



wwPDB EM Validation Summary Report ⓘ

Jun 18, 2026 – 12:12 pm BST

PDB ID : 7PJZ / pdb_00007pjz
EMDB ID : EMD-13465
Title : Structure of the 70S-EF-G-GDP ribosome complex with tRNAs in chimeric state 2 (CHI2-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 : 6.00 Å (reported)
Based on initial models : 5LZD, 4AQY, 5J9Z, 6YSS

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

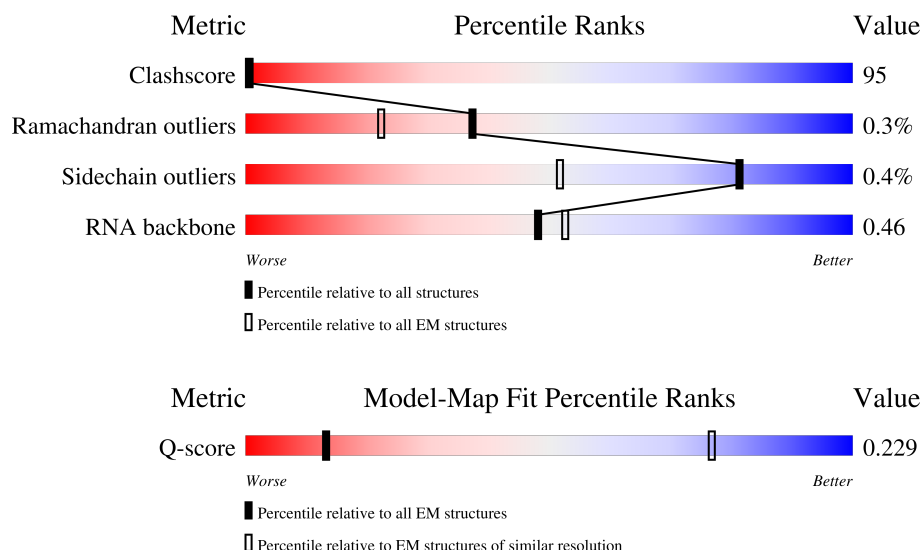
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

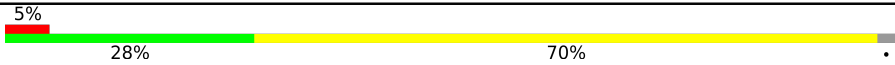
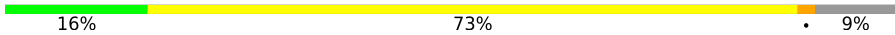
The reported resolution of this entry is 6.00 Å.

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



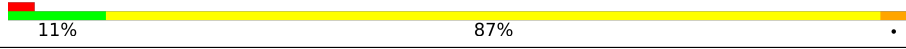
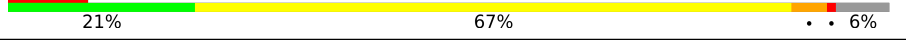
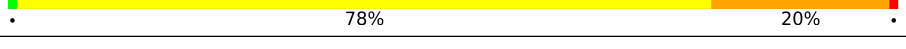
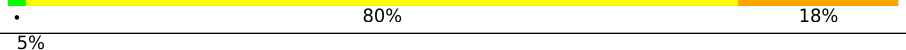
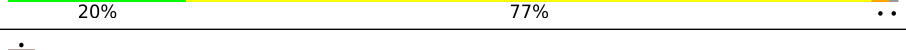
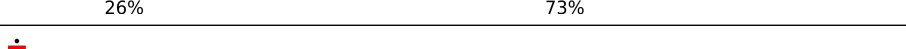
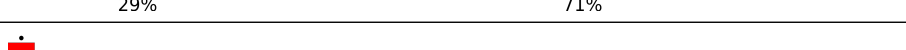
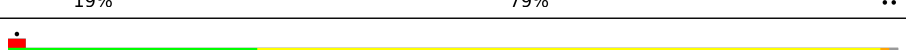
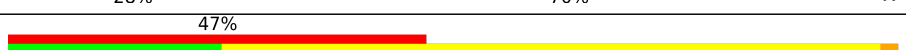
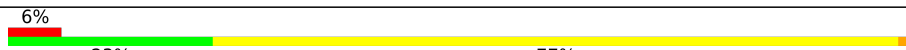
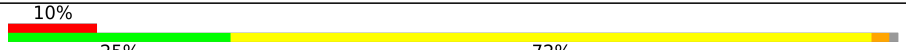
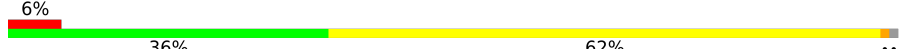
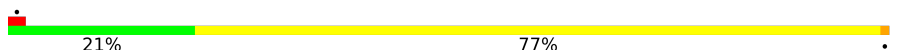
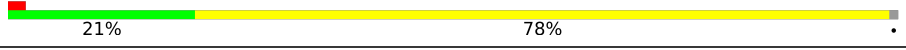
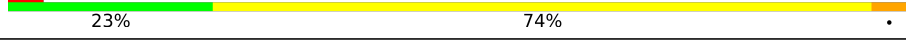
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	525 (5.50 - 6.50)

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	

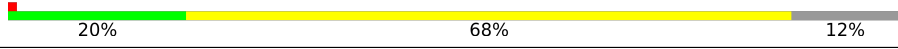
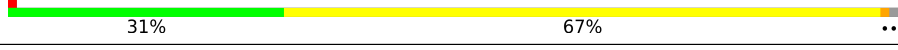
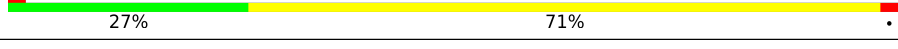
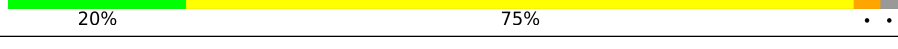
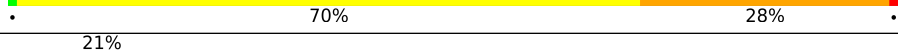
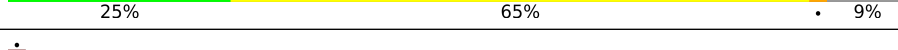
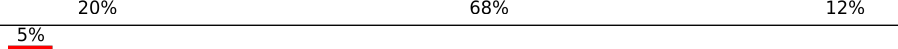
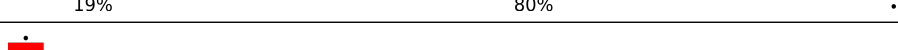
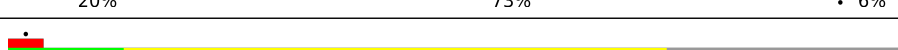
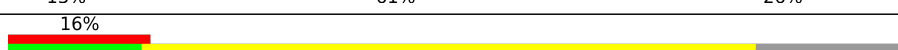
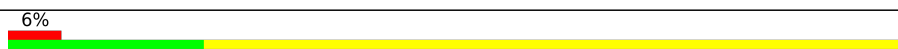
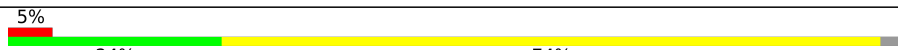
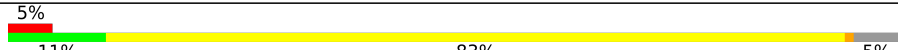
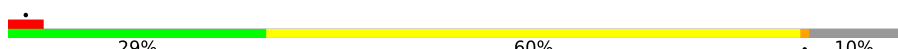
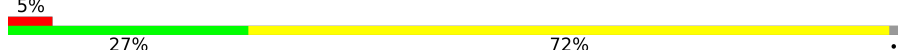
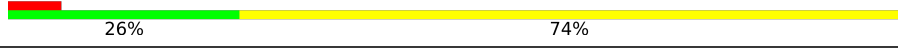
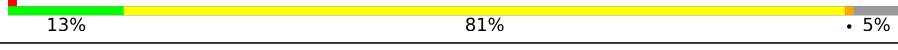
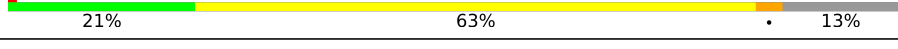
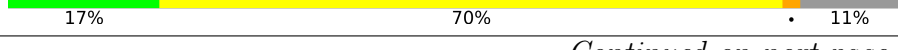
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Mol	Chain	Length	Quality of chain
3	2	46	
4	3	65	
5	4	38	
6	5	165	
7	6	70	
8	A	2903	
9	B	120	
10	C	273	
11	D	209	
12	E	201	
13	F	179	
14	G	177	
15	H	149	
16	I	142	
17	J	142	
18	K	123	
19	L	144	
20	M	136	
21	N	127	
22	O	117	
23	P	115	
24	Q	118	
25	R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

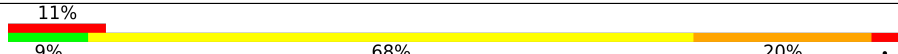
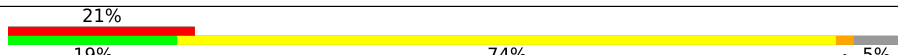
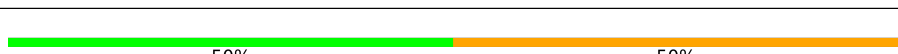
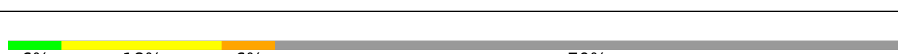
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Mol	Chain	Length	Quality of chain
28	U	104	
29	V	94	
30	W	85	
31	X	78	
32	Y	63	
33	Z	59	
34	a	1542	
35	b	240	
36	c	233	
37	d	206	
38	e	167	
39	f	135	
40	g	179	
41	h	130	
42	i	130	
43	j	103	
44	k	129	
45	l	124	
46	m	118	
47	n	102	
48	o	89	
49	p	82	
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
34	2MG	a	1207	-	-	X	-
34	4OC	a	1402	-	-	X	-
34	UR3	a	1498	-	-	X	-
34	MA6	a	1518	-	-	X	-
34	MA6	a	1519	-	-	X	-
34	PSU	a	516	-	-	X	-
55	PSU	v	55	-	-	X	-
56	MIA	w	37	-	-	X	-
56	PSU	w	39	-	-	X	-
62	GDP	x	801	-	-	X	-
8	PSU	A	1917	-	-	X	-
8	5MC	A	1962	-	-	X	-
8	2MG	A	2445	-	-	X	-
8	OMU	A	2552	-	-	X	-
8	PSU	A	2580	-	-	X	-
8	PSU	A	2604	-	-	X	-
8	PSU	A	2605	-	-	X	-
8	1MG	A	745	-	-	X	-
8	PSU	A	955	-	-	X	-

2 Entry composition

There are 62 unique types of molecules in this entry. The entry contains 152440 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	0	0
			779	492	146	141		

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

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

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

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

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

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

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

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

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

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

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

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

- 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	669	Total	C	N	O	S	1	0
			5192	3275	900	994	23		

- 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	10	Total	C	N	O	P	0	0
			208	93	29	76	10		

- Molecule 60 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
60	6	1	Total	Zn	0
			1	1	

- Molecule 61 is APRAMYCIN (CCD ID: AM2) (formula: C₂₁H₄₁N₅O₁₁).



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

- Molecule 62 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $\text{C}_{10}\text{H}_{15}\text{N}_5\text{O}_{11}\text{P}_2$).

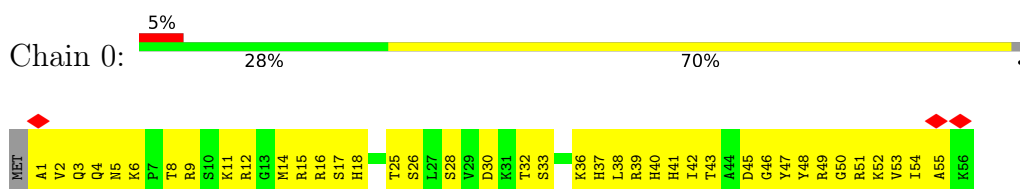


Mol	Chain	Residues	Atoms					AltConf
62	x	1	Total 28	C 10	N 5	O 11	P 2	0

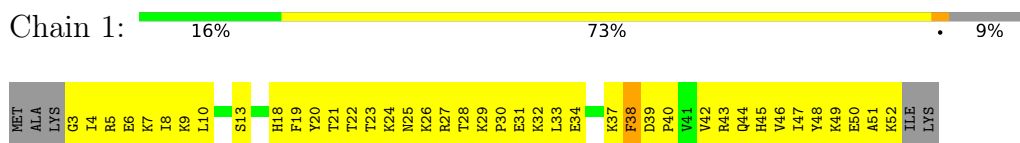
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

