



wwPDB EM Validation Summary Report ⓘ

Jun 21, 2026 – 04:48 am BST

PDB ID : 7PJX / pdb_00007pjax
EMDB ID : EMD-13463
Title : Structure of the 70S-EF-G-GDP ribosome complex with tRNAs in hybrid state 1 (H1-EF-G-GDP)
Authors : Petrychenko, V.; Peng, B.Z.; Schwarzer, A.C.; Peske, F.; Rodnina, M.V.; Fischer, N.
Deposited on : 2021-08-24
Resolution : 6.50 Å(reported)
Based on initial models : 5LZD, 6YSS, 4AQY, 5J9Z

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:

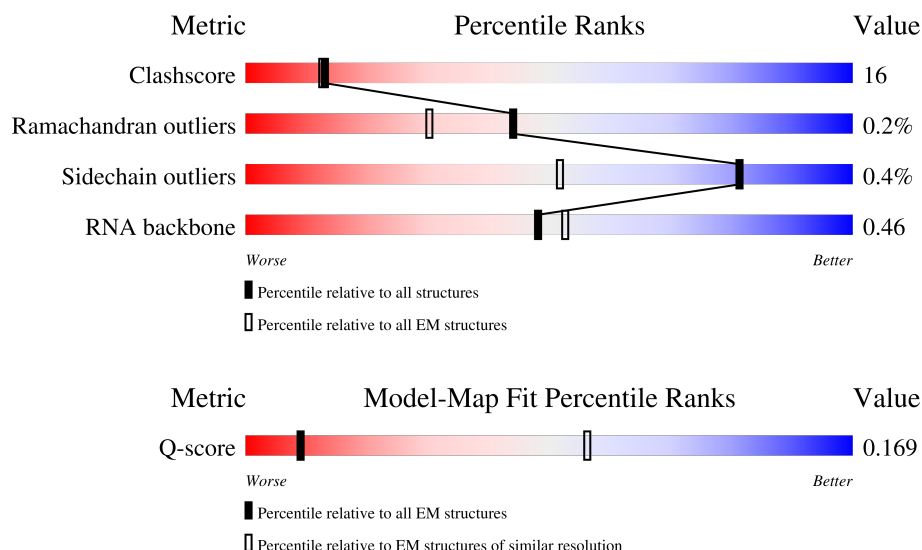
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 6.50 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.



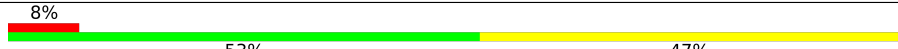
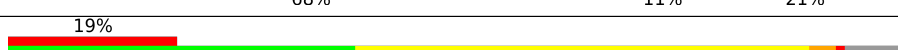
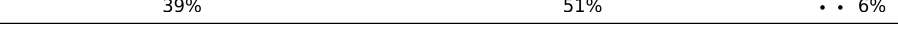
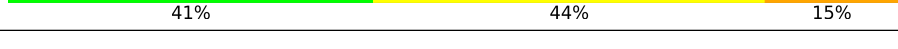
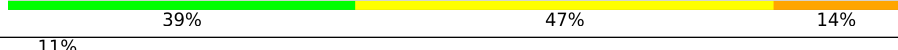
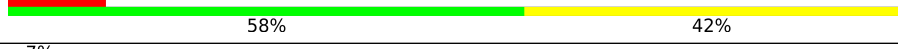
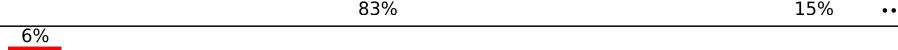
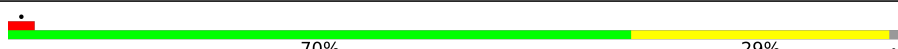
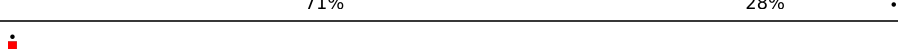
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	556 (6.00 - 7.00)

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	0	57	
2	1	55	

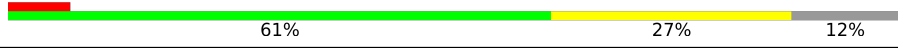
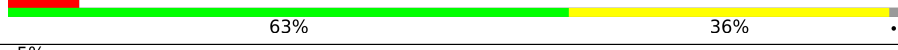
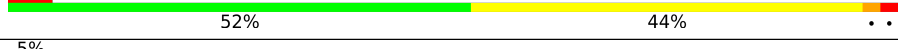
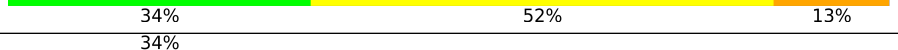
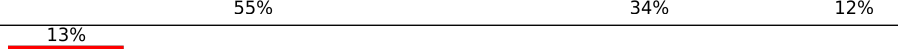
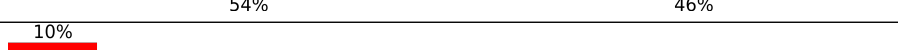
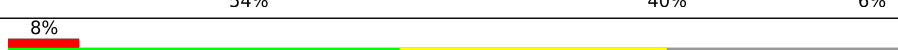
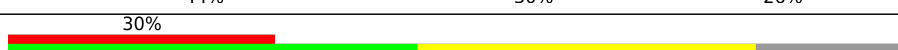
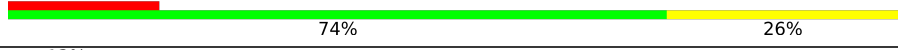
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Mol	Chain	Length	Quality of chain
3	2	46	
4	3	65	
5	4	38	
6	5	165	
7	6	70	
8	A	2903	
9	B	120	
10	C	273	
11	D	209	
12	E	201	
13	F	179	
14	G	177	
15	H	149	
16	I	142	
17	J	142	
18	K	123	
19	L	144	
20	M	136	
21	N	127	
22	O	117	
23	P	115	
24	Q	118	
25	R	103	
26	S	110	
27	T	100	

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Mol	Chain	Length	Quality of chain
28	U	104	
29	V	94	
30	W	85	
31	X	78	
32	Y	63	
33	Z	59	
34	a	1542	
35	b	240	
36	c	233	
37	d	206	
38	e	167	
39	f	135	
40	g	179	
41	h	130	
42	i	130	
43	j	103	
44	k	129	
45	l	124	
46	m	118	
47	n	102	
48	o	89	
49	p	82	
50	q	84	
51	r	75	
52	s	92	

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Mol	Chain	Length	Quality of chain
53	t	87	
54	u	71	
55	v	77	
56	w	76	
57	x	704	
58	y	2	
59	z	33	

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
61	GDP	x	801	-	-	X	-

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 151321 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 L32.

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

- Molecule 2 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 3 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 4 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 5 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 6 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	5	131	Total	C	N	O	0	0
			647	385	131	131		

- Molecule 7 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 8 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A	2903	Total	C	N	O	P	0	0
			62338	27816	11471	20148	2903		

- Molecule 9 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	B	120	Total	C	N	O	P	0	0
			2570	1144	468	838	120		

- Molecule 10 is a protein called 50S ribosomal protein L2.

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

- Molecule 11 is a protein called 50S ribosomal protein L3.

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

- Molecule 12 is a protein called 50S ribosomal protein L4.

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

- Molecule 13 is a protein called 50S ribosomal protein L5.

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

- Molecule 14 is a protein called 50S ribosomal protein L6.

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

- Molecule 15 is a protein called 50S ribosomal protein L9.

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

- Molecule 16 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	I	141	Total	C	N	O	S	0	0
			693	411	141	141			

- Molecule 17 is a protein called 50S ribosomal protein L13.

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

- Molecule 18 is a protein called 50S ribosomal protein L14.

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

- Molecule 19 is a protein called 50S ribosomal protein L15.

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

- Molecule 20 is a protein called 50S ribosomal protein L16.

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

- Molecule 21 is a protein called 50S ribosomal protein L17.

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

- Molecule 22 is a protein called 50S ribosomal protein L18.

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

- Molecule 23 is a protein called 50S ribosomal protein L19.

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

- Molecule 24 is a protein called 50S ribosomal protein L20.

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

- Molecule 25 is a protein called 50S ribosomal protein L21.

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

- Molecule 26 is a protein called 50S ribosomal protein L22.

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

- Molecule 27 is a protein called 50S ribosomal protein L23.

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

- Molecule 28 is a protein called 50S ribosomal protein L24.

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

- Molecule 29 is a protein called 50S ribosomal protein L25.

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

- Molecule 30 is a protein called 50S ribosomal protein L27.

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

- Molecule 31 is a protein called 50S ribosomal protein L28.

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

- Molecule 32 is a protein called 50S ribosomal protein L29.

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

- Molecule 33 is a protein called 50S ribosomal protein L30.

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

- Molecule 34 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	a	1540	Total	C	N	O	P		
			33050	14748	6057	10705	1540	0	0

- Molecule 35 is a protein called 30S ribosomal protein S2.

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

- Molecule 36 is a protein called 30S ribosomal protein S3.

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

- Molecule 37 is a protein called 30S ribosomal protein S4.

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

- Molecule 38 is a protein called 30S ribosomal protein S5.

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

- Molecule 39 is a protein called 30S ribosomal protein S6.

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

- Molecule 40 is a protein called 30S ribosomal protein S7.

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

- Molecule 41 is a protein called 30S ribosomal protein S8.

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

- Molecule 42 is a protein called 30S ribosomal protein S9.

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

- Molecule 43 is a protein called 30S ribosomal protein S10.

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

- Molecule 44 is a protein called 30S ribosomal protein S11.

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

- Molecule 45 is a protein called 30S ribosomal protein S12.

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

- Molecule 46 is a protein called 30S ribosomal protein S13.

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

- Molecule 47 is a protein called 30S ribosomal protein S14.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	35	ALA	-	insertion	UNP C3SR07

- Molecule 48 is a protein called 30S ribosomal protein S15.

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

- Molecule 49 is a protein called 30S ribosomal protein S16.

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

- Molecule 50 is a protein called 30S ribosomal protein S17.

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

- Molecule 51 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	r	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 52 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	s	82	Total	C	N	O	S	0	0
			658	421	125	110	2		

- Molecule 53 is a protein called 30S ribosomal protein S20.

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

- Molecule 54 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	u	65	Total	C	N	O	S	0	0
			506	313	105	87	1		

- Molecule 55 is a RNA chain called P-site tRNA(fMet).

Mol	Chain	Residues	Atoms						AltConf	Trace
55	v	77	Total	C	N	O	P	S	0	0
			1642	733	297	534	77	1		

- Molecule 56 is a RNA chain called P-site fMet-Phe-tRNA(Phe).

Mol	Chain	Residues	Atoms						AltConf	Trace
56	w	76	Total	C	N	O	P	S	0	0
			1631	731	291	531	76	2		

- Molecule 57 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms						AltConf	Trace
57	x	522	Total	C	N	O	S		0	0
			4052	2546	702	783	21			

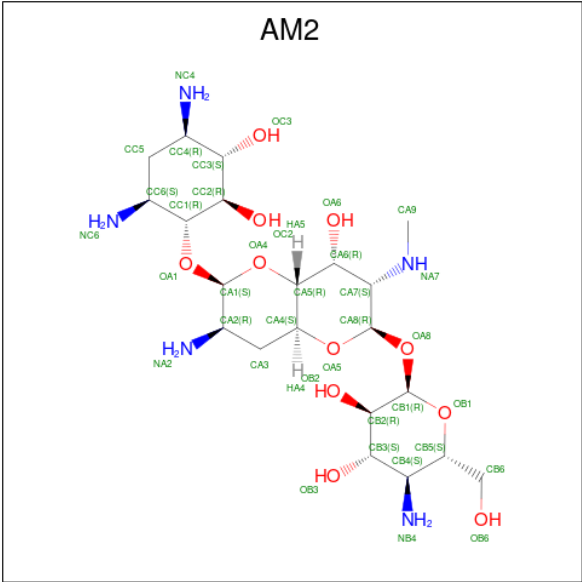
- Molecule 58 is a protein called Dipeptide (FME-PHE).

Mol	Chain	Residues	Atoms					AltConf	Trace
58	y	2	Total	C	N	O	S	0	0
			21	15	2	3	1		

- Molecule 59 is a RNA chain called mRNA.

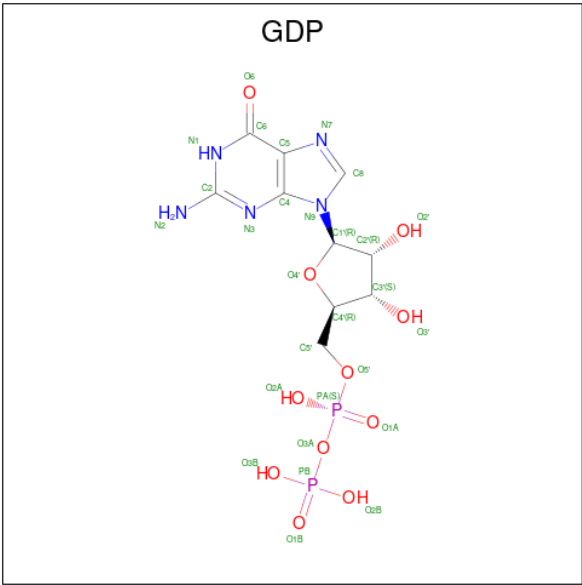
Mol	Chain	Residues	Atoms					AltConf	Trace
59	z	11	Total	C	N	O	P	0	0
			230	103	35	81	11		

- Molecule 60 is APRAMYCIN (CCD ID: AM2) (formula: C₂₁H₄₁N₅O₁₁).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
60	a	1	37	21	5	11	0

- Molecule 61 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).

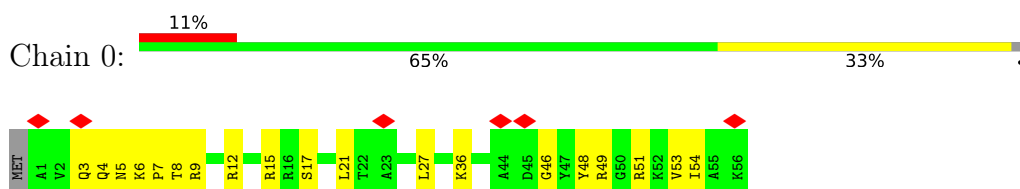


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
61	x	1	28	10	5	11	2	0

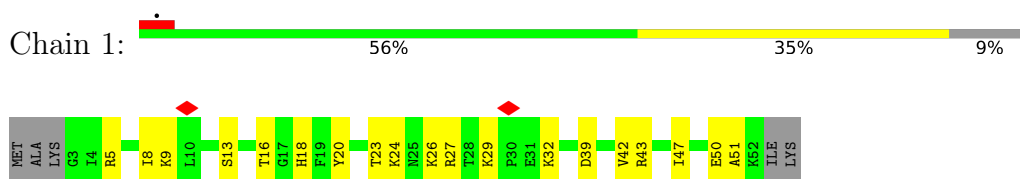
3 Residue-property plots [i](#)

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.

