



wwPDB EM Validation Summary Report ⓘ

Jun 17, 2026 – 07:42 pm BST

PDB ID : 7PJV / pdb_00007pjb
EMDB ID : EMD-13461
Title : Structure of the 70S-EF-G-GDP-Pi ribosome complex with tRNAs in hybrid state 1 (H1-EF-G-GDP-Pi)
Authors : Petrychenko, V.; Peng, B.Z.; Schwarzer, A.C.; Peske, F.; Rodnina, M.V.; Fischer, N.
Deposited on : 2021-08-24
Resolution : 3.10 Å (reported)
Based on initial models : 5LZD, 5J9Z, 4AQY, 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:

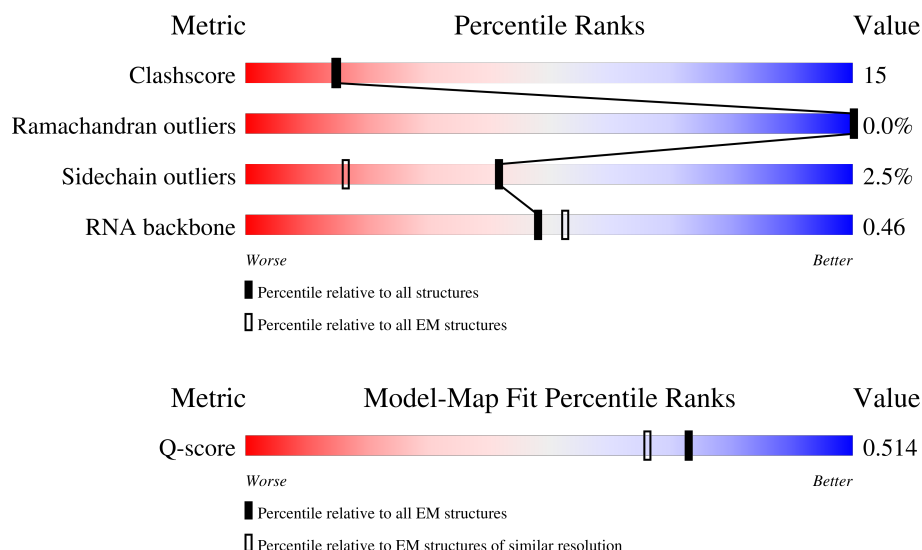
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.10 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	14724 (2.60 - 3.60)

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	 67% 32% .
2	1	55	 65% 24% . 9%

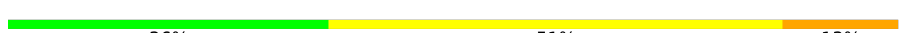
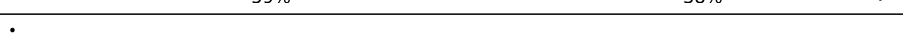
Continued on next page...

Continued from previous page...

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	

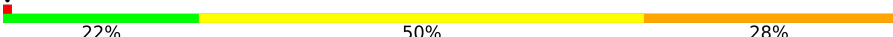
Continued on next page...

Continued from previous page...

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	

Continued on next page...

Continued from previous page...

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
65	PO4	x	802	-	-	X	-

2 Entry composition

There are 65 unique types of molecules in this entry. The entry contains 153165 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, fully modified isoform.

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 P0AG59

- 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	703	Total	C	N	O	S	0	0
			5444	3429	942	1048	25		

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

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

- Molecule 59 is a RNA chain called mRNA.

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

- Molecule 60 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
60	0	1	Total	Mg	0
			1	1	
60	A	262	Total	Mg	0
			262	262	
60	B	7	Total	Mg	0
			7	7	
60	C	3	Total	Mg	0
			3	3	
60	D	1	Total	Mg	0
			1	1	
60	O	1	Total	Mg	0
			1	1	

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
60	P	1	Total 1	Mg 1	0
60	Q	1	Total 1	Mg 1	0
60	Z	1	Total 1	Mg 1	0
60	a	85	Total 85	Mg 85	0
60	m	1	Total 1	Mg 1	0
60	n	1	Total 1	Mg 1	0
60	v	1	Total 1	Mg 1	0
60	w	1	Total 1	Mg 1	0
60	x	1	Total 1	Mg 1	0
60	z	1	Total 1	Mg 1	0

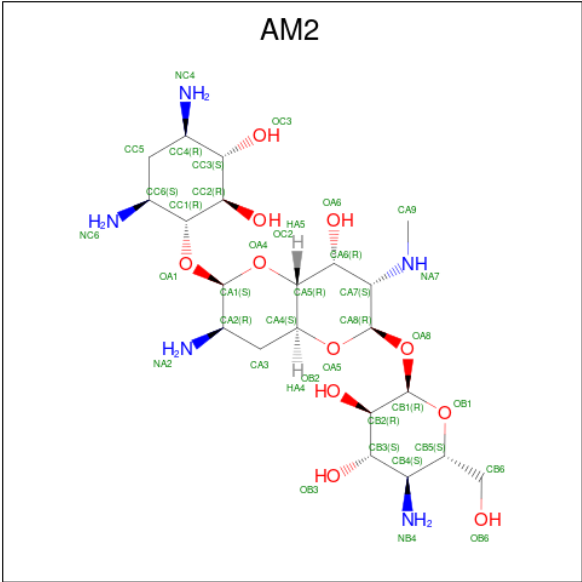
- Molecule 61 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
61	4	1	Total 1	Zn 1	0
61	6	1	Total 1	Zn 1	0

- Molecule 62 is SODIUM ION (CCD ID: NA) (formula: Na).

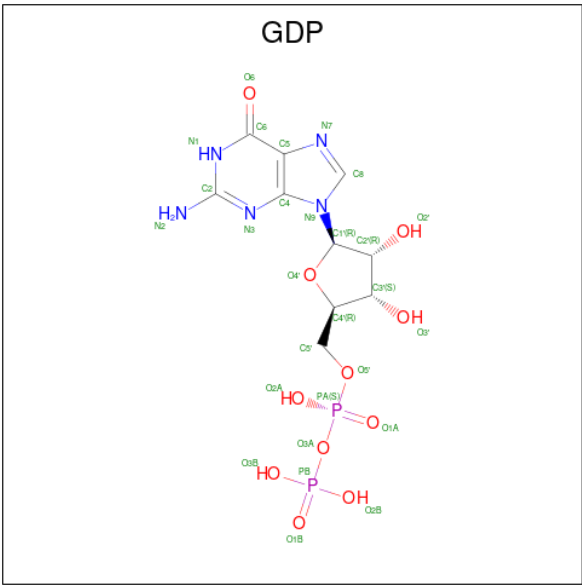
Mol	Chain	Residues	Atoms		AltConf
62	A	1	Total 1	Na 1	0
62	B	1	Total 1	Na 1	0

- Molecule 63 is APRAMYCIN (CCD ID: AM2) (formula: C₂₁H₄₁N₅O₁₁).



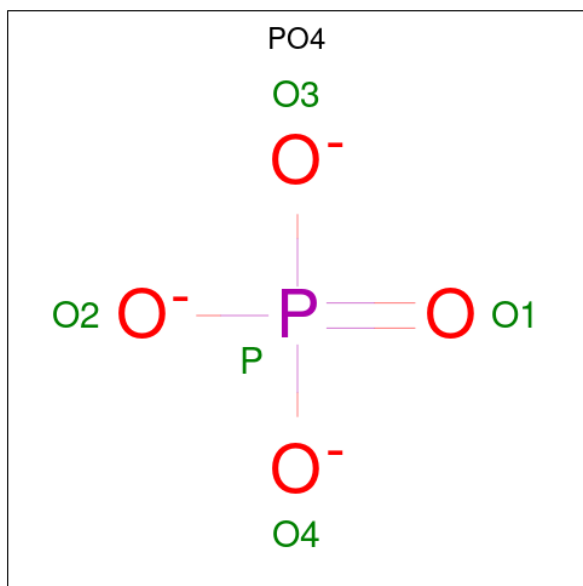
Mol	Chain	Residues	Atoms				AltConf
63	a	1	Total	C	N	O	0
			37	21	5	11	
63	a	1	Total	C	N	O	0
			37	21	5	11	
63	a	1	Total	C	N	O	0
			37	21	5	11	

- Molecule 64 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



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

- Molecule 65 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			AltConf
			Total	O	P	
65	x	1	5	4	1	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

Chain 0: 



- Molecule 2: 50S ribosomal protein L33

Chain 1: 



- Molecule 3: 50S ribosomal protein L34

Chain 2: 



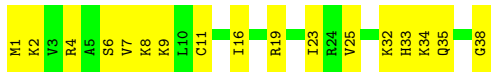
- Molecule 4: 50S ribosomal protein L35

Chain 3: 

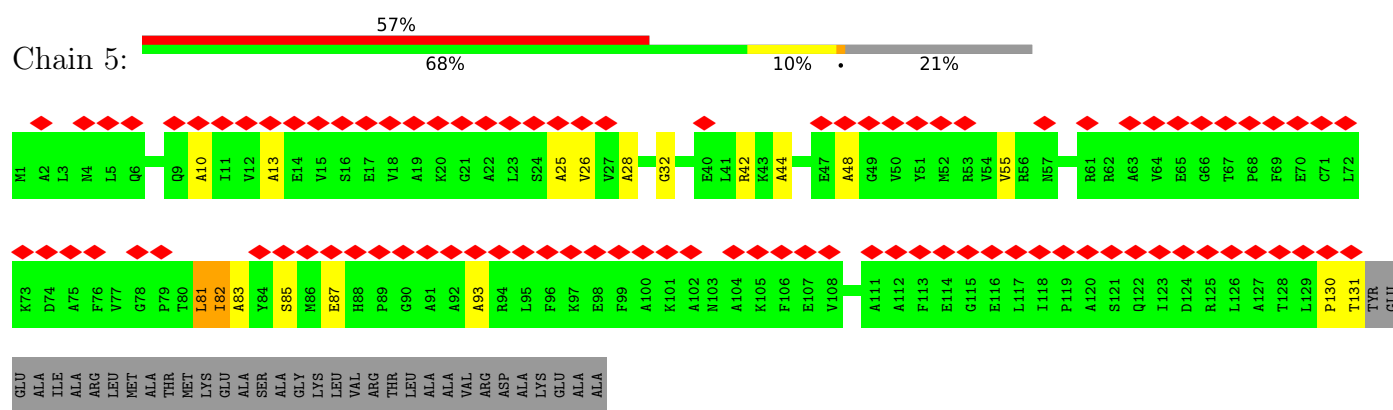


- Molecule 5: 50S ribosomal protein L36

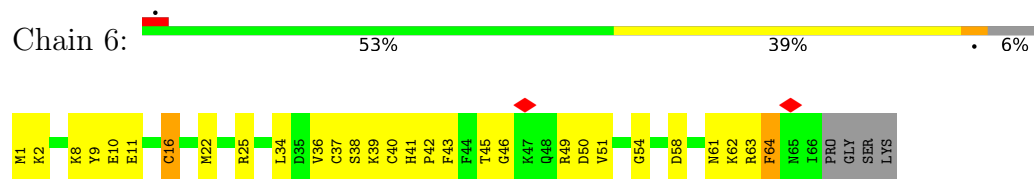
Chain 4: 



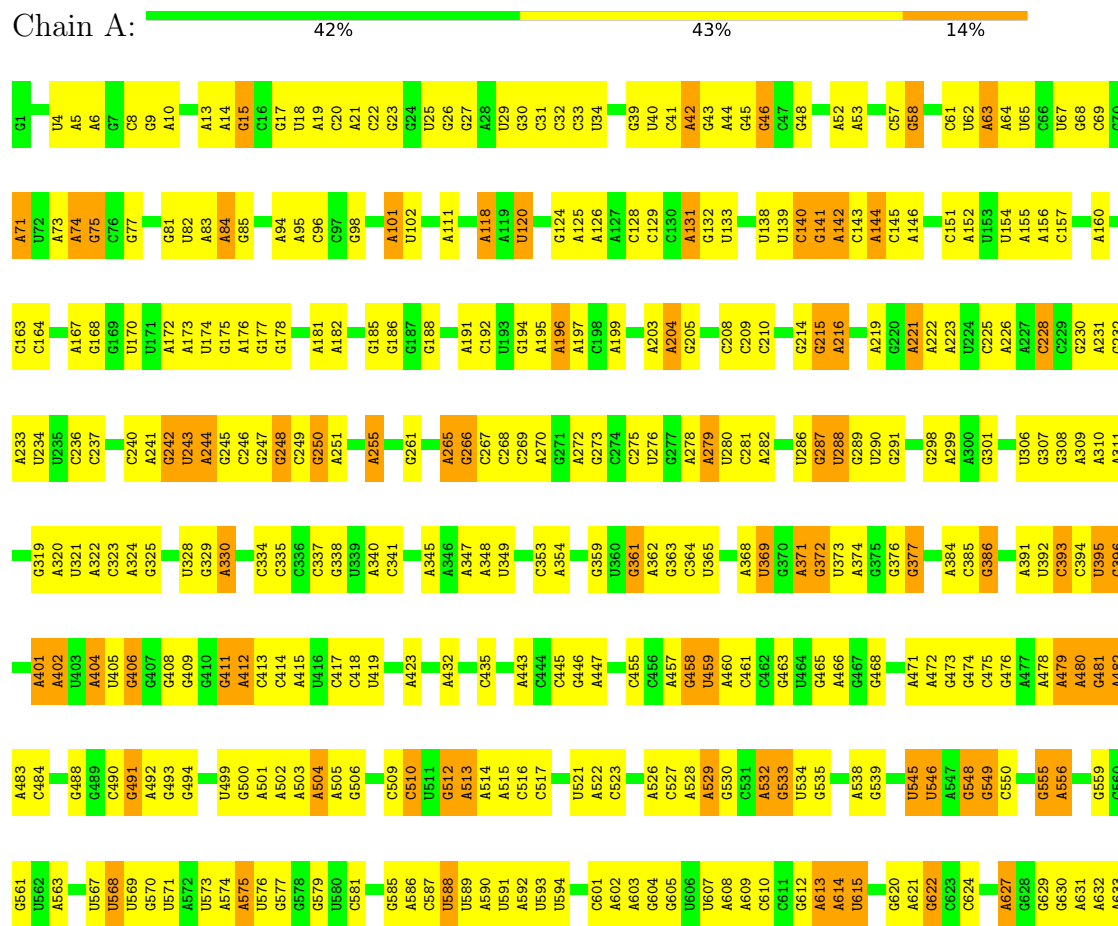
- Molecule 6: 50S ribosomal protein L10



• Molecule 7: 50S ribosomal protein L31



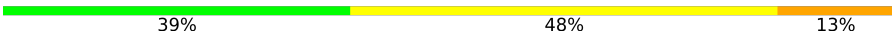
• Molecule 8: 23S ribosomal RNA

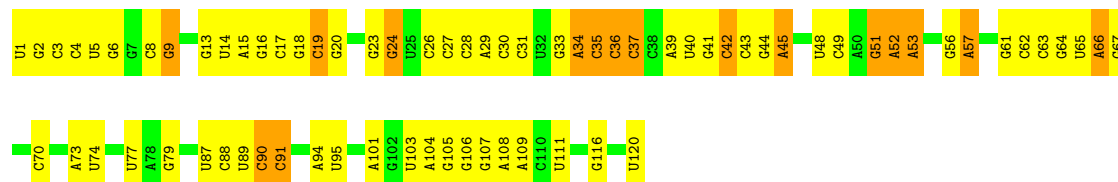


A1762	G1682	U1599	G1436	C1363	G1279	U1203	A1111	G1051	A980	C888	G809	C717	G636
G1763	U1683	C1600	C1437	G1364	U1282	A1203	G1112	C1052	A981	C889	U810	A718	A637
C1764	G1601	A1522	U1438	A1366	U1283	A1205	U1113	A1053	C982	C890	U811	C719	G638
U1769	U1523	U1524	G1441	A1367	A1284	G1210	G1115	A1054	A984	G891	U813	U720	U639
G1770	C1604	G1524	U1442	G1368	A1285	G1211	G1116	G1055	G989	A892	C814	A721	C640
C1771	G1606	G1530	U1443	C1376	A1286	C1212	U1119	A1057	U899	U894	C723	C722	U641
A1772	C1607	C1531	U1444	G1377	A1287	A1213	G1120	U1058	A990	C893	C817	G726	A644
A1773	A1608	C1533	G1445	A1378	G1288	A1214	C1121	U1060	C991	U895	G818	A727	C645
C1774	U1534	U1534	C1451	U1379	G1292	G1215	G1122	U1061	G992	A896	A819	G728	U646
U1775	A1535	A1535	G1452	G1380	C1293	G1216	C1125	G1062	C994	C898	A825	G729	G647
U1779	C1536	C1536	A1453	A1383	U1294	U1219	A1126	G1063	C995	A899	U826	A730	G648
U1782	G1537	G1537	U1458	A1384	U1297	G1220	U1129	C1064	A996	A900	U827	G734	U652
U1783	U1538	U1538	G1459	A1385	C1298	G1221	A1130	U1065	A1000	C901	U828	A734	U653
A1784	G1540	C1541	U1460	C1386	C1299	U1222	U1130	A1066	A1001	C902	A829	A742	A654
C1788	C1541	U1542	C1461	A1387	G1300	G1223	G1131	A1067	G1002	C903	G830	A743	A655
U1789	U1542	G1543	U1466	A1393	A1301	U1224	U1132	G1068	U906	U906	G831	G744	G656
C1790	G1543	C1544	U1467	U1394	A1302	G1225	A1133	A1069	U1004	G907	U832	U745	U657
A1791	A1545	A1545	U1468	A1395	C1306	G1227	A1134	A1070	C1005	A910	G834	G746	U658
U1794	A1549	A1549	U1469	A1396	U1318	U1230	G1136	C1071	C1006	A911	C835	C747	G659
C1795	U1554	U1554	G1471	U1397	C1319	U1231	G1139	A1073	A1009	G916	U839	A752	G669
U1796	G1555	G1555	U1474	C1398	G1311	U1234	G1140	G1074	A1010	A920	C840	G757	A670
C1797	C1556	C1556	U1475	U1400	U1312	G1235	U1141	C1075	G1011	C921	G843	U762	C671
U1798	C1557	C1557	U1476	A1401	G1317	U1239	A1142	A1077	U1012	C922	A844	C672	C672
G1799	C1558	C1558	G1477	U1402	U1318	G1239	A1151	C1078	A1013	G917	U846	A764	G674
A1801	G1564	C1564	U1478	U1405	C1319	A1247	C1152	A1080	U1019	U931	U847	C879	C879
C1802	C1565	C1565	G1482	U1406	A1322	G1248	C1153	U1081	U1023	A941	C848	U773	G680
A1803	A1566	A1566	G1483	G1407	C1323	U1249	G1154	U1082	G1024	C942	A849	G774	G681
C1806	G1569	G1569	U1484	U1409	G1327	G1250	A1155	U1083	U1029	G943	U850	G775	G682
A1808	U1570	A1570	U1485	G1410	A1328	C1251	G1168	A1085	G1026	A936	U852	G776	U683
A1809	A1571	A1571	U1486	U1411	A1328	G1252	A1169	A1086	A1027	G937	G856	G777	G684
U1810	U1578	U1578	U1487	U1412	G1331	A1254	C1170	U1087	A1028	G940	G857	G778	A685
G1811	A1579	A1579	C1488	C1413	U1334	U1255	C1171	A1088	U1029	A941	G857	G779	U686
C1816	A1580	A1580	C1489	U1414	G1334	G1256	U1172	A1089	A1030	C942	G858	G780	A689
U1817	G1581	G1581	U1491	U1415	G1334	A1260	U1176	A1090	G1031	G943	G859	A781	G690
U1818	C1582	C1582	A1494	G1417	U1338	C1261	A1175	A1091	G1032	A944	U860	A782	C691
A1821	A1583	A1583	A1495	U1418	U1340	A1262	C1177	G1092	U1033	A945	G861	G783	C692
U1822	C1584	C1584	U1496	U1420	G1341	U1263	U1177	G1093	G1034	C946	G862	G784	A693
G1823	U1585	U1585	U1497	G1421	G1341	A1264	A1178	U1094	U1035	A947	U870	G785	G694
U1824	A1586	A1586	G1501	U1422	U1344	A1265	G1179	A1095	G1036	C948	U871	C786	U694
U1827	G1587	G1587	G1501	G1423	C1345	G1266	U1181	A1096	G1037	C948	U872	C787	G697
U1828	U1588	U1588	A1504	G1426	C1351	A1269	U1182	U1097	G1038	G954	U873	A788	C698
A1829	A1590	A1590	A1505	A1427	U1352	C1270	U1183	A1098	A1039	U955	U874	A789	A699
U1835	U1591	U1591	G1505	C1428	A1353	G1271	G1186	G1099	A1040	G956	A877	C791	G700
G1835	C1592	C1592	U1509	G1429	A1353	A1272	U1187	U1101	G1042	C961	A878	A792	U703
A1754	A1593	A1593	G1510	G1430	C1357	U1273	U1188	C1102	C1043	G965	G881	A793	G704
U1757	U1594	U1594	U1513	A1431	G1358	A1274	U1188	A1103	C1044	C965	G882	G799	G711
G1839	C1595	C1595	G1514	G1432	A1359	A1275	C1196	C1104	C1045	A973	G883	A800	G712
U1840	A1596	A1596	U1515	A1433	G1360	A1276	G1197	U1105	G1047	G974	U884	G713	G713
U1841	U1597	U1597	G1516	A1434	G1361	G1277	U1197	G1106	A1048	A975	C885	U714	U714
G1842	A1598	A1598	G1516	G1435	C1362	C1278	U1198	U1107	C1049	G976	A886	C806	A715
							U1199	C1109	A1050		A887		A716

