



wwPDB EM Validation Summary Report ⓘ

Jun 18, 2026 – 12:45 pm BST

PDB ID : 7PJT / pdb_00007pjt
EMDB ID : EMD-13459
Title : Structure of the 70S ribosome with tRNAs in hybrid state 1 (H1)
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 : 4AQY, 5LZD, 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:

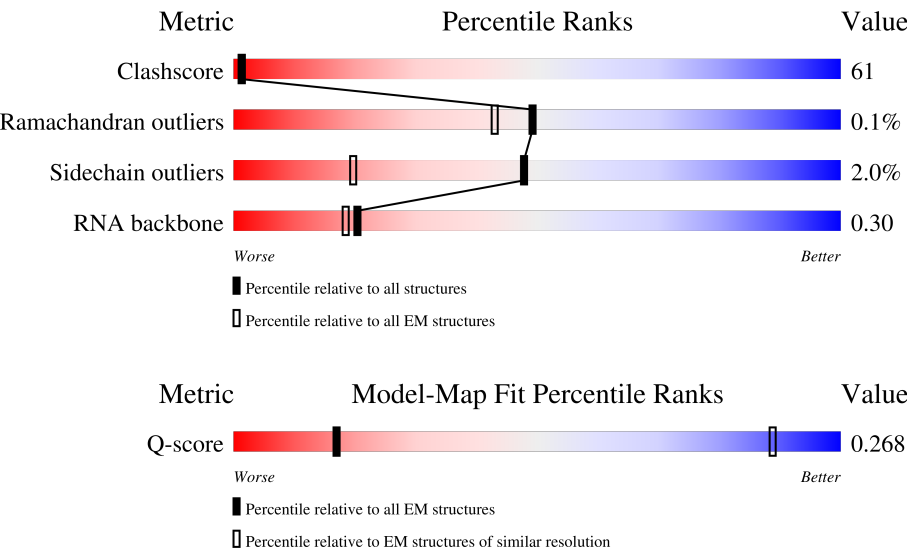
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

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.



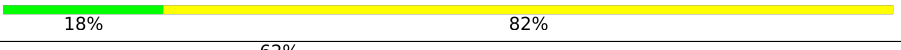
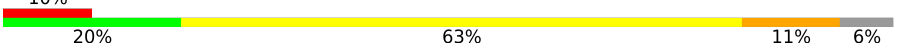
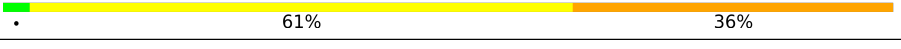
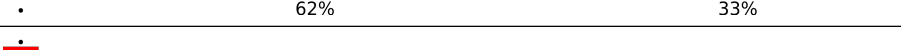
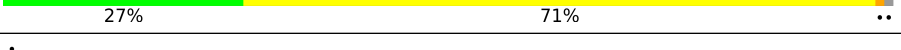
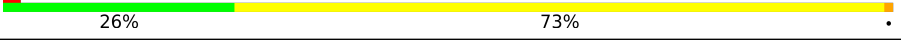
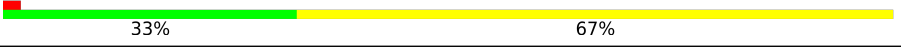
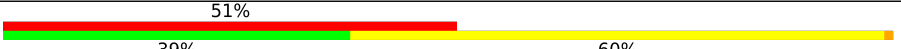
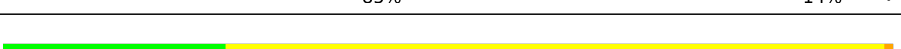
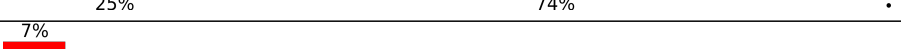
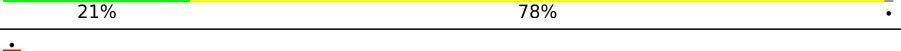
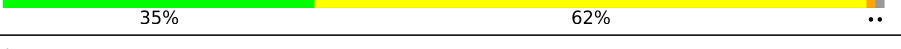
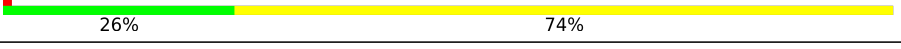
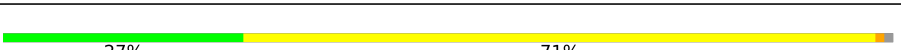
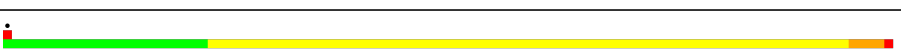
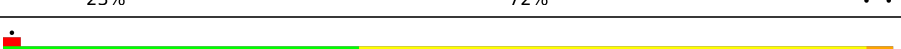
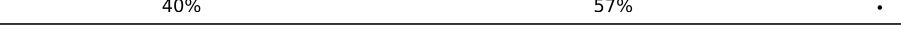
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	525 (5.50 - 6.50)

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	35% 56% 7%
2	1	55	7% 25% 65% 9%
3	2	46	17% 80%

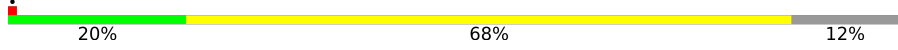
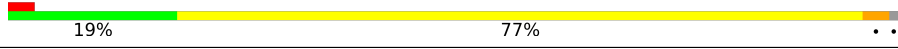
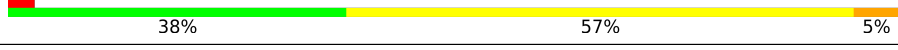
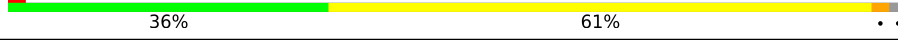
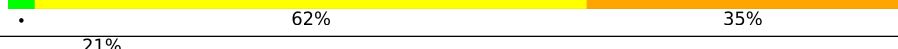
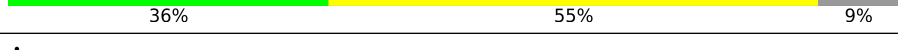
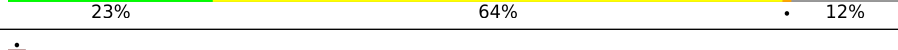
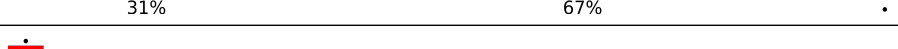
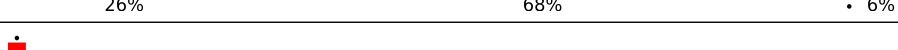
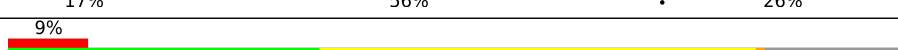
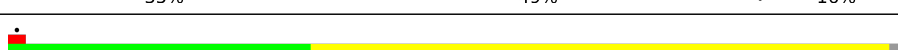
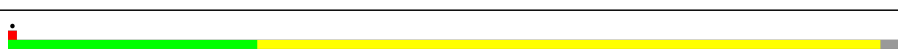
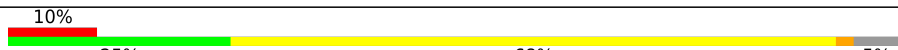
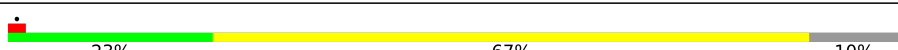
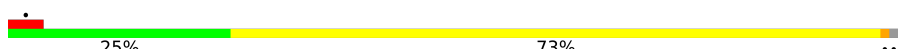
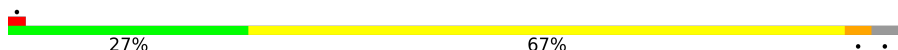
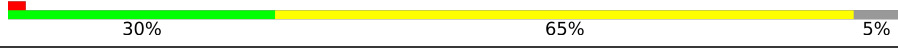
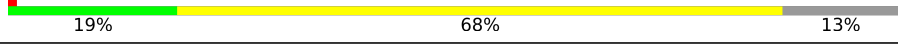
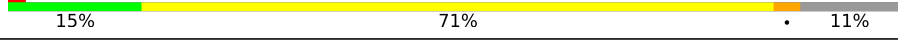
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Mol	Chain	Length	Quality of chain
4	3	65	
5	4	38	
6	5	165	
7	6	70	
8	A	2903	
9	B	120	
10	C	273	
11	D	209	
12	E	201	
13	F	179	
14	G	177	
15	H	149	
16	I	142	
17	J	142	
18	K	123	
19	L	144	
20	M	136	
21	N	127	
22	O	117	
23	P	115	
24	Q	118	
25	R	103	
26	S	110	
27	T	100	
28	U	104	

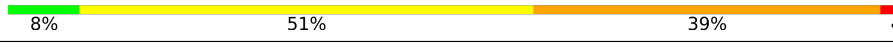
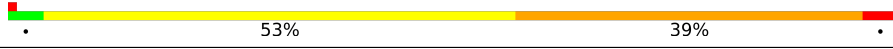
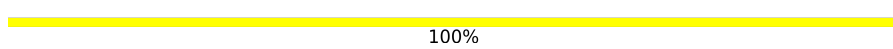
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Mol	Chain	Length	Quality of chain
29	V	94	
30	W	85	
31	X	78	
32	Y	63	
33	Z	59	
34	a	1542	
35	b	240	
36	c	233	
37	d	206	
38	e	167	
39	f	135	
40	g	179	
41	h	130	
42	i	130	
43	j	103	
44	k	129	
45	l	124	
46	m	118	
47	n	102	
48	o	89	
49	p	82	
50	q	84	
51	r	75	
52	s	92	
53	t	87	

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Mol	Chain	Length	Quality of chain
54	u	71	
55	v	77	
56	w	76	
57	y	2	
58	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	2MG	a	1516	-	-	X	-
34	PSU	a	516	-	-	X	-
8	2MG	A	2445	-	-	X	-

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 147222 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	2902	Total	C	N	O	P	0	0
			62317	27806	11469	20140	2902		

- 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 Dipeptide (FME-PHE).

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

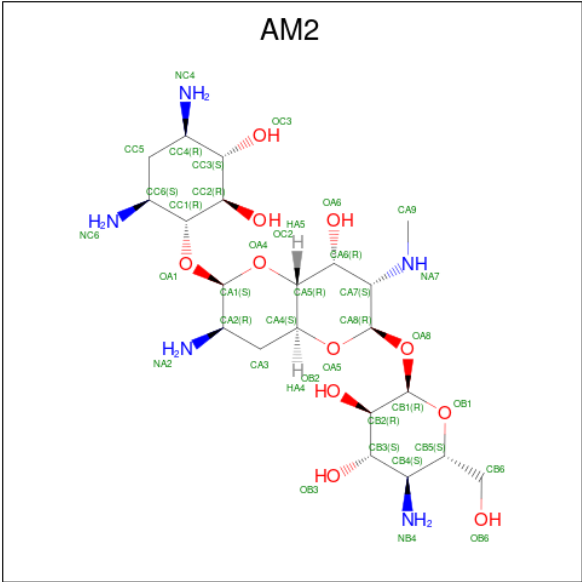
- Molecule 58 is a RNA chain called mRNA.

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

- Molecule 59 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
59	4	1	Total	Zn	0
			1	1	
59	6	1	Total	Zn	0
			1	1	

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

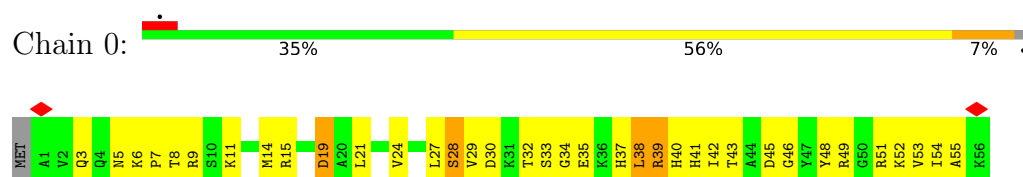


Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
60	a	1	37	21	5	11	0

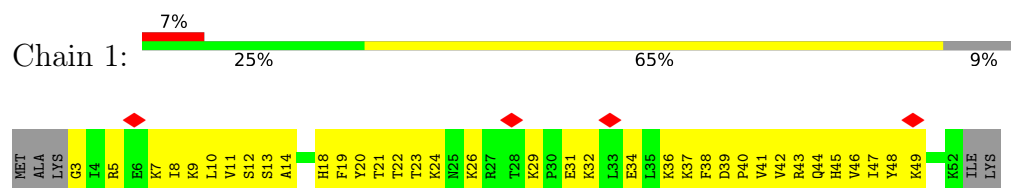
3 Residue-property plots [i](#)

