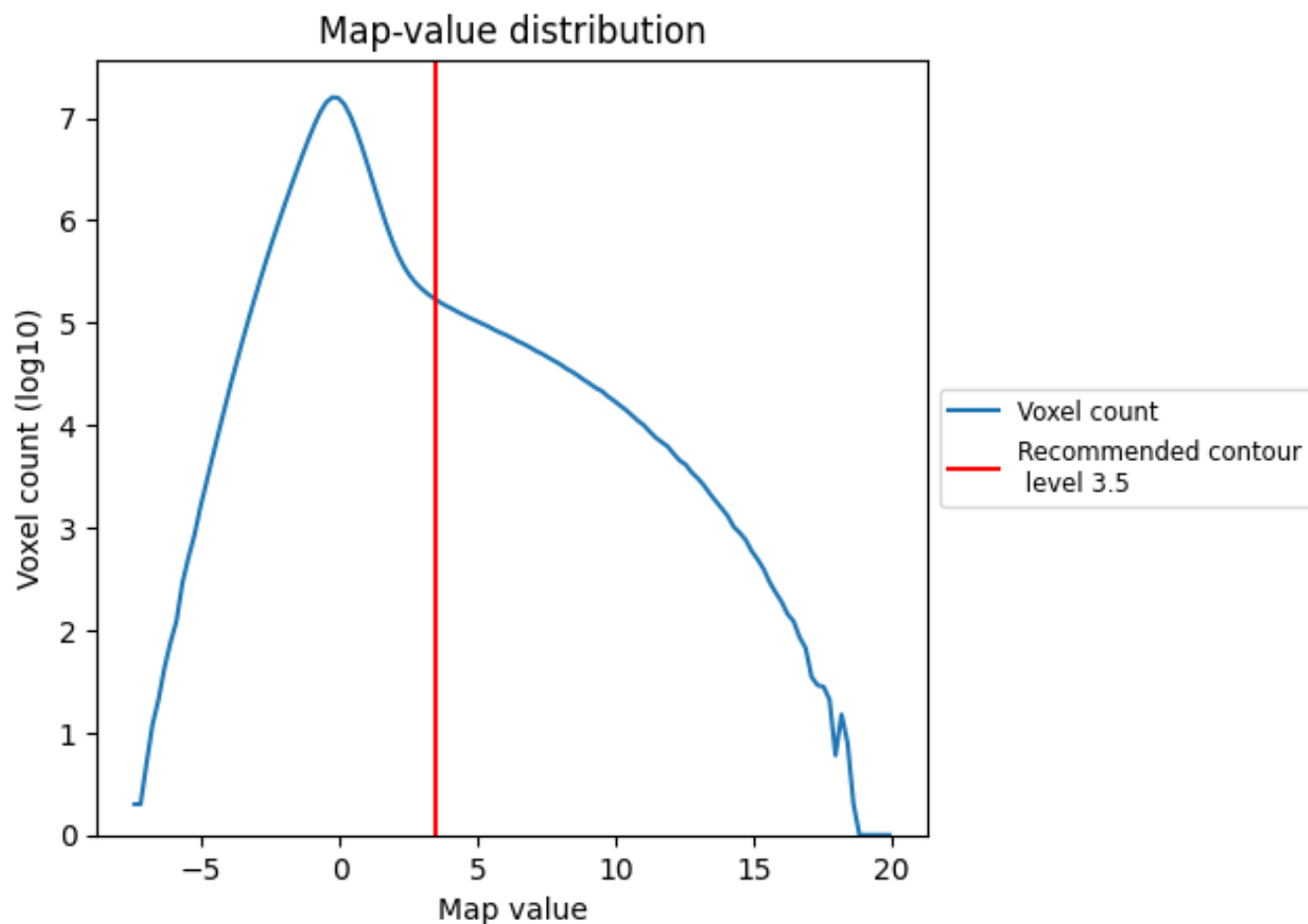
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