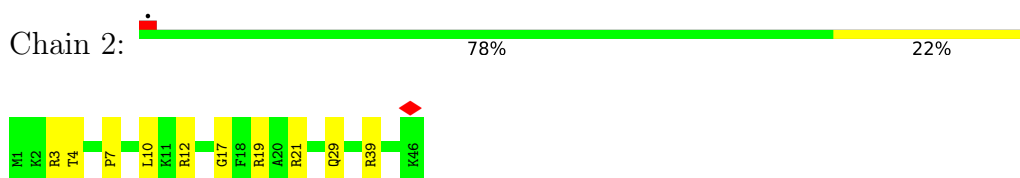
- Molecule 1: 50S ribosomal protein L32



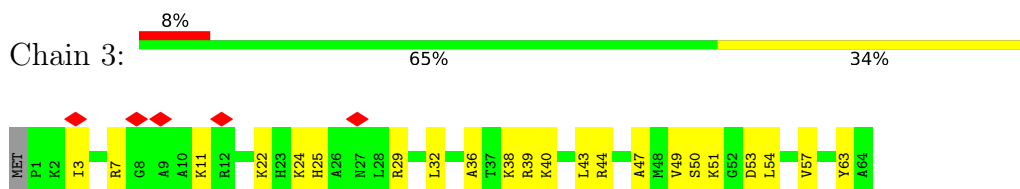
- Molecule 2: 50S ribosomal protein L33



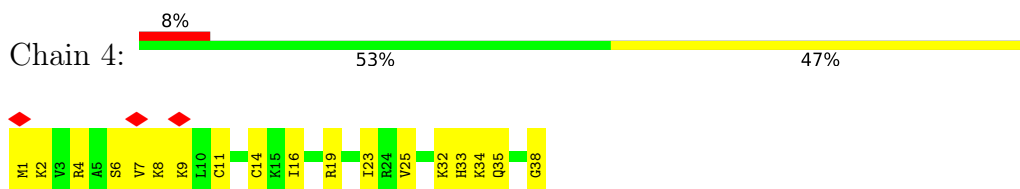
- Molecule 3: 50S ribosomal protein L34



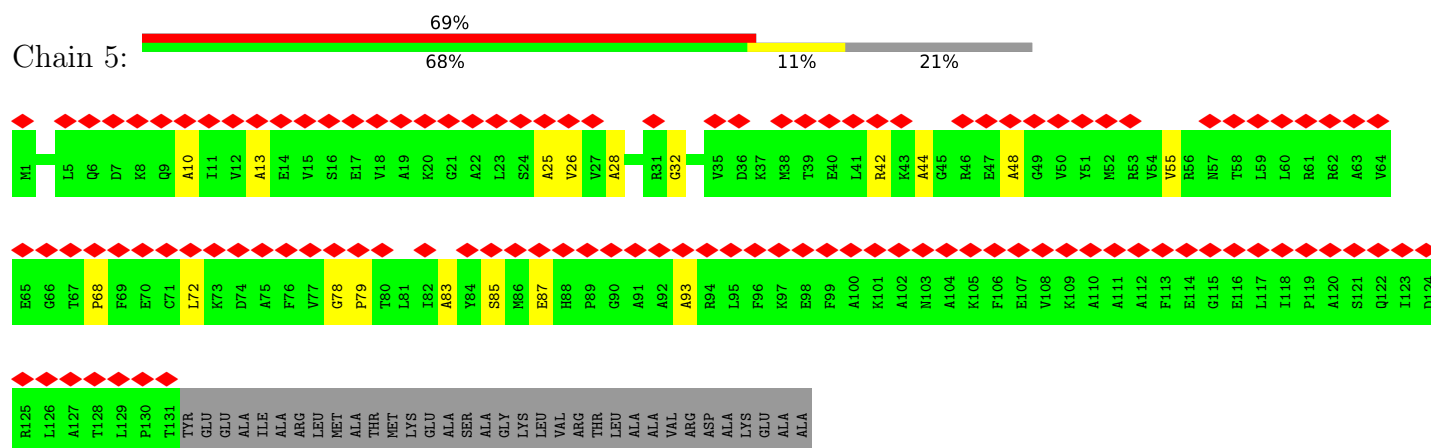
- Molecule 4: 50S ribosomal protein L35



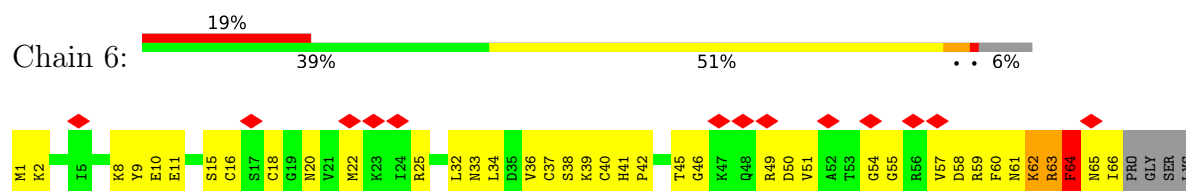
- Molecule 5: 50S ribosomal protein L36



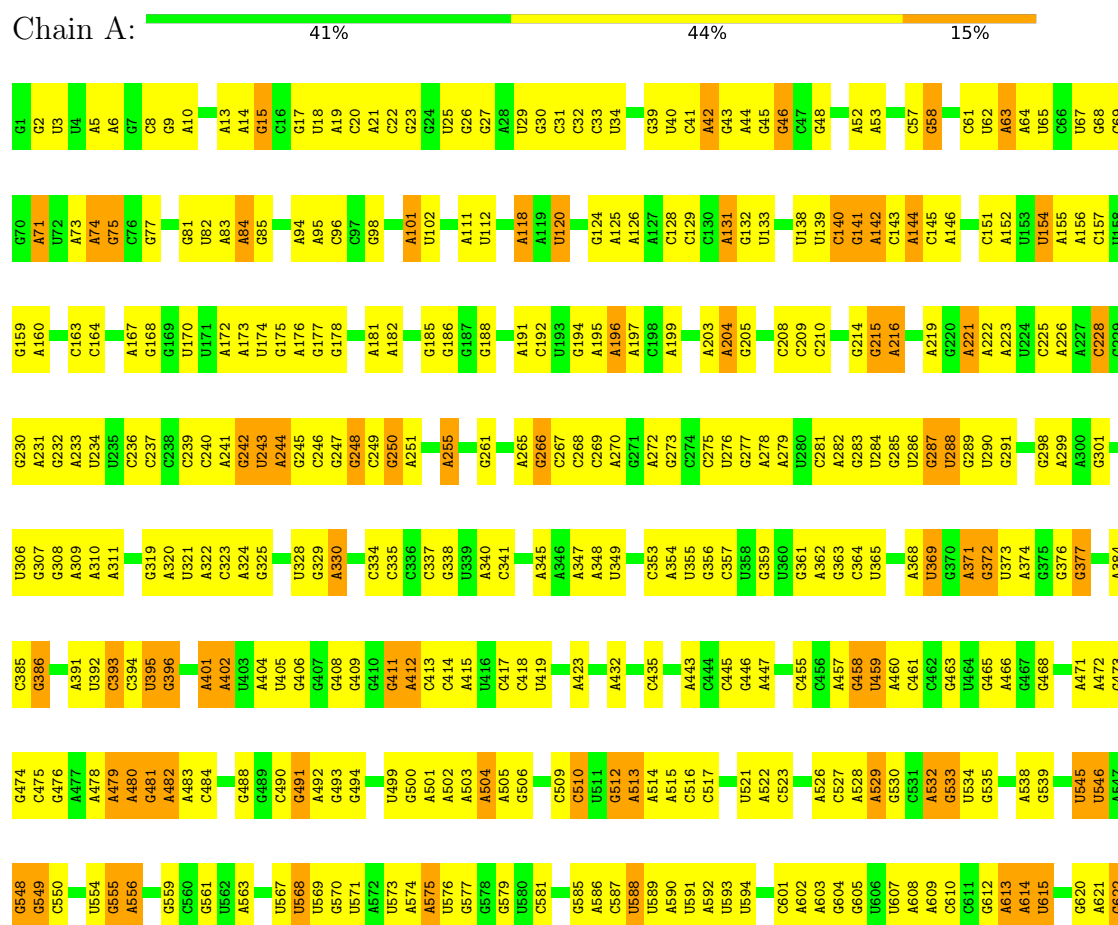
- Molecule 6: 50S ribosomal protein L10



- Molecule 7: 50S ribosomal protein L31

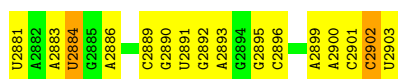


- Molecule 8: 23S ribosomal RNA



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A1754	G1667	A1590	G1428	C1427	U1352	G1271	G1186	C1104	C1044	C961	G879	G704	A627
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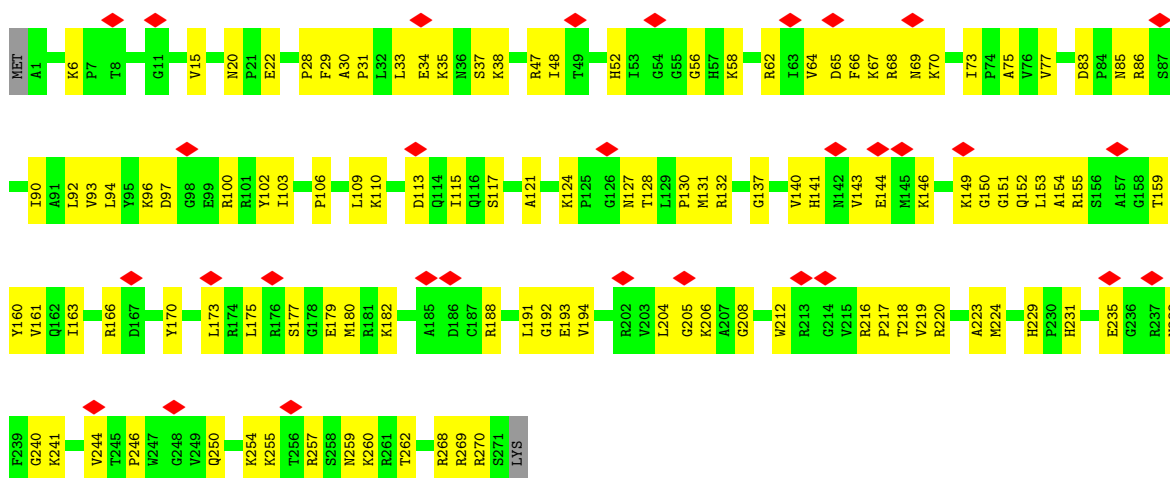
• Molecule 9: 5S ribosomal RNA

Chain B: 39% 47% 14%



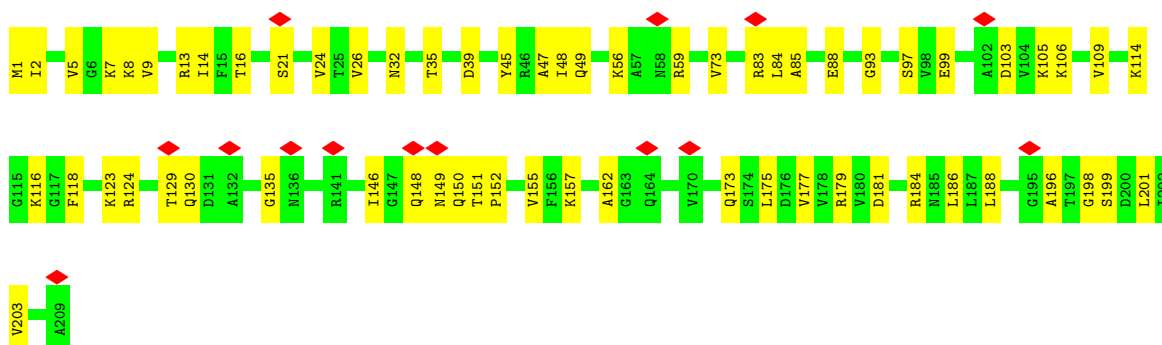
• Molecule 10: 50S ribosomal protein L2

Chain C: 11% 58% 42%



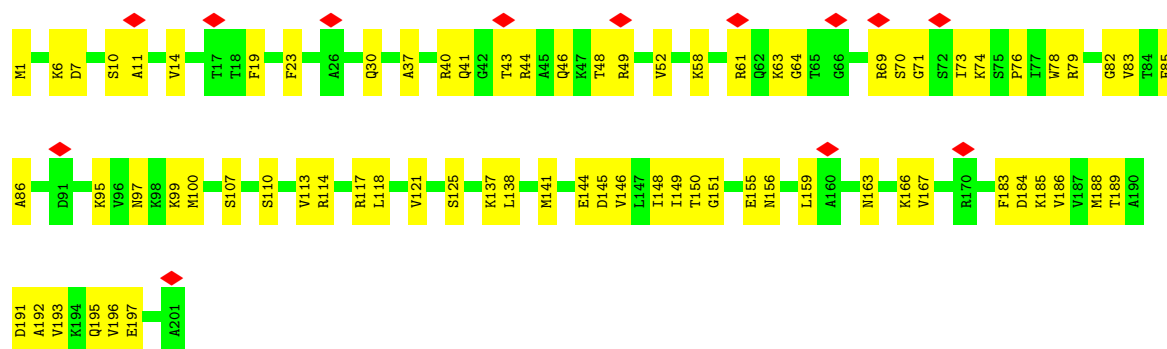
• Molecule 11: 50S ribosomal protein L3

Chain D: 7% 70% 30%

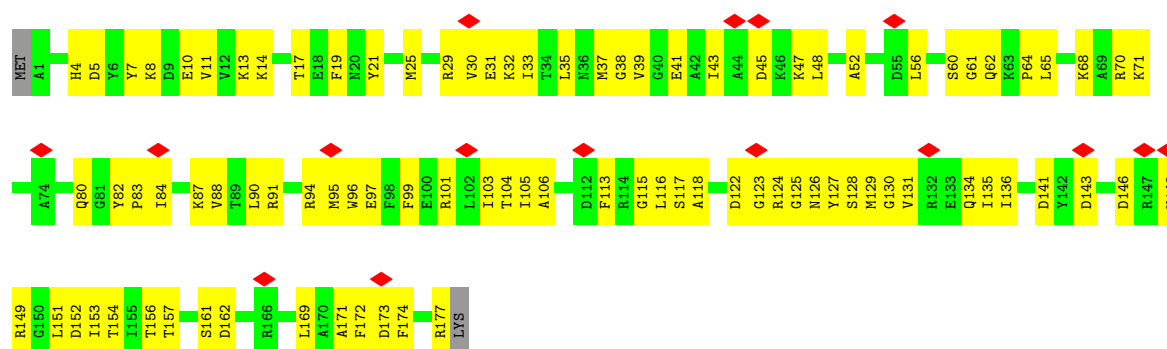


• Molecule 12: 50S ribosomal protein L4

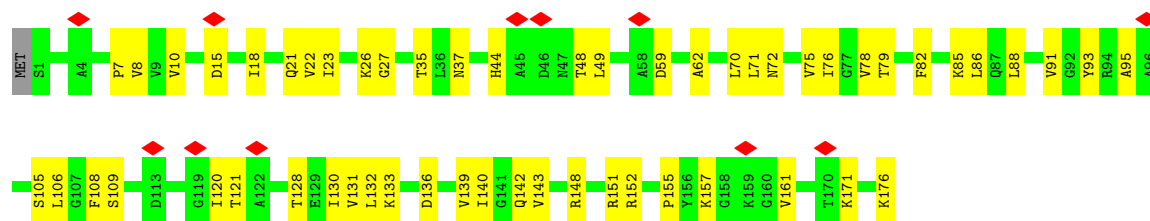
Chain E: 6% 63% 37%



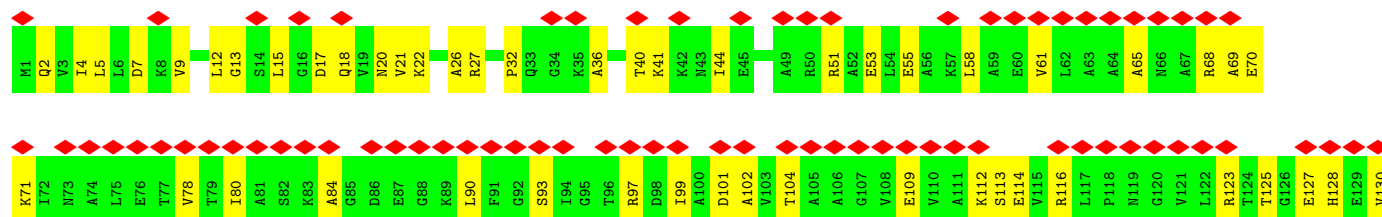
• Molecule 13: 50S ribosomal protein L5

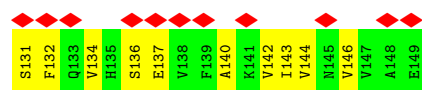


• Molecule 14: 50S ribosomal protein L6

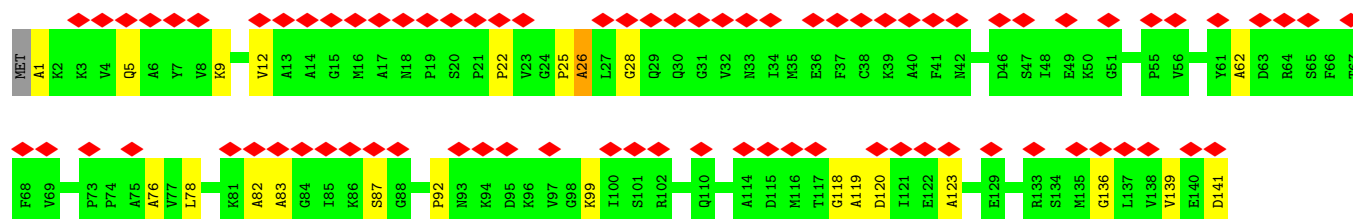
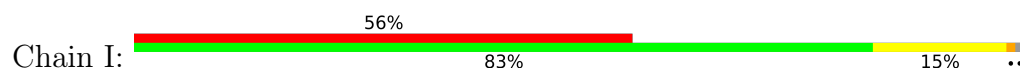


• Molecule 15: 50S ribosomal protein L9

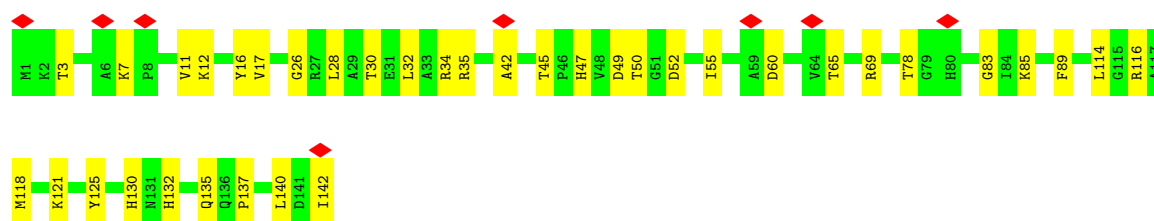
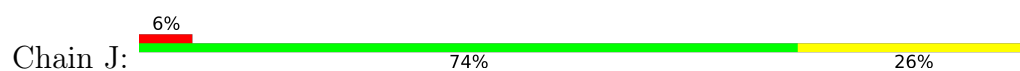




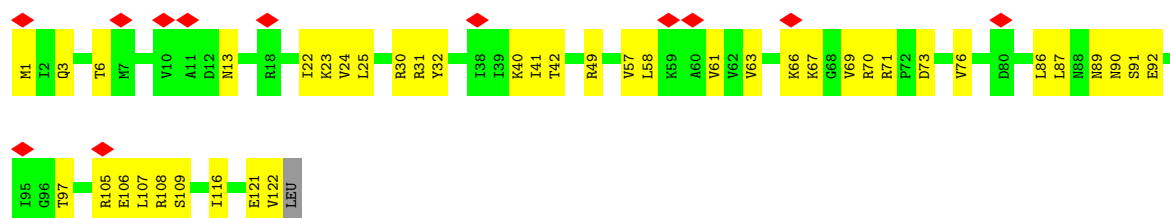
- Molecule 16: 50S ribosomal protein L11



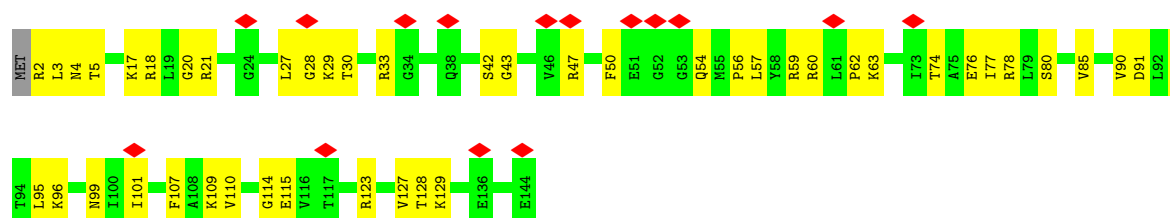
- Molecule 17: 50S ribosomal protein L13



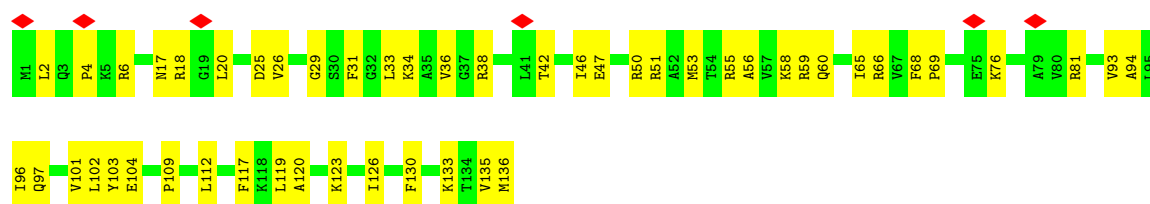
- Molecule 18: 50S ribosomal protein L14



