



wwPDB EM Validation Summary Report ⓘ

Mar 22, 2026 – 03:44 PM UTC

PDB ID : 5AFI / pdb_00005afi
EMDB ID : EMD-2847
Title : 2.9Å Structure of E. coli ribosome-EF-TU complex by cs-corrected cryo-EM
Authors : Fischer, N.; Neumann, P.; Konevega, A.L.; Bock, L.V.; Ficner, R.; Rodnina, M.V.; Stark, H.
Deposited on : 2015-01-22
Resolution : 2.90 Å(reported)

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:

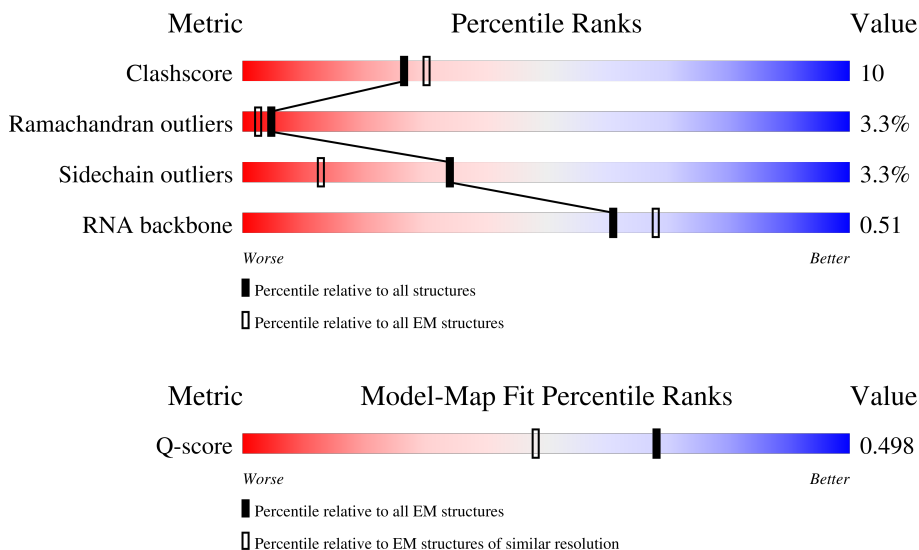
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 i

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

The reported resolution of this entry is 2.90 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	13054 (2.40 - 3.40)

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	a	1539	
2	b	240	
3	c	233	

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Mol	Chain	Length	Quality of chain
4	d	206	16% 66% 31% .
5	e	167	8% 56% 32% 6% . 6%
6	f	135	9% 43% 26% . . 26%
7	g	179	12% 51% 30% . 16%
8	h	130	5% 72% 27% .
9	i	130	10% 56% 40% . .
10	j	103	22% 47% 42% 6% . 5%
11	k	129	5% 56% 29% 5% 10%
12	l	124	9% 67% 29% . .
13	m	118	16% 67% 26% . .
14	n	102	11% 69% 25% 5% .
15	o	89	6% 76% 21% . .
16	p	82	11% 65% 33% .
17	q	84	10% 55% 37% . 5%
18	r	75	11% 55% 29% . 13%
19	s	92	7% 46% 37% . 14%
20	t	87	5% 68% 28% . .
21	u	71	30% 58% 31% . 8%
22	v	77	6% 52% 35% 13%
22	w	77	48% 43% 51% .
23	x	11	9% 55% 45%
24	y	77	6% 48% 34% 16% .
25	z	393	13% 58% 35% . 6%
26	A	2903	5% 54% 37% 9%
27	B	120	. 54% 42% .

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Mol	Chain	Length	Quality of chain
28	C	273	76% 22%
29	D	209	73% 26% 5%
30	E	201	74% 24% 8%
31	F	179	59% 36% 16%
32	G	177	77% 21% 14%
33	H	149	80% 18% 80%
34	I	142	61% 34% 85%
35	J	142	73% 26% 5%
36	K	123	66% 31% 2%
37	L	144	63% 33% 6%
38	M	136	73% 25% 2%
39	N	127	66% 27% 6% 6%
40	O	117	82% 16% 11%
41	P	115	78% 19% 10%
42	Q	118	74% 25% 2%
43	R	103	76% 24% 8%
44	S	110	69% 28% 6%
45	T	100	65% 26% 9% 7%
46	U	104	70% 27% 17%
47	V	94	73% 26% 11%
48	W	85	72% 16% 5% 12%
49	X	78	78% 19% 8%
50	Y	63	75% 24% 16%
51	Z	59	80% 19% 7%
52	0	57	68% 26% 7%

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Mol	Chain	Length	Quality of chain
53	1	55	
54	2	46	
55	3	65	
56	4	38	
57	5	165	
58	6	70	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
22	H2U	w	20	-	-	X	-
61	FME	v	105	-	-	X	-

2 Entry composition [i](#)

There are 66 unique types of molecules in this entry. The entry contains 152717 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	a	1539	33029	14738	6052	10700	1539	0	0

- Molecule 2 is a protein called 30S ribosomal protein S2.

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

- Molecule 3 is a protein called 30S ribosomal protein S3.

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

- Molecule 4 is a protein called 30S ribosomal protein S4.

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

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	e	157	1141	709	218	208	6	0	0

- Molecule 6 is a protein called 30S ribosomal protein S6.

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

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	g	151	1181	735	227	215	4	0	0

- Molecule 8 is a protein called 30S ribosomal protein S8.

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

- Molecule 9 is a protein called 30S ribosomal protein S9.

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

- Molecule 10 is a protein called 30S ribosomal protein S10.

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

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	k	116	869	535	173	158	3	0	0

- Molecule 12 is a protein called 30S ribosomal protein S12.

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

- Molecule 13 is a protein called 30S ribosomal protein S13.

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

- Molecule 14 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	n	101	799	498	165	133	3	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	35	ALA	-	insertion	UNP P0AG59

- Molecule 15 is a protein called 30S ribosomal protein S15.

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

- Molecule 16 is a protein called 30S ribosomal protein S16.

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

- Molecule 17 is a protein called 30S ribosomal protein S17.

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

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
18	r	65	504	317	96	91	0	0

- Molecule 19 is a protein called 30S ribosomal protein S19.

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

- Molecule 20 is a protein called 30S ribosomal protein S20.

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

- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	u	65	Total	C	N	O	S	0	0
			495	307	100	87	1		

- Molecule 22 is a RNA chain called P-site fMet-tRNA^{fMet}.

Mol	Chain	Residues	Atoms					AltConf	Trace	
22	v	77	Total	C	N	O	P	S	0	0
			1644	733	297	536	77	1		
22	w	77	Total	C	N	O	P	S	0	0
			1644	733	297	536	77	1		

- Molecule 23 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	x	11	Total	C	N	O	P	0	0
			234	105	41	77	11		

- Molecule 24 is a RNA chain called A/T-site Phe-tRNA^{Phe}.

Mol	Chain	Residues	Atoms					AltConf	Trace	
24	y	77	Total	C	N	O	P	S	0	0
			1643	740	291	534	76	2		

- Molecule 25 is a protein called Elongation factor Tu 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	z	371	Total	C	N	O	S	1	0
			2881	1824	495	549	13		

- Molecule 26 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	A	2900	Total	C	N	O	P	0	0
			62276	27788	11460	20128	2900		

- Molecule 27 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
27	B	120	2572	1145	471	836	120	0	0

- Molecule 28 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	C	271	2082	1288	423	364	7	0	0

- Molecule 29 is a protein called 50S ribosomal protein L3.

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

- Molecule 30 is a protein called 50S ribosomal protein L4.

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

- Molecule 31 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	F	177	1410	899	249	256	6	0	0

- Molecule 32 is a protein called 50S ribosomal protein L6.

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

- Molecule 33 is a protein called 50S ribosomal protein L9.

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

- Molecule 34 is a protein called 50S ribosomal protein L11.

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

- Molecule 35 is a protein called 50S ribosomal protein L13.

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

- Molecule 36 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	K	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 37 is a protein called 50S ribosomal protein L15.

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

- Molecule 38 is a protein called 50S ribosomal protein L16.

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

- Molecule 39 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	N	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 40 is a protein called 50S ribosomal protein L18.

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

- Molecule 41 is a protein called 50S ribosomal protein L19.

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

- Molecule 42 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	Q	117	947	604	192	151		0	0

- Molecule 43 is a protein called 50S ribosomal protein L21.

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

- Molecule 44 is a protein called 50S ribosomal protein L22.

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

- Molecule 45 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	T	93	738	466	139	131	2	0	0

- Molecule 46 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	U	102	779	492	146	141		0	0

- Molecule 47 is a protein called 50S ribosomal protein L25.

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

- Molecule 48 is a protein called 50S ribosomal protein L27.

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

- Molecule 49 is a protein called 50S ribosomal protein L28.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L30.

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

- Molecule 52 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 53 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	1	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 54 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 55 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 56 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 57 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	5	131	Total	C	N	O	S	0	0
			988	625	175	183	5		

- Molecule 58 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	6	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

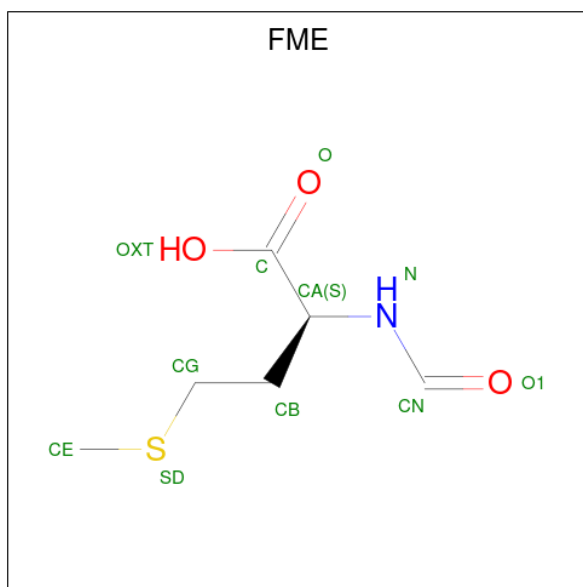
- Molecule 59 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
59	a	83	Total	Mg	0
			83	83	
59	v	4	Total	Mg	0
			4	4	
59	z	1	Total	Mg	0
			1	1	
59	A	234	Total	Mg	0
			234	234	
59	B	7	Total	Mg	0
			7	7	
59	N	2	Total	Mg	0
			2	2	
59	0	1	Total	Mg	0
			1	1	
59	4	1	Total	Mg	0
			1	1	

- Molecule 60 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

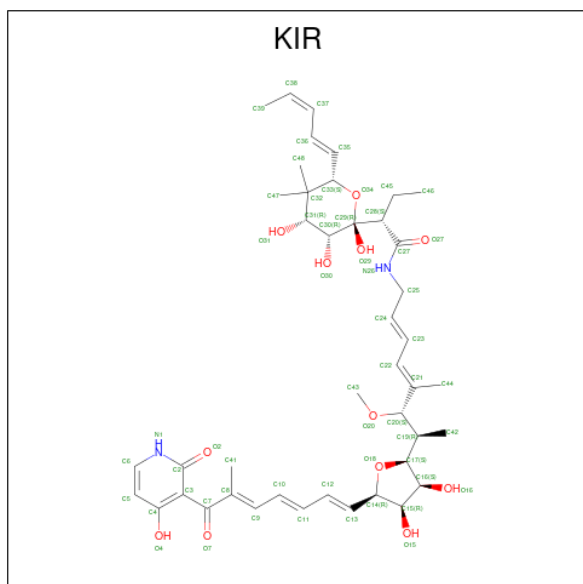
Mol	Chain	Residues	Atoms	AltConf
60	a	1	Total Cl 1 1	0
60	A	1	Total Cl 1 1	0

- Molecule 61 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: $C_6H_{11}NO_3S$).



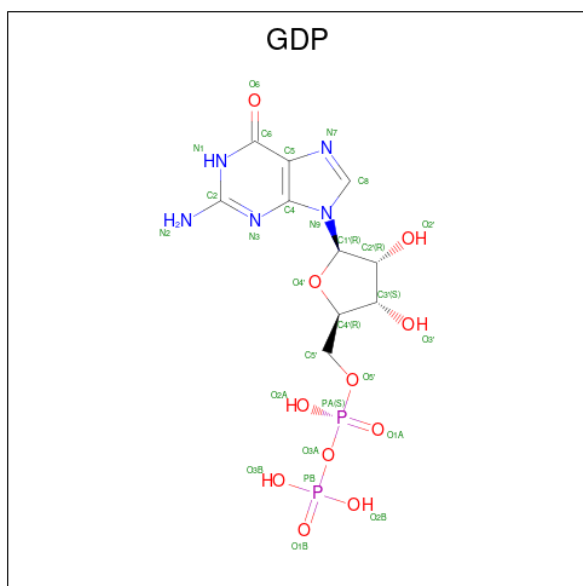
Mol	Chain	Residues	Atoms	AltConf
61	v	1	Total C N O S 10 6 1 2 1	0

- Molecule 62 is KIRROMYCIN (CCD ID: KIR) (formula: $C_{43}H_{60}N_2O_{12}$).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
62	z	1	57	43	2	12	0

- Molecule 63 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
63	z	1	28	10	5	11	2	0

- Molecule 64 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		AltConf
			Total	Na	
64	A	1	1	1	0
64	B	1	1	1	0

- Molecule 65 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
65	4	1	1	1	0
65	6	1	1	1	0

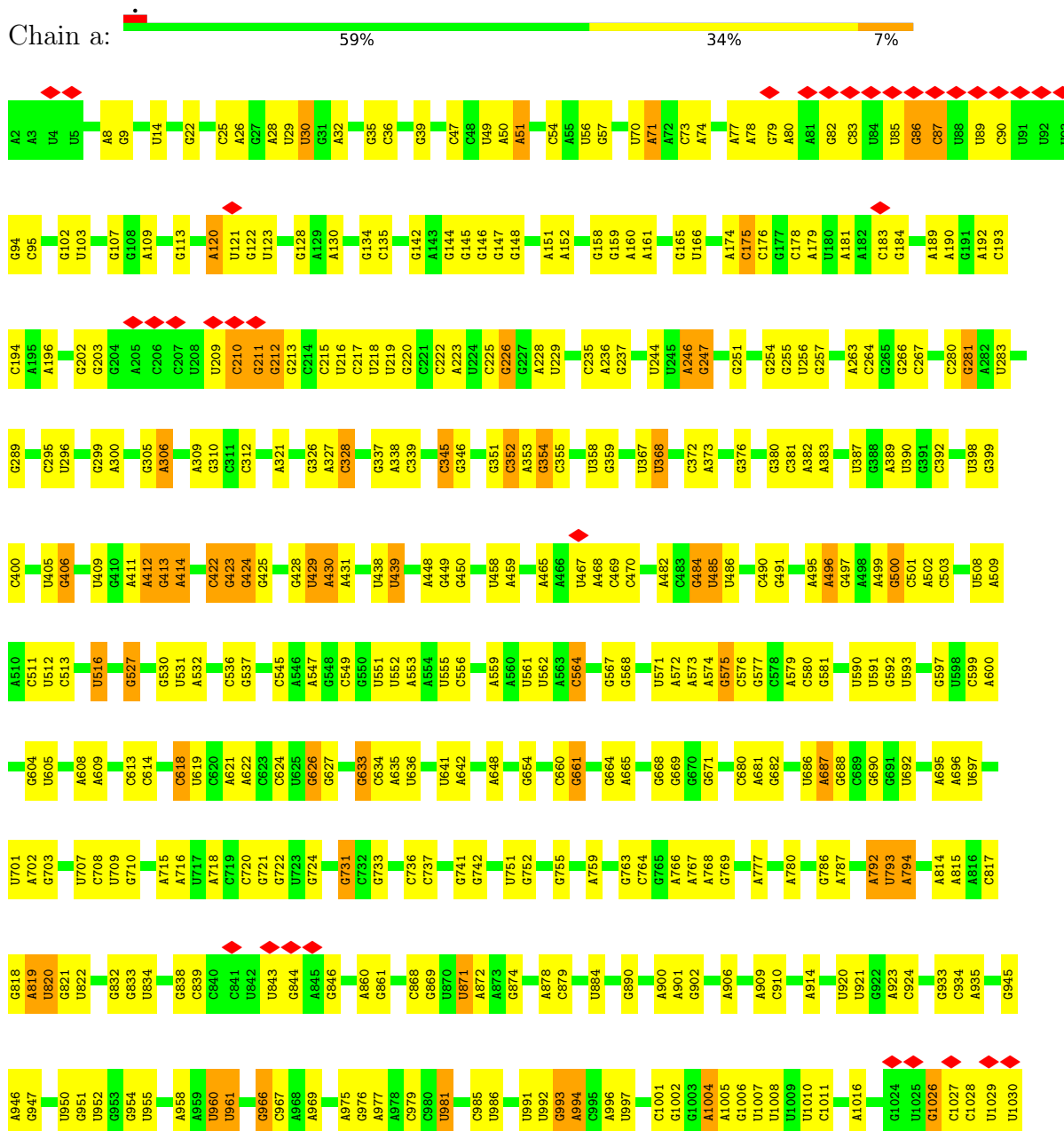
- Molecule 66 is water.