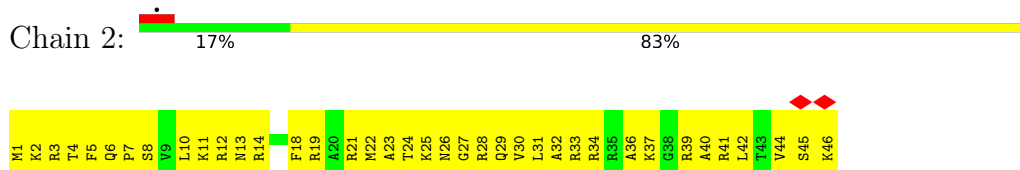
- Molecule 1: 50S ribosomal protein L32



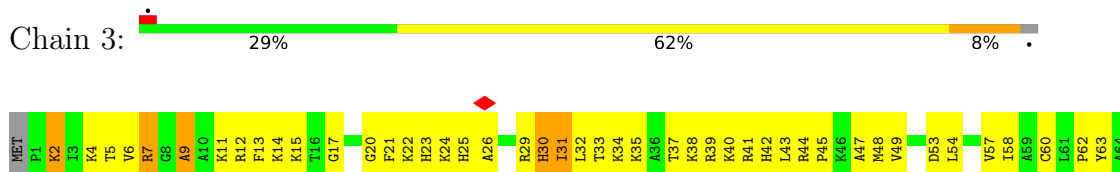
- Molecule 2: 50S ribosomal protein L33



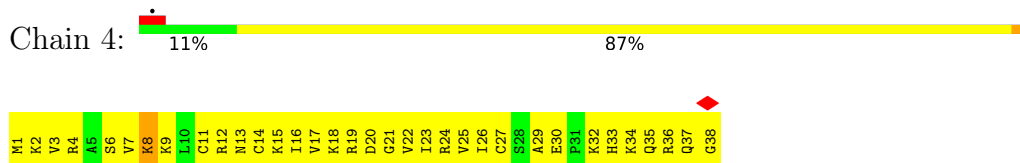
- Molecule 3: 50S ribosomal protein L34



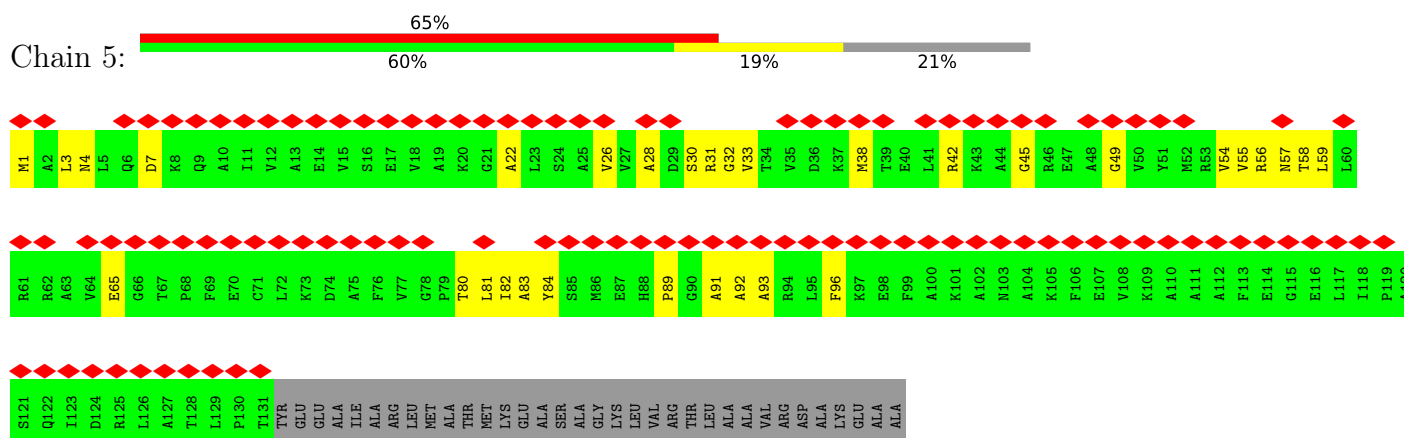
- Molecule 4: 50S ribosomal protein L35



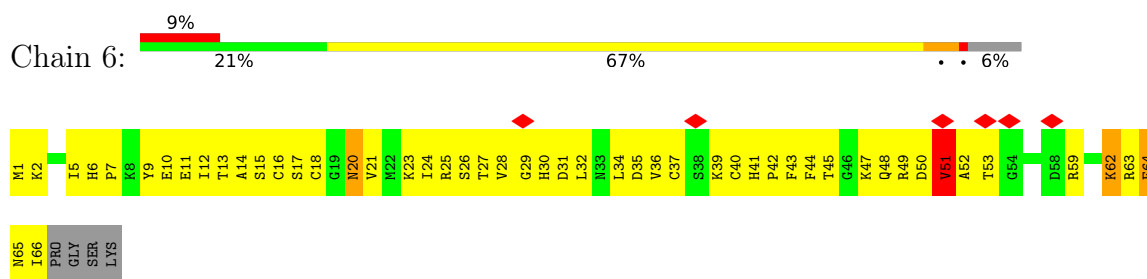
- Molecule 5: 50S ribosomal protein L36



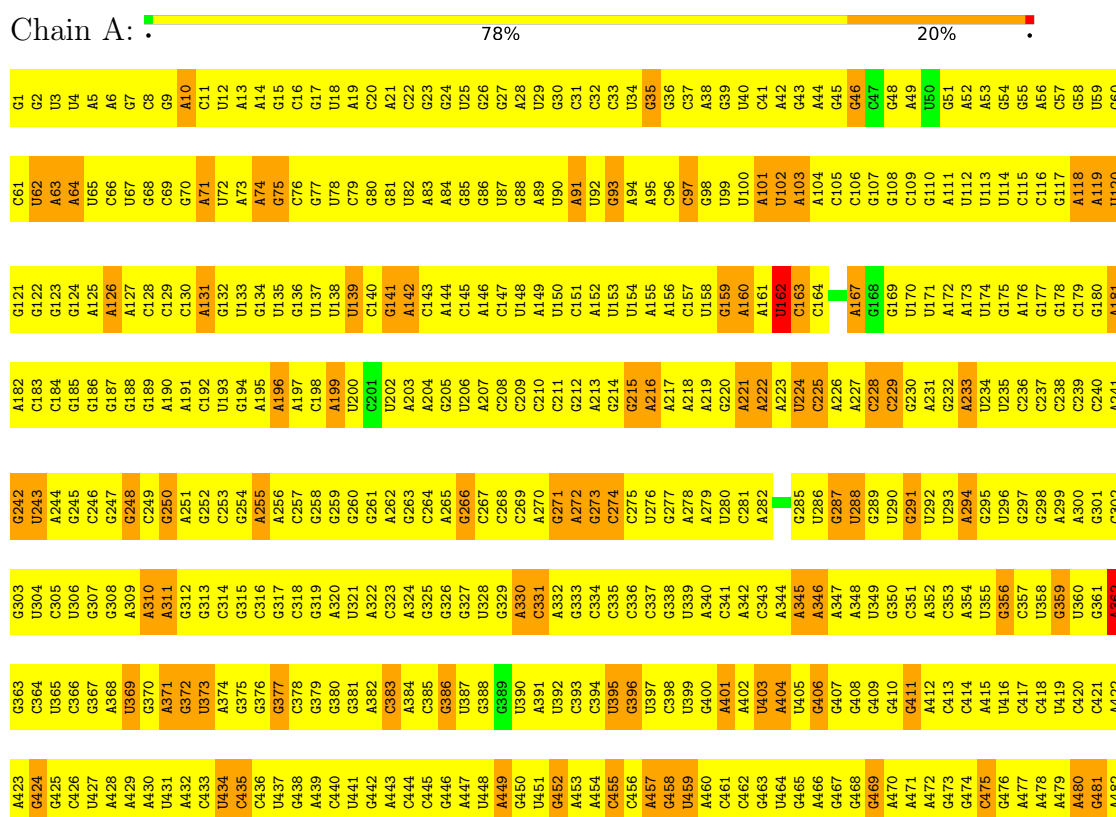
- Molecule 6: 50S ribosomal protein L10



- Molecule 7: 50S ribosomal protein L31



- Molecule 8: 23S ribosomal RNA



A1503	U1443	A1383	G1323	U1263	U1203	A1143	U1083	U1023	U963	C903	G843	A783	C723	G663	A603	G543	A483
A1504	G1444	A1384	G1324	A1264	A1204	A1144	A1084	G1024	C964	G904	A844	G784	U724	G664	G604	C544	C484
A1505	G1445	A1385	U1325	A1265	A1205	C1145	A1085	G1025	C965	A905	A845	G785	G725	G665	G605	C545	C485
A1506	G1446	A1386	U1326	G1266	G1206	C1146	A1086	G1026	C966	U906	A846	G786	G726	U666	C606	U546	C486
A1507	C1447	A1387	A1327	U1267	C1207	U1147	A1087	A1027	U967	U907	C847	G787	U727	U667	U607	C547	C487
A1508	G1448	A1388	A1328	U1268	C1208	U1148	A1088	A1028	C968	C908	C848	G788	G728	U668	A608	G548	C488
A1509	G1449	A1389	U1329	A1269	U1209	U1149	A1089	A1029	C969	A909	A849	U789	G729	G669	A609	G549	C489
G1510	G1450	U1390	C1330	C1270	G1210	C1150	A1090	C1030	U970	A910	U850	U790	A730	C670	C610	C550	C490
G1511	G1451	U1391	G1331	C1271	G1211	A1151	G1091	G1031	C971	A911	C851	C791	C731	C671	C611	C551	C491
G1512	G1452	A1392	G1332	A1272	G1212	C1152	C1092	U1032	A972	C912	C852	U792	C732	C672	G612	U552	A492
G1513	G1453	A1393	G1333	U1273	A1213	C1153	G1093	U1033	A973	C913	C853	A793	G733	C673	A613	G453	G493
G1514	G1454	U1394	G1334	A1274	A1214	U1154	U1094	G1034	G974	G914	C854	G794	A734	G674	U614	U554	G494
A1515	G1455	A1395	G1335	A1275	G1215	A1155	A1095	U1035	A975	C915	C855	C795	A735	A675	U615	G555	G495
G1516	G1456	U1396	A1336	A1276	G1216	A1156	A1096	G1036	C976	G916	C856	C796	C736	A676	A616	A556	G496
G1517	U1457	U1397	G1337	G1277	U1217	G1157	U1097	G1037	G977	A917	C857	G797	C737	A677	G617	C557	A497
G1518	U1458	A1398	G1338	C1278	G1218	C1158	A1098	U1038	C978	A918	C858	G798	C738	U678	U558	U598	G498
G1519	G1459	C1399	G1339	U1279	U1219	U1159	G1099	A1039	A979	U919	C859	G799	G739	G679	G619	G559	U499
U1520	U1460	U1400	U1340	G1280	G1220	U1160	C1100	A1040	A980	U920	U860	A800	C740	C680	C620	C560	G500
G1521	G1461	G1401	G1341	U1281	C1221	C1161	U1101	G1041	A981	C921	A861	C801	U741	G681	A621	G561	A501
A1522	C1462	U1402	A1342	U1282	U1222	G1162	C1102	G1042	C982	C922	C862	A802	A742	G682	G622	U562	A502
U1523	C1463	A1403	G1343	G1283	G1223	C1163	A1103	C1043	A983	G923	C863	U803	A743	U683	C623	A563	A503
A1524	G1464	C1404	U1344	A1284	U1224	C1164	C1104	C1044	A984	G924	C864	A804	U744	C684	C624	C564	A504
A1525	G1465	U1405	G1345	A1285	G1225	A1165	U1105	C1045	C985	A925	C865	A805	G745	A685	G625	C565	A505
G1526	U1466	U1406	G1346	A1286	A1226	G1166	G1106	A1046	C986	G926	A866	C806	U746	U686	A626	U566	G506
G1527	U1467	G1407	A1347	U1287	G1227	C1167	G1107	G1047	C987	A927	C867	U807	C747	C687	A627	U567	A507
A1528	U1468	G1408	C1348	G1288	G1228	G1168	U1108	A1048	A988	A928	U868	C808	G748	U688	G628	U568	A508
G1529	U1469	U1409	C1349	C1289	C1229	A1169	G1109	C1049	C989	U929	C869	C809	A749	A689	G629	U569	C509
U1530	A1470	A1410	U1350	U1290	A1230	C1170	G1110	A1050	A990	G930	U870	U810	A750	G690	C630	G570	C510
C1531	G1471	U1411	C1351	C1291	U1231	G1171	A1111	G1051	C991	U931	U871	U811	A751	U691	A631	U571	U511
A1532	C1472	U1412	G1352	G1292	G1232	C1172	G1112	C1052	C992	U932	U872	C812	A752	C692	A632	A572	G512
C1533	G1473	A1413	A1353	C1293	C1233	U1173	U1113	C1053	C993	A933	C873	U813	A753	A693	A633	U573	A513
U1534	U1474	C1414	A1354	U1294	U1234	U1174	C1114	A1054	C994	U934	C874	C814	U754	U694	C634	A574	A514
A1535	G1475	U1415	G1355	C1295	G1235	U1175	G1115	G1055	C995	C935	C875	C815	U755	G695	C635	A575	A515
G1536	U1476	A1416	G1356	G1296	G1236	U1176	C1116	A1056	A996	A936	C876	C816	A756	G696	G636	U576	C516
G1537	A1477	C1417	C1357	G1297	A1237	G1177	C1117	A1057	C997	G937	A877	C817	G757	G697	A637	G577	C517
G1538	G1478	G1418	G1358	C1298	G1238	C1178	C1118	U1058	C998	G938	A878	C818	C758	C698	G638	G578	G518
U1539	G1479	A1419	A1359	G1299	U1239	G1179	U1119	G1059	U999	G939	C879	A819	G759	A699	U639	G579	U519
G1540	U1480	A1420	G1360	G1300	U1240	U1180	G1120	U1060	A1000	G940	C880	A820	G760	G700	C640	U580	G520
C1541	U1481	G1421	G1361	A1301	A1241	U1181	C1121	U1061	A941	A941	C881	A821	A761	G701	U641	C581	U521
U1542	G1482	G1422	C1362	A1302	U1242	G1182	G1122	G1062	G1002	G942	C882	G822	U762	U702	U642	A582	A522
G1543	U1483	G1423	C1363	G1303	C1243	U1183	C1123	C1063	G1003	A943	C883	C823	G763	G703	A643	G583	C523
A1544	U1484	G1424	A1364	A1304	A1244	U1184	G1124	C1064	U1004	C944	U884	U824	A764	G704	A644	C584	G524
A1545	U1485	G1425	A1365	C1305	G1245	G1185	G1125	U1065	C1005	A945	C885	A825	G765	A705	G645	G585	U525
G1546	U1486	G1426	A1366	C1306	A1246	G1186	A1126	U1066	C1006	C946	A886	U826	U766	A706	U646	A586	A526
U1547	U1487	A1427	A1367	A1307	A1247	G1187	A1127	A1067	C1007	A947	A887	U827	U767	G707	G647	C587	C527
A1548	C1488	C1428	G1368	A1308	G1248	U1188	G1128	G1068	C948	C948	C888	U828	G768	G708	G648	U588	A528
A1549	U1489	G1429	G1369	U1309	U1249	A1189	A1129	A1069	A1009	G949	C889	A829	U769	U709	G649	U589	A529
A1550	A1490	G1430	C1370	G1310	G1250	G1190	U1130	A1070	G950	C950	C890	G830	G770	U710	C650	A590	G530
A1551	G1491	A1431	G1371	C1311	C1251	G1191	G1131	G1071	G1011	C951	C891	G831	G771	G711	G651	U591	C531
A1552	G1492	G1432	U1372	U1312	G1252	U1192	U1132	C1072	U1012	C952	A892	U832	C772	G712	U652	A592	A532
A1553	C1493	A1433	A1373	U1313	A1253	G1193	A1133	C1073	C1013	G953	C893	A833	U773	G713	U653	U593	G533
A1554	A1494	A1434	G1374	C1314	U1254	A1194	A1134	G1074	A1014	G954	U894	U834	G774	U714	A654	U594	U534
A1555	A1495	G1435	U1375	C1315	U1255	G1195	C1135	C1075	U1015	U955	U895	C835	G775	A715	A655	C595	G535
C1556	A1496	A1436	C1376	G1316	G1256	C1196	G1136	C1076	G1016	G956	A896	G836	G776	A716	G656	U596	G536
A1557	U1497	C1437	G1377	G1317	C1257	U1197	G1137	A1077	G1017	C957	C897	C837	G777	G717	U657	G597	G537
C1558	U1498	A1438	A1378	U1318	U1258	U1198	G1138	U1078	U1018	U958	C898	C838	G778	A718	U658	U598	A538
G1559	C1499	A1439	U1379	C1319	G1259	U1199	G1139	C1079	U1019	A959	A899	U839	U779	C719	G659	A599	G539
U1560	G1500	U1440	G1380	A1260	U1260	C1200	C1140	A1080	A1020	A900	A890	C840	G780	U720	C660	G600	C540
C1561	G1501	U1441	A1381	C1261	U1261	U1201	U1141	A1081	A1021	C961	C901	A841	A781	U721	A661	C601	A541
U1562	A1502	U1442	G1382	A1262	G1202	C1202	A1142	U1082	G1022	G962	C902	U842	A782	A722	G662	A602	C542

C2466	A2406	U2344	G2224	C2164	C2104	C2044	G1984	C1924	U1864	C1804	G1743	U1683	G1623	U1563
C2467	A2407	G2345	A2225	C2165	U2105	C2045	C1985	C1925	U1865	A1805	A1744	G1684	U1624	C1564
A2468	U2408	C2346	C2226	U2166	U2106	G2046	A1866	U1926	A1866	C1806	A1745	C1685	C1625	C1565
A2469	A2409	C2347	C2227	U2167	G2107	C2047	A1867	A1927	G1867	U1807	A1746	C1686	A1626	A1566
A2470	G2410	U2348	A2228	C2168	A2108	G2048	C1868	G1928	C1868	A1808	U1747	G1687	G1627	G1567
A2471	G2411	G2349	U2229	A2169	U2109	G2049	G1869	A1929	A1809	U1809	C1748	U1688	G1628	G1568
A2472	A2412	C2350	G2230	A2170	G2110	C2050	C1990	G1930	C1870	A1810	A1749	A1689	U1629	A1569
G2473	G2413	G2351	U2231	A2171	U2111	A2051	U1991	U1931	A1871	G1811	U1750	A1690	A1630	A1570
G2474	G2414	A2352	U2232	U2172	G2112	A2052	C1992	A1932	A1872	U1812	U1751	C1691	G1631	A1571
G2475	G2415	G2353	G2233	A2173	U2113	G2053	U1993	G1933	C1873	G1813	C1752	U1692	A1632	A1572
A2476	A2416	C2354	G2234	C2174	A2114	A2054	C1994	C1934	G1874	G1814	G1753	U1693	G1633	G1573
A2477	G2417	G2355	G2235	C2175	G2115	G2055	U1995	A1935	A1875	A1815	A1754	C1694	A1634	C1574
A2478	A2418	U2356	G2236	A2176	G2116	G2056	C1996	G1936	A1876	C1816	A1755	G1695	C1635	C1575
U2479	U2419	G2357	G2237	C2177	A2117	G2057	C1997	A1937	A1877	G1817	G1756	G1696	U1636	U1576
G2480	G2420	A2358	G2238	C2178	U2118	A2058	A1998	U1938	G1878	U1818	A1757	G1697	A1637	C1577
G2481	C2421	U2359	G2239	C2179	A2119	A2059	C1999	A1939	C1879	A1819	U1758	A1698	C1638	U1578
A2482	A2422	U2360	U2240	U2180	G2120	A2060	C2000	U1940	U1880	U1820	A1759	G1699	C1639	A1579
A2483	U2423	G2361	A2241	U2181	G2121	G2061	C2001	C1941	C1881	A1821	C1760	A1700	A1640	A1580
A2484	C2424	C2362	G2242	U2182	U2122	A2062	G2002	C1942	U1882	G1822	C1761	A1701	A1641	G1581
G2485	A2425	G2363	U2243	A2183	G2123	C2063	A2003	U1943	U1883	G1823	A1762	G1702	G1642	A1582
G2486	A2426	G2364	U2244	A2184	G2124	C2064	G2004	U1944	A1884	G1824	G1763	G1703	G1643	A1583
G2487	G2427	U2365	U2245	U2185	G2125	C2065	A2005	U1945	A1885	U1825	U1764	C1704	G1644	U1584
G2488	G2428	C2366	G2246	G2186	A2126	C2066	C2006	U1946	U1886	G1826	U1765	A1705	G1645	C1585
U2489	G2429	A2367	A2247	U2187	G2127	G2067	U2007	C1947	G1887	U1827	G1766	C1706	G1646	A1586
G2490	A2430	G2370	C2248	U2188	G2128	U2068	C2008	G1948	G1888	G1828	G1767	G1707	U1647	G1587
U2491	U2431	A2371	U2249	U2189	G2129	C2069	A2009	G1949	A1889	A1829	C1768	C1708	U1648	G1588
U2492	A2432	U2372	G2250	G2190	A2130	A2070	C2010	U1950	A1890	G1830	U1769	U1709	G1649	A1589
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G2494	A2434	U2374	G2252	U2192	U2132	C2072	G2012	A1952	C1892	C1832	C1771	U1711	A1651	A1591
G2495	A2435	G2375	G2253	G2193	G2133	C2073	A2013	A1953	C1893	G1833	A1772	U1712	A1652	C1592
G2496	G2436	A2376	C2254	U2194	A2134	U2074	A2014	U1954	C1894	U1834	A1773	U1713	G1653	A1593
A2497	G2437	U2377	G2255	U2195	U2135	U2075	A2015	U1955	C1895	C1835	C1774	U1714	A1654	U1594
G2498	A2378	G2315	G2256	C2196	A2135	G2076	U2016	U1956	G1896	G1836	U1775	G1715	A1655	C1595
G2499	A2439	G2379	U2257	U2197	U2137	A2077	G2017	C1957	G1897	C1837	G1776	U1716	C1656	A1596
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C2501	U2441	U2381	U2259	A2199	U2139	U2079	A2019	G1959	A1899	G1839	U1778	G1718	C1658	A1598
G2502	C2442	G2382	C2260	C2200	G2140	A2080	A2020	C1960	A1900	G1840	U1779	G1719	G1659	U1599
A2503	C2443	G2383	C2261	G2201	G2141	U2081	C2021	C1961	A1901	U1841	A1780	U1720	G1660	C1600
U2504	G2444	U2384	U2262	U2202	A2142	A2082	U2022	C1962	C1902	G1842	U1781	G1721	G1661	G1601
G2505	A2445	C2385	C2263	U2203	C2143	G2083	C2023	U1963	G1903	C1843	U1782	A1722	U1662	A1602
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U2511	A2451	G2391	G2269	G2209	U2149	C2089	A2030	A1969	C1909	G1849	C1788	C1728	A1668	A1608
C2512	C2452	A2392	A2270	U2210	C2150	A2090	A2031	U1971	G1910	G1850	A1789	U1729	A1669	A1609
A2513	A2453	U2393	G2271	A2211	U2151	C2091	G2032	U1972	U1911	U1851	C1790	C1730	C1670	A1610
U2514	G2454	C2394	G2272	A2212	G2152	U2092	G2033	G1973	A1912	U1852	A1791	G1731	U1671	C1611
C2515	G2455	G2395	A2273	U2213	C2153	G2093	A2034	C1974	A1913	A1853		C1732	A1672	C1612
A2516	C2456	G2396	A2274	C2214	A2154	A2094	U2034	C1975	C1914	U1854	A1794	G1733	G1673	G1613
C2517	U2457	G2397	C2275	G2215	U2155	A2095	G2035	U1976	3TD1915	U1855	C1795	G1734	G1674	A1614
A2518	G2458	U2398	G2276	G2216	G2156	C2096	C2036	A1977	A1916	U1856	U1796	A1735	C1675	C1615
U2519	A2459	G2399	G2277	G2217	G2157	A2097	U1917	G1978	U1917	G1857	U1797	U1736	A1676	A1616
C2520	U2460	G2400	G2278	G2218	A2158	U2098	G2038	U1979	A1918	A1858	U1798	G1737	A1677	C1617
C2521	A2461	U2401	G2279	U2219	A2159	U2099	U2039	U1979	A1919	U1859	G1799	G1738	A1678	A1618
U2522	C2462	U2402	G2280	U2220	G2160	G2100	G2040	G1980	C1920	G1860	C1800	A1739	A1679	G1619
G2523	G2463	C2403	A2281	G2221	A2101	U2041	U2041	A1981	G1921	G1861	A1801	G1740	U1680	G1620
G2524	G2464	U2404	G2282	C2222	G2162	G2102	A2042	U1982	G1922	G1862	A1802	G1741	G1681	U1621
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G2526	A2586	C2646	A2706	A2766	A2826	A2886
C2527	A2587	U2647	U2707	C2767	C2827	A2887
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G2529	A2589	C2649	C2709	U2769	A2829	C2889
A2530	A2590	U2650	U2710	G2770	G2830	U2890
A2531	C2591	C2651	A2711	C2771	G2831	U2891
G2532	G2592	U2652	C2712	C2772	U2832	G2892
U2533	U2593	U2653	U2713	C2773	U2833	A2893
A2534	C2594	A2654	G2714	C2774	U2834	G2894
G2535	U2595	U2655	C2715	G2775	A2835	U2895
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U2537	G2597	A2657	C2717	C2777	A2837	U2897
U2538	A2598	C2658	G2718	A2778	U2838	U2898
C2539	G2599	G2659	C2719	U2779	U2839	A2899
U2540	A2600	A2660	U2720	G2780	C2840	A2900
A2541	C2601	G2661	A2721	G2781	C2841	C2901
A2542	A2602	A2662	G2722	G2782	G2842	C2902
G2543	G2603	G2663	C2723	U2783	G2843	U2903
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G2545	U2605	A2665	A2725	C2785	U2845	
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A2547	G2607	C2667	A2727	C2787	U2847	
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C2556	U2616	C2676	A2736	U2796	A2856	
G2557	U2617	C2677	G2737	U2797	G2857	
U2558	U2618	C2678	A2738	U2798	C2858	
C2559	C2619	A2679	U2739	A2800	G2859	
A2560	C2620	U2680	A2740	U2801	A2860	
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U2563	G2623	C2683	U2743	U2804	C2863	
A2564	G2624	U2684	G2744	U2805	G2864	
A2565	G2625	U2685	C2745	C2806	U2865	
A2566	G2626	C2686	U2746	U2807	U2866	
U2567	G2627	U2687	G2747	U2808	G2867	
U2568	C2628	U2688	A2748	U2809	A2868	
G2569	U2629	U2689	A2749	A2810	C2869	
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U2571	C2631	C2691	G2751	G2812	U2871	
A2572	A2632	G2692	C2752	A2813	A2872	
G2573	G2633	G2693	A2753	A2814	A2873	
C2574	A2634	A2694	U2754	C2815	C2874	
G2575	A2635	U2695	C2755	G2816	C2875	
G2576	U2636	U2696	U2756	U2817	G2876	
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C2579	C2639	C2699	A2759	U2820	A2879	
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G2581	G2641	U2701	A2761	G2822	A2881	
G2582	G2642	G2702	C2762	A2823	A2882	
U2583	G2643	C2703	G2763	A2824	A2883	
U2584	G2644	A2764	C2704	U2884	U2884	
U2585	G2645	A2705	A2765	G2825	U2885	

• Molecule 9: 5S ribosomal RNA

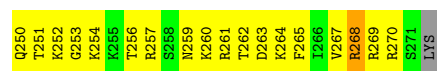
Chain B:  80% 18%

U1	G61
G2	C62
C3	G63
C4	G64
U5	U65
G6	A66
G7	G67
C8	C68
G9	G69
C10	C70
C11	C71
C12	G72
G13	A73
U14	U74
A15	G75
G16	G76
C17	U77
G18	A78
C19	G79
G20	U80
C21	G81
U22	U82
G23	G83
G24	G84
U25	G85
C26	G86
C27	U87
C28	C88
A29	U89
C30	C90
C31	C91
U32	C92
G33	C93
C34	A94
C35	U95
C36	G96
C37	C97
C38	G98
A39	A99
U40	G100
G41	A101
C42	G102
C43	U103
A44	A104
A45	G105
A46	G106
C47	G107
U48	A108
C49	A109
A50	C110
G51	U111
A52	G112
A53	C113
G54	C114
U55	A115
G56	G116
A57	G117
A58	C118
A59	U119
C60	U120