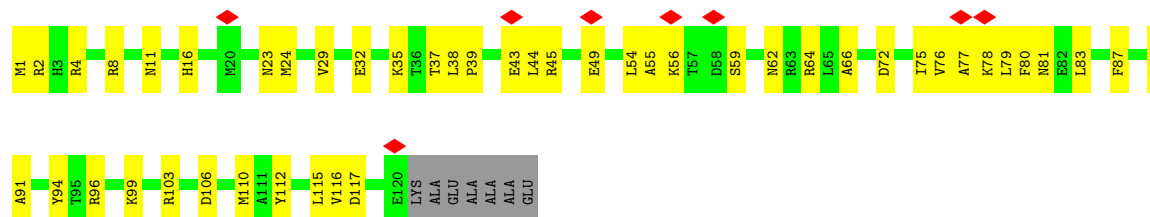
- Molecule 19: 50S ribosomal protein L15



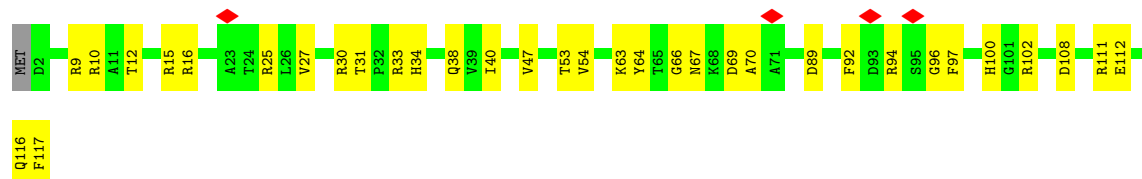
- Molecule 20: 50S ribosomal protein L16



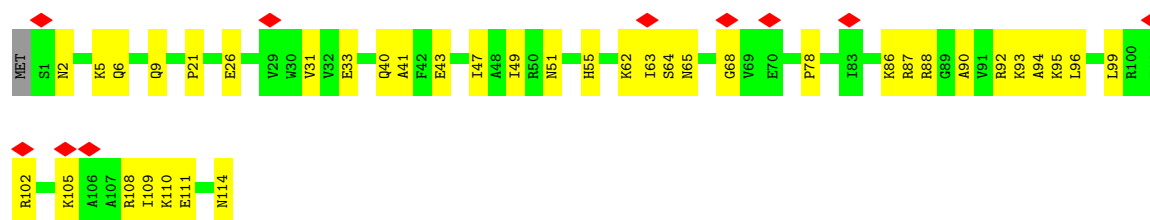
- Molecule 21: 50S ribosomal protein L17



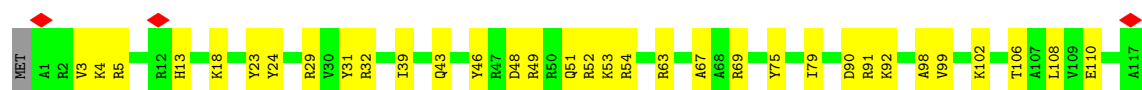
- Molecule 22: 50S ribosomal protein L18



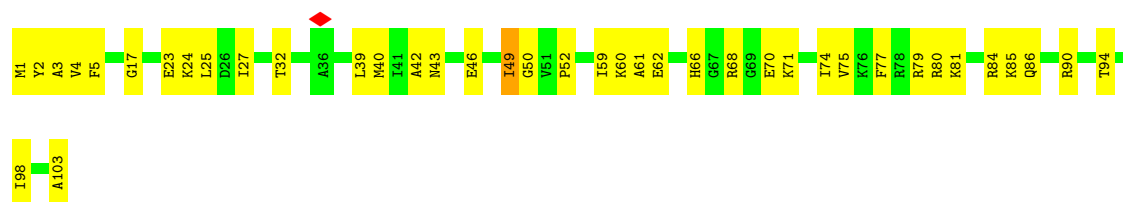
- Molecule 23: 50S ribosomal protein L19



- Molecule 24: 50S ribosomal protein L20



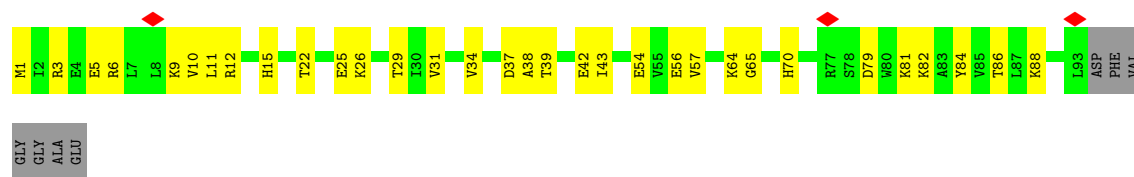
- Molecule 25: 50S ribosomal protein L21



- Molecule 26: 50S ribosomal protein L22



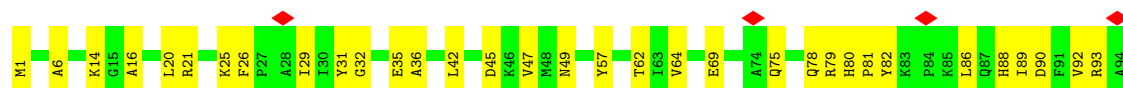
- Molecule 27: 50S ribosomal protein L23



- Molecule 28: 50S ribosomal protein L24



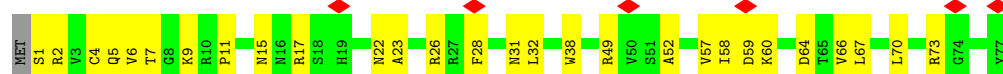
- Molecule 29: 50S ribosomal protein L25



- Molecule 30: 50S ribosomal protein L27



- Molecule 31: 50S ribosomal protein L28



- Molecule 32: 50S ribosomal protein L29



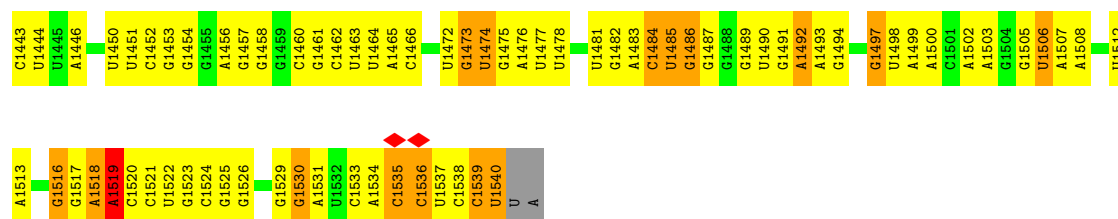
- Molecule 33: 50S ribosomal protein L30



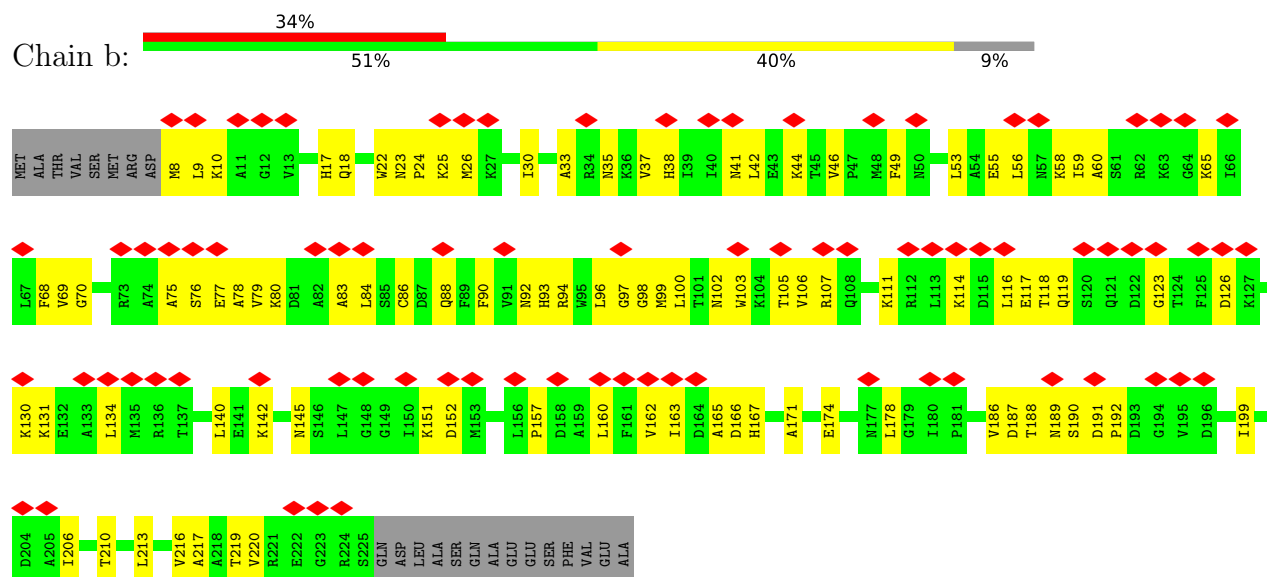
- Molecule 34: 16S ribosomal RNA



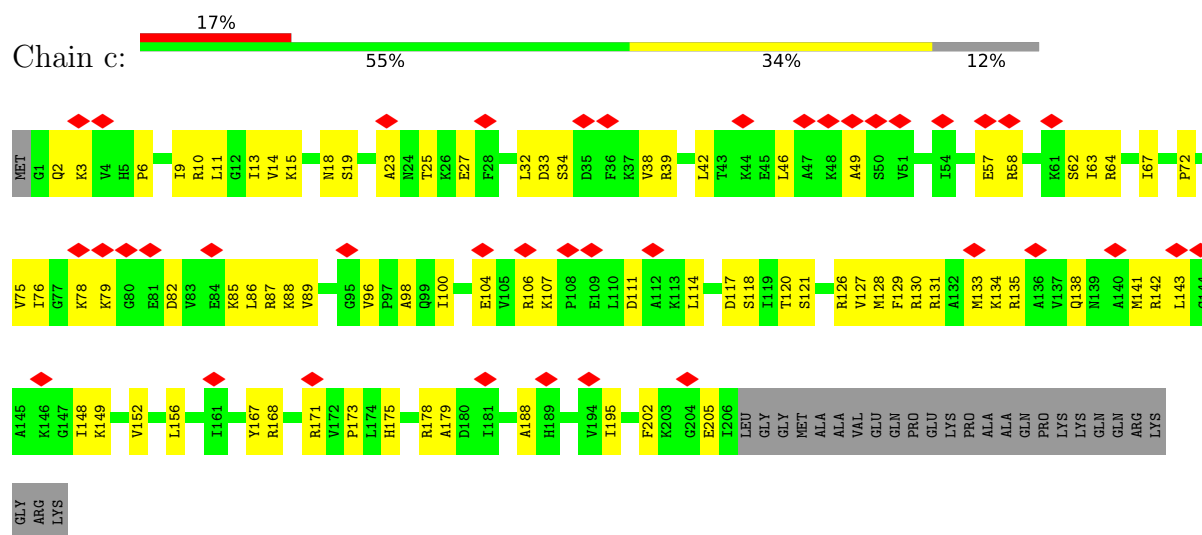
U1372	U1308	C1243	G1175	A1102	C1031	A969	C896	G821	G737	G664	C582	G515	A448	U365
G1373	G1309	G1244	G1176	C1103	G1032	C970	A900	U822	C738	A665	C586	U516	G449	U368
U1376	G1310	A1250	G1177	C1107	G1033	G971	G902	C826	C739	G666	G587	C518	G450	U369
A1377	G1312	A1251	G1178	A1035	A1036	A974	A906	G829	G742	A673	G592	G521	A455	C370
G1378	U1313	A1252	A1179	G1109	C1037	A975	A907	U834	G743	G674	U593	C522	A456	C371
G1379	C1314	G1253	A1180	C1112	G1038	G976	A908	U835	G744	A675	U594	A524	A457	C372
C1382	U1315	G1254	G1181	A1117	U1040	A977	A909	U836	G745	A676	U595	G525	A458	C373
C1383	C1317	G1255	G1182	C1118	U1041	A978	C910	U837	G746	A677	A596	C526	A459	A374
U1386	A1318	A1256	G1183	C1119	U1042	C979	C911	U838	G747	A678	A597	G527	A460	U375
U1391	C1320	G1257	G1184	G1119	A1043	C980	U911	G839	G748	C679	A600	C361	A461	C381
G1392	U1321	G1260	G1190	C1120	U1044	U981	C912	C840	A753	C680	A601	U463	A462	A382
U1393	C1322	A1261	A1196	U1121	A1045	U982	A913	C841	C754	A681	A602	U464	A465	A383
A1397	A1197	C1262	A1197	U1122	C1046	C983	A914	U842	G755	G682	U603	U465	A384	C385
C1398	G1198	C1263	G1198	U1123	A1047	C984	U921	U843	G756	G683	G604	A468	A389	G388
C1399	U1199	U1264	U1125	G1124	U985	C985	G922	C844	C758	U686	U605	C469	U390	G391
C1400	C1200	C1265	U1126	U1126	G987	C986	A923	A845	A759	A687	G606	C470	A471	G398
C1401	G1201	A1201	G1127	G1127	G988	C988	C924	C846	G763	G688	A607	U472	A473	U399
C1402	C1203	C1203	A1130	A1130	U991	U991	G925	C847	C764	C689	A608	U473	G474	U400
G1403	G1204	A1204	G1131	U1054	U992	U992	G926	C848	C765	G690	A609	U474	A475	U401
C1404	U1205	G1132	G1132	U1055	U993	U993	G927	C849	G766	G691	U610	U475	A476	U402
G1405	G1206	G1133	G1133	U1056	G994	A994	G928	U850	A767	U692	C613	U476	C477	C401
C1406	C1207	G1134	G1134	C1057	C995	C995	C932	G851	A768	G693	C614	U477	C478	G402
C1407	C1208	C1137	C1137	C1058	A996	A996	G933	U852	G769	A694	G615	C479	U479	G403
A1408	C1209	U1137	U1137	U1060	C999	C999	C934	U855	G773	A695	G616	C545	U480	G404
U1412	G1210	G1138	G1138	U1061	U1000	A1000	C935	C856	A777	U701	C620	C547	U481	U405
U1413	U1211	U1139	U1139	U1062	C1001	C1001	A937	G859	C778	G703	A621	C548	U482	G406
U1414	C1212	G1140	G1140	U1063	G1002	G1002	A938	A860	C779	A704	A622	C549	U483	U407
G1415	U1213	G1141	G1141	U1064	U1003	U1003	G939	U780	G781	G705	U625	C550	C483	G410
G1416	C1214	G1142	G1142	U1065	A1004	A1004	C940	A865	A781	U706	A626	A553	A487	A411
G1417	G1215	G1143	G1143	C1070	U1005	U1005	G941	C866	C789	A707	G626	U554	C488	A412
G1418	C1216	G1144	G1144	C1071	A1006	A1006	G942	C867	U789	A712	G627	U555	A489	G413
A1418	C1217	G1145	G1145	C1072	U1007	U1007	G943	C868	C790	G713	G628	C556	A490	A414
G1419	C1218	G1146	G1146	U1073	U1008	U1008	G944	C869	C791	G714	A629	A559	A491	A415
A1349	A1219	U1148	U1148	G1074	U1009	U1009	G945	U870	G792	A715	U632	A560	A492	G416
A1350	C1220	C1149	C1149	U1075	U1010	U1010	A946	U871	A792	A716	G633	U561	A493	G417
U1420	G1221	U1150	U1150	U1076	C1011	C1011	G947	A872	U793	U717	C634	U562	A494	U420
G1421	C1222	A1151	A1151	G1078	A1012	A1012	C948	A873	A794	U718	C635	A563	A495	U421
G1422	G1223	G1152	G1152	G1079	G1013	G1013	A949	G874	C795	A719	U636	C564	A496	U422
G1423	U1224	G1153	G1153	A1080	A1014	A1014	U950	U875	C796	C720	C637	C565	A497	C423
U1424	A1225	A1157	A1157	G1084	G1015	G1015	G954	A878	C797	G721	U638	U566	A498	G424
U1425	C1226	C1158	C1158	U1085	A1016	A1016	U955	C879	G803	U722	G639	G567	A499	U425
G1426	U1227	U1159	U1159	U1086	U1017	U1017	U956	C880	U804	G723	A640	C501	U426	G426
C1427	A1228	G1160	G1160	G1087	G1018	G1018	U957	C881	G804	G724	U641	A502	U427	U427
A1428	C1229	C1161	C1161	G1088	A1019	A1019	U958	C882	C810	G725	A642	A503	U428	A429
A1429	C1230	G1162	G1162	U1089	G1020	G1020	A958	C883	C811	C726	C504	A504	U429	A430
A1430	G1231	A1163	A1163	A1092	A1021	A1021	A959	C884	C812	G727	A505	A505	U430	A431
A1431	C1234	G1164	G1164	A1093	A1022	A1022	U960	U884	G813	A728	A506	A506	U431	G432
A1432	U1235	U1165	U1165	G1094	U1023	U1023	U961	C885	U813	A729	A507	A507	U432	A433
A1433	A1236	G1166	G1166	U1095	G1024	G1024	C962	U886	A814	A730	A508	A508	U433	A434
A1434	C1237	A1167	A1167	C1096	U1025	U1025	C963	G890	A815	G730	C651	A509	U434	G435
A1435	U1238	U1168	U1168	C1097	U1026	U1026	A964	U891	A816	C731	U652	A510	U435	U436
A1436	A1239	A1169	A1169	C1098	U1027	U1027	U965	A892	C817	G733	U653	A511	U436	A437
C1369	U1240	A1170	A1170	C1099	G1028	G1028	G966	C893	G818	G734	U662	A512	U437	U440
G1370	G1241	A1171	A1171	C1100	U1029	U1029	C967	C894	G819	C735	U663	A513	U438	A441
G1442	G1242	C1172	C1172	A1101	U1030	U1030	A968	C895	U820	C736	A663	G581	U439	G442