C2827	C2828	A2750	A2751	C2876	C2877	A2600	C2601	C2817	C2818	G2445	G2446	A2366	U2296	G2224	U2151	A2090	C2021	A1932	C1843
G2829	G2830	C2750	C2751	C2676	C2677	C2602	C2603	A2518	A2519	G2447	G2448	G2370	A2297	A2225	G2152	C2091	U2022	G1933	C1844
G2831	G2832	U2604	U2605	U2522	U2523	G2604	G2605	U2524	U2525	G2449	G2450	G2371	U2298	G2226	C2153	U2092	C2023	A1936	G1847
G2833	G2834	U2606	U2607	U2526	U2527	U2608	U2609	U2528	U2529	U2451	U2452	G2372	U2299	G2227	C2154	A2094	C2024	A1937	A1848
G2835	G2836	U2610	U2611	U2530	U2531	U2612	U2613	U2532	U2533	U2453	U2454	G2373	U2300	G2228	C2155		C2025	U1938	A1853
G2837	G2838	C2614	C2615	G2534	G2535	C2616	C2617	G2536	G2537	U2455	U2456	G2374	U2301	G2229	C2156	A2097	C2026	U1940	A1854
G2839	G2840	U2765	U2766	U2538	U2539	U2618	U2619	U2540	U2541	U2457	U2458	G2375	U2302	G2230	C2157	U2098	G2027	U1941	U1855
G2841	G2842	U2767	U2768	G2542	G2543	U2620	U2621	G2544	G2545	U2459	U2460	G2376	U2303	G2231	C2158	U2099	A2030	U1942	U1856
G2843	G2844	G2770	G2771	U2546	U2547	U2622	U2623	G2548	G2549	U2461	U2462	G2377	U2304	G2232	C2159	A2101	G2032	U1943	G1857
G2845	G2846	G2772	G2773	U2550	U2551	C2624	C2625	G2552	G2553	U2463	U2464	G2378	U2305	G2233	C2160	A2102	G2033	U1944	A1858
G2847	G2848	A2776	A2777	U2554	U2555	C2626	C2627	U2556	U2557	U2465	U2466	G2379	U2306	G2234	C2161	A2103	U2034	U1946	A1866
G2849	G2850	A2778	A2779	U2558	U2559	C2628	C2629	U2560	U2561	U2467	U2468	G2380	U2307	G2235	C2162	A2104	G2035	U1947	
G2851	G2852	G2780	G2781	U2562	U2563	U2700	U2701	U2564	U2565	U2469	U2470	G2381	U2308	G2236	C2163	A2105	G2036	A1952	G1869
G2853	G2854	U2786	U2787	U2566	U2567	G2624	G2625	U2568	U2569	U2471	U2472	G2382	U2309	G2237	C2164	A2106	G2037	A1953	G1874
G2855	G2856	C2787	C2788	U2570	U2571	G2626	G2627	U2572	U2573	U2473	U2474	G2383	U2310	G2238	C2165	A2107	G2038	A1954	G1875
G2857	G2858	G2789	G2790	U2574	U2575	U2630	U2631	U2576	U2577	U2475	U2476	G2384	U2311	G2239	C2166	A2108	G2039	A1955	U1967
G2859	G2860	A2791	A2792	U2578	U2579	U2632	U2633	U2580	U2581	U2477	U2478	G2385	U2312	G2240	C2167	A2109	U2040	U1968	C1879
G2861	G2862	G2793	G2794	U2582	U2583	U2634	U2635	U2584	U2585	U2479	U2480	G2386	U2313	G2241	C2168	A2110	G2041	U1969	U1880
G2863	G2864	C2795	C2796	U2586	U2587	A2636	A2637	U2588	U2589	U2481	U2482	G2387	U2314	G2242	C2169	A2111	G2042	U1970	G1884
G2865	G2866	U2797	U2798	U2590	U2591	U2638	U2639	U2592	U2593	U2483	U2484	G2388	U2315	G2243	C2170	A2112	G2043	U1971	A1885
G2867	G2868	G2799	G2800	U2594	U2595	U2640	U2641	U2596	U2597	U2485	U2486	G2389	U2316	G2244	C2171	A2113	G2044	U1972	C1894
G2869	G2870	A2801	A2802	U2598	U2599	U2642	U2643	U2599	U2600	U2487	U2488	G2390	U2317	G2245	C2172	A2114	G2045	U1973	C1895
G2871	G2872	C2801	C2802	U2602	U2603	U2644	U2645	U2604	U2605	U2489	U2490	G2391	U2318	G2246	C2173	A2115	G2046	U1974	A1900
G2873	G2874	U2803	U2804	U2606	U2607	U2646	U2647	U2608	U2609	U2491	U2492	G2392	U2319	G2247	C2174	A2116	G2047	U1975	A1901
G2875	G2876	C2805	C2806	U2610	U2611	U2648	U2649	U2612	U2613	U2493	U2494	G2393	U2320	G2248	C2175	A2117	G2048	U1976	G1906
G2877	G2878	U2807	U2808	U2614	U2615	U2650	U2651	U2616	U2617	U2495	U2496	G2394	U2321	G2249	C2176	A2118	G2049	U1977	G1907
G2879	G2880	A2809	A2810	U2618	U2619	C2652	C2653	U2618	U2619	U2497	U2498	G2395	U2322	G2250	C2177	A2119	G2050	U1978	G1908
G2881	G2882	C2811	C2812	U2620	U2621	U2654	U2655	U2622	U2623	U2499	U2500	G2396	U2323	G2251	C2178	A2120	G2051	U1979	G1909
G2883	G2884	U2813	U2814	U2624	U2625	U2656	U2657	U2626	U2627	U2502	U2503	G2397	U2324	G2252	C2179	A2121	G2052	U1980	G1910
G2885	G2886	C2815	C2816	U2628	U2629	U2658	U2659	U2628	U2629	U2504	U2505	G2398	U2325	G2253	C2180	A2122	G2053	U1981	A1912
G2887	G2888	U2817	U2818	U2630	U2631	U2660	U2661	U2632	U2633	U2506	U2507	G2399	U2326	G2254	C2181	A2123	G2054	U1982	G1922
G2889	G2890	G2819	G2820	U2634	U2635	U2662	U2663	U2636	U2637	U2508	U2509	G2400	U2327	G2255	C2182	A2124	G2055	U1983	G1923
G2891	G2892	A2821	A2822	U2638	U2639	U2664	U2665	U2640	U2641	U2510	U2511	G2401	U2328	G2256	C2183	A2125	G2056	U1984	C1924
G2893	G2894	C2823	C2824	U2642	U2643	U2666	U2667	U2642	U2643	U2512	U2513	G2402	U2329	G2257	C2184	A2126	G2057	U1985	C1925
G2895	G2896	U2825	U2826	U2646	U2647	U2668	U2669	U2646	U2647	U2514	U2515	G2403	U2330	G2258	C2185	A2127	G2058	U1986	U1926
G2897	G2898	A2827	A2828	U2650	U2651	U2670	U2671	U2650	U2651	U2516	U2517	G2404	U2331	G2259	C2186	A2128	G2059	U1987	A1927
G2899	G2900	C2829	C2830	U2654	U2655	U2672	U2673	U2654	U2655	U2518	U2519	G2405	U2332	G2260	C2187	A2129	G2060	U1988	A1928
G2901	G2902	U2829	U2830	U2658	U2659	U2674	U2675	U2658	U2659	U2520	U2521	G2406	U2333	G2261	C2188	A2130	G2061	U1989	G1929
G2903	G2904	A2831	A2832	U2662	U2663	U2676	U2677	U2662	U2663	U2522	U2523	G2407	U2334	G2262	C2189	A2131	G2062	U1990	A1931
G2905	G2906	C2833	C2834	U2666	U2667	U2678	U2679	U2666	U2667	U2524	U2525	G2408	U2335	G2263	C2190	A2132	G2063	U1991	G1906
G2907	G2908	U2835	U2836	U2670	U2671	U2680	U2681	U2670	U2671	U2526	U2527	G2409	U2336	G2264	C2191	A2133	G2064	U1992	G1907
G2909	G2910	A2837	A2838	U2674	U2675	U2682	U2683	U2674	U2675	U2528	U2529	G2410	U2337	G2265	C2192	A2134	G2065	U1993	G1908
G2911	G2912	C2839	C2840	U2678	U2679	U2684	U2685	U2678	U2679	U2530	U2531	G2411	U2338	G2266	C2193	A2135	G2066	U1994	G1909
G2913	G2914	U2839	U2840	U2680	U2681	U2686	U2687	U2680	U2681	U2532	U2533	G2412	U2339	G2267	C2194	A2136	G2067	U1995	G1910
G2915	G2916	A2841	A2842	U2684	U2685	U2688	U2689	U2684	U2685	U2534	U2535	G2413	U2340	G2268	C2195	A2137	G2068	U1996	A1912
G2917	G2918	C2843	C2844	U2688	U2689	U2690	U2691	U2688	U2689	U2536	U2537	G2414	U2341	G2269	C2196	A2138	G2069	U1997	3TD1915
G2919	G2920	U2843	U2844	U2692	U2693	U2692	U2693	U2692	U2693	U2538	U2539	G2415	U2342	G2270	C2197	A2139	G2070	U1998	A1916
G2921	G2922	A2845	A2846	U2696	U2697	U2694	U2695	U2696	U2697	U2540	U2541	G2416	U2343	G2271	C2198	A2140	G2071	U1999	U1917
G2923	G2924	C2847	C2848	U2698	U2699	U2696	U2697	U2698	U2699	U2542	U2543	G2417	U2344	G2272	C2199	A2141	G2072	U2000	A1918
G2925	G2926	U2847	U2848	U2700	U2701	U2698	U2699	U2700	U2701	U2544	U2545	G2418	U2345	G2273	C2200	A2142	G2073	U2001	A1919
G2927	G2928	A2849	A2850	U2702	U2703	U2700	U2701	U2702	U2703	U2546	U2547	G2419	U2346	G2274	C2201	A2143	G2074	U2002	G1920
G2929	G2930	C2849	C2850	U2704	U2705	U2702	U2703	U2704	U2705	U2548	U2549	G2420	U2347	G2275	C2202	A2144	G2075	U2003	G1921
G2931	G2932	U2849	U2850	U2706	U2707	U2704	U2705	U2706	U2707	U2550	U2551	G2421	U2348	G2276	C2203	A2145	G2076	U2004	G1922
G2933	G2934	A2851	A2852	U2708	U2709	U2706	U2707	U2708	U2709	U2552	U2553	G2422	U2349	G2277	C2204	A2146	G2077	U2005	U1923
G2935	G2936	C2853	C2854	U2710	U2711	U2708	U2709	U2710	U2711	U2554	U2555	G2423	U2350	G2278	C2205	A2147	G2078	U2006	C2006
G2937	G2938	U2853	U2854	U2712	U2713	U2710	U2711	U2712	U2713	U2556	U2557	G2424	U2351	G2279	C2206	A2148	G2079	U2007	G2012
G2939	G2940	A2855	A2856	U2714	U2715	U2712	U2713	U2714	U2715	U2558	U2559	G2425	U2352	G2280	C2207	A2149	G2080	U2008	C1924
G2941	G2942	C2857	C2858	U2716	U2717	U2714	U2715	U2716	U2717	U2560	U2561	G2426	U2353	G2281	C2208	A2150	G2081	U2009	C1925
G2943	G2944	U2857	U2858	U2718	U2719	U2716	U2717	U2718	U2719	U2562	U2563	G2427	U2354	G2282	C2209	A2151	G2082	U2010	U1926
G2945	G2946	A2859	A2860	U2720	U2721	U2718	U2719	U2720	U2721	U2564	U2565	G2428	U2355	G2283	C2210	A2152	G2083	U2011	A2082
G2947	G2948	C2859	C2860	U2722	U2723	U2720	U2721	U2722	U2723	U2566	U2567	G2429	U2356	G2284	C2211	A2153	G2084	U2012	C2012
G2949	G2950	U2859	U2860	U2724	U2725	U2722	U2723	U2724	U2725	U2568	U2569	G2430	U2357	G2285	C2212	A2154	G2085	U2013	A2013
G2951	G2952	A2861	A2862	U2726	U2727	U2724	U2725	U2726	U2727	U2570	U2571	G2431	U2358	G2286	C2213	A2155	G2086	U2014	A2014
G2953	G2954	C2863	C286																

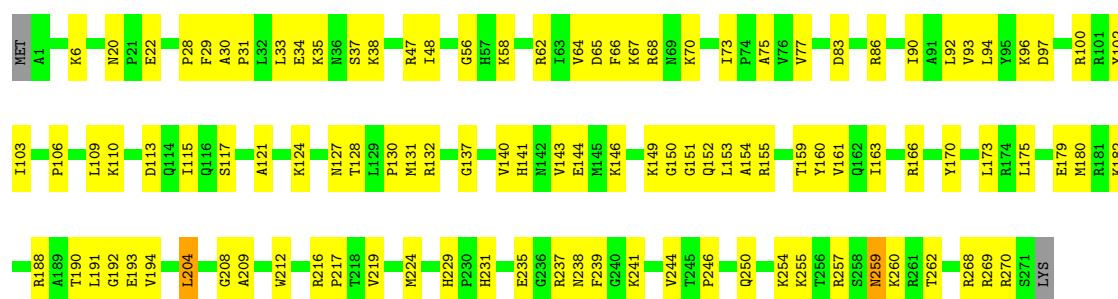
- Molecule 9: 5S ribosomal RNA

Chain B: 



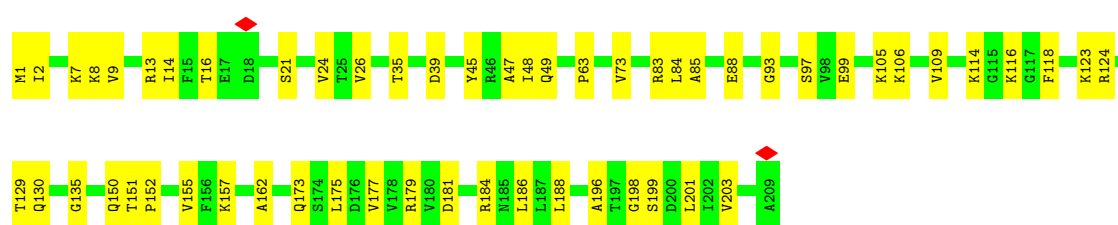
- Molecule 10: 50S ribosomal protein L2

Chain C: 



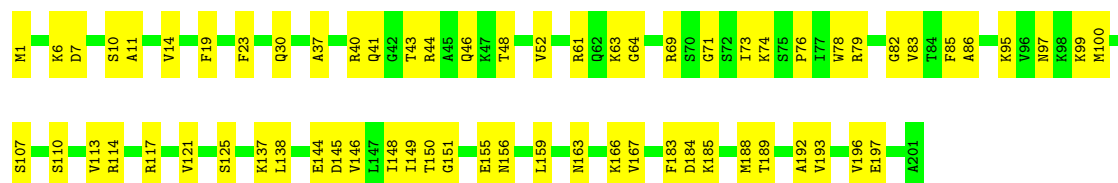
- Molecule 11: 50S ribosomal protein L3

Chain D: 



- Molecule 12: 50S ribosomal protein L4

Chain E: 

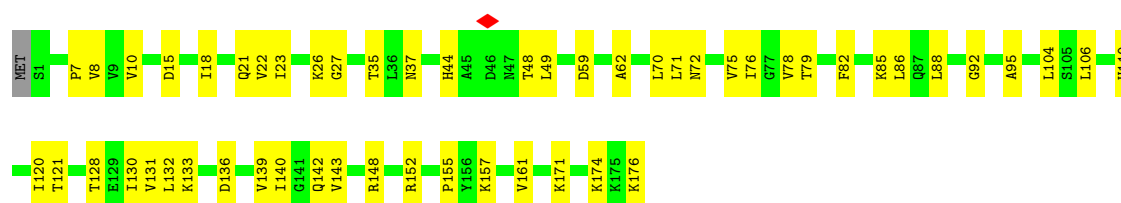


- Molecule 13: 50S ribosomal protein L5

Chain F: 



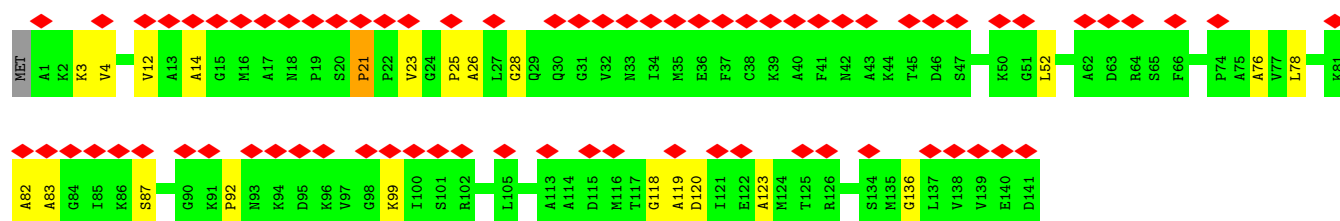
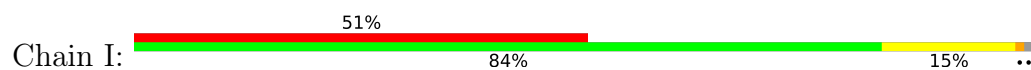
- Molecule 14: 50S ribosomal protein L6