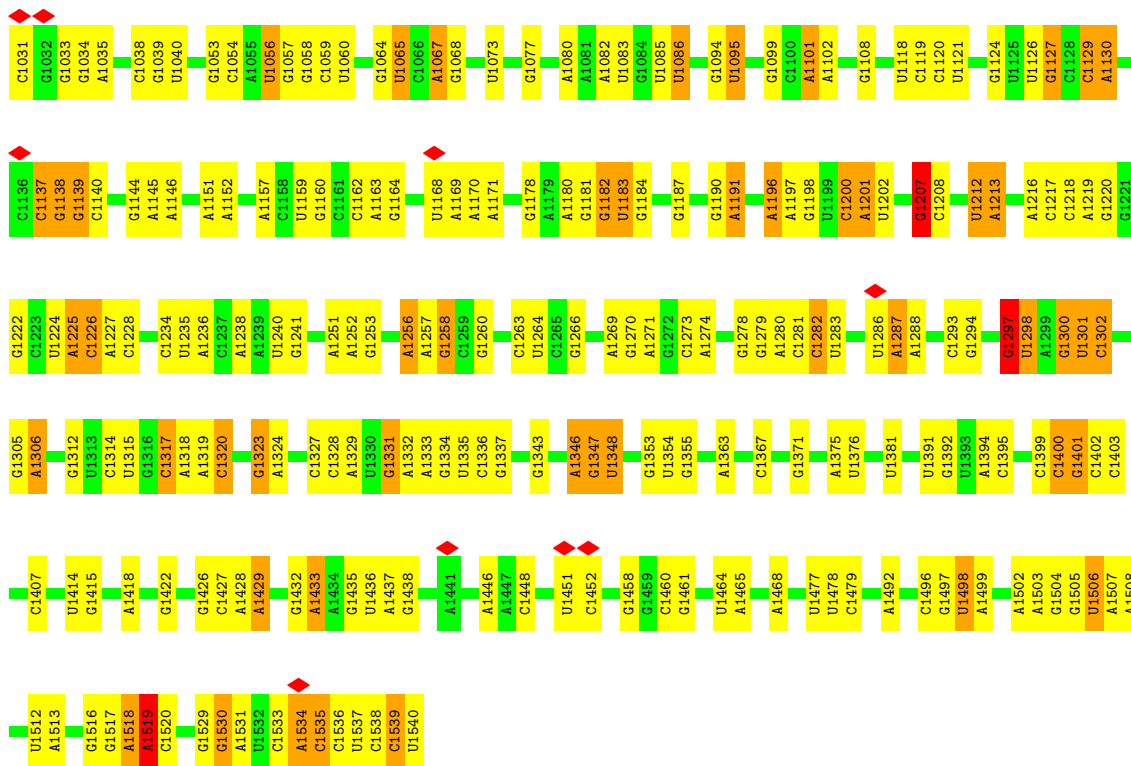
Mol	Chain	Residues	Atoms	AltConf
66	a	9	Total O 9 9	0
66	A	9	Total O 9 9	0
66	D	2	Total O 2 2	0
66	K	1	Total O 1 1	0

3 Residue-property plots i

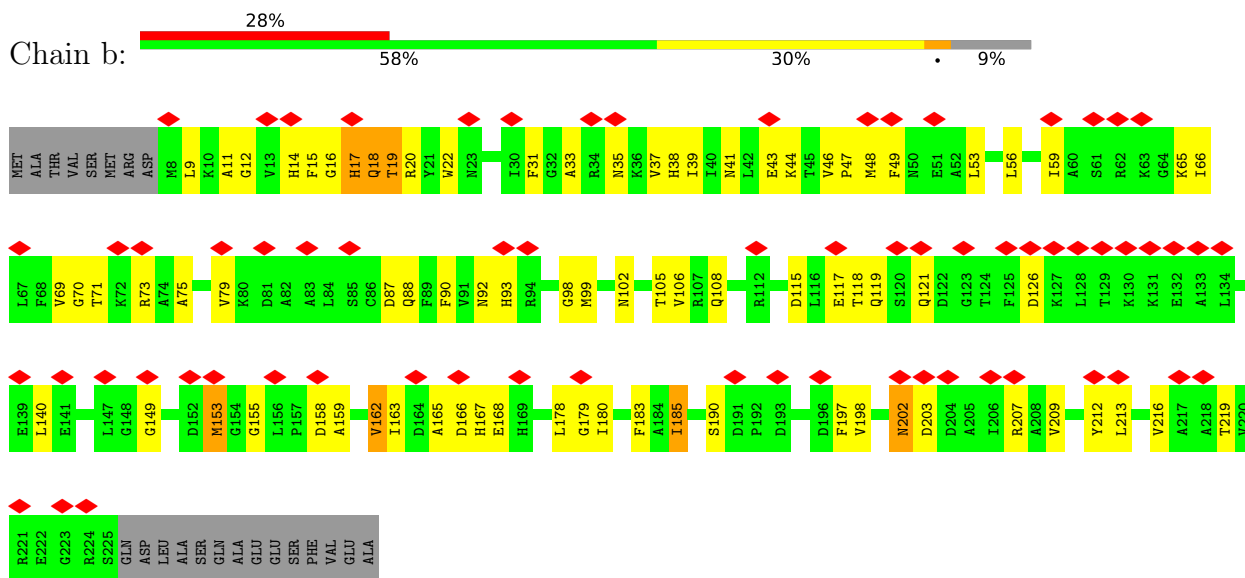
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 16S ribosomal RNA

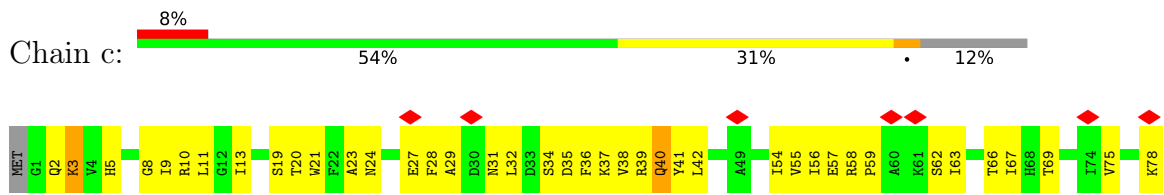


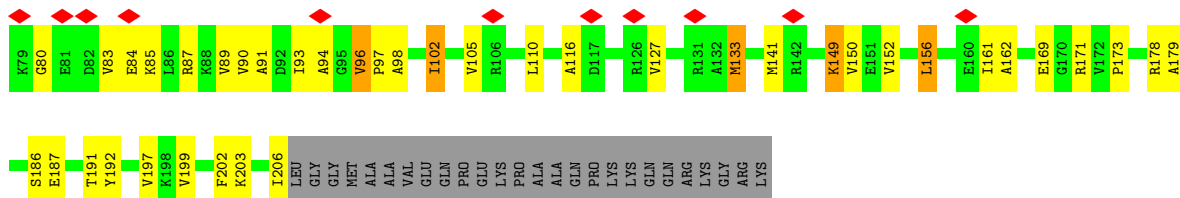


• Molecule 2: 30S ribosomal protein S2

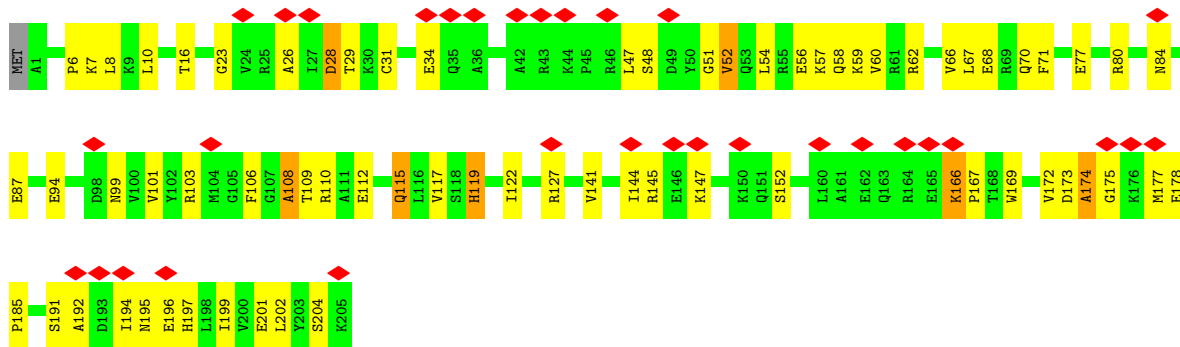


• Molecule 3: 30S ribosomal protein S3

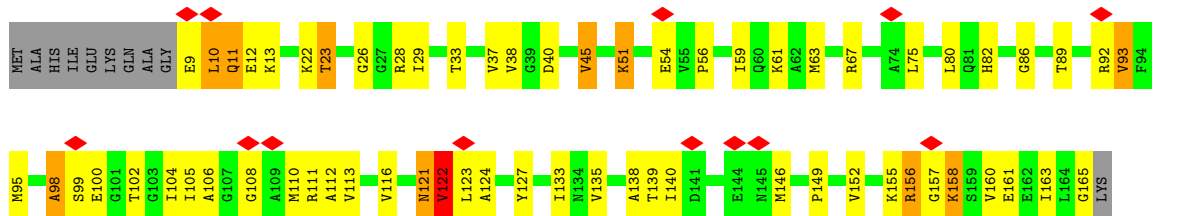




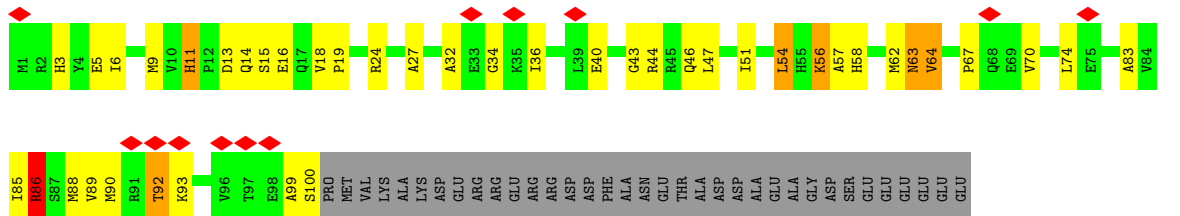
• Molecule 4: 30S ribosomal protein S4



• Molecule 5: 30S ribosomal protein S5

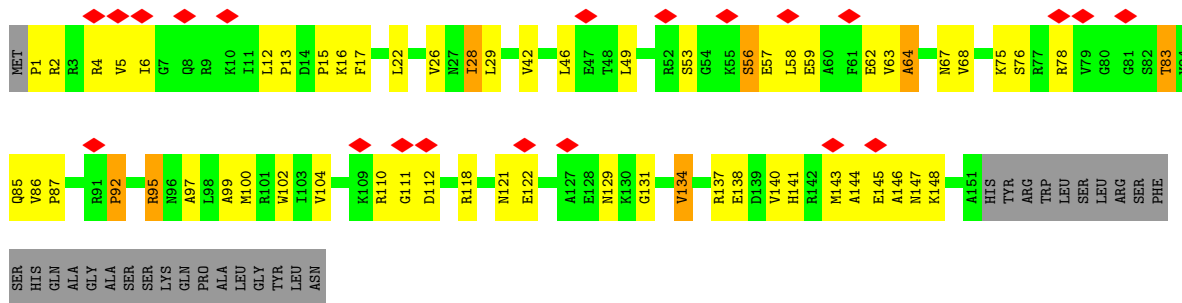


• Molecule 6: 30S ribosomal protein S6

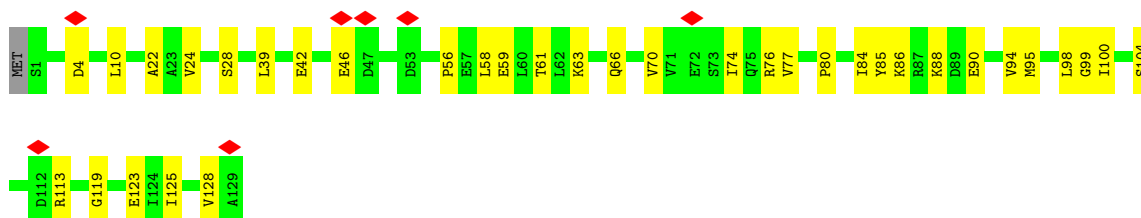


• Molecule 7: 30S ribosomal protein S7

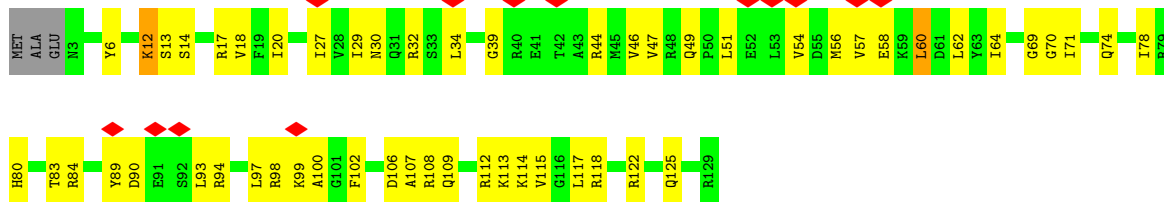




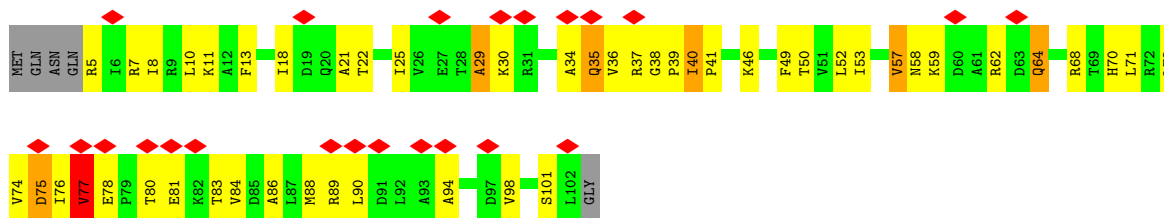
• Molecule 8: 30S ribosomal protein S8



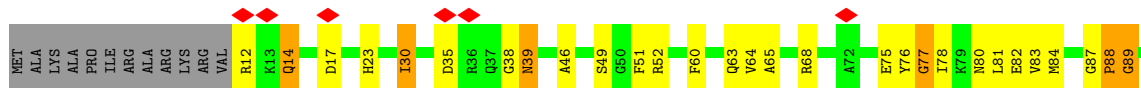
• Molecule 9: 30S ribosomal protein S9



• Molecule 10: 30S ribosomal protein S10

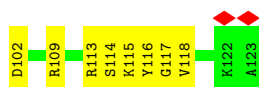


• Molecule 11: 30S ribosomal protein S11

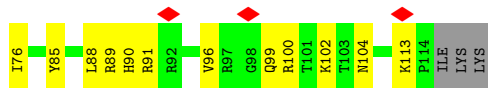




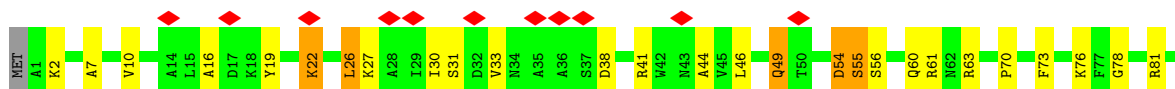
- Molecule 12: 30S ribosomal protein S12



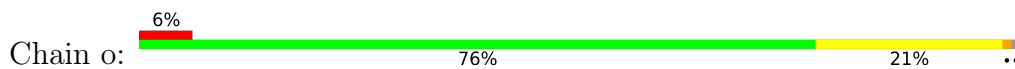
- Molecule 13: 30S ribosomal protein S13



- Molecule 14: 30S ribosomal protein S14



- Molecule 15: 30S ribosomal protein S15



- Molecule 16: 30S ribosomal protein S16

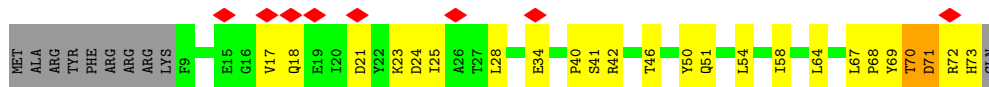




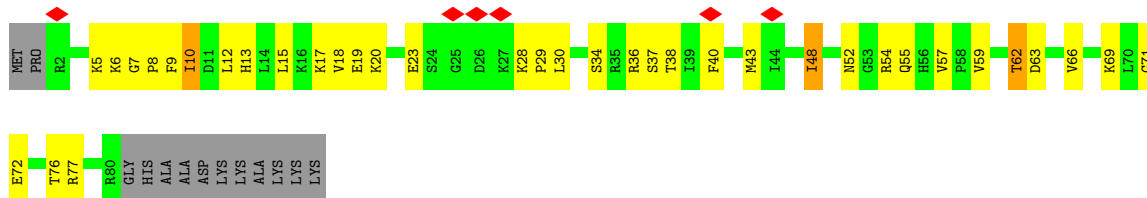
• Molecule 17: 30S ribosomal protein S17



• Molecule 18: 30S ribosomal protein S18



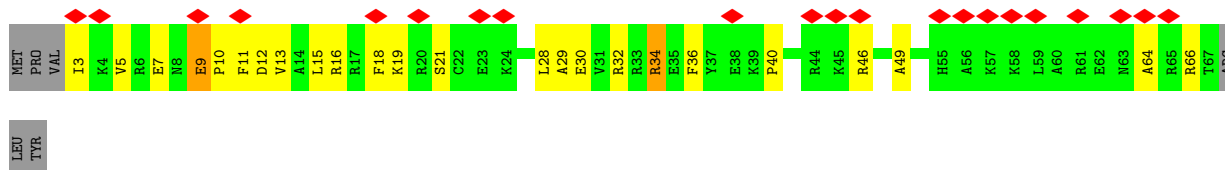
• Molecule 19: 30S ribosomal protein S19