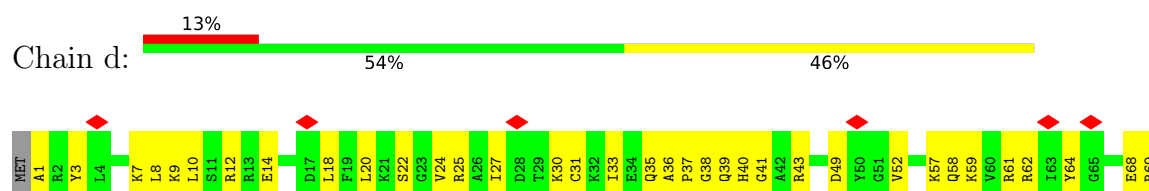
• Molecule 35: 30S ribosomal protein S2

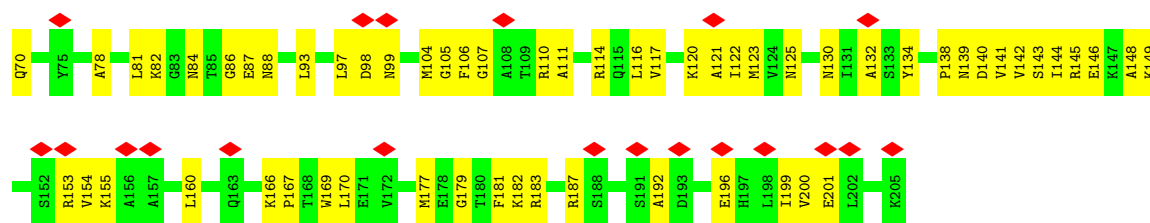


• Molecule 36: 30S ribosomal protein S3

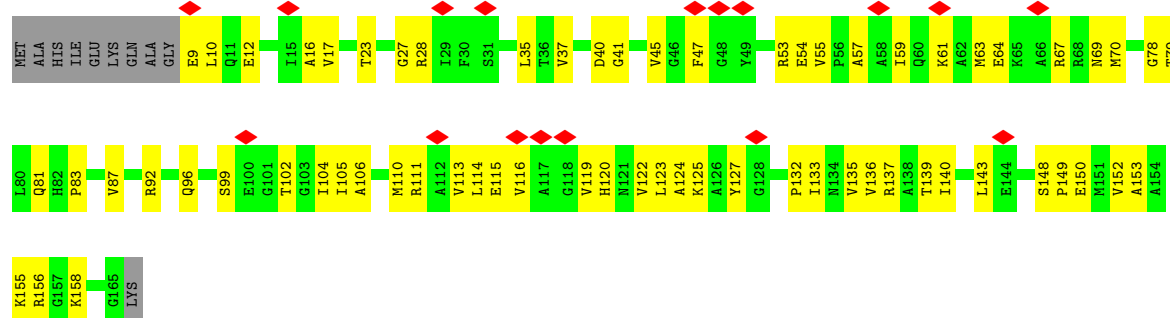


• Molecule 37: 30S ribosomal protein S4

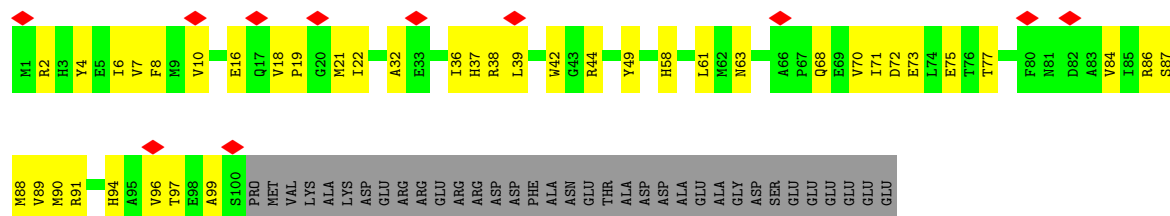




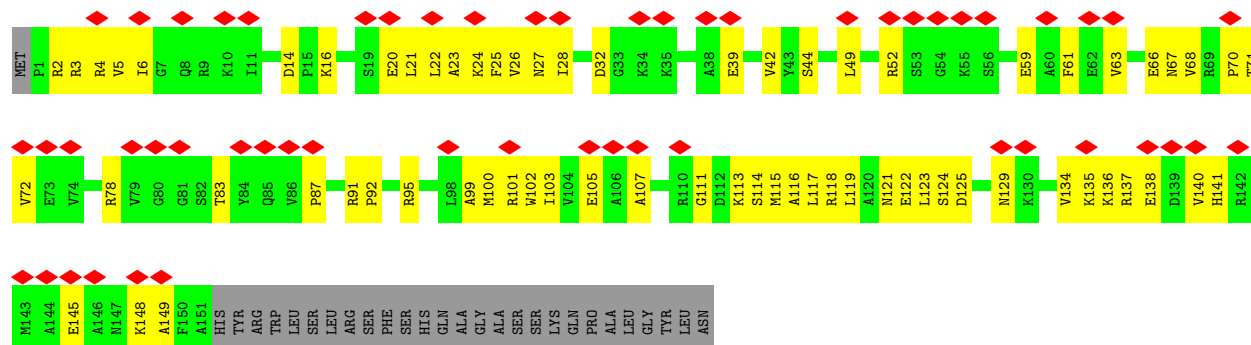
• Molecule 38: 30S ribosomal protein S5



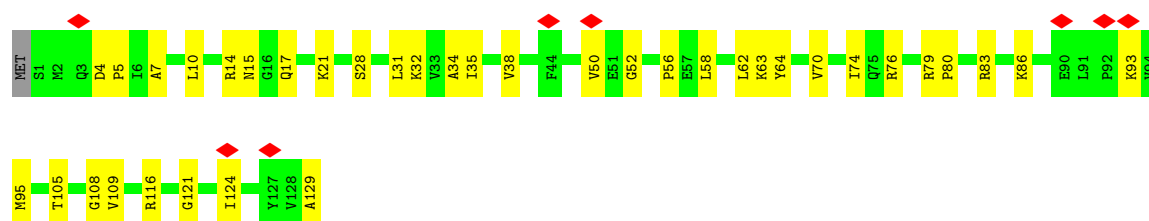
• Molecule 39: 30S ribosomal protein S6



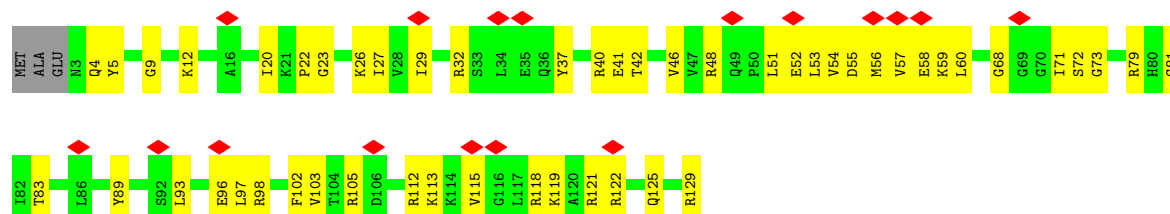
• Molecule 40: 30S ribosomal protein S7



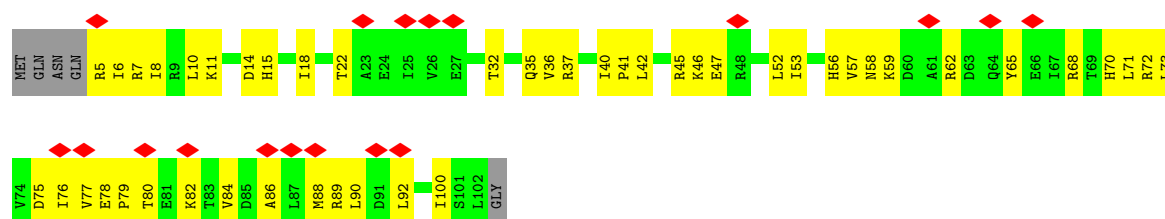
• Molecule 41: 30S ribosomal protein S8



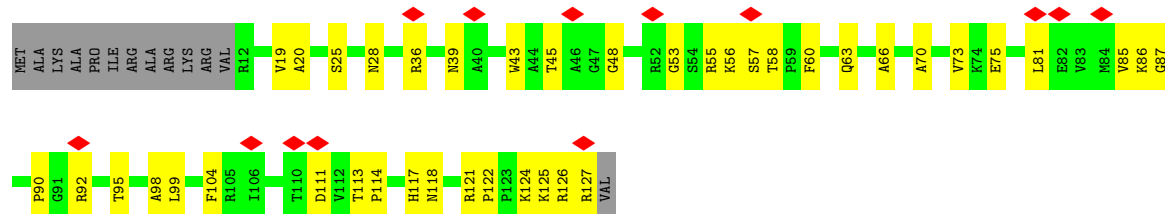
- Molecule 42: 30S ribosomal protein S9



- Molecule 43: 30S ribosomal protein S10

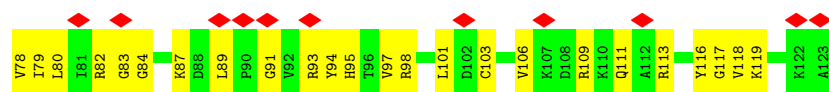


- Molecule 44: 30S ribosomal protein S11

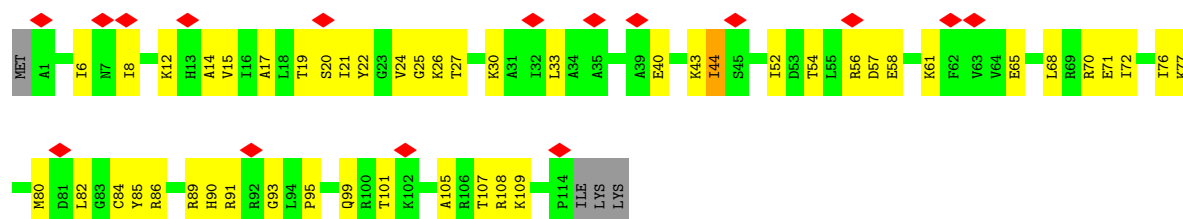


- Molecule 45: 30S ribosomal protein S12

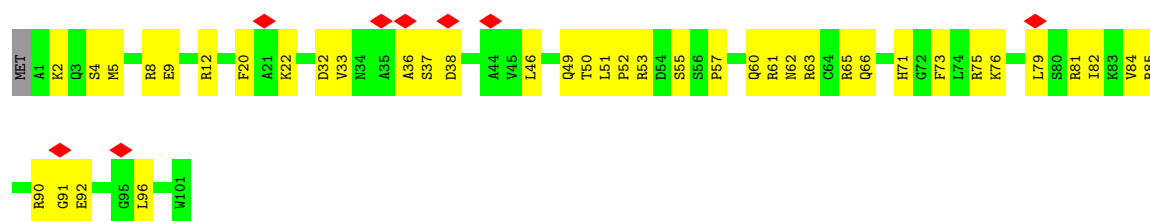




- Molecule 46: 30S ribosomal protein S13



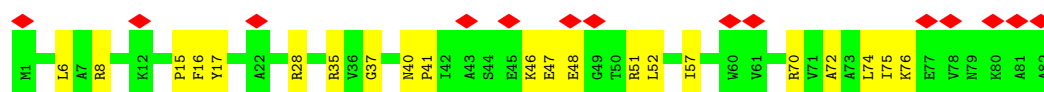
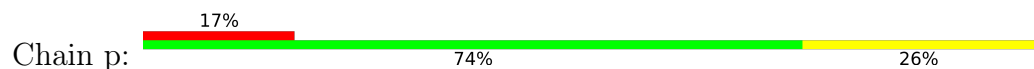
- Molecule 47: 30S ribosomal protein S14



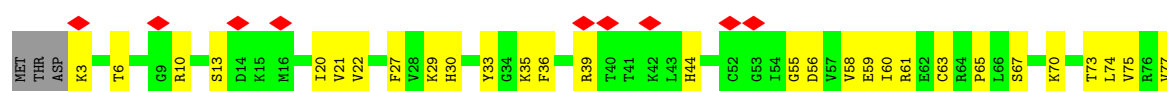
- Molecule 48: 30S ribosomal protein S15

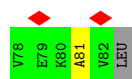


- Molecule 49: 30S ribosomal protein S16

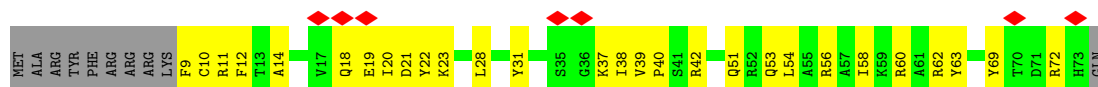


- Molecule 50: 30S ribosomal protein S17

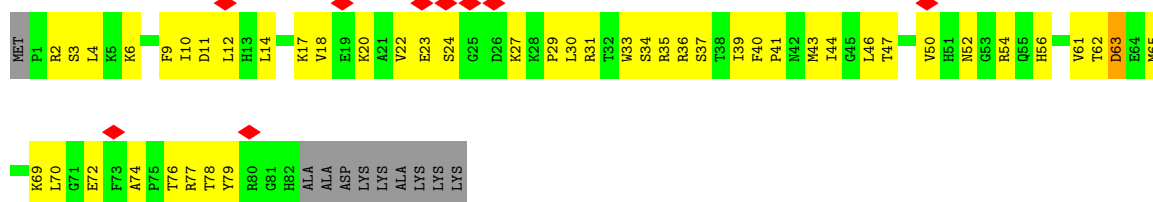




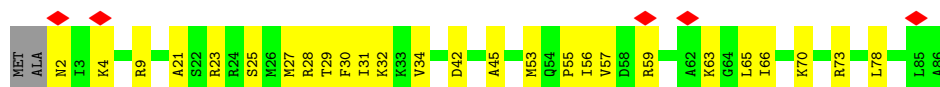
- Molecule 51: 30S ribosomal protein S18



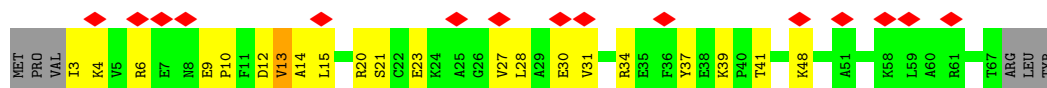
- Molecule 52: 30S ribosomal protein S19



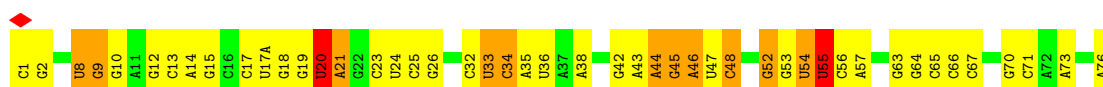
- Molecule 53: 30S ribosomal protein S20



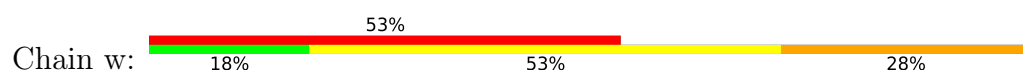
- Molecule 54: 30S ribosomal protein S21

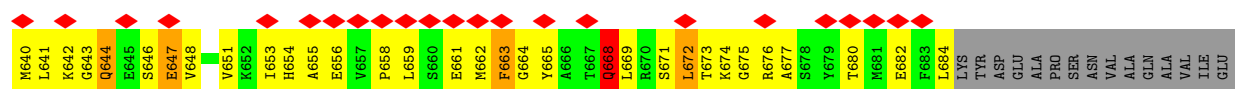


- Molecule 55: P-site tRNA(fMet)



- Molecule 56: P-site fMet-Phe-tRNA(Phe)





ARG
GLY
LYS

● Molecule 58: Dipeptide (FME-PHE)



M101
F102

● Molecule 59: mRNA



G U U U A A A C C A G G U U A A U A C A U A-2 C-1 U0 A1 U4 U5 U6 G7 U8 U A U U U A C

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	6412	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 ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1200	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	10.657	Depositor
Minimum map value	-5.451	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	1.5	Depositor
Map size (Å)	334.08, 334.08, 334.08	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.16, 1.16, 1.16	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MIA, 4SU, OMC, GDP, 5MC, 2MA, 2MG, 5MU, PSU, FME, UR3, 3TD, 6MZ, OMG, G7M, AM2, OMU, H2U, 1MG, MA6, 4OC

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	0	0.38	0/450	0.40	0/599
2	1	0.28	0/416	0.37	0/554
3	2	0.41	0/380	0.44	0/498
4	3	0.46	0/513	0.63	0/676
5	4	0.37	0/303	0.46	0/397
6	5	0.18	0/646	0.44	0/898
7	6	0.37	0/531	0.74	3/709 (0.4%)
8	A	0.40	0/69266	0.38	0/108055
9	B	0.33	0/2873	0.36	0/4478
10	C	0.38	0/2121	0.49	0/2852
11	D	0.36	0/1586	0.44	0/2134
12	E	0.35	0/1571	0.42	0/2113
13	F	0.26	0/1434	0.43	0/1926
14	G	0.27	0/1343	0.43	0/1816
15	H	0.20	0/1122	0.48	0/1515
16	I	0.28	0/692	0.57	1/960 (0.1%)
17	J	0.36	0/1152	0.41	0/1551
18	K	0.34	0/947	0.46	0/1268
19	L	0.36	0/1054	0.51	0/1403
20	M	0.34	0/1093	0.44	0/1460
21	N	0.37	0/973	0.51	0/1301
22	O	0.29	0/902	0.43	0/1209
23	P	0.33	0/929	0.41	0/1242
24	Q	0.42	0/960	0.48	0/1278
25	R	0.42	0/829	0.55	2/1107 (0.2%)
26	S	0.35	0/864	0.45	0/1156
27	T	0.30	0/744	0.40	0/994
28	U	0.34	0/787	0.66	3/1051 (0.3%)
29	V	0.30	0/766	0.41	0/1025
30	W	0.36	0/582	0.43	0/769
31	X	0.37	0/635	0.45	0/848

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Y	0.37	0/510	0.79	4/677 (0.6%)
33	Z	0.33	0/453	0.40	0/605
34	a	0.34	0/36725	0.39	4/57285 (0.0%)
35	b	0.23	0/1735	0.45	0/2338
36	c	0.28	0/1651	0.41	0/2225
37	d	0.28	0/1665	0.54	0/2227
38	e	0.29	0/1154	0.45	0/1554
39	f	0.26	0/835	0.42	0/1128
40	g	0.22	0/1195	0.45	0/1602
41	h	0.30	0/989	0.43	0/1326
42	i	0.25	0/1034	0.48	0/1375
43	j	0.27	0/796	0.56	0/1077
44	k	0.30	0/885	0.50	0/1195
45	l	0.34	0/969	0.49	0/1300
46	m	0.23	0/892	0.51	1/1193 (0.1%)
47	n	0.37	0/811	0.57	0/1081
48	o	0.28	0/722	0.41	0/964
49	p	0.30	0/659	0.47	0/884
50	q	0.31	0/657	0.49	0/881
51	r	0.26	0/544	0.49	0/731
52	s	0.31	0/675	0.54	1/908 (0.1%)
53	t	0.28	0/671	0.41	0/888
54	u	0.23	0/512	0.67	2/683 (0.3%)
55	v	0.31	0/1745	0.42	0/2716
56	w	0.31	1/1650 (0.1%)	0.41	0/2569
57	x	0.42	0/4120	0.68	4/5573 (0.1%)
58	y	0.33	0/11	0.30	0/13
59	z	0.34	0/255	0.32	0/394
All	All	0.36	1/162984 (0.0%)	0.42	25/243234 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	w	46	G7M	O3'-P	5.02	1.61	1.56

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	a	154	U	C4'-C3'-O3'	10.98	129.48	113.00
28	U	98	ASN	N-CA-C	-9.63	90.28	110.80
34	a	154	U	C2'-C3'-O3'	-8.87	100.39	113.70
54	u	13	VAL	N-CA-C	-8.10	104.70	111.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	a	159	G	C4'-C3'-O3'	7.61	124.42	113.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	444	0	461	23	0
2	1	409	0	440	16	0
3	2	377	0	418	11	0
4	3	504	0	574	18	0
5	4	302	0	343	14	0
6	5	647	0	336	13	0
7	6	522	0	524	49	0
8	A	62338	0	31373	1419	0
9	B	2570	0	1301	64	0
10	C	2082	0	2157	92	0
11	D	1565	0	1616	49	0
12	E	1552	0	1618	60	0
13	F	1410	0	1447	81	0
14	G	1323	0	1374	43	0
15	H	1111	0	1148	42	0
16	I	693	0	347	18	0
17	J	1129	0	1162	32	0
18	K	938	0	1012	36	0
19	L	1045	0	1117	42	0
20	M	1074	0	1157	36	0
21	N	960	0	1000	39	0
22	O	892	0	923	28	0
23	P	917	0	965	31	0
24	Q	947	0	1022	31	0
25	R	816	0	839	28	0
26	S	857	0	922	29	0
27	T	738	0	807	24	0
28	U	779	0	834	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	V	753	0	780	28	0
30	W	575	0	592	20	0
31	X	625	0	655	25	0
32	Y	509	0	543	23	0
33	Z	449	0	491	10	0
34	a	33050	0	16655	913	0
35	b	1704	0	1732	75	0
36	c	1624	0	1699	53	0
37	d	1643	0	1710	74	0
38	e	1141	0	1170	46	0
39	f	817	0	808	32	0
40	g	1181	0	1240	56	0
41	h	979	0	1034	29	0
42	i	1022	0	1070	45	0
43	j	786	0	828	43	0
44	k	869	0	878	39	0
45	l	955	0	1019	45	0
46	m	883	0	944	39	0
47	n	799	0	841	38	0
48	o	714	0	737	23	0
49	p	649	0	666	13	0
50	q	648	0	691	20	0
51	r	535	0	552	20	0
52	s	658	0	685	53	0
53	t	665	0	714	23	0
54	u	506	0	502	18	0
55	v	1642	0	839	45	0
56	w	1631	0	838	78	0
57	x	4052	0	4038	243	0
58	y	21	0	19	2	0
59	z	230	0	116	10	0
60	a	37	0	41	3	0
61	x	28	0	12	13	0
All	All	151321	0	102376	4024	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 16.