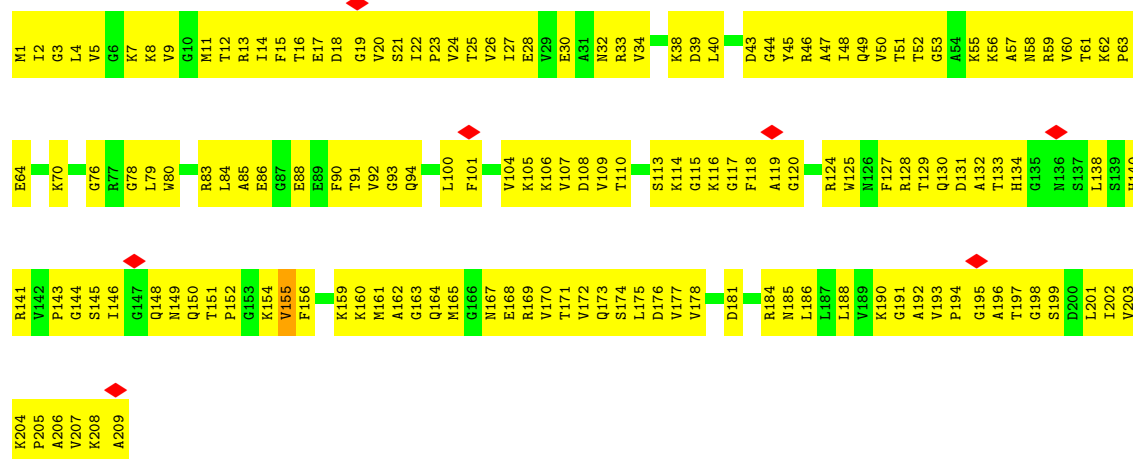
• Molecule 10: 50S ribosomal protein L2

Chain C:  5% 20% 77%

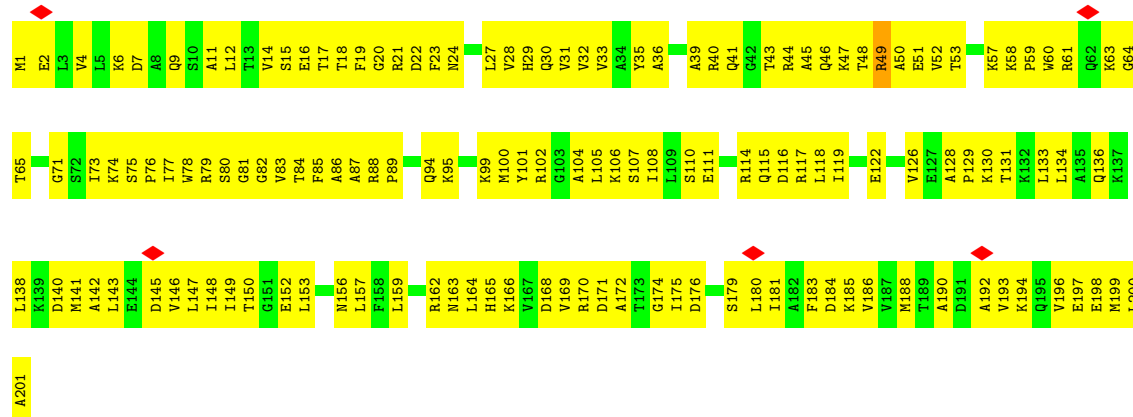
MET	K67	N127	K187
A1	R68	T128	R188
V2	N69	T129	A189
V3	K70	P130	T190
K4	D71	M131	L191
C5	G72	R132	G192
K6	T73	N133	E193
P7	P74	I134	V194
T8	A75	G135	G195
S9	V76	V136	N196
P10	V77	G137	A197
G11	E78	S138	E198
R12	R79	T139	H199
R13	L80	V140	M200
H14	E81	H141	L201
R15	Y82	N142	R202
V16	D83	V143	V203
K17	P84	E144	L204
V18	N85	M145	G205
V19	R86	K146	K206
N20	S87	P147	A207
L23	A88	G148	G208
H24	N89	K149	A209
K27	I90	G150	A210
P28	L92	G151	R211
P29	V93	Q152	W212
F29	L94	L153	R213
A30	Y95	A154	G214
P31	K96	R155	V215
L32	D97	S156	R216
L33	G98	A157	P217
N36	E99	G158	G221
G40	R100	T159	M224
G41	R101	V160	N225
R42	Y102	V161	P226
N43	I103	I163	V227
G46	L104	V164	D228
R47	A105	A165	H229
I48	K107	R166	P230
T49	G108	D167	H231
T50	L109	G168	G232
R51	K110	A169	G233
H52	A111	Y170	G234
I53	G112	V171	E235
G54	D113	T172	G236
G55	Q114	L173	R237
G56	I115	R174	N238
H57	Q116	L175	F239
S117	S117	R176	G240
V119	G118	S177	K241
D120	V119	G178	H242
A121	M180	E179	P243
A122	A121	M181	V244
K182	I123	T245	T246
V183	K182	W247	W247
E184	E184	G248	G248
A185	A185	V249	V249



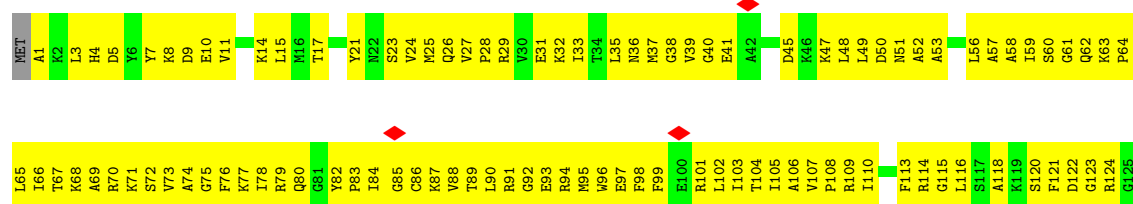
• Molecule 11: 50S ribosomal protein L3

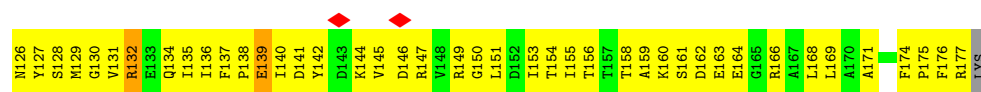


• Molecule 12: 50S ribosomal protein L4

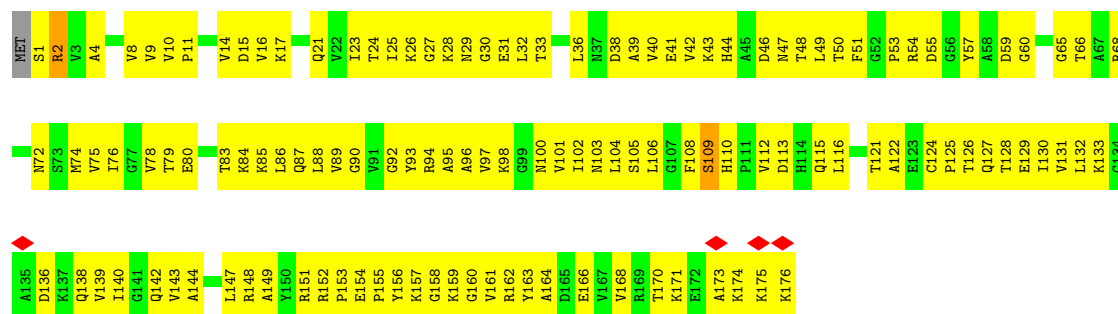
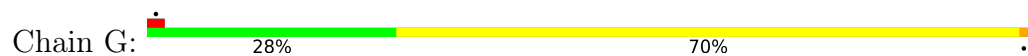


• Molecule 13: 50S ribosomal protein L5

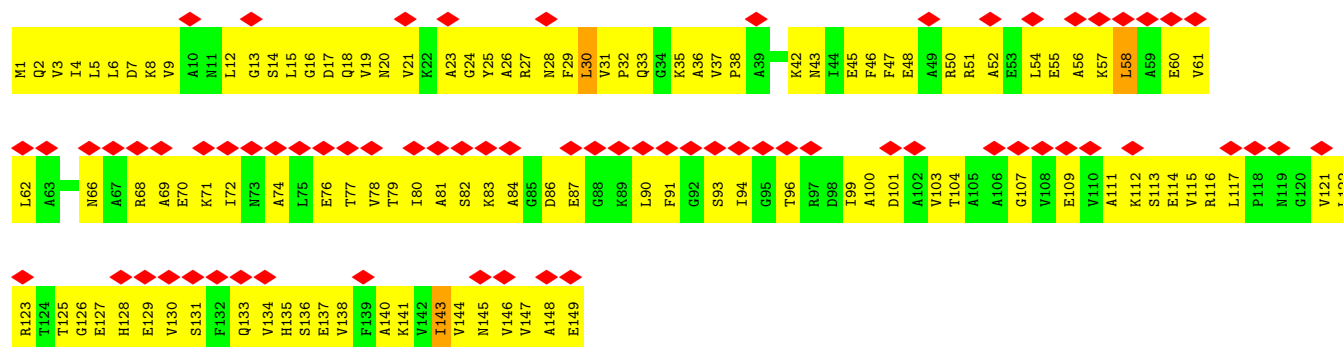




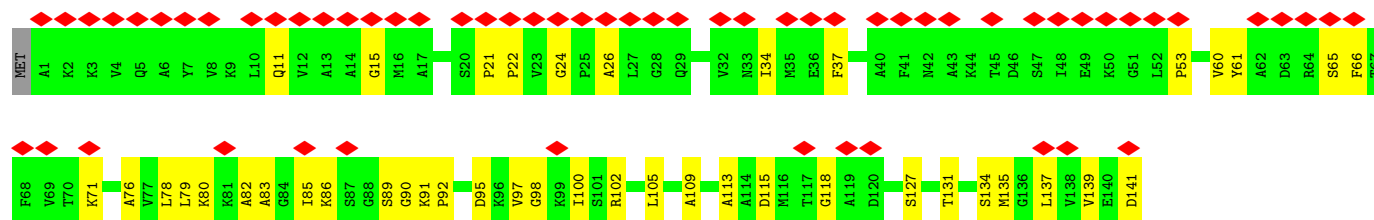
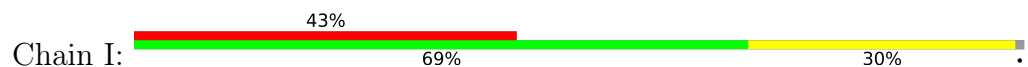
• Molecule 14: 50S ribosomal protein L6



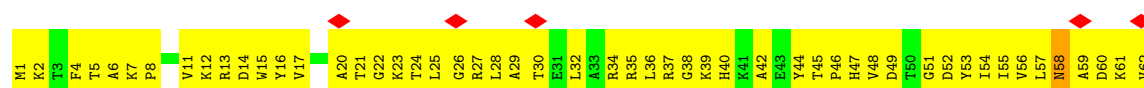
• Molecule 15: 50S ribosomal protein L9

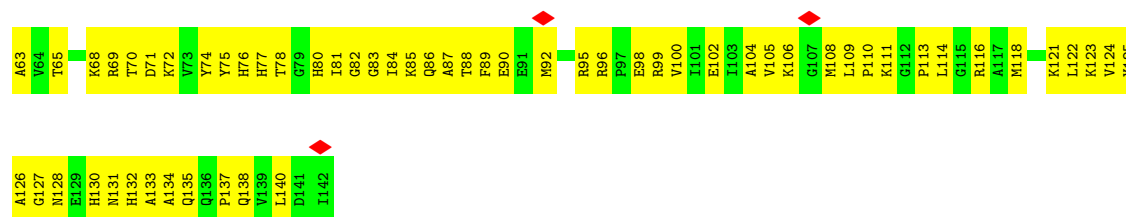


• Molecule 16: 50S ribosomal protein L11

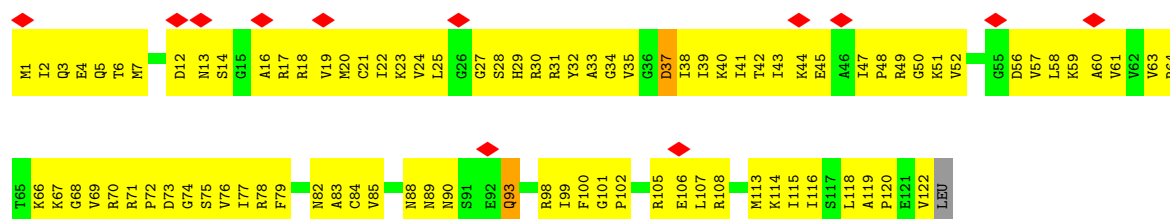


• Molecule 17: 50S ribosomal protein L13

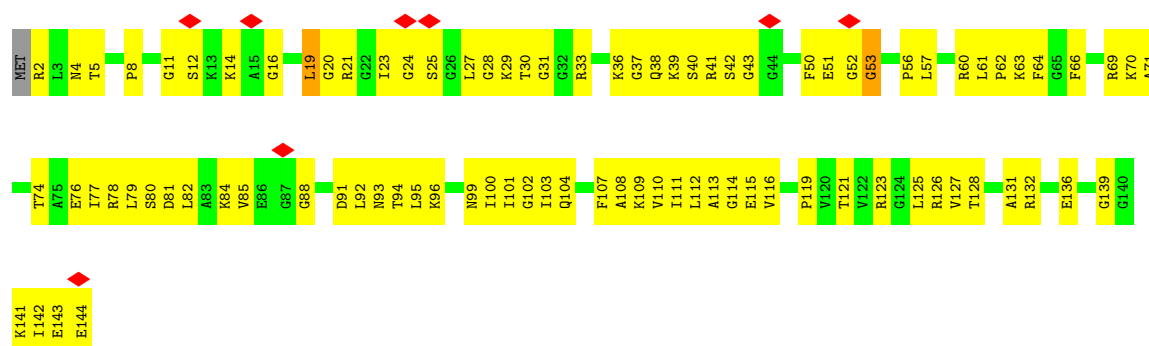




• Molecule 18: 50S ribosomal protein L14



• Molecule 19: 50S ribosomal protein L15



• Molecule 20: 50S ribosomal protein L16



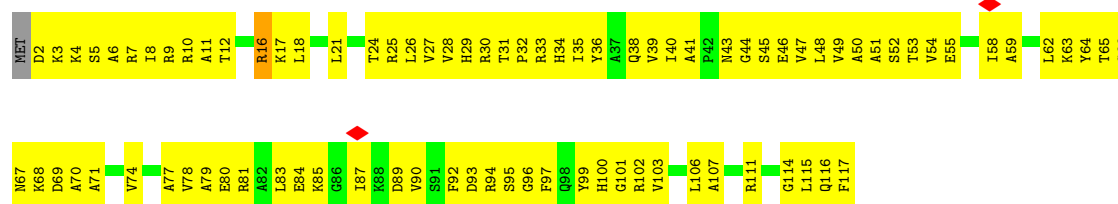
• Molecule 21: 50S ribosomal protein L17

Chain N:  20% 74% 6%

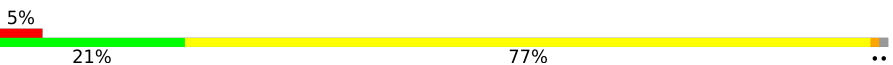


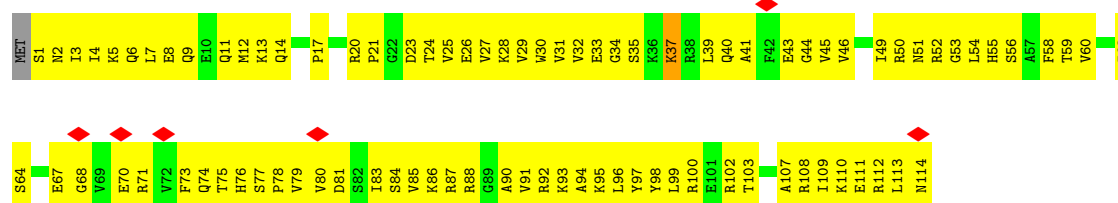
- Molecule 22: 50S ribosomal protein L18

Chain O:  25% 74% 1%



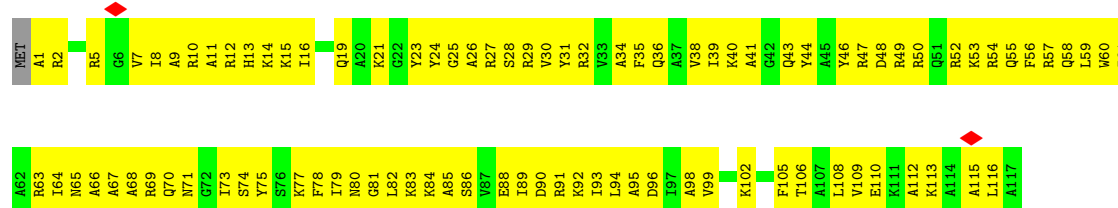
- Molecule 23: 50S ribosomal protein L19

Chain P:  5% 21% 77%



- Molecule 24: 50S ribosomal protein L20

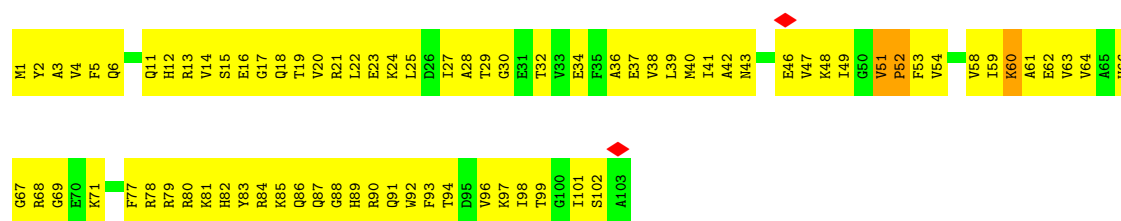
Chain Q:  21% 78% 1%



- Molecule 25: 50S ribosomal protein L21

Chain R:  23% 74% 3%





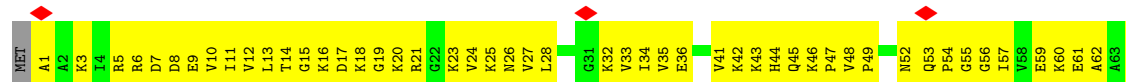
• Molecule 26: 50S ribosomal protein L22



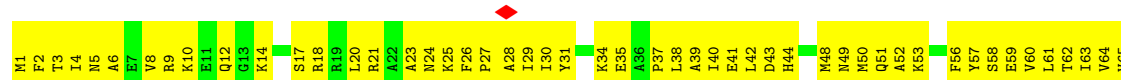
• Molecule 27: 50S ribosomal protein L23

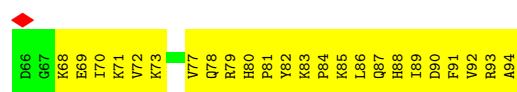


• Molecule 28: 50S ribosomal protein L24

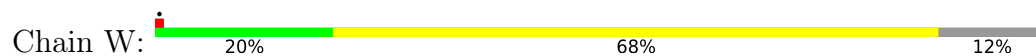


• Molecule 29: 50S ribosomal protein L25

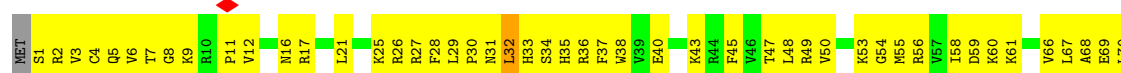




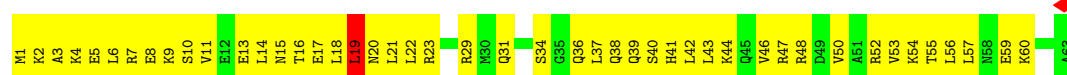
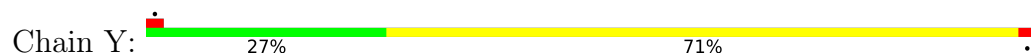
• Molecule 30: 50S ribosomal protein L27



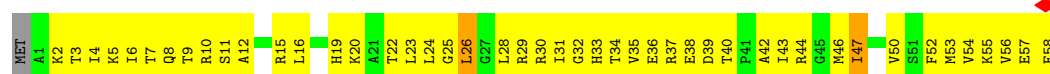
• Molecule 31: 50S ribosomal protein L28



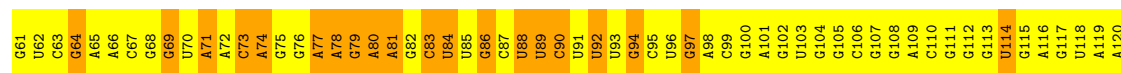
• Molecule 32: 50S ribosomal protein L29



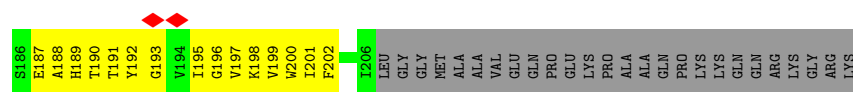
• Molecule 33: 50S ribosomal protein L30