• Molecule 20: 30S ribosomal protein S20

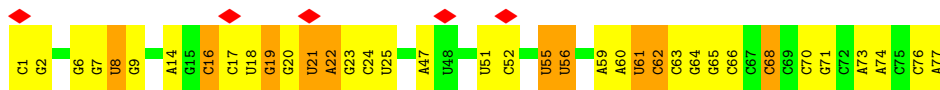


• Molecule 21: 30S ribosomal protein S21

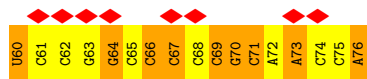


• Molecule 22: P-site fMet-tRNAfMet





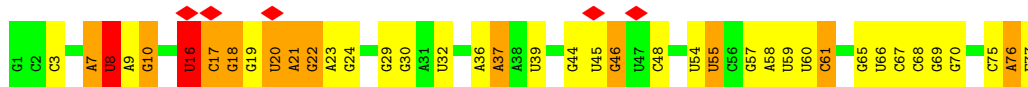
• Molecule 22: P-site fMet-tRNAfMet



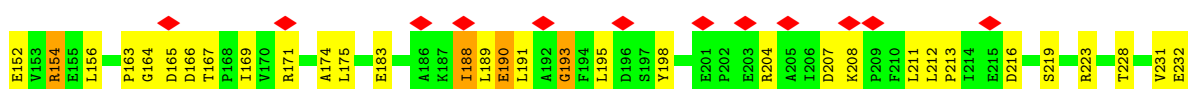
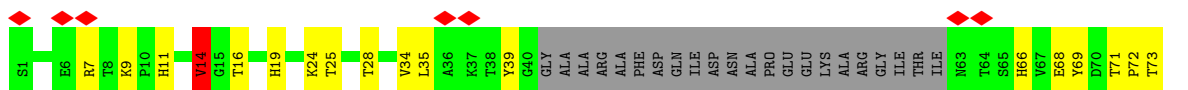
• Molecule 23: mRNA

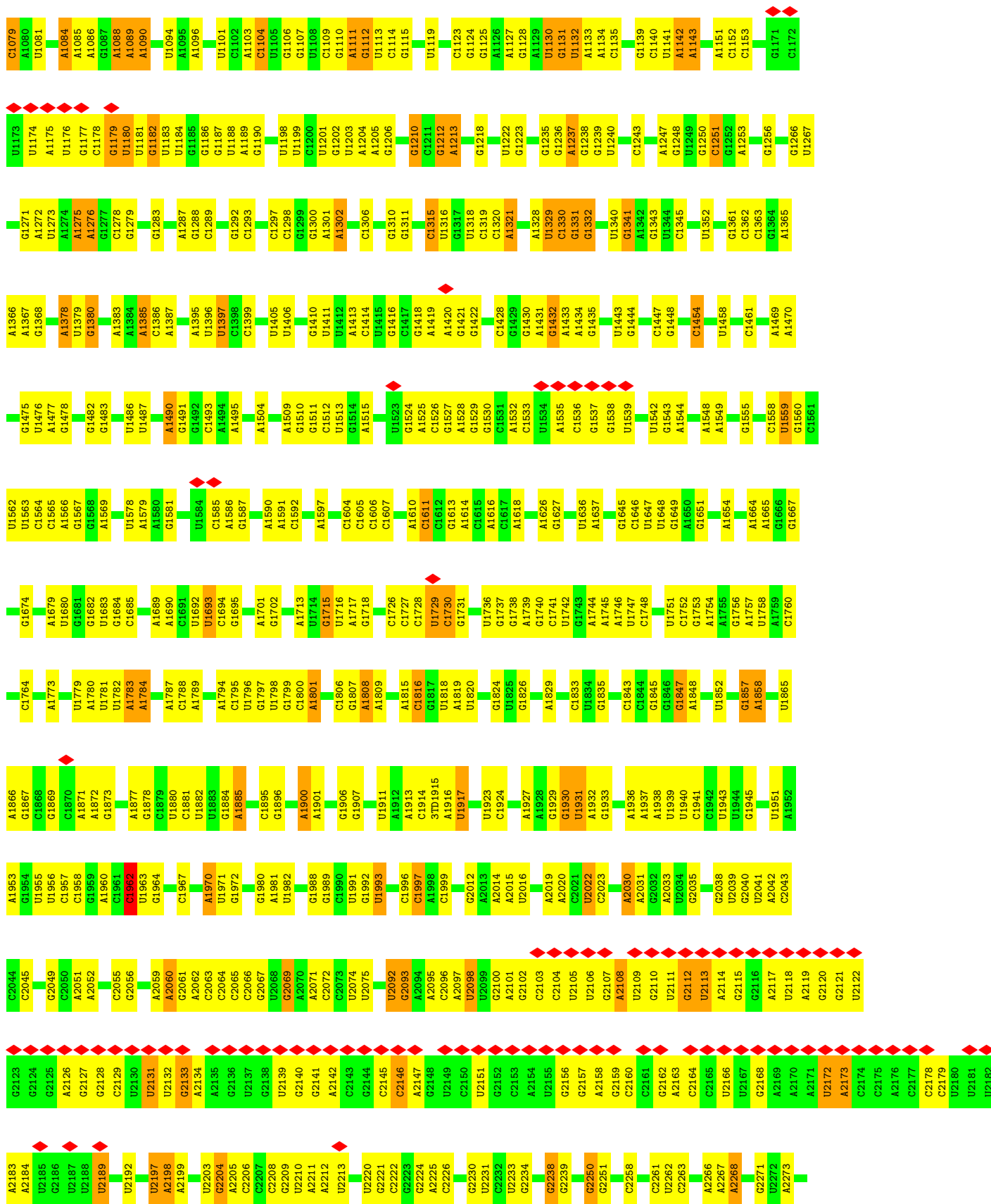


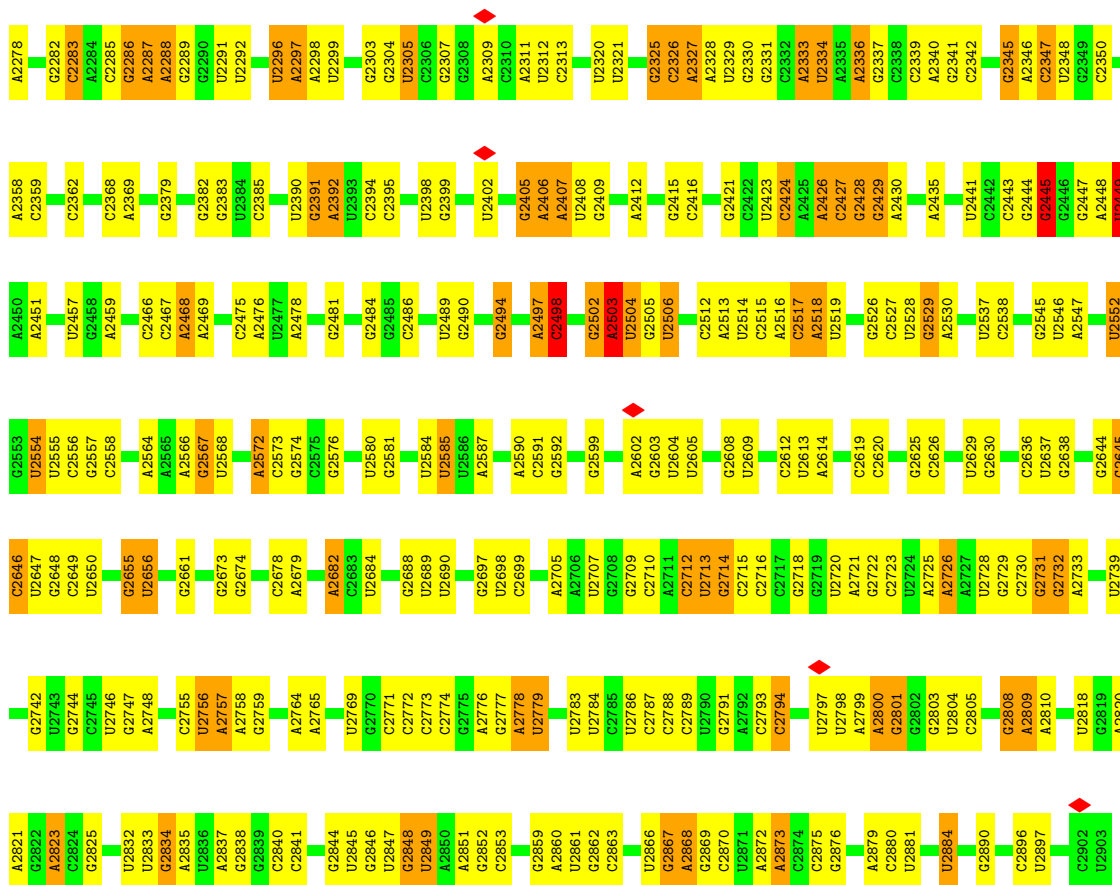
• Molecule 24: A/T-site Phe-tRNA^{Phe}



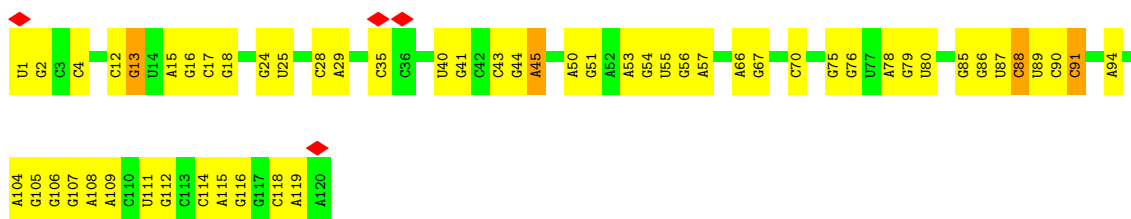
• Molecule 25: Elongation factor Tu 2



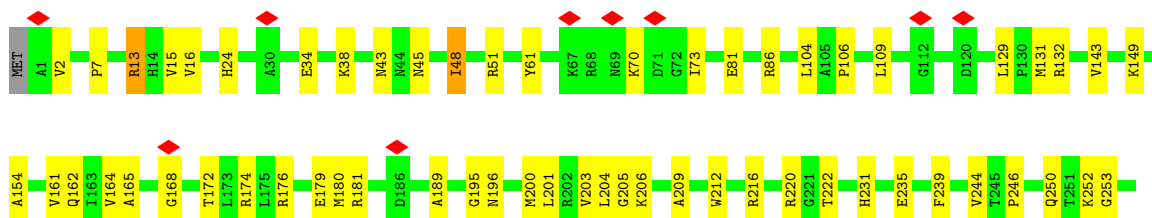
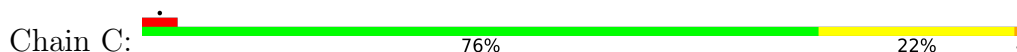


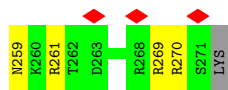


• Molecule 27: 5S ribosomal RNA

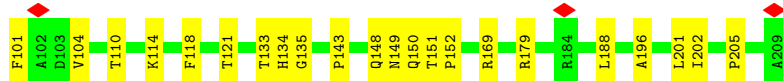
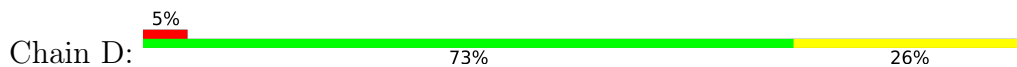


• Molecule 28: 50S ribosomal protein L2

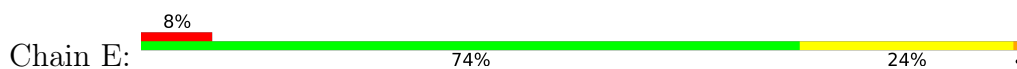




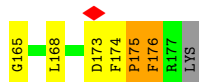
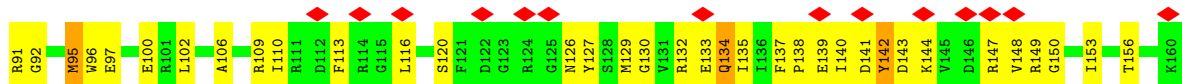
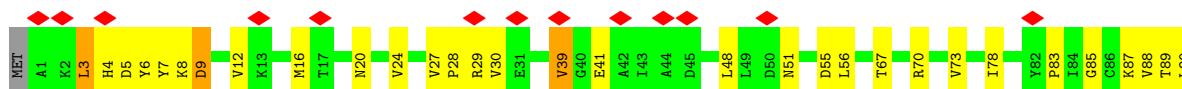
• Molecule 29: 50S ribosomal protein L3



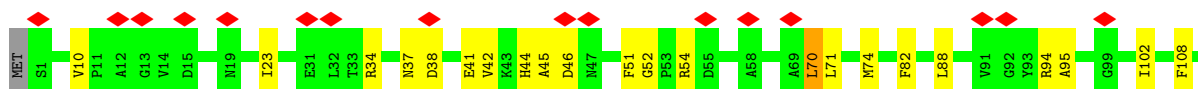
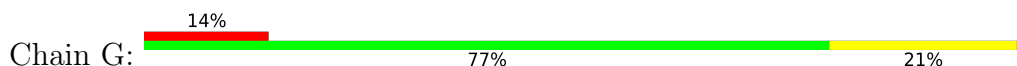
• Molecule 30: 50S ribosomal protein L4