- Molecule 15: 50S ribosomal protein L9

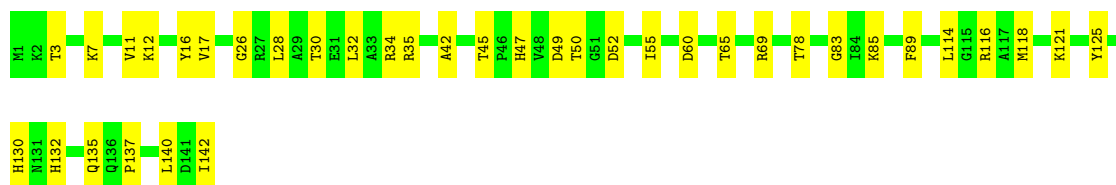


- Molecule 16: 50S ribosomal protein L11



- Molecule 17: 50S ribosomal protein L13





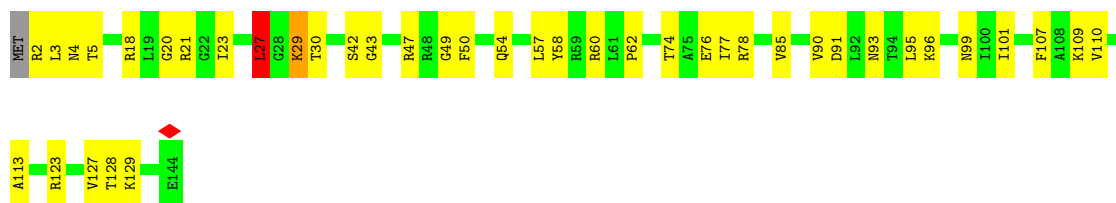
- Molecule 18: 50S ribosomal protein L14

Chain K: 72% 27%



- Molecule 19: 50S ribosomal protein L15

Chain L: 71% 27%



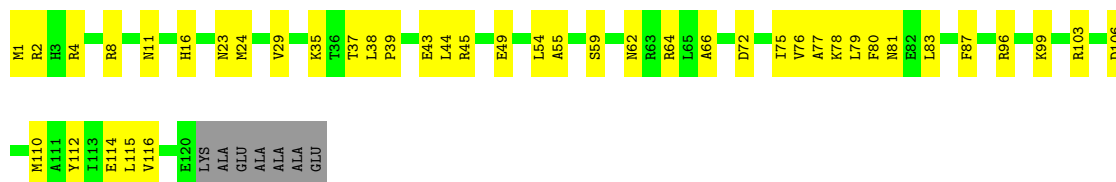
- Molecule 20: 50S ribosomal protein L16

Chain M: 65% 35%



- Molecule 21: 50S ribosomal protein L17

Chain N: 61% 33% 6%



- Molecule 22: 50S ribosomal protein L18

Chain O: 74% 25%



- Molecule 23: 50S ribosomal protein L19



- Molecule 24: 50S ribosomal protein L20



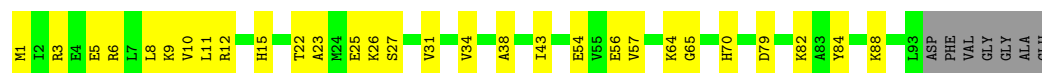
- Molecule 25: 50S ribosomal protein L21



- Molecule 26: 50S ribosomal protein L22

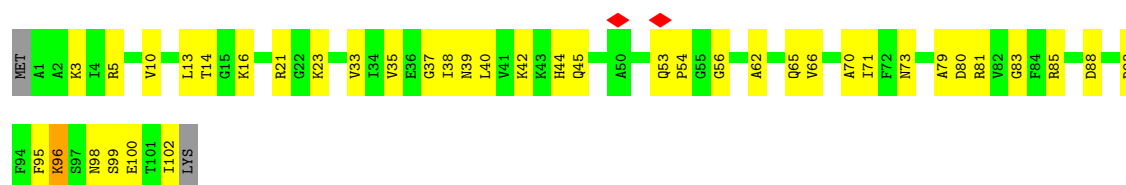


- Molecule 27: 50S ribosomal protein L23

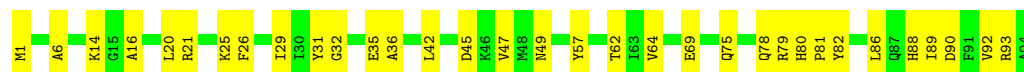


- Molecule 28: 50S ribosomal protein L24





- Molecule 29: 50S ribosomal protein L25



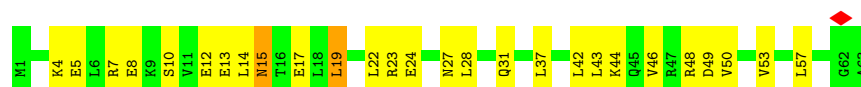
- Molecule 30: 50S ribosomal protein L27



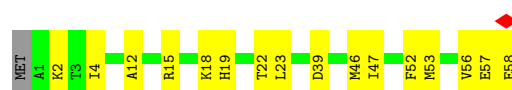
- Molecule 31: 50S ribosomal protein L28



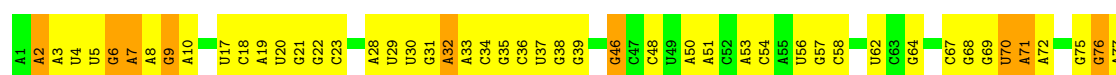
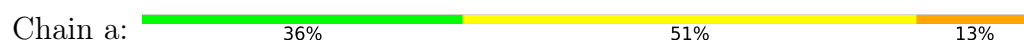
- Molecule 32: 50S ribosomal protein L29



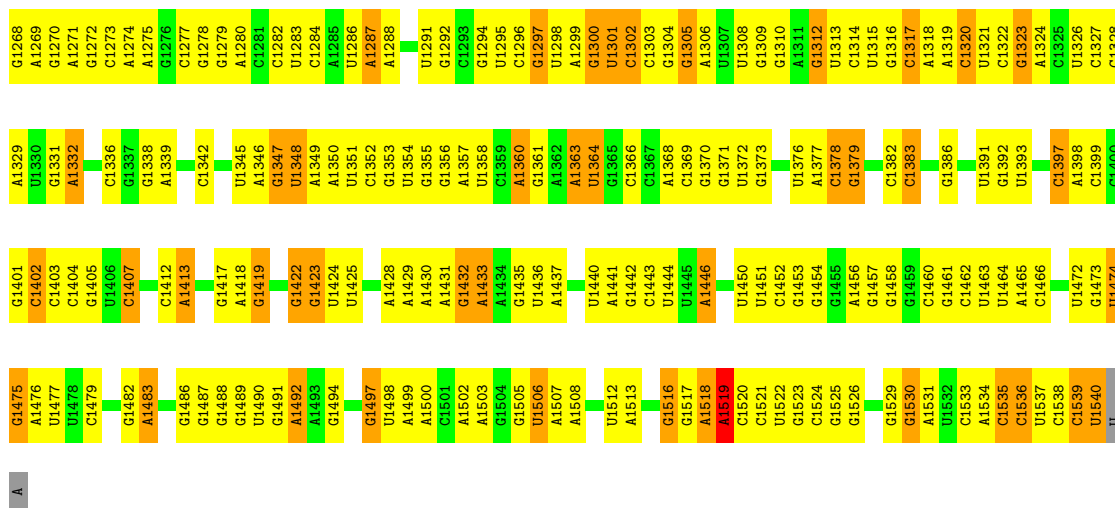
- Molecule 33: 50S ribosomal protein L30



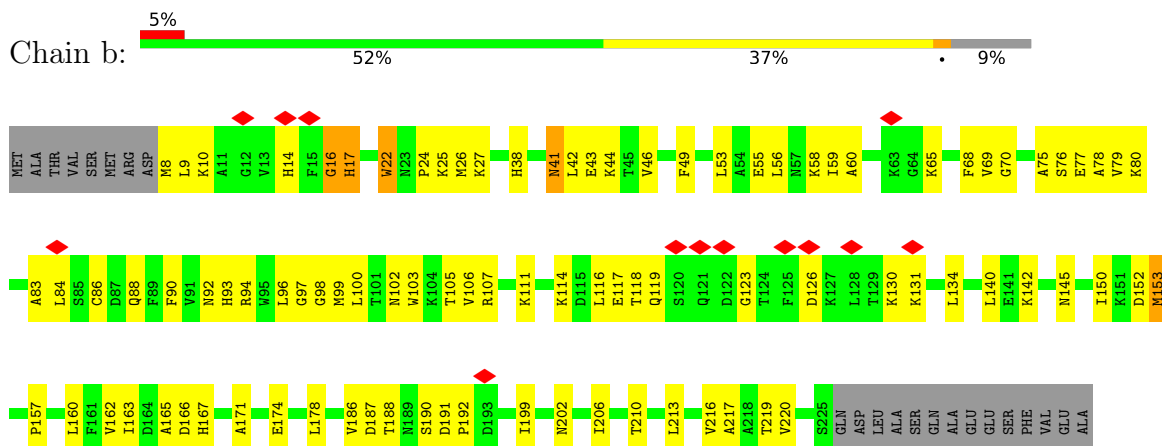
- Molecule 34: 16S ribosomal RNA



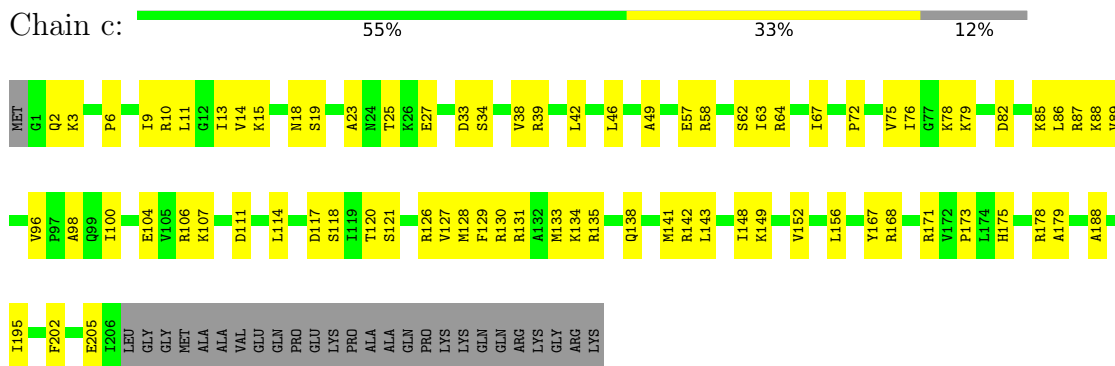
G1203	A1130	G1054	U986	U842	G756	U757	A681	A600	G530	A485	A383	A298	G227	G27	A78
A1204	G1131	A1055	G987	U843	U757	G758	G683	G601	U531	A488	G384	G299	A228	G79	G163
U1205	C1132	U1056	G988	G844	G758	C758	G683	A602	A532	A468	C385	A303	U229	A80	G164
G1206	G1133	G1057		A845	A759			U603		C469			G230	A81	G165
G1207	G1134	G1058	U991	G846	U686		U686	G604	A535	C470	G388	A309	U231	G82	A167
C1208		C1059	U992	G847	G687		G687	U605	C536	U471	A389		G232	C83	U166
C1209	G1137	U1060	G993	C848	C764			U606	A539	U472	U390		C233	U84	G168
G1210	G1138	G1061	A994	G849	G765		G691	A607	A539	U473	G391		C234	U85	C169
U1211	G1139	U1062	A995	U850	G766		U692	A608	G540	U474			C235	C87	G86
U1212		C1063	A996	G851	A767		G693	U609	G541	U475	A397		C236	C88	U173
A1213	G1142	G1064		G852	G768		A694	U610	G542	U476			G237	U88	U174
C1214	G1143	U1065			G769		A695		U543	C477	C401	A320	G240	U89	C175
G1215	G1144	G933	C999	U855	G773		U701	C613	G544	A478	C402	A321		C90	C176
A1216	A1145	C934	C1001	C856			A702	C614	C545	U479	C403	C322	G241	U91	G177
C1217	A1146	A935			G773			G615	A546	U480	G404	U323		U92	C178
C1218	C1147	A937	G936	G859	A777		G703		A547	U481	U405	G324	A243	U93	U179
A1219	U1148	U938	A1004	A860	G778		A704	C620	G548	A482	U406	U325	U244	G94	
G1220	C1149	A1005	A1005	G879	C779		G705	A621	C549	C483	U407	G326	U245	C95	
A1221	A1150	C940		A865	A780		A706	A622	G550	G484		A327	U246	C96	
G1222				C866	A781		U707		U551		G410	C328	G247	U96	
A1223	G1152	G944		G867				U625	U552	A487	A411	A329	G251	C97	
U1224	G1153	A945		C868	U789		A712	U626	A553	C488	A412	C330	U252	A98	
A1225		A946		G869	A790		G713	G627	A554		A413	G331	A253	C99	
C1226	A1157	C947		U870	G791		G714		U555		A414	G332			
A1227	U1085	A948		U871	A792		A715	A629	C556		A415		U256	U103	
G1228	U1159	A949		A872	U793		A716				A416		C257	G104	
A1229	C1160	U950		A873	U794			U632	A559		U420	A336	C257	G105	
C1230	G1162			G874	C795		G719	C634	A560	A496	U421	A338	G259	C106	
G1231		G954		U875	C796		G720	A641	G567	A498	U422		U261	G107	
		U955			C797					A499	G423		A262	G108	
U1234	A1163	U956		A878			G721		G504	G500		C344	A263	A109	
A1235	U1165	U957		C879	G803		G722		U571	C501	U427	C345	A264	C110	
C1237	G1166	A958		C880	U804		U723		A572	C507	U437	A352	C267	G111	
A1238	U1167	U959		G881			G724		A573	U508	U438	A353	C268	G112	
A1239	A1168	U960		C882	C810		G725		A574	A509	U439	C354	A270	G113	
C1240	U1169	U961		C883	C811		G726		G575	A510	C440	C355	C272	A130	
A1241	A1170	C962		U884	G812		G727		C576	C511	G444	A356	A274	A131	
G1242	C1171	G963		G885	U813		A728	A642	G577	U512	G445			C132	
C1243		A964		G890	U814		G729		C578	C513	G446	G359	U208	U133	
G1244		U965		U891	A815		G730	A648	A579	C514	G447	G360	U209	G134	
	U1175			A892	A816		G733	A649	G579	C515	G448	G361	C210		
A1250	A1176	C967		C893	C817		G734	C651	G579	C516	G449	G362	C211	U137	
A1251	G1177	A968		C894	G818		G735	U652	C577	U517	G450		G212		
A1252	C1178	A969		G895	U820		G736	U653	C578	U518	G451	U365	A282	G141	
G1253	A1179	C970		C896	U821		C737		A579	C519	G452	A366	U283		
A1254	A1180	G971			U822		C738	A663	G581	U516	G453	U367	C284	G144	
G1255	G1182	C972			U822		C739	C664	C582	C518	G454	U368	C285	G145	
A1256	U1183	G973		A900	C826		G742	A665			G455	U369	C286	G146	
A1257	G1184	U974		G902			A743	G667	C586	G521	G456			G147	
G1258		A975		A906	G829		C744		G587	C522	A457	C372	C289	A149	
C1259		G976		A907	U834		G745			C523	A459	A373	G289	C221	
A1260	A1196	A978		A908	U835		A746	A673	G592	A524	A459	A374		A223	
C1261	C1045	C979		A909	U836		A747	A675	U593	C525	A460	U375		C224	
C1262	U1047	G980		A910	G837		G748	A676	U594	G526	A461		U294	A159	
G1263	G1048	U981		C910	U837			U677	A595	G527	G462		C295	G158	
U1264		U982		U911	G838			U678	A596	C528	U463	C381	U296	G159	
C1265		A983		C912	C839		A753	U679	G597	G529				C225	
A1266	A1201	C984		A913	C840		C754	C690			U464	A382	G297	A160	
C1267	U1202			A914	G755										



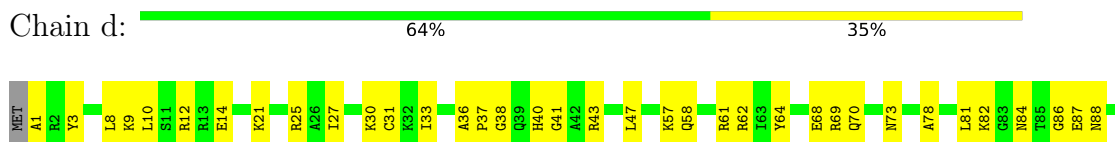
- Molecule 35: 30S ribosomal protein S2

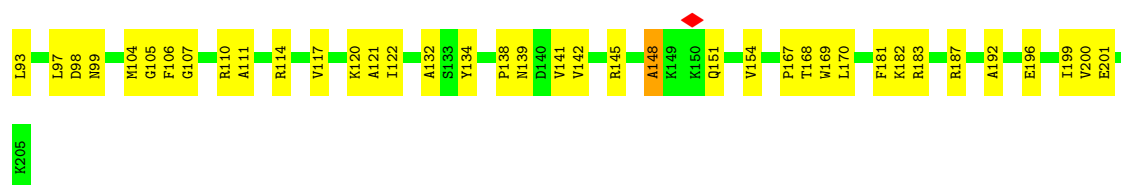


- Molecule 36: 30S ribosomal protein S3



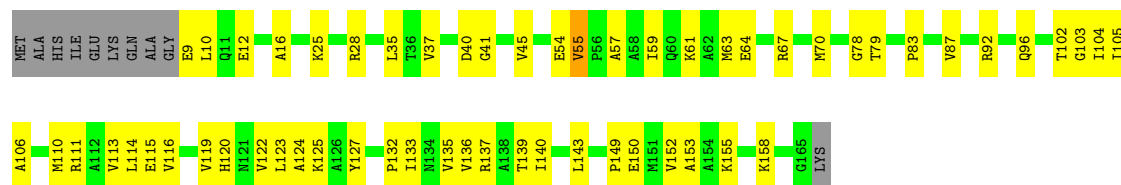
- Molecule 37: 30S ribosomal protein S4





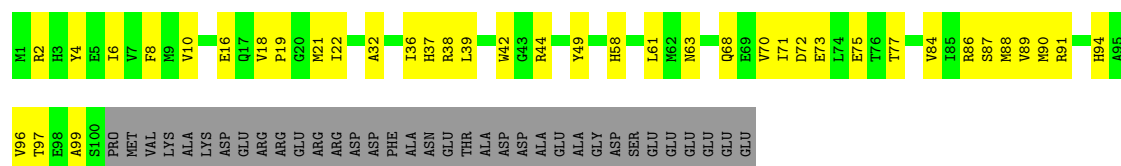
- Molecule 38: 30S ribosomal protein S5

Chain e: 59% 34% 6%



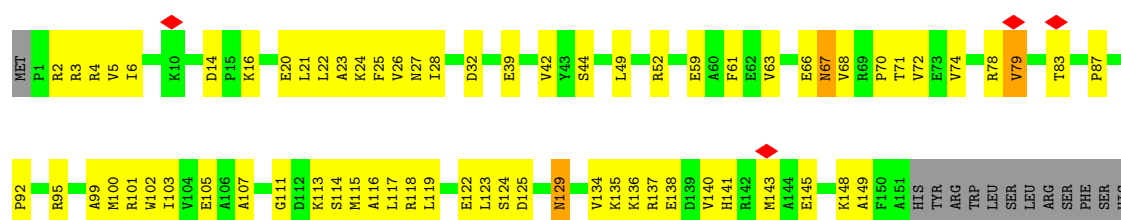
- Molecule 39: 30S ribosomal protein S6, fully modified isoform