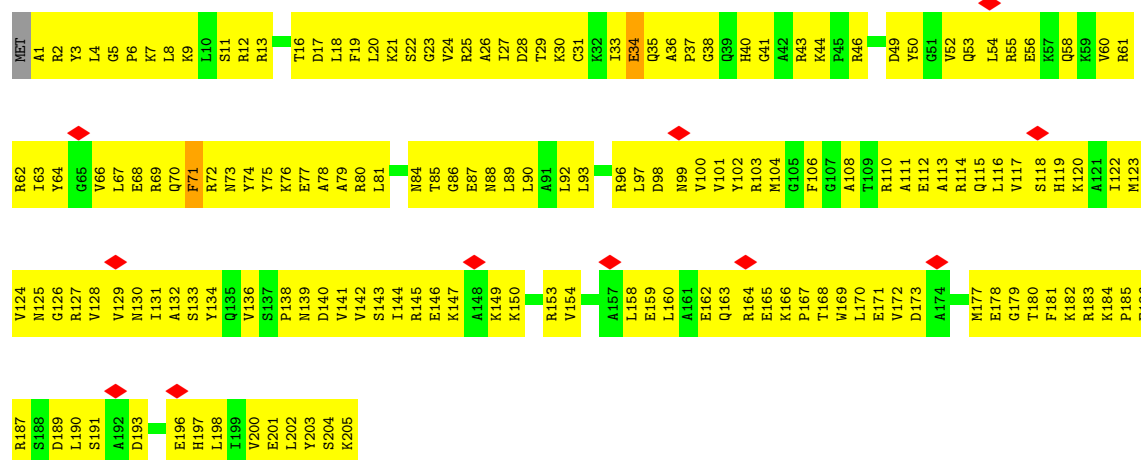
• Molecule 34: 16S ribosomal RNA



C1141	A1081	A1021	U961	A901	C941	A781	G721	G661	G541	G481	U421	G361	G301	G241	A181	U121
G1142	A1082	A1022	C962	G902	U942	A782	G722	U662	G542	A482	C422	G362	G302	G242	A182	G122
G1143	U1083	U1023	G963	G903	U943	C783	U723	A663	G543	C483	G423	A363	A303	A243	C183	U123
G1144	G1084	G1024	A964	U904	G944	A784	G724	G664	G544	G484	G424	A364	A304	A244	G184	U124
A1145	U1085	U1025	U965	U905	A945	G785	G725	A665	G545	U485	U425	U365	G305	U245	U185	U125
A1146	U1086	G1026	G966	A906	G946	G786	G726	G666	A546	A486	U426	A366	A306	A246	C186	G126
C1147	G1087	C1027	C967	A907	G947	A787	G727	G667	A547	A487	U427	U367	C307	G247	G187	G127
U1148	G1088	G1028	A968	A908	C948	U788	A728	G668	G548	C488	G428	U368	C308	C248	C188	G128
C1149	U1089	U1029	A969	A909	C949	U789	A729	G669	G549	C489	U429	U369	A309	U249	A189	A129
A1150	U1090	U1030	C970	C910	U950	A790	G730	G670	G550	C490	A430	C370	A310	A250	A190	A130
A1151	U1091	C1031	G971	U911	U951	G791	G731	G671	U551	C491	A431	C371	C311	A251	G191	A131
A1152	A1092	G1032	C972	C912	G952	A792	G732	U672	U552	C492	A432	C372	A312	U252	A192	C132
G1153	A1093	G1033	G973	A913	C953	U793	G733	A673	A553	A493	C433	A373	A313	A253	C193	U133
G1154	G1094	G1034	A974	A914	U954	A794	G734	G674	A554	G494	U434	A374	C314	G254	C194	G134
U1155	U1095	A1035	U975	U915	U955	C795	C735	A675	U555	A495	A435	U375	A315	G255	A195	C135
G1156	C1096	A1036	G976	U916	C956	C796	C736	A676	C556	A496	A436	G376	A316	G256	A196	C136
A1157	C1097	C1037	A977	A917	C957	U797	C737	U677	G557	C497	U437	G377	A317	G257	A197	U137
C1158	C1098	C1038	A978	A918	G958	U798	C738	G678	G558	A498	U438	G378	G318	G258	G198	G138
U1159	G1099	G1039	C979	A919	G959	G799	C739	C679	A559	A499	U439	C379	G319	G259	A199	A139
G1160	C1100	U1040	C980	U920	A860	G800	U740	G680	A560	G500	C440	C380	A320	G260	G200	U140
C1161	A1101	G1041	U981	U921	A861	G801	G741	C681	U561	C501	A441	C381	A321	U261	G201	G141
C1162	U1042	A1042	U982	G922	C862	A802	G742	G682	U562	A502	C442	A382	G322	A262	G202	G142
A1163	C1103	G1043	A983	A923	U863	G803	A743	G683	A563	C503	C443	A383	U323	A263	G203	A143
G1164	G1104	A1044	C984	C924	A864	U804	G744	G684	C564	C504	G444	G384	G324	G264	G204	G144
U1165	A1105	G1045	C985	G925	A865	C805	G745	G685	U565	G505	G445	G385	A325	G265	A205	G145
G1166	G1106	A1046	U986	G926	C866	C806	A746	U686	G566	G506	G446	C386	G326	G266	C206	G146
A1167	C1107	G1047	G987	G927	U867	A807	A747	A687	G567	C507	G447	U387	A327	G267	C207	G147
U1168	U1048	G1048	C988	G928	C868	G808	G748	G688	G568	U508	A448	C388	U208	G278	U218	G148
A1169	U1049	U1049	U989	G929	G869	G809	A749	C689	C569	A509	A449	A389	A329	C269	U209	A149
A1170	A1110	G1050	C990	C930	U870	C810	C750	G690	G570	A510	C450	U390	C210	A270	U150	U150
C1171	A1111	C1051	U991	C931	U871	C811	U751	G691	U571	C511	A451	G391	G331	G271	G211	A151
C1172	C1112	U1052	U992	C932	A872	G812	G752	U692	A572	U512	A452	C392	G332	C272	G212	A152
U1173	C1113	G1053	G993	G933	A873	U813	A753	G693	A573	C513	C453	A393	U333	U273	G213	C153
G1174	C1114	A1054	A994	C934	G874	A814	G754	A694	A574	C514	G454	G394	C334	A274	C214	U154
G1175	U1115	U1055	C995	A935	U875	A815	G755	A695	G575	A515	G455	C395	G335	G275	C215	A155
A1176	U1116	U1056	A996	C936	C876	A816	C756	A696	C576	U516	A456	C396	A336	G276	U216	C156
G1177	A1117	G1057	U997	A937	G877	C817	U757	U697	G577	G517	G457	A397	G337	C277	C217	U157
G1178	U1118	G1058	C998	A938	A878	G818	C758	G698	C578	C518	U458	U398	A338	G278	U218	G158
A1179	C1119	C1059	C999	G939	C879	A819	A759	C699	A579	C519	A459	G399	C339	A279	U219	G159
A1180	C1120	U1060	A1000	C940	C880	U820	G760	G700	C580	A520	A460	C400	U340	C280	G220	A160
G1181	G1061	G1061	C1001	G941	G881	G821	G761	U701	G581	C521	A461	C401	C341	G281	C221	A161
G1182	U1122	U1062	G1002	G942	C882	U822	U762	A702	C582	C522	A462	C402	C342	A282	C222	A162
U1183	G1123	C1063	G1003	U943	C883	G823	G763	G703	A583	A523	U463	C403	U343	U283	A223	C163
G1184	G1124	A1064	U1004	G944	U884	G824	C764	A704	G584	G524	U464	C404	A344	C284	U224	G164
G1185	U1125	U1065	A1005	G945	G885	A825	G765	G705	G585	C525	A465	U405	C345	C285	C225	G165
U1186	U1126	C1066	G1006	A946	G886	C826	A766	A706	G586	C526	A466	C406	G346	C286	G226	U166
G1187	G1127	A1067	U1007	G947	G887	U827	A767	U707	G587	G527	U467	U407	G347	U287	A167	G167
A1188	U1068	G1068	U1008	C948	G888	U828	A768	C708	G588	C528	A468	U408	G348	A288	G168	G168
U1189	C1129	C1069	U1009	A949	A889	G829	G769	U709	U589	G529	C469	U409	A349	G289	U229	C169
G1190	A1130	U1070	U1010	U950	G890	G830	C770	G710	U590	G530	C470	G410	G350	C290	U170	G170
A1191	G1131	C1071	C1011	G951	U891	A831	G771	G711	U591	U531	U471	A411	G351	U291	U231	A171
C1192	C1132	G1072	A1012	U952	A892	G832	A772	A712	G592	A532	U472	A412	C352	G292	G232	A172
G1193	G1133	U1073	G1013	G953	C893	C833	G773	G713	U593	A533	U473	G413	A353	G293	C233	U173
U1194	G1134	G1074	A1014	G954	G894	U834	G774	G714	U594	U534	G474	A414	A354	U294	G234	A174
C1195	U1135	U1075	G1015	U955	G895	U835	G775	A715	A595	A535	U475	A415	C355	C295	C235	C175
A1196	A1136	U1076	A1016	U956	C896	G836	G776	A716	A596	A536	U476	A416	A356	U296	A236	C176
A1197	C1137	G1077	U1017	U957	C897	U837	A777	U717	G597	C537	C477	G417	G357	G297	G237	G177
G1198	G1138	U1078	G1018	A958	G898	G838	G778	A718	U598	G538	A478	C418	U358	A298	A238	C178
U1199	C1139	G1079	A1019	A959	C899	C839	C779	C719	U599	G539	U479	C419	G359	G299	G239	A179
C1200	C1140	A1080	G1020	U960	A900	C940	U780	C720	A600	G540	U480	U420	G360	A300	G240	U180



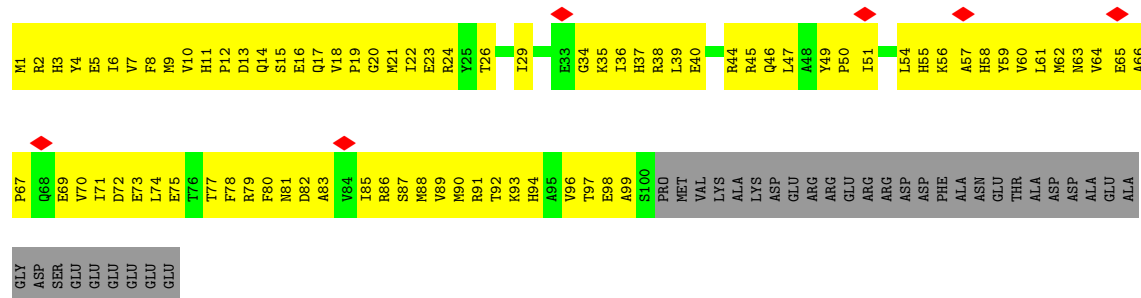
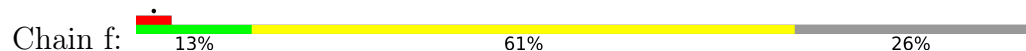
• Molecule 37: 30S ribosomal protein S4



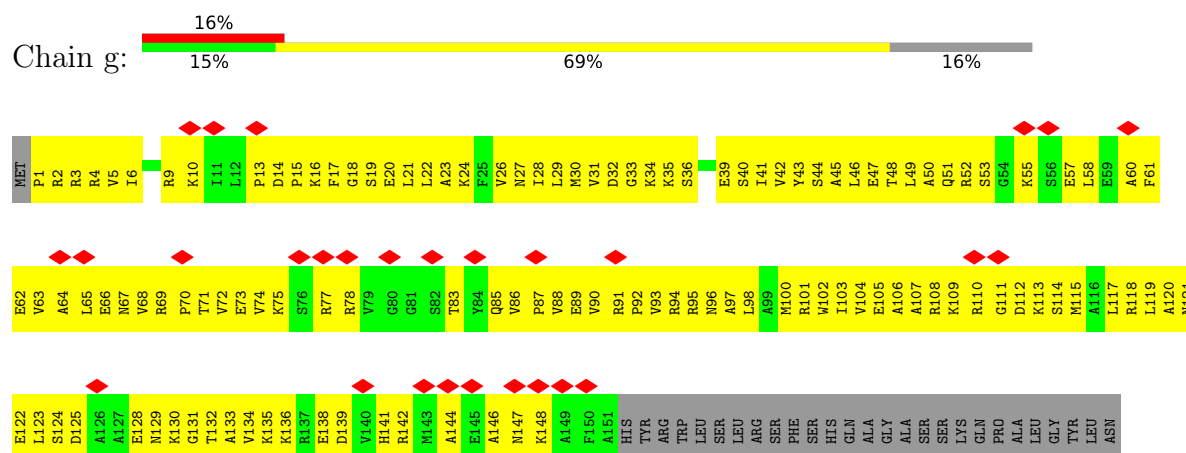
• Molecule 38: 30S ribosomal protein S5



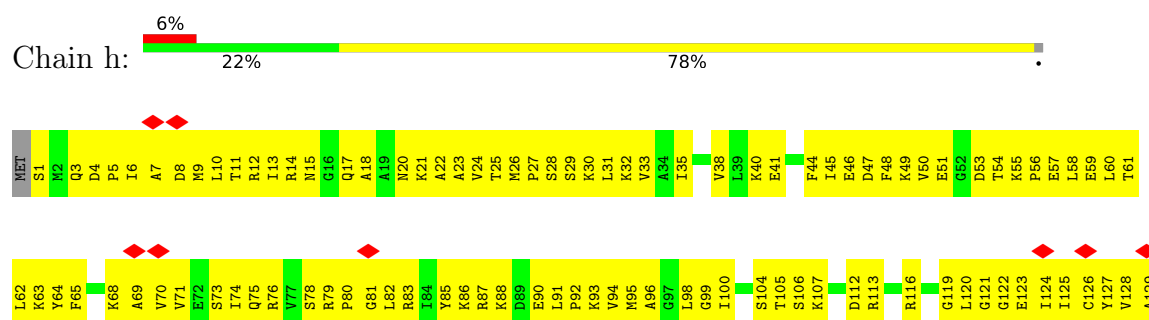
• Molecule 39: 30S ribosomal protein S6



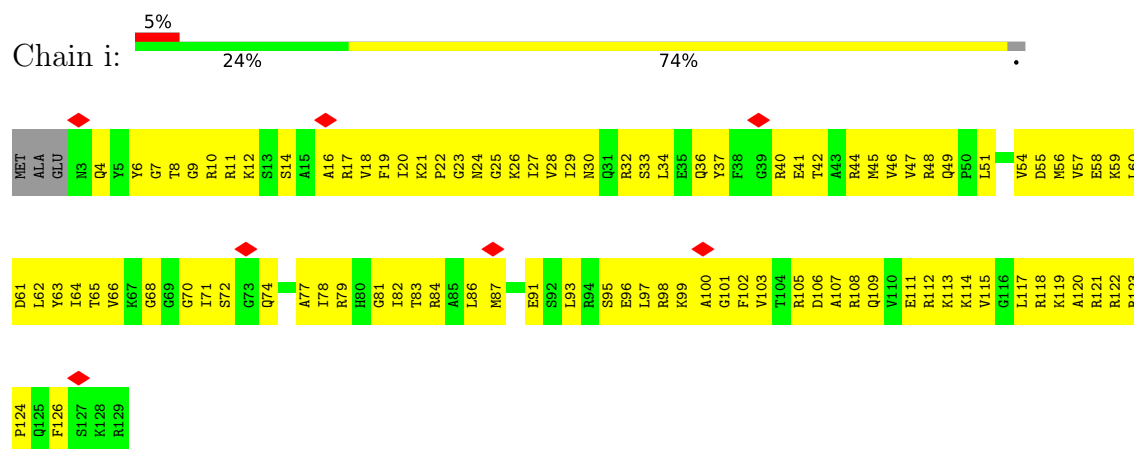
- Molecule 40: 30S ribosomal protein S7



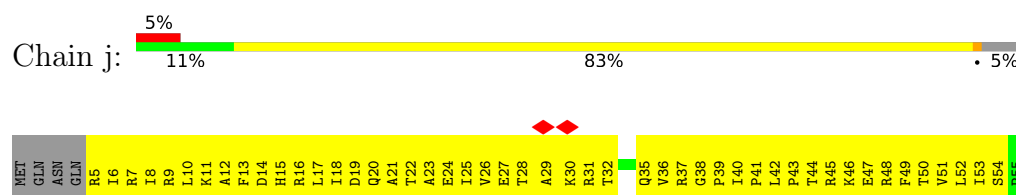
- Molecule 41: 30S ribosomal protein S8



- Molecule 42: 30S ribosomal protein S9

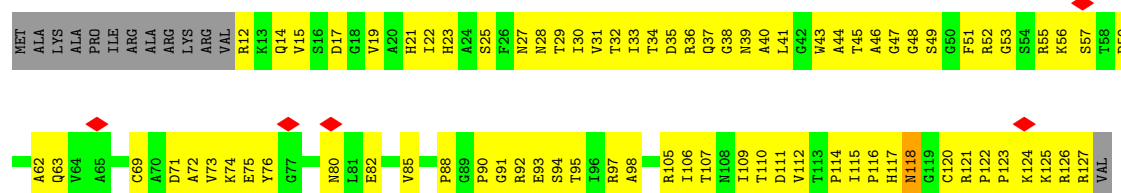
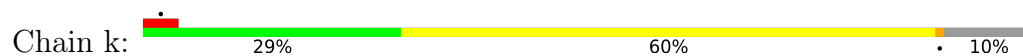


- Molecule 43: 30S ribosomal protein S10





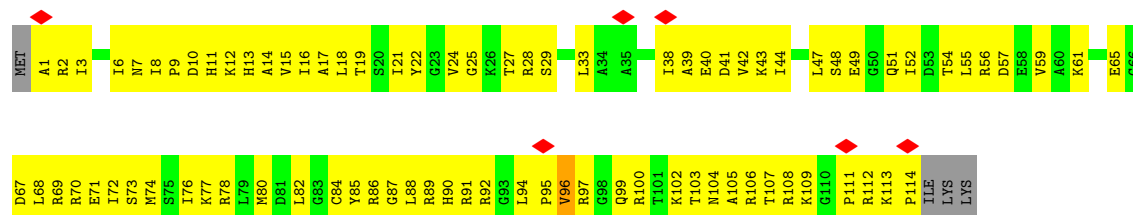
- Molecule 44: 30S ribosomal protein S11



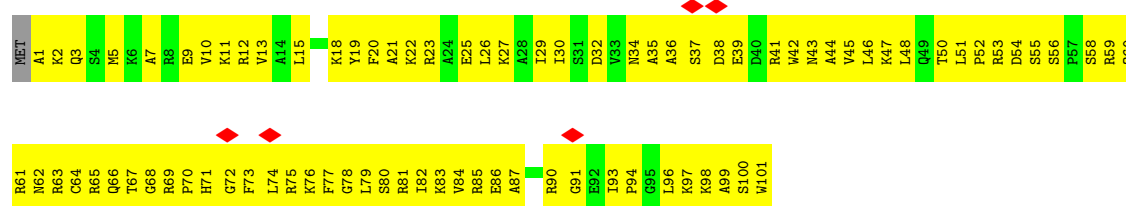
- Molecule 45: 30S ribosomal protein S12



- Molecule 46: 30S ribosomal protein S13



- Molecule 47: 30S ribosomal protein S14



- Molecule 48: 30S ribosomal protein S15

Chain o: 

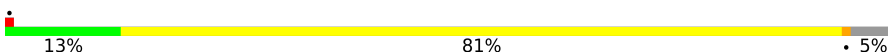


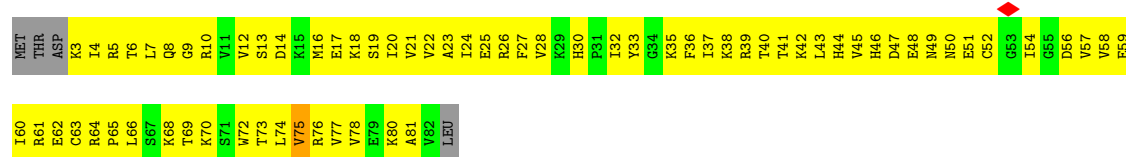
- Molecule 49: 30S ribosomal protein S16

Chain p: 