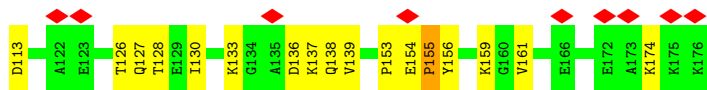


• Molecule 31: 50S ribosomal protein L5

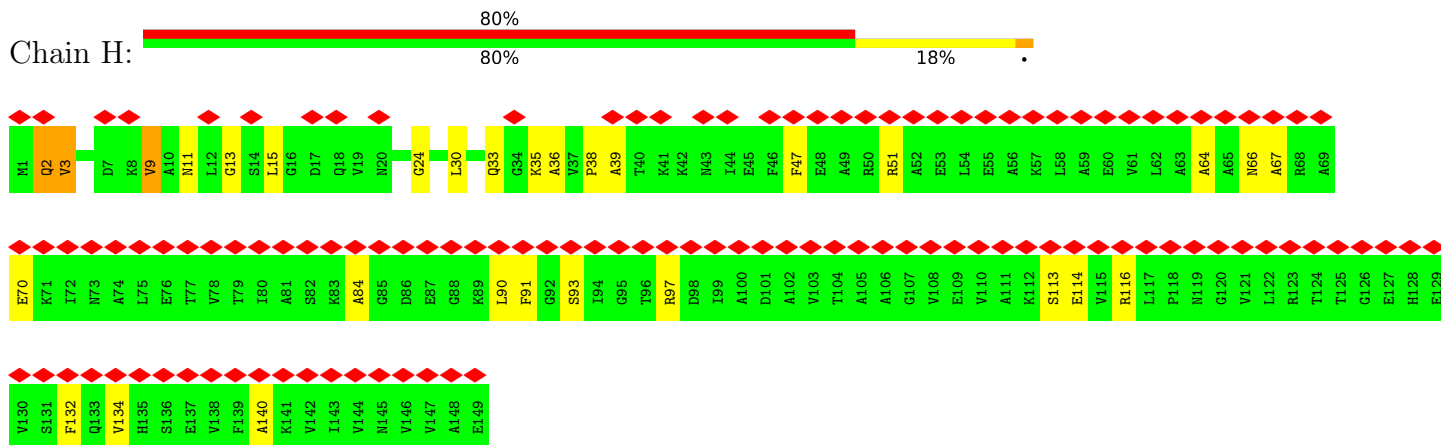


• Molecule 32: 50S ribosomal protein L6

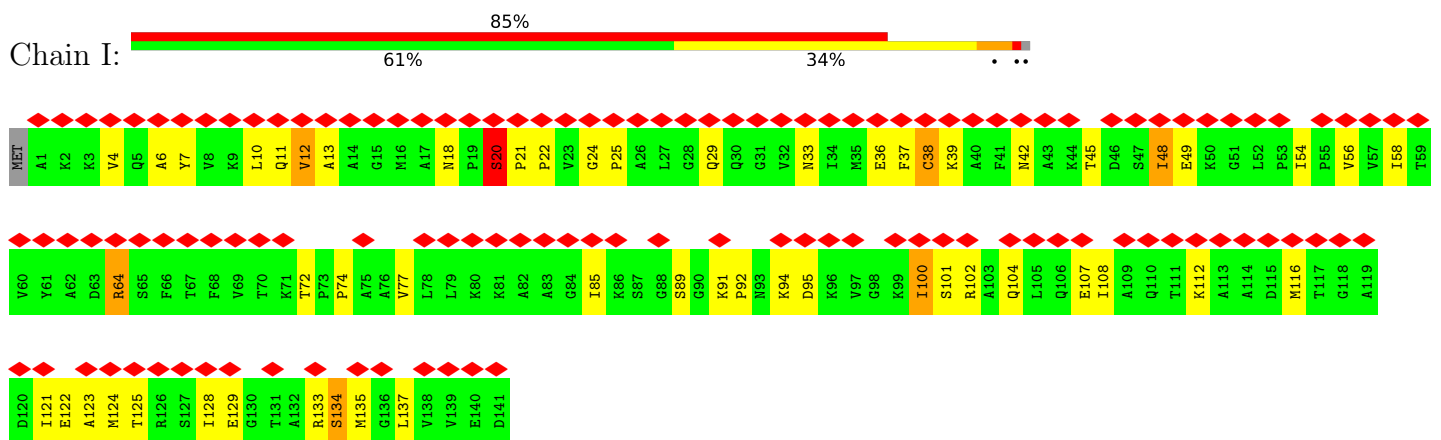




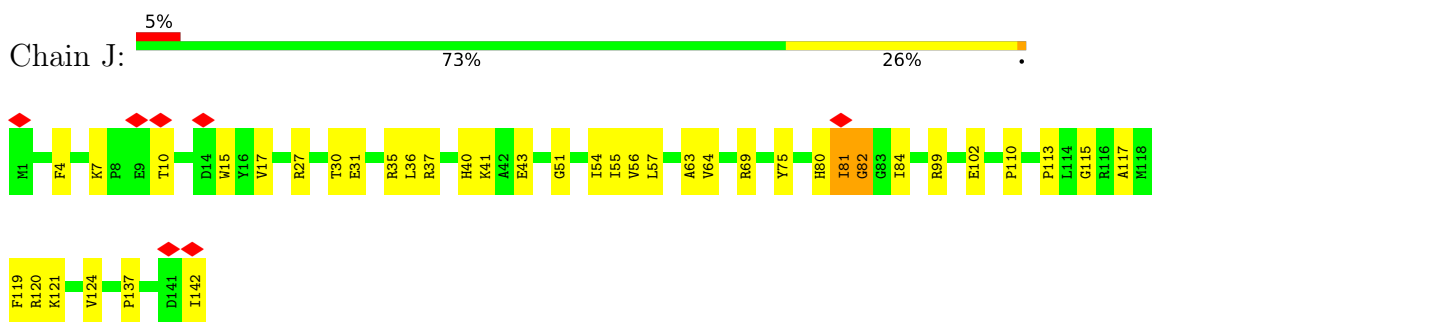
• Molecule 33: 50S ribosomal protein L9



• Molecule 34: 50S ribosomal protein L11

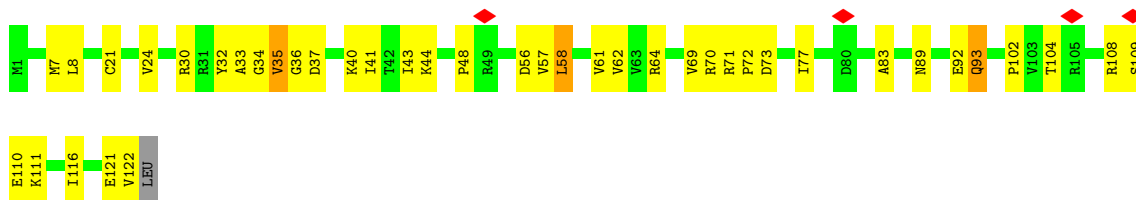


• Molecule 35: 50S ribosomal protein L13

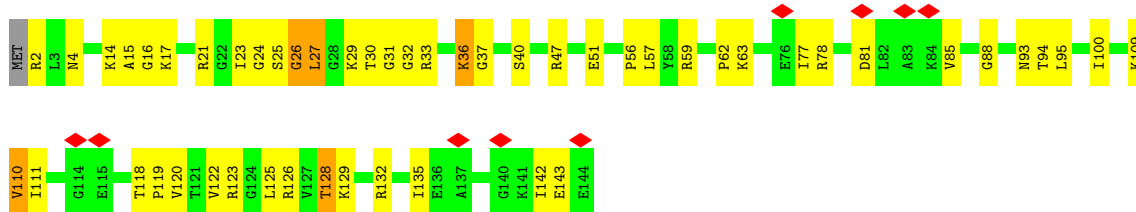


• Molecule 36: 50S ribosomal protein L14

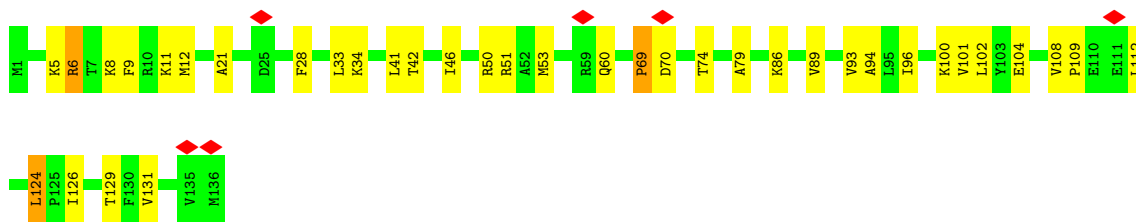




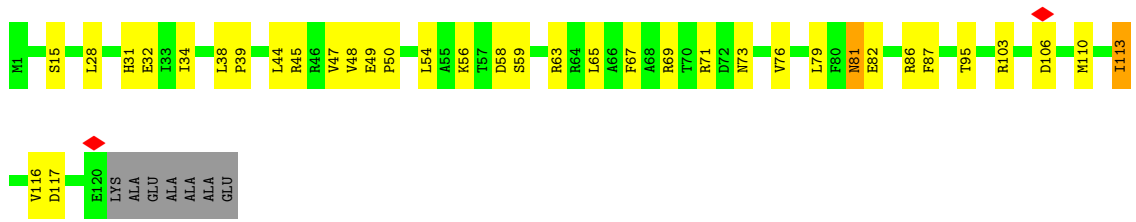
• Molecule 37: 50S ribosomal protein L15



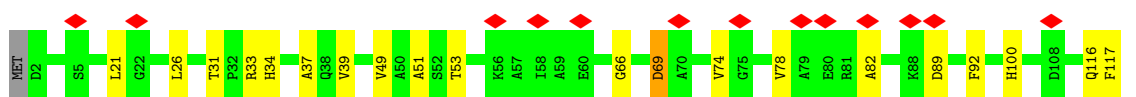
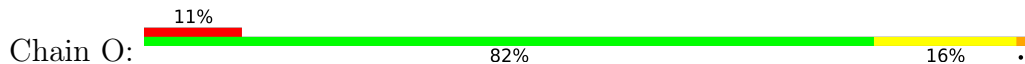
• Molecule 38: 50S ribosomal protein L16



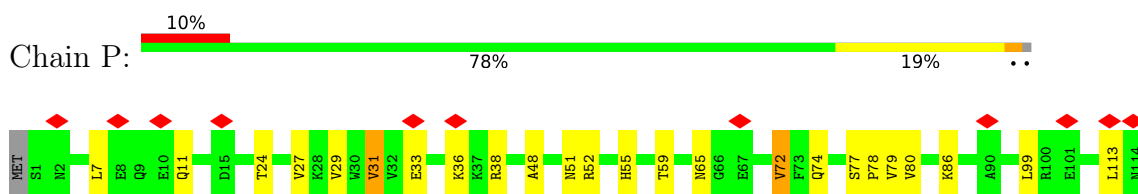
• Molecule 39: 50S ribosomal protein L17



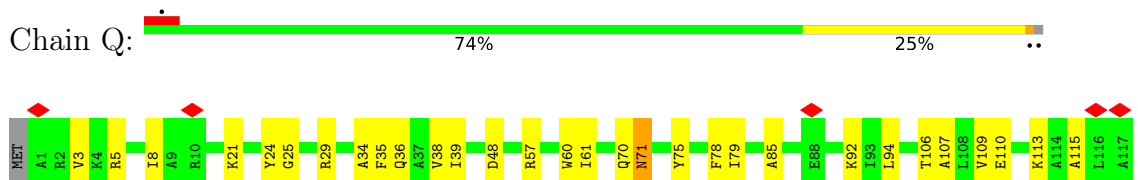
• Molecule 40: 50S ribosomal protein L18



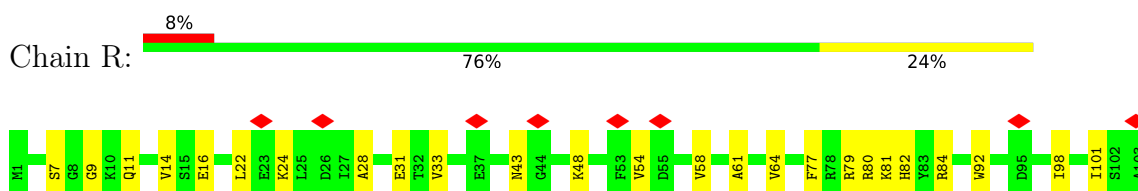
• Molecule 41: 50S ribosomal protein L19



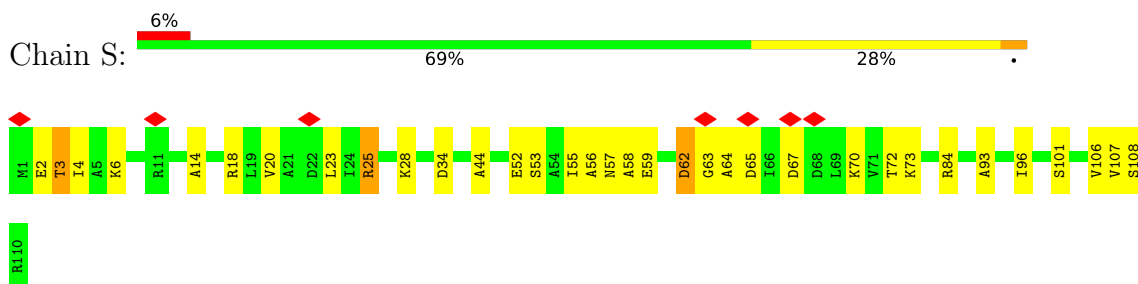
- Molecule 42: 50S ribosomal protein L20



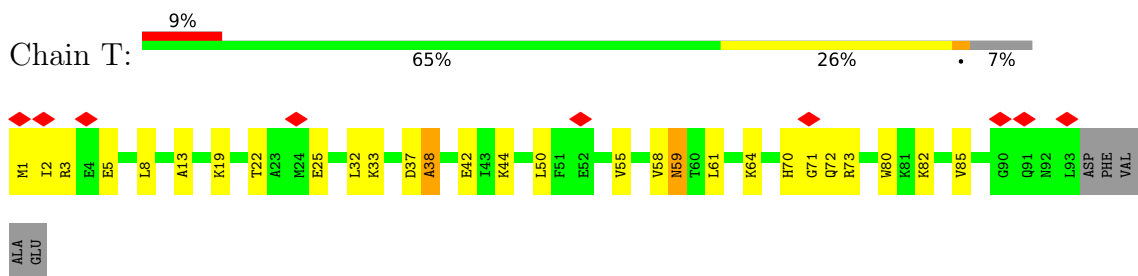
- Molecule 43: 50S ribosomal protein L21



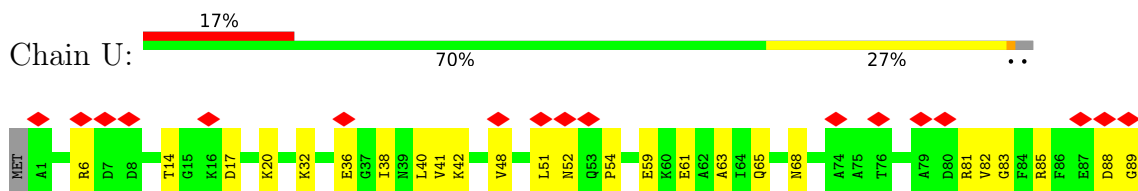
- Molecule 44: 50S ribosomal protein L22

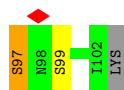


- Molecule 45: 50S ribosomal protein L23

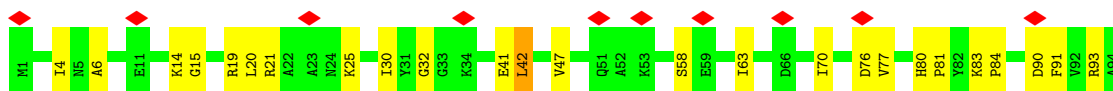
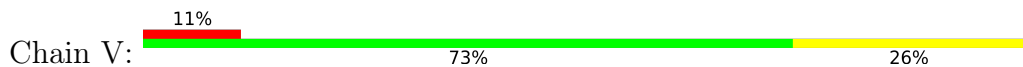


- Molecule 46: 50S ribosomal protein L24





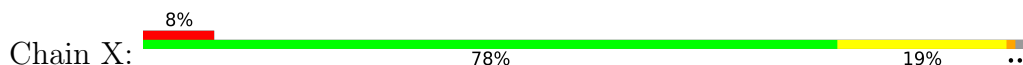
- Molecule 47: 50S ribosomal protein L25



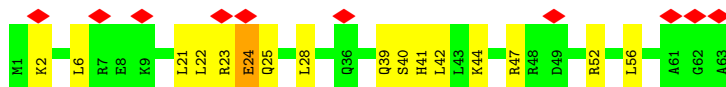
- Molecule 48: 50S ribosomal protein L27



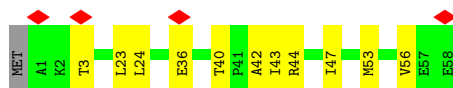
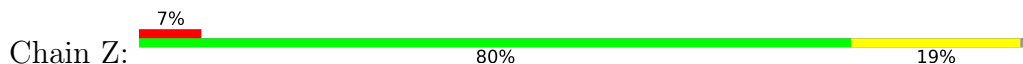
- Molecule 49: 50S ribosomal protein L28



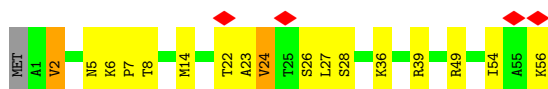
- Molecule 50: 50S ribosomal protein L29



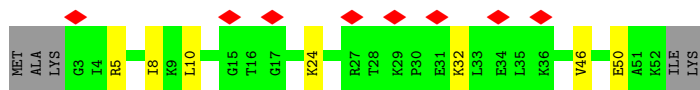
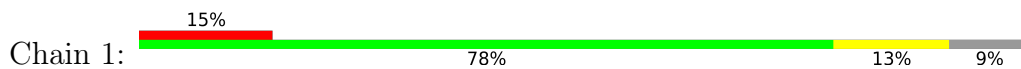
- Molecule 51: 50S ribosomal protein L30



- Molecule 52: 50S ribosomal protein L32



- Molecule 53: 50S ribosomal protein L33



• Molecule 54: 50S ribosomal protein L34



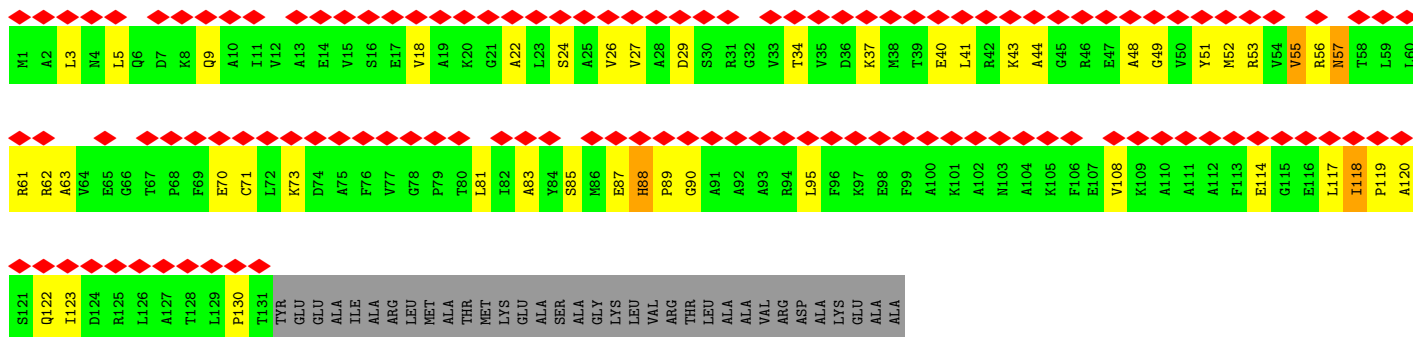
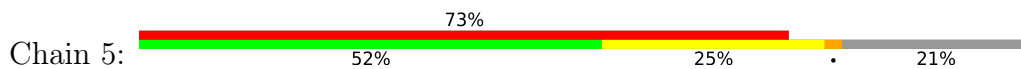
• Molecule 55: 50S ribosomal protein L35



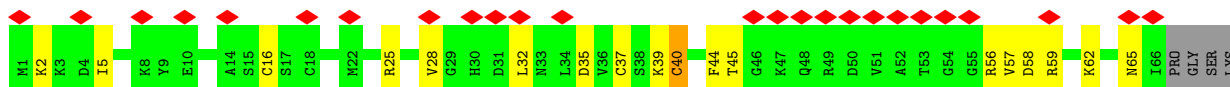
• Molecule 56: 50S ribosomal protein L36



• Molecule 57: 50S ribosomal protein L10



• Molecule 58: 50S ribosomal protein L31



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	417201	Depositor
Resolution determination method	Not provided	
CTF correction method	LOCAL CTF CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	192000	Depositor
Image detector	FEI FALCON I (4k x 4k)	Depositor
Maximum map value	4.711	Depositor
Minimum map value	-2.426	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.214	Depositor
Recommended contour level	0.43	Depositor
Map size (\AA)	317.205, 317.205, 317.205	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.75525, 0.75525, 0.75525	Depositor