Chain f: 45% 29% 26%



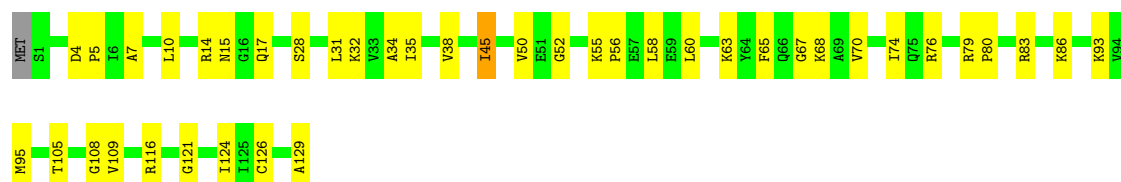
- Molecule 40: 30S ribosomal protein S7

Chain g: 45% 37% 16%

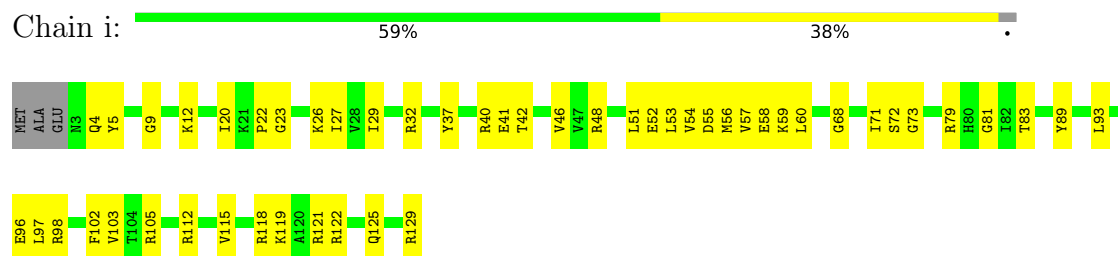


- Molecule 41: 30S ribosomal protein S8

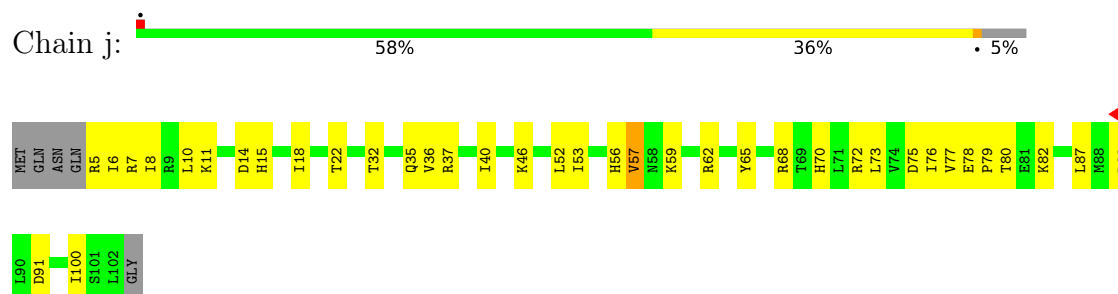
Chain h: 68% 31% 1%



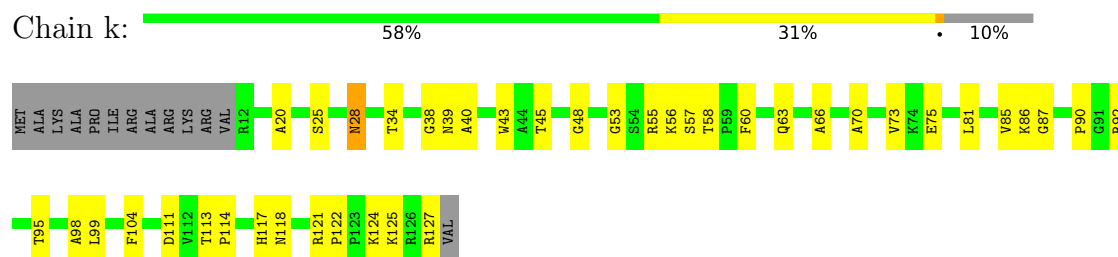
- Molecule 42: 30S ribosomal protein S9



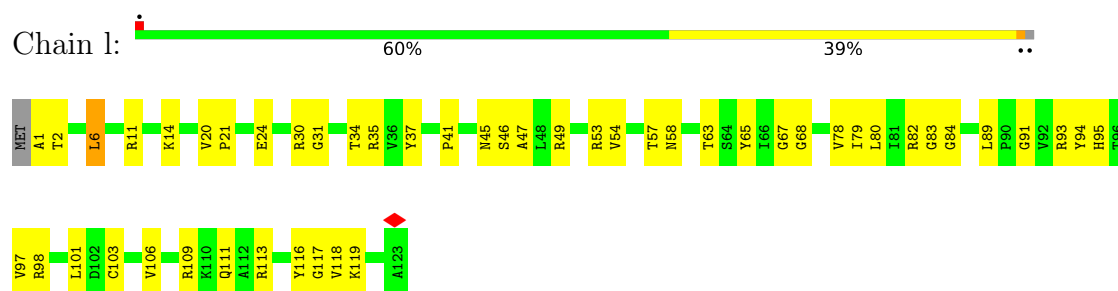
- Molecule 43: 30S ribosomal protein S10



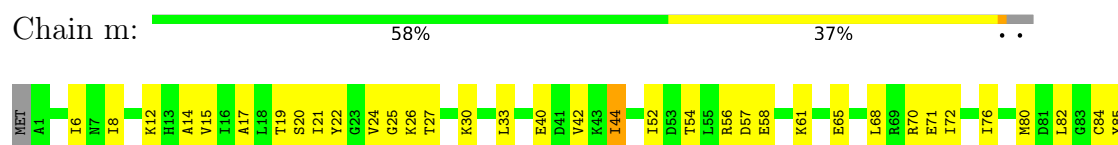
- Molecule 44: 30S ribosomal protein S11



- Molecule 45: 30S ribosomal protein S12



- Molecule 46: 30S ribosomal protein S13





- Molecule 47: 30S ribosomal protein S14

Chain n: 64% 35%



- Molecule 48: 30S ribosomal protein S15

Chain o: 70% 29%



- Molecule 49: 30S ribosomal protein S16

Chain p: 77% 23%



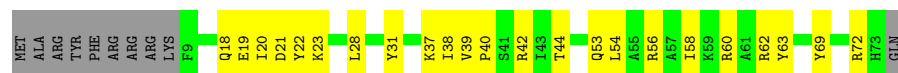
- Molecule 50: 30S ribosomal protein S17

Chain q: 62% 32% 5%



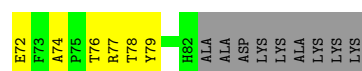
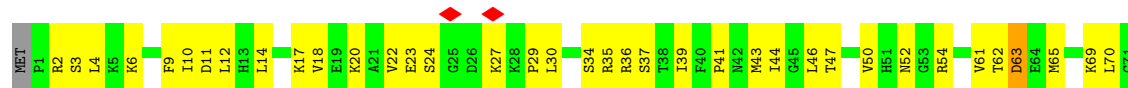
- Molecule 51: 30S ribosomal protein S18

Chain r: 56% 31% 13%



- Molecule 52: 30S ribosomal protein S19

Chain s: 42% 46% 11%

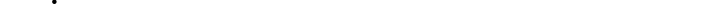


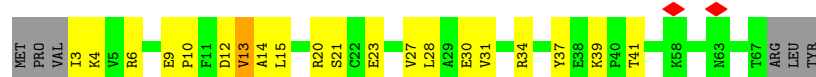
- Molecule 53: 30S ribosomal protein S20

Chain t: 68% 30%



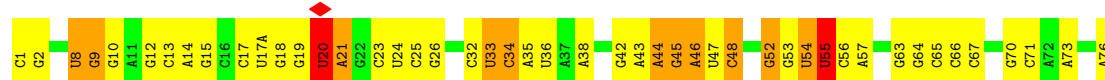
- Molecule 54: 30S ribosomal protein S21

Chain u:  63% 27% 8%

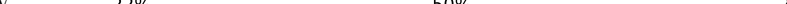


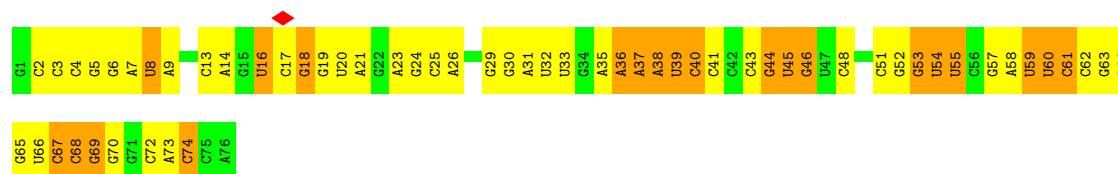
- Molecule 55: P-site tRNA(fMet)

Chain v:

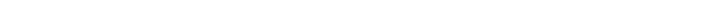


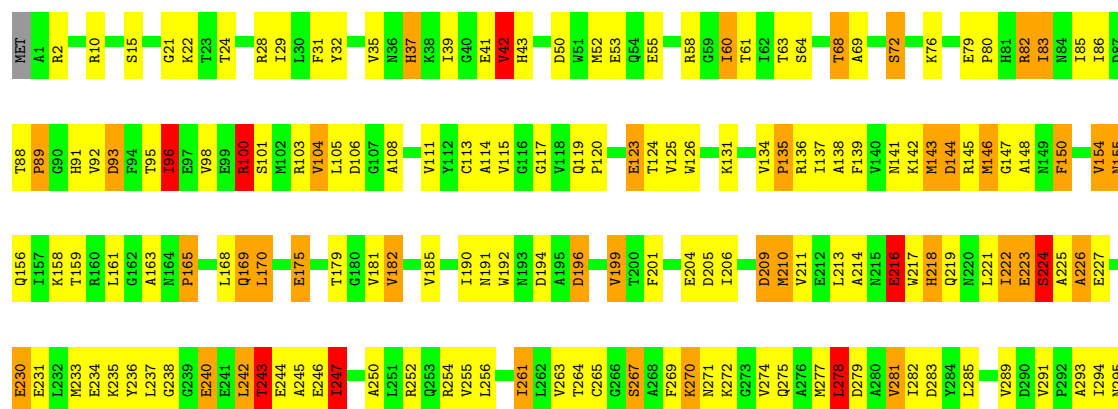
- Molecule 56: P-site fMet-Phe-tRNA(Phe)

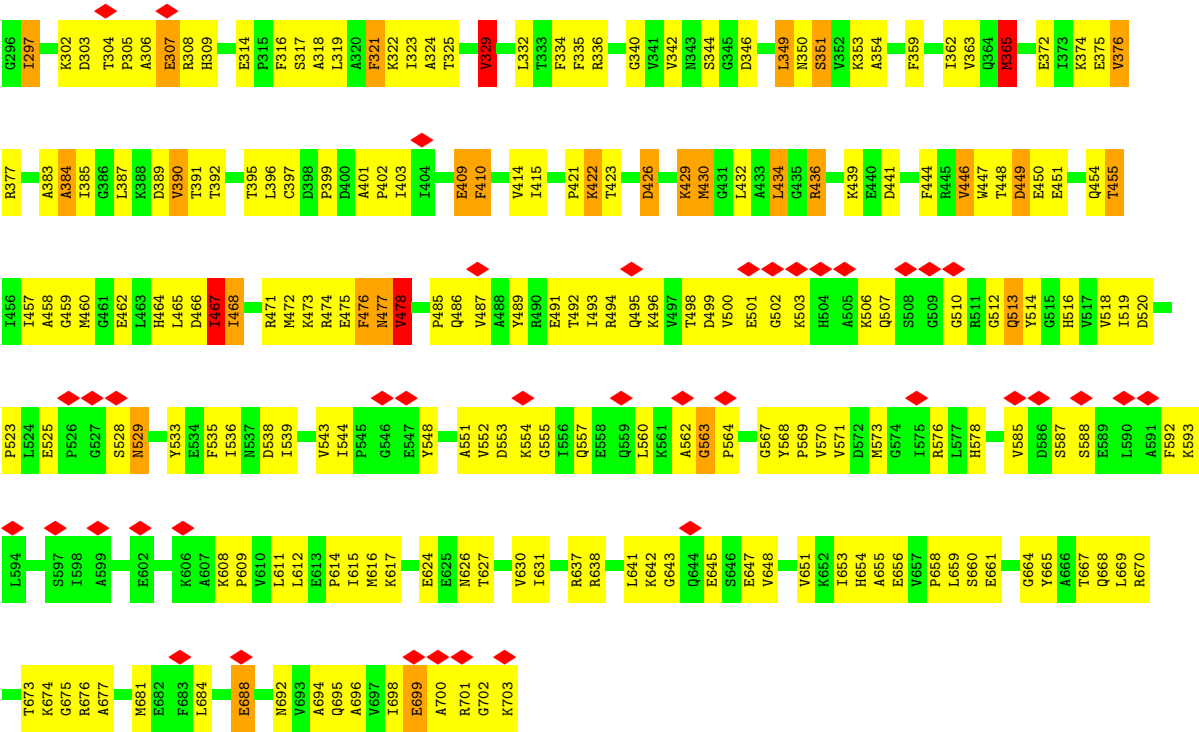
Chain w: 



- Molecule 57: Elongation factor G

Chain x: 





• Molecule 58: Dipeptide (FME-PHE)



• Molecule 59: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	24313	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	16.323	Depositor
Minimum map value	-7.685	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	1.5	Depositor
Map size (Å)	334.08, 334.08, 334.08	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.6525, 0.6525, 0.6525	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 1MG, 4OC, FME, PO4, G7M, MIA, H2U, AM2, OMC, OMG, MG, 3TD, 4SU, ZN, 2MA, PSU, NA, UR3, MA6, 2MG, 5MC, OMU, GDP, 5MU, 6MZ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.38	0/450	0.40	0/599
2	1	0.36	0/416	0.47	0/554
3	2	0.41	0/380	0.44	0/498
4	3	0.41	0/513	0.78	2/676 (0.3%)
5	4	0.37	0/303	0.45	0/397
6	5	0.35	0/646	0.83	2/898 (0.2%)
7	6	0.33	0/531	0.68	0/709
8	A	0.40	0/69266	0.40	6/108055 (0.0%)
9	B	0.33	0/2873	0.36	0/4478
10	C	0.42	0/2121	0.60	3/2852 (0.1%)
11	D	0.39	0/1586	0.51	1/2134 (0.0%)
12	E	0.37	0/1571	0.46	0/2113
13	F	0.29	0/1434	0.55	1/1926 (0.1%)
14	G	0.26	0/1343	0.44	0/1816
15	H	0.24	0/1122	0.60	2/1515 (0.1%)
16	I	0.36	0/692	0.79	3/960 (0.3%)
17	J	0.36	0/1152	0.41	0/1551
18	K	0.43	0/947	0.69	3/1268 (0.2%)
19	L	0.43	0/1054	0.66	1/1403 (0.1%)
20	M	0.38	0/1093	0.50	0/1460
21	N	0.40	0/973	0.57	0/1301
22	O	0.34	0/902	0.56	0/1209
23	P	0.36	0/929	0.51	0/1242
24	Q	0.40	0/960	0.43	0/1278
25	R	0.41	0/829	0.74	4/1107 (0.4%)
26	S	0.34	0/864	0.44	0/1156
27	T	0.34	0/744	0.55	1/994 (0.1%)
28	U	0.33	0/787	0.66	2/1051 (0.2%)
29	V	0.30	0/766	0.41	0/1025
30	W	0.35	0/582	0.43	0/769
31	X	0.37	0/635	0.45	0/848

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Y	0.35	0/510	0.49	1/677 (0.1%)
33	Z	0.33	0/453	0.40	0/605
34	a	0.34	0/36725	0.39	1/57285 (0.0%)
35	b	0.27	0/1735	0.69	3/2338 (0.1%)
36	c	0.27	0/1651	0.41	0/2225
37	d	0.34	0/1665	0.69	3/2227 (0.1%)
38	e	0.37	0/1154	0.61	1/1554 (0.1%)
39	f	0.26	0/835	0.42	0/1128
40	g	0.25	0/1195	0.57	1/1602 (0.1%)
41	h	0.31	0/989	0.55	2/1326 (0.2%)
42	i	0.25	0/1034	0.48	0/1375
43	j	0.36	0/796	0.74	2/1077 (0.2%)
44	k	0.35	0/885	0.57	1/1195 (0.1%)
45	l	0.40	0/969	0.55	0/1300
46	m	0.29	0/892	0.64	2/1193 (0.2%)
47	n	0.30	0/811	0.52	0/1081
48	o	0.31	0/722	0.42	0/964
49	p	0.38	0/659	0.58	0/884
50	q	0.40	0/657	0.71	2/881 (0.2%)
51	r	0.35	0/544	0.54	0/731
52	s	0.25	0/675	0.43	0/908
53	t	0.27	0/671	0.41	0/888
54	u	0.23	0/512	0.67	2/683 (0.3%)
55	v	0.31	0/1745	0.42	0/2716
56	w	0.33	0/1650	0.49	2/2569 (0.1%)
57	x	0.83	7/5546 (0.1%)	1.43	78/7504 (1.0%)
58	y	0.33	0/11	0.31	0/13
59	z	0.34	0/255	0.32	0/394
All	All	0.39	7/164410 (0.0%)	0.51	132/245165 (0.1%)

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	x	317	SER	CA-CB	-6.74	1.41	1.53
57	x	267	SER	CA-CB	-5.81	1.44	1.53
57	x	89	PRO	C-O	-5.31	1.17	1.23
57	x	224	SER	CA-CB	-5.30	1.44	1.53
57	x	344	SER	CA-CB	-5.26	1.44	1.53

The worst 5 of 132 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	b	16	GLY	N-CA-C	19.51	136.09	112.48
37	d	148	ALA	N-CA-C	-12.59	98.40	113.88
28	U	98	ASN	N-CA-C	-12.13	90.89	108.60
57	x	563	GLY	N-CA-C	11.93	136.68	112.34
40	g	79	VAL	N-CA-C	-11.34	99.88	110.53

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	444	0	461	21	0
2	1	409	0	440	12	0
3	2	377	0	418	12	0
4	3	504	0	574	17	0
5	4	302	0	340	14	0
6	5	647	0	336	13	0
7	6	522	0	521	27	0
8	A	62338	0	31369	1341	0
9	B	2570	0	1301	64	0
10	C	2082	0	2157	85	0
11	D	1565	0	1616	43	0
12	E	1552	0	1619	54	0
13	F	1410	0	1447	75	0
14	G	1323	0	1374	39	0
15	H	1111	0	1148	37	0
16	I	693	0	347	18	0
17	J	1129	0	1162	31	0
18	K	938	0	1012	27	0
19	L	1045	0	1117	36	0
20	M	1074	0	1157	37	0
21	N	960	0	1000	34	0
22	O	892	0	923	24	0
23	P	917	0	965	29	0
24	Q	947	0	1022	31	0
25	R	816	0	839	23	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	S	857	0	922	31	0
27	T	738	0	807	22	0
28	U	779	0	834	27	0
29	V	753	0	780	29	0
30	W	575	0	592	20	0
31	X	625	0	655	24	0
32	Y	509	0	543	19	0
33	Z	449	0	491	9	0
34	a	33050	0	16652	827	0
35	b	1704	0	1732	70	0
36	c	1624	0	1699	53	0
37	d	1643	0	1710	58	0
38	e	1141	0	1170	38	0
39	f	817	0	808	30	0
40	g	1181	0	1240	58	0
41	h	979	0	1034	30	0
42	i	1022	0	1070	43	0
43	j	786	0	828	39	0
44	k	869	0	878	35	0
45	l	955	0	1019	42	0
46	m	883	0	944	33	0
47	n	799	0	841	33	0
48	o	714	0	737	23	0
49	p	649	0	666	10	0
50	q	648	0	691	17	0
51	r	535	0	552	16	0
52	s	658	0	685	47	0
53	t	665	0	714	23	0
54	u	506	0	502	17	0
55	v	1642	0	839	45	0
56	w	1631	0	837	55	0
57	x	5444	0	5416	235	0
58	y	21	0	19	0	0
59	z	230	0	116	4	0
60	0	1	0	0	0	0
60	A	262	0	0	0	0
60	B	7	0	0	0	0
60	C	3	0	0	0	0
60	D	1	0	0	0	0
60	O	1	0	0	0	0
60	P	1	0	0	0	0
60	Q	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	Z	1	0	0	0	0
60	a	85	0	0	0	0
60	m	1	0	0	0	0
60	n	1	0	0	0	0
60	v	1	0	0	0	0
60	w	1	0	0	0	0
60	x	1	0	0	0	0
60	z	1	0	0	0	0
61	4	1	0	0	0	0
61	6	1	0	0	0	0
62	A	1	0	0	0	0
62	B	1	0	0	0	0
63	a	111	0	123	2	0
64	x	28	0	12	3	0
65	x	5	0	0	2	0
All	All	153165	0	103823	3743	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 15.