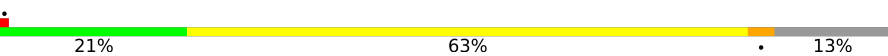


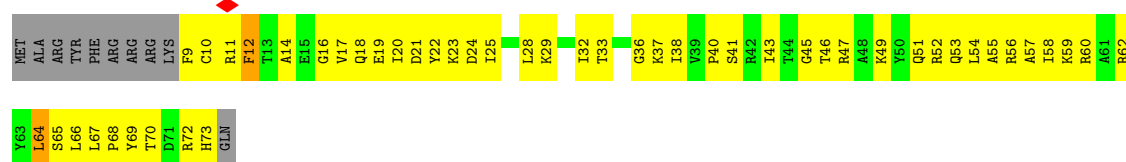
- Molecule 50: 30S ribosomal protein S17

Chain q: 

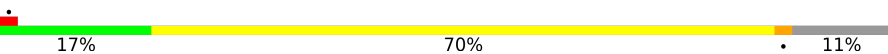


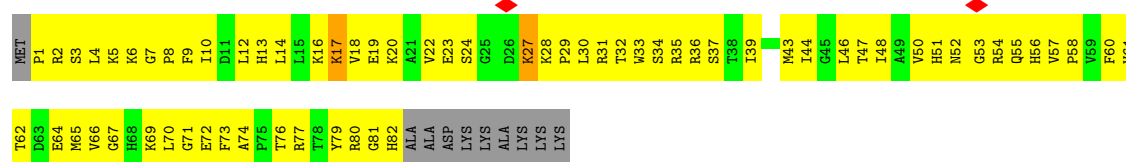
- Molecule 51: 30S ribosomal protein S18

Chain r: 



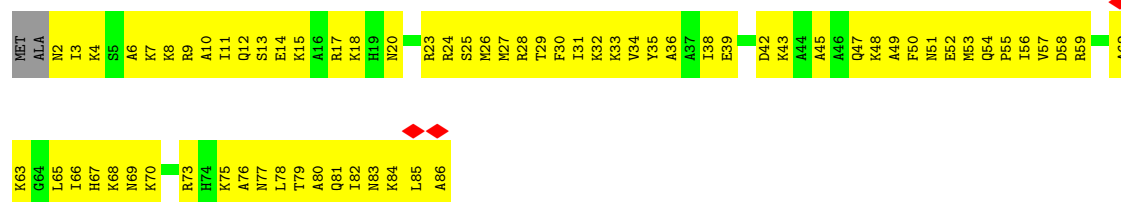
- Molecule 52: 30S ribosomal protein S19

Chain s: 



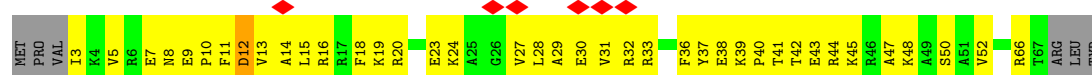
- Molecule 53: 30S ribosomal protein S20

Chain t: 



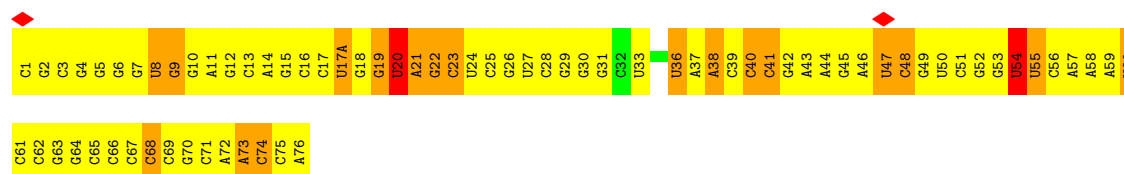
- Molecule 54: 30S ribosomal protein S21

Chain u: 

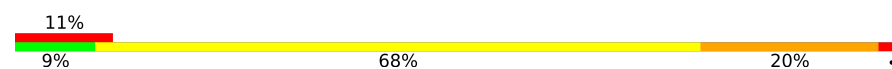


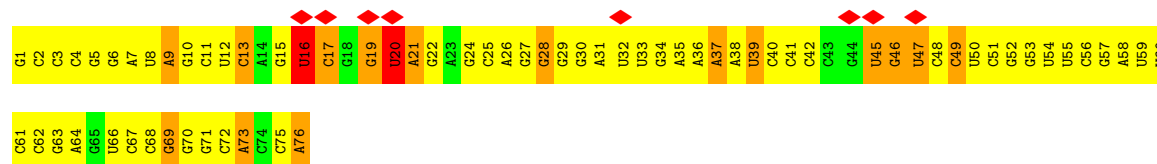
- Molecule 55: P-site tRNA(fMet)

Chain v: 



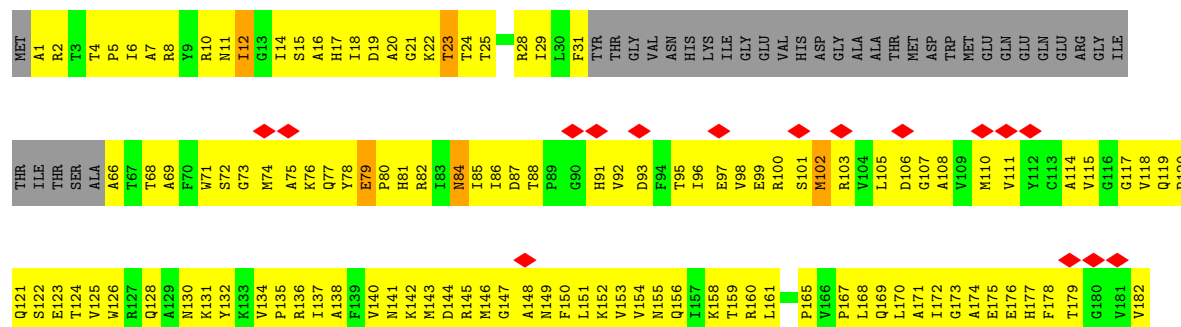
- Molecule 56: P-site fMet-Phe-tRNA(Phe)

Chain w: 



- Molecule 57: Elongation factor G

Chain x: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	6168	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	10.963	Depositor
Minimum map value	-5.358	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	1.5	Depositor
Map size ($\text{\AA}$)	334.08, 334.08, 334.08	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	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: OMC, MIA, 3TD, 5MC, 2MG, 4OC, GDP, MA6, PSU, FME, 5MU, 4SU, 6MZ, ZN, 2MA, UR3, G7M, 1MG, AM2, OMU, OMG, H2U

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	0.85	0/450	1.22	0/599
2	1	0.83	0/416	1.34	2/554 (0.4%)
3	2	0.91	0/380	1.21	0/498
4	3	0.91	0/513	1.26	3/676 (0.4%)
5	4	0.83	0/303	1.40	2/397 (0.5%)
6	5	0.31	0/646	0.76	0/898
7	6	0.78	0/531	1.24	1/709 (0.1%)
8	A	0.84	0/69266	0.89	44/108055 (0.0%)
9	B	0.87	0/2873	0.92	0/4478
10	C	0.80	0/2121	1.17	4/2852 (0.1%)
11	D	0.79	0/1586	1.09	1/2134 (0.0%)
12	E	0.82	0/1571	1.13	1/2113 (0.0%)
13	F	0.83	0/1434	1.11	2/1926 (0.1%)
14	G	0.83	0/1343	1.17	5/1816 (0.3%)
15	H	0.64	0/1122	1.03	2/1515 (0.1%)
16	I	0.41	0/692	0.90	1/960 (0.1%)
17	J	0.89	0/1152	1.17	1/1551 (0.1%)
18	K	0.79	0/947	1.17	1/1268 (0.1%)
19	L	0.80	0/1054	1.33	3/1403 (0.2%)
20	M	0.87	0/1093	1.18	2/1460 (0.1%)
21	N	0.87	1/973 (0.1%)	1.26	2/1301 (0.2%)
22	O	0.79	0/902	1.04	1/1209 (0.1%)
23	P	0.86	0/929	1.14	1/1242 (0.1%)
24	Q	0.99	0/960	1.18	1/1278 (0.1%)
25	R	0.82	0/829	1.11	1/1107 (0.1%)
26	S	0.91	0/864	1.23	5/1156 (0.4%)
27	T	0.91	0/744	1.20	0/994
28	U	0.97	0/787	1.23	0/1051
29	V	0.98	0/766	1.11	0/1025
30	W	0.82	0/582	1.20	0/769
31	X	0.90	0/635	1.25	1/848 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Y	0.95	0/510	1.20	0/677
33	Z	0.96	0/453	1.24	3/605 (0.5%)
34	a	0.77	2/36725 (0.0%)	0.85	25/57285 (0.0%)
35	b	0.64	0/1735	0.93	0/2338
36	c	0.78	0/1651	1.00	1/2225 (0.0%)
37	d	0.74	0/1665	1.06	0/2227
38	e	0.80	0/1154	1.11	1/1554 (0.1%)
39	f	0.75	0/835	0.99	0/1128
40	g	0.68	0/1195	0.96	1/1602 (0.1%)
41	h	0.72	0/989	0.95	0/1326
42	i	0.70	0/1034	1.07	0/1375
43	j	0.72	0/796	1.00	1/1077 (0.1%)
44	k	0.73	0/885	1.04	0/1195
45	l	0.84	0/969	1.23	0/1300
46	m	0.76	0/892	1.02	1/1193 (0.1%)
47	n	0.73	0/811	1.08	0/1081
48	o	0.78	0/722	1.04	0/964
49	p	0.75	0/659	1.04	0/884
50	q	0.83	0/657	1.08	1/881 (0.1%)
51	r	0.76	1/544 (0.2%)	1.08	1/731 (0.1%)
52	s	0.69	0/675	1.16	4/908 (0.4%)
53	t	0.99	0/671	1.05	0/888
54	u	0.65	0/512	1.08	0/683
55	v	0.73	0/1745	0.87	0/2716
56	w	0.59	0/1650	0.95	12/2569 (0.5%)
57	x	0.75	0/5288	1.09	7/7152 (0.1%)
58	y	0.31	0/11	0.86	0/13
59	z	0.50	0/230	0.80	1/355 (0.3%)
All	All	0.81	4/164127 (0.0%)	0.95	146/244774 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
4	3	0	1
25	R	0	1
28	U	0	1
32	Y	0	1
35	b	0	1
37	d	0	3

Continued on next page...

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Mol	Chain	#Chirality outliers	#Planarity outliers
54	u	0	1
57	x	0	1
All	All	0	10

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	a	1081	A	O3'-P	6.75	1.71	1.61
51	r	64	LEU	CA-C	-5.76	1.42	1.52
21	N	107	ASN	C-N	-5.35	1.22	1.33
34	a	921	U	C5'-C4'	5.15	1.58	1.51

The worst 5 of 146 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	w	9	A	C4'-C3'-O3'	12.57	128.25	109.40
8	A	2381	A	C4'-C3'-O3'	12.54	131.81	113.00
8	A	1789	A	C2'-C3'-O3'	11.62	131.13	113.70
56	w	45	U	C4'-C3'-O3'	10.83	125.64	109.40
8	A	2289	G	C3'-C2'-O2'	10.02	125.73	110.70

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	3	30	HIS	Peptide
25	R	51	VAL	Peptide
28	U	97	SER	Peptide
32	Y	19	LEU	Peptide
35	b	87	ASP	Peptide

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	90	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	1	409	0	440	89	0
3	2	377	0	418	93	0
4	3	504	0	574	86	0
5	4	302	0	341	71	0
6	5	647	0	336	49	0
7	6	522	0	521	128	0
8	A	62338	0	31367	10600	0
9	B	2570	0	1301	492	0
10	C	2082	0	2157	391	0
11	D	1565	0	1616	278	0
12	E	1552	0	1619	218	0
13	F	1410	0	1447	286	0
14	G	1323	0	1374	202	0
15	H	1111	0	1148	184	0
16	I	693	0	347	51	0
17	J	1129	0	1162	197	0
18	K	938	0	1012	149	0
19	L	1045	0	1117	208	0
20	M	1074	0	1157	185	0
21	N	960	0	1000	185	0
22	O	892	0	923	147	0
23	P	917	0	965	158	0
24	Q	947	0	1022	162	0
25	R	816	0	839	140	0
26	S	857	0	922	151	0
27	T	738	0	807	119	0
28	U	779	0	834	177	0
29	V	753	0	780	149	0
30	W	575	0	592	103	0
31	X	625	0	655	96	0
32	Y	509	0	543	80	0
33	Z	449	0	491	74	0
34	a	33050	0	16651	5697	0
35	b	1704	0	1732	238	0
36	c	1624	0	1699	280	0
37	d	1643	0	1710	309	0
38	e	1141	0	1170	209	0
39	f	817	0	808	132	0
40	g	1181	0	1240	189	0
41	h	979	0	1034	161	0
42	i	1022	0	1070	169	0
43	j	786	0	828	161	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	k	869	0	878	116	0
45	l	955	0	1019	164	0
46	m	883	0	944	156	0
47	n	799	0	841	151	0
48	o	714	0	737	108	0
49	p	649	0	666	100	0
50	q	648	0	691	128	0
51	r	535	0	552	74	0
52	s	658	0	685	127	0
53	t	665	0	714	112	0
54	u	506	0	502	63	0
55	v	1642	0	839	202	0
56	w	1631	0	837	153	0
57	x	5192	0	5187	883	0
58	y	21	0	19	5	0
59	z	208	0	104	19	0
60	6	1	0	0	0	0
61	a	37	0	41	4	0
62	x	28	0	11	13	0
All	All	152440	0	103497	23374	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 95.

The worst 5 of 23374 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)
5:4:11:CYS:SG	5:4:27:CYS:SG	1.34	1.33
56:w:5:G:N2	56:w:68:C:O2	1.70	1.24
34:a:246:A:C8	34:a:281:G:N2	2.09	1.21
8:A:529:A:N6	8:A:2041:U:O2	1.78	1.17
8:A:1915:3TD:O4'	8:A:1915:3TD:C1'	1.67	1.17

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%)	46 (96%)	2 (4%)	0	100	100
3	2	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
4	3	62/65 (95%)	56 (90%)	5 (8%)	1 (2%)	7	37
5	4	36/38 (95%)	31 (86%)	5 (14%)	0	100	100
6	5	129/165 (78%)	107 (83%)	22 (17%)	0	100	100
7	6	64/70 (91%)	57 (89%)	5 (8%)	2 (3%)	3	22
10	C	269/273 (98%)	245 (91%)	24 (9%)	0	100	100
11	D	207/209 (99%)	190 (92%)	17 (8%)	0	100	100
12	E	199/201 (99%)	191 (96%)	8 (4%)	0	100	100
13	F	175/179 (98%)	157 (90%)	18 (10%)	0	100	100
14	G	174/177 (98%)	163 (94%)	11 (6%)	0	100	100
15	H	147/149 (99%)	126 (86%)	21 (14%)	0	100	100
16	I	139/142 (98%)	124 (89%)	14 (10%)	1 (1%)	18	56
17	J	140/142 (99%)	134 (96%)	6 (4%)	0	100	100
18	K	120/123 (98%)	109 (91%)	11 (9%)	0	100	100
19	L	141/144 (98%)	124 (88%)	17 (12%)	0	100	100
20	M	134/136 (98%)	122 (91%)	12 (9%)	0	100	100
21	N	118/127 (93%)	109 (92%)	9 (8%)	0	100	100
22	O	114/117 (97%)	107 (94%)	7 (6%)	0	100	100
23	P	112/115 (97%)	101 (90%)	11 (10%)	0	100	100
24	Q	115/118 (98%)	113 (98%)	2 (2%)	0	100	100
25	R	101/103 (98%)	91 (90%)	9 (9%)	1 (1%)	12	48
26	S	108/110 (98%)	99 (92%)	9 (8%)	0	100	100
27	T	91/100 (91%)	81 (89%)	9 (10%)	1 (1%)	11	46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	U	100/104 (96%)	89 (89%)	10 (10%)	1 (1%)	12	48
29	V	92/94 (98%)	92 (100%)	0	0	100	100
30	W	73/85 (86%)	68 (93%)	5 (7%)	0	100	100
31	X	75/78 (96%)	70 (93%)	5 (7%)	0	100	100
32	Y	61/63 (97%)	57 (93%)	3 (5%)	1 (2%)	7	37
33	Z	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
35	b	216/240 (90%)	180 (83%)	35 (16%)	1 (0%)	24	63
36	c	204/233 (88%)	193 (95%)	11 (5%)	0	100	100
37	d	203/206 (98%)	172 (85%)	30 (15%)	1 (0%)	24	63
38	e	155/167 (93%)	140 (90%)	15 (10%)	0	100	100
39	f	98/135 (73%)	89 (91%)	9 (9%)	0	100	100
40	g	149/179 (83%)	134 (90%)	15 (10%)	0	100	100
41	h	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
42	i	125/130 (96%)	106 (85%)	19 (15%)	0	100	100
43	j	96/103 (93%)	78 (81%)	18 (19%)	0	100	100
44	k	114/129 (88%)	103 (90%)	11 (10%)	0	100	100
45	l	121/124 (98%)	104 (86%)	16 (13%)	1 (1%)	16	54
46	m	112/118 (95%)	100 (89%)	12 (11%)	0	100	100
47	n	99/102 (97%)	90 (91%)	9 (9%)	0	100	100
48	o	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
49	p	80/82 (98%)	68 (85%)	12 (15%)	0	100	100
50	q	78/84 (93%)	65 (83%)	13 (17%)	0	100	100
51	r	63/75 (84%)	54 (86%)	9 (14%)	0	100	100
52	s	80/92 (87%)	72 (90%)	8 (10%)	0	100	100
53	t	83/87 (95%)	82 (99%)	1 (1%)	0	100	100
54	u	63/71 (89%)	51 (81%)	12 (19%)	0	100	100
57	x	666/704 (95%)	588 (88%)	71 (11%)	7 (1%)	11	46
All	All	6516/6924 (94%)	5877 (90%)	621 (10%)	18 (0%)	37	72

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	6	64	PHE

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Mol	Chain	Res	Type
57	x	387	LEU
57	x	545	PRO
57	x	546	GLY
4	3	31	ILE

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%)	214 (99%)	2 (1%)	70	78
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%)	136 (99%)	1 (1%)	76	81
15	H	114/114 (100%)	112 (98%)	2 (2%)	51	68
17	J	116/116 (100%)	116 (100%)	0	100	100
18	K	103/104 (99%)	99 (96%)	4 (4%)	28	49
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	R	84/84 (100%)	84 (100%)	0	100	100
26	S	93/93 (100%)	92 (99%)	1 (1%)	65	76
27	T	80/84 (95%)	80 (100%)	0	100	100
28	U	83/85 (98%)	83 (100%)	0	100	100
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%)	55 (100%)	0	100	100
33	Z	48/49 (98%)	48 (100%)	0	100	100
35	b	180/198 (91%)	178 (99%)	2 (1%)	65	76
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%)	113 (99%)	1 (1%)	70	78
39	f	87/116 (75%)	87 (100%)	0	100	100
40	g	124/147 (84%)	123 (99%)	1 (1%)	73	80
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%)	88 (99%)	1 (1%)	65	76
45	l	103/104 (99%)	102 (99%)	1 (1%)	68	78
46	m	92/96 (96%)	92 (100%)	0	100	100
47	n	79/84 (94%)	79 (100%)	0	100	100
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%)	72 (100%)	0	100	100
53	t	65/66 (98%)	65 (100%)	0	100	100
54	u	46/61 (75%)	46 (100%)	0	100	100
57	x	551/578 (95%)	546 (99%)	5 (1%)	70	78
58	y	1/1 (100%)	1 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	5178/5408 (96%)	5155 (100%)	23 (0%)	81 84

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	e	81	GLN
45	l	46	SER
44	k	118	ASN
57	x	23	THR
15	H	143	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
52	s	68	HIS
57	x	504	HIS
23	P	11	GLN
22	O	98	GLN
57	x	513	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	a	1539/1542 (99%)	448 (29%)	0
55	v	76/77 (98%)	20 (26%)	0
56	w	75/76 (98%)	23 (30%)	0
59	z	9/33 (27%)	3 (33%)	0
8	A	2902/2903 (99%)	594 (20%)	39 (1%)
9	B	119/120 (99%)	21 (17%)	3 (2%)
All	All	4720/4751 (99%)	1109 (23%)	42 (0%)

5 of 1109 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	A	10	A
8	A	34	U
8	A	35	G
8	A	46	G
8	A	62	U

5 of 42 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	A	2287	A
8	A	2406	A
8	A	2308	G
8	A	2346	A
8	A	2750	A