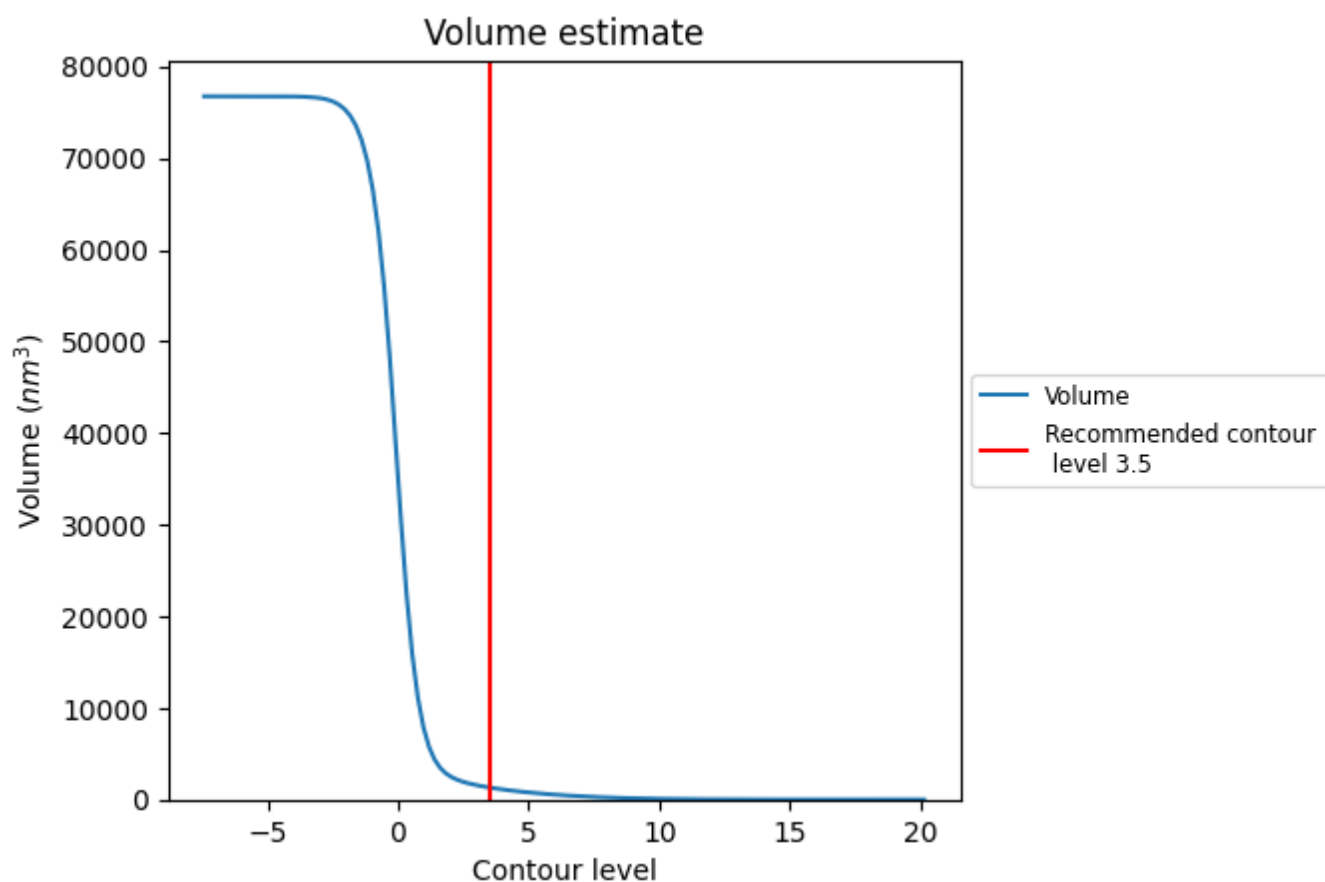
This section contains the results of statistical analysis of the map.

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.