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

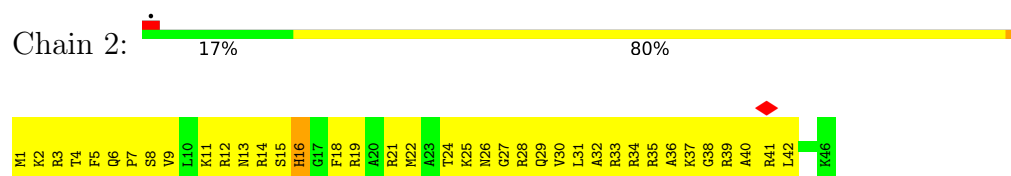
- Molecule 1: 50S ribosomal protein L32



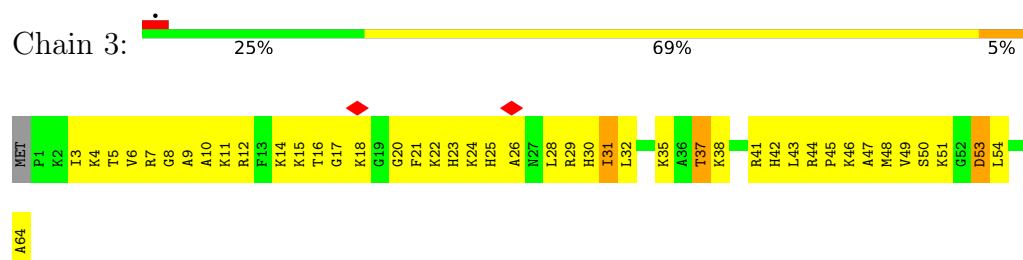
- Molecule 2: 50S ribosomal protein L33



- Molecule 3: 50S ribosomal protein L34



- Molecule 4: 50S ribosomal protein L35

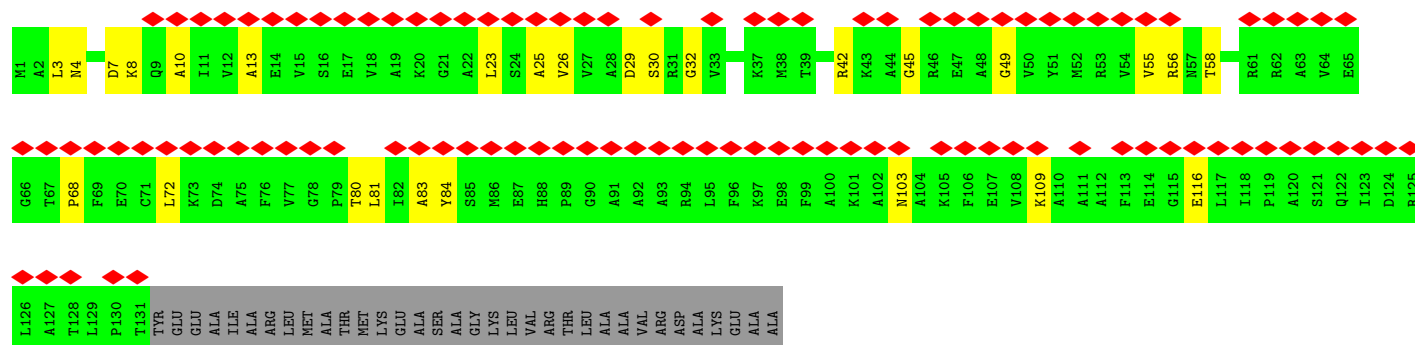


- Molecule 5: 50S ribosomal protein L36

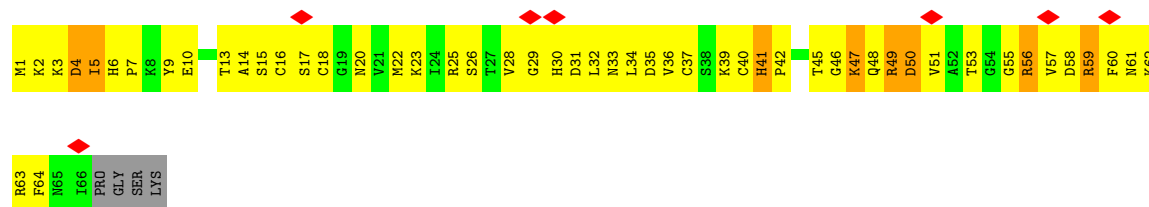




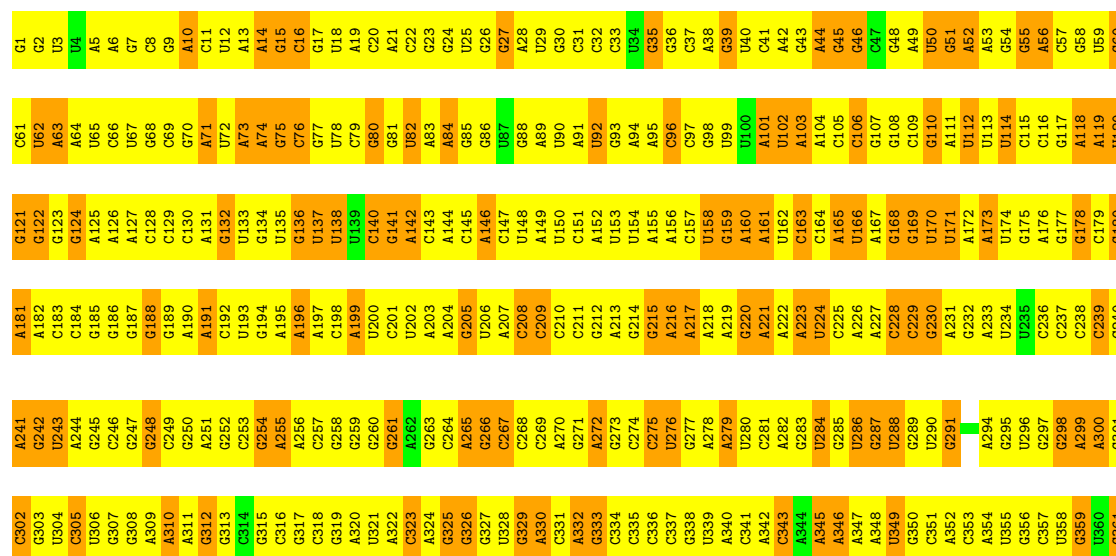
• Molecule 6: 50S ribosomal protein L10



• Molecule 7: 50S ribosomal protein L31



• Molecule 8: 23S ribosomal RNA

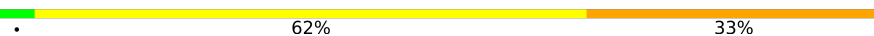


A1322	A1262	G1202	G962	C902	U842	A782	A722	G662	A602	C542	A482	A422	A362
C1323	U1263	U1023	U963	C903	G843	A783	C723	G663	A603	G543	A483	A423	G363
A1324	A1264	G1204	C964	G904	A844	G784	U724	G664	A604	C544	A484	A424	C364
U1325	A1265	G1205	C965	G905	A845	G785	G725	U665	G605	U545	C485	G425	U365
U1326	G1266	G1026	G966	U906	U846	G786	G726	A666	U606	U546	C486	U426	C366
A1327	U1267	A1027	G967	G907	U847	G787	U727	U667	U607	U547	C487	G427	G367
A1328	A1268	A1028	C968	C908	C848	A788	G728	A668	A608	G548	G488	A428	A368
U1329	A1269	A1029	G969	A909	A849	A789	G729	A669	A609	C549	C489	A429	U369
C1330	C1270	C1210	U970	A910	U850	U790	A730	A670	C610	C550	C490	G370	G370
G1331	G1271	G1031	G971	A911	C851	C791	C731	C671	C611	U551	A491	U431	A371
G1332	A1272	A1032	A972	C912	U852	A792	C732	C672	C612	U552	A492	G372	G372
G1333	U1273	U1033	G973	U913	C853	A793	G733	C673	A613	G553	G493	U373	U373
G1334	A1274	G1034	C974	G914	C854	A794	A734	G674	A614	U554	G494	U434	A374
C1335	A1275	U1035	A975	C915	C855	C795	A735	A675	U615	G555	G495	C435	G375
A1336	A1276	G1036	G976	G916	G856	C796	G736	A676	A616	A556	G496	C436	G376
G1337	G1277	G1037	G977	A917	C857	G797	G737	A677	G617	C557	A497	U437	G377
G1338	A1278	G1038	G978	U918	C858	G798	G738	C678	G618	U558	G498	G438	C378
G1339	U1279	A1039	A979	U919	C859	G799	A739	C679	G619	U559	U499	A439	G379
U1340	G1280	A1040	A980	A920	U860	A800	C740	C680	G620	C560	G500	C440	G380
G1341	G1281	G1041	A981	C921	A861	G801	U741	C681	A621	G561	A501	U441	C381
A1342	U1282	G1042	C982	C922	G862	A802	A742	C682	G622	U562	A502	G442	A382
G1343	G1283	C1043	A983	G923	A863	U803	A743	U683	C623	A563	A503	A443	C383
U1344	A1284	C1044	A984	G924	C864	A804	U744	C684	C624	C564	A504	C444	C384
C1345	A1285	C1045	C985	A925	C865	G805	G745	A685	G625	C565	A505	C445	C385
G1346	A1286	A1046	C986	G926	A866	C806	U746	U686	A626	U566	G506	G446	G386
A1347	A1287	G1047	C987	A927	C867	U807	G747	C687	A627	U567	A507	A447	U387
G1348	G1288	A1048	A988	A928	U868	G808	A748	U688	G628	U568	A508	U448	G388
C1349	A1289	C1049	G989	U929	C869	G809	A749	A689	G629	U569	C509	A449	C389
C1350	G1290	A1050	A990	G930	U870	U810	A750	C690	G630	U570	C510	G450	U390
C1351	C1291	G1051	C991	U931	U871	U811	A751	C691	A631	U571	U511	U451	A391
U1352	G1292	C1052	C992	U932	U872	C812	A752	C692	A632	A572	G512	G452	U392
A1353	C1293	C1053	G993	A933	C873	U813	A753	A693	A633	U573	A513	A453	C393
A1354	U1294	A1054	C994	U934	A874	C814	U754	U694	C634	U574	A514	A454	C394
G1355	G1295	G1055	A995	C935	C875	C815	A755	G695	C635	A575	A515	C455	U395
G1356	G1296	G1056	A996	A936	C876	C816	A756	G696	C636	U576	C516	C456	G396
C1357	C1297	A1057	G997	C937	A877	C817	G757	C697	A637	A577	C517	A457	U397
G1358	G1298	U1058	C998	G938	A878	C818	C758	C698	G638	G578	G518	G458	C398
A1359	G1299	G1059	U999	C939	C879	A819	G759	A699	U639	U579	U519	U459	U399
G1360	G1300	U1060	A1000	G940	C880	A820	G760	G699	C640	U580	G520	A460	G400
G1361	A1241	U1061	A1001	A941	C881	A821	A761	G701	U641	C581	U521	C461	A401
C1362	G1242	G1062	G1002	G942	C882	G822	U762	U702	U642	A582	A522	C462	A402
G1363	C1243	G1063	G1003	A943	C883	G823	G763	U703	G643	C583	C523	G463	U403
G1364	A1244	C1064	U1004	C944	U884	U824	A764	G704	A644	C584	G524	U464	A404
A1365	C1305	U1065	C1005	A945	C885	A825	C765	A705	C645	G585	U525	G465	U405
A1366	G1246	U1066	C1006	C946	A886	U826	U766	A706	U646	A586	A526	A466	G406
A1367	A1247	A1067	C1007	A947	A887	U827	U767	G707	G647	C587	C527	G467	G407
G1368	G1248	G1068	A1008	C948	C888	U828	G768	G708	G648	U588	A528	G468	G408
G1369	U1249	A1069	G949	C949	C889	A829	U769	U709	G649	U589	A529	G469	G409
C1370	G1250	A1070	A1010	G950	C890	G830	G770	U710	C650	A590	G530	A470	G410
G1371	C1251	G1071	C951	C951	C891	G831	G771	G711	G651	U591	C531	A471	G411
U1372	G1252	C1072	G952	G952	A892	U832	C772	G712	U652	A592	A532	A472	A412
C1373	A1253	A1073	C1013	G953	C893	A833	U773	G713	C653	U593	G533	G473	C413
G1374	C1254	G1074	U1014	G954	U894	G834	G774	U714	A654	U594	A534	G474	C414
C1375	U1255	C1075	U1015	U955	U895	C835	G775	A715	A655	C595	G535	C475	A415
G1376	G1256	C1076	G1016	G956	A896	G836	G776	C716	G656	U596	G536	G476	U416
G1377	C1257	A1077	G1017	C957	C897	C837	G777	A717	U657	G597	G537	A477	C417
A1378	U1258	U1078	U958	U958	C898	C838	G778	A718	U658	U598	A538	A478	C418
U1379	G1259	C1079	A1019	A959	A899	U839	U779	C719	G659	A599	G539	A479	U419
G1380	C1260	A1080	A960	A960	A900	U840	G780	C720	C660	U600	C540	A480	C420
G1381	C1261	U1081	A1021	C961	C901	G841	A781	A721	A661	C601	A541	G481	C421

A2287	A2288	G2228	G2229	G2230	G2231	G2232	G2233	G2234	G2235	G2236	G2237	G2238	G2239	G2240	A2241	A2242	G2243	G2244	G2245	G2246	G2247	U2187	U2188	U2189	G2190	A2191	U2192	G2193	U2194	U2195	G2196	U2197	A2198	A2199	G2200	G2201	G2202	G2203	G2204	A2205	G2206	G2207	G2208	G2209	U2210	A2211	G2212	G2213	G2214	G2215	G2216	G2217	G2218	U2219	U2220	G2221	G2222	G2223	A2224	G2225	G2226																		
A2287	A2288	G2228	G2229	G2230	G2231	G2232	G2233	G2234	G2235	G2236	G2237	G2238	G2239	G2240	A2241	A2242	G2243	G2244	G2245	G2246	G2247	U2187	U2188	U2189	G2190	A2191	U2192	G2193	U2194	U2195	G2196	U2197	A2198	A2199	G2200	G2201	G2202	G2203	G2204	A2205	G2206	G2207	G2208	G2209	U2210	A2211	G2212	G2213	G2214	G2215	G2216	G2217	G2218	U2219	U2220	G2221	G2222	G2223	A2224	G2225	G2226																		
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A1746	U1747	C1748	A1749	U1750	G1751	C1752	G1753	U1754	A1755	G1756	U1757	A1758	A1759	C1760	U1761	G1762	G1763	C1764	U1765	G1766	G1767	C1768	U1769	G1770	C1771	U1772	A1773	C1774	U1775	G1776	U1777	G1778	U1779	A1780	U1781	U1782	U1783	A1784	A1785	U1786	A1787	G1788	U1789	C1790	U1791	G1792	G1793	A1794	C1795	U1796	U1797	U1798	U1799	G1800	G1801	A1802	A1803	C1804	A1805																				
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U2349	G2349	U2407	G2409	A2469	A2470	G2629	A2588	C2649	G2709	U2769	A2829	C2889
C2350	A2410	G2410	G2411	A2471	A2472	A2530	A2590	U2850	C2710	G2770	G2830	C2890
G2351	A2411	A2412	A2412	A2473	A2474	A2531	C2591	U2851	A2711	C2771	G2831	C2891
A2352	G2413	G2413	G2414	A2475	C2475	U2532	U2593	U2852	C2712	C2772	U2832	G2892
G2353	G2414	G2415	G2415	A2476	C2476	A2533	C2594	U2853	G2713	C2773	G2833	G2893
C2354	G2416	G2417	G2417	A2477	C2477	U2534	G2595	A2854	C2714	C2774	G2834	G2894
U2355	G2418	G2419	G2419	A2478	C2478	A2535	U2596	U2855	C2715	A2775	A2835	G2895
G2356	U2419	U2420	U2420	A2479	C2479	U2536	G2597	U2856	C2716	A2776	U2836	C2896
A2358	U2419	U2420	U2420	A2480	C2480	U2537	U2598	A2857	C2717	A2777	G2837	U2897
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G2365	A2426	A2427	A2427	A2487	C2487	U2544	G2605	A2665	U2724	U2785	U2844	
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A2377	A2441	A2442	A2442	U2499	C2499	U2555	U2616	A2676	A2735	U2796	G2856	
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G2379	A2444	A2445	A2445	U2501	C2501	U2557	U2618	A2678	A2737	U2798	G2858	
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G2381	A2448	A2449	A2449	U2503	C2503	U2559	U2620	U2680	A2739	A2800	A2860	
G2382	A2450	A2451	A2451	U2504	C2504	U2560	G2621	U2681	A2740	G2801	U2861	
G2383	A2452	A2453	A2453	U2505	C2505	U2561	U2622	A2682	A2741	G2802	G2862	
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G2391	A2455	A2456	A2456	U2513	C2513	U2569	G2631	C2691	U2750	A2810	C2870	
A2392	A2457	A2458	A2458	U2514	C2514	U2570	A2632	G2692	C2751	G2811	U2871	
G2393	A2459	A2460	A2460	U2515	C2515	U2571	U2633	G2693	C2752	G2812	A2872	
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A2396	G2463	G2464	G2464	U2518	C2518	U2574	G2636	U2696	C2755	G2815	G2875	
U2397	G2465	G2466	G2466	U2519	C2519	U2575	U2637	U2697	U2756	U2816	G2876	
G2398	A2467	A2468	A2468	U2520	C2520	U2576	U2638	U2698	A2757	U2817	G2877	
G2399	A2469	A2470	A2470	U2521	C2521	U2577	G2639	U2699	U2758	U2818	U2878	
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U2401	G2471	G2472	G2472	U2523	C2523	U2579	U2640	U2701	U2760	A2820	C2880	
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G2403	G2464	G2465	G2465	U2525	C2525	U2581	G2642	G2703	C2762	G2822	A2882	
U2404	G2466	G2467	G2467	U2526	C2526	U2582	G2643	G2704	C2763	G2823	A2883	
G2405	G2467	G2468	G2468	U2527	C2527	U2583	G2644	U2705	A2764	C2824	U2884	
A2406	G2467	G2468	G2468	U2528	C2528	U2584	G2645	U2706	A2765	G2825	A2885	
						A2585	G2646	A2707	A2766	A2826	A2886	
						U2586	G2647	U2707	C2767	C2827	A2887	

• Molecule 9: 5S ribosomal RNA

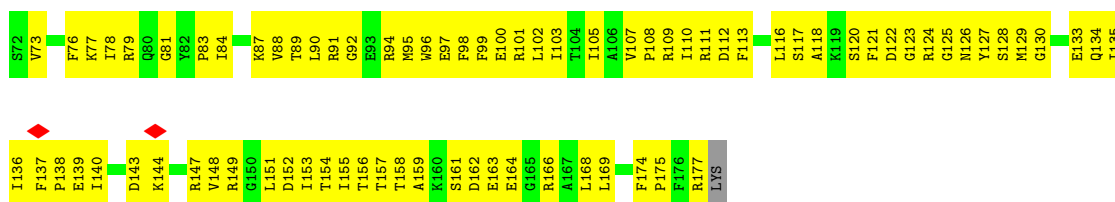
Chain B:  62% 33%

U1	C62	C63	G64	U65	A66	G67	C68	G69	C70	C71	G72	A73	U74	G75	G76	U77	A78	G79	U80	G81	U82	G83	G84	G85	G86	U87	C88	U89	G90	C91	C92	C93	A94	U95	G96	C97	G98	A99	G100	A101	G102	U103	A104	G105	G106	G107	A108	U109	C110	U111	G112	C113	C114	A115	G116	G117	C118	A119	U120	G121
C2	C3	C4	U5	G6	G7	C8	G9	C10	C11	C12	G13	U14	A15	G16	C17	G18	C19	G20	G21	U22	G23	G24	U25	C26	C27	C28	A29	C30	C31	U32	G33	A34	C35	C36	C37	C38	A39	U40	G41	C42	C43	G44	A45	A46	C47	U48	C49	A50	G51	A52	A53	G54	U55	G56	A57	A58	C59			

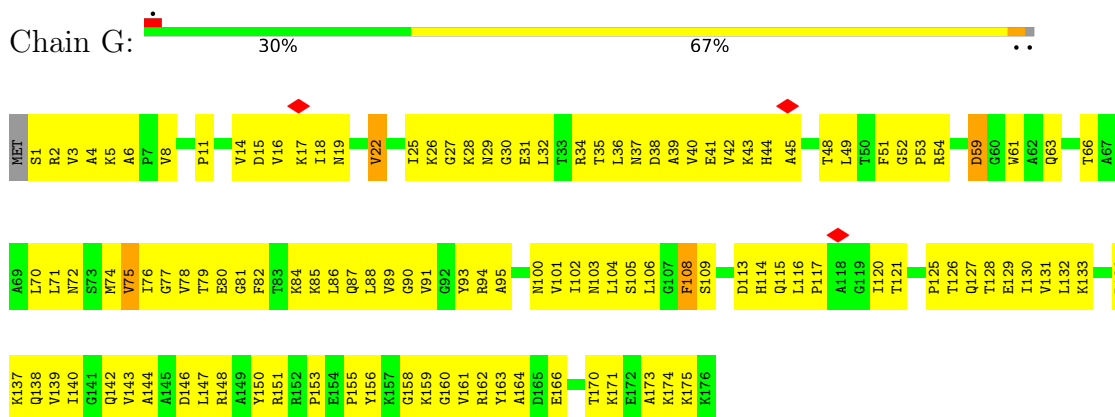
• Molecule 10: 50S ribosomal protein L2

Chain C:  27% 71%

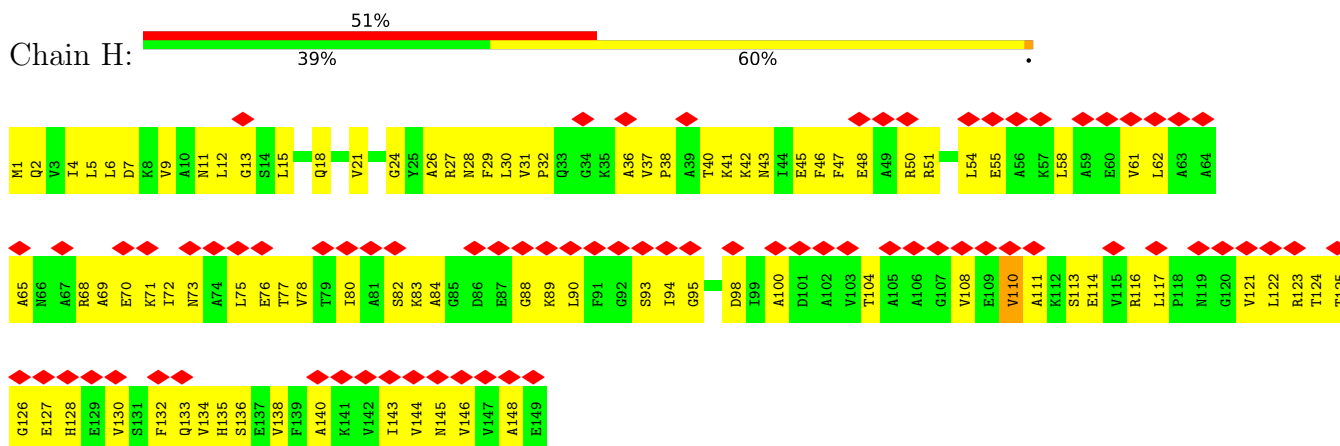
MET	A1	K4	C5	K6	S9	R12	R13	H14	V15	V16	K17	V18	V19	N20	L23	K27	P28	F29	A30	P31	L32	L33	E34	K35	N36	G40	G41	R42	N43	N44	N45	G46	R47	T48	T49	T50	R51	H52	F53	G54	G55	G56	H57	K58	G59	A60	Y61	R62	I63	V64	D65	F66	G67	R68	M69	I73	P74	A75	V76	V77	E78	R79	L80	E81	Y82	D83	P84	N85	R86	S87	A88	N89	I90	A91	L92	V93	L94	Y95	A96	D97	G98	E99	R100	R101	I102	I103	L104	A105	P106	K107	G108	L109	K110	A111	G112	D113	Q114	T115	Q116	S117	G118	N127	T128	L129	P130	M131	R132	N133	I134	G137
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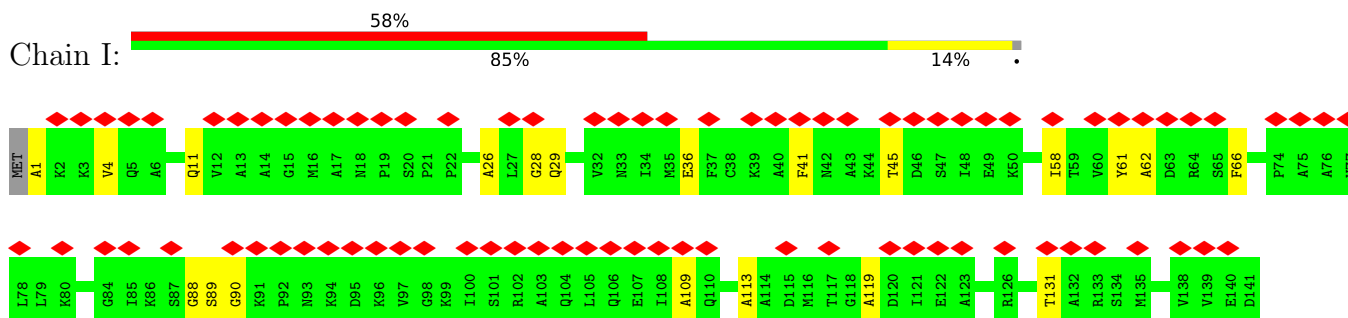
• Molecule 14: 50S ribosomal protein L6