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
8	OMU	A	2552	8	19,22,23	2.66	5 (26%)	26,31,34	2.07	6 (23%)
8	OMG	A	2251	56,8	23,26,27	2.43	7 (30%)	33,38,41	2.48	11 (33%)
8	1MG	A	745	8	22,26,27	2.48	7 (31%)	33,39,42	1.94	9 (27%)
8	2MA	A	2503	8	22,25,26	3.54	9 (40%)	33,37,40	2.12	13 (39%)
8	OMC	A	2498	8	19,22,23	3.08	8 (42%)	26,31,34	0.84	0
34	UR3	a	1498	34	19,22,23	2.46	6 (31%)	26,32,35	1.12	2 (7%)
8	5MC	A	747	8	18,22,23	3.41	7 (38%)	26,32,35	1.39	2 (7%)
34	4OC	a	1402	34	20,23,24	3.16	8 (40%)	26,32,35	1.13	3 (11%)
55	4SU	v	8	55	18,21,22	3.41	8 (44%)	26,30,33	2.15	4 (15%)
55	5MU	v	54	55	19,22,23	4.60	7 (36%)	28,32,35	3.73	10 (35%)
8	6MZ	A	2030	8	22,25,26	2.32	7 (31%)	30,36,39	2.66	12 (40%)
34	2MG	a	966	34	23,26,27	1.25	3 (13%)	32,38,41	2.26	7 (21%)
8	PSU	A	955	8	18,21,22	3.55	7 (38%)	22,30,33	1.98	4 (18%)
8	5MC	A	1962	8	18,22,23	2.96	7 (38%)	26,32,35	1.34	2 (7%)
34	MA6	a	1519	34	23,26,27	1.71	5 (21%)	34,38,41	3.25	14 (41%)
34	G7M	a	527	34	23,26,27	2.27	5 (21%)	35,39,42	3.43	12 (34%)
56	4SU	w	8	56	18,21,22	1.89	5 (27%)	26,30,33	2.11	6 (23%)
8	PSU	A	2457	8	18,21,22	3.52	8 (44%)	22,30,33	2.16	4 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
56	PSU	w	39	56	18,21,22	3.75	6 (33%)	22,30,33	2.22	5 (22%)
34	5MC	a	967	34	18,22,23	3.28	7 (38%)	26,32,35	1.29	4 (15%)
56	PSU	w	55	56	18,21,22	1.43	3 (16%)	22,30,33	1.91	5 (22%)
8	6MZ	A	1618	8	22,25,26	2.29	8 (36%)	30,36,39	2.76	11 (36%)
8	2MG	A	2445	8	23,26,27	2.43	7 (30%)	32,38,41	1.66	8 (25%)
55	H2U	v	20	55	18,21,22	3.58	3 (16%)	21,30,33	2.03	5 (23%)
8	PSU	A	2504	8	18,21,22	3.85	7 (38%)	22,30,33	1.84	4 (18%)
34	2MG	a	1207	34	23,26,27	2.47	8 (34%)	32,38,41	1.95	11 (34%)
8	3TD	A	1915	8	18,22,23	7.27	11 (61%)	22,32,35	1.73	2 (9%)
8	PSU	A	2605	8	18,21,22	3.48	7 (38%)	22,30,33	2.27	6 (27%)
8	5MU	A	1939	8	19,22,23	4.63	7 (36%)	28,32,35	3.83	9 (32%)
34	PSU	a	516	34	18,21,22	3.65	7 (38%)	22,30,33	1.90	5 (22%)
56	PSU	w	32	56	18,21,22	3.91	6 (33%)	22,30,33	1.85	6 (27%)
56	MIA	w	37	56	28,31,32	2.53	8 (28%)	40,44,47	2.60	14 (35%)
56	G7M	w	46	56	23,26,27	4.12	16 (69%)	35,39,42	2.90	15 (42%)
8	PSU	A	1917	8	18,21,22	3.68	6 (33%)	22,30,33	1.92	5 (22%)
56	5MU	w	54	56	19,22,23	1.38	6 (31%)	28,32,35	2.21	9 (32%)
58	FME	y	101	58	8,9,10	1.03	1 (12%)	7,9,11	1.05	1 (14%)
34	2MG	a	1516	34	23,26,27	2.69	9 (39%)	32,38,41	2.08	10 (31%)
8	PSU	A	2604	8	18,21,22	3.51	8 (44%)	22,30,33	2.41	6 (27%)
8	PSU	A	2580	8	18,21,22	3.28	7 (38%)	22,30,33	2.54	6 (27%)
34	MA6	a	1518	34	23,26,27	1.64	5 (21%)	34,38,41	3.18	13 (38%)
34	5MC	a	1407	34	18,22,23	3.16	7 (38%)	26,32,35	1.09	2 (7%)
55	PSU	v	55	55	18,21,22	3.82	6 (33%)	22,30,33	1.89	5 (22%)
8	2MG	A	1835	8	23,26,27	2.57	8 (34%)	32,38,41	2.39	8 (25%)
8	PSU	A	746	8	18,21,22	3.74	6 (33%)	22,30,33	1.68	5 (22%)
8	PSU	A	1911	8	18,21,22	3.58	7 (38%)	22,30,33	1.96	5 (22%)
8	G7M	A	2069	8	23,26,27	2.18	7 (30%)	35,39,42	3.22	13 (37%)

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
8	OMU	A	2552	8	-	2/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	OMG	A	2251	56,8	-	0/9/27/28	0/3/3/3
8	1MG	A	745	8	-	0/7/25/26	0/3/3/3
8	2MA	A	2503	8	-	2/7/25/26	0/3/3/3
8	OMC	A	2498	8	-	2/9/27/28	0/2/2/2
34	UR3	a	1498	34	-	2/7/25/26	0/2/2/2
8	5MC	A	747	8	-	2/7/25/26	0/2/2/2
34	4OC	a	1402	34	-	0/9/29/30	0/2/2/2
55	4SU	v	8	55	-	0/7/25/26	0/2/2/2
55	5MU	v	54	55	-	3/7/25/26	0/2/2/2
8	6MZ	A	2030	8	-	3/9/27/28	0/3/3/3
34	2MG	a	966	34	-	3/9/27/28	0/3/3/3
8	PSU	A	955	8	-	0/7/25/26	0/2/2/2
8	5MC	A	1962	8	-	0/7/25/26	0/2/2/2
34	MA6	a	1519	34	-	4/11/29/30	0/3/3/3
34	G7M	a	527	34	-	2/7/25/26	0/3/3/3
56	4SU	w	8	56	-	0/7/25/26	0/2/2/2
8	PSU	A	2457	8	-	0/7/25/26	0/2/2/2
56	PSU	w	39	56	-	3/7/25/26	0/2/2/2
34	5MC	a	967	34	-	2/7/25/26	0/2/2/2
56	PSU	w	55	56	-	1/7/25/26	0/2/2/2
8	6MZ	A	1618	8	-	2/9/27/28	0/3/3/3
8	2MG	A	2445	8	-	2/9/27/28	0/3/3/3
55	H2U	v	20	55	-	1/7/38/39	0/2/2/2
8	PSU	A	2504	8	-	0/7/25/26	0/2/2/2
34	2MG	a	1207	34	-	0/9/27/28	0/3/3/3
8	3TD	A	1915	8	-	2/7/25/26	0/2/2/2
8	PSU	A	2605	8	-	0/7/25/26	0/2/2/2
8	5MU	A	1939	8	-	2/7/25/26	0/2/2/2
34	PSU	a	516	34	-	0/7/25/26	0/2/2/2
56	PSU	w	32	56	-	2/7/25/26	0/2/2/2
56	MIA	w	37	56	-	3/15/33/34	0/3/3/3
56	G7M	w	46	56	-	1/7/25/26	0/3/3/3
8	PSU	A	1917	8	-	0/7/25/26	0/2/2/2
56	5MU	w	54	56	-	0/7/25/26	0/2/2/2
58	FME	y	101	58	-	4/7/9/11	-
34	2MG	a	1516	34	-	0/9/27/28	0/3/3/3
8	PSU	A	2604	8	-	1/7/25/26	0/2/2/2
8	PSU	A	2580	8	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	MA6	a	1518	34	-	0/11/29/30	0/3/3/3
34	5MC	a	1407	34	-	0/7/25/26	0/2/2/2
55	PSU	v	55	55	-	2/7/25/26	0/2/2/2
8	2MG	A	1835	8	-	2/9/27/28	0/3/3/3
8	PSU	A	746	8	-	1/7/25/26	0/2/2/2
8	PSU	A	1911	8	-	0/7/25/26	0/2/2/2
8	G7M	A	2069	8	-	1/7/25/26	0/3/3/3

The worst 5 of 313 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1915	3TD	O4'-C1'	17.31	1.67	1.43
8	A	1915	3TD	C2'-C1'	-15.67	1.33	1.53
8	A	1915	3TD	C6-C5	13.05	1.50	1.35
55	v	20	H2U	C2-N1	12.16	1.53	1.35
8	A	1939	5MU	C2-N1	10.72	1.55	1.38

The worst 5 of 319 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	1939	5MU	C5-C4-N3	13.01	126.41	115.31
34	a	1519	MA6	N1-C6-N6	-12.48	103.44	117.08
34	a	1518	MA6	N1-C6-N6	-12.13	103.82	117.08
55	v	54	5MU	C5-C4-N3	12.04	125.59	115.31
34	a	527	G7M	CN7-N7-C5	10.69	140.05	126.77

There are no chirality outliers.

5 of 57 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
34	a	967	5MC	O4'-C4'-C5'-O5'
34	a	967	5MC	C3'-C4'-C5'-O5'
34	a	1498	UR3	O4'-C1'-N1-C6
34	a	1498	UR3	O4'-C1'-N1-C2
34	a	1519	MA6	C5-C6-N6-C9

There are no ring outliers.

41 monomers are involved in 274 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	2552	OMU	13	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	2251	OMG	8	0
8	A	745	1MG	9	0
8	A	2503	2MA	5	0
8	A	2498	OMC	2	0
34	a	1498	UR3	10	0
8	A	747	5MC	3	0
34	a	1402	4OC	15	0
55	v	8	4SU	6	0
55	v	54	5MU	3	0
8	A	2030	6MZ	5	0
34	a	966	2MG	1	0
8	A	955	PSU	7	0
8	A	1962	5MC	7	0
34	a	1519	MA6	20	0
34	a	527	G7M	5	0
8	A	2457	PSU	3	0
56	w	39	PSU	12	0
34	a	967	5MC	6	0
8	A	1618	6MZ	5	0
8	A	2445	2MG	10	0
55	v	20	H2U	2	0
8	A	2504	PSU	1	0
34	a	1207	2MG	11	0
8	A	1915	3TD	1	0
8	A	2605	PSU	9	0
8	A	1939	5MU	2	0
34	a	516	PSU	9	0
56	w	37	MIA	12	0
8	A	1917	PSU	7	0
58	y	101	FME	5	0
34	a	1516	2MG	7	0
8	A	2604	PSU	9	0
8	A	2580	PSU	15	0
34	a	1518	MA6	13	0
34	a	1407	5MC	5	0
55	v	55	PSU	7	0
8	A	1835	2MG	7	0
8	A	746	PSU	3	0
8	A	1911	PSU	4	0
8	A	2069	G7M	7	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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	$\# Z > 2$
61	AM2	a	2001	-	40,40,40	0.24	0	53,60,60	0.60	2 (3%)
62	GDP	x	801	-	28,30,30	3.62	12 (42%)	44,47,47	1.78	14 (31%)

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
61	AM2	a	2001	-	-	4/12/84/84	0/4/4/4
62	GDP	x	801	-	-	7/16/32/32	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)
62	x	801	GDP	C3'-C4'	-10.01	1.27	1.53
62	x	801	GDP	C2'-C1'	-8.16	1.27	1.53
62	x	801	GDP	O4'-C1'	5.66	1.55	1.42
62	x	801	GDP	C4-N3	5.53	1.47	1.34
62	x	801	GDP	C2-N2	4.96	1.46	1.34

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	x	801	GDP	N2-C2-N1	4.60	126.50	116.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	x	801	GDP	N2-C2-N3	-3.20	113.50	119.73
62	x	801	GDP	N9-C8-N7	-3.09	107.57	113.39
62	x	801	GDP	C2-N3-C4	3.08	117.79	112.30
62	x	801	GDP	C5-C4-N3	-2.73	124.03	128.46

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

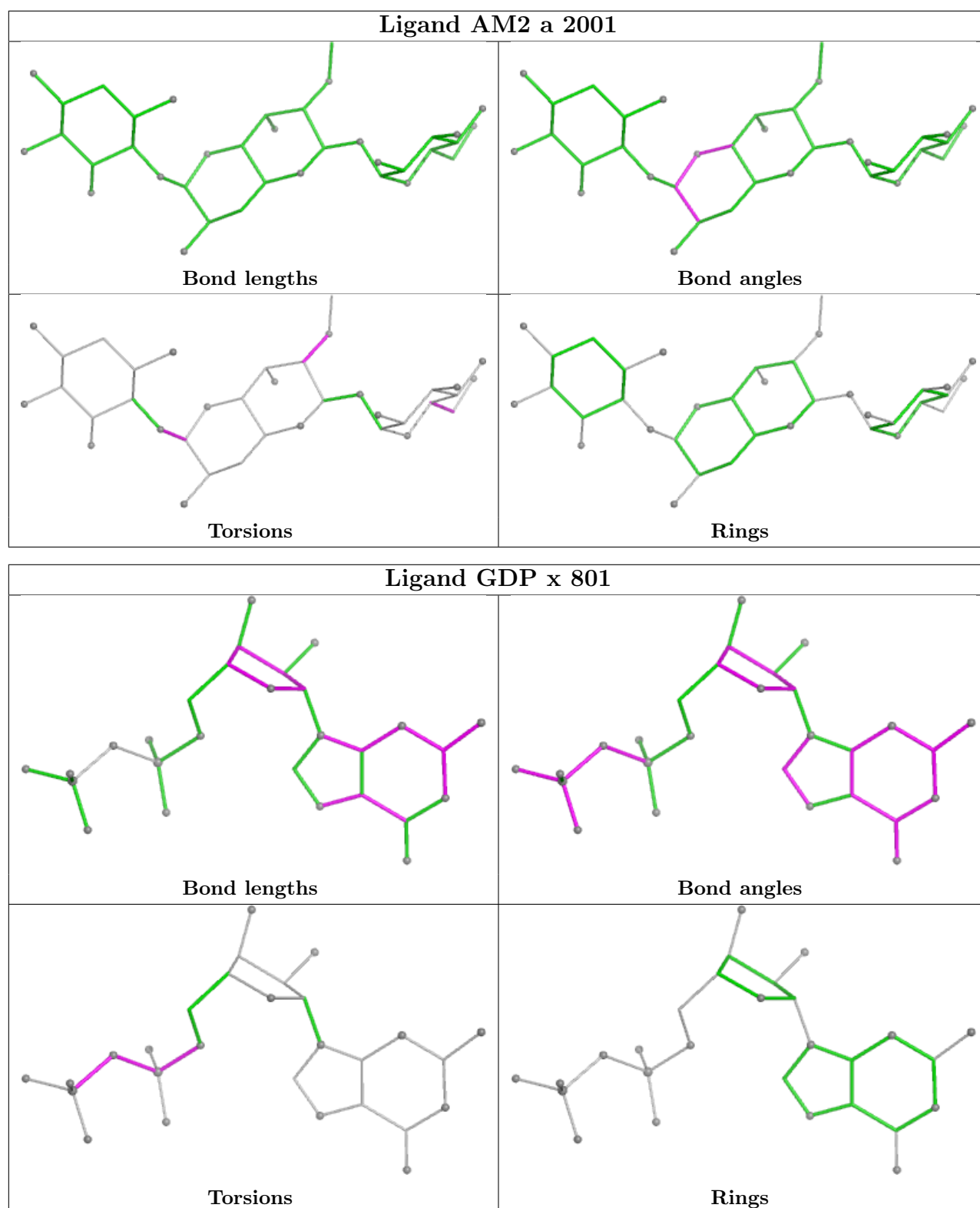
Mol	Chain	Res	Type	Atoms
61	a	2001	AM2	CA8-CA7-NA7-CA9
62	x	801	GDP	C5'-O5'-PA-O3A
61	a	2001	AM2	OB1-CB5-CB6-OB6
62	x	801	GDP	PA-O3A-PB-O3B
61	a	2001	AM2	OA4-CA1-OA1-CC1

There are no ring outliers.

2 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
61	a	2001	AM2	4	0
62	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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

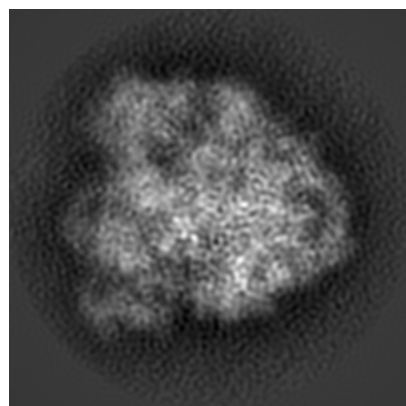
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13465. These allow visual inspection of the internal detail of the map and identification of artifacts.

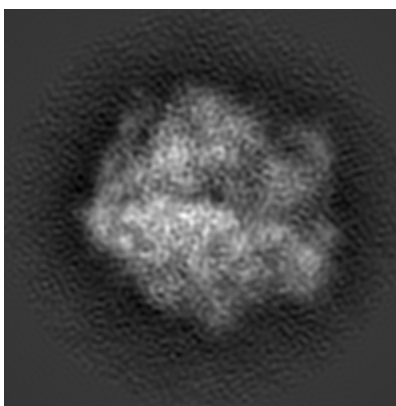
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

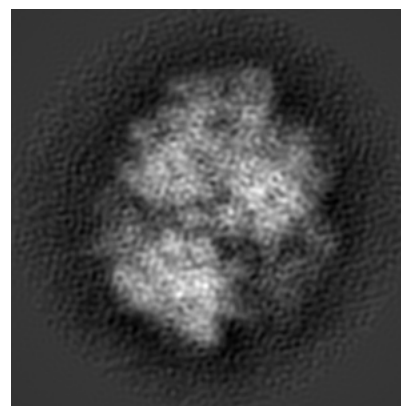
6.1.1 Primary map



X

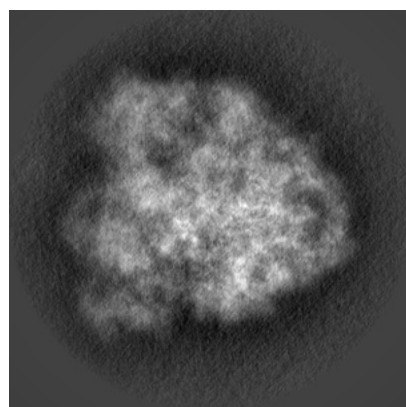


Y

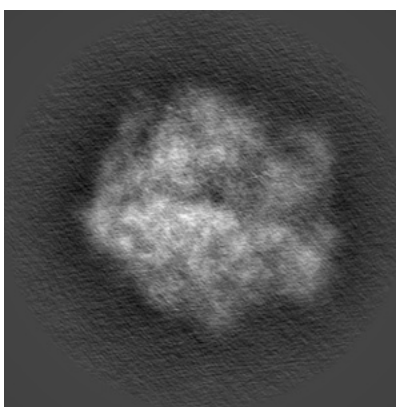


Z

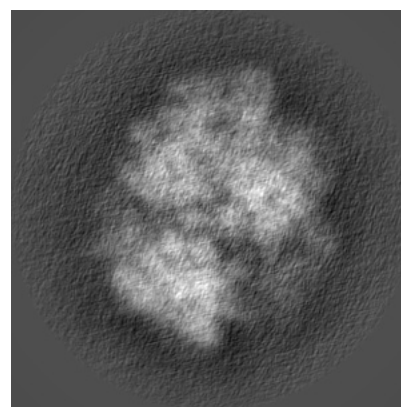
6.1.2 Raw map



X



Y

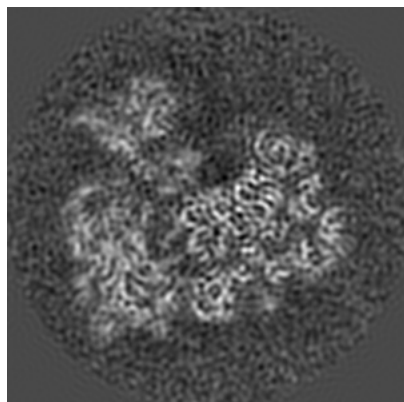


Z

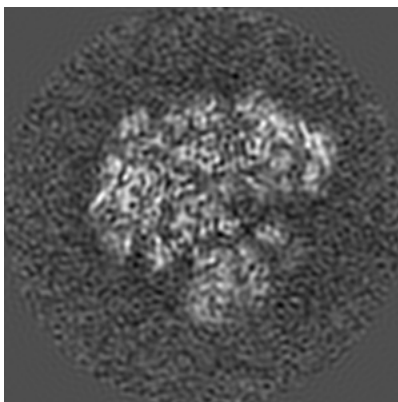
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