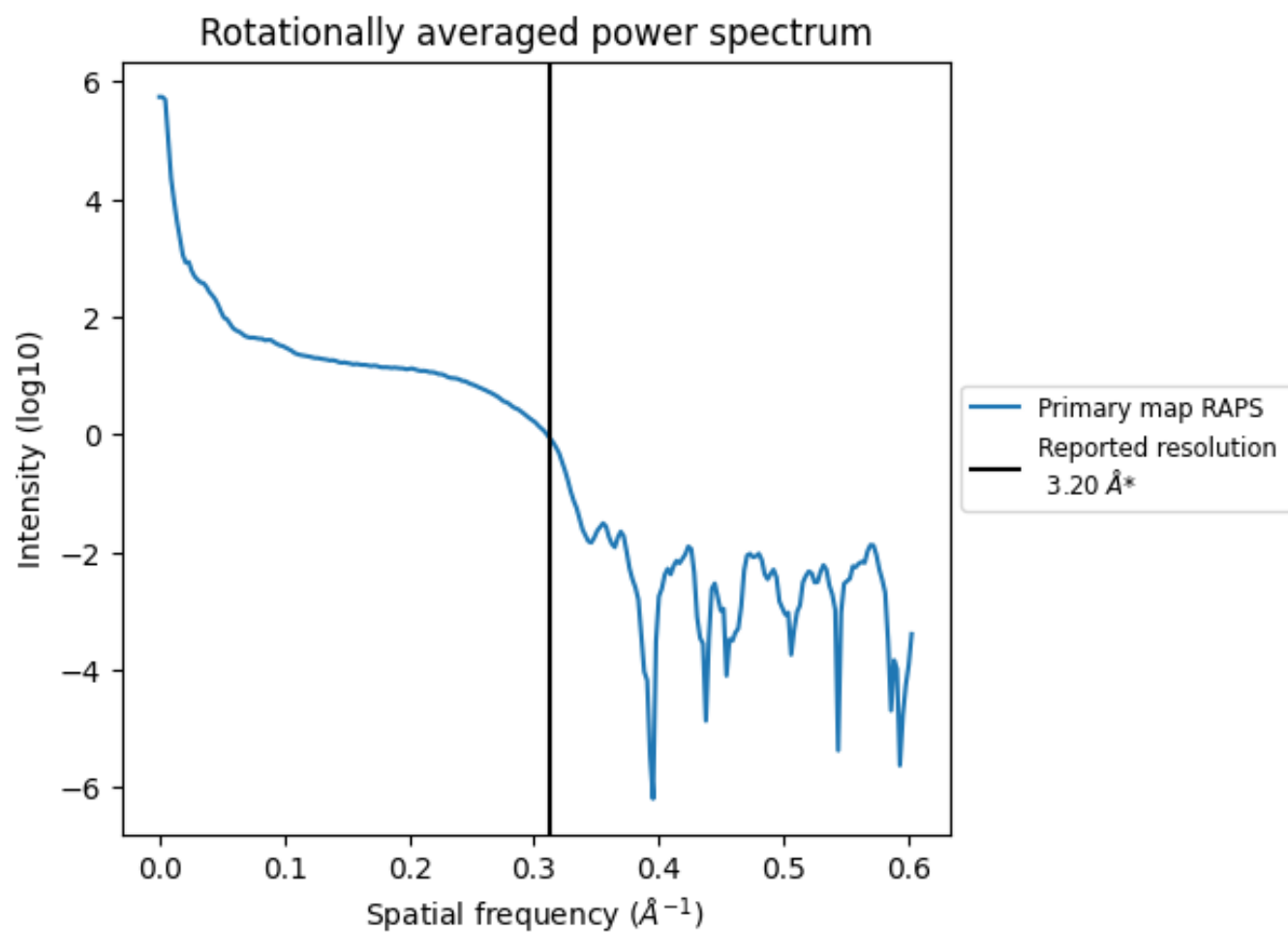
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1314 nm³; this corresponds to an approximate mass of 1187 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 0.312 Å⁻¹