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: NA, 7MG, ZN, MG, 2MA, FME, 1MG, UR3, OMU, 4OC, OMC, 5MC, H2U, PSU, 3TD, OMG, GDP, MA6, CL, KIR, 4SU, 6MZ, 5MU, 2MG, MIA

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	a	0.20	0/36701	0.32	2/57246 (0.0%)
2	b	0.40	0/1735	0.76	1/2338 (0.0%)
3	c	0.43	0/1651	0.76	0/2225
4	d	0.34	0/1665	0.79	0/2227
5	e	0.41	0/1154	0.80	1/1554 (0.1%)
6	f	0.46	0/835	0.85	3/1128 (0.3%)
7	g	0.50	1/1195 (0.1%)	0.85	0/1602
8	h	0.35	0/989	0.77	0/1326
9	i	0.35	0/1034	0.75	0/1375
10	j	0.51	0/796	0.88	2/1077 (0.2%)
11	k	0.37	0/885	0.85	2/1195 (0.2%)
12	l	0.36	0/969	0.80	1/1300 (0.1%)
13	m	0.50	0/892	0.85	0/1193
14	n	0.33	0/811	0.75	0/1081
15	o	0.43	0/722	0.72	0/964
16	p	0.43	0/659	0.84	0/884
17	q	0.32	0/657	0.79	0/881
18	r	0.35	0/511	0.71	0/689
19	s	0.35	0/652	0.73	0/877
20	t	0.50	0/671	0.82	1/888 (0.1%)
21	u	0.39	0/500	0.77	0/668
22	v	0.22	1/1747 (0.1%)	0.33	0/2721
22	w	0.46	0/1747	0.62	1/2721 (0.0%)
23	x	0.43	1/261 (0.4%)	0.27	0/404
24	y	0.20	1/1618 (0.1%)	0.31	0/2514
25	z	0.45	4/2935 (0.1%)	0.78	0/3970
26	A	0.23	1/69174 (0.0%)	0.34	0/107910
27	B	0.16	0/2876	0.32	0/4483
28	C	0.42	0/2121	0.82	0/2852
29	D	0.45	0/1586	0.83	1/2134 (0.0%)
30	E	0.33	0/1571	0.70	2/2113 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	F	0.39	0/1434	0.78	0/1926
32	G	0.47	0/1343	0.84	1/1816 (0.1%)
33	H	0.34	0/1122	0.73	0/1515
34	I	0.37	0/1046	0.79	2/1410 (0.1%)
35	J	0.36	0/1152	0.73	0/1551
36	K	0.36	0/947	0.72	0/1268
37	L	0.35	0/1054	0.77	1/1403 (0.1%)
38	M	0.40	0/1093	0.77	2/1460 (0.1%)
39	N	0.36	0/973	0.76	0/1301
40	O	0.42	0/902	0.74	0/1209
41	P	0.34	0/929	0.75	0/1242
42	Q	0.40	0/960	0.77	0/1278
43	R	0.43	0/829	0.82	1/1107 (0.1%)
44	S	0.37	0/864	0.83	1/1156 (0.1%)
45	T	0.35	0/744	0.79	0/994
46	U	0.47	1/787 (0.1%)	0.78	1/1051 (0.1%)
47	V	0.36	0/766	0.78	0/1025
48	W	0.39	0/582	0.83	2/769 (0.3%)
49	X	0.34	0/635	0.69	0/848
50	Y	0.43	0/510	0.73	0/677
51	Z	0.31	0/453	0.67	0/605
52	0	0.32	0/450	0.72	0/599
53	1	0.34	0/416	0.74	0/554
54	2	0.35	0/380	0.79	0/498
55	3	0.33	0/513	0.80	2/676 (0.3%)
56	4	0.33	0/303	0.77	0/397
57	5	0.37	0/1001	0.79	0/1350
58	6	0.45	0/531	0.89	0/709
All	All	0.29	10/164039 (0.0%)	0.50	30/244934 (0.0%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	z	189	LEU	C-O	6.81	1.32	1.24
46	U	41	VAL	C-O	6.51	1.31	1.24
25	z	188	ILE	C-O	6.24	1.32	1.24
23	x	14	U	C1'-N1	5.80	1.57	1.48
25	z	193	GLY	N-CA	5.78	1.53	1.45

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	w	19	G	C4'-C3'-O3'	-7.12	98.72	109.40
37	L	36	LYS	CB-CA-C	-6.12	108.51	115.79
6	f	11	HIS	CA-C-N	5.83	127.13	119.84
6	f	11	HIS	C-N-CA	5.83	127.13	119.84
48	W	69	GLY	CA-C-N	5.80	125.00	118.97

There are no chirality outliers.

There are no planarity outliers.

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	a	33029	0	16645	377	0
2	b	1704	0	1732	45	0
3	c	1624	0	1699	53	0
4	d	1643	0	1710	49	0
5	e	1141	0	1170	37	0
6	f	817	0	808	26	0
7	g	1181	0	1240	33	0
8	h	979	0	1034	17	0
9	i	1022	0	1070	32	0
10	j	786	0	828	38	0
11	k	869	0	878	31	0
12	l	955	0	1019	25	0
13	m	883	0	944	25	0
14	n	799	0	841	20	0
15	o	714	0	737	16	0
16	p	649	0	666	22	0
17	q	648	0	691	28	0
18	r	504	0	502	14	0
19	s	637	0	665	28	0
20	t	665	0	714	19	0
21	u	495	0	486	18	0
22	v	1644	0	839	20	0
22	w	1644	0	840	154	0
23	x	234	0	118	3	0
24	y	1643	0	850	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	z	2881	0	2894	98	0
26	A	62276	0	31346	847	0
27	B	2572	0	1302	27	0
28	C	2082	0	2157	42	0
29	D	1565	0	1616	39	0
30	E	1552	0	1619	31	0
31	F	1410	0	1447	48	0
32	G	1323	0	1374	23	0
33	H	1111	0	1148	18	0
34	I	1032	0	1088	35	0
35	J	1129	0	1162	31	0
36	K	938	0	1012	23	0
37	L	1045	0	1117	35	0
38	M	1074	0	1157	22	0
39	N	960	0	1000	26	0
40	O	892	0	923	11	0
41	P	917	0	965	17	0
42	Q	947	0	1022	22	0
43	R	816	0	839	15	0
44	S	857	0	922	22	0
45	T	738	0	807	20	0
46	U	779	0	834	17	0
47	V	753	0	780	15	0
48	W	575	0	592	9	0
49	X	625	0	655	12	0
50	Y	509	0	543	11	0
51	Z	449	0	491	7	0
52	0	444	0	461	15	0
53	1	409	0	440	4	0
54	2	377	0	418	20	0
55	3	504	0	574	16	0
56	4	302	0	341	12	0
57	5	988	0	1025	32	0
58	6	522	0	520	14	0
59	0	1	0	0	0	0
59	4	1	0	0	0	0
59	A	234	0	0	0	0
59	B	7	0	0	0	0
59	N	2	0	0	0	0
59	a	83	0	0	0	0
59	v	4	0	0	0	0
59	z	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	A	1	0	0	0	0
60	a	1	0	0	0	0
61	v	10	0	10	7	0
62	z	57	0	60	5	0
63	z	28	0	12	3	0
64	A	1	0	0	0	0
64	B	1	0	0	0	0
65	4	1	0	0	0	0
65	6	1	0	0	0	0
66	A	9	0	0	1	0
66	D	2	0	0	0	0
66	K	1	0	0	0	0
66	a	9	0	0	0	0
All	All	152717	0	103399	2498	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 10.

The worst 5 of 2498 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)
22:w:18:G:H21	22:w:58:A:C5'	1.23	1.47
22:w:18:G:N2	22:w:58:A:C5'	2.03	1.21
22:w:18:G:N2	22:w:58:A:O5'	1.75	1.17
22:w:20:H2U:C5'	26:A:2112:G:H21	1.64	1.10
22:w:20:H2U:H5'	26:A:2112:G:H21	1.15	1.05

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	
2	b	216/240 (90%)	183 (85%)	23 (11%)	10 (5%)	2	7
3	c	204/233 (88%)	184 (90%)	18 (9%)	2 (1%)	12	39
4	d	203/206 (98%)	172 (85%)	21 (10%)	10 (5%)	1	6
5	e	155/167 (93%)	130 (84%)	16 (10%)	9 (6%)	1	4
6	f	98/135 (73%)	81 (83%)	11 (11%)	6 (6%)	1	4
7	g	149/179 (83%)	124 (83%)	15 (10%)	10 (7%)	1	3
8	h	127/130 (98%)	110 (87%)	14 (11%)	3 (2%)	4	18
9	i	125/130 (96%)	98 (78%)	19 (15%)	8 (6%)	1	3
10	j	96/103 (93%)	74 (77%)	16 (17%)	6 (6%)	1	3
11	k	114/129 (88%)	92 (81%)	16 (14%)	6 (5%)	1	5
12	l	121/124 (98%)	96 (79%)	20 (16%)	5 (4%)	2	9
13	m	112/118 (95%)	99 (88%)	8 (7%)	5 (4%)	2	8
14	n	99/102 (97%)	82 (83%)	12 (12%)	5 (5%)	1	6
15	o	86/89 (97%)	71 (83%)	10 (12%)	5 (6%)	1	4
16	p	80/82 (98%)	67 (84%)	11 (14%)	2 (2%)	4	17
17	q	78/84 (93%)	65 (83%)	8 (10%)	5 (6%)	1	3
18	r	63/75 (84%)	53 (84%)	5 (8%)	5 (8%)	1	2
19	s	77/92 (84%)	66 (86%)	11 (14%)	0	100	100
20	t	83/87 (95%)	77 (93%)	4 (5%)	2 (2%)	4	18
21	u	63/71 (89%)	44 (70%)	14 (22%)	5 (8%)	1	2
25	z	368/393 (94%)	327 (89%)	35 (10%)	6 (2%)	7	27
28	C	269/273 (98%)	243 (90%)	21 (8%)	5 (2%)	6	23
29	D	207/209 (99%)	185 (89%)	20 (10%)	2 (1%)	12	39
30	E	199/201 (99%)	172 (86%)	20 (10%)	7 (4%)	3	12
31	F	175/179 (98%)	149 (85%)	20 (11%)	6 (3%)	3	12
32	G	174/177 (98%)	148 (85%)	21 (12%)	5 (3%)	3	15
33	H	147/149 (99%)	128 (87%)	15 (10%)	4 (3%)	4	16
34	I	139/142 (98%)	110 (79%)	20 (14%)	9 (6%)	1	3
35	J	140/142 (99%)	129 (92%)	9 (6%)	2 (1%)	9	30
36	K	120/123 (98%)	103 (86%)	14 (12%)	3 (2%)	4	17
37	L	141/144 (98%)	110 (78%)	20 (14%)	11 (8%)	1	2
38	M	134/136 (98%)	117 (87%)	14 (10%)	3 (2%)	5	20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	N	118/127 (93%)	103 (87%)	12 (10%)	3 (2%)	4	17
40	O	114/117 (97%)	102 (90%)	11 (10%)	1 (1%)	14	41
41	P	112/115 (97%)	93 (83%)	18 (16%)	1 (1%)	14	41
42	Q	115/118 (98%)	110 (96%)	5 (4%)	0	100	100
43	R	101/103 (98%)	82 (81%)	17 (17%)	2 (2%)	6	22
44	S	108/110 (98%)	90 (83%)	12 (11%)	6 (6%)	1	4
45	T	91/100 (91%)	77 (85%)	11 (12%)	3 (3%)	3	13
46	U	100/104 (96%)	80 (80%)	17 (17%)	3 (3%)	3	14
47	V	92/94 (98%)	78 (85%)	12 (13%)	2 (2%)	5	20
48	W	73/85 (86%)	66 (90%)	6 (8%)	1 (1%)	9	30
49	X	75/78 (96%)	69 (92%)	5 (7%)	1 (1%)	9	32
50	Y	61/63 (97%)	55 (90%)	5 (8%)	1 (2%)	7	27
51	Z	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
52	0	54/57 (95%)	49 (91%)	4 (7%)	1 (2%)	6	23
53	1	48/55 (87%)	43 (90%)	5 (10%)	0	100	100
54	2	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
55	3	62/65 (95%)	54 (87%)	7 (11%)	1 (2%)	7	27
56	4	36/38 (95%)	28 (78%)	8 (22%)	0	100	100
57	5	129/165 (78%)	100 (78%)	22 (17%)	7 (5%)	1	5
58	6	64/70 (91%)	53 (83%)	10 (16%)	1 (2%)	7	27
All	All	6215/6613 (94%)	5318 (86%)	691 (11%)	206 (3%)	5	13

5 of 206 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	c	156	LEU
5	e	122	VAL
6	f	63	ASN
9	i	12	LYS
9	i	71	ILE

5.3.2 Protein sidechains [i](#)

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	
2	b	180/198 (91%)	173 (96%)	7 (4%)	28	63
3	c	170/190 (90%)	159 (94%)	11 (6%)	15	44
4	d	172/173 (99%)	166 (96%)	6 (4%)	32	66
5	e	114/126 (90%)	104 (91%)	10 (9%)	9	29
6	f	87/116 (75%)	82 (94%)	5 (6%)	18	49
7	g	124/147 (84%)	119 (96%)	5 (4%)	28	62
8	h	104/105 (99%)	103 (99%)	1 (1%)	68	89
9	i	105/107 (98%)	103 (98%)	2 (2%)	50	79
10	j	86/90 (96%)	82 (95%)	4 (5%)	23	56
11	k	89/99 (90%)	86 (97%)	3 (3%)	32	66
12	l	103/104 (99%)	99 (96%)	4 (4%)	28	63
13	m	92/96 (96%)	88 (96%)	4 (4%)	26	60
14	n	79/84 (94%)	75 (95%)	4 (5%)	21	53
15	o	76/77 (99%)	75 (99%)	1 (1%)	61	86
16	p	65/65 (100%)	61 (94%)	4 (6%)	16	46
17	q	74/78 (95%)	72 (97%)	2 (3%)	39	73
18	r	48/65 (74%)	47 (98%)	1 (2%)	47	77
19	s	70/79 (89%)	65 (93%)	5 (7%)	13	40
20	t	65/66 (98%)	63 (97%)	2 (3%)	35	69
21	u	44/61 (72%)	44 (100%)	0	100	100
25	z	311/326 (95%)	298 (96%)	13 (4%)	26	60
28	C	216/218 (99%)	210 (97%)	6 (3%)	38	72
29	D	164/164 (100%)	163 (99%)	1 (1%)	78	93
30	E	165/165 (100%)	161 (98%)	4 (2%)	43	75
31	F	148/150 (99%)	138 (93%)	10 (7%)	14	42
32	G	137/138 (99%)	136 (99%)	1 (1%)	76	92
33	H	114/114 (100%)	114 (100%)	0	100	100
34	I	109/110 (99%)	103 (94%)	6 (6%)	19	50
35	J	116/116 (100%)	114 (98%)	2 (2%)	53	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	K	103/104 (99%)	98 (95%)	5 (5%)	22	54
37	L	102/103 (99%)	100 (98%)	2 (2%)	48	78
38	M	109/109 (100%)	108 (99%)	1 (1%)	70	90
39	N	100/103 (97%)	97 (97%)	3 (3%)	36	70
40	O	86/87 (99%)	84 (98%)	2 (2%)	44	76
41	P	99/100 (99%)	94 (95%)	5 (5%)	21	53
42	Q	89/90 (99%)	85 (96%)	4 (4%)	24	58
43	R	84/84 (100%)	82 (98%)	2 (2%)	43	75
44	S	93/93 (100%)	90 (97%)	3 (3%)	34	68
45	T	80/84 (95%)	78 (98%)	2 (2%)	42	74
46	U	83/85 (98%)	81 (98%)	2 (2%)	43	75
47	V	78/78 (100%)	77 (99%)	1 (1%)	61	86
48	W	57/63 (90%)	56 (98%)	1 (2%)	51	80
49	X	67/68 (98%)	67 (100%)	0	100	100
50	Y	55/55 (100%)	54 (98%)	1 (2%)	51	80
51	Z	48/49 (98%)	48 (100%)	0	100	100
52	0	47/48 (98%)	45 (96%)	2 (4%)	26	60
53	1	45/49 (92%)	44 (98%)	1 (2%)	45	77
54	2	38/38 (100%)	37 (97%)	1 (3%)	40	73
55	3	51/52 (98%)	50 (98%)	1 (2%)	48	78
56	4	34/34 (100%)	33 (97%)	1 (3%)	37	71
57	5	100/123 (81%)	97 (97%)	3 (3%)	36	70
58	6	59/62 (95%)	58 (98%)	1 (2%)	53	82
All	All	5134/5388 (95%)	4966 (97%)	168 (3%)	34	67

5 of 168 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	G	10	VAL
42	Q	48	ASP
34	I	95	ASP
37	L	110	VAL
44	S	107	VAL

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

Mol	Chain	Res	Type
34	I	29	GLN
47	V	75	GLN
36	K	3	GLN
44	S	7	HIS
52	0	5	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1538/1539 (99%)	244 (15%)	0
22	v	76/77 (98%)	18 (23%)	0
22	w	76/77 (98%)	43 (56%)	0
23	x	10/11 (90%)	1 (10%)	0
24	y	75/77 (97%)	19 (25%)	0
26	A	2898/2903 (99%)	549 (18%)	90 (3%)
27	B	119/120 (99%)	18 (15%)	4 (3%)
All	All	4792/4804 (99%)	892 (18%)	94 (1%)