• Molecule 15: 50S ribosomal protein L9

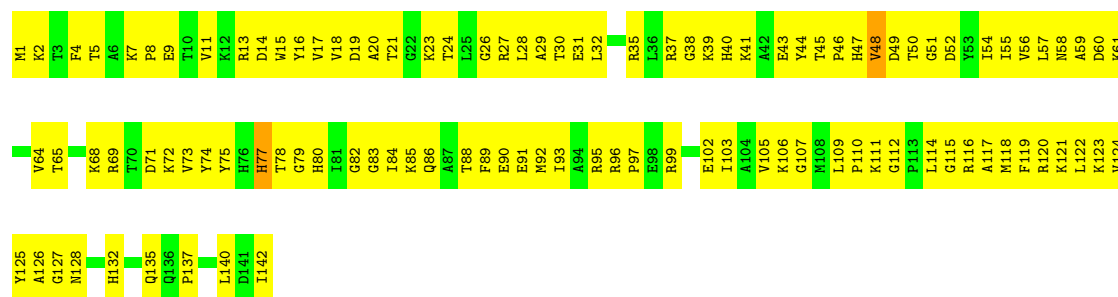


• Molecule 16: 50S ribosomal protein L11

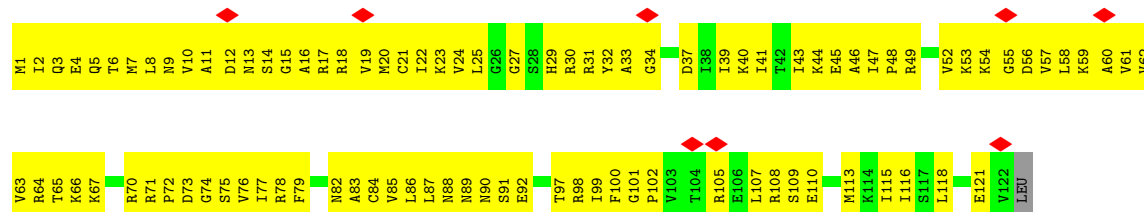


• Molecule 17: 50S ribosomal protein L13

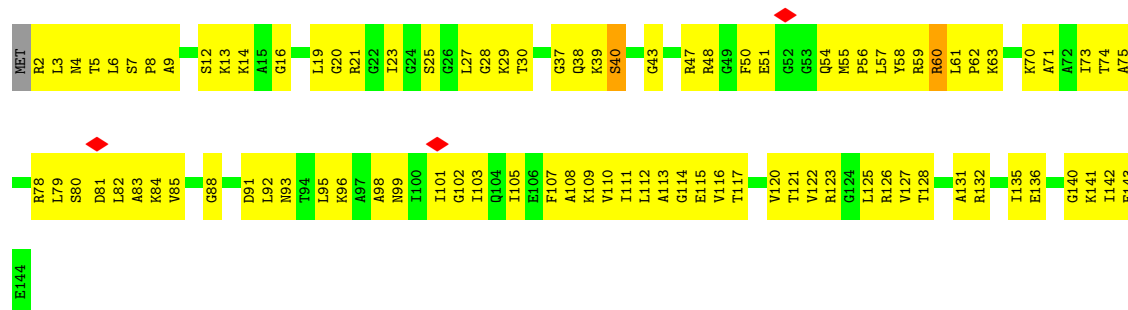




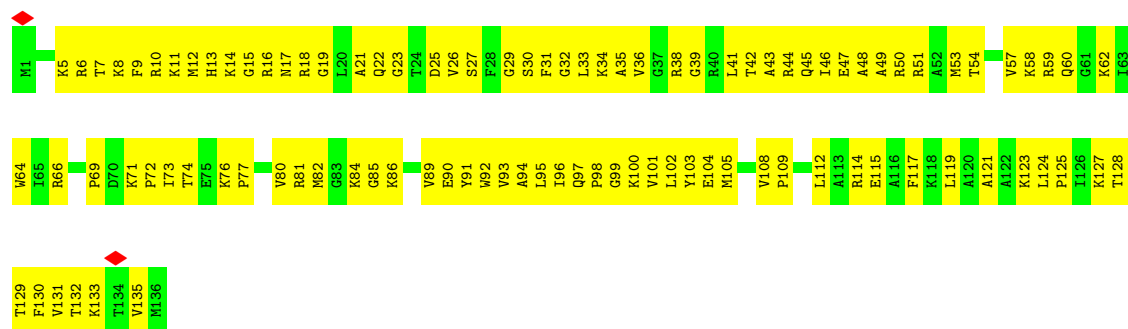
- Molecule 18: 50S ribosomal protein L14



- Molecule 19: 50S ribosomal protein L15

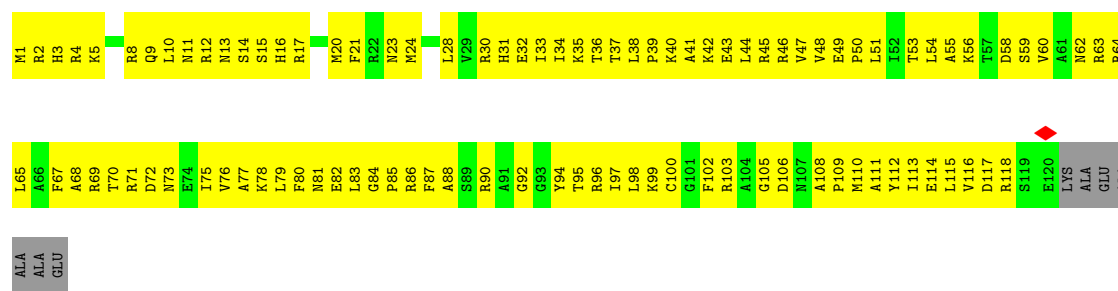


- Molecule 20: 50S ribosomal protein L16

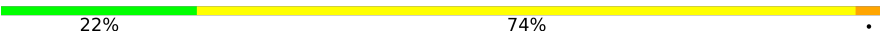


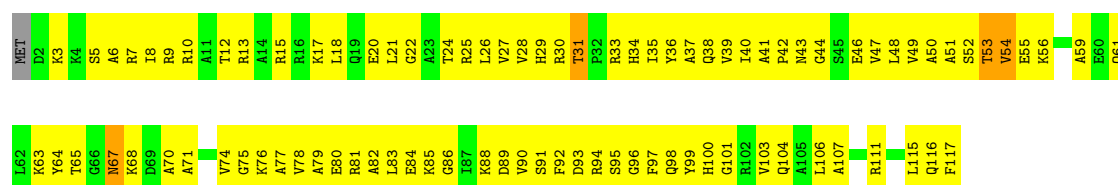
- Molecule 21: 50S ribosomal protein L17

Chain N:  17% 77% 6%



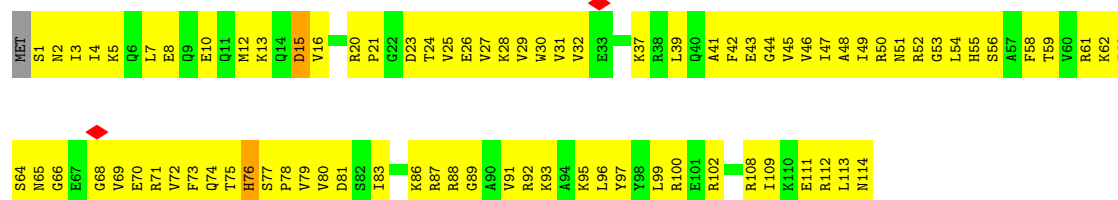
- Molecule 22: 50S ribosomal protein L18

Chain O:  22% 74% 4%

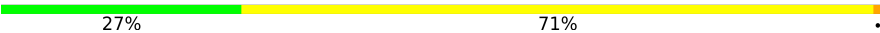


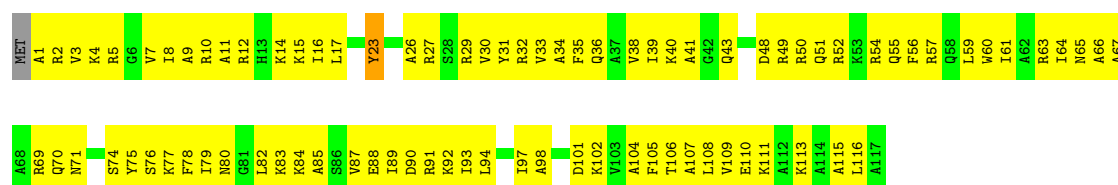
- Molecule 23: 50S ribosomal protein L19

Chain P:  26% 71% 3%

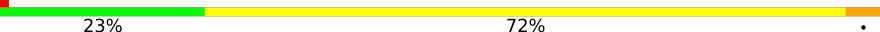


- Molecule 24: 50S ribosomal protein L20

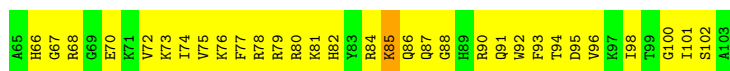
Chain Q:  27% 71% 2%



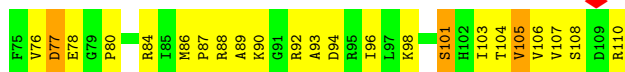
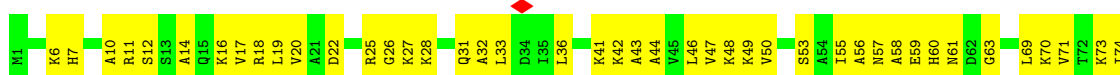
- Molecule 25: 50S ribosomal protein L21

Chain R:  23% 72% 5%

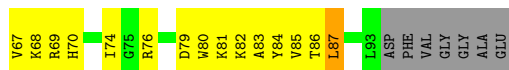
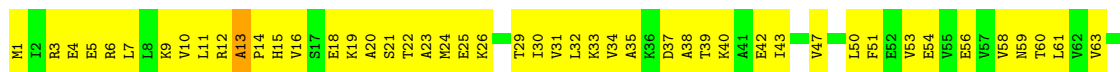




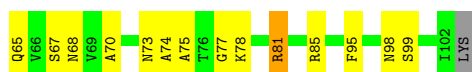
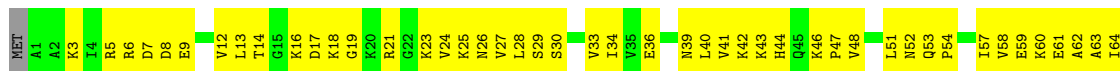
- Molecule 26: 50S ribosomal protein L22



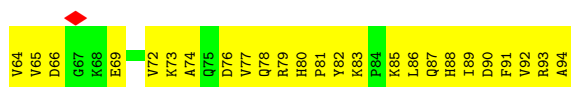
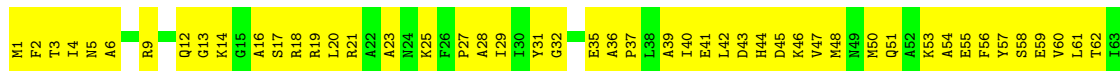
- Molecule 27: 50S ribosomal protein L23



- Molecule 28: 50S ribosomal protein L24

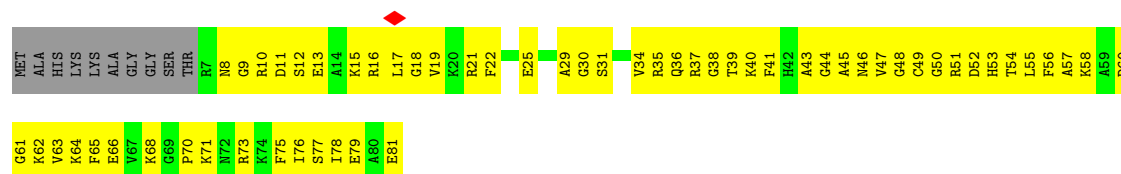


- Molecule 29: 50S ribosomal protein L25

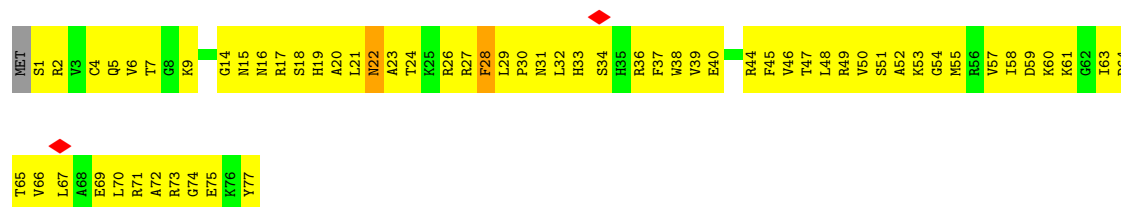


- Molecule 30: 50S ribosomal protein L27





• Molecule 31: 50S ribosomal protein L28



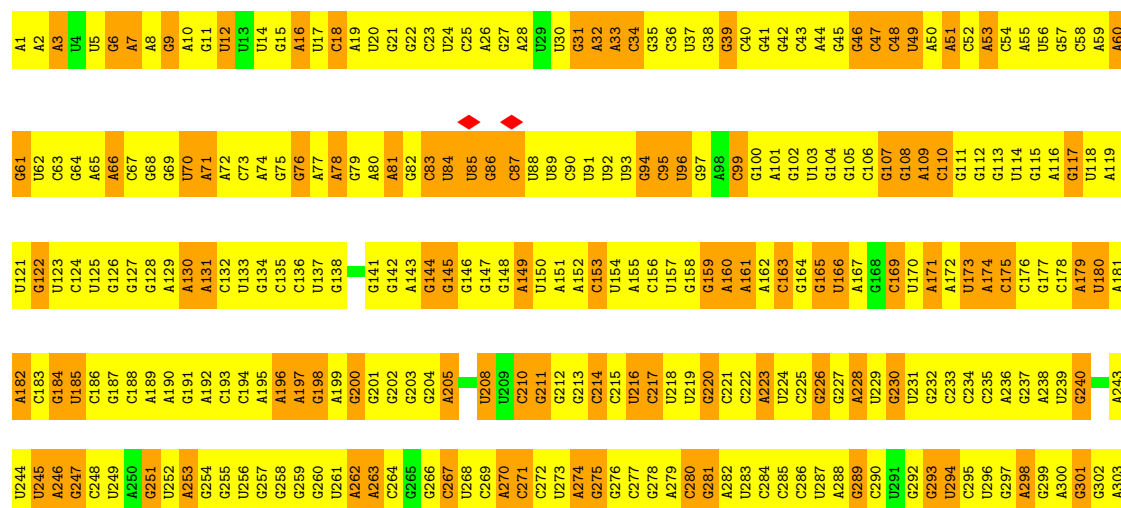
• Molecule 32: 50S ribosomal protein L29



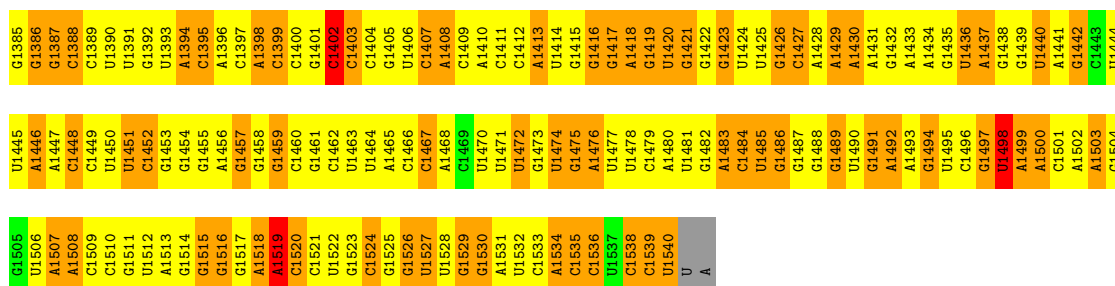
• Molecule 33: 50S ribosomal protein L30