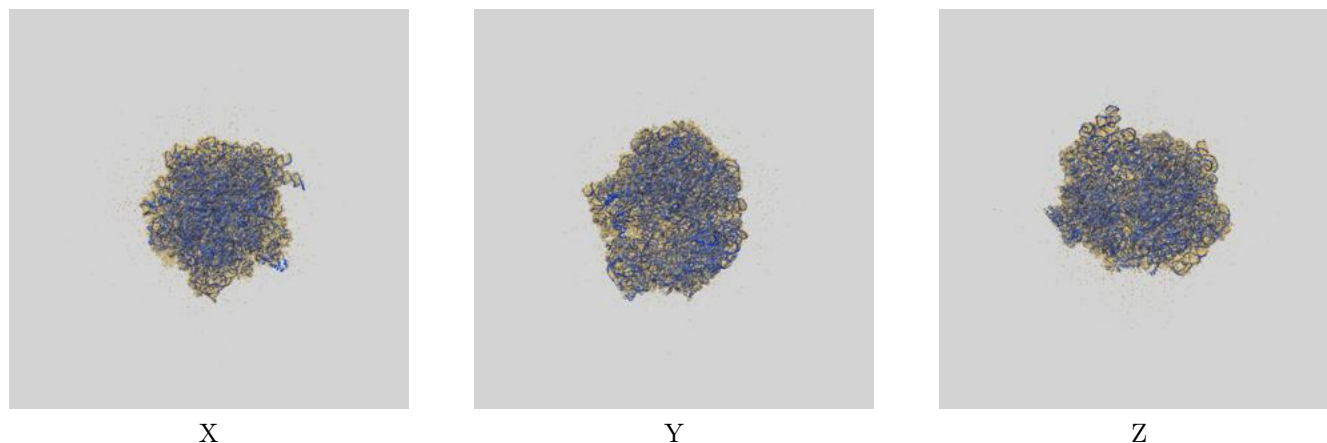
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

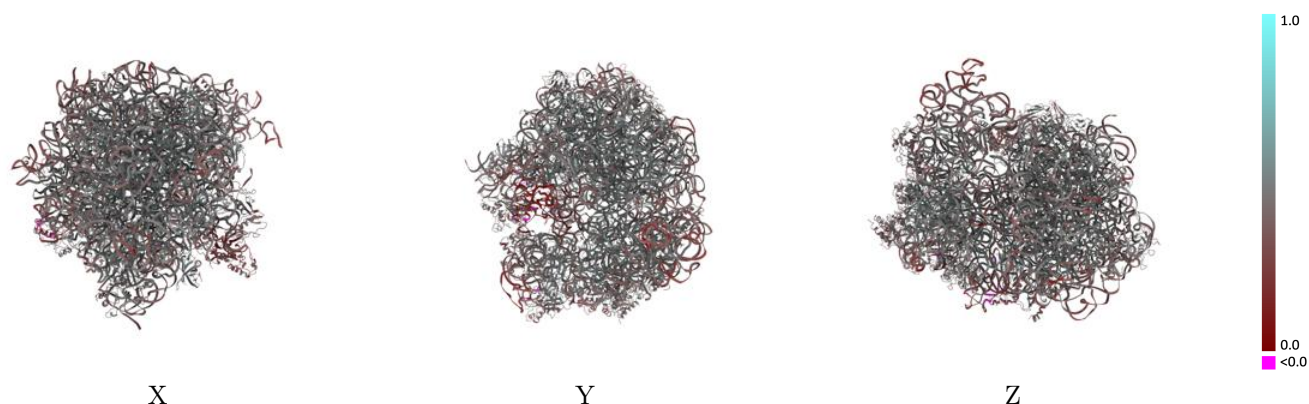
This section contains information regarding the fit between EMDB map EMD-23528 and PDB model 7LV0. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