5 of 892 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	9	G
1	a	14	U
1	a	22	G
1	a	30	U
1	a	32	A

5 of 94 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
26	A	1399	C
26	A	2282	G
26	A	1626	A
26	A	1930	G
26	A	2333	A

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

52 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
26	2MG	A	1835	26	23,26,27	1.30	4 (17%)	33,38,41	2.24	8 (24%)
26	1MG	A	745	26	23,26,27	1.19	1 (4%)	33,39,42	1.86	7 (21%)
26	OMG	A	2251	22,26	23,26,27	1.26	3 (13%)	32,38,41	1.81	5 (15%)
24	5MU	y	54	24	19,22,23	1.38	5 (26%)	27,32,35	2.24	7 (25%)
26	6MZ	A	2030	26	22,25,26	1.60	4 (18%)	29,36,39	2.26	10 (34%)
1	5MC	a	1407	1	19,22,23	1.54	3 (15%)	26,32,35	1.16	3 (11%)
26	PSU	A	2504	26	18,21,22	1.35	2 (11%)	21,30,33	1.98	3 (14%)
24	PSU	y	32	24	18,21,22	1.35	2 (11%)	21,30,33	2.04	4 (19%)
26	7MG	A	2069	26	23,26,27	1.36	4 (17%)	27,39,42	2.63	7 (25%)
26	PSU	A	955	26	18,21,22	1.44	4 (22%)	21,30,33	2.17	4 (19%)
1	MA6	a	1519	1	23,26,27	1.52	5 (21%)	33,38,41	2.35	14 (42%)
1	4OC	a	1402	1	20,23,24	0.77	0	25,32,35	0.93	0
1	PSU	a	516	1,59	18,21,22	1.47	4 (22%)	21,30,33	2.31	5 (23%)
22	5MU	w	54	22	19,22,23	1.27	3 (15%)	27,32,35	2.36	10 (37%)
24	7MG	y	46	24	23,26,27	1.31	3 (13%)	27,39,42	2.64	7 (25%)
26	PSU	A	746	26,59	18,21,22	1.35	3 (16%)	21,30,33	1.98	4 (19%)
22	PSU	w	55	22	18,21,22	1.51	3 (16%)	21,30,33	2.32	5 (23%)
26	2MG	A	2445	26	23,26,27	1.33	4 (17%)	33,38,41	1.95	6 (18%)
26	H2U	A	2449	26	18,21,22	0.92	2 (11%)	19,30,33	1.11	2 (10%)
24	H2U	y	20	24	18,21,22	0.95	2 (11%)	19,30,33	0.89	1 (5%)
26	PSU	A	2580	26	18,21,22	1.44	3 (16%)	21,30,33	2.19	4 (19%)
22	5MU	v	55	22	19,22,23	1.37	5 (26%)	27,32,35	2.26	5 (18%)
26	3TD	A	1915	26	19,22,23	1.35	3 (15%)	23,32,35	2.07	4 (17%)
1	2MG	a	966	1	23,26,27	1.26	4 (17%)	33,38,41	2.30	8 (24%)
26	PSU	A	1911	26	18,21,22	1.35	2 (11%)	21,30,33	2.12	4 (19%)
24	4SU	y	8	24	18,21,22	1.86	4 (22%)	25,30,33	2.45	5 (20%)
1	2MG	a	1516	1	23,26,27	1.27	4 (17%)	33,38,41	2.15	7 (21%)
26	6MZ	A	1618	26	22,25,26	1.68	5 (22%)	29,36,39	2.31	9 (31%)
24	PSU	y	39	24	18,21,22	1.33	2 (11%)	21,30,33	2.04	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
22	4SU	w	8	22	18,21,22	1.89	4 (22%)	25,30,33	2.42	4 (16%)
1	MA6	a	1518	1	23,26,27	1.67	5 (21%)	33,38,41	2.26	9 (27%)
1	2MG	a	1207	1	23,26,27	1.27	4 (17%)	33,38,41	2.25	8 (24%)
26	OMU	A	2552	26	19,22,23	1.24	3 (15%)	25,31,34	2.28	7 (28%)
24	H2U	y	16	24	18,21,22	0.97	2 (11%)	19,30,33	0.98	1 (5%)
26	PSU	A	1917	26	18,21,22	1.38	2 (11%)	21,30,33	2.00	3 (14%)
22	H2U	v	21	22	18,21,22	0.92	2 (11%)	19,30,33	1.03	2 (10%)
26	OMC	A	2498	26,59	19,22,23	0.81	1 (5%)	25,31,34	0.88	0
26	5MC	A	747	26	19,22,23	1.53	3 (15%)	26,32,35	1.38	3 (11%)
26	PSU	A	2605	26	18,21,22	1.43	3 (16%)	21,30,33	1.96	5 (23%)
1	UR3	a	1498	1	19,22,23	0.93	1 (5%)	26,32,35	1.95	4 (15%)
1	7MG	a	527	1	23,26,27	1.34	4 (17%)	27,39,42	2.57	7 (25%)
22	4SU	v	8	22	18,21,22	1.77	4 (22%)	25,30,33	2.36	6 (24%)
24	PSU	y	55	24	18,21,22	1.39	2 (11%)	21,30,33	2.01	3 (14%)
26	PSU	A	2604	26	18,21,22	1.38	3 (16%)	21,30,33	2.05	5 (23%)
26	5MU	A	1939	26	19,22,23	1.36	4 (21%)	27,32,35	2.28	6 (22%)
1	5MC	a	967	1	19,22,23	1.52	2 (10%)	26,32,35	1.08	2 (7%)
26	2MA	A	2503	26,59	22,25,26	1.47	5 (22%)	32,37,40	2.32	9 (28%)
24	MIA	y	37	24	28,31,32	2.36	6 (21%)	38,44,47	3.05	15 (39%)
22	PSU	v	56	22	18,21,22	1.38	3 (16%)	21,30,33	2.00	4 (19%)
26	5MC	A	1962	26	19,22,23	1.58	3 (15%)	26,32,35	1.10	2 (7%)
26	PSU	A	2457	26	18,21,22	1.36	3 (16%)	21,30,33	2.23	4 (19%)
22	H2U	w	20	22	18,21,22	1.35	3 (16%)	19,30,33	1.87	3 (15%)

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
26	2MG	A	1835	26	-	0/9/27/28	0/3/3/3
26	1MG	A	745	26	-	0/7/25/26	0/3/3/3
26	OMG	A	2251	22,26	-	0/9/27/28	0/3/3/3
24	5MU	y	54	24	-	0/7/25/26	0/2/2/2
26	6MZ	A	2030	26	-	2/9/27/28	0/3/3/3
1	5MC	a	1407	1	-	0/7/25/26	0/2/2/2
26	PSU	A	2504	26	-	2/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	PSU	y	32	24	-	0/7/25/26	0/2/2/2
26	7MG	A	2069	26	-	0/7/37/38	0/3/3/3
26	PSU	A	955	26	-	0/7/25/26	0/2/2/2
1	MA6	a	1519	1	-	2/11/29/30	0/3/3/3
1	4OC	a	1402	1	-	0/9/29/30	0/2/2/2
1	PSU	a	516	1,59	-	2/7/25/26	0/2/2/2
22	5MU	w	54	22	-	2/7/25/26	0/2/2/2
24	7MG	y	46	24	-	3/7/37/38	0/3/3/3
26	PSU	A	746	26,59	-	1/7/25/26	0/2/2/2
22	PSU	w	55	22	-	2/7/25/26	0/2/2/2
26	2MG	A	2445	26	-	2/9/27/28	0/3/3/3
26	H2U	A	2449	26	-	0/7/38/39	0/2/2/2
24	H2U	y	20	24	-	5/7/38/39	0/2/2/2
26	PSU	A	2580	26	-	0/7/25/26	0/2/2/2
22	5MU	v	55	22	-	0/7/25/26	0/2/2/2
26	3TD	A	1915	26	-	3/7/25/26	0/2/2/2
1	2MG	a	966	1	-	2/9/27/28	0/3/3/3
26	PSU	A	1911	26	-	0/7/25/26	0/2/2/2
24	4SU	y	8	24	-	0/7/25/26	0/2/2/2
1	2MG	a	1516	1	-	0/9/27/28	0/3/3/3
26	6MZ	A	1618	26	-	0/9/27/28	0/3/3/3
24	PSU	y	39	24	-	0/7/25/26	0/2/2/2
22	4SU	w	8	22	-	5/7/25/26	0/2/2/2
1	MA6	a	1518	1	-	6/11/29/30	0/3/3/3
1	2MG	a	1207	1	-	2/9/27/28	0/3/3/3
26	OMU	A	2552	26	-	2/9/27/28	0/2/2/2
24	H2U	y	16	24	-	0/7/38/39	0/2/2/2
26	PSU	A	1917	26	-	0/7/25/26	0/2/2/2
22	H2U	v	21	22	-	1/7/38/39	0/2/2/2
26	OMC	A	2498	26,59	-	1/9/27/28	0/2/2/2
26	5MC	A	747	26	-	0/7/25/26	0/2/2/2
26	PSU	A	2605	26	-	0/7/25/26	0/2/2/2
1	UR3	a	1498	1	-	2/7/25/26	0/2/2/2
1	7MG	a	527	1	-	3/7/37/38	0/3/3/3
22	4SU	v	8	22	-	0/7/25/26	0/2/2/2
24	PSU	y	55	24	-	0/7/25/26	0/2/2/2
26	PSU	A	2604	26	-	0/7/25/26	0/2/2/2
26	5MU	A	1939	26	-	0/7/25/26	0/2/2/2
1	5MC	a	967	1	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
26	2MA	A	2503	26,59	-	2/7/25/26	0/3/3/3
24	MIA	y	37	24	-	3/15/33/34	0/3/3/3
22	PSU	v	56	22	-	2/7/25/26	0/2/2/2
26	5MC	A	1962	26	-	1/7/25/26	0/2/2/2
26	PSU	A	2457	26	-	0/7/25/26	0/2/2/2
22	H2U	w	20	22	-	1/7/38/39	0/2/2/2

The worst 5 of 165 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	y	37	MIA	C2-S10	-7.43	1.69	1.75
24	y	37	MIA	C13-C14	6.90	1.53	1.32
26	A	1618	6MZ	C5-C4	5.73	1.49	1.39
26	A	1962	5MC	C5-C4	5.55	1.48	1.44
1	a	1407	5MC	C5-C4	5.41	1.48	1.44

The worst 5 of 274 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	y	37	MIA	C12-C13-C14	-9.96	109.14	127.01
24	y	46	7MG	N9-C4-N3	9.02	138.69	125.46
26	A	2069	7MG	N9-C4-N3	8.77	138.32	125.46
1	a	527	7MG	N9-C4-N3	8.73	138.26	125.46
24	y	37	MIA	C5-C4-N3	-8.31	118.43	127.18

There are no chirality outliers.

5 of 59 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	a	1207	2MG	O4'-C4'-C5'-O5'
1	a	1207	2MG	C3'-C4'-C5'-O5'
1	a	1518	MA6	C5-C6-N6-C9
1	a	1518	MA6	C5-C6-N6-C10
1	a	1518	MA6	N1-C6-N6-C9

There are no ring outliers.

26 monomers are involved in 45 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
26	A	2030	6MZ	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
26	A	955	PSU	1	0
1	a	1519	MA6	2	0
1	a	1402	4OC	2	0
1	a	516	PSU	1	0
22	w	54	5MU	2	0
22	w	55	PSU	3	0
26	A	2445	2MG	1	0
26	A	2449	H2U	1	0
22	v	55	5MU	1	0
24	y	8	4SU	2	0
22	w	8	4SU	4	0
1	a	1518	MA6	1	0
1	a	1207	2MG	2	0
26	A	2552	OMU	1	0
24	y	16	H2U	1	0
26	A	1917	PSU	1	0
26	A	2498	OMC	1	0
26	A	747	5MC	1	0
1	a	1498	UR3	1	0
24	y	55	PSU	1	0
26	A	2503	2MA	1	0
24	y	37	MIA	1	0
22	v	56	PSU	1	0
26	A	1962	5MC	1	0
22	w	20	H2U	12	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 342 ligands modelled in this entry, 339 are monoatomic - leaving 3 for Mogul analysis.

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
63	GDP	z	402	59	29,30,30	1.11	2 (6%)	45,47,47	1.82	7 (15%)
61	FME	v	105	-	8,9,10	0.87	0	8,9,11	1.41	2 (25%)
62	KIR	z	401	-	56,59,59	0.97	4 (7%)	60,84,84	1.74	11 (18%)

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
63	GDP	z	402	59	-	1/16/32/32	0/3/3/3
61	FME	v	105	-	-	2/7/9/11	-
62	KIR	z	401	-	-	24/54/98/98	0/3/3/3

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	z	401	KIR	C3-C4	4.00	1.49	1.41
63	z	402	GDP	C5-C4	3.03	1.47	1.38
63	z	402	GDP	C6-N1	-2.33	1.34	1.38
62	z	401	KIR	C3-C2	2.32	1.49	1.44
62	z	401	KIR	C6-C5	2.26	1.40	1.35

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	z	401	KIR	C23-C22-C21	-6.12	118.50	127.37
63	z	402	GDP	C5-C4-N3	-5.90	119.00	128.39
63	z	402	GDP	C2-N3-C4	4.96	120.84	112.30
63	z	402	GDP	N9-C4-N3	4.69	135.33	125.95
62	z	401	KIR	C15-C14-C13	-4.44	107.29	114.60

There are no chirality outliers.

5 of 27 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
61	v	105	FME	O1-CN-N-CA
62	z	401	KIR	C2-C3-C7-C8
62	z	401	KIR	C4-C3-C7-C8
62	z	401	KIR	C3-C7-C8-C41

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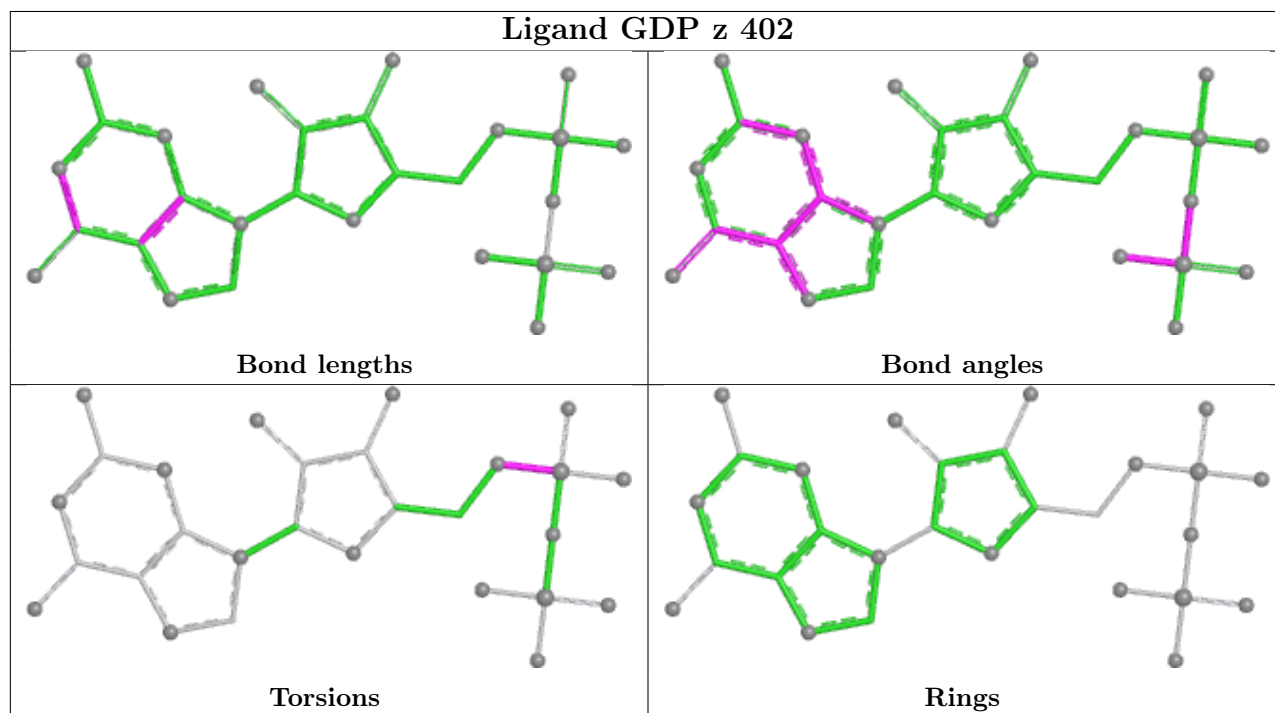
Mol	Chain	Res	Type	Atoms
62	z	401	KIR	C17-C19-C20-C21