The worst 5 of 3743 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:879:C:OP2	45:l:1:ALA:HB2	1.31	1.31
34:a:81:A:H61	34:a:86:G:N2	1.41	1.19
34:a:879:C:OP2	45:l:1:ALA:CB	2.02	1.08
34:a:765:G:H1	34:a:812:G:HO2'	1.04	1.01
55:v:44:A:H5''	55:v:44:A:H8	1.24	1.01

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	54/57 (95%)	53 (98%)	1 (2%)	0	100	100
2	1	48/55 (87%)	45 (94%)	3 (6%)	0	100	100
3	2	44/46 (96%)	40 (91%)	4 (9%)	0	100	100
4	3	62/65 (95%)	57 (92%)	5 (8%)	0	100	100
5	4	36/38 (95%)	31 (86%)	5 (14%)	0	100	100
6	5	129/165 (78%)	110 (85%)	19 (15%)	0	100	100
7	6	64/70 (91%)	54 (84%)	10 (16%)	0	100	100
10	C	269/273 (98%)	247 (92%)	22 (8%)	0	100	100
11	D	207/209 (99%)	186 (90%)	21 (10%)	0	100	100
12	E	199/201 (99%)	190 (96%)	9 (4%)	0	100	100
13	F	175/179 (98%)	153 (87%)	22 (13%)	0	100	100
14	G	174/177 (98%)	162 (93%)	12 (7%)	0	100	100
15	H	147/149 (99%)	122 (83%)	25 (17%)	0	100	100
16	I	139/142 (98%)	114 (82%)	25 (18%)	0	100	100
17	J	140/142 (99%)	133 (95%)	7 (5%)	0	100	100
18	K	120/123 (98%)	109 (91%)	11 (9%)	0	100	100
19	L	141/144 (98%)	131 (93%)	10 (7%)	0	100	100
20	M	134/136 (98%)	123 (92%)	11 (8%)	0	100	100
21	N	118/127 (93%)	111 (94%)	7 (6%)	0	100	100
22	O	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
23	P	112/115 (97%)	103 (92%)	9 (8%)	0	100	100
24	Q	115/118 (98%)	110 (96%)	5 (4%)	0	100	100
25	R	101/103 (98%)	92 (91%)	9 (9%)	0	100	100
26	S	108/110 (98%)	98 (91%)	10 (9%)	0	100	100
27	T	91/100 (91%)	87 (96%)	4 (4%)	0	100	100
28	U	100/104 (96%)	91 (91%)	9 (9%)	0	100	100
29	V	92/94 (98%)	86 (94%)	6 (6%)	0	100	100
30	W	73/85 (86%)	67 (92%)	6 (8%)	0	100	100
31	X	75/78 (96%)	70 (93%)	5 (7%)	0	100	100
32	Y	61/63 (97%)	58 (95%)	3 (5%)	0	100	100
33	Z	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
35	b	216/240 (90%)	197 (91%)	19 (9%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	c	204/233 (88%)	194 (95%)	10 (5%)	0	100	100
37	d	203/206 (98%)	176 (87%)	27 (13%)	0	100	100
38	e	155/167 (93%)	144 (93%)	11 (7%)	0	100	100
39	f	98/135 (73%)	88 (90%)	10 (10%)	0	100	100
40	g	149/179 (83%)	139 (93%)	10 (7%)	0	100	100
41	h	127/130 (98%)	120 (94%)	7 (6%)	0	100	100
42	i	125/130 (96%)	109 (87%)	16 (13%)	0	100	100
43	j	96/103 (93%)	83 (86%)	13 (14%)	0	100	100
44	k	114/129 (88%)	98 (86%)	16 (14%)	0	100	100
45	l	121/124 (98%)	107 (88%)	14 (12%)	0	100	100
46	m	112/118 (95%)	100 (89%)	12 (11%)	0	100	100
47	n	99/102 (97%)	92 (93%)	7 (7%)	0	100	100
48	o	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
49	p	80/82 (98%)	71 (89%)	9 (11%)	0	100	100
50	q	78/84 (93%)	71 (91%)	7 (9%)	0	100	100
51	r	63/75 (84%)	57 (90%)	6 (10%)	0	100	100
52	s	80/92 (87%)	76 (95%)	4 (5%)	0	100	100
53	t	83/87 (95%)	81 (98%)	2 (2%)	0	100	100
54	u	63/71 (89%)	55 (87%)	8 (13%)	0	100	100
57	x	701/704 (100%)	652 (93%)	48 (7%)	1 (0%)	48	78
All	All	6551/6924 (95%)	5985 (91%)	565 (9%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
57	x	165	PRO

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%)	44 (98%)	1 (2%)	45	71
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%)	56 (95%)	3 (5%)	21	52
10	C	216/218 (99%)	214 (99%)	2 (1%)	70	80
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%)	146 (99%)	2 (1%)	59	76
14	G	137/138 (99%)	137 (100%)	0	100	100
15	H	114/114 (100%)	114 (100%)	0	100	100
17	J	116/116 (100%)	116 (100%)	0	100	100
18	K	103/104 (99%)	102 (99%)	1 (1%)	68	79
19	L	102/103 (99%)	100 (98%)	2 (2%)	48	72
20	M	109/109 (100%)	108 (99%)	1 (1%)	70	80
21	N	100/103 (97%)	100 (100%)	0	100	100
22	O	86/87 (99%)	85 (99%)	1 (1%)	63	78
23	P	99/100 (99%)	98 (99%)	1 (1%)	68	79
24	Q	89/90 (99%)	88 (99%)	1 (1%)	65	78
25	R	84/84 (100%)	79 (94%)	5 (6%)	17	47
26	S	93/93 (100%)	93 (100%)	0	100	100
27	T	80/84 (95%)	80 (100%)	0	100	100
28	U	83/85 (98%)	81 (98%)	2 (2%)	43	69
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%)	53 (96%)	2 (4%)	31	62
33	Z	48/49 (98%)	48 (100%)	0	100	100
35	b	180/198 (91%)	176 (98%)	4 (2%)	45	71
36	c	170/190 (90%)	170 (100%)	0	100	100
37	d	172/173 (99%)	170 (99%)	2 (1%)	63	78

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	e	114/126 (90%)	113 (99%)	1 (1%)	70	80
39	f	87/116 (75%)	87 (100%)	0	100	100
40	g	124/147 (84%)	121 (98%)	3 (2%)	43	69
41	h	104/105 (99%)	103 (99%)	1 (1%)	68	79
42	i	105/107 (98%)	105 (100%)	0	100	100
43	j	86/90 (96%)	85 (99%)	1 (1%)	63	78
44	k	89/99 (90%)	87 (98%)	2 (2%)	45	71
45	l	103/104 (99%)	101 (98%)	2 (2%)	50	73
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%)	63 (97%)	2 (3%)	35	64
50	q	74/78 (95%)	73 (99%)	1 (1%)	59	76
51	r	56/65 (86%)	55 (98%)	1 (2%)	51	73
52	s	72/79 (91%)	71 (99%)	1 (1%)	59	76
53	t	65/66 (98%)	65 (100%)	0	100	100
54	u	46/61 (75%)	46 (100%)	0	100	100
57	x	577/578 (100%)	491 (85%)	86 (15%)	3	13
58	y	1/1 (100%)	1 (100%)	0	100	100
All	All	5204/5408 (96%)	5073 (98%)	131 (2%)	42	69

5 of 131 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
57	x	446	VAL
57	x	455	THR
57	x	701	ARG
57	x	39	ILE
57	x	35	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
27	T	70	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
57	x	504	HIS
31	X	19	HIS
52	s	51	HIS
28	U	73	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	a	1539/1542 (99%)	336 (21%)	0
55	v	76/77 (98%)	17 (22%)	0
56	w	75/76 (98%)	23 (30%)	0
59	z	10/33 (30%)	4 (40%)	0
8	A	2902/2903 (99%)	648 (22%)	45 (1%)
9	B	119/120 (99%)	29 (24%)	3 (2%)
All	All	4721/4751 (99%)	1057 (22%)	48 (1%)

5 of 1057 RNA backbone outliers are listed below:

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

5 of 48 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	A	1730	C
8	A	2319	G
8	A	1907	G
8	A	2192	U
8	A	2405	G

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

46 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	PSU	A	2457	8	18,21,22	1.06	3 (16%)	22,30,33	1.82	5 (22%)
34	MA6	a	1518	34	23,26,27	1.45	5 (21%)	34,38,41	2.82	12 (35%)
8	1MG	A	745	8	22,26,27	2.58	6 (27%)	33,39,42	2.01	7 (21%)
8	PSU	A	1917	8	18,21,22	0.95	1 (5%)	22,30,33	1.77	4 (18%)
8	PSU	A	955	8	18,21,22	1.05	2 (11%)	22,30,33	1.89	4 (18%)
58	FME	y	101	58	8,9,10	0.99	1 (12%)	7,9,11	0.86	0
34	5MC	a	1407	34	18,22,23	3.62	7 (38%)	26,32,35	1.02	1 (3%)
8	6MZ	A	1618	8	22,25,26	2.95	5 (22%)	30,36,39	4.35	14 (46%)
8	OMG	A	2251	8,56	23,26,27	1.76	6 (26%)	33,38,41	2.17	10 (30%)
56	PSU	w	32	56	18,21,22	1.06	1 (5%)	22,30,33	1.75	4 (18%)
56	G7M	w	46	56	23,26,27	4.07	16 (69%)	35,39,42	2.38	10 (28%)
56	MIA	w	37	56	28,31,32	3.03	10 (35%)	40,44,47	3.50	19 (47%)
55	5MU	v	54	55	19,22,23	4.78	7 (36%)	28,32,35	3.60	9 (32%)
8	5MU	A	1939	8	19,22,23	4.64	7 (36%)	28,32,35	3.79	9 (32%)
8	G7M	A	2069	60,8	23,26,27	4.08	15 (65%)	35,39,42	2.46	11 (31%)
8	5MC	A	747	8	18,22,23	3.56	7 (38%)	26,32,35	1.23	2 (7%)
8	PSU	A	1911	8	18,21,22	1.15	2 (11%)	22,30,33	1.95	6 (27%)
56	4SU	w	8	56	18,21,22	1.95	4 (22%)	26,30,33	2.31	4 (15%)
56	5MU	w	54	56	19,22,23	1.43	6 (31%)	28,32,35	2.10	9 (32%)
8	PSU	A	2580	60,8	18,21,22	1.10	3 (16%)	22,30,33	1.92	6 (27%)
8	6MZ	A	2030	8	22,25,26	3.05	5 (22%)	30,36,39	4.51	14 (46%)
8	5MC	A	1962	8	18,22,23	0.95	2 (11%)	26,32,35	1.33	3 (11%)
34	MA6	a	1519	34	23,26,27	1.46	4 (17%)	34,38,41	2.77	11 (32%)
8	PSU	A	2504	60,8	18,21,22	1.03	2 (11%)	22,30,33	1.75	4 (18%)
8	OMC	A	2498	60,8	19,22,23	2.84	7 (36%)	26,31,34	0.86	1 (3%)
8	PSU	A	2605	8	18,21,22	1.03	2 (11%)	22,30,33	1.85	3 (13%)
56	PSU	w	55	56	18,21,22	1.40	2 (11%)	22,30,33	1.87	3 (13%)
8	2MG	A	1835	8	23,26,27	2.93	8 (34%)	32,38,41	2.14	10 (31%)
8	PSU	A	2604	8	18,21,22	1.06	2 (11%)	22,30,33	2.01	4 (18%)
8	2MG	A	2445	8	23,26,27	1.36	4 (17%)	32,38,41	2.30	9 (28%)
8	3TD	A	1915	8	18,22,23	4.24	5 (27%)	22,32,35	1.72	3 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
55	4SU	v	8	55	18,21,22	3.59	7 (38%)	26,30,33	2.19	4 (15%)
55	PSU	v	55	55	18,21,22	1.09	1 (5%)	22,30,33	1.72	4 (18%)
34	2MG	a	966	34	23,26,27	3.03	7 (30%)	32,38,41	2.26	8 (25%)
8	PSU	A	746	60,8	18,21,22	1.03	2 (11%)	22,30,33	1.72	4 (18%)
34	2MG	a	1516	34	23,26,27	2.88	9 (39%)	32,38,41	2.31	12 (37%)
55	H2U	v	20	55	18,21,22	3.15	5 (27%)	21,30,33	1.96	5 (23%)
34	4OC	a	1402	34	20,23,24	2.97	8 (40%)	26,32,35	0.90	2 (7%)
34	PSU	a	516	60,34	18,21,22	0.96	1 (5%)	22,30,33	1.66	5 (22%)
34	UR3	a	1498	60,34	19,22,23	2.57	7 (36%)	26,32,35	1.34	3 (11%)
34	2MG	a	1207	34	23,26,27	2.92	8 (34%)	32,38,41	2.24	11 (34%)
8	OMU	A	2552	60,8	19,22,23	2.86	8 (42%)	26,31,34	1.78	5 (19%)
56	PSU	w	39	56	18,21,22	1.11	1 (5%)	22,30,33	1.84	4 (18%)
34	G7M	a	527	34	23,26,27	4.10	15 (65%)	35,39,42	2.36	11 (31%)
8	2MA	A	2503	60,8	22,25,26	3.63	9 (40%)	33,37,40	2.12	8 (24%)
34	5MC	a	967	34	18,22,23	3.68	7 (38%)	26,32,35	1.02	1 (3%)

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	PSU	A	2457	8	-	0/7/25/26	0/2/2/2
34	MA6	a	1518	34	-	0/11/29/30	0/3/3/3
8	1MG	A	745	8	-	0/7/25/26	0/3/3/3
8	PSU	A	1917	8	-	3/7/25/26	0/2/2/2
8	PSU	A	955	8	-	0/7/25/26	0/2/2/2
58	FME	y	101	58	-	7/7/9/11	-
34	5MC	a	1407	34	-	0/7/25/26	0/2/2/2
8	6MZ	A	1618	8	-	0/9/27/28	0/3/3/3
8	OMG	A	2251	8,56	-	2/9/27/28	0/3/3/3
56	PSU	w	32	56	-	3/7/25/26	0/2/2/2
56	G7M	w	46	56	-	1/7/25/26	0/3/3/3
56	MIA	w	37	56	-	3/15/33/34	0/3/3/3
55	5MU	v	54	55	-	0/7/25/26	0/2/2/2
8	5MU	A	1939	8	-	2/7/25/26	0/2/2/2
8	G7M	A	2069	60,8	-	2/7/25/26	0/3/3/3

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	5MC	A	747	8	-	1/7/25/26	0/2/2/2
8	PSU	A	1911	8	-	0/7/25/26	0/2/2/2
56	4SU	w	8	56	-	0/7/25/26	0/2/2/2
56	5MU	w	54	56	-	0/7/25/26	0/2/2/2
8	PSU	A	2580	60,8	-	0/7/25/26	0/2/2/2
8	6MZ	A	2030	8	-	2/9/27/28	0/3/3/3
8	5MC	A	1962	8	-	0/7/25/26	0/2/2/2
34	MA6	a	1519	34	-	3/11/29/30	0/3/3/3
8	PSU	A	2504	60,8	-	0/7/25/26	0/2/2/2
8	OMC	A	2498	60,8	-	1/9/27/28	0/2/2/2
8	PSU	A	2605	8	-	0/7/25/26	0/2/2/2
56	PSU	w	55	56	-	0/7/25/26	0/2/2/2
8	2MG	A	1835	8	-	2/9/27/28	0/3/3/3
8	PSU	A	2604	8	-	0/7/25/26	0/2/2/2
8	2MG	A	2445	8	-	0/9/27/28	0/3/3/3
8	3TD	A	1915	8	-	2/7/25/26	0/2/2/2
55	4SU	v	8	55	-	0/7/25/26	0/2/2/2
55	PSU	v	55	55	-	1/7/25/26	0/2/2/2
34	2MG	a	966	34	-	2/9/27/28	0/3/3/3
8	PSU	A	746	60,8	-	4/7/25/26	0/2/2/2
34	2MG	a	1516	34	-	0/9/27/28	0/3/3/3
55	H2U	v	20	55	-	7/7/38/39	0/2/2/2
34	4OC	a	1402	34	-	1/9/29/30	0/2/2/2
34	PSU	a	516	60,34	-	0/7/25/26	0/2/2/2
34	UR3	a	1498	60,34	-	2/7/25/26	0/2/2/2
34	2MG	a	1207	34	-	0/9/27/28	0/3/3/3
8	OMU	A	2552	60,8	-	3/9/27/28	0/2/2/2
56	PSU	w	39	56	-	3/7/25/26	0/2/2/2
34	G7M	a	527	34	-	1/7/25/26	0/3/3/3
8	2MA	A	2503	60,8	-	1/7/25/26	0/3/3/3
34	5MC	a	967	34	-	0/7/25/26	0/2/2/2

The worst 5 of 252 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1915	3TD	C6-C5	12.88	1.50	1.35
8	A	2030	6MZ	C6-N6	12.20	1.47	1.34
56	w	37	MIA	C2-S10	-11.90	1.65	1.75
8	A	1618	6MZ	C6-N6	11.86	1.47	1.34
8	A	2069	G7M	C2'-C3'	-11.59	1.21	1.53

The worst 5 of 298 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	2030	6MZ	C4-N9-C8	14.44	121.38	105.73
8	A	1618	6MZ	C4-N9-C8	13.24	120.08	105.73
8	A	1939	5MU	C5-C4-N3	12.35	125.85	115.31
55	v	54	5MU	C5-C4-N3	11.91	125.48	115.31
8	A	2030	6MZ	N9-C8-N7	-11.39	98.34	113.91

There are no chirality outliers.