9.1 Map-model overlay [i](#)



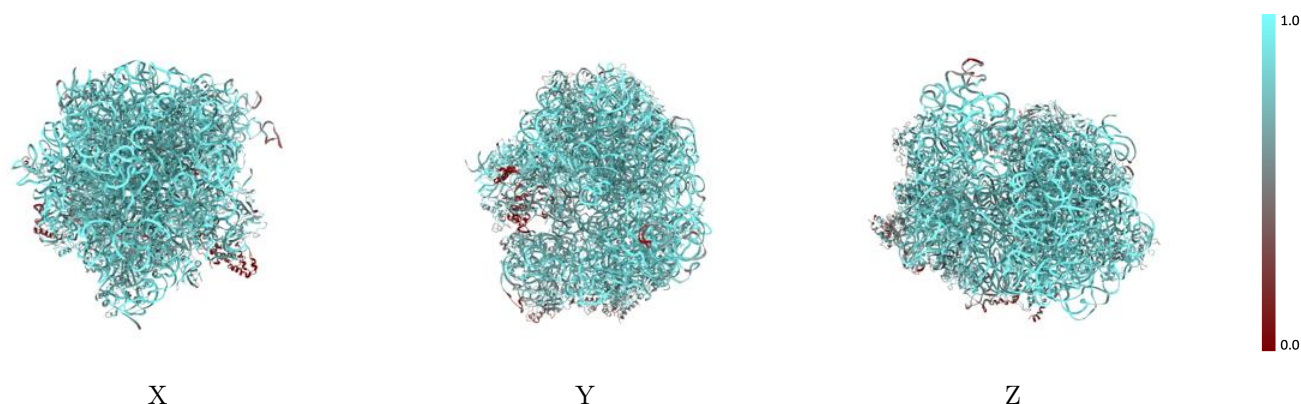
The images above show the 3D surface view of the map at the recommended contour level 3.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



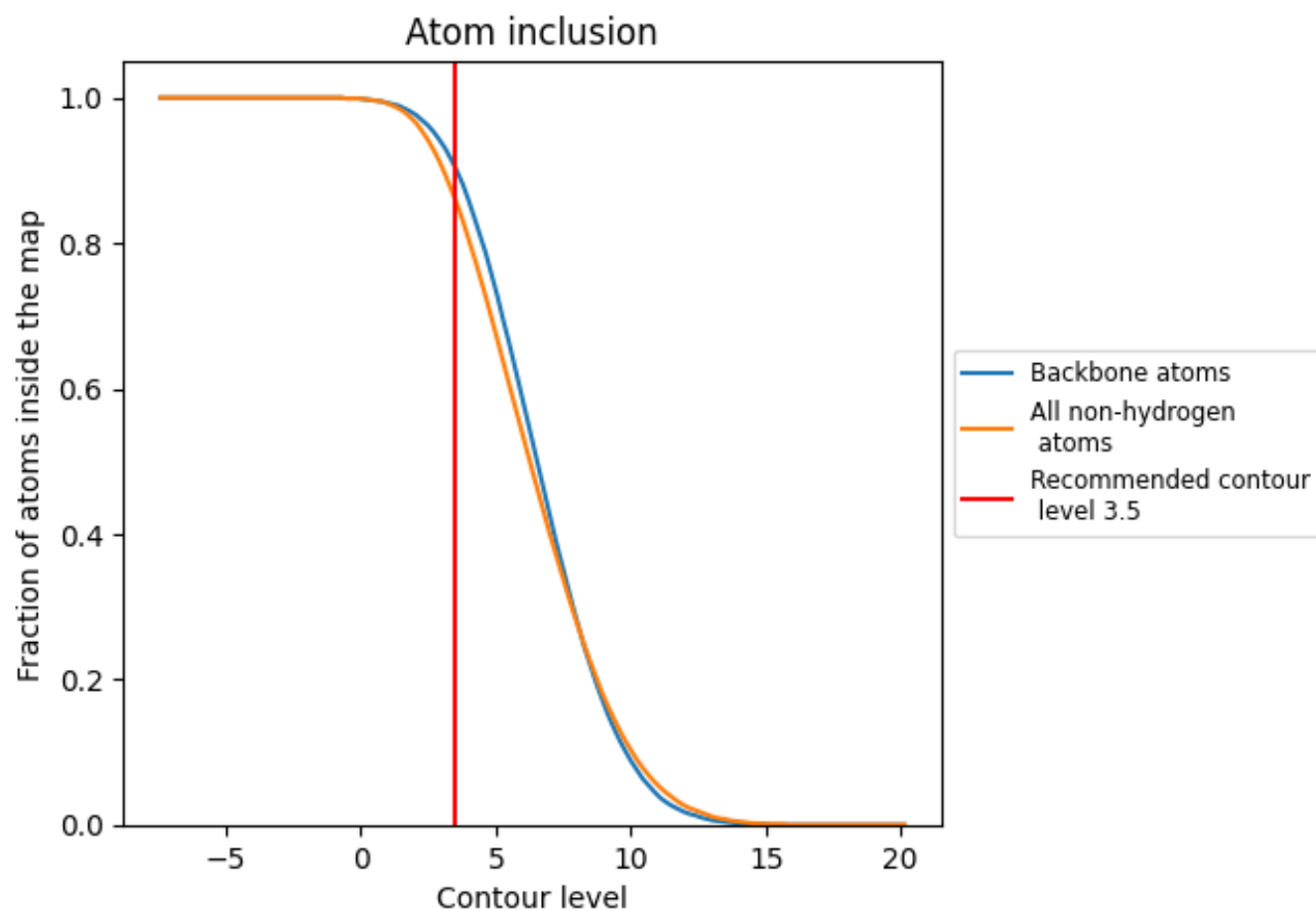
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.5).