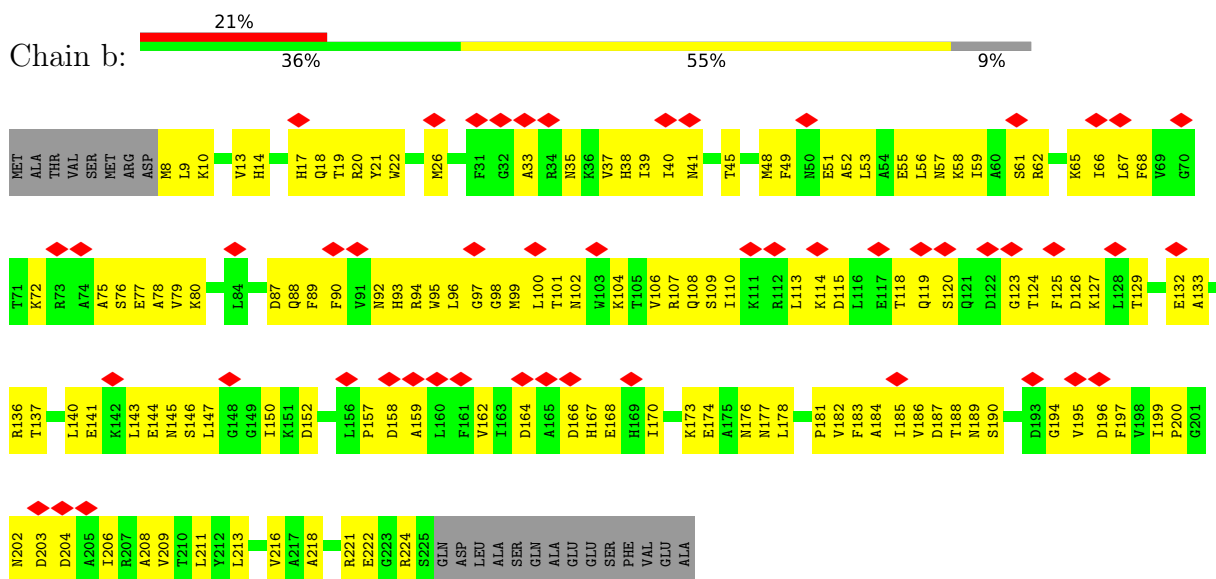
• Molecule 34: 16S ribosomal RNA



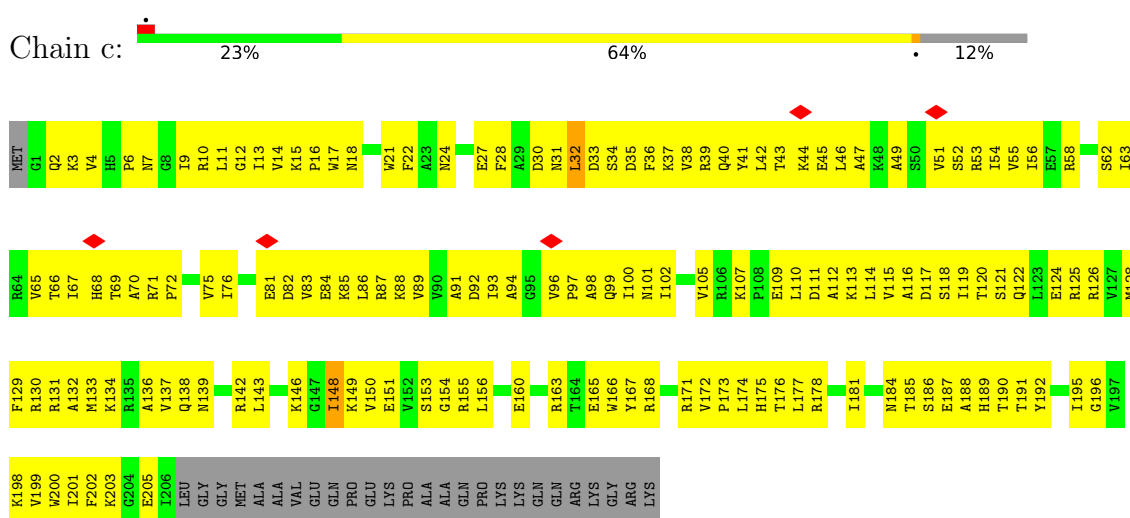
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U1326	G1266	G1206	A1146	U1086	G1026	G966	A906	G846	G786	G726	G666	G606	A546	U486	G425	U365	G305
C1327	G1267	G1207	C1147	G1087	C1027	C957	A907	G847	A787	G727	G667	A607	A547	A487	U426	A366	A306
C1328	G1268	C1208	U1148	G1088	U1028	A968	A908	C848	U788	A728	G668	A608	G548	U368	U427	U367	C307
A1329	G1269	C1209	C1149	G1089	U1029	A969	A909	G849	U789	A729	G669	A609	C549	U369	G428	U368	C308
U1330	G1270	C1210	A1150	U1090	U1030	C970	C910	U850	A790	G730	G670	U610	G550	C490	U429	G369	A309
G1331	A1271	U1211	A1151	U1091	C1031	G971	U911	G851	G791	G731	G671	C611	U551	C491	A430	C370	G310
A1332	G1272	U1212	A1152	A1092	G1032	C972	C912	G852	A792	G732	U672	C612	U552	C492	A431	A371	C311
A1333	C1273	U1213	G1153	A1093	U1033	G973	A913	C853	U793	G733	A673	C613	A553	A493	A432	C372	C312
G1334	A1274	C1214	A1154	U1094	G1034	A974	A914	U854	A794	G734	G674	C614	U554	G494	A433	A373	A313
U1335	A1275	U1095	A1155	U1095	A1035	A975	A915	U855	C795	G735	A675	C615	U555	A495	U434	A374	A314
G1336	G1276	A1216	A1156	C1096	A1036	G976	U916	C856	U796	G736	A676	G616	C556	A496	A435	U375	A315
G1337	G1277	C1217	A1157	C1097	C1037	A977	G917	C857	C797	G737	U677	C617	G557	G497	C436	G376	C316
G1338	G1278	C1218	C1158	C1098	C1038	A978	A918	G858	U798	G738	U678	C618	G558	A498	U437	G377	U317
A1339	G1279	A1219	U1159	G1099	G1039	C979	A919	G859	G799	C739	C679	U619	A559	A499	U438	G378	G318
A1340	G1280	G1220	G1160	U1100	U1040	C980	U920	G860	C800	U740	C680	C620	G560	A500	U439	C379	G319
U1341	C1281	G1221	A1161	A1101	G1041	U981	U921	G861	U801	G741	A681	A621	C501	C440	C440	G380	A320
C1342	G1282	U1222	C1162	A1102	A1042	U982	G922	C862	A802	G742	G682	U562	A502	A441	A441	C381	A321
G1343	U1283	C1223	A1163	C1103	G1043	A983	A923	U863	C803	A743	G683	C623	C503	G442	G442	A382	C322
C1344	C1284	U1224	A1164	G1104	A1044	C984	C924	A864	U804	G744	U684	C624	C504	C443	C443	A383	U323
U1345	A1285	A1225	U1165	A1105	U1045	C985	G925	A865	C805	G745	G685	U625	G505	G444	G444	G384	G324
A1346	U1286	C1226	G1166	G1106	A1046	U986	G926	C866	C806	A746	U686	G626	G506	G445	G445	C385	A325
G1347	A1287	A1227	A1167	C1107	G1047	G987	G927	G867	A807	A747	A687	G627	C507	G446	G446	C386	G326
A1348	A1288	C1228	U1168	G1108	U1048	G988	G928	C868	C808	G748	G688	G628	G508	G447	G447	U387	A327
U1349	A1289	A1229	A1169	C1109	U1049	U989	G929	G869	C809	A749	C689	A629	C509	G448	G448	G388	C328
A1350	G1290	C1230	A1170	A1110	G1050	C990	C930	U870	C810	C750	G690	A630	G570	A510	G449	A389	A329
U1351	U1291	G1231	A1171	A1111	U1051	U991	C931	U871	C811	U751	G691	C631	U571	C511	G450	U390	C330
C1352	G1292	U1232	C1172	C1112	U1052	U992	C932	A872	G812	G752	U692	U632	A572	U512	A451	G391	G331
G1353	C1293	G1233	U1173	G993	A1053	C993	G933	A873	U813	A753	G693	G633	C513	C452	A452	C392	A332
U1354	A1294	C1234	C1174	C1113	C1054	A994	C934	G874	A814	G754	A694	C634	A574	C514	G453	A393	U333
G1355	U1295	U1235	G1175	U1115	A1055	C995	A935	U875	A815	G755	A695	A635	G575	G515	G454	G394	C334
C1356	C1296	A1236	U1176	U1116	U1056	A996	C936	C876	A816	G756	A696	U636	C576	U516	G455	C395	C335
A1357	G1297	C1237	G1177	A1117	U1057	U997	A937	G877	C817	U757	U697	C637	A577	C457	A456	A396	A336
U1358	U1298	A1238	C1178	U1118	G1058	C998	A938	A878	G818	G758	G698	U638	C578	C458	U457	A397	G337
C1359	A1299	C1239	A1179	C1119	U1059	C999	G939	C879	A819	A759	C699	G639	A579	U459	G458	U398	A338
A1360	G1300	U1240	A1180	C1120	U1060	A1000	C940	C880	U820	G760	G700	A640	C580	A520	A459	G399	C339
G1361	U1301	G1241	G1181	U1121	G1061	C1001	G941	C881	G821	G761	U701	A641	G581	G521	A460	C400	U340
A1362	C1302	U1242	G1182	U1122	U1062	G1002	G942	C882	U822	U762	A702	A642	C582	C522	A461	C401	C341
A1363	G1303	G1243	U1183	U1123	C1063	G1003	U943	C883	C823	G763	G703	C643	A583	A523	G462	G402	C342
U1364	A1304	G1244	A1184	G1124	G1064	A1004	G944	U884	G824	G764	A704	U644	G584	G524	U463	C403	U343
G1365	G1305	C1245	G1185	U1125	U1065	A1005	G945	C885	A825	G765	G705	G645	G585	C525	U464	G404	A344
C1366	A1306	A1246	G1186	U1126	C1066	G1006	A946	C886	C826	A766	A706	G646	C586	C526	A465	U405	C345
G1367	U1307	U1247	G1187	G1127	U1067	U1007	G947	C887	U827	A767	U707	C647	G587	G527	A466	G406	G346
A1368	U1308	A1248	A1188	C1128	G1068	U1008	C948	C888	U828	A768	C708	A648	G588	C528	U467	U407	G347
C1369	G1309	C1249	U1189	C1129	C1069	U1009	A949	A889	G829	G769	U709	A649	U589	G529	A468	A408	G348
G1370	U1310	A1250	G1190	A1130	U1070	U1010	U950	C890	G830	C770	G710	G650	U590	G530	C469	U409	A349
A1371	C1311	A1251	A1191	C1131	C1071	C1011	G951	U891	G831	G771	G711	C651	U591	U531	C470	G410	G350
U1372	G1312	A1252	C1192	C1132	G1072	A1012	U952	A892	G832	U772	A712	U652	G592	A532	A471	A411	G351
G1373	U1313	G1253	G1193	G1133	U1073	G1013	G953	C893	G833	G773	G713	U653	U593	A533	U472	A412	C352
A1374	C1314	A1254	U1194	G1134	G1074	A1014	G954	C894	U834	G774	G714	G654	U594	U534	G473	G413	A353
U1375	U1315	G1255	C1195	U1135	U1075	G1015	U955	C895	U835	G775	A715	A655	A595	A535	C474	A414	G354
G1376	G1316	A1256	A1196	C1136	U1076	A1016	U956	C896	G836	G776	A716	G656	A596	C536	U476	A415	C355
A1377	C1317	U1257	A1197	U1017	G1077	U1017	U957	C897	U837	A777	U717	U657	G597	G537	U477	G416	A356
C1378	A1318	G1258	G1198	G1138	U1078	A1018	A958	C898	G838	G778	A718	C658	U598	G538	A478	G417	G357
G1379	U1319	C1259	U1199	A1019	G1079	A1019	A959	C899	C839	C779	G719	U659	C599	A539	U479	C418	U358
U1380	C1320	G1260	C1200	G1140	A1080	U1020	U960	A900	C840	A780	C720	C660	A600	G540	U480	C419	G359
A1381	U1321	A1261	A1201	C1141	A1081	U1021	U961	A901	C841	A781	G721	G661	G601	G541	C481	U420	G360
C1382	C1322	C1262	U1202	G1142	A1082	A1022	C962	G902	U842	A782	G722	U662	A602	G542	A482	U421	G361
G1383	U1323	C1263	C1203	G1143	U1083	U1023	G963	G903	U843	A783	G723	U663	U603	G543	G483	C422	G362
C1384	A1324	U1264	A1204	G1144	G1084	G1024	A964	U904	G844	A784	G724	G664	G604	G544	G484	G423	A363



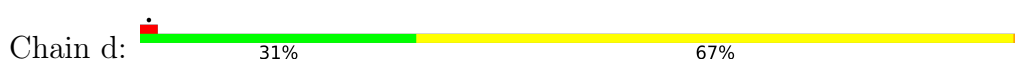
• Molecule 35: 30S ribosomal protein S2

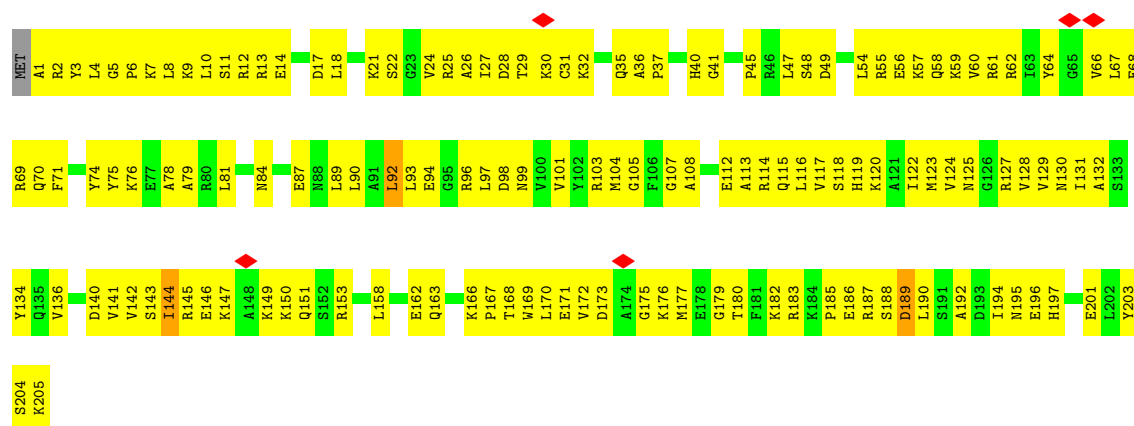


• Molecule 36: 30S ribosomal protein S3

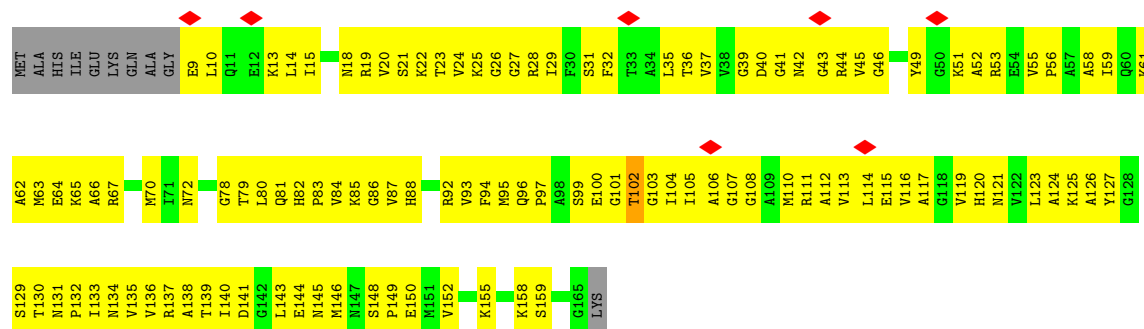


• Molecule 37: 30S ribosomal protein S4

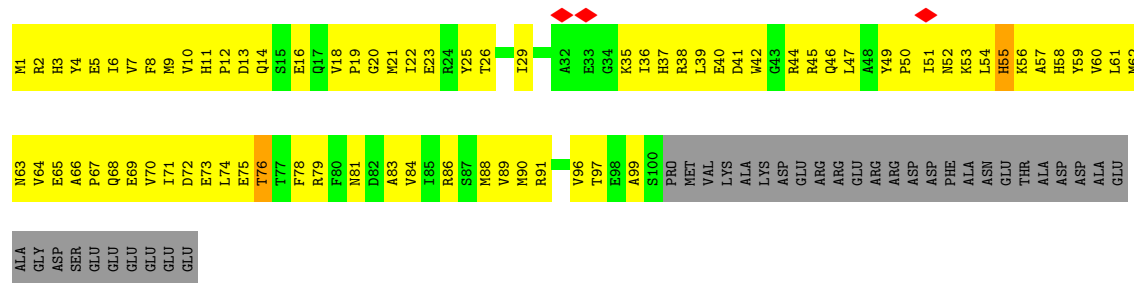
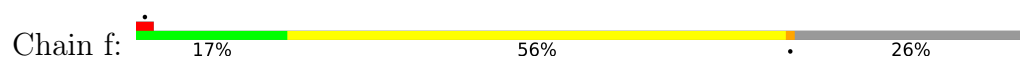




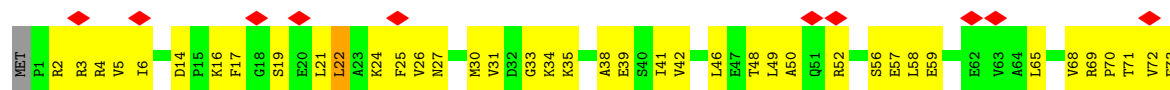
• Molecule 38: 30S ribosomal protein S5

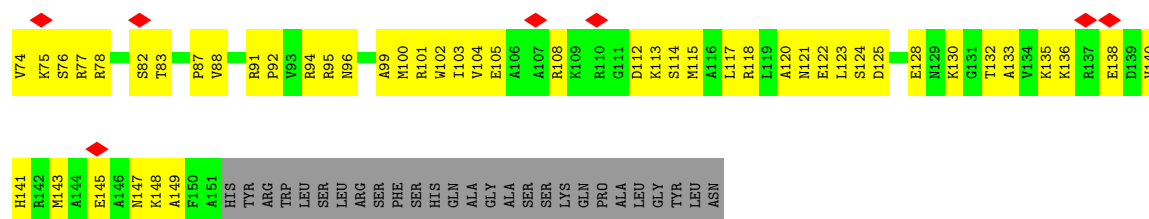


• Molecule 39: 30S ribosomal protein S6

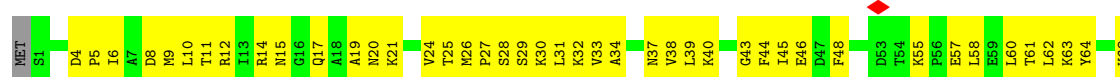


• Molecule 40: 30S ribosomal protein S7

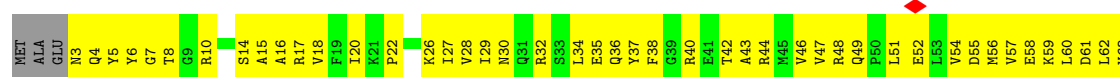




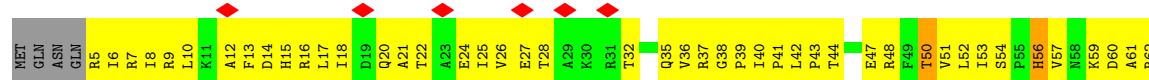
• Molecule 41: 30S ribosomal protein S8



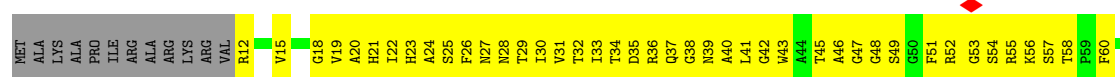
• Molecule 42: 30S ribosomal protein S9



• Molecule 43: 30S ribosomal protein S10



• Molecule 44: 30S ribosomal protein S11





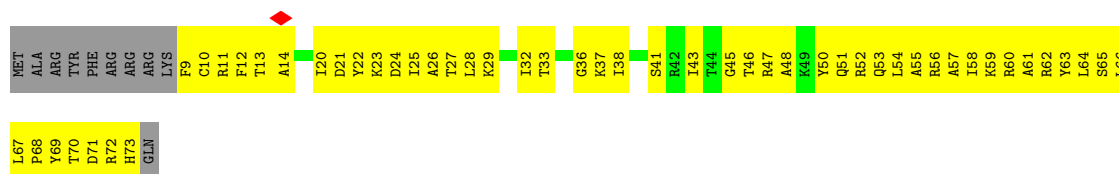
- Molecule 50: 30S ribosomal protein S17