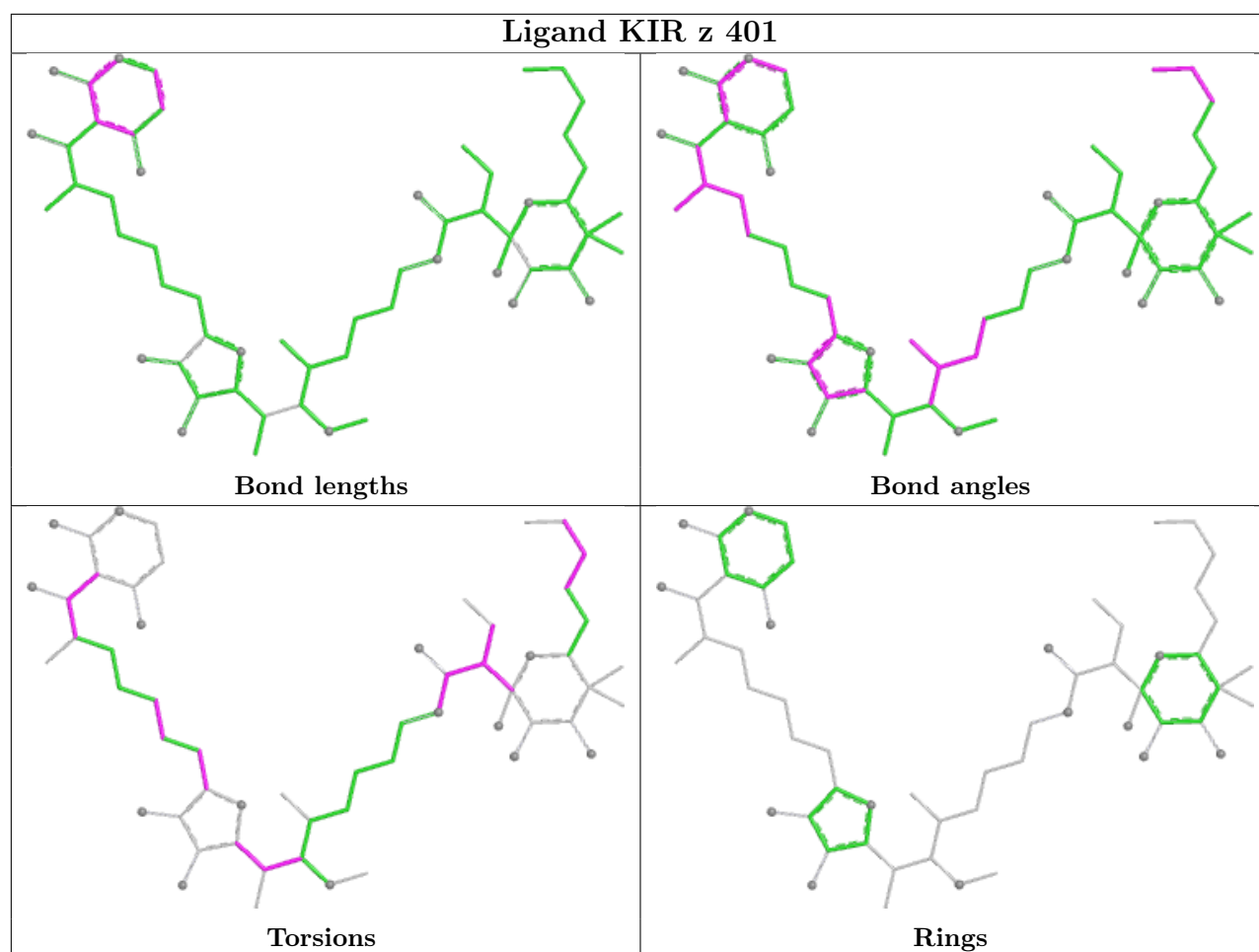
There are no ring outliers.

3 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
63	z	402	GDP	3	0
61	v	105	FME	7	0
62	z	401	KIR	5	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 [i](#)

There are no chain breaks in this entry.

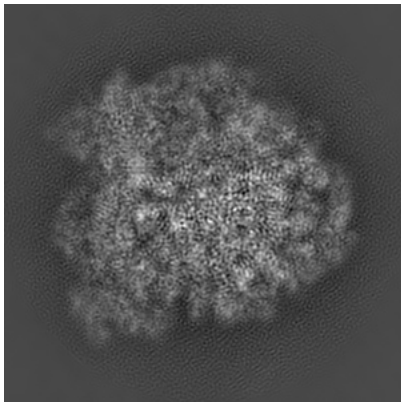
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2847. These allow visual inspection of the internal detail of the map and identification of artifacts.

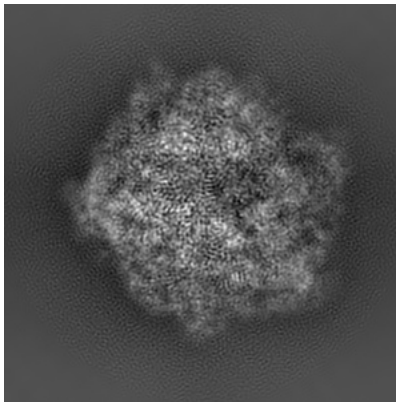
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

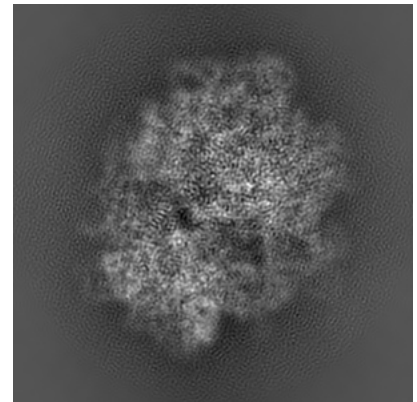
6.1.1 Primary map



X



Y

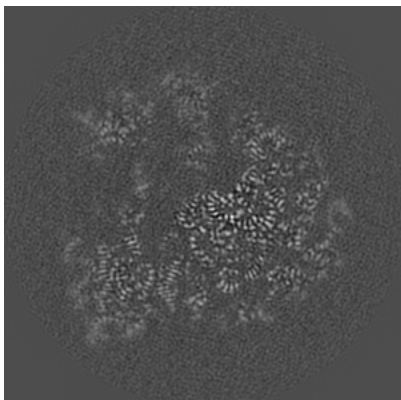


Z

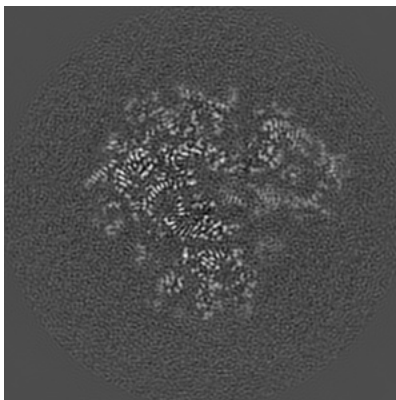
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

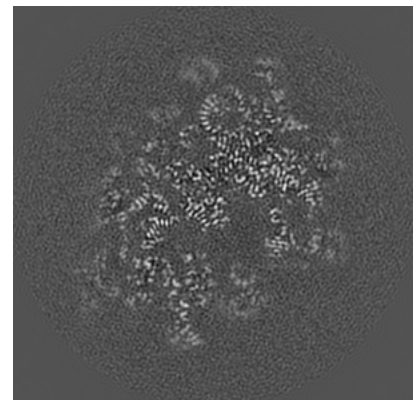
6.2.1 Primary map



X Index: 210



Y Index: 210

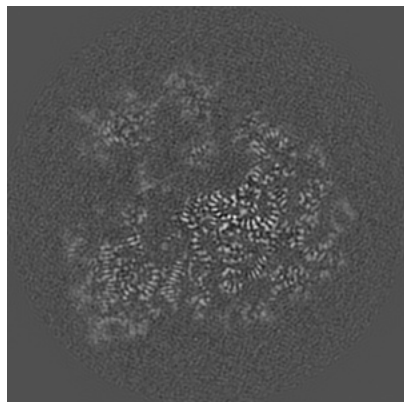


Z Index: 210

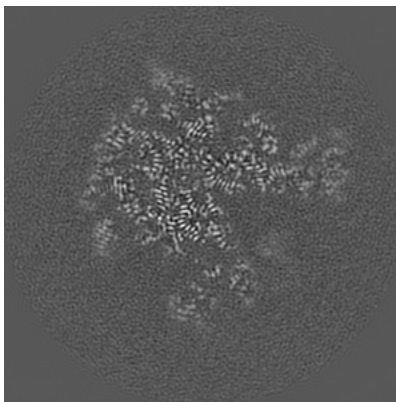
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

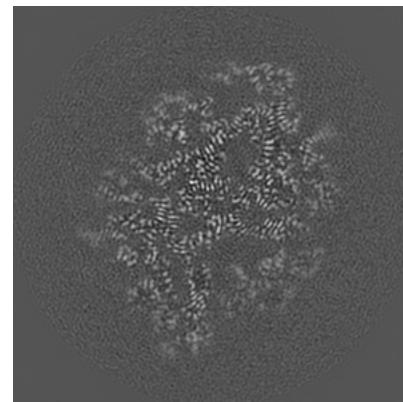
6.3.1 Primary map



X Index: 209



Y Index: 228

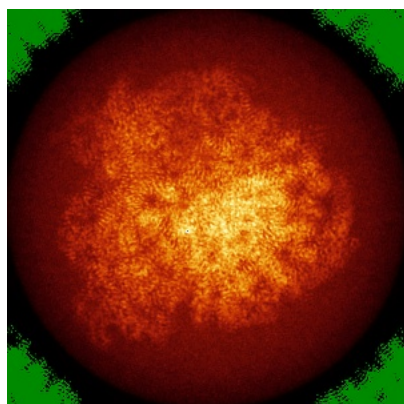


Z Index: 189

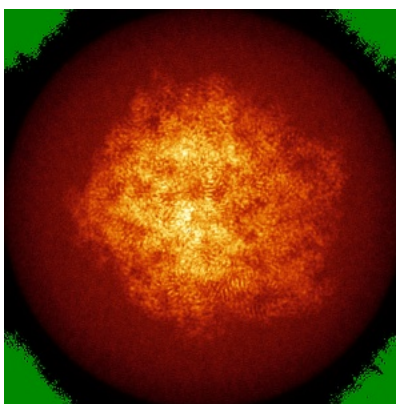
The images above show the largest variance slices of the map in three orthogonal directions.

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

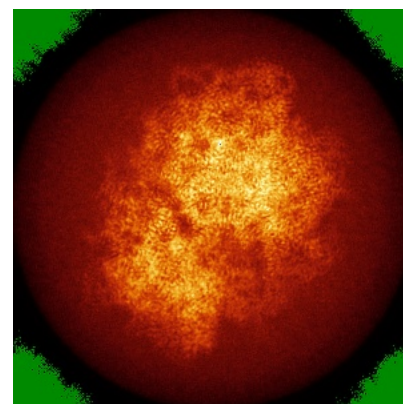
6.4.1 Primary map



X



Y

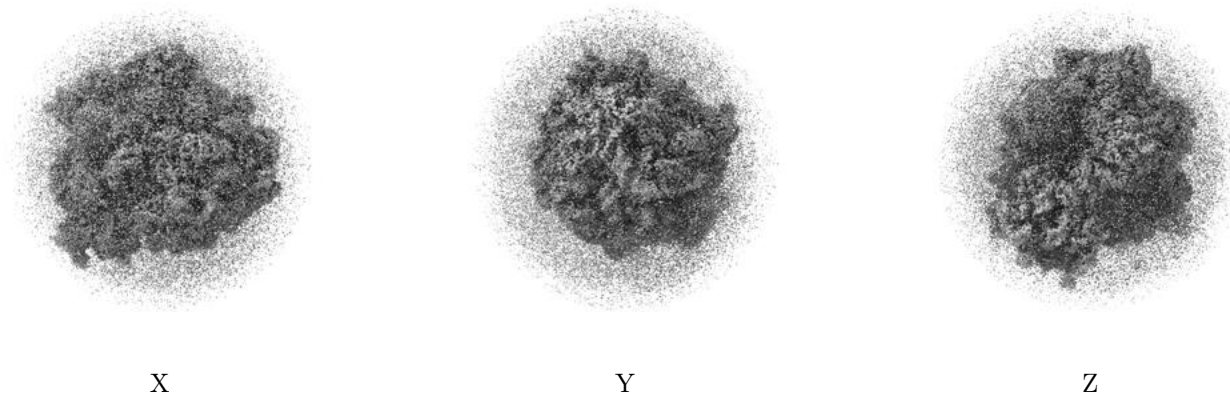


Z

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

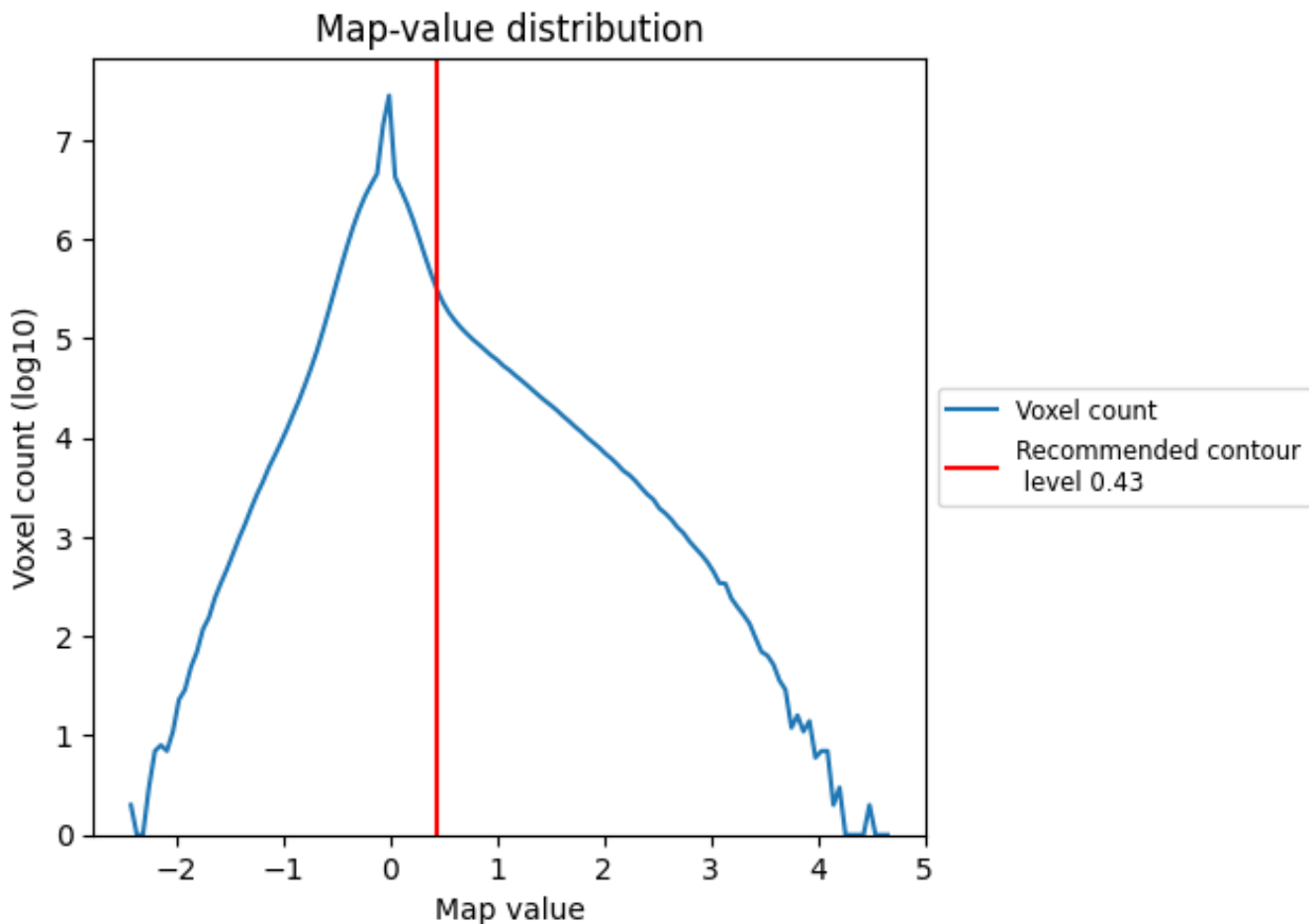
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

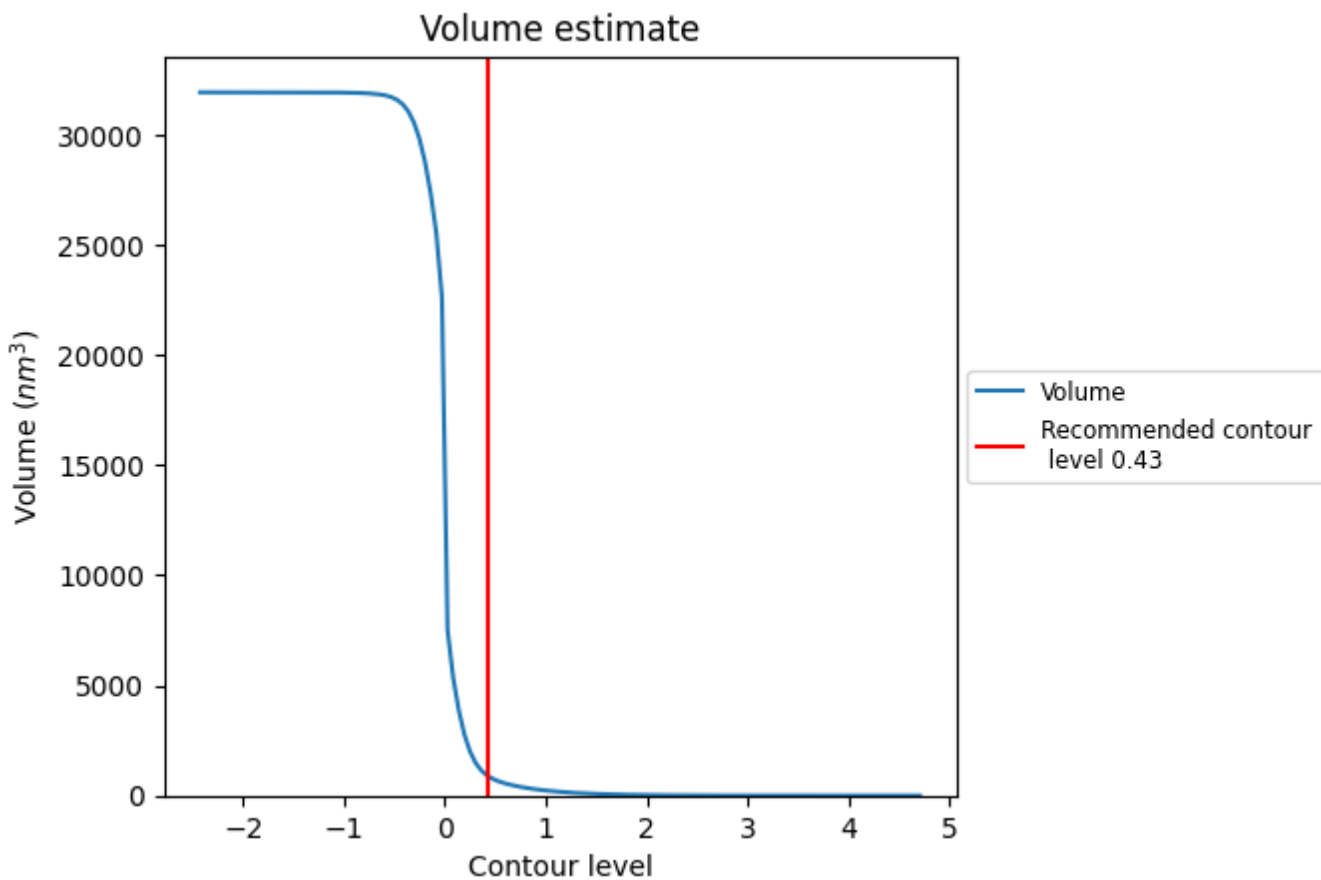
This section contains the results of statistical analysis of the map.