5 of 59 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
34	a	966	2MG	O4'-C4'-C5'-O5'
34	a	966	2MG	C3'-C4'-C5'-O5'
34	a	1498	UR3	O4'-C1'-N1-C2
55	v	20	H2U	O4'-C4'-C5'-O5'
55	v	20	H2U	O4'-C1'-N1-C6

There are no ring outliers.

29 monomers are involved in 40 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
34	a	1518	MA6	1	0
8	A	745	1MG	1	0
8	A	1917	PSU	3	0
34	a	1407	5MC	1	0
8	A	2251	OMG	1	0
56	w	37	MIA	2	0
55	v	54	5MU	2	0
8	A	1939	5MU	1	0
8	A	1911	PSU	1	0
56	w	54	5MU	1	0
8	A	2030	6MZ	1	0
34	a	1519	MA6	2	0
8	A	2504	PSU	1	0
8	A	2498	OMC	2	0
56	w	55	PSU	1	0
8	A	2445	2MG	1	0
8	A	1915	3TD	1	0
55	v	8	4SU	1	0
55	v	55	PSU	2	0
34	a	966	2MG	1	0
8	A	746	PSU	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
34	a	1516	2MG	1	0
55	v	20	H2U	2	0
34	a	1402	4OC	2	0
34	a	516	PSU	3	0
34	a	1207	2MG	1	0
8	A	2552	OMU	2	0
56	w	39	PSU	3	0
8	A	2503	2MA	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 378 ligands modelled in this entry, 373 are monoatomic - leaving 5 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
63	AM2	a	1648	-	40,40,40	0.54	0	53,60,60	0.93	1 (1%)
63	AM2	a	1657	-	40,40,40	0.51	0	53,60,60	0.87	2 (3%)
64	GDP	x	801	60	28,30,30	1.38	4 (14%)	44,47,47	2.10	16 (36%)
65	PO4	x	802	60	4,4,4	4.81	2 (50%)	6,6,6	1.00	0
63	AM2	a	1652	-	40,40,40	0.52	0	53,60,60	1.00	3 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
63	AM2	a	1657	-	-	2/12/84/84	0/4/4/4

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
63	AM2	a	1652	-	-	2/12/84/84	0/4/4/4
64	GDP	x	801	60	-	0/16/32/32	0/3/3/3
63	AM2	a	1648	-	-	0/12/84/84	0/4/4/4

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
65	x	802	PO4	P-O1	9.16	1.72	1.50
64	x	801	GDP	C6-N1	-3.56	1.32	1.38
64	x	801	GDP	C5-N7	-2.66	1.33	1.39
64	x	801	GDP	C4-N9	-2.64	1.31	1.38
64	x	801	GDP	C5-C4	2.30	1.45	1.38

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
64	x	801	GDP	C5-C4-N3	-4.95	120.42	128.46
64	x	801	GDP	PA-O3A-PB	-4.50	117.39	132.83
64	x	801	GDP	C2-N3-C4	4.37	120.08	112.30
64	x	801	GDP	O3'-C3'-C4'	-4.25	98.75	111.05
64	x	801	GDP	N9-C4-N3	3.94	133.85	125.94

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
63	a	1652	AM2	OA5-CA8-OA8-CB1
63	a	1657	AM2	CA6-CA7-NA7-CA9
63	a	1657	AM2	OB1-CB5-CB6-OB6
63	a	1652	AM2	OA4-CA1-OA1-CC1

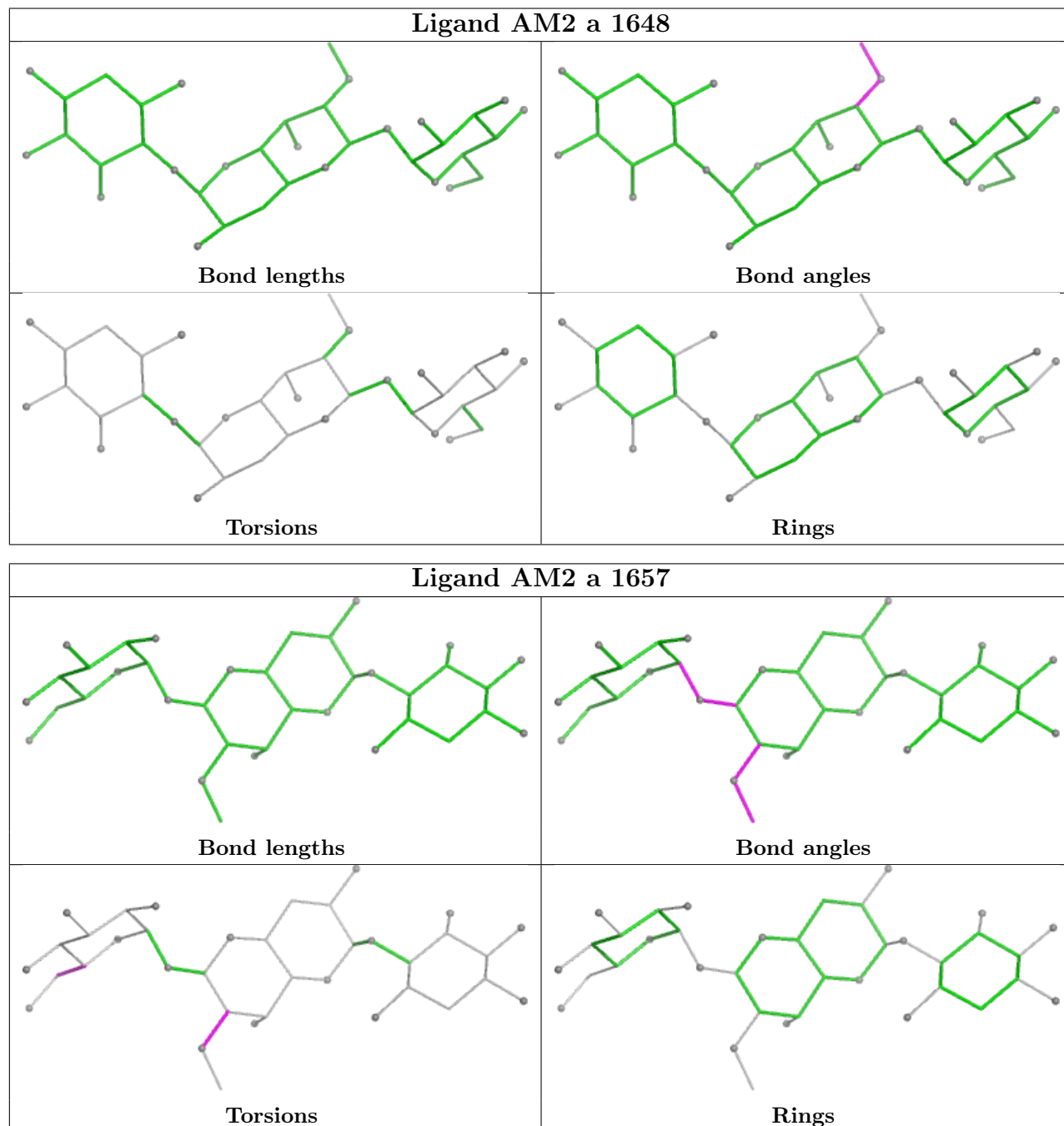
There are no ring outliers.

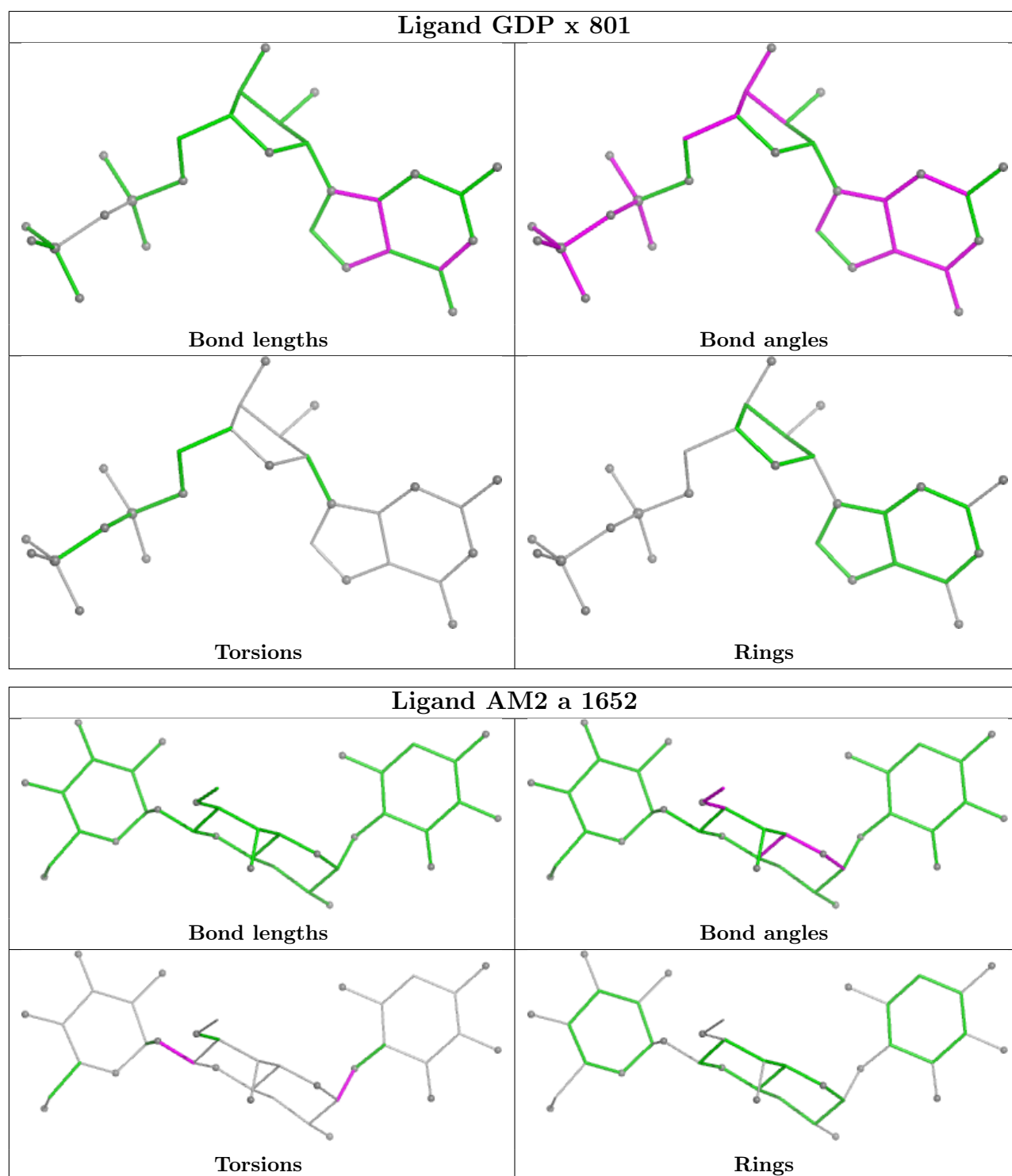
3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
63	a	1648	AM2	2	0
64	x	801	GDP	3	0
65	x	802	PO4	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

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





5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

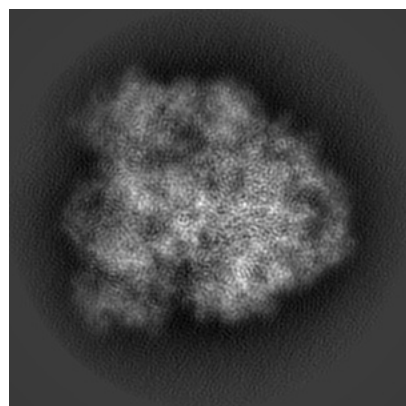
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13461. These allow visual inspection of the internal detail of the map and identification of artifacts.

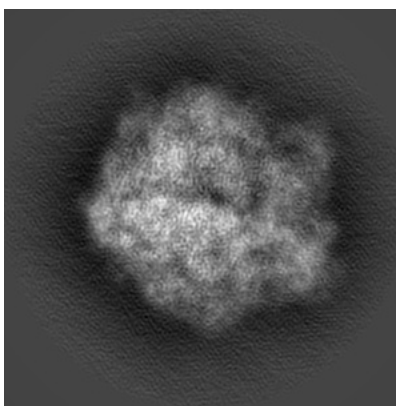
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

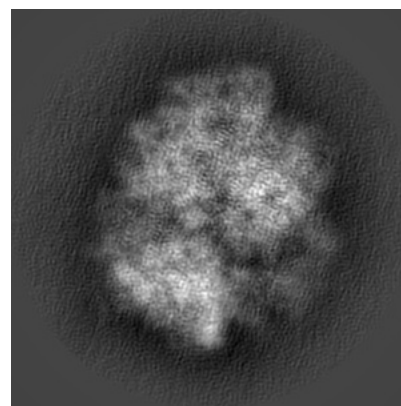
6.1.1 Primary map



X

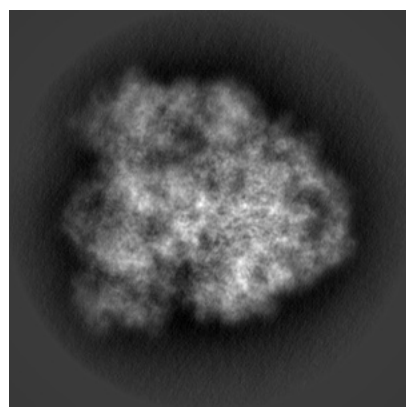


Y

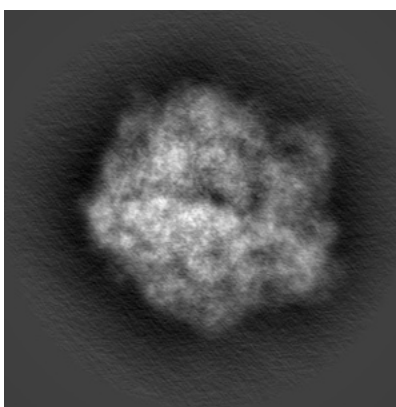


Z

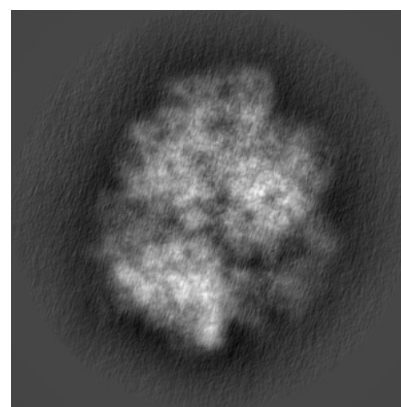
6.1.2 Raw map



X



Y

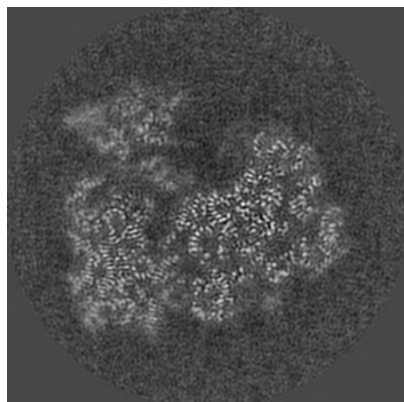


Z

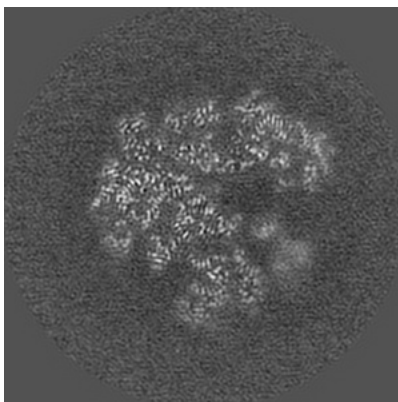
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

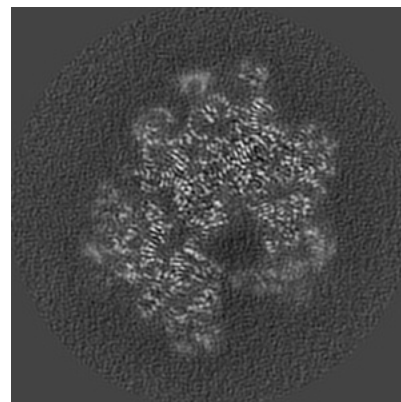
6.2.1 Primary map



X Index: 256

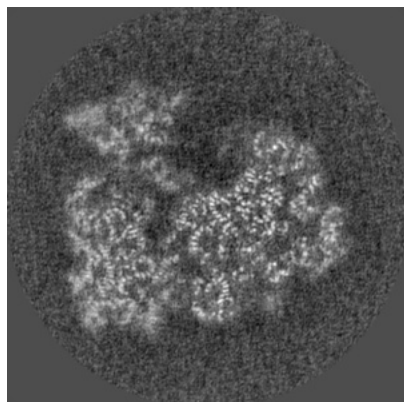


Y Index: 256

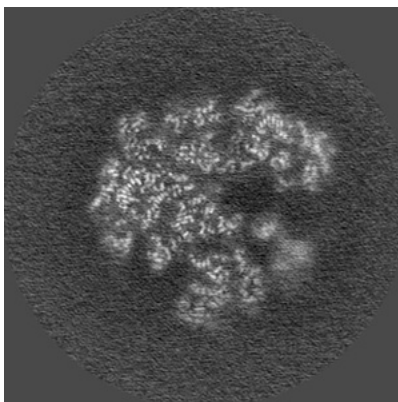


Z Index: 256

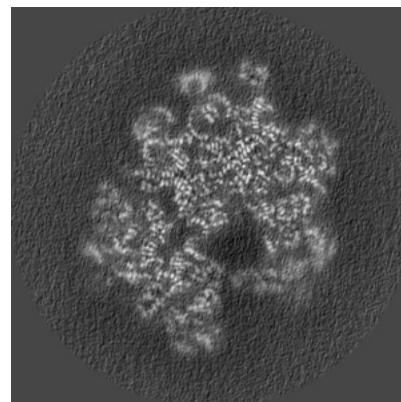
6.2.2 Raw map



X Index: 144



Y Index: 144

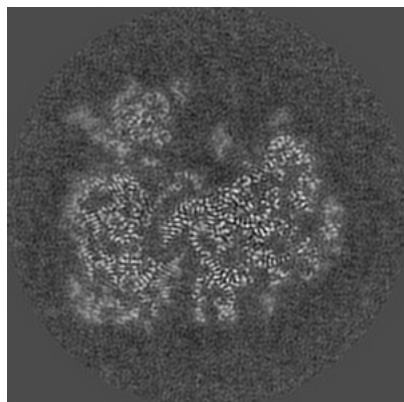


Z Index: 144

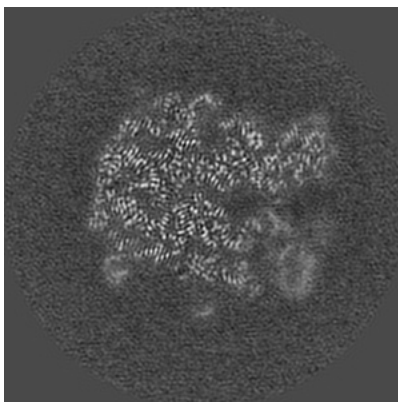
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