Chain q: 30% 65% 5%



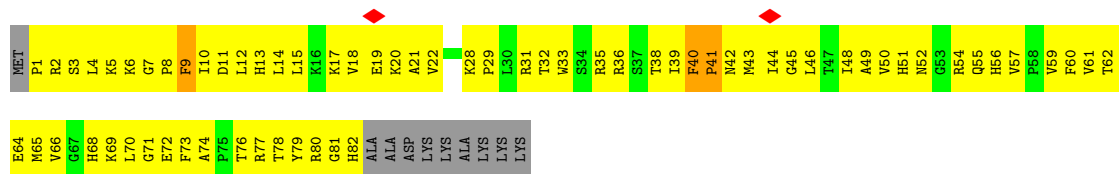
- Molecule 51: 30S ribosomal protein S18

Chain r: 19% 68% 13%



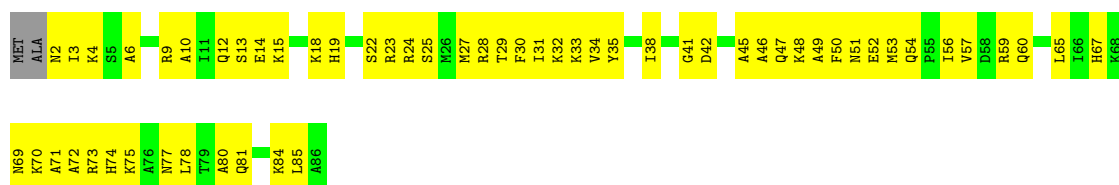
- Molecule 52: 30S ribosomal protein S19

Chain s: 15% 71% 11%



- Molecule 53: 30S ribosomal protein S20

Chain t: 32% 66% 2%

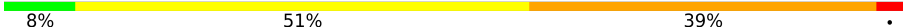


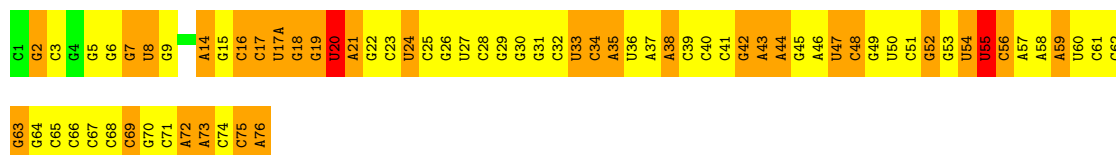
- Molecule 54: 30S ribosomal protein S21

Chain u:  56% 34% 8%



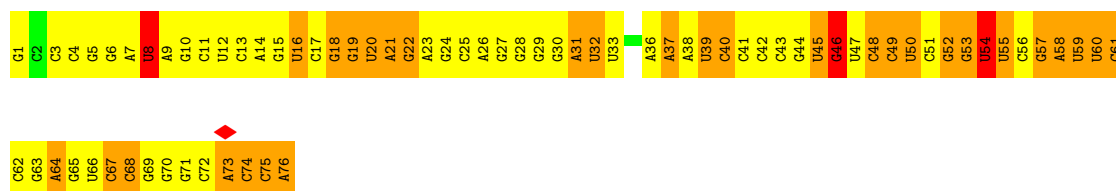
- Molecule 55: P-site tRNA(fMet)

Chain v:  8% 51% 39%

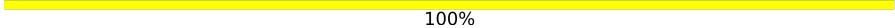


- Molecule 56: P-site fMet-Phe-tRNA(Phe)

Chain w:  53% 39%



- Molecule 57: Dipeptide (FME-PHE)

Chain y:  100%



- Molecule 58: mRNA

Chain z:  18% 15% 67%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	6937	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	11.607	Depositor
Minimum map value	-7.178	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	1.5	Depositor
Map size (Å)	334.08, 334.08, 334.08	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.16, 1.16, 1.16	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.59	0/450	0.79	1/599 (0.2%)
2	1	0.34	0/416	0.61	0/554
3	2	0.52	0/380	0.80	0/498
4	3	0.60	0/513	1.01	2/676 (0.3%)
5	4	0.43	0/303	0.66	0/397
6	5	0.24	0/646	0.64	0/898
7	6	0.64	1/531 (0.2%)	1.04	2/709 (0.3%)
8	A	0.49	0/69266	0.53	9/108055 (0.0%)
9	B	0.42	0/2873	0.49	0/4478
10	C	0.51	0/2121	0.78	2/2852 (0.1%)
11	D	0.48	0/1586	0.77	2/2134 (0.1%)
12	E	0.46	0/1571	0.64	0/2113
13	F	0.47	0/1434	0.72	0/1926
14	G	0.40	0/1343	0.70	2/1816 (0.1%)
15	H	0.39	0/1122	0.76	2/1515 (0.1%)
16	I	0.26	0/692	0.67	0/960
17	J	0.46	0/1152	0.64	0/1551
18	K	0.41	0/947	0.72	0/1268
19	L	0.54	0/1054	0.88	3/1403 (0.2%)
20	M	0.47	0/1093	0.69	0/1460
21	N	0.45	0/973	0.74	0/1301
22	O	0.49	0/902	0.79	1/1209 (0.1%)
23	P	0.49	0/929	0.75	2/1242 (0.2%)
24	Q	0.58	0/960	0.76	1/1278 (0.1%)
25	R	0.52	0/829	0.89	5/1107 (0.5%)
26	S	0.59	0/864	0.90	0/1156
27	T	0.48	0/744	0.82	1/994 (0.1%)
28	U	0.50	0/787	0.86	2/1051 (0.2%)
29	V	0.42	0/766	0.60	0/1025
30	W	0.43	0/582	0.69	0/769
31	X	0.48	0/635	0.97	2/848 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Y	0.53	0/510	1.08	2/677 (0.3%)
33	Z	0.41	0/453	0.63	0/605
34	a	0.44	1/36725 (0.0%)	0.52	6/57285 (0.0%)
35	b	0.41	0/1735	0.65	0/2338
36	c	0.38	0/1651	0.64	0/2225
37	d	0.40	0/1665	0.77	3/2227 (0.1%)
38	e	0.41	0/1154	0.65	0/1554
39	f	0.34	0/835	0.66	0/1128
40	g	0.38	0/1195	0.67	0/1602
41	h	0.44	0/989	0.69	0/1326
42	i	0.47	0/1034	0.81	0/1375
43	j	0.44	1/796 (0.1%)	0.76	0/1077
44	k	0.42	0/885	0.70	0/1195
45	l	0.41	0/969	0.70	0/1300
46	m	0.42	0/892	0.79	1/1193 (0.1%)
47	n	0.53	0/811	1.05	5/1081 (0.5%)
48	o	0.42	0/722	0.68	0/964
49	p	0.37	0/659	0.71	0/884
50	q	0.40	0/657	0.67	0/881
51	r	0.41	0/544	0.70	0/731
52	s	0.63	0/675	1.07	3/908 (0.3%)
53	t	0.45	0/671	0.62	0/888
54	u	0.47	0/512	0.83	0/683
55	v	0.39	0/1745	0.48	0/2716
56	w	0.41	1/1650 (0.1%)	0.53	0/2569
57	y	0.40	0/11	0.41	0/13
58	z	0.41	0/255	0.71	1/394 (0.3%)
All	All	0.47	4/158864 (0.0%)	0.59	60/237661 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	6	5	ILE	C-N	-7.07	1.23	1.33
56	w	46	G7M	O3'-P	6.58	1.62	1.56
34	a	1498	UR3	O3'-P	6.00	1.62	1.56
43	j	56	HIS	N-CA	5.76	1.50	1.46

The worst 5 of 60 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	a	1196	A	C2'-C3'-O3'	14.57	131.35	109.50
31	X	28	PHE	CA-C-N	-13.96	99.47	122.65

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	X	28	PHE	C-N-CA	-13.96	99.47	122.65
34	a	1053	G	O3'-P-O5'	-12.34	85.50	104.00
47	n	39	GLU	N-CA-C	-10.28	99.49	114.39

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	43	0
2	1	409	0	440	52	0
3	2	377	0	418	62	0
4	3	504	0	574	71	0
5	4	302	0	341	46	0
6	5	647	0	336	19	0
7	6	522	0	521	68	0
8	A	62317	0	31359	6655	0
9	B	2570	0	1301	238	0
10	C	2082	0	2157	313	0
11	D	1565	0	1616	233	0
12	E	1552	0	1619	174	0
13	F	1410	0	1447	169	0
14	G	1323	0	1374	135	0
15	H	1111	0	1148	101	0
16	I	693	0	347	17	0
17	J	1129	0	1162	129	0
18	K	938	0	1012	137	0
19	L	1045	0	1117	134	0
20	M	1074	0	1157	131	0
21	N	960	0	1000	155	0
22	O	892	0	923	95	0
23	P	917	0	965	130	0
24	Q	947	0	1022	126	0
25	R	816	0	839	106	0
26	S	857	0	922	77	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	T	738	0	807	83	0
28	U	779	0	834	78	0
29	V	753	0	780	85	0
30	W	575	0	592	81	0
31	X	625	0	655	94	0
32	Y	509	0	543	37	0
33	Z	449	0	491	39	0
34	a	33050	0	16655	3445	0
35	b	1704	0	1732	140	0
36	c	1624	0	1699	185	0
37	d	1643	0	1710	198	0
38	e	1141	0	1170	130	0
39	f	817	0	808	108	0
40	g	1181	0	1240	85	0
41	h	979	0	1034	94	0
42	i	1022	0	1070	121	0
43	j	786	0	828	101	0
44	k	869	0	878	130	0
45	l	955	0	1019	131	0
46	m	883	0	944	109	0
47	n	799	0	841	86	0
48	o	714	0	737	81	0
49	p	649	0	666	67	0
50	q	648	0	691	67	0
51	r	535	0	552	83	0
52	s	658	0	685	91	0
53	t	665	0	714	79	0
54	u	506	0	502	27	0
55	v	1642	0	839	168	0
56	w	1631	0	838	142	0
57	y	21	0	19	3	0
58	z	230	0	116	12	0
59	4	1	0	0	0	0
59	6	1	0	0	0	0
60	a	37	0	41	4	0
All	All	147222	0	98308	14599	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 61.

The worst 5 of 14599 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)
8:A:524:G:H2'	8:A:525:U:C5'	0.90	1.38
7:6:61:ASN:ND2	7:6:64:PHE:CD1	1.94	1.34
8:A:524:G:C2'	8:A:525:U:H5''	0.84	1.31
8:A:53:A:H62	8:A:117:G:N2	1.26	1.29
8:A:1299:G:N2	8:A:1641:A:H62	1.25	1.29

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%)	42 (78%)	12 (22%)	0	100	100
2	1	48/55 (87%)	38 (79%)	10 (21%)	0	100	100
3	2	44/46 (96%)	27 (61%)	17 (39%)	0	100	100
4	3	62/65 (95%)	48 (77%)	14 (23%)	0	100	100
5	4	36/38 (95%)	28 (78%)	8 (22%)	0	100	100
6	5	129/165 (78%)	100 (78%)	29 (22%)	0	100	100
7	6	64/70 (91%)	54 (84%)	10 (16%)	0	100	100
10	C	269/273 (98%)	213 (79%)	56 (21%)	0	100	100
11	D	207/209 (99%)	172 (83%)	34 (16%)	1 (0%)	24	63
12	E	199/201 (99%)	165 (83%)	34 (17%)	0	100	100
13	F	175/179 (98%)	153 (87%)	22 (13%)	0	100	100
14	G	174/177 (98%)	149 (86%)	25 (14%)	0	100	100
15	H	147/149 (99%)	117 (80%)	30 (20%)	0	100	100
16	I	139/142 (98%)	104 (75%)	35 (25%)	0	100	100
17	J	140/142 (99%)	109 (78%)	31 (22%)	0	100	100
18	K	120/123 (98%)	101 (84%)	19 (16%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	L	141/144 (98%)	108 (77%)	33 (23%)	0	100	100
20	M	134/136 (98%)	109 (81%)	24 (18%)	1 (1%)	18	56
21	N	118/127 (93%)	87 (74%)	31 (26%)	0	100	100
22	O	114/117 (97%)	101 (89%)	13 (11%)	0	100	100
23	P	112/115 (97%)	98 (88%)	14 (12%)	0	100	100
24	Q	115/118 (98%)	102 (89%)	13 (11%)	0	100	100
25	R	101/103 (98%)	87 (86%)	14 (14%)	0	100	100
26	S	108/110 (98%)	89 (82%)	19 (18%)	0	100	100
27	T	91/100 (91%)	74 (81%)	17 (19%)	0	100	100
28	U	100/104 (96%)	81 (81%)	19 (19%)	0	100	100
29	V	92/94 (98%)	79 (86%)	13 (14%)	0	100	100
30	W	73/85 (86%)	56 (77%)	17 (23%)	0	100	100
31	X	75/78 (96%)	63 (84%)	12 (16%)	0	100	100
32	Y	61/63 (97%)	49 (80%)	12 (20%)	0	100	100
33	Z	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
35	b	216/240 (90%)	184 (85%)	32 (15%)	0	100	100
36	c	204/233 (88%)	181 (89%)	23 (11%)	0	100	100
37	d	203/206 (98%)	160 (79%)	42 (21%)	1 (0%)	24	63
38	e	155/167 (93%)	119 (77%)	36 (23%)	0	100	100
39	f	98/135 (73%)	88 (90%)	10 (10%)	0	100	100
40	g	149/179 (83%)	130 (87%)	19 (13%)	0	100	100
41	h	127/130 (98%)	107 (84%)	20 (16%)	0	100	100
42	i	125/130 (96%)	98 (78%)	27 (22%)	0	100	100
43	j	96/103 (93%)	76 (79%)	19 (20%)	1 (1%)	12	48
44	k	114/129 (88%)	92 (81%)	22 (19%)	0	100	100
45	l	121/124 (98%)	96 (79%)	25 (21%)	0	100	100
46	m	112/118 (95%)	99 (88%)	13 (12%)	0	100	100
47	n	99/102 (97%)	87 (88%)	12 (12%)	0	100	100
48	o	86/89 (97%)	74 (86%)	12 (14%)	0	100	100
49	p	80/82 (98%)	61 (76%)	19 (24%)	0	100	100
50	q	78/84 (93%)	68 (87%)	10 (13%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	r	63/75 (84%)	49 (78%)	14 (22%)	0	100	100
52	s	80/92 (87%)	70 (88%)	10 (12%)	0	100	100
53	t	83/87 (95%)	66 (80%)	17 (20%)	0	100	100
54	u	63/71 (89%)	50 (79%)	13 (21%)	0	100	100
All	All	5850/6220 (94%)	4809 (82%)	1037 (18%)	4 (0%)	49	83

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
43	j	60	ASP
37	d	144	ILE
11	D	138	LEU
20	M	59	ARG

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%)	42 (89%)	5 (11%)	6	21
2	1	45/49 (92%)	45 (100%)	0	100	100
3	2	38/38 (100%)	37 (97%)	1 (3%)	40	61
4	3	51/52 (98%)	46 (90%)	5 (10%)	7	24
5	4	34/34 (100%)	33 (97%)	1 (3%)	37	58
7	6	59/62 (95%)	49 (83%)	10 (17%)	2	10
10	C	216/218 (99%)	215 (100%)	1 (0%)	81	83
11	D	164/164 (100%)	163 (99%)	1 (1%)	78	82
12	E	165/165 (100%)	165 (100%)	0	100	100
13	F	148/150 (99%)	143 (97%)	5 (3%)	32	54
14	G	137/138 (99%)	133 (97%)	4 (3%)	37	58
15	H	114/114 (100%)	114 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	J	116/116 (100%)	113 (97%)	3 (3%)	40	61
18	K	103/104 (99%)	103 (100%)	0	100	100
19	L	102/103 (99%)	100 (98%)	2 (2%)	48	66
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%)	82 (95%)	4 (5%)	23	44
23	P	99/100 (99%)	98 (99%)	1 (1%)	68	78
24	Q	89/90 (99%)	89 (100%)	0	100	100
25	R	84/84 (100%)	80 (95%)	4 (5%)	23	44
26	S	93/93 (100%)	88 (95%)	5 (5%)	20	41
27	T	80/84 (95%)	79 (99%)	1 (1%)	61	74
28	U	83/85 (98%)	82 (99%)	1 (1%)	63	75
29	V	78/78 (100%)	78 (100%)	0	100	100
30	W	57/63 (90%)	57 (100%)	0	100	100
31	X	67/68 (98%)	66 (98%)	1 (2%)	57	72
32	Y	55/55 (100%)	50 (91%)	5 (9%)	9	27
33	Z	48/49 (98%)	47 (98%)	1 (2%)	47	65
35	b	180/198 (91%)	180 (100%)	0	100	100
36	c	170/190 (90%)	168 (99%)	2 (1%)	63	75
37	d	172/173 (99%)	169 (98%)	3 (2%)	53	69
38	e	114/126 (90%)	112 (98%)	2 (2%)	51	68
39	f	87/116 (75%)	85 (98%)	2 (2%)	44	64
40	g	124/147 (84%)	121 (98%)	3 (2%)	43	63
41	h	104/105 (99%)	103 (99%)	1 (1%)	68	78
42	i	105/107 (98%)	103 (98%)	2 (2%)	50	67
43	j	86/90 (96%)	85 (99%)	1 (1%)	63	75
44	k	89/99 (90%)	89 (100%)	0	100	100
45	l	103/104 (99%)	102 (99%)	1 (1%)	68	78
46	m	92/96 (96%)	89 (97%)	3 (3%)	33	55
47	n	79/84 (94%)	74 (94%)	5 (6%)	16	37
48	o	76/77 (99%)	76 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	p	65/65 (100%)	65 (100%)	0	100	100
50	q	74/78 (95%)	73 (99%)	1 (1%)	59	72
51	r	56/65 (86%)	56 (100%)	0	100	100
52	s	72/79 (91%)	67 (93%)	5 (7%)	14	36
53	t	65/66 (98%)	65 (100%)	0	100	100
54	u	46/61 (75%)	45 (98%)	1 (2%)	45	64
57	y	1/1 (100%)	1 (100%)	0	100	100
All	All	4627/4830 (96%)	4534 (98%)	93 (2%)	48	66