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.

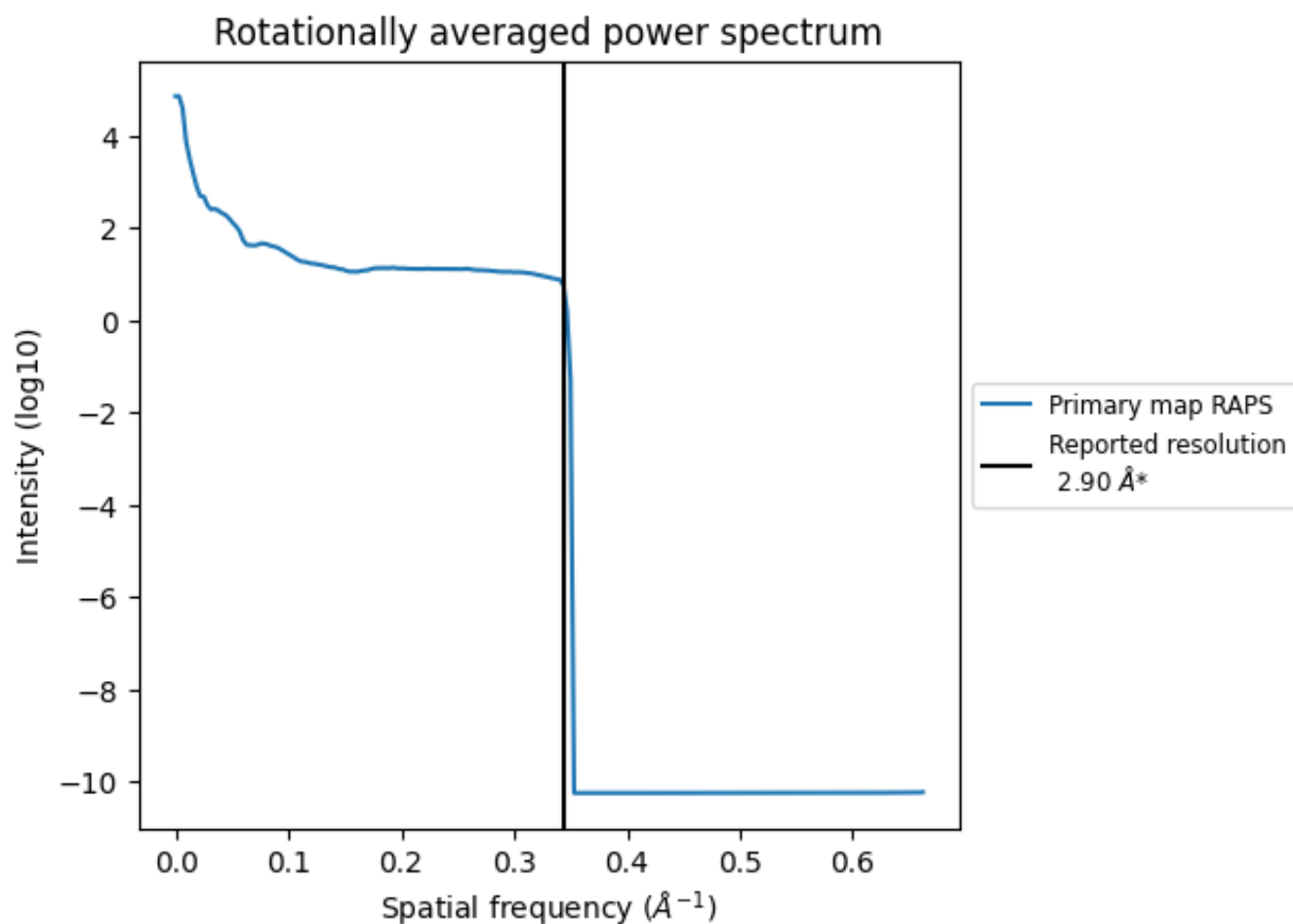
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 882 nm³; this corresponds to an approximate mass of 797 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 [\(i\)](#)



*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

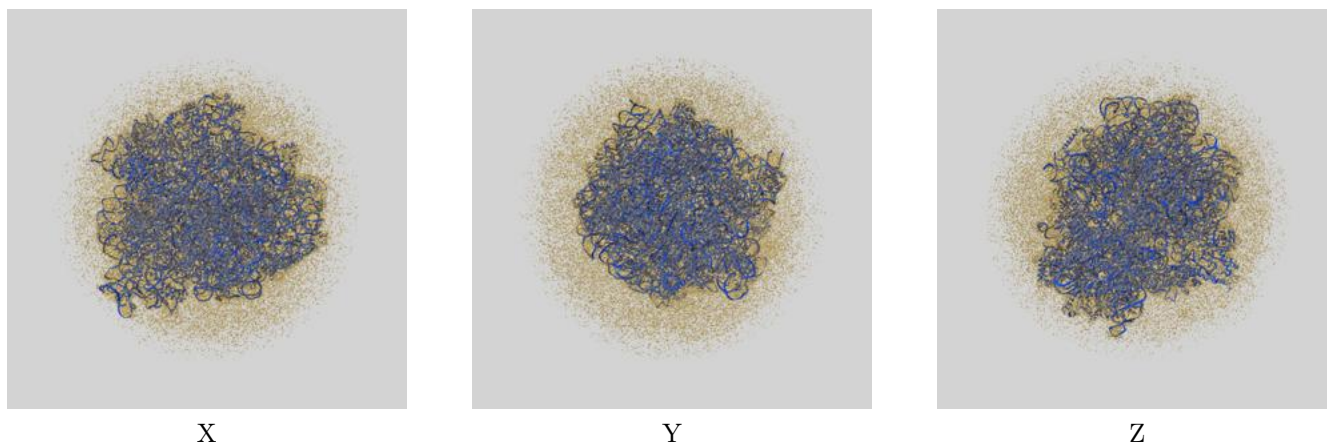
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

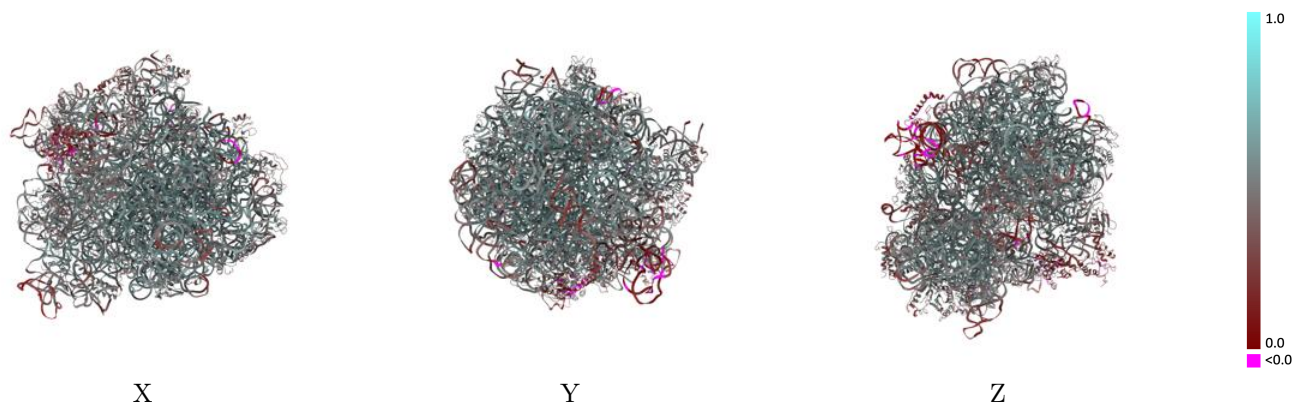
This section contains information regarding the fit between EMDB map EMD-2847 and PDB model 5AFI. Per-residue inclusion information can be found in section 3 on page 18.

9.1 Map-model overlay [i](#)



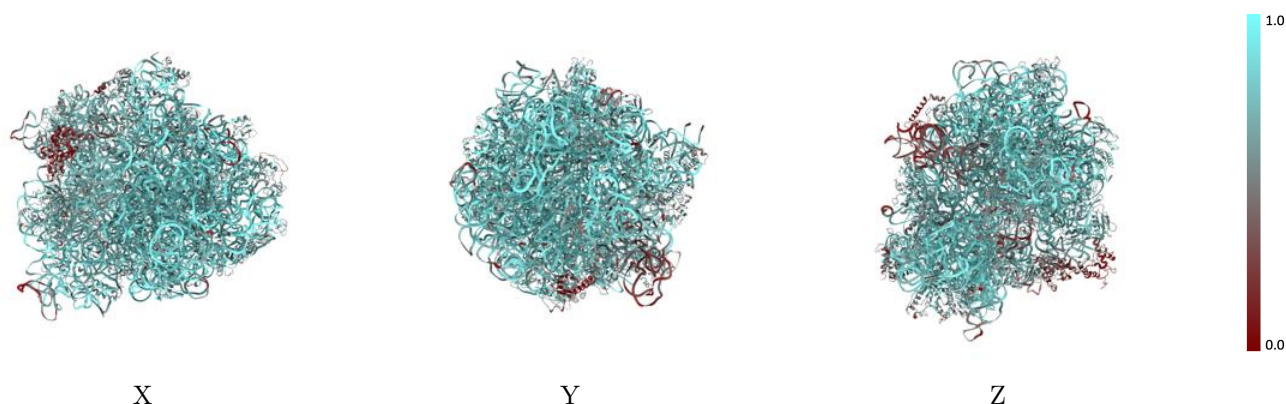
The images above show the 3D surface view of the map at the recommended contour level 0.43 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



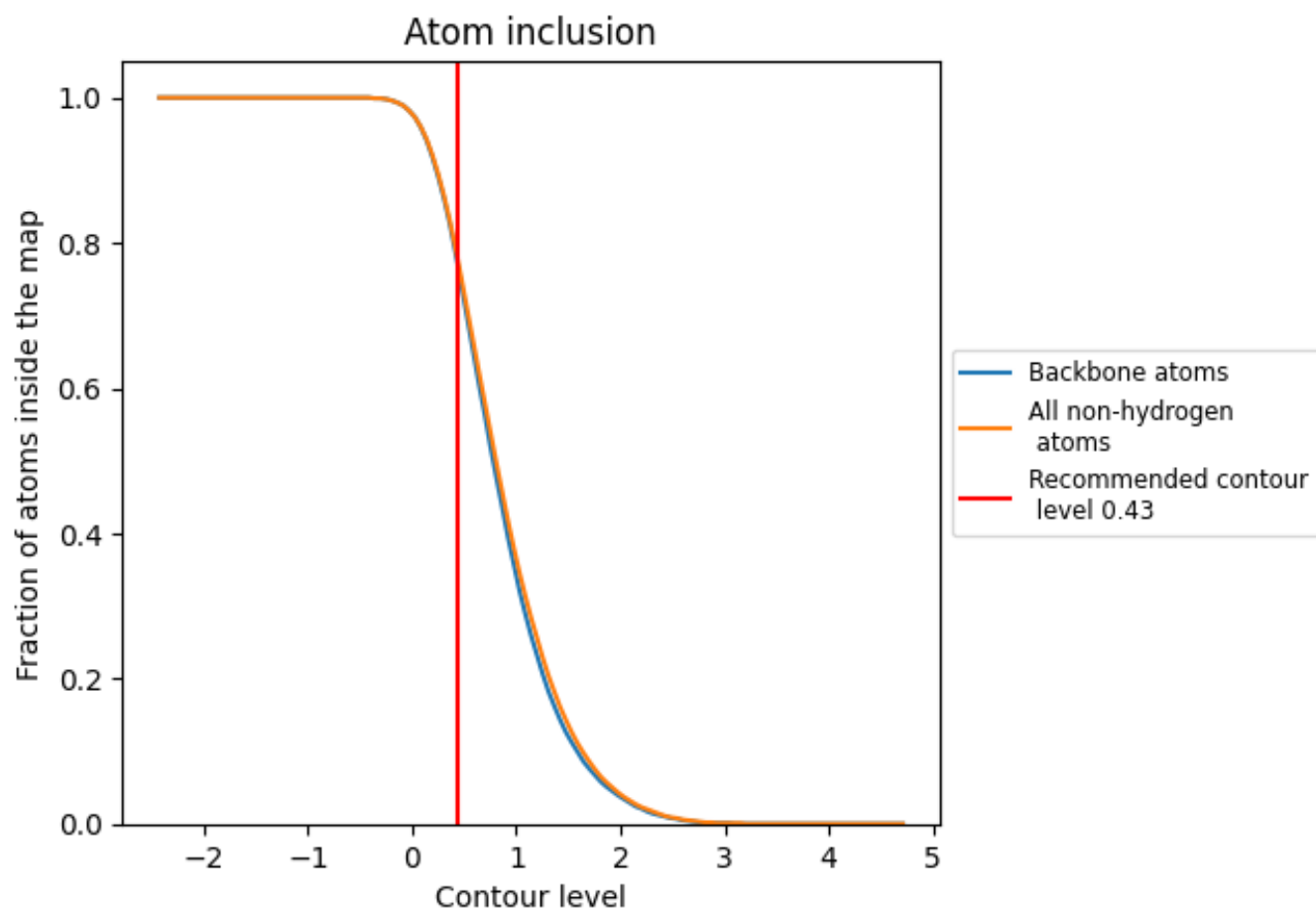
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.43).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 78% 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 (0.43) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7830	 0.4980
0	 0.7530	 0.5130
1	 0.6360	 0.4690
2	 0.8060	 0.5360
3	 0.7900	 0.5620
4	 0.7620	 0.5050
5	 0.1590	 0.1980
6	 0.4510	 0.3410
A	 0.8600	 0.5270
B	 0.8250	 0.4790
C	 0.7710	 0.5200
D	 0.7480	 0.5180
E	 0.6730	 0.4760
F	 0.5920	 0.4100
G	 0.6110	 0.4260
H	 0.2150	 0.1780
I	 0.2040	 0.2050
J	 0.7470	 0.5070
K	 0.7400	 0.5320
L	 0.7170	 0.4870
M	 0.7390	 0.5040
N	 0.7740	 0.5320
O	 0.6560	 0.4530
P	 0.7060	 0.4940
Q	 0.7770	 0.5360
R	 0.7130	 0.4760
S	 0.7390	 0.5170
T	 0.6840	 0.4660
U	 0.6210	 0.4460
V	 0.6730	 0.4530
W	 0.7460	 0.5280
X	 0.7190	 0.4930
Y	 0.6300	 0.4170
Z	 0.7070	 0.4910
a	 0.8650	 0.5260



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Chain	Atom inclusion	Q-score
b	 0.4970	 0.3890
c	 0.6730	 0.4720
d	 0.6460	 0.4540
e	 0.7340	 0.4940
f	 0.6390	 0.3820
g	 0.6320	 0.4330
h	 0.7180	 0.4990
i	 0.6570	 0.4350
j	 0.5900	 0.4150
k	 0.7340	 0.4820
l	 0.7450	 0.5170
m	 0.6380	 0.4230
n	 0.6860	 0.4650
o	 0.7300	 0.4770
p	 0.6790	 0.4660
q	 0.6800	 0.4650
r	 0.7300	 0.4930
s	 0.6600	 0.4580
t	 0.6720	 0.4770
u	 0.5290	 0.3610
v	 0.7680	 0.4980
w	 0.4290	 0.3010
x	 0.7610	 0.4850
y	 0.7630	 0.4810
z	 0.6080	 0.4350