The worst 5 of 4024 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:1416:G:H1	34:a:1483:A:N6	1.36	1.21
34:a:81:A:H61	34:a:86:G:N2	1.41	1.19
57:x:404:ILE:HD11	57:x:408:MET:HE3	1.24	1.16
8:A:2901:C:N4	8:A:2902:C:H41	1.42	1.15
8:A:2901:C:N4	8:A:2902:C:N4	1.95	1.15

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	0	54/57 (95%)	53 (98%)	1 (2%)	0	100	100
2	1	48/55 (87%)	45 (94%)	3 (6%)	0	100	100
3	2	44/46 (96%)	40 (91%)	4 (9%)	0	100	100
4	3	62/65 (95%)	58 (94%)	4 (6%)	0	100	100
5	4	36/38 (95%)	31 (86%)	5 (14%)	0	100	100
6	5	129/165 (78%)	97 (75%)	32 (25%)	0	100	100
7	6	64/70 (91%)	51 (80%)	12 (19%)	1 (2%)	7	38
10	C	269/273 (98%)	241 (90%)	27 (10%)	1 (0%)	30	67
11	D	207/209 (99%)	184 (89%)	23 (11%)	0	100	100
12	E	199/201 (99%)	189 (95%)	10 (5%)	0	100	100
13	F	175/179 (98%)	149 (85%)	26 (15%)	0	100	100
14	G	174/177 (98%)	161 (92%)	13 (8%)	0	100	100
15	H	147/149 (99%)	117 (80%)	30 (20%)	0	100	100
16	I	139/142 (98%)	104 (75%)	34 (24%)	1 (1%)	18	56
17	J	140/142 (99%)	132 (94%)	8 (6%)	0	100	100
18	K	120/123 (98%)	101 (84%)	19 (16%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	L	141/144 (98%)	122 (86%)	19 (14%)	0	100	100
20	M	134/136 (98%)	118 (88%)	15 (11%)	1 (1%)	18	56
21	N	118/127 (93%)	107 (91%)	11 (9%)	0	100	100
22	O	114/117 (97%)	103 (90%)	11 (10%)	0	100	100
23	P	112/115 (97%)	100 (89%)	12 (11%)	0	100	100
24	Q	115/118 (98%)	109 (95%)	6 (5%)	0	100	100
25	R	101/103 (98%)	88 (87%)	13 (13%)	0	100	100
26	S	108/110 (98%)	98 (91%)	10 (9%)	0	100	100
27	T	91/100 (91%)	80 (88%)	11 (12%)	0	100	100
28	U	100/104 (96%)	87 (87%)	11 (11%)	2 (2%)	6	31
29	V	92/94 (98%)	86 (94%)	6 (6%)	0	100	100
30	W	73/85 (86%)	67 (92%)	6 (8%)	0	100	100
31	X	75/78 (96%)	70 (93%)	5 (7%)	0	100	100
32	Y	61/63 (97%)	55 (90%)	6 (10%)	0	100	100
33	Z	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
35	b	216/240 (90%)	190 (88%)	26 (12%)	0	100	100
36	c	204/233 (88%)	194 (95%)	10 (5%)	0	100	100
37	d	203/206 (98%)	165 (81%)	37 (18%)	1 (0%)	24	63
38	e	155/167 (93%)	140 (90%)	15 (10%)	0	100	100
39	f	98/135 (73%)	88 (90%)	10 (10%)	0	100	100
40	g	149/179 (83%)	138 (93%)	11 (7%)	0	100	100
41	h	127/130 (98%)	117 (92%)	10 (8%)	0	100	100
42	i	125/130 (96%)	108 (86%)	17 (14%)	0	100	100
43	j	96/103 (93%)	78 (81%)	17 (18%)	1 (1%)	12	48
44	k	114/129 (88%)	95 (83%)	19 (17%)	0	100	100
45	l	121/124 (98%)	105 (87%)	16 (13%)	0	100	100
46	m	112/118 (95%)	95 (85%)	17 (15%)	0	100	100
47	n	99/102 (97%)	90 (91%)	8 (8%)	1 (1%)	12	48
48	o	86/89 (97%)	79 (92%)	7 (8%)	0	100	100
49	p	80/82 (98%)	70 (88%)	10 (12%)	0	100	100
50	q	78/84 (93%)	66 (85%)	12 (15%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	r	63/75 (84%)	52 (82%)	11 (18%)	0	100	100
52	s	80/92 (87%)	76 (95%)	4 (5%)	0	100	100
53	t	83/87 (95%)	81 (98%)	2 (2%)	0	100	100
54	u	63/71 (89%)	55 (87%)	8 (13%)	0	100	100
57	x	516/704 (73%)	441 (86%)	71 (14%)	4 (1%)	16	54
All	All	6366/6924 (92%)	5619 (88%)	734 (12%)	13 (0%)	44	78

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	6	64	PHE
28	U	98	ASN
28	U	99	SER
57	x	663	PHE
47	n	37	SER

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	0	47/48 (98%)	47 (100%)	0	100	100
2	1	45/49 (92%)	45 (100%)	0	100	100
3	2	38/38 (100%)	38 (100%)	0	100	100
4	3	51/52 (98%)	51 (100%)	0	100	100
5	4	34/34 (100%)	34 (100%)	0	100	100
7	6	59/62 (95%)	57 (97%)	2 (3%)	32	54
10	C	216/218 (99%)	216 (100%)	0	100	100
11	D	164/164 (100%)	164 (100%)	0	100	100
12	E	165/165 (100%)	165 (100%)	0	100	100
13	F	148/150 (99%)	148 (100%)	0	100	100
14	G	137/138 (99%)	137 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	H	114/114 (100%)	114 (100%)	0	100	100
17	J	116/116 (100%)	116 (100%)	0	100	100
18	K	103/104 (99%)	103 (100%)	0	100	100
19	L	102/103 (99%)	102 (100%)	0	100	100
20	M	109/109 (100%)	109 (100%)	0	100	100
21	N	100/103 (97%)	100 (100%)	0	100	100
22	O	86/87 (99%)	86 (100%)	0	100	100
23	P	99/100 (99%)	99 (100%)	0	100	100
24	Q	89/90 (99%)	89 (100%)	0	100	100
25	R	84/84 (100%)	83 (99%)	1 (1%)	63	75
26	S	93/93 (100%)	93 (100%)	0	100	100
27	T	80/84 (95%)	80 (100%)	0	100	100
28	U	83/85 (98%)	82 (99%)	1 (1%)	63	75
29	V	78/78 (100%)	78 (100%)	0	100	100
30	W	57/63 (90%)	57 (100%)	0	100	100
31	X	67/68 (98%)	67 (100%)	0	100	100
32	Y	55/55 (100%)	54 (98%)	1 (2%)	51	68
33	Z	48/49 (98%)	48 (100%)	0	100	100
35	b	180/198 (91%)	180 (100%)	0	100	100
36	c	170/190 (90%)	170 (100%)	0	100	100
37	d	172/173 (99%)	172 (100%)	0	100	100
38	e	114/126 (90%)	114 (100%)	0	100	100
39	f	87/116 (75%)	87 (100%)	0	100	100
40	g	124/147 (84%)	124 (100%)	0	100	100
41	h	104/105 (99%)	104 (100%)	0	100	100
42	i	105/107 (98%)	105 (100%)	0	100	100
43	j	86/90 (96%)	86 (100%)	0	100	100
44	k	89/99 (90%)	89 (100%)	0	100	100
45	l	103/104 (99%)	103 (100%)	0	100	100
46	m	92/96 (96%)	92 (100%)	0	100	100
47	n	79/84 (94%)	79 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
48	o	76/77 (99%)	76 (100%)	0	100	100
49	p	65/65 (100%)	65 (100%)	0	100	100
50	q	74/78 (95%)	74 (100%)	0	100	100
51	r	56/65 (86%)	56 (100%)	0	100	100
52	s	72/79 (91%)	71 (99%)	1 (1%)	59	72
53	t	65/66 (98%)	65 (100%)	0	100	100
54	u	46/61 (75%)	46 (100%)	0	100	100
57	x	433/578 (75%)	421 (97%)	12 (3%)	38	60
58	y	1/1 (100%)	1 (100%)	0	100	100
All	All	5060/5408 (94%)	5042 (100%)	18 (0%)	81	84

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
57	x	636	ARG
57	x	672	LEU
57	x	668	GLN
57	x	329	VAL
57	x	407	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 85 such sidechains are listed below:

Mol	Chain	Res	Type
40	g	96	ASN
52	s	42	ASN
41	h	17	GLN
45	l	45	ASN
57	x	119	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	a	1539/1542 (99%)	343 (22%)	0
55	v	76/77 (98%)	17 (22%)	0
56	w	75/76 (98%)	26 (34%)	0
59	z	10/33 (30%)	4 (40%)	0
8	A	2902/2903 (99%)	642 (22%)	46 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
9	B	119/120 (99%)	29 (24%)	3 (2%)
All	All	4721/4751 (99%)	1061 (22%)	49 (1%)

5 of 1061 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	A	10	A
8	A	15	G
8	A	23	G
8	A	34	U
8	A	42	A

5 of 49 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	A	1490	A
8	A	2287	A
8	A	1715	G
8	A	1926	U
8	A	2319	G

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

46 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	$\# Z > 2$
56	4SU	w	8	56	18,21,22	3.59	7 (38%)	26,30,33	2.33	5 (19%)
8	PSU	A	2580	8	18,21,22	1.11	3 (16%)	22,30,33	1.93	6 (27%)
8	3TD	A	1915	8	18,22,23	4.25	5 (27%)	22,32,35	1.71	3 (13%)
8	PSU	A	2504	8	18,21,22	1.02	2 (11%)	22,30,33	1.74	4 (18%)
34	UR3	a	1498	34	19,22,23	2.57	7 (36%)	26,32,35	1.34	3 (11%)
55	5MU	v	54	55	19,22,23	4.78	7 (36%)	28,32,35	3.60	9 (32%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	5MC	A	747	8	18,22,23	3.55	7 (38%)	26,32,35	1.23	2 (7%)
8	OMU	A	2552	8	19,22,23	2.86	8 (42%)	26,31,34	1.78	5 (19%)
8	OMC	A	2498	8	19,22,23	2.85	7 (36%)	26,31,34	0.86	1 (3%)
56	PSU	w	32	56	18,21,22	1.07	1 (5%)	22,30,33	1.74	4 (18%)
56	G7M	w	46	56	23,26,27	2.60	8 (34%)	35,39,42	2.25	10 (28%)
34	5MC	a	967	34	18,22,23	3.68	7 (38%)	26,32,35	1.02	1 (3%)
56	5MU	w	54	56	19,22,23	1.46	6 (31%)	28,32,35	2.10	8 (28%)
8	OMG	A	2251	56,8	23,26,27	2.37	8 (34%)	33,38,41	1.83	9 (27%)
8	2MA	A	2503	8	22,25,26	3.64	9 (40%)	33,37,40	2.11	8 (24%)
34	PSU	a	516	34	18,21,22	0.95	1 (5%)	22,30,33	1.68	5 (22%)
8	5MU	A	1939	8	19,22,23	4.65	7 (36%)	28,32,35	3.80	10 (35%)
8	G7M	A	2069	8	23,26,27	2.53	8 (34%)	35,39,42	2.28	10 (28%)
8	6MZ	A	1618	8	22,25,26	2.95	5 (22%)	30,36,39	4.36	14 (46%)
8	PSU	A	1917	8	18,21,22	0.94	1 (5%)	22,30,33	1.77	4 (18%)
8	2MG	A	2445	8	23,26,27	2.87	8 (34%)	32,38,41	2.24	11 (34%)
34	G7M	a	527	34	23,26,27	2.59	8 (34%)	35,39,42	2.27	10 (28%)
34	5MC	a	1407	34	18,22,23	3.62	7 (38%)	26,32,35	1.02	1 (3%)
8	PSU	A	2604	8	18,21,22	1.06	2 (11%)	22,30,33	2.01	4 (18%)
8	PSU	A	955	8	18,21,22	1.06	2 (11%)	22,30,33	1.90	4 (18%)
55	PSU	v	55	55	18,21,22	1.09	1 (5%)	22,30,33	1.71	4 (18%)
34	MA6	a	1519	34	23,26,27	1.46	4 (17%)	34,38,41	2.77	11 (32%)
8	PSU	A	746	8	18,21,22	1.01	2 (11%)	22,30,33	1.73	4 (18%)
55	H2U	v	20	55	18,21,22	3.15	5 (27%)	21,30,33	1.98	5 (23%)
55	4SU	v	8	55	18,21,22	3.58	7 (38%)	26,30,33	2.19	4 (15%)
8	PSU	A	2457	8	18,21,22	1.07	3 (16%)	22,30,33	1.82	5 (22%)
34	4OC	a	1402	34	20,23,24	2.97	8 (40%)	26,32,35	0.90	2 (7%)
34	2MG	a	966	34	23,26,27	3.03	7 (30%)	32,38,41	2.25	8 (25%)
56	PSU	w	39	56	18,21,22	1.09	1 (5%)	22,30,33	1.86	5 (22%)
8	PSU	A	1911	8	18,21,22	1.16	2 (11%)	22,30,33	1.95	6 (27%)
34	2MG	a	1516	34	23,26,27	2.89	9 (39%)	32,38,41	2.31	12 (37%)
58	FME	y	101	58	8,9,10	1.01	1 (12%)	7,9,11	0.87	0
34	MA6	a	1518	34	23,26,27	1.45	5 (21%)	34,38,41	2.83	12 (35%)
8	1MG	A	745	8	22,26,27	2.58	6 (27%)	33,39,42	2.00	7 (21%)
8	6MZ	A	2030	8	22,25,26	3.06	5 (22%)	30,36,39	4.50	14 (46%)
8	PSU	A	2605	8	18,21,22	1.02	2 (11%)	22,30,33	1.85	3 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
34	2MG	a	1207	34	23,26,27	2.91	8 (34%)	32,38,41	2.25	11 (34%)
56	MIA	w	37	56	28,31,32	2.55	6 (21%)	40,44,47	3.27	15 (37%)
8	2MG	A	1835	8	23,26,27	2.94	8 (34%)	32,38,41	2.15	11 (34%)
8	5MC	A	1962	8	18,22,23	3.64	7 (38%)	26,32,35	1.02	1 (3%)
56	PSU	w	55	56	18,21,22	1.34	2 (11%)	22,30,33	1.90	4 (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
56	4SU	w	8	56	-	0/7/25/26	0/2/2/2
8	PSU	A	2580	8	-	0/7/25/26	0/2/2/2
8	3TD	A	1915	8	-	2/7/25/26	0/2/2/2
8	PSU	A	2504	8	-	0/7/25/26	0/2/2/2
34	UR3	a	1498	34	-	2/7/25/26	0/2/2/2
55	5MU	v	54	55	-	0/7/25/26	0/2/2/2
8	5MC	A	747	8	-	1/7/25/26	0/2/2/2
8	OMU	A	2552	8	-	3/9/27/28	0/2/2/2
8	OMC	A	2498	8	-	1/9/27/28	0/2/2/2
56	PSU	w	32	56	-	3/7/25/26	0/2/2/2
56	G7M	w	46	56	-	0/7/25/26	0/3/3/3
34	5MC	a	967	34	-	0/7/25/26	0/2/2/2
56	5MU	w	54	56	-	0/7/25/26	0/2/2/2
8	OMG	A	2251	56,8	-	1/9/27/28	0/3/3/3
8	2MA	A	2503	8	-	1/7/25/26	0/3/3/3
34	PSU	a	516	34	-	0/7/25/26	0/2/2/2
8	5MU	A	1939	8	-	2/7/25/26	0/2/2/2
8	G7M	A	2069	8	-	1/7/25/26	0/3/3/3
8	6MZ	A	1618	8	-	0/9/27/28	0/3/3/3
8	PSU	A	1917	8	-	3/7/25/26	0/2/2/2
8	2MG	A	2445	8	-	2/9/27/28	0/3/3/3
34	G7M	a	527	34	-	1/7/25/26	0/3/3/3
34	5MC	a	1407	34	-	0/7/25/26	0/2/2/2
8	PSU	A	2604	8	-	0/7/25/26	0/2/2/2
8	PSU	A	955	8	-	0/7/25/26	0/2/2/2
55	PSU	v	55	55	-	1/7/25/26	0/2/2/2
34	MA6	a	1519	34	-	3/11/29/30	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	PSU	A	746	8	-	4/7/25/26	0/2/2/2
55	H2U	v	20	55	-	7/7/38/39	0/2/2/2
55	4SU	v	8	55	-	0/7/25/26	0/2/2/2
8	PSU	A	2457	8	-	0/7/25/26	0/2/2/2
34	4OC	a	1402	34	-	1/9/29/30	0/2/2/2
34	2MG	a	966	34	-	2/9/27/28	0/3/3/3
56	PSU	w	39	56	-	3/7/25/26	0/2/2/2
8	PSU	A	1911	8	-	0/7/25/26	0/2/2/2
34	2MG	a	1516	34	-	0/9/27/28	0/3/3/3
58	FME	y	101	58	-	7/7/9/11	-
34	MA6	a	1518	34	-	0/11/29/30	0/3/3/3
8	1MG	A	745	8	-	0/7/25/26	0/3/3/3
8	6MZ	A	2030	8	-	2/9/27/28	0/3/3/3
8	PSU	A	2605	8	-	0/7/25/26	0/2/2/2
34	2MG	a	1207	34	-	0/9/27/28	0/3/3/3
56	MIA	w	37	56	-	3/15/33/34	0/3/3/3
8	2MG	A	1835	8	-	2/9/27/28	0/3/3/3
8	5MC	A	1962	8	-	0/7/25/26	0/2/2/2
56	PSU	w	55	56	-	0/7/25/26	0/2/2/2

The worst 5 of 240 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1915	3TD	C6-C5	12.86	1.50	1.35
8	A	2030	6MZ	C6-N6	12.27	1.47	1.34
8	A	1618	6MZ	C6-N6	11.91	1.47	1.34
8	A	2503	2MA	C4-N3	11.42	1.48	1.34
55	v	54	5MU	C2-N1	10.76	1.55	1.38

The worst 5 of 295 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	2030	6MZ	C4-N9-C8	14.40	121.33	105.73
8	A	1618	6MZ	C4-N9-C8	13.22	120.06	105.73
8	A	1939	5MU	C5-C4-N3	12.31	125.82	115.31
55	v	54	5MU	C5-C4-N3	11.89	125.46	115.31
8	A	2030	6MZ	N9-C8-N7	-11.36	98.37	113.91

There are no chirality outliers.