5 of 93 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	Y	18	LEU
40	g	22	LEU
32	Y	57	LEU
37	d	189	ASP
42	i	58	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 102 such sidechains are listed below:

Mol	Chain	Res	Type
32	Y	45	GLN
40	g	121	ASN
53	t	51	ASN
35	b	17	HIS
37	d	70	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	a	1539/1542 (99%)	578 (37%)	0
55	v	76/77 (98%)	30 (39%)	0
56	w	75/76 (98%)	33 (44%)	0
58	z	10/33 (30%)	6 (60%)	0
8	A	2900/2903 (99%)	1096 (37%)	86 (2%)
9	B	119/120 (99%)	46 (38%)	2 (1%)
All	All	4719/4751 (99%)	1789 (37%)	88 (1%)

5 of 1789 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	A	10	A
8	A	14	A
8	A	15	G
8	A	16	C
8	A	23	G

5 of 88 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	A	1921	G
8	A	2405	G
8	A	2015	A
8	A	2192	U
8	A	2474	U

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

45 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	2604	8	18,21,22	1.06	2 (11%)	22,30,33	2.03	5 (22%)
56	5MU	w	54	56	19,22,23	1.45	6 (31%)	28,32,35	2.26	7 (25%)
8	PSU	A	746	8	18,21,22	1.09	1 (5%)	22,30,33	1.78	4 (18%)
8	PSU	A	2457	8	18,21,22	1.05	2 (11%)	22,30,33	1.99	5 (22%)
56	G7M	w	46	56	23,26,27	2.55	8 (34%)	35,39,42	2.30	10 (28%)
56	4SU	w	8	56	18,21,22	3.57	8 (44%)	26,30,33	2.31	4 (15%)
57	FME	y	101	57	8,9,10	0.90	0	7,9,11	1.14	0
8	5MC	A	1962	8	18,22,23	3.49	7 (38%)	26,32,35	1.34	4 (15%)
8	PSU	A	955	8	18,21,22	1.05	1 (5%)	22,30,33	1.88	5 (22%)
34	PSU	a	516	34	18,21,22	1.07	1 (5%)	22,30,33	1.62	3 (13%)
56	PSU	w	32	56	18,21,22	1.06	1 (5%)	22,30,33	1.65	5 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
34	MA6	a	1519	34	23,26,27	1.51	5 (21%)	34,38,41	2.66	10 (29%)
34	2MG	a	966	34	23,26,27	2.93	8 (34%)	32,38,41	2.27	12 (37%)
56	PSU	w	39	56	18,21,22	1.10	1 (5%)	22,30,33	1.74	3 (13%)
8	6MZ	A	1618	8	22,25,26	4.15	10 (45%)	30,36,39	4.42	16 (53%)
34	UR3	a	1498	34	19,22,23	2.48	6 (31%)	26,32,35	1.27	1 (3%)
55	H2U	v	20	55	18,21,22	2.95	5 (27%)	21,30,33	2.17	5 (23%)
8	5MU	A	1939	8	19,22,23	4.76	7 (36%)	28,32,35	3.71	13 (46%)
34	G7M	a	527	34	23,26,27	2.62	7 (30%)	35,39,42	2.38	10 (28%)
34	4OC	a	1402	34	20,23,24	2.94	8 (40%)	26,32,35	1.24	5 (19%)
34	2MG	a	1516	34	23,26,27	2.87	6 (26%)	32,38,41	2.13	10 (31%)
8	PSU	A	2605	8	18,21,22	1.00	1 (5%)	22,30,33	2.05	4 (18%)
8	PSU	A	1911	8	18,21,22	1.07	2 (11%)	22,30,33	2.15	6 (27%)
8	1MG	A	745	8	22,26,27	2.60	5 (22%)	33,39,42	2.05	8 (24%)
8	2MA	A	2503	8	22,25,26	3.50	10 (45%)	33,37,40	2.30	9 (27%)
8	G7M	A	2069	8	23,26,27	2.50	8 (34%)	35,39,42	2.47	11 (31%)
55	4SU	v	8	55	18,21,22	3.56	7 (38%)	26,30,33	2.08	6 (23%)
8	6MZ	A	2030	8	22,25,26	4.12	11 (50%)	30,36,39	4.44	14 (46%)
8	PSU	A	1917	8	18,21,22	0.97	1 (5%)	22,30,33	1.88	4 (18%)
8	OMG	A	2251	8,56	23,26,27	2.43	8 (34%)	33,38,41	1.94	8 (24%)
34	2MG	a	1207	34	23,26,27	2.79	9 (39%)	32,38,41	2.11	10 (31%)
8	2MG	A	1835	8	23,26,27	2.92	7 (30%)	32,38,41	2.33	11 (34%)
8	PSU	A	2580	8	18,21,22	1.32	2 (11%)	22,30,33	2.23	7 (31%)
56	MIA	w	37	56	28,31,32	2.47	6 (21%)	40,44,47	3.18	15 (37%)
34	5MC	a	1407	34	18,22,23	3.44	7 (38%)	26,32,35	1.18	3 (11%)
8	OMC	A	2498	8	19,22,23	0.95	1 (5%)	26,31,34	1.49	2 (7%)
55	PSU	v	55	55	18,21,22	1.11	1 (5%)	22,30,33	1.80	4 (18%)
8	PSU	A	2504	8	18,21,22	1.10	3 (16%)	22,30,33	2.17	5 (22%)
8	OMU	A	2552	8	19,22,23	2.90	7 (36%)	26,31,34	1.95	6 (23%)
56	PSU	w	55	56	18,21,22	1.43	3 (16%)	22,30,33	1.89	7 (31%)
34	5MC	a	967	34	18,22,23	3.66	7 (38%)	26,32,35	1.18	3 (11%)
8	5MC	A	747	8	18,22,23	3.51	7 (38%)	26,32,35	1.50	2 (7%)
34	MA6	a	1518	34	23,26,27	1.54	5 (21%)	34,38,41	2.35	11 (32%)
55	5MU	v	54	55	19,22,23	4.80	7 (36%)	28,32,35	3.54	11 (39%)
8	2MG	A	2445	8	23,26,27	2.89	8 (34%)	32,38,41	2.29	9 (28%)

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	2604	8	-	0/7/25/26	0/2/2/2
56	5MU	w	54	56	-	3/7/25/26	0/2/2/2
8	PSU	A	746	8	-	1/7/25/26	0/2/2/2
8	PSU	A	2457	8	-	0/7/25/26	0/2/2/2
56	G7M	w	46	56	-	3/7/25/26	0/3/3/3
56	4SU	w	8	56	-	2/7/25/26	0/2/2/2
57	FME	y	101	57	-	6/7/9/11	-
8	5MC	A	1962	8	-	4/7/25/26	0/2/2/2
8	PSU	A	955	8	-	0/7/25/26	0/2/2/2
34	PSU	a	516	34	-	1/7/25/26	0/2/2/2
56	PSU	w	32	56	-	2/7/25/26	0/2/2/2
34	MA6	a	1519	34	-	4/11/29/30	0/3/3/3
34	2MG	a	966	34	-	1/9/27/28	0/3/3/3
56	PSU	w	39	56	-	5/7/25/26	0/2/2/2
8	6MZ	A	1618	8	-	5/9/27/28	0/3/3/3
34	UR3	a	1498	34	-	4/7/25/26	0/2/2/2
55	H2U	v	20	55	-	5/7/38/39	0/2/2/2
8	5MU	A	1939	8	-	1/7/25/26	0/2/2/2
34	G7M	a	527	34	-	1/7/25/26	0/3/3/3
34	4OC	a	1402	34	-	3/9/29/30	0/2/2/2
34	2MG	a	1516	34	-	0/9/27/28	0/3/3/3
8	PSU	A	2605	8	-	0/7/25/26	0/2/2/2
8	PSU	A	1911	8	-	1/7/25/26	0/2/2/2
8	1MG	A	745	8	-	0/7/25/26	0/3/3/3
8	2MA	A	2503	8	-	3/7/25/26	0/3/3/3
8	G7M	A	2069	8	-	2/7/25/26	0/3/3/3
55	4SU	v	8	55	-	0/7/25/26	0/2/2/2
8	6MZ	A	2030	8	-	2/9/27/28	0/3/3/3
8	PSU	A	1917	8	-	0/7/25/26	0/2/2/2
8	OMG	A	2251	8,56	-	3/9/27/28	0/3/3/3
34	2MG	a	1207	34	-	0/9/27/28	0/3/3/3
8	2MG	A	1835	8	-	2/9/27/28	0/3/3/3
8	PSU	A	2580	8	-	2/7/25/26	0/2/2/2
56	MIA	w	37	56	-	3/15/33/34	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	5MC	a	1407	34	-	0/7/25/26	0/2/2/2
8	OMC	A	2498	8	-	3/9/27/28	0/2/2/2
55	PSU	v	55	55	-	3/7/25/26	0/2/2/2
8	PSU	A	2504	8	-	0/7/25/26	0/2/2/2
8	OMU	A	2552	8	-	6/9/27/28	0/2/2/2
56	PSU	w	55	56	-	1/7/25/26	0/2/2/2
34	5MC	a	967	34	-	1/7/25/26	0/2/2/2
8	5MC	A	747	8	-	2/7/25/26	0/2/2/2
34	MA6	a	1518	34	-	3/11/29/30	0/3/3/3
55	5MU	v	54	55	-	2/7/25/26	0/2/2/2
8	2MG	A	2445	8	-	2/9/27/28	0/3/3/3

The worst 5 of 233 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1618	6MZ	C6-N6	12.21	1.47	1.34
8	A	2030	6MZ	C6-N6	11.92	1.47	1.34
55	v	54	5MU	C2-N1	11.24	1.56	1.38
8	A	1939	5MU	C2-N1	11.04	1.56	1.38
8	A	2503	2MA	C4-N3	10.36	1.47	1.34

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	1618	6MZ	C4-N9-C8	13.46	120.31	105.73
8	A	2030	6MZ	C4-N9-C8	13.00	119.81	105.73
8	A	1939	5MU	C5-C4-N3	11.77	125.36	115.31
55	v	54	5MU	C5-C4-N3	11.06	124.75	115.31
8	A	1618	6MZ	N9-C8-N7	-10.72	99.26	113.91

There are no chirality outliers.

5 of 92 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
55	v	20	H2U	O4'-C1'-N1-C6
55	v	20	H2U	C2'-C1'-N1-C2
55	v	20	H2U	C2'-C1'-N1-C6
8	A	747	5MC	C3'-C4'-C5'-O5'
8	A	1618	6MZ	C5-C6-N6-C9

There are no ring outliers.

42 monomers are involved in 168 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
56	w	54	5MU	2	0
8	A	746	PSU	2	0
8	A	2457	PSU	4	0
56	w	46	G7M	1	0
56	w	8	4SU	6	0
57	y	101	FME	3	0
8	A	1962	5MC	3	0
8	A	955	PSU	4	0
34	a	516	PSU	8	0
56	w	32	PSU	3	0
34	a	1519	MA6	6	0
34	a	966	2MG	1	0
56	w	39	PSU	2	0
34	a	1498	UR3	3	0
55	v	20	H2U	4	0
8	A	1939	5MU	3	0
34	a	527	G7M	2	0
34	a	1402	4OC	4	0
34	a	1516	2MG	11	0
8	A	2605	PSU	1	0
8	A	1911	PSU	2	0
8	A	745	1MG	5	0
8	A	2503	2MA	3	0
8	A	2069	G7M	7	0
55	v	8	4SU	3	0
8	A	1917	PSU	6	0
8	A	2251	OMG	6	0
34	a	1207	2MG	9	0
8	A	1835	2MG	5	0
8	A	2580	PSU	5	0
56	w	37	MIA	4	0
34	a	1407	5MC	6	0
8	A	2498	OMC	2	0
55	v	55	PSU	3	0
8	A	2504	PSU	2	0
8	A	2552	OMU	4	0
56	w	55	PSU	5	0
34	a	967	5MC	4	0
8	A	747	5MC	4	0
34	a	1518	MA6	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
55	v	54	5MU	5	0
8	A	2445	2MG	9	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 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	$\# Z > 2$
60	AM2	a	2001	-	40,40,40	1.66	10 (25%)	53,60,60	1.71	11 (20%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
60	AM2	a	2001	-	-	8/12/84/84	0/4/4/4

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	a	2001	AM2	OA4-CA1	4.04	1.52	1.41
60	a	2001	AM2	CB3-CB4	-3.69	1.48	1.53
60	a	2001	AM2	OA5-CA8	3.20	1.50	1.41
60	a	2001	AM2	OA5-CA4	3.08	1.51	1.44
60	a	2001	AM2	OB1-CB1	2.89	1.49	1.41

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	a	2001	AM2	CA1-OA1-CC1	-5.36	104.71	117.96
60	a	2001	AM2	CA8-CA7-NA7	-3.99	103.86	111.00
60	a	2001	AM2	CB1-OA8-CA8	-3.84	107.56	114.42
60	a	2001	AM2	CA9-NA7-CA7	-3.31	109.57	114.38
60	a	2001	AM2	OA1-CA1-CA2	3.21	113.61	108.23

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

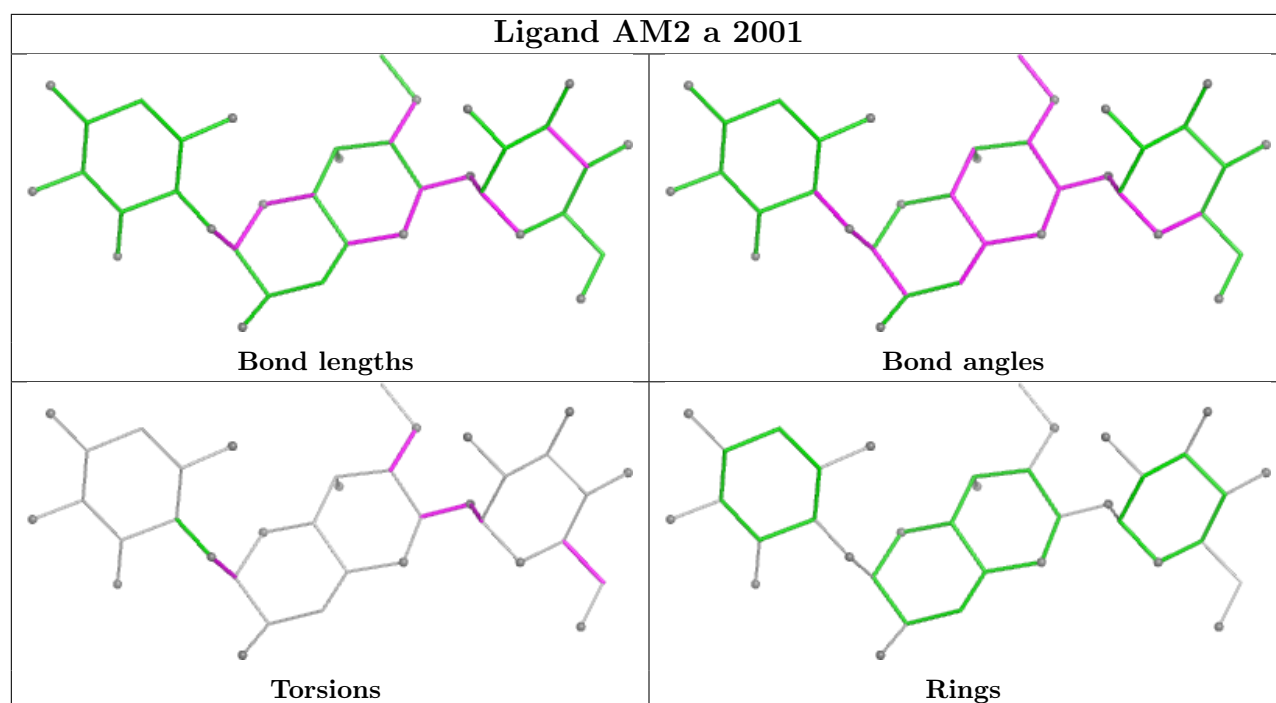
Mol	Chain	Res	Type	Atoms
60	a	2001	AM2	CA7-CA8-OA8-CB1
60	a	2001	AM2	OA5-CA8-OA8-CB1
60	a	2001	AM2	OB1-CB5-CB6-OB6
60	a	2001	AM2	CB4-CB5-CB6-OB6
60	a	2001	AM2	OB1-CB1-OA8-CA8

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	a	2001	AM2	4	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

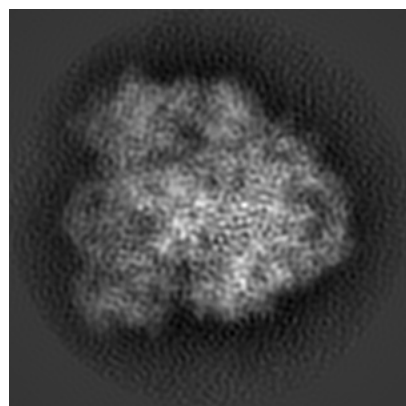
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13459. These allow visual inspection of the internal detail of the map and identification of artifacts.