9.4 Atom inclusion ⓘ



At the recommended contour level, 90% of all backbone atoms, 86% 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 (3.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8600	 0.4370
1	 0.9270	 0.4380
2	 0.9080	 0.4150
3	 0.9020	 0.4310
4	 0.6570	 0.3070
5	 0.7050	 0.2740
6	 0.9050	 0.3510
A	 0.5710	 0.3670
B	 0.8390	 0.4880
C	 0.7090	 0.4790
D	 0.8900	 0.5110
E	 0.8980	 0.5100
F	 0.8560	 0.5040
G	 0.4840	 0.3990
H	 0.6850	 0.4550
I	 0.6820	 0.4320
J	 0.8030	 0.4770
K	 0.7630	 0.4250
L	 0.6200	 0.4110
M	 0.7920	 0.4840
N	 0.6540	 0.4230
O	 0.5310	 0.4210
P	 0.8480	 0.4650
Q	 0.8650	 0.4790
R	 0.7010	 0.4140
S	 0.7390	 0.4500
T	 0.8550	 0.4610
U	 0.7750	 0.4500
V	 0.8250	 0.4710
W	 0.7920	 0.4580
X	 0.7590	 0.4320
Y	 0.7390	 0.4260
Z	 0.6720	 0.4040
a	 0.3450	 0.2710
b	 0.9170	 0.5150



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Chain	Atom inclusion	Q-score
c	 0.8090	 0.4900
d	 0.7280	 0.4600
e	 0.7140	 0.4080
f	 0.7400	 0.4240
g	 0.5700	 0.4120
h	 0.1070	 0.2860
i	 0.1700	 0.2860
j	 0.8350	 0.4880
k	 0.8400	 0.4870
l	 0.8360	 0.4790
m	 0.8480	 0.4850
n	 0.8440	 0.4870
o	 0.7650	 0.4520
p	 0.8110	 0.4760
q	 0.8460	 0.4830
r	 0.7370	 0.4740
s	 0.7890	 0.4820
t	 0.7880	 0.4660
u	 0.7060	 0.4460
v	 0.7980	 0.4610
w	 0.8500	 0.5050
x	 0.8880	 0.4880
y	 0.7200	 0.4110
z	 0.8030	 0.4840