5 of 58 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
55	v	20	H2U	O4'-C4'-C5'-O5'
55	v	20	H2U	O4'-C1'-N1-C6
8	A	746	PSU	C2'-C1'-C5-C4
8	A	746	PSU	C2'-C1'-C5-C6
8	A	1915	3TD	O4'-C1'-C5-C4

There are no ring outliers.

32 monomers are involved in 51 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
56	w	8	4SU	1	0
8	A	1915	3TD	2	0
8	A	2504	PSU	1	0
55	v	54	5MU	2	0
8	A	2552	OMU	2	0
8	A	2498	OMC	2	0
56	w	54	5MU	1	0
8	A	2251	OMG	2	0
8	A	2503	2MA	1	0
34	a	516	PSU	3	0
8	A	1939	5MU	1	0
8	A	1917	PSU	3	0
8	A	2445	2MG	1	0
34	a	527	G7M	1	0
34	a	1407	5MC	1	0
55	v	55	PSU	2	0
34	a	1519	MA6	2	0
8	A	746	PSU	1	0
55	v	20	H2U	2	0
55	v	8	4SU	1	0
34	a	1402	4OC	2	0
34	a	966	2MG	1	0
56	w	39	PSU	2	0
8	A	1911	PSU	1	0
34	a	1516	2MG	1	0
58	y	101	FME	2	0
34	a	1518	MA6	1	0
8	A	745	1MG	1	0
8	A	2030	6MZ	1	0
34	a	1207	2MG	1	0
56	w	37	MIA	8	0
56	w	55	PSU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
60	AM2	a	2001	-	40,40,40	1.61	9 (22%)	53,60,60	1.18	3 (5%)
61	GDP	x	801	-	28,30,30	1.11	3 (10%)	44,47,47	2.04	12 (27%)

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
60	AM2	a	2001	-	-	2/12/84/84	0/4/4/4
61	GDP	x	801	-	-	6/16/32/32	0/3/3/3

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	a	2001	AM2	OA4-CA1	4.19	1.52	1.41
60	a	2001	AM2	OB1-CB1	3.40	1.50	1.41
60	a	2001	AM2	CB3-CB4	-3.28	1.49	1.53
60	a	2001	AM2	OA5-CA8	3.27	1.50	1.41
60	a	2001	AM2	OA5-CA4	2.96	1.51	1.44

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
61	x	801	GDP	C5-C4-N3	-6.57	117.81	128.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
61	x	801	GDP	C2-N3-C4	5.28	121.71	112.30
60	a	2001	AM2	CA9-NA7-CA7	-4.71	107.52	114.38
61	x	801	GDP	N9-C4-N3	4.62	135.21	125.94
61	x	801	GDP	C6-C5-N7	3.48	136.72	130.25

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

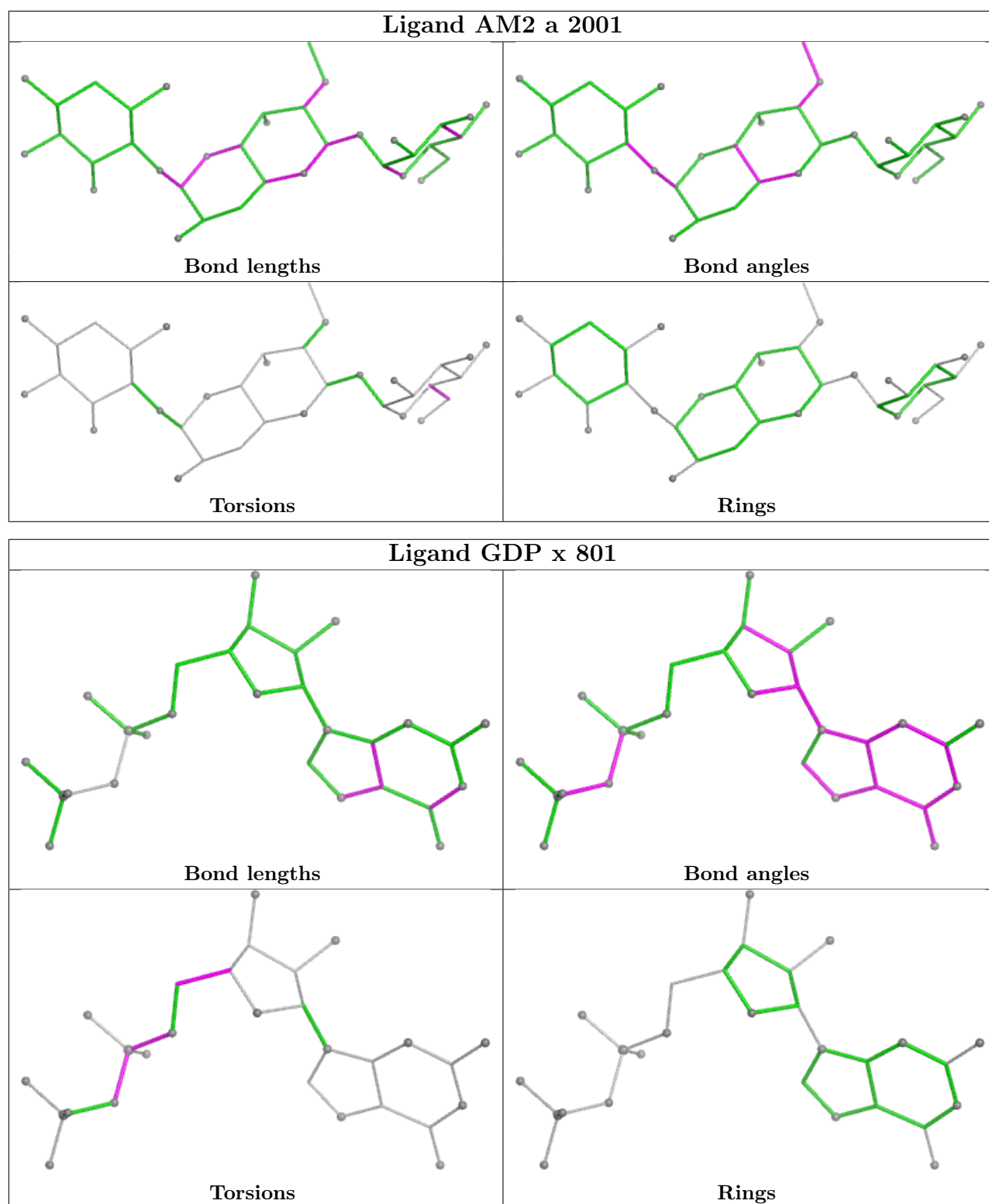
Mol	Chain	Res	Type	Atoms
61	x	801	GDP	C5'-O5'-PA-O3A
61	x	801	GDP	O4'-C4'-C5'-O5'
61	x	801	GDP	C3'-C4'-C5'-O5'
60	a	2001	AM2	OB1-CB5-CB6-OB6
61	x	801	GDP	C5'-O5'-PA-O1A

There are no ring outliers.

2 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	a	2001	AM2	3	0
61	x	801	GDP	13	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

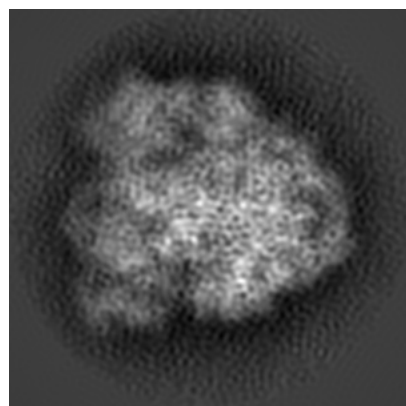
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13463. These allow visual inspection of the internal detail of the map and identification of artifacts.

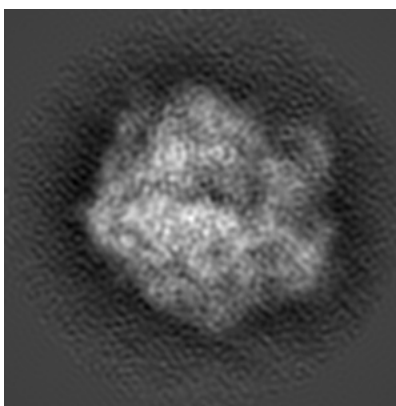
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

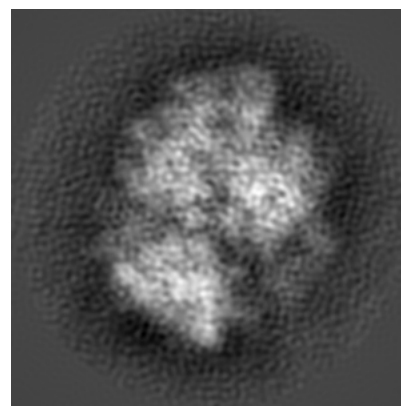
6.1.1 Primary map



X

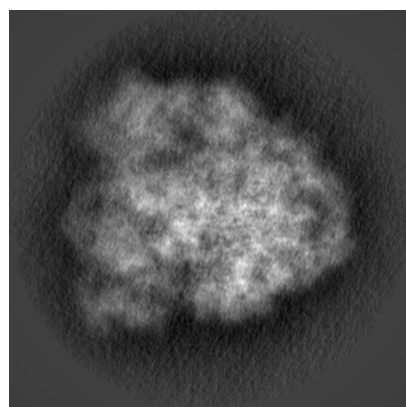


Y

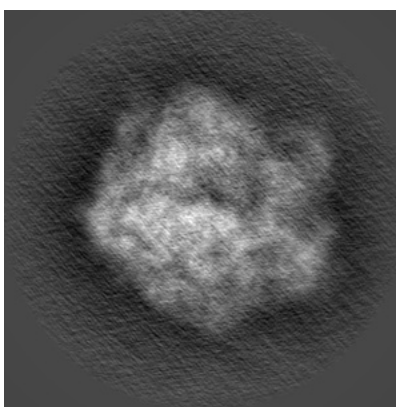


Z

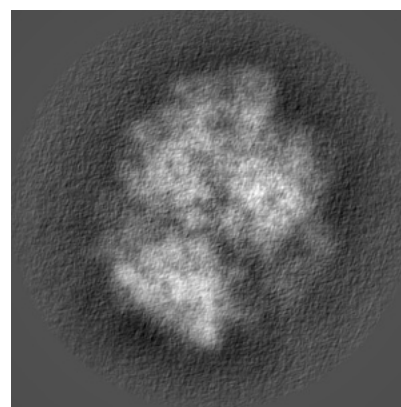
6.1.2 Raw map



X



Y

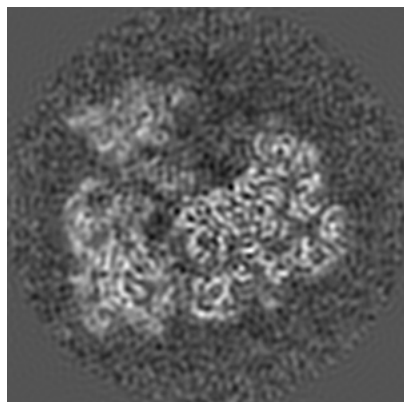


Z

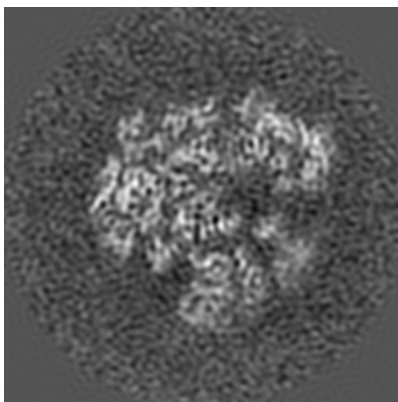
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

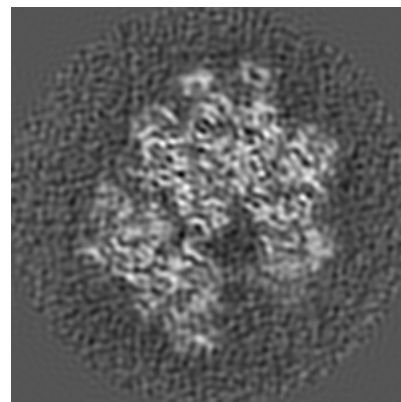
6.2.1 Primary map



X Index: 144

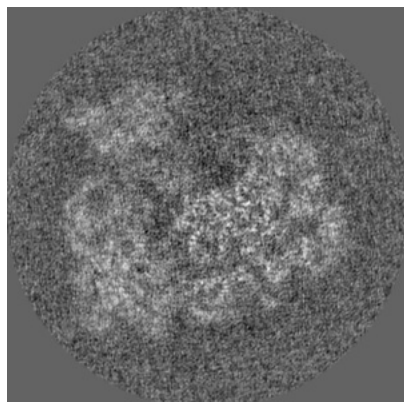


Y Index: 144

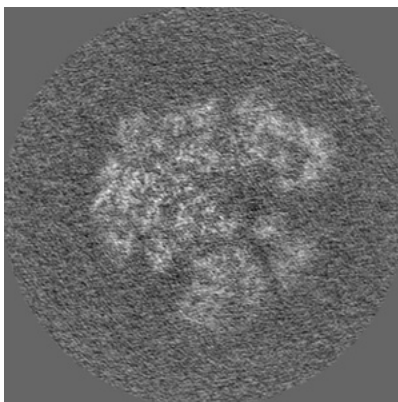


Z Index: 144

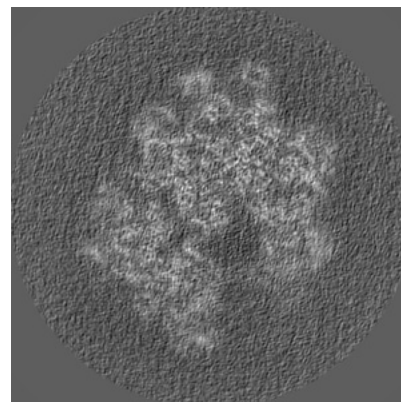
6.2.2 Raw map



X Index: 144



Y Index: 144

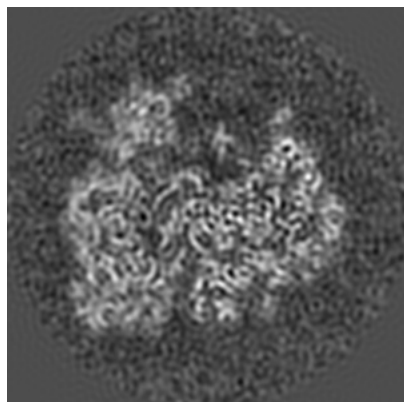


Z Index: 144

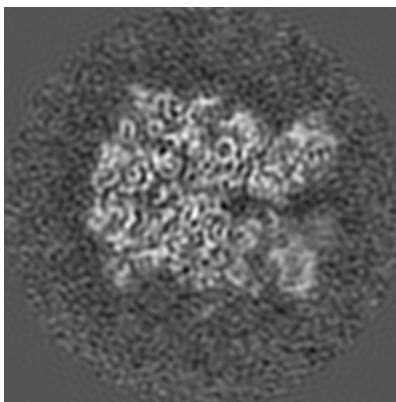
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