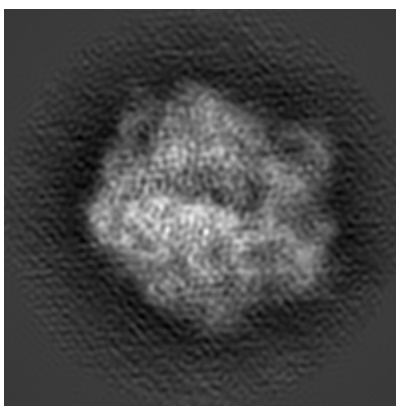
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

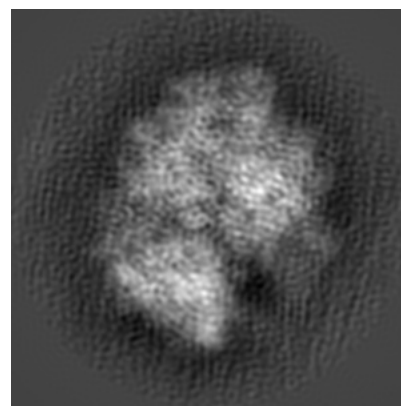
6.1.1 Primary map



X

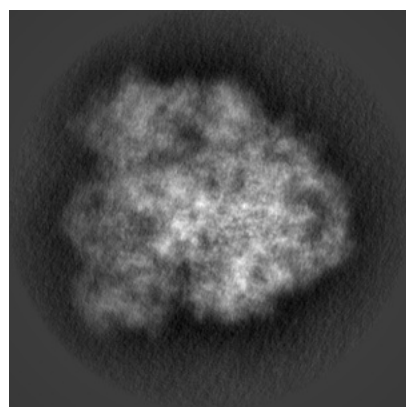


Y

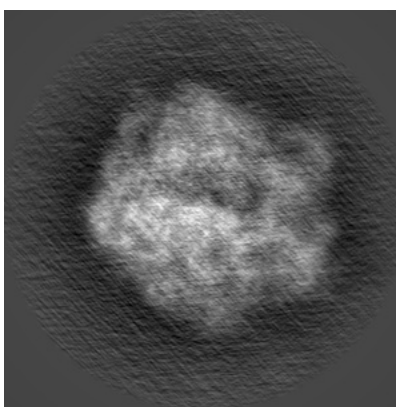


Z

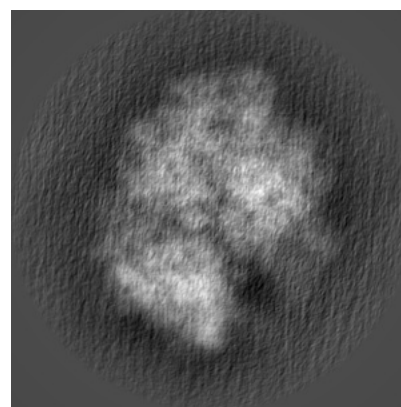
6.1.2 Raw map



X



Y

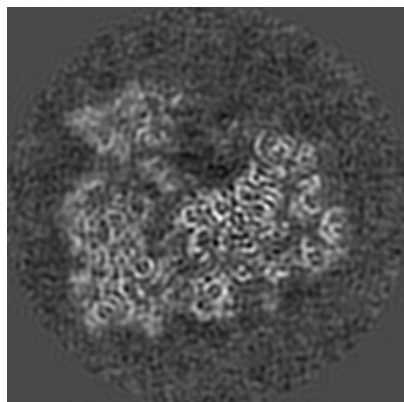


Z

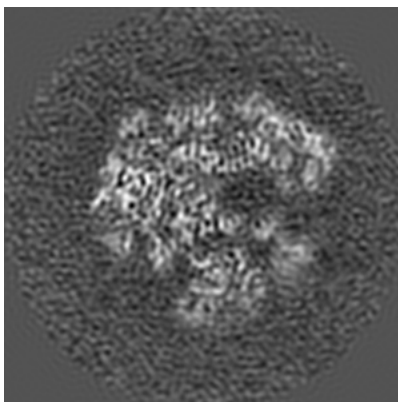
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

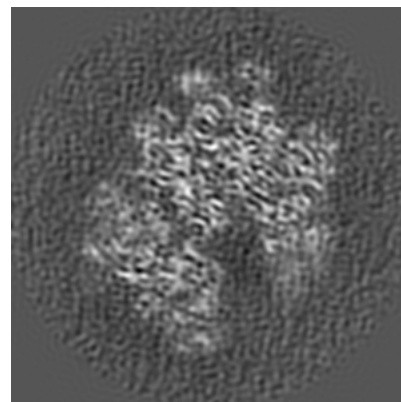
6.2.1 Primary map



X Index: 144

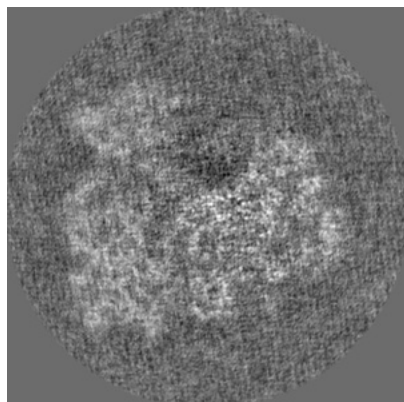


Y Index: 144

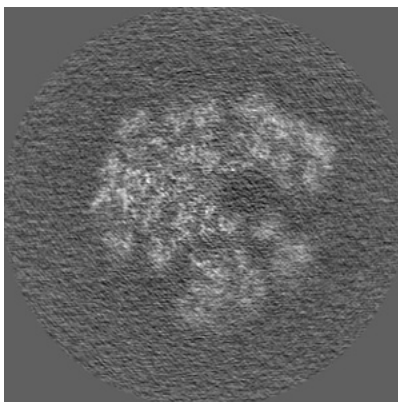


Z Index: 144

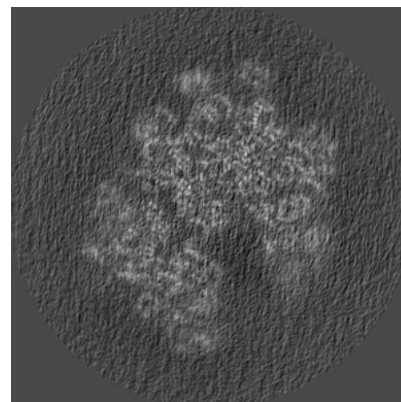
6.2.2 Raw map



X Index: 144



Y Index: 144

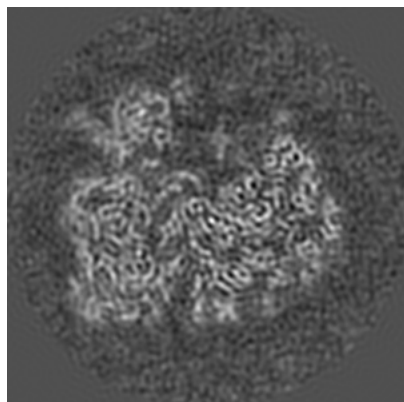


Z Index: 144

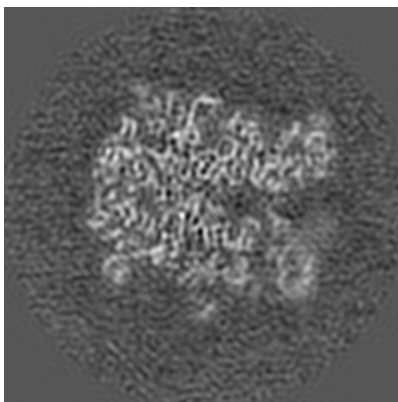
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

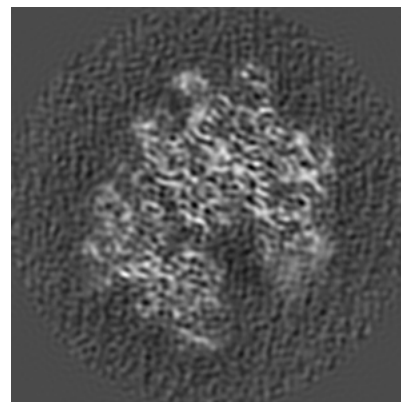
6.3.1 Primary map



X Index: 139

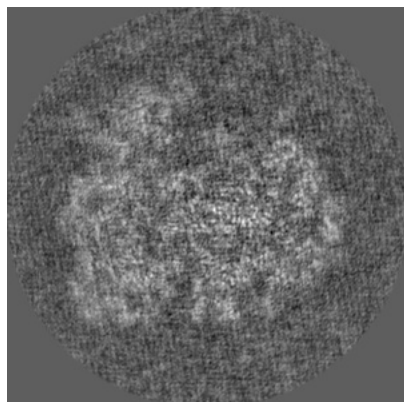


Y Index: 158

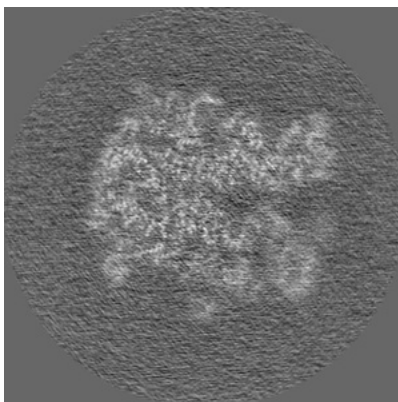


Z Index: 146

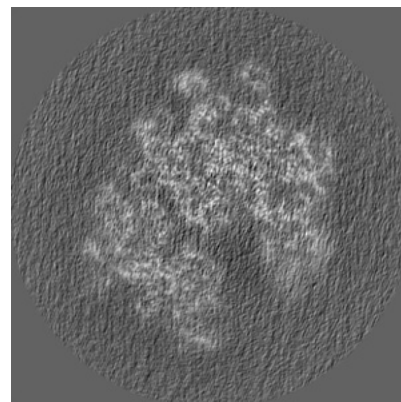
6.3.2 Raw map



X Index: 138



Y Index: 157

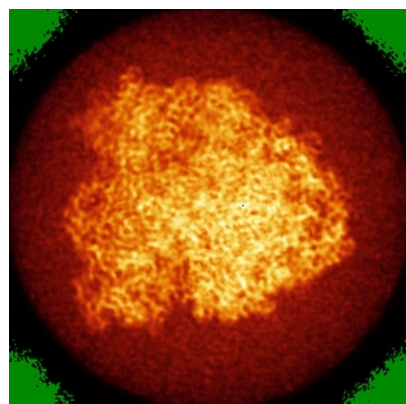


Z Index: 146

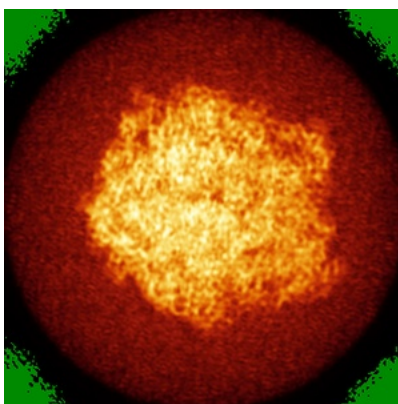
The images above show the largest variance slices of the map in three orthogonal directions.

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

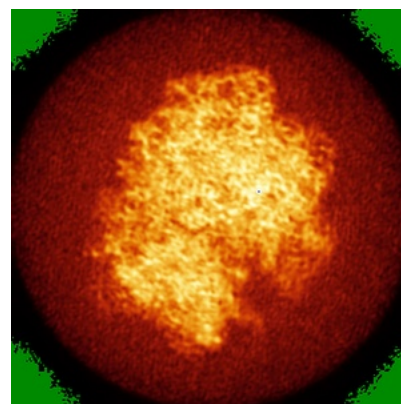
6.4.1 Primary map



X

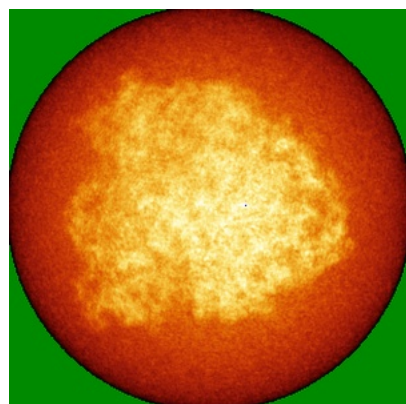


Y

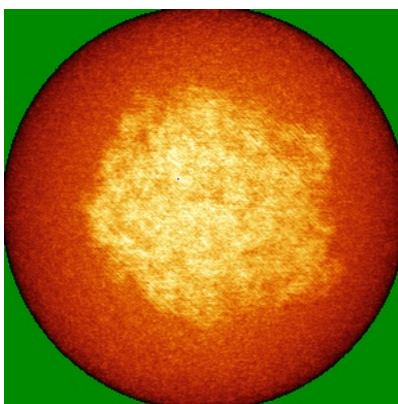


Z

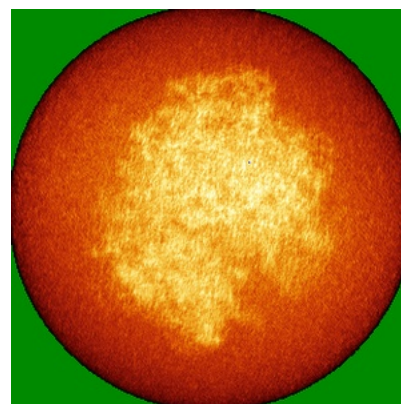
6.4.2 Raw map



X



Y

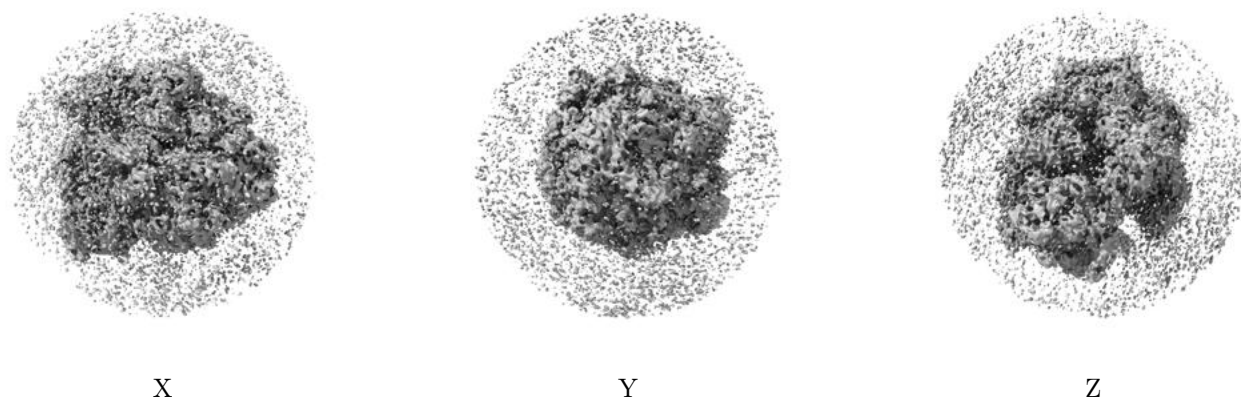


Z

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.

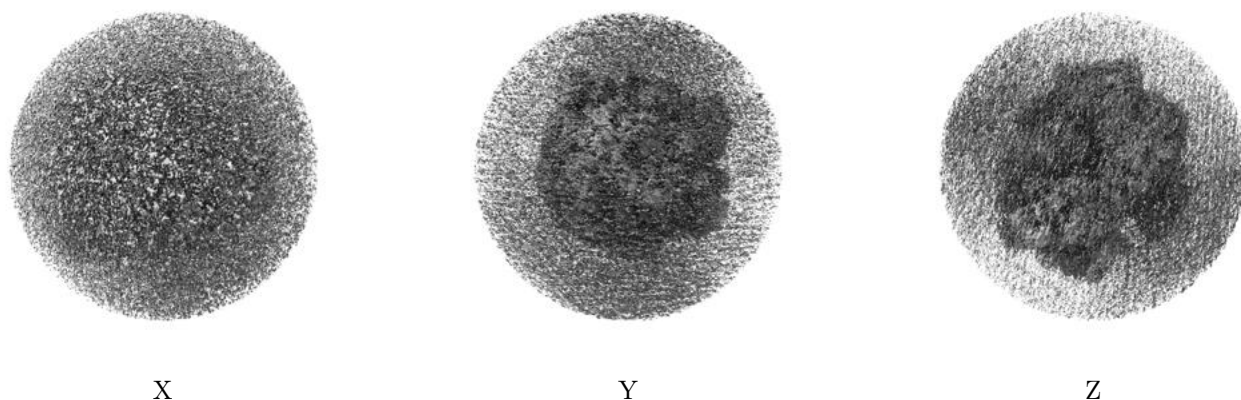
6.5 Orthogonal surface views [i](#)

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.

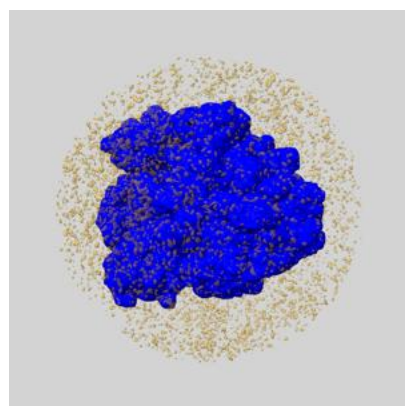
6.6 Mask visualisation [i](#)

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

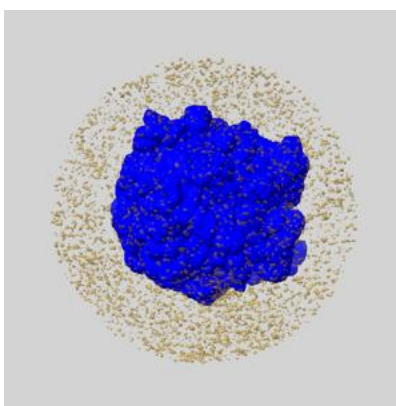
A mask typically either:

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

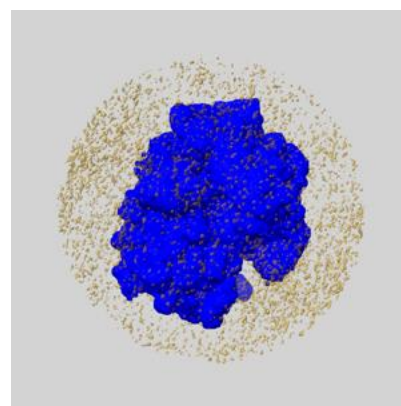
6.6.1 emd_13459_msk_1.map [i](#)



X



Y

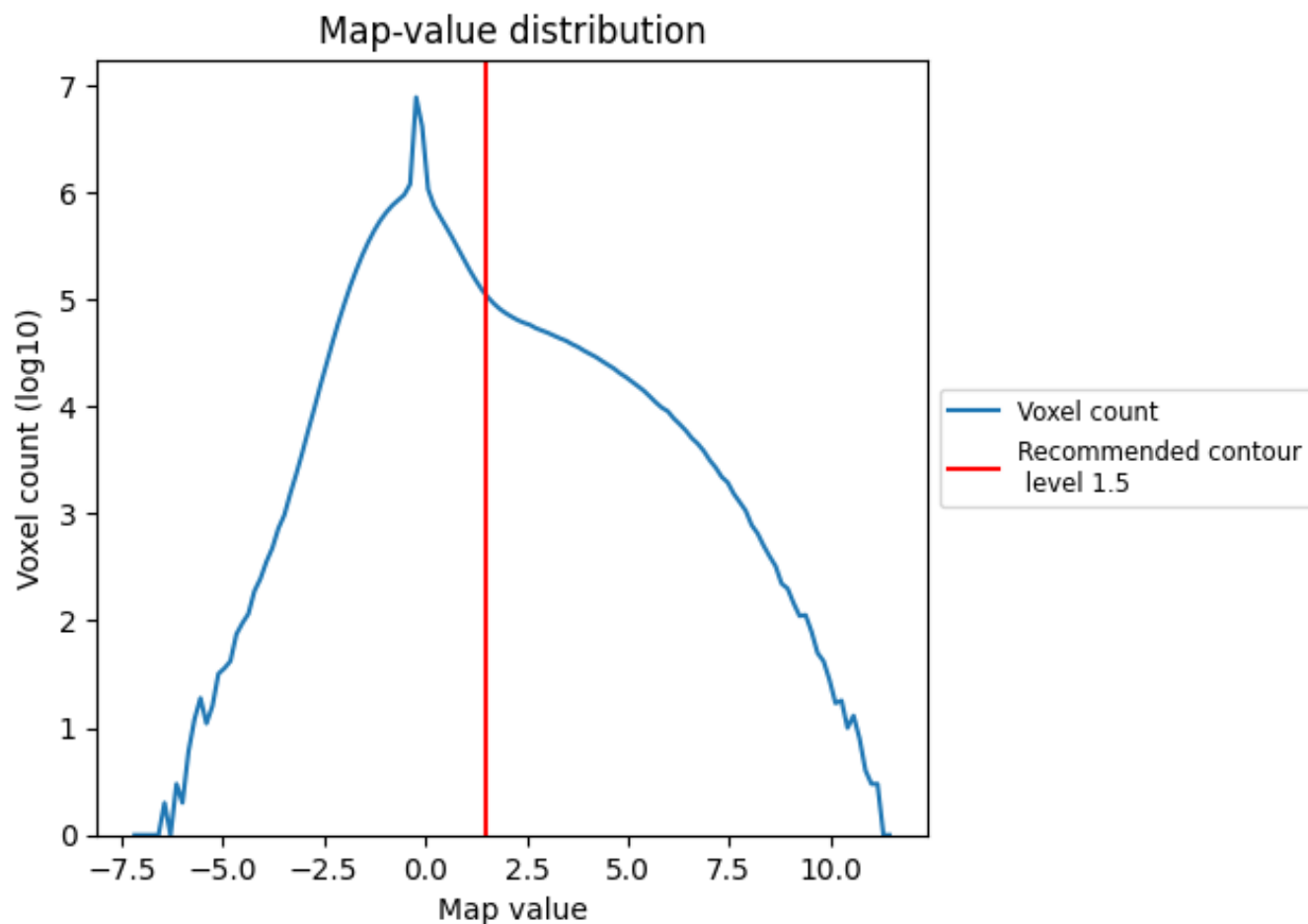


Z

7 Map analysis [i](#)

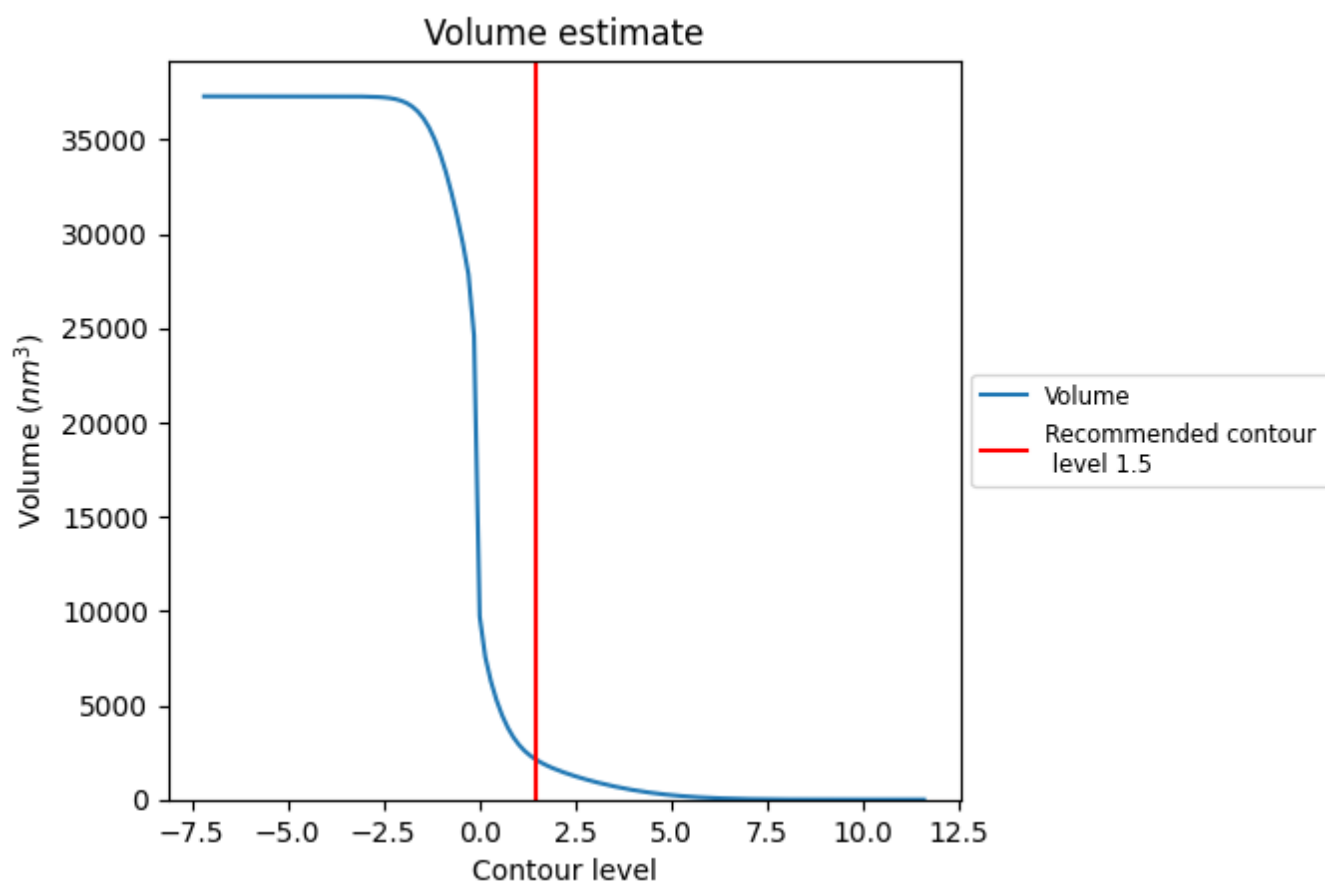
This section contains the results of statistical analysis of the map.

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.

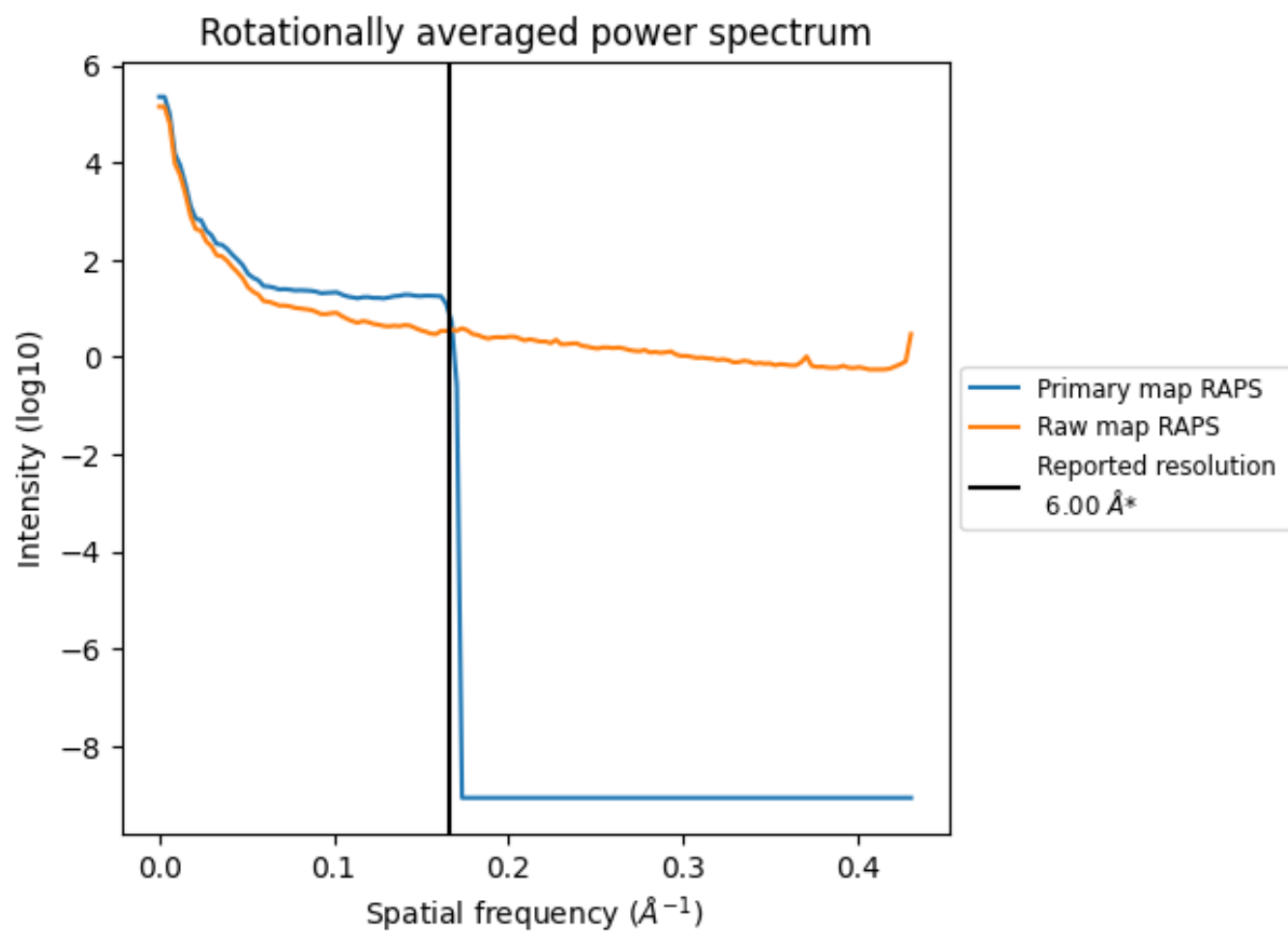
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2098 nm³; this corresponds to an approximate mass of 1895 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 ⓘ

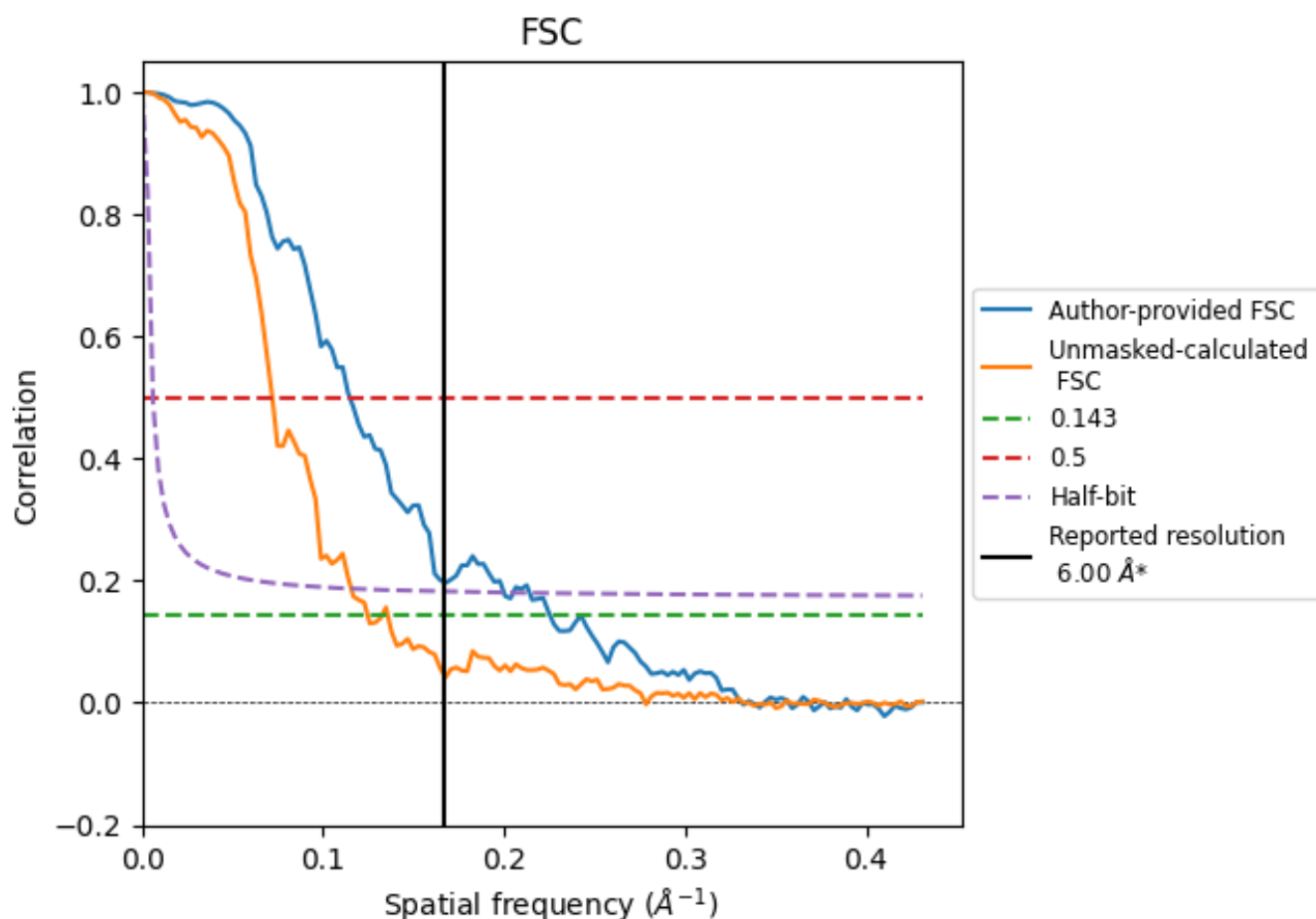


*Reported resolution corresponds to spatial frequency of 0.167 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.167 \text{ \AA}^{-1}$

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	4.44	8.72	5.00
Unmasked-calculated*	8.03	13.91	8.65

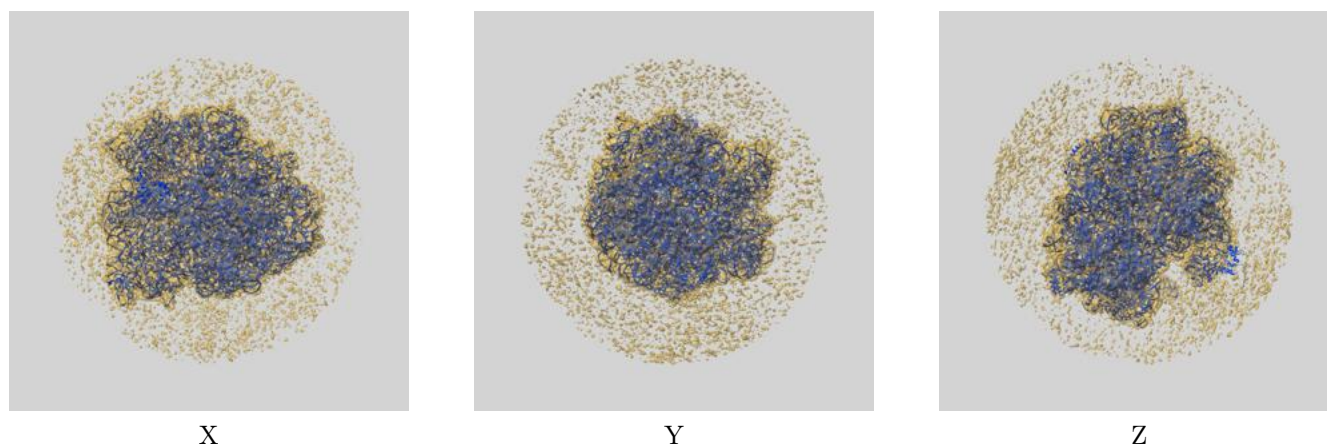
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 4.44 differs from the reported value 6.0 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 8.03 differs from the reported value 6.0 by more than 10 %

9 Map-model fit [i](#)

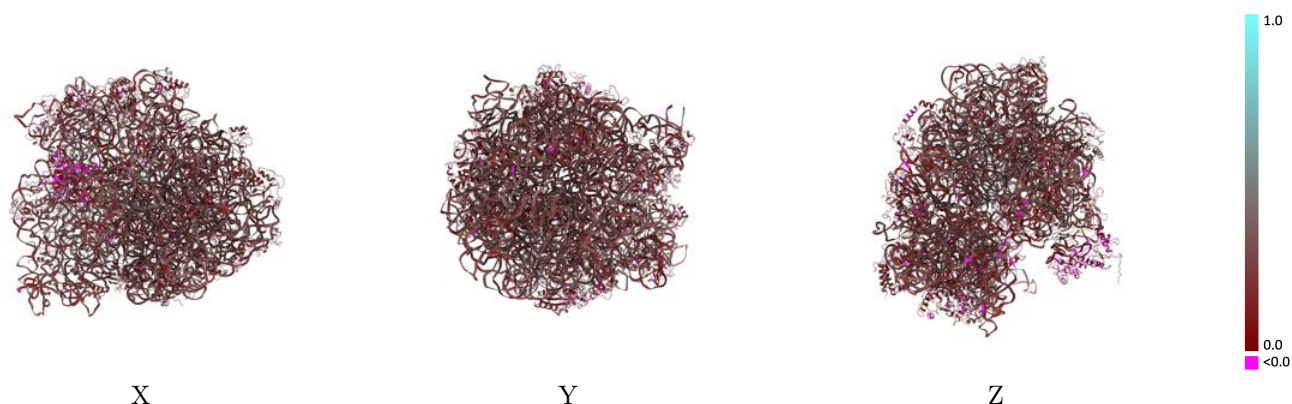
This section contains information regarding the fit between EMDB map EMD-13459 and PDB model 7PJT. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