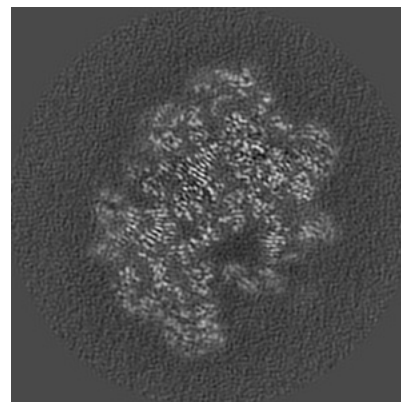
6.3.1 Primary map



X Index: 248

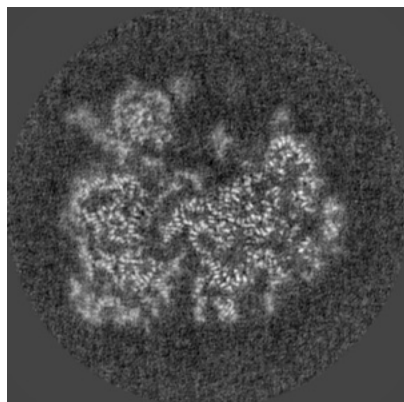


Y Index: 280

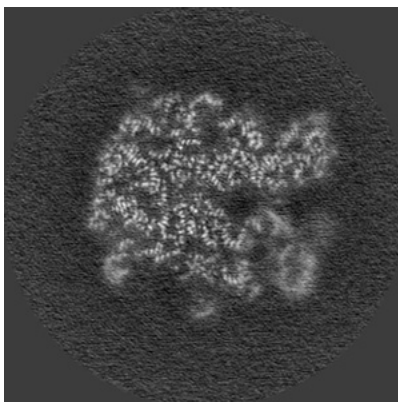


Z Index: 239

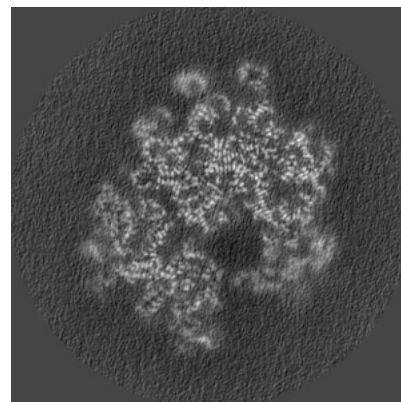
6.3.2 Raw map



X Index: 139



Y Index: 157

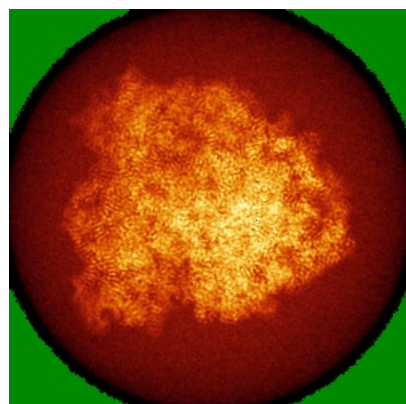


Z Index: 146

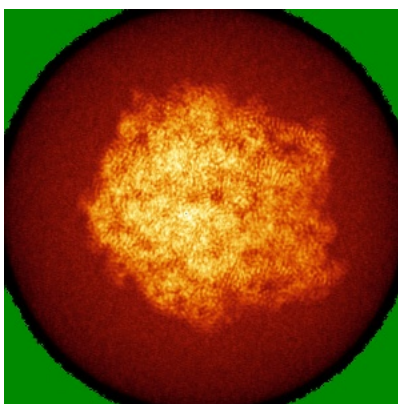
The images above show the largest variance slices of the map in three orthogonal directions.

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

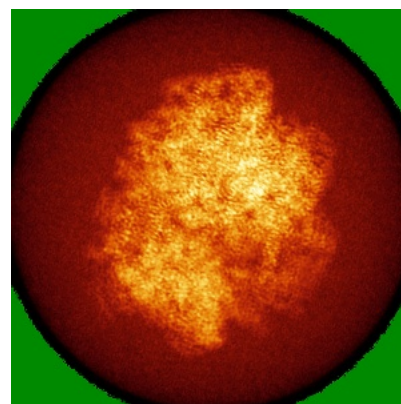
6.4.1 Primary map



X

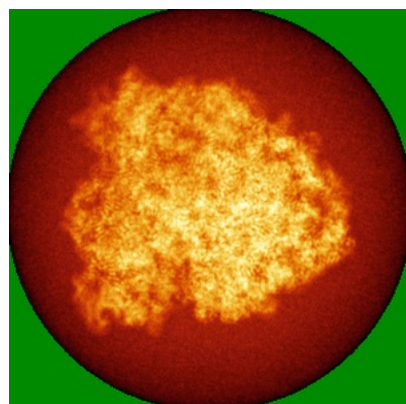


Y

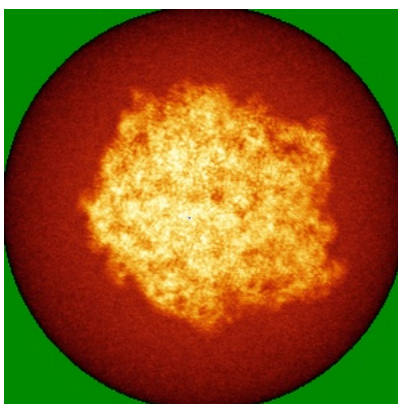


Z

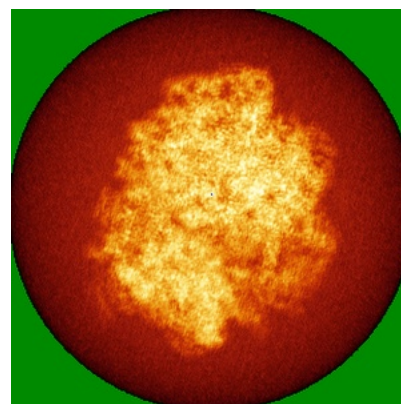
6.4.2 Raw map



X



Y

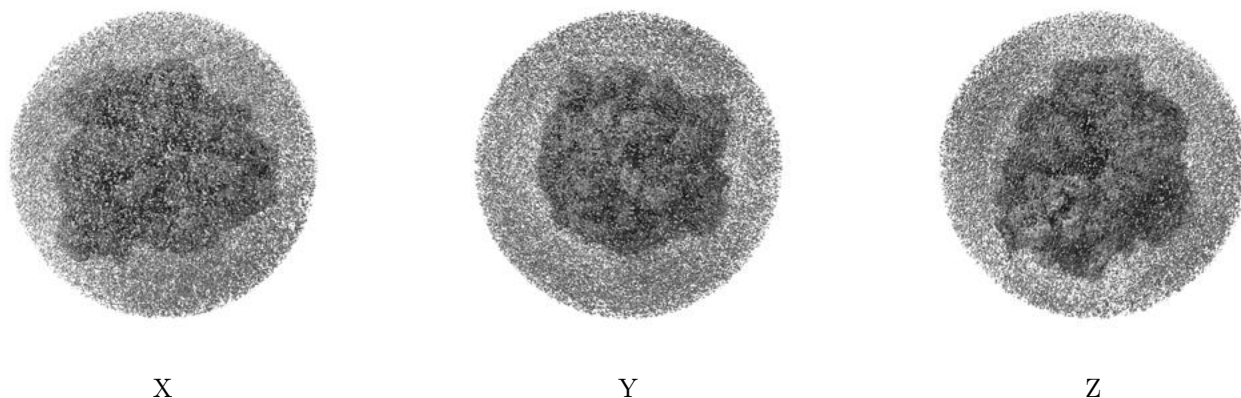


Z

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.

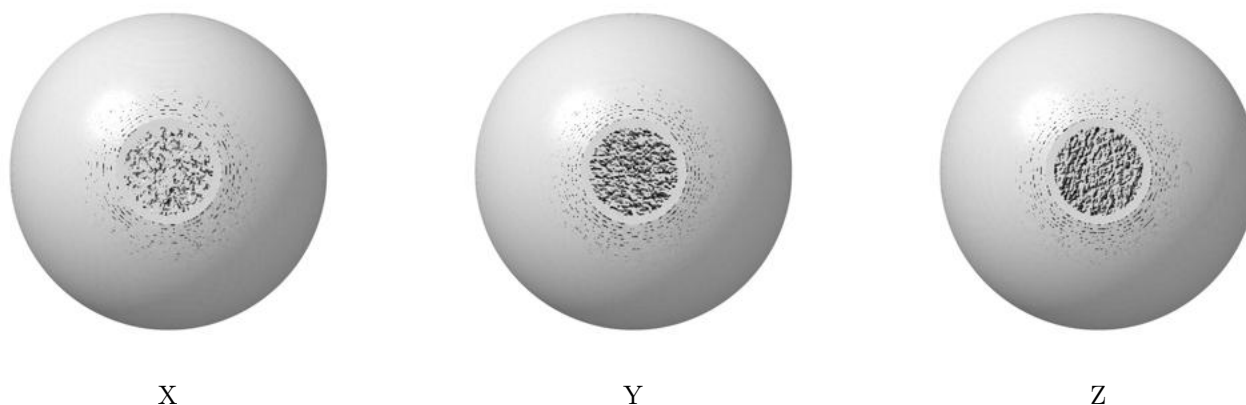
6.5 Orthogonal surface views [i](#)

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.

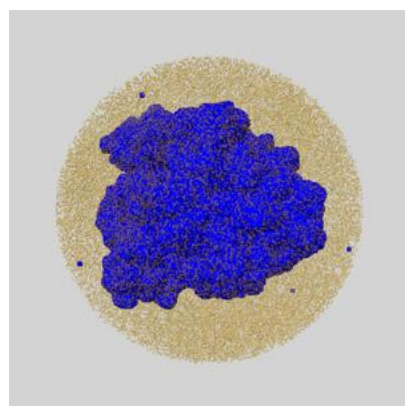
6.6 Mask visualisation [i](#)

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

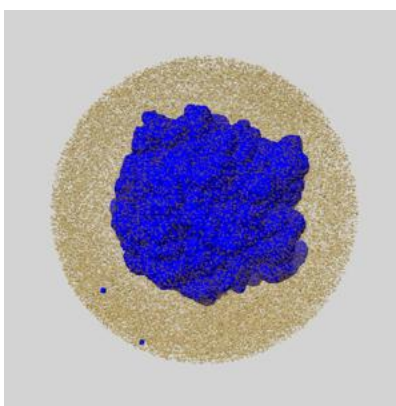
A mask typically either:

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

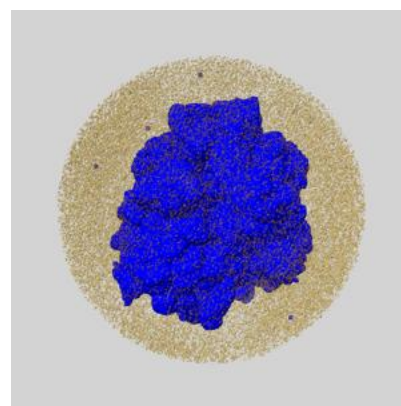
6.6.1 emd_13461_msk_1.map [i](#)



X



Y

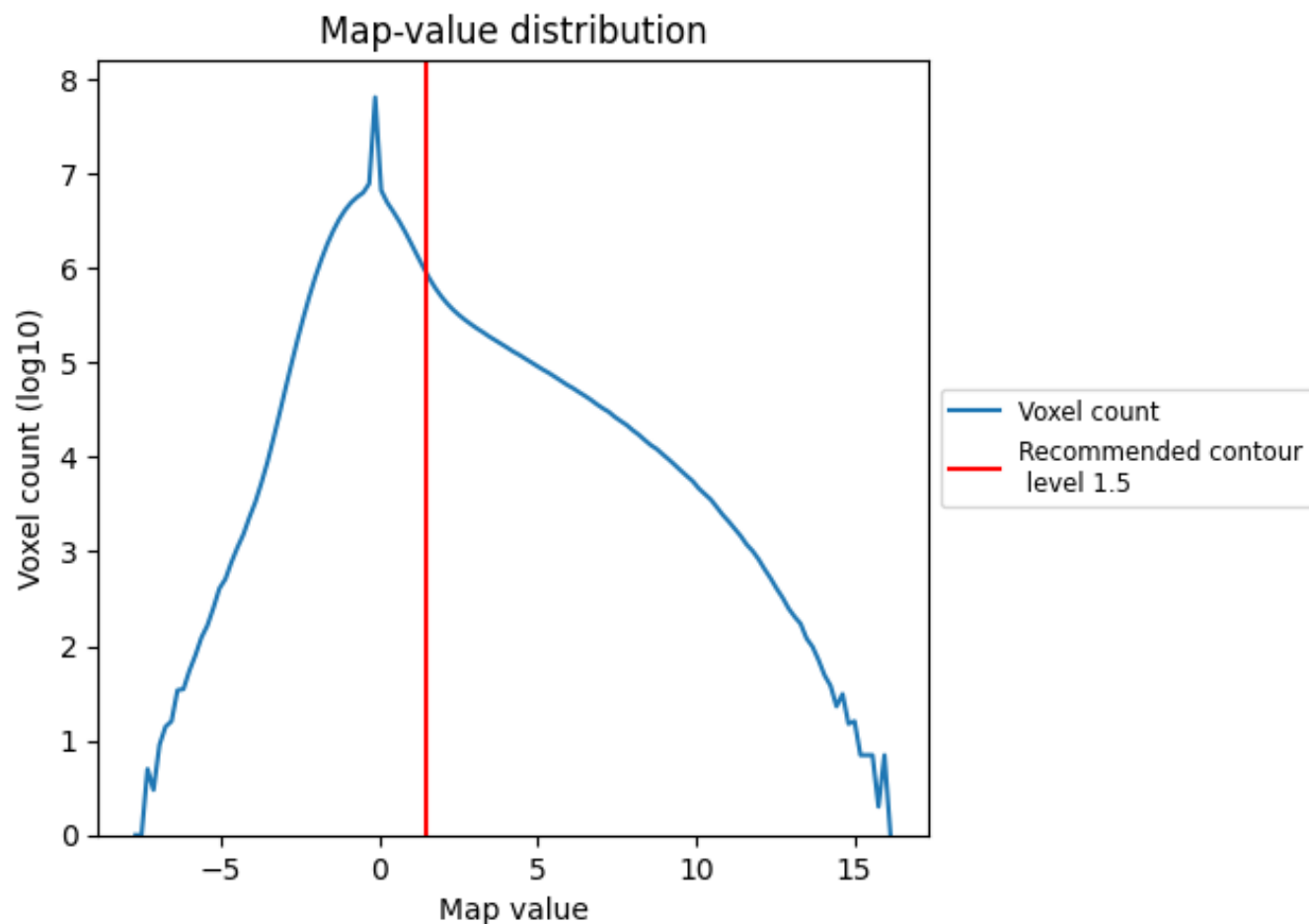


Z

7 Map analysis [i](#)

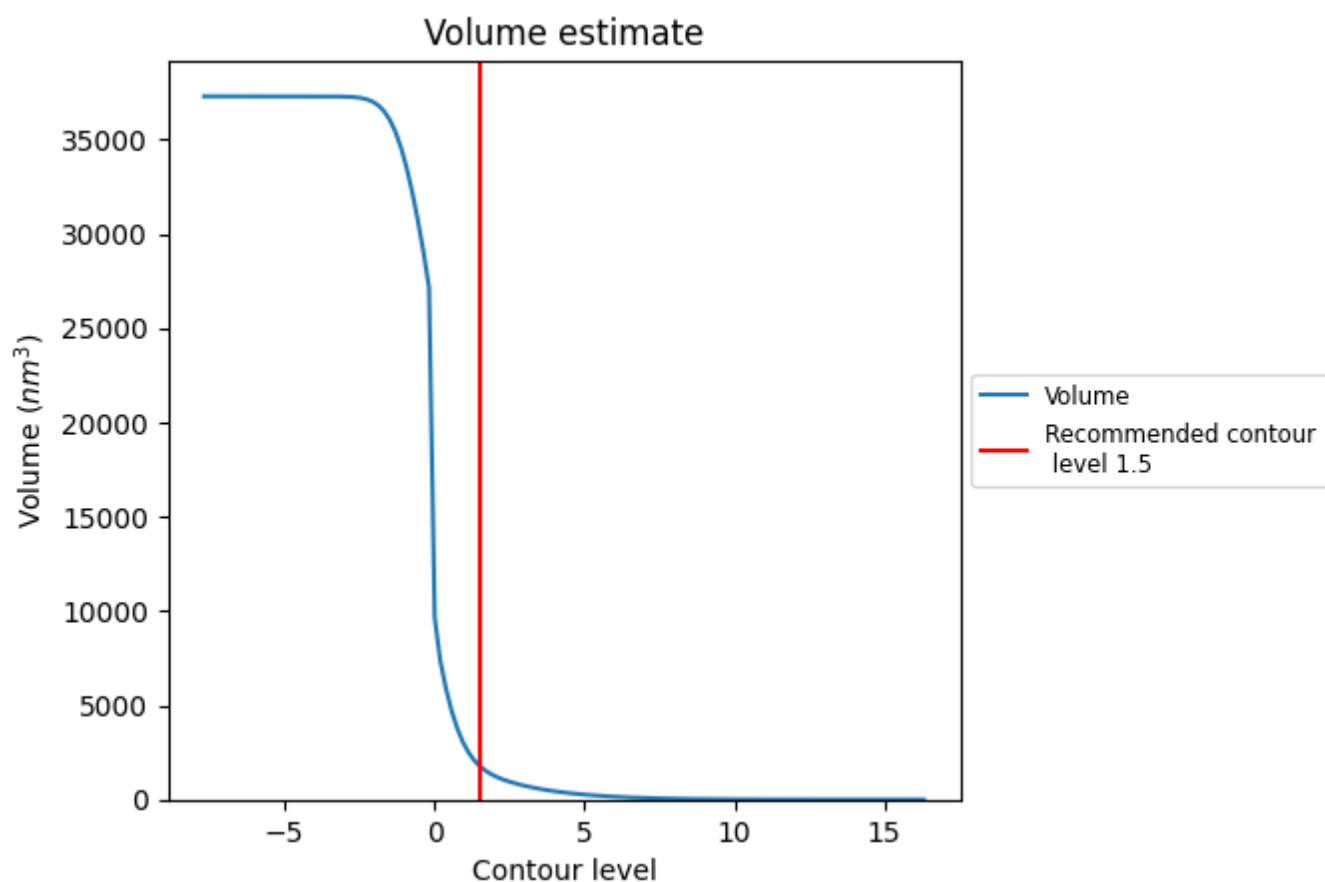
This section contains the results of statistical analysis of the map.