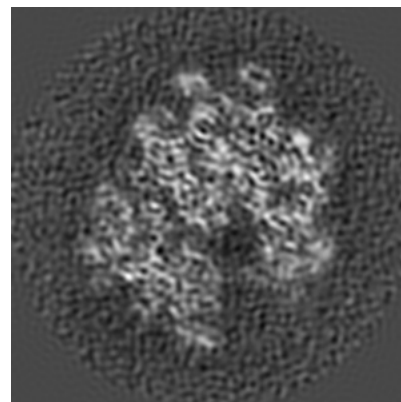
6.3.1 Primary map



X Index: 138

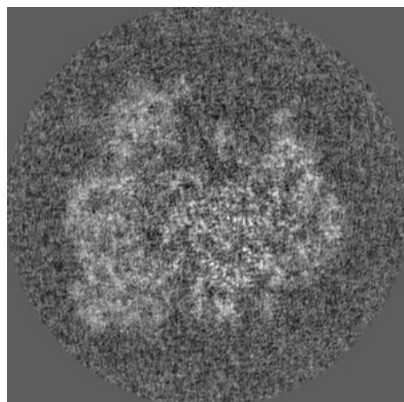


Y Index: 160

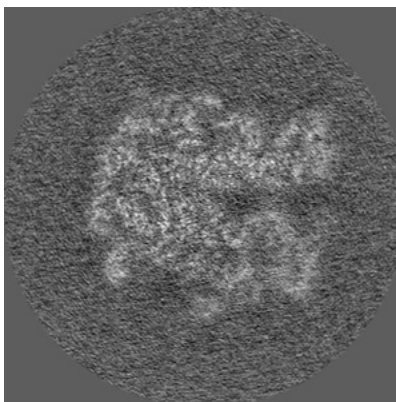


Z Index: 146

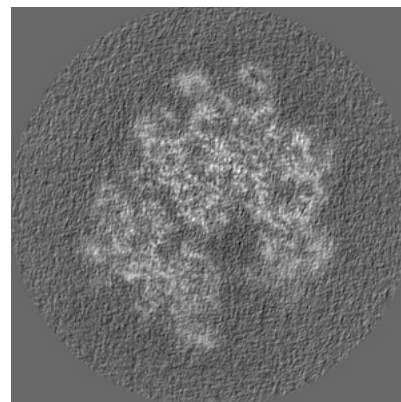
6.3.2 Raw map



X Index: 138



Y Index: 156

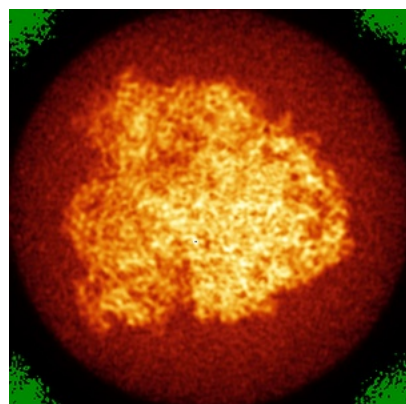


Z Index: 146

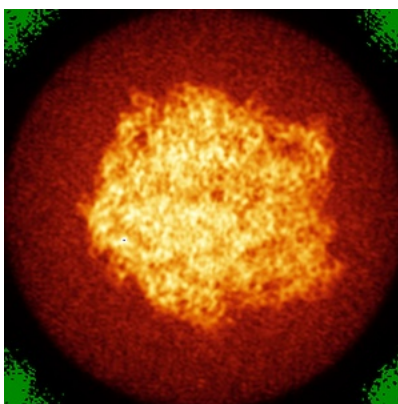
The images above show the largest variance slices of the map in three orthogonal directions.

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

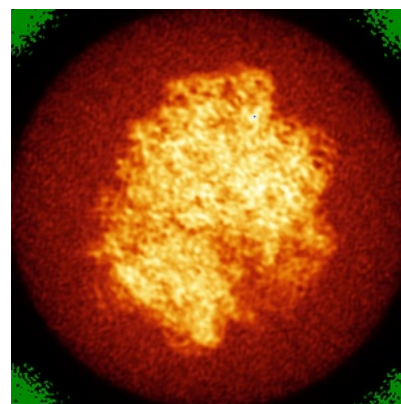
6.4.1 Primary map



X

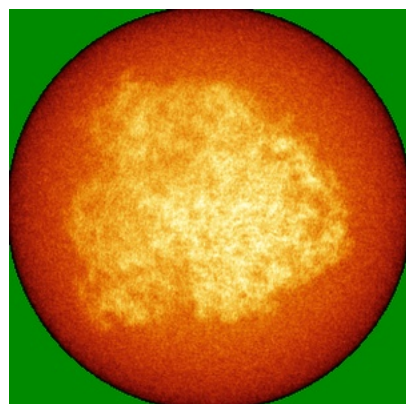


Y

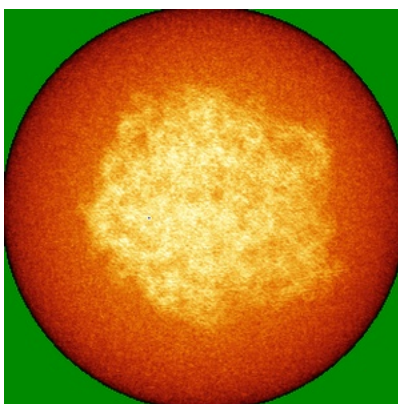


Z

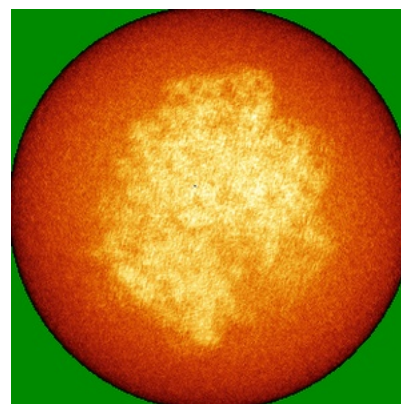
6.4.2 Raw map



X



Y

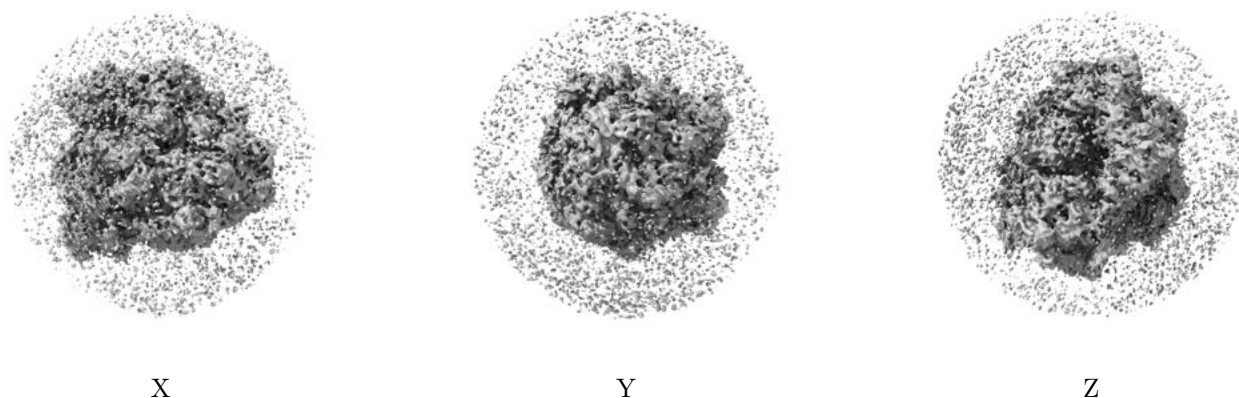


Z

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.

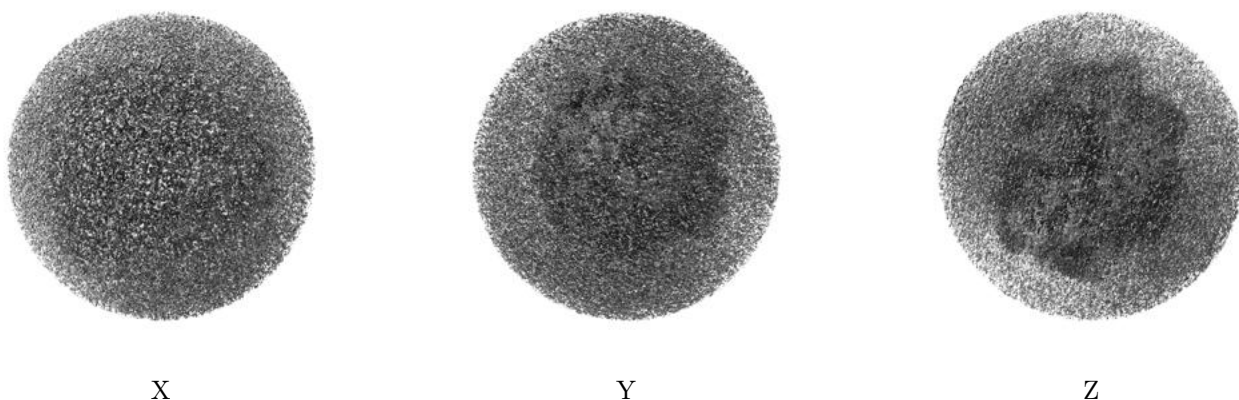
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

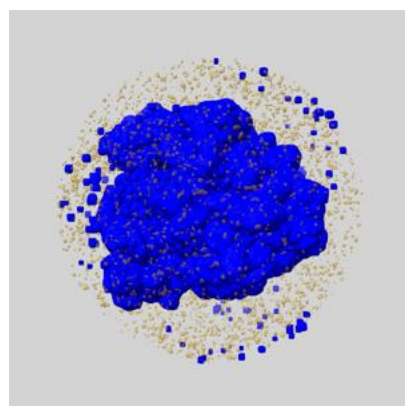
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

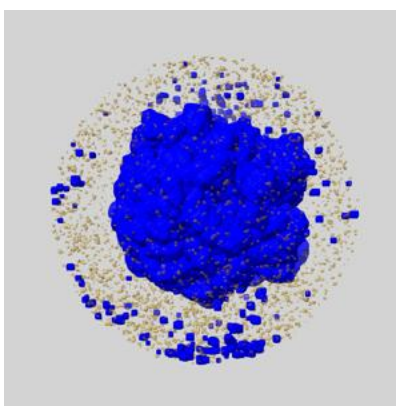
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

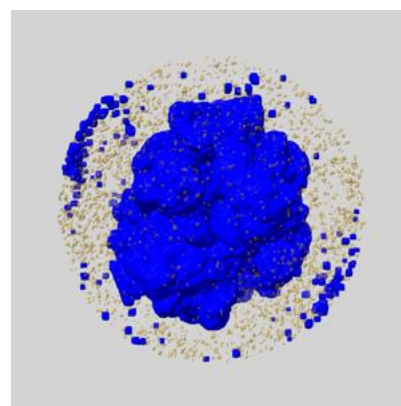
6.6.1 emd_13463_msk_1.map [i](#)



X



Y

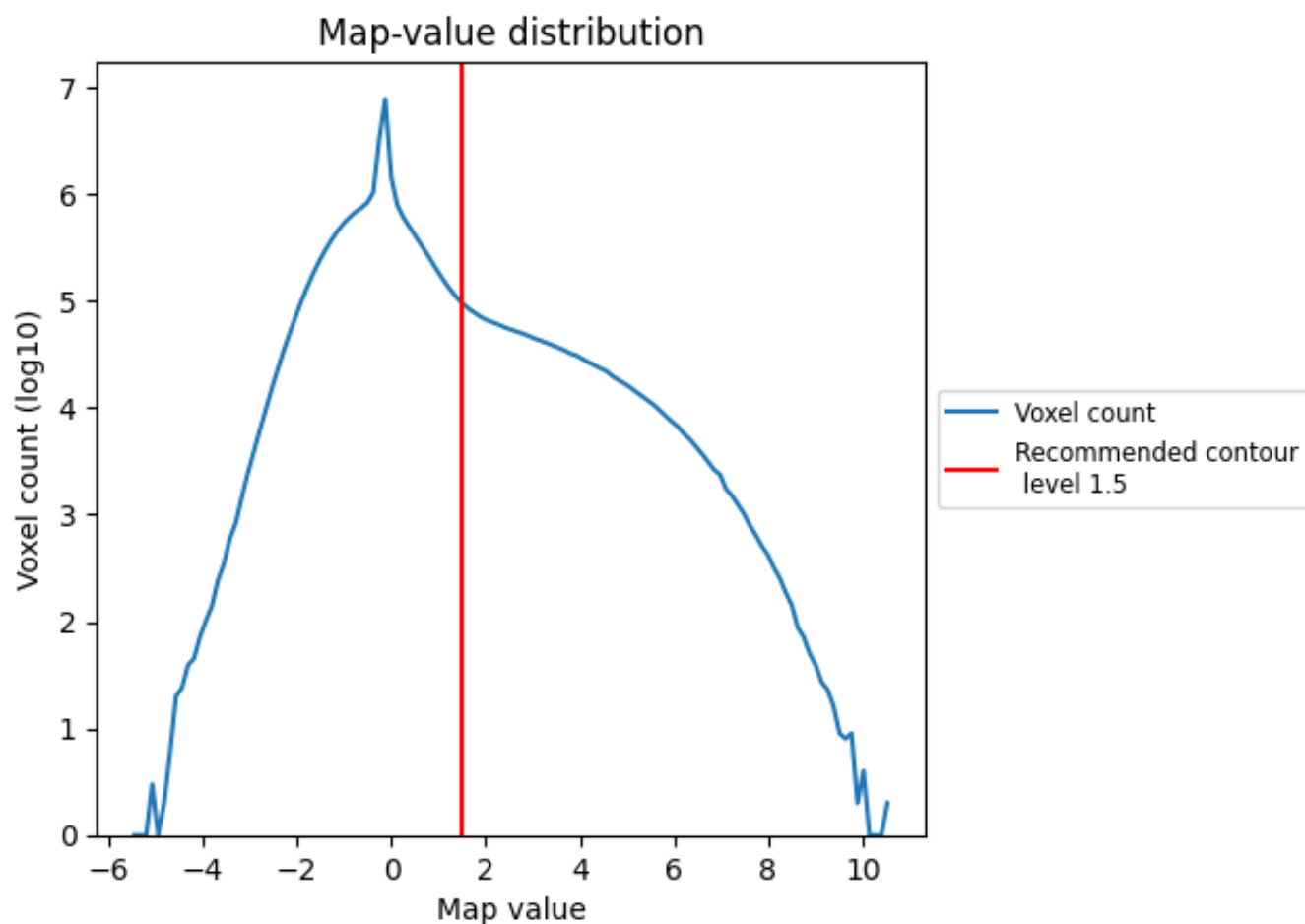


Z

7 Map analysis [i](#)

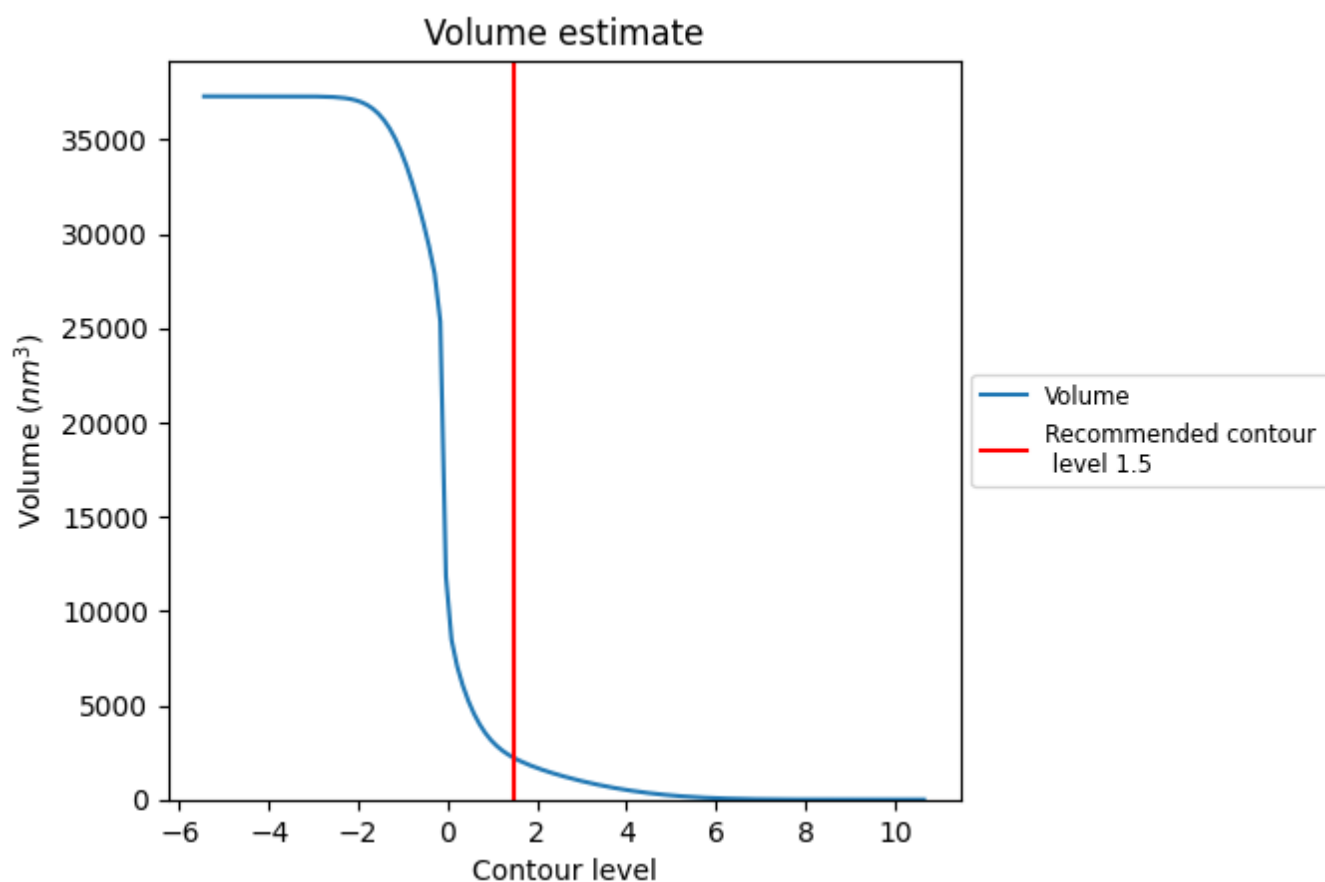
This section contains the results of statistical analysis of the map.

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.