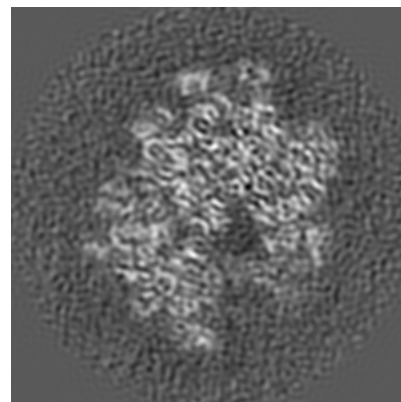
6.2.1 Primary map



X Index: 144

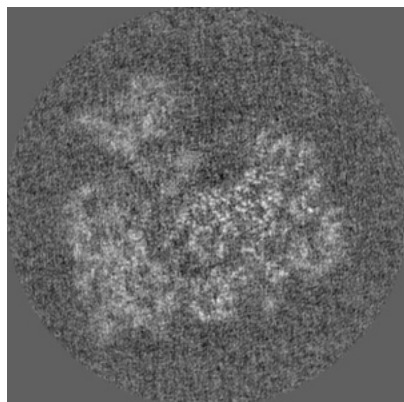


Y Index: 144

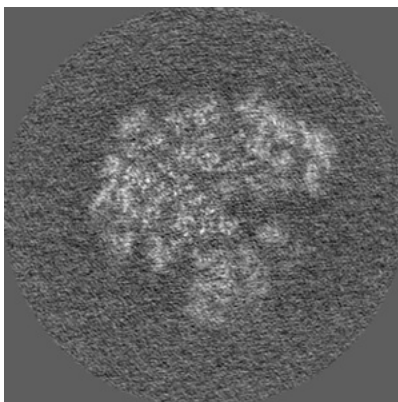


Z Index: 144

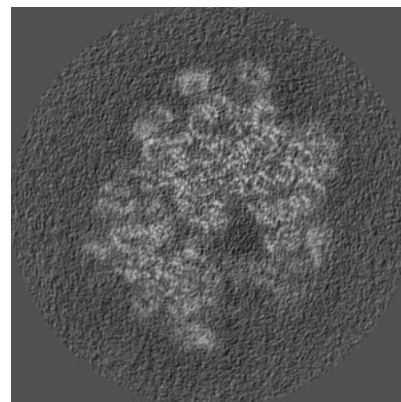
6.2.2 Raw map



X Index: 144



Y Index: 144

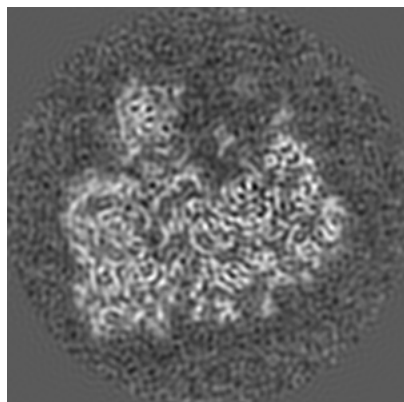


Z Index: 144

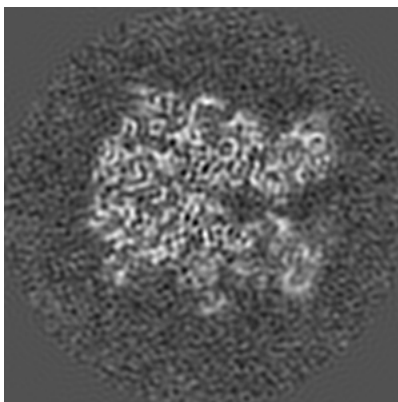
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

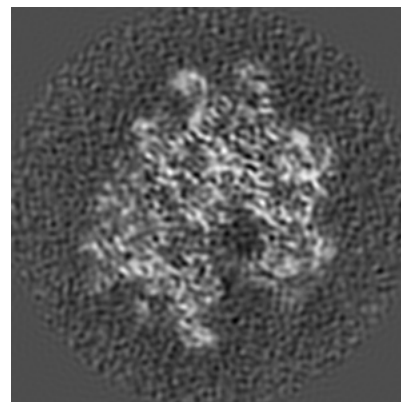
6.3.1 Primary map



X Index: 138

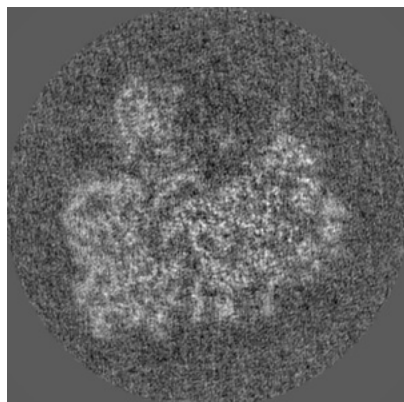


Y Index: 159

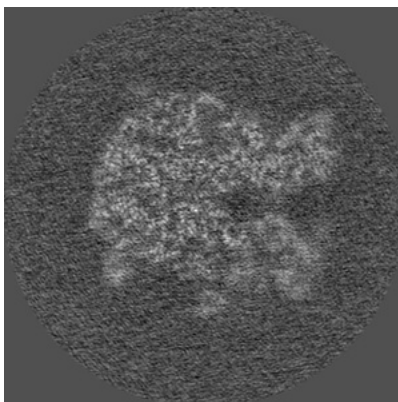


Z Index: 147

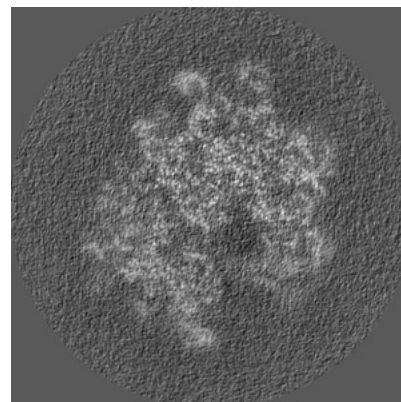
6.3.2 Raw map



X Index: 139



Y Index: 157

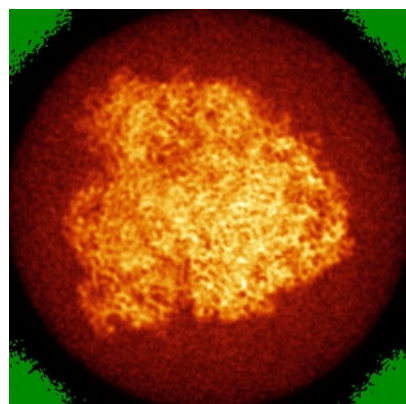


Z Index: 146

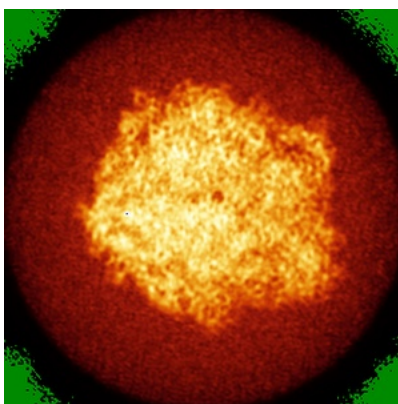
The images above show the largest variance slices of the map in three orthogonal directions.

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

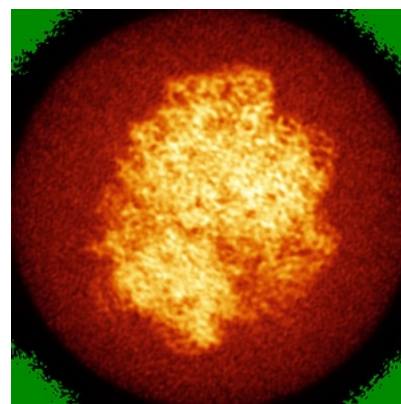
6.4.1 Primary map



X

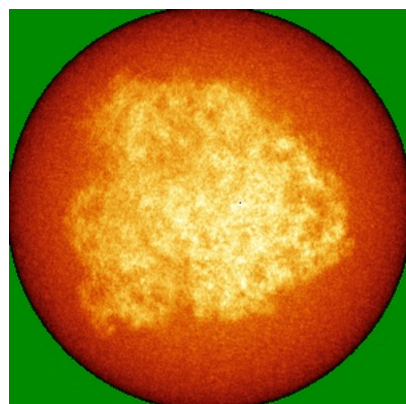


Y

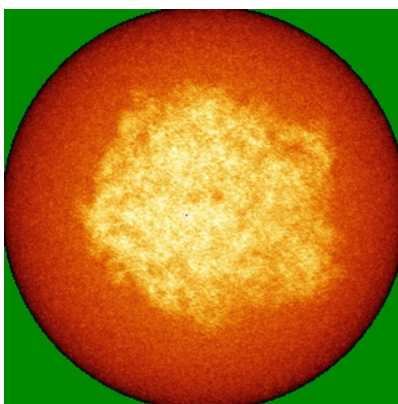


Z

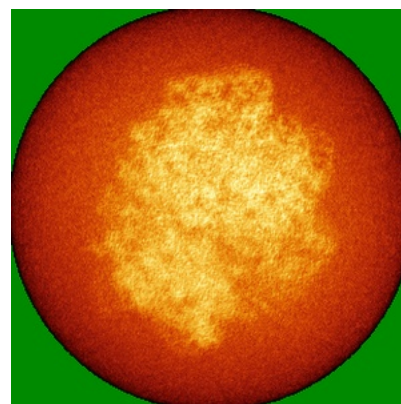
6.4.2 Raw map



X



Y

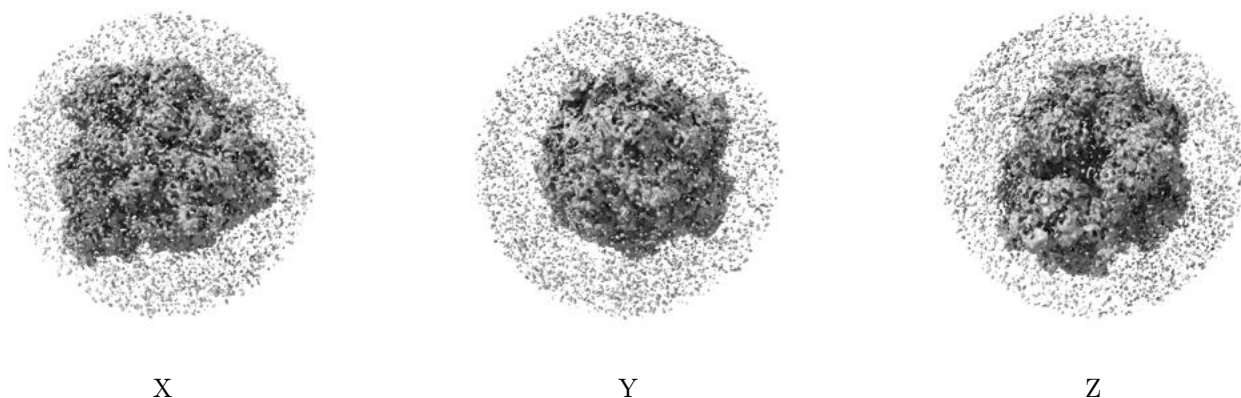


Z

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.

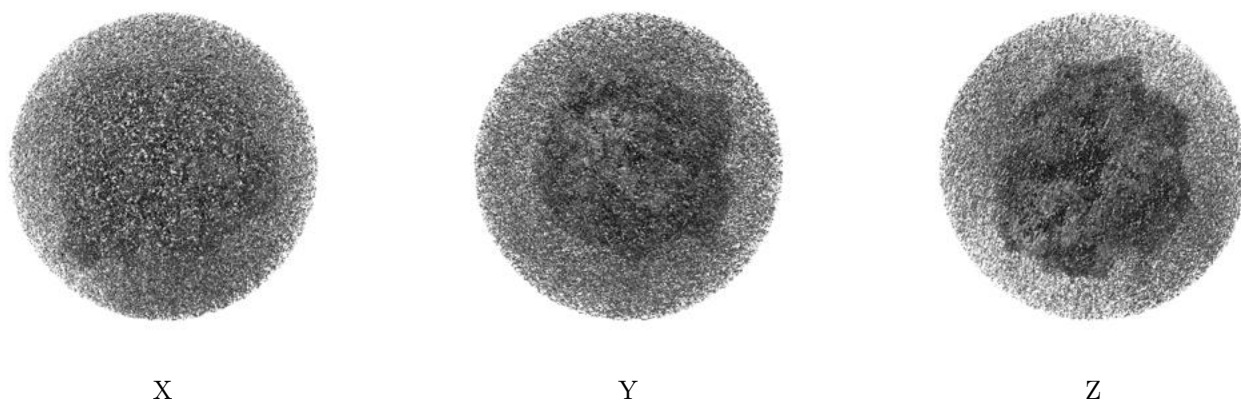
6.5 Orthogonal surface views [i](#)

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.

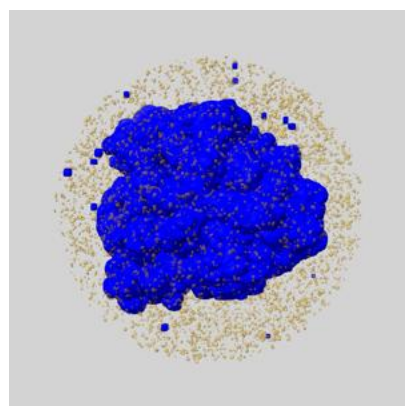
6.6 Mask visualisation [i](#)

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

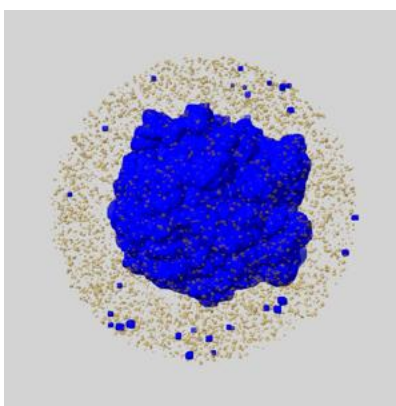
A mask typically either:

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

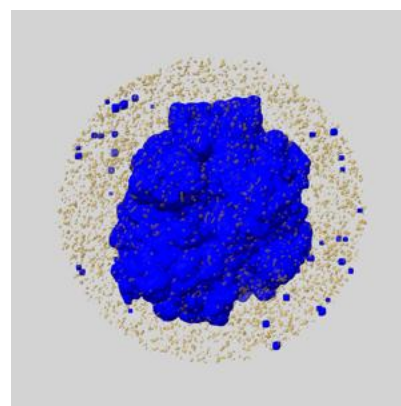
6.6.1 emd_13465_msk_1.map [i](#)



X



Y

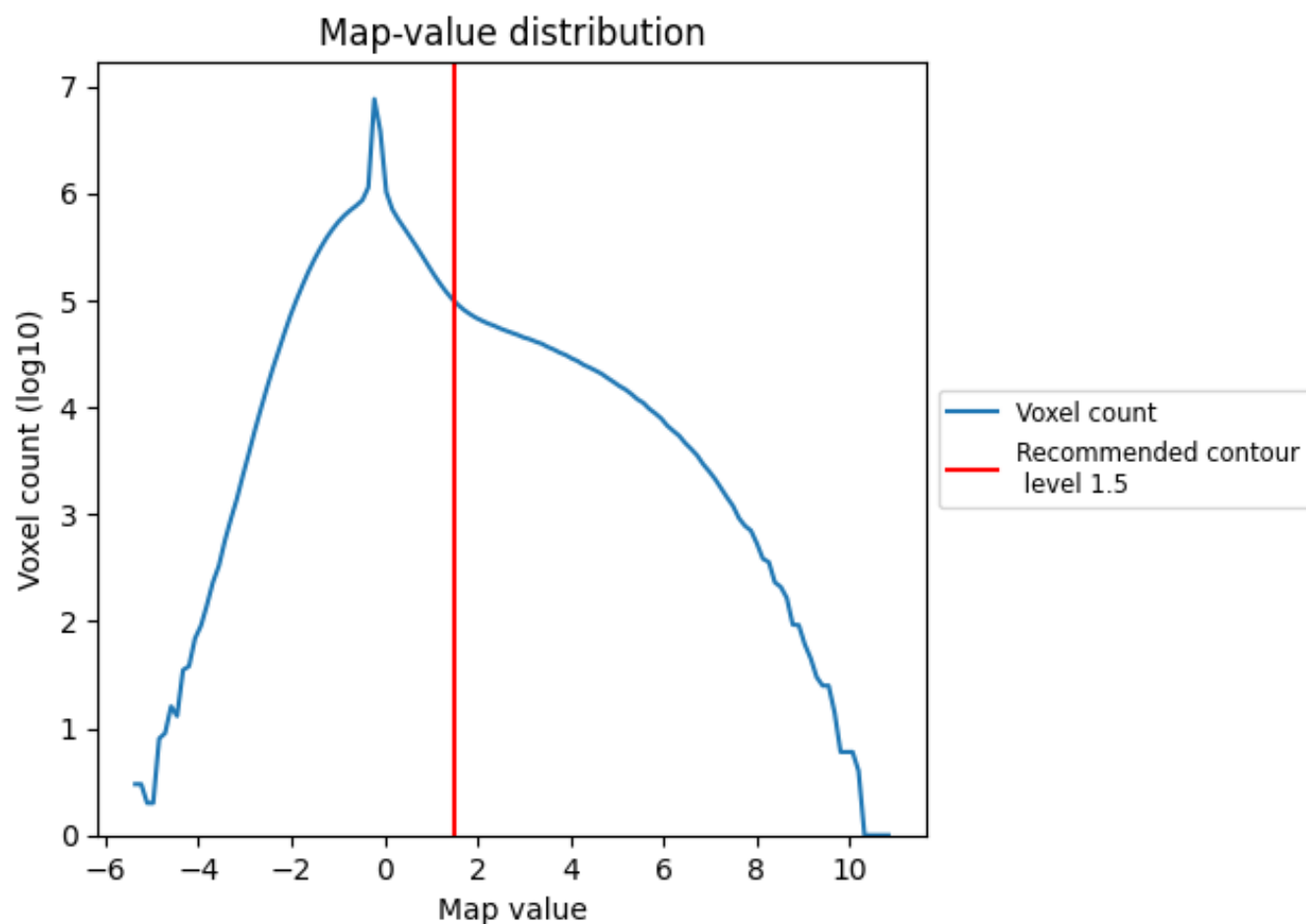


Z

7 Map analysis [i](#)

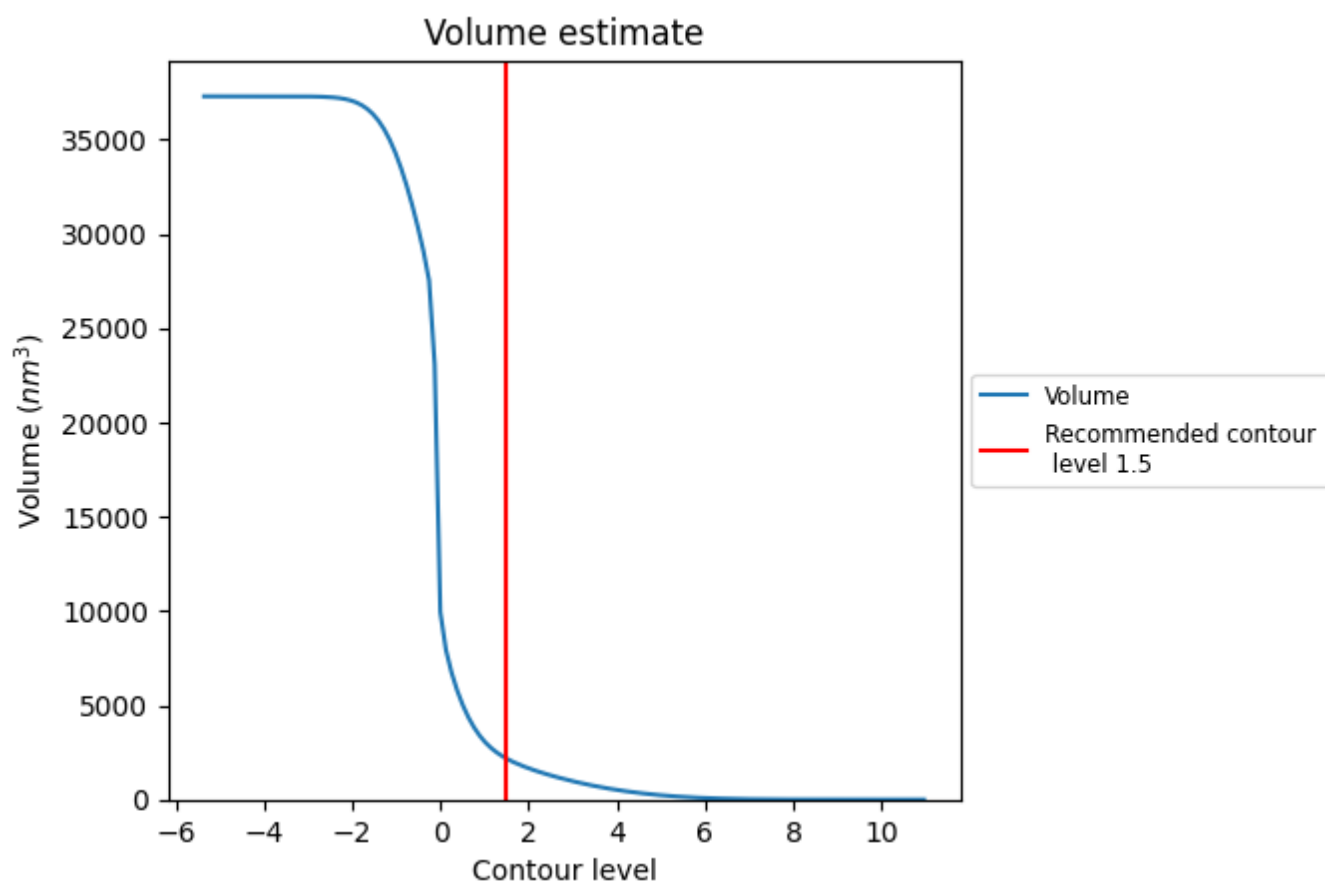
This section contains the results of statistical analysis of the map.