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.

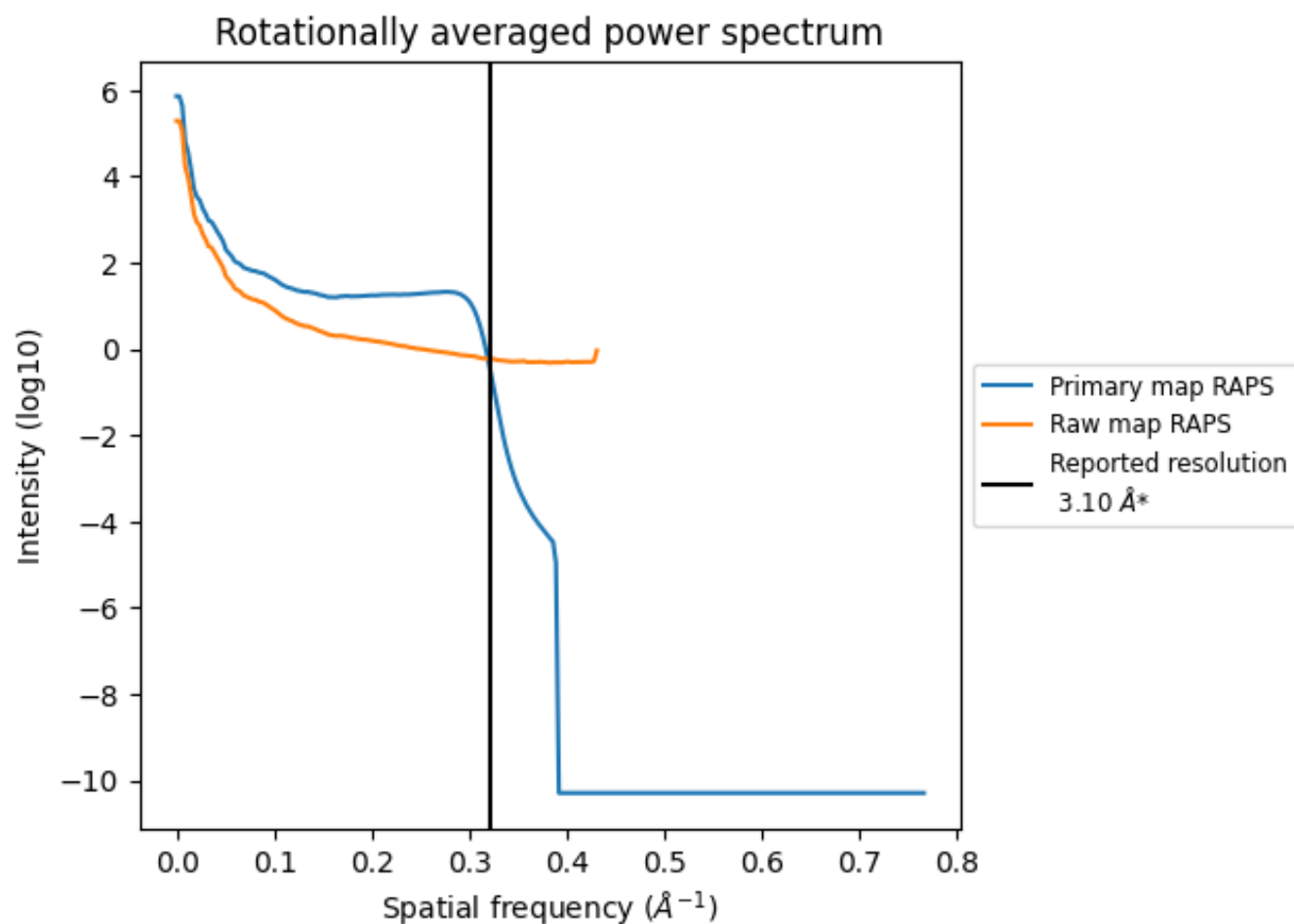
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1787 nm³; this corresponds to an approximate mass of 1614 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 ⓘ

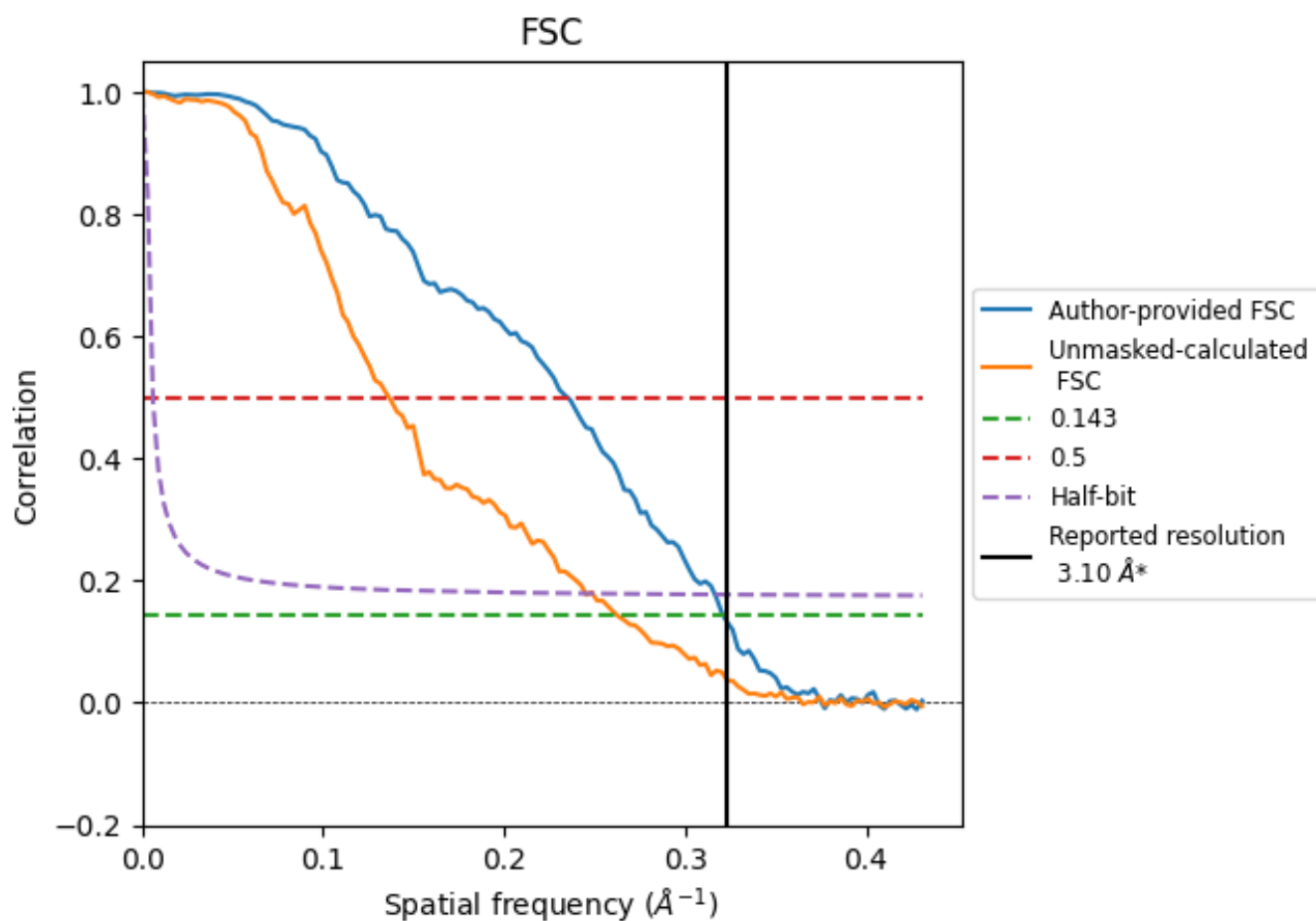


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

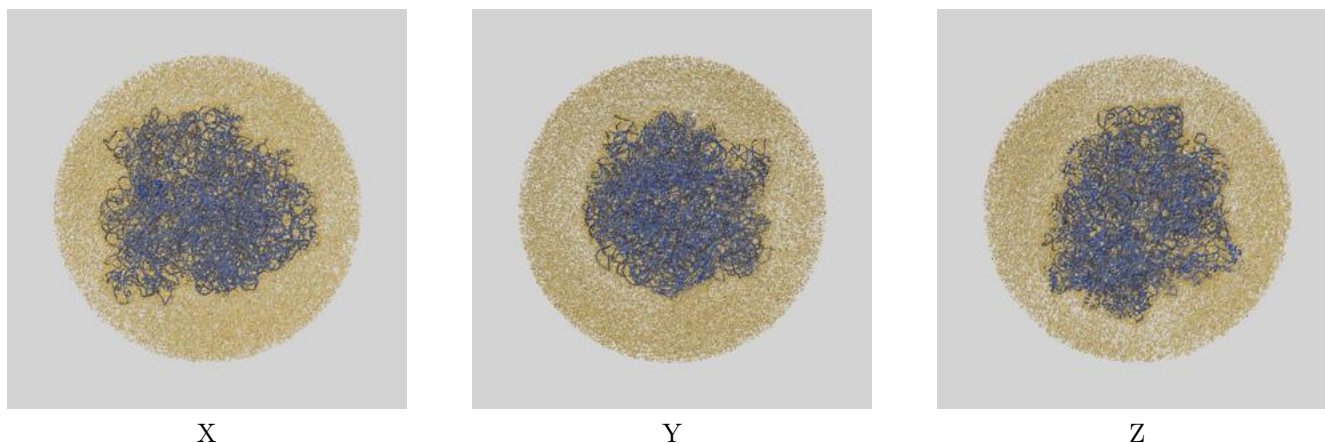
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.11	4.26	3.16
Unmasked-calculated*	3.81	7.34	4.08

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.81 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

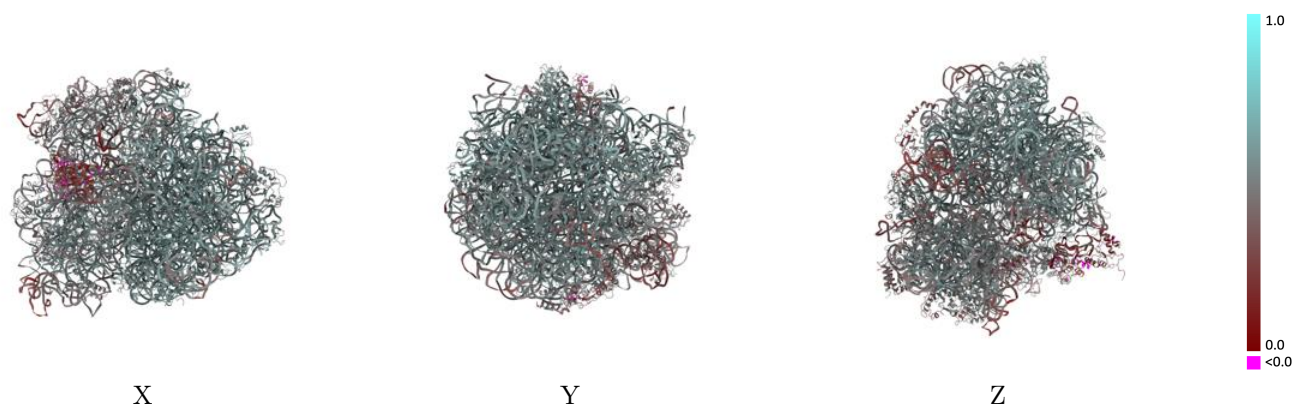
This section contains information regarding the fit between EMDB map EMD-13461 and PDB model 7PJV. Per-residue inclusion information can be found in section [3](#) on page [18](#).

9.1 Map-model overlay [i](#)



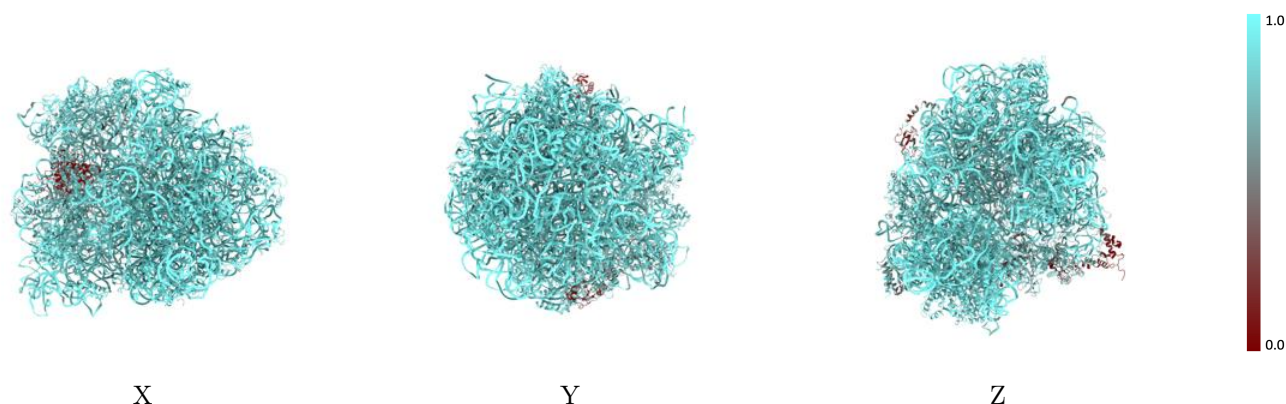
The images above show the 3D surface view of the map at the recommended contour level 1.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



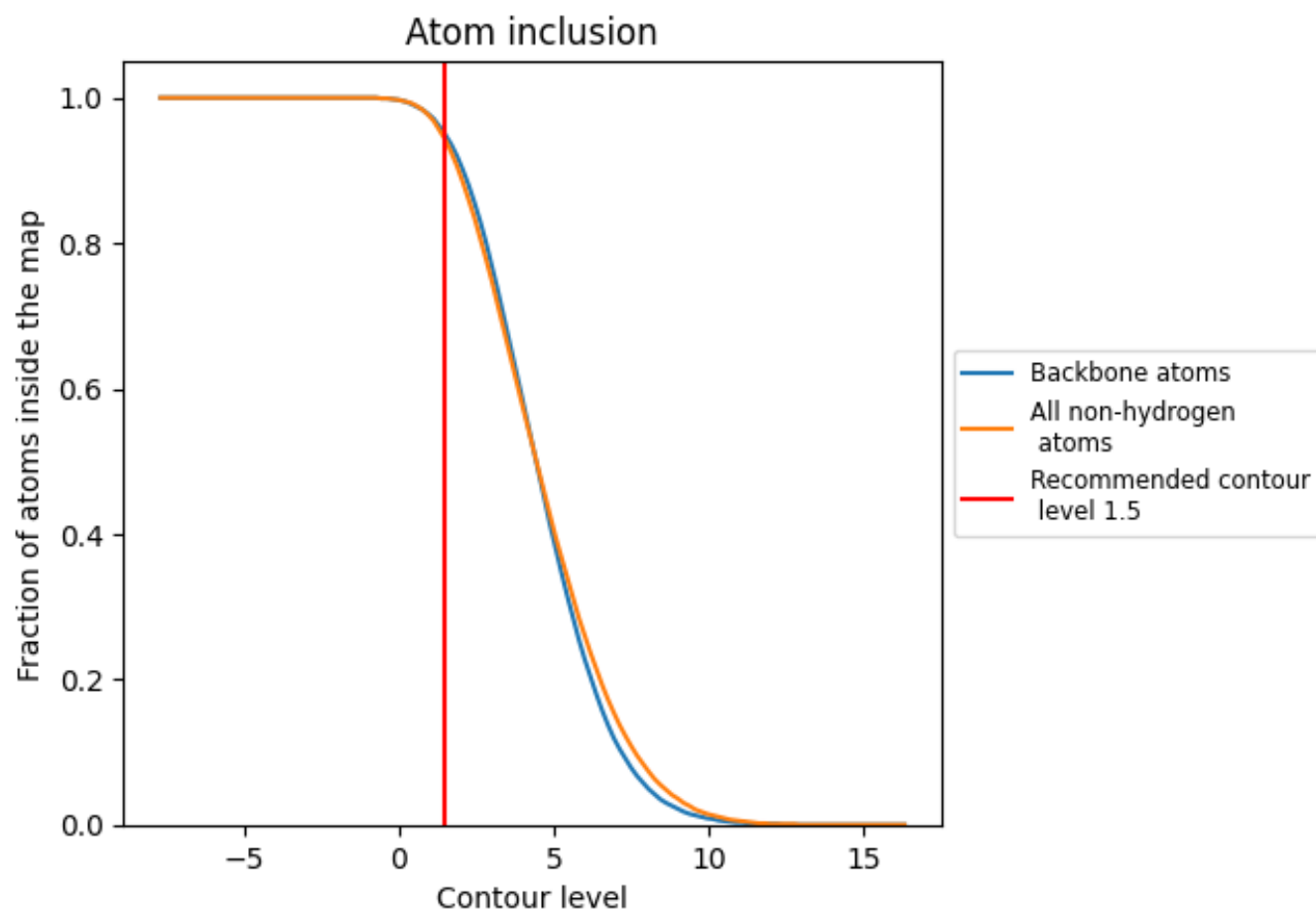
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 95% of all backbone atoms, 94% 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	 0.9420	 0.5140
0	 0.9440	 0.5580
1	 0.9080	 0.5550
2	 0.9490	 0.5850
3	 0.9630	 0.5910
4	 0.9590	 0.5540
5	 0.3090	 0.2560
6	 0.8630	 0.4130
A	 0.9770	 0.5320
B	 0.9810	 0.5230
C	 0.9350	 0.5620
D	 0.9440	 0.5640
E	 0.9370	 0.5430
F	 0.8910	 0.4740
G	 0.8980	 0.4980
H	 0.4570	 0.3710
I	 0.4560	 0.2230
J	 0.9580	 0.5680
K	 0.9100	 0.5550
L	 0.9400	 0.5510
M	 0.9420	 0.5600
N	 0.9570	 0.5630
O	 0.9540	 0.5240
P	 0.9100	 0.5560
Q	 0.9740	 0.5680
R	 0.9250	 0.5330
S	 0.9340	 0.5610
T	 0.9420	 0.5310
U	 0.9320	 0.5130
V	 0.9390	 0.5300
W	 0.9610	 0.5760
X	 0.9280	 0.5560
Y	 0.9210	 0.5020
Z	 0.9380	 0.5690
a	 0.9760	 0.5070



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
b	 0.7380	 0.4420
c	 0.9120	 0.5020
d	 0.9010	 0.4830
e	 0.9390	 0.5380
f	 0.8840	 0.4600
g	 0.7770	 0.4170
h	 0.9270	 0.5350
i	 0.9220	 0.4800
j	 0.8760	 0.4390
k	 0.9090	 0.5120
l	 0.9010	 0.5370
m	 0.9080	 0.4610
n	 0.9400	 0.4970
o	 0.9350	 0.5170
p	 0.9200	 0.5160
q	 0.9220	 0.5160
r	 0.9100	 0.5110
s	 0.8880	 0.4540
t	 0.9310	 0.5060
u	 0.8330	 0.4820
v	 0.9340	 0.4530
w	 0.8620	 0.4000
x	 0.8090	 0.4470
y	 0.8090	 0.5250
z	 0.9350	 0.5320