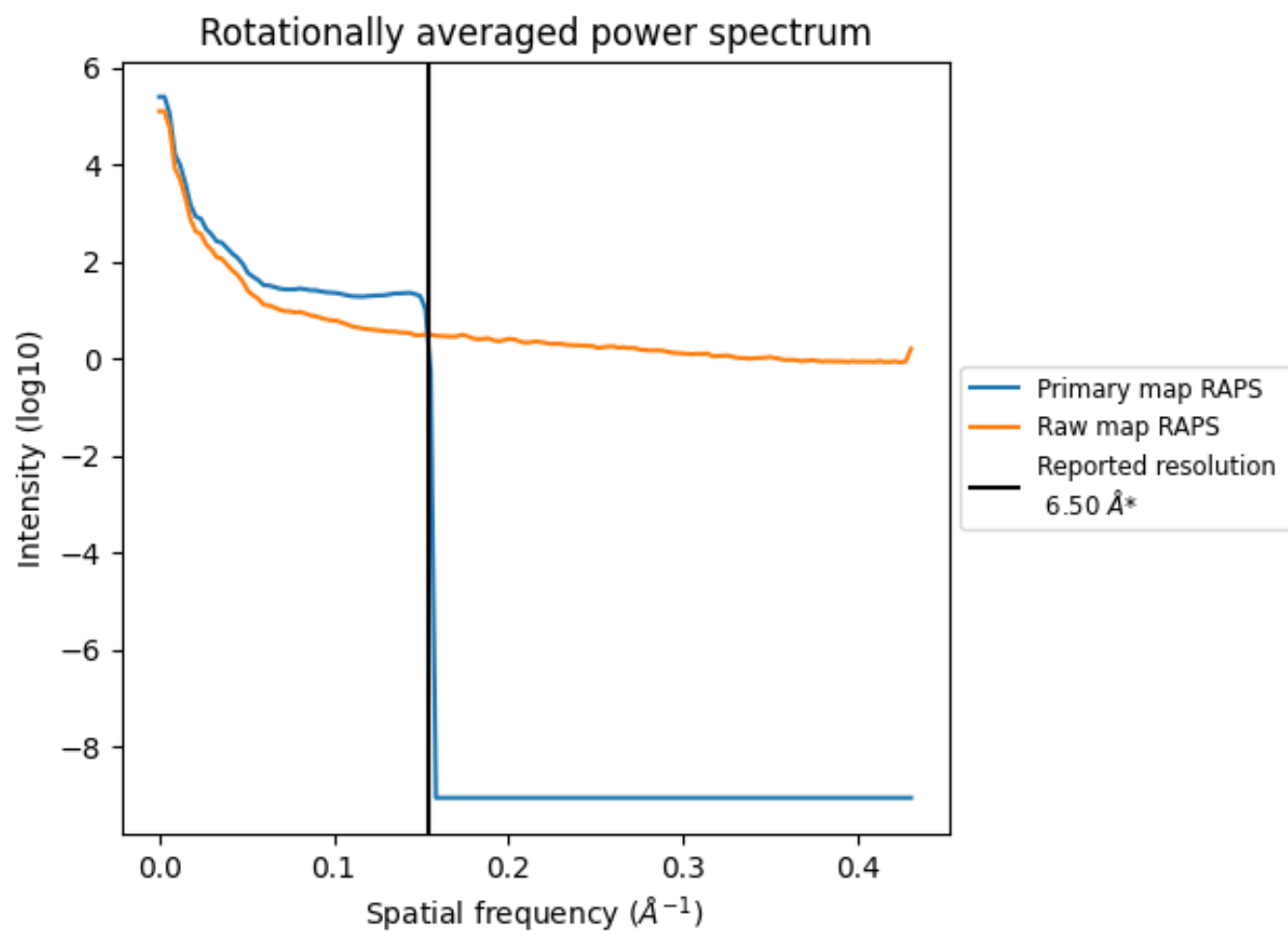
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2187 nm³; this corresponds to an approximate mass of 1976 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 ⓘ

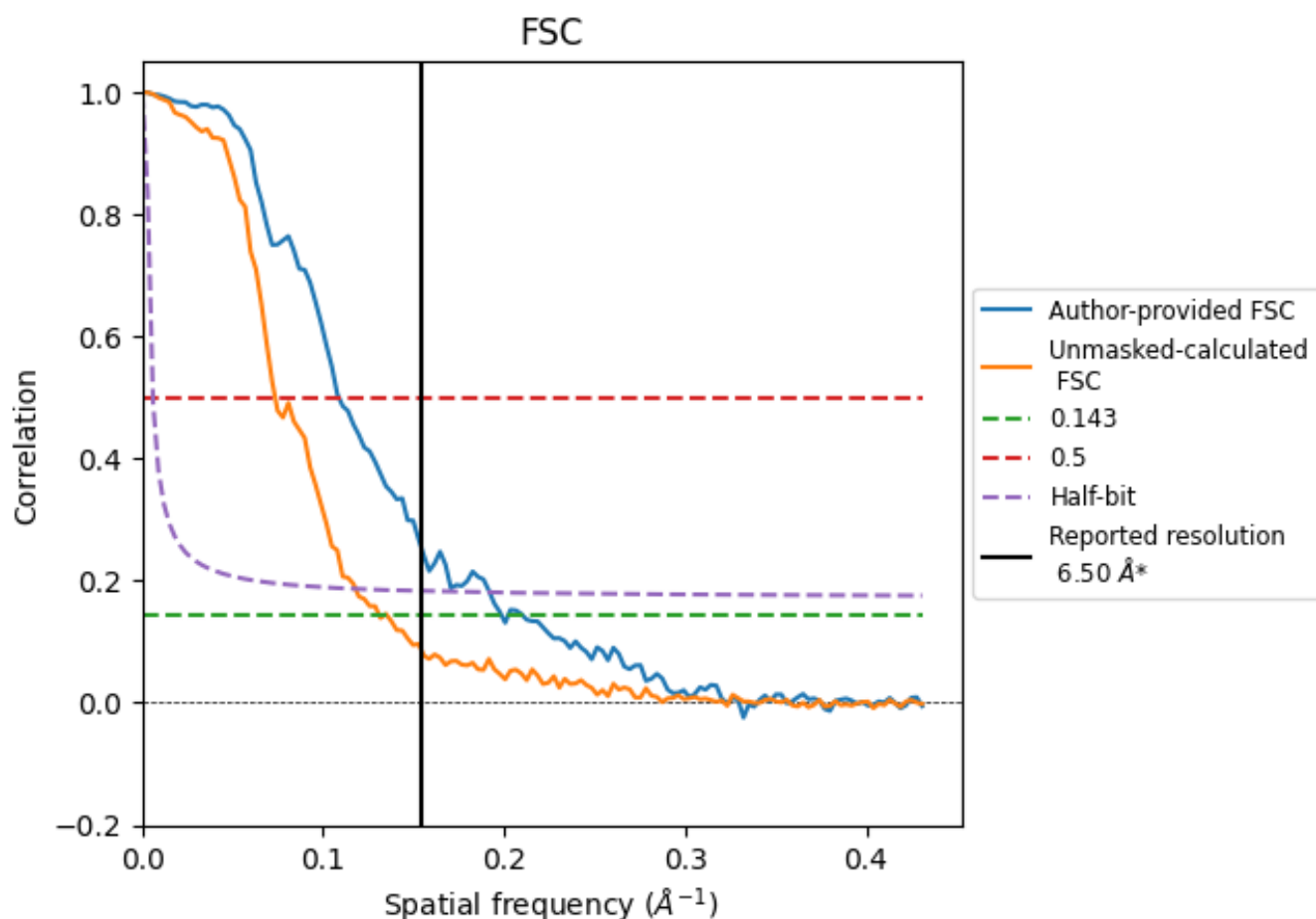


*Reported resolution corresponds to spatial frequency of 0.154 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.154 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.50	-	-
Author-provided FSC curve	5.04	9.21	5.21
Unmasked-calculated*	7.63	13.61	8.48

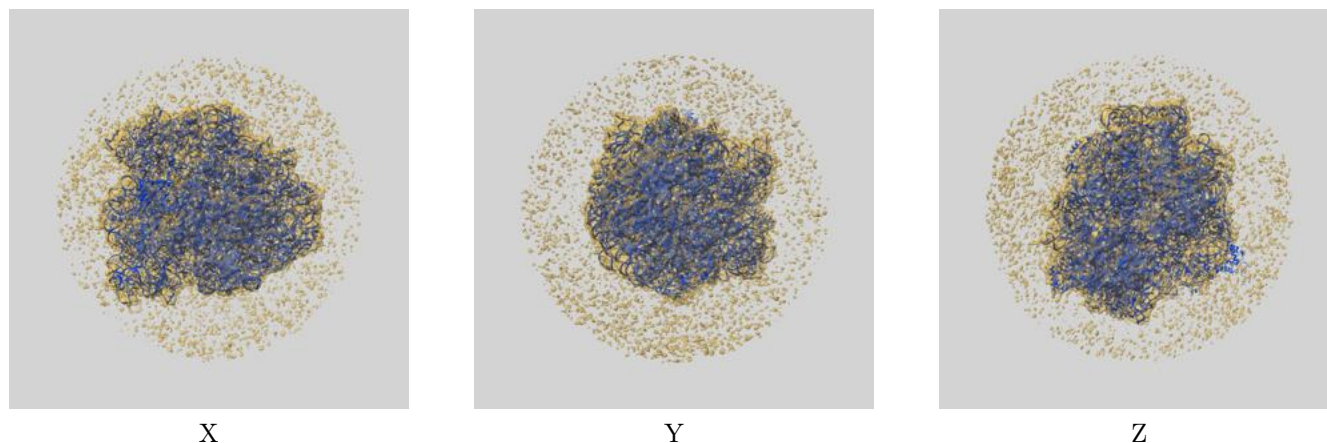
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 5.04 differs from the reported value 6.5 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.63 differs from the reported value 6.5 by more than 10 %

9 Map-model fit [i](#)

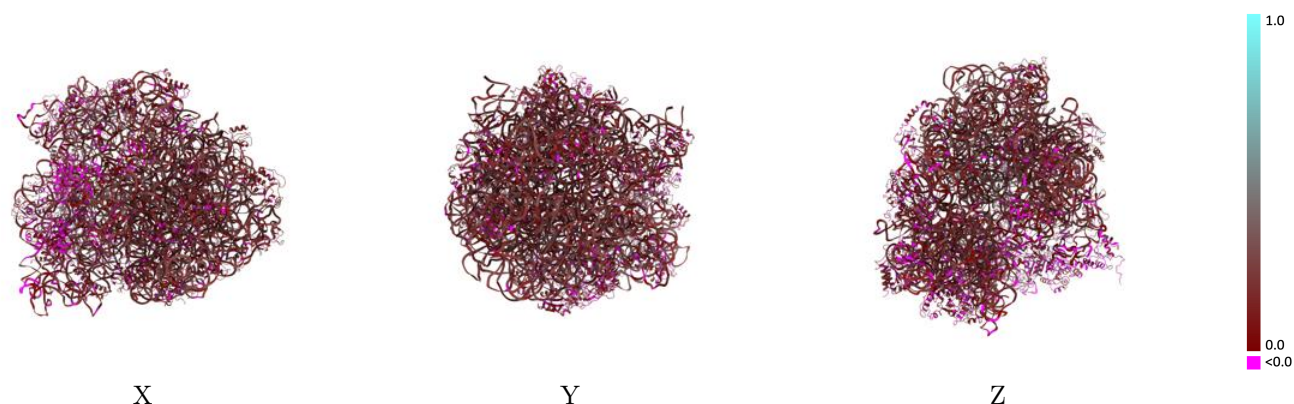
This section contains information regarding the fit between EMDB map EMD-13463 and PDB model 7PJX. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



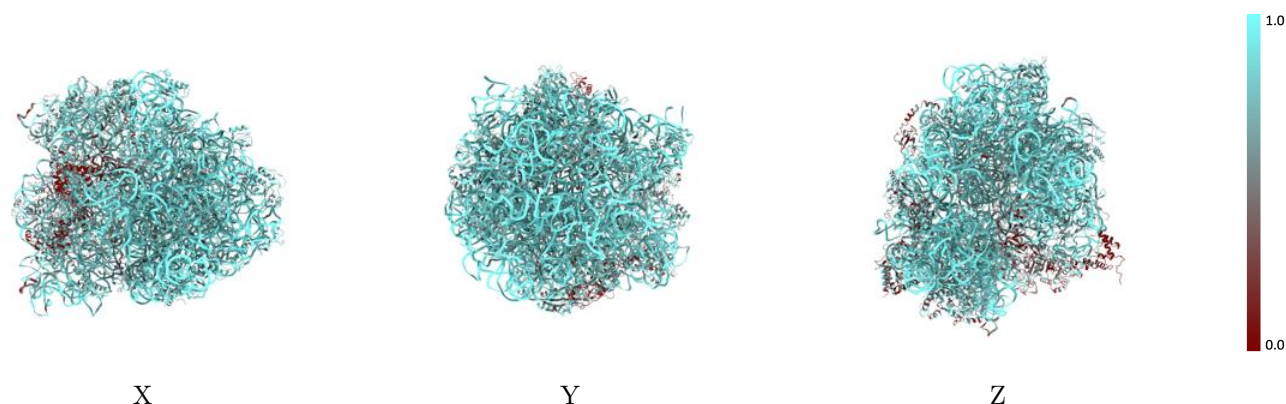
The images above show the 3D surface view of the map at the recommended contour level 1.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



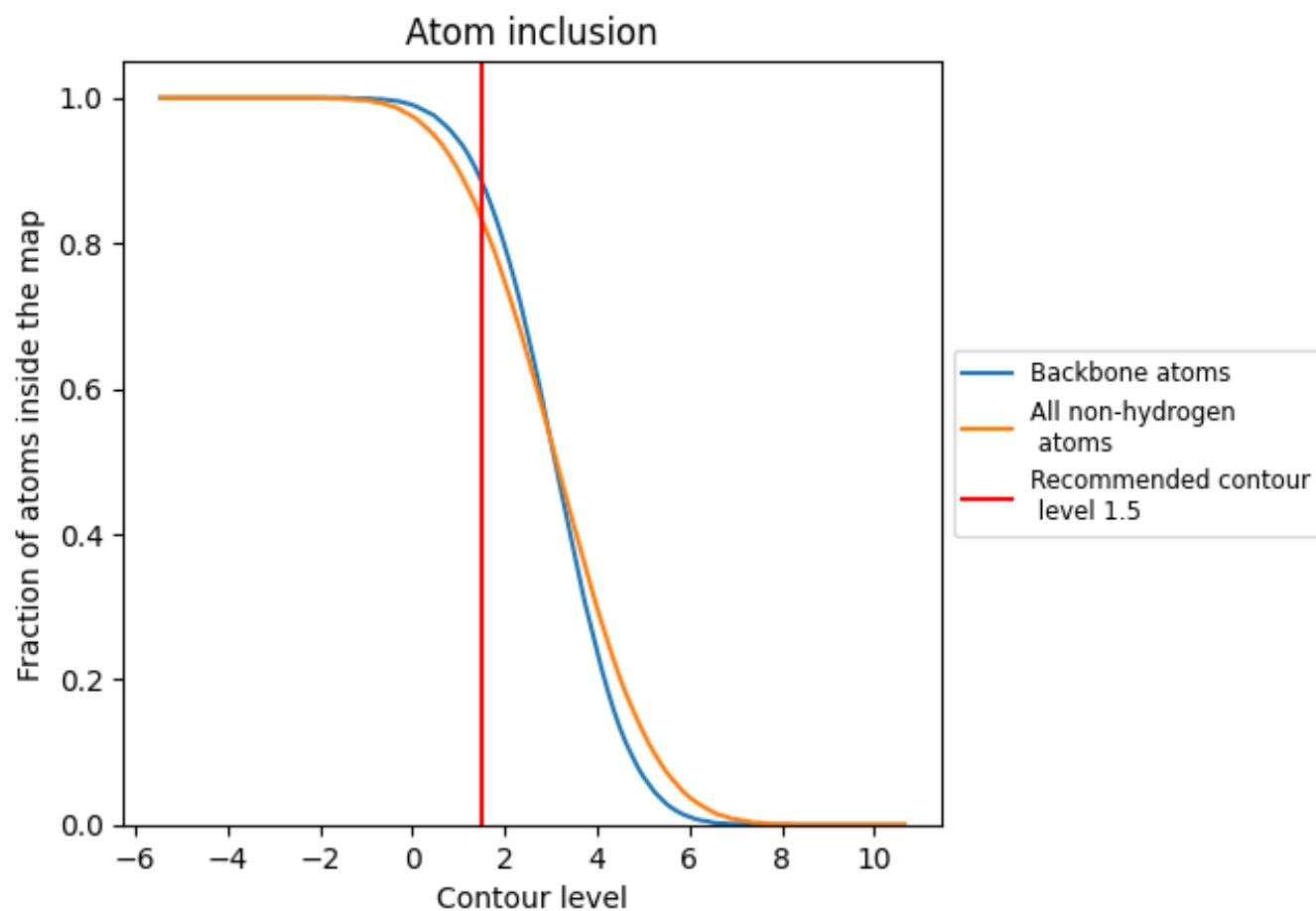
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 83% 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 (1.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8330	 0.1690
0	 0.7360	 0.1780
1	 0.7110	 0.1560
2	 0.7380	 0.1440
3	 0.6880	 0.1400
4	 0.7430	 0.1240
5	 0.1380	 0.0340
6	 0.6630	 0.0900
A	 0.9390	 0.2010
B	 0.9530	 0.1970
C	 0.6910	 0.1380
D	 0.7190	 0.1370
E	 0.7280	 0.1490
F	 0.7280	 0.1330
G	 0.7460	 0.1460
H	 0.3480	 0.0730
I	 0.4080	 0.0520
J	 0.7530	 0.1520
K	 0.6470	 0.1540
L	 0.7000	 0.1380
M	 0.6860	 0.1420
N	 0.7220	 0.1280
O	 0.8170	 0.1200
P	 0.6940	 0.1570
Q	 0.7350	 0.1290
R	 0.7820	 0.1450
S	 0.7070	 0.1290
T	 0.7440	 0.1570
U	 0.8030	 0.1530
V	 0.7630	 0.1450
W	 0.7370	 0.1170
X	 0.7010	 0.1420
Y	 0.7730	 0.1500
Z	 0.7460	 0.1580
a	 0.9070	 0.1740



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Chain	Atom inclusion	Q-score
b	 0.4940	 0.1280
c	 0.6690	 0.1300
d	 0.7090	 0.1180
e	 0.6880	 0.1410
f	 0.7260	 0.1310
g	 0.5100	 0.1120
h	 0.7150	 0.1320
i	 0.7300	 0.1090
j	 0.6710	 0.1180
k	 0.7210	 0.1240
l	 0.5990	 0.1260
m	 0.6620	 0.1190
n	 0.7380	 0.1090
o	 0.7440	 0.1400
p	 0.6700	 0.1100
q	 0.6880	 0.0930
r	 0.6790	 0.1050
s	 0.7370	 0.1080
t	 0.7150	 0.1180
u	 0.5770	 0.1190
v	 0.8140	 0.1710
w	 0.4090	 0.1130
x	 0.4260	 0.0760
y	 0.4290	 0.0510
z	 0.7260	 0.1250