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.

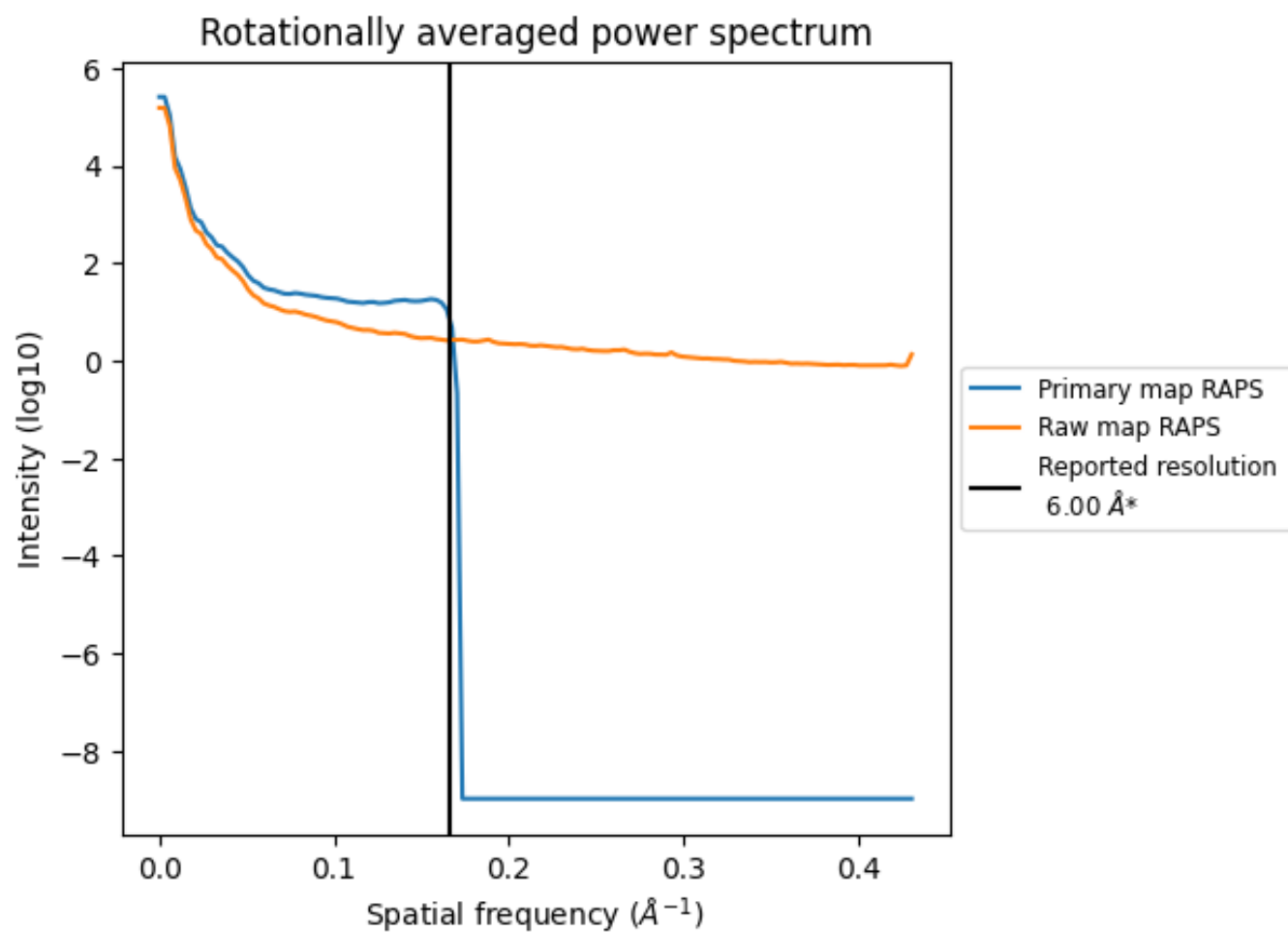
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2172 nm³; this corresponds to an approximate mass of 1962 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 ⓘ

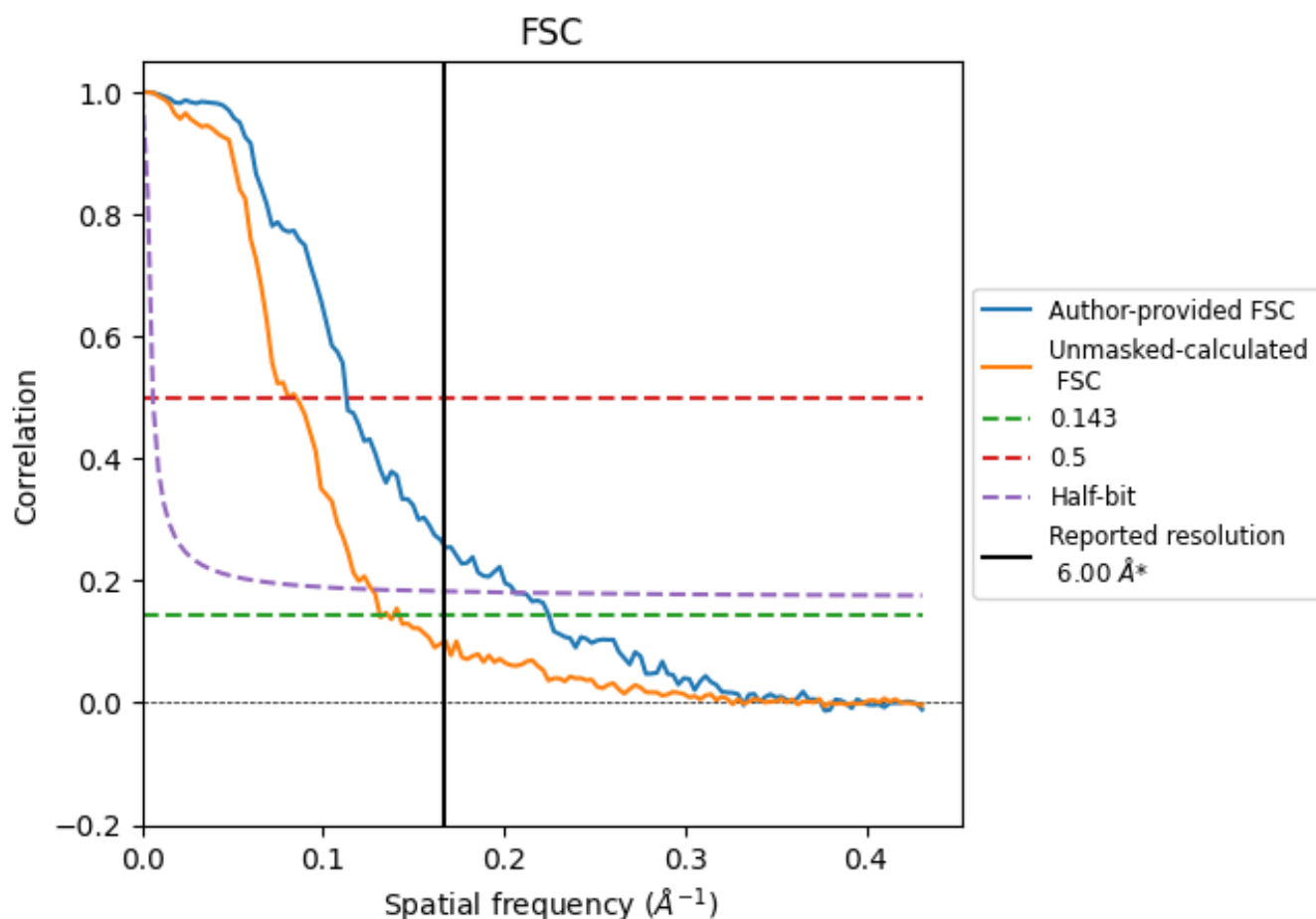


*Reported resolution corresponds to spatial frequency of 0.167 Å⁻¹

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 $0.167 \text{ \AA}^{-1}$

8.2 Resolution estimates

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.00	-	-
Author-provided FSC curve	4.45	8.86	4.85
Unmasked-calculated*	7.61	12.39	7.87

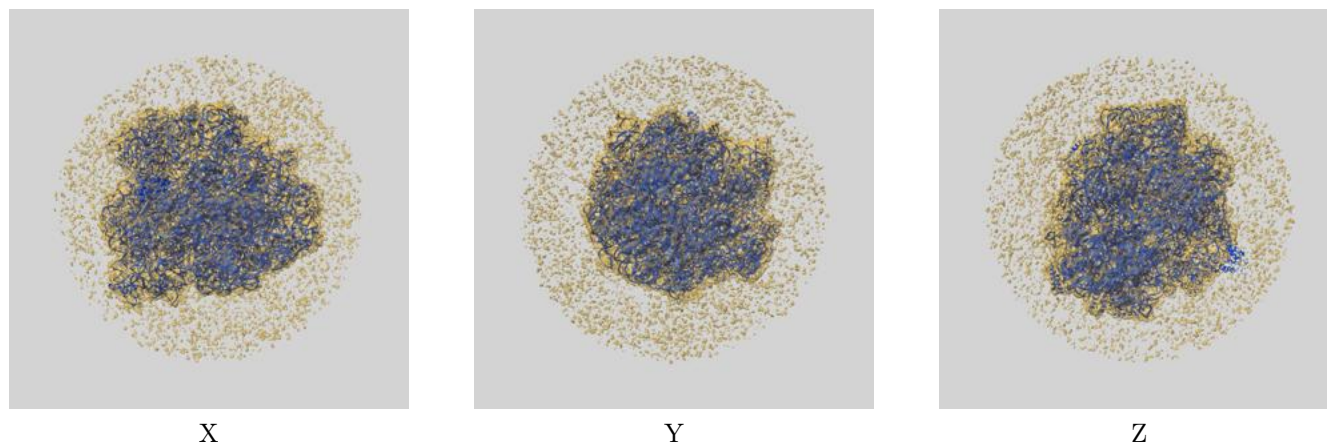
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 4.45 differs from the reported value 6.0 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.61 differs from the reported value 6.0 by more than 10 %

9 Map-model fit [i](#)

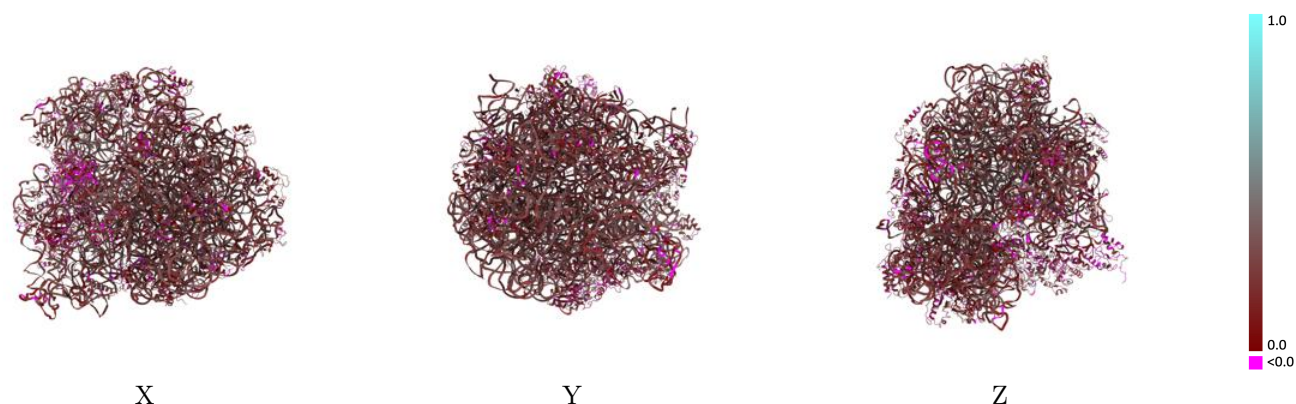
This section contains information regarding the fit between EMDB map EMD-13465 and PDB model 7PJZ. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



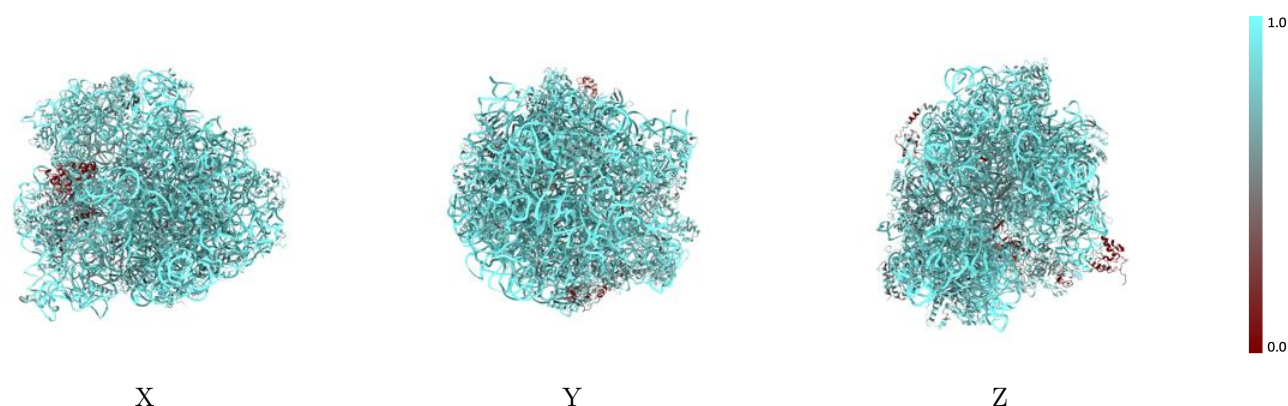
The images above show the 3D surface view of the map at the recommended contour level 1.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



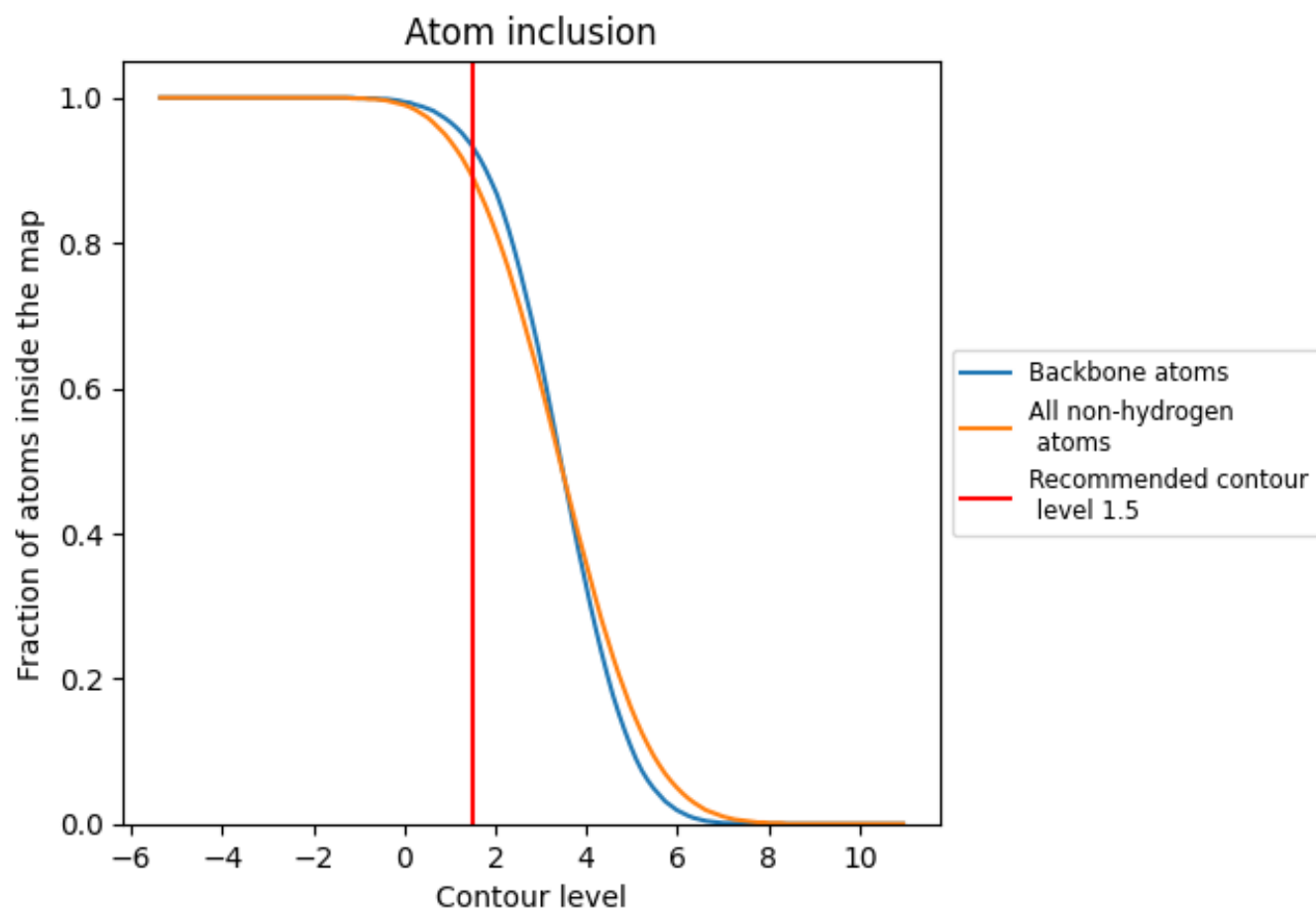
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 93% of all backbone atoms, 89% 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	 0.8910	 0.2290
0	 0.8200	 0.2180
1	 0.8030	 0.1790
2	 0.8170	 0.2260
3	 0.7900	 0.1990
4	 0.7910	 0.1960
5	 0.2040	 0.0550
6	 0.7750	 0.1830
A	 0.9630	 0.2580
B	 0.9830	 0.2580
C	 0.7770	 0.2080
D	 0.7790	 0.1960
E	 0.8000	 0.2120
F	 0.8140	 0.1870
G	 0.8280	 0.2000
H	 0.4640	 0.1680
I	 0.5470	 0.0990
J	 0.7740	 0.1970
K	 0.7310	 0.2030
L	 0.7960	 0.2050
M	 0.7970	 0.2110
N	 0.8210	 0.1900
O	 0.8780	 0.1880
P	 0.7810	 0.1970
Q	 0.8120	 0.1760
R	 0.8190	 0.1980
S	 0.7420	 0.1830
T	 0.8350	 0.2030
U	 0.8540	 0.1950
V	 0.8390	 0.1850
W	 0.8530	 0.1850
X	 0.8090	 0.2120
Y	 0.8290	 0.1740
Z	 0.8420	 0.2060
a	 0.9620	 0.2400



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Chain	Atom inclusion	Q-score
b	 0.5880	 0.1850
c	 0.7970	 0.1980
d	 0.8110	 0.1770
e	 0.7740	 0.1860
f	 0.7760	 0.1750
g	 0.6770	 0.1790
h	 0.7950	 0.1910
i	 0.8110	 0.1880
j	 0.7780	 0.1740
k	 0.7740	 0.1880
l	 0.7760	 0.2030
m	 0.7630	 0.1710
n	 0.8400	 0.1760
o	 0.7830	 0.1800
p	 0.8180	 0.1890
q	 0.7960	 0.1760
r	 0.7900	 0.1640
s	 0.8080	 0.1830
t	 0.8050	 0.1780
u	 0.7460	 0.1970
v	 0.9020	 0.2410
w	 0.7110	 0.2060
x	 0.6490	 0.1570
y	 0.9050	 0.3130
z	 0.8650	 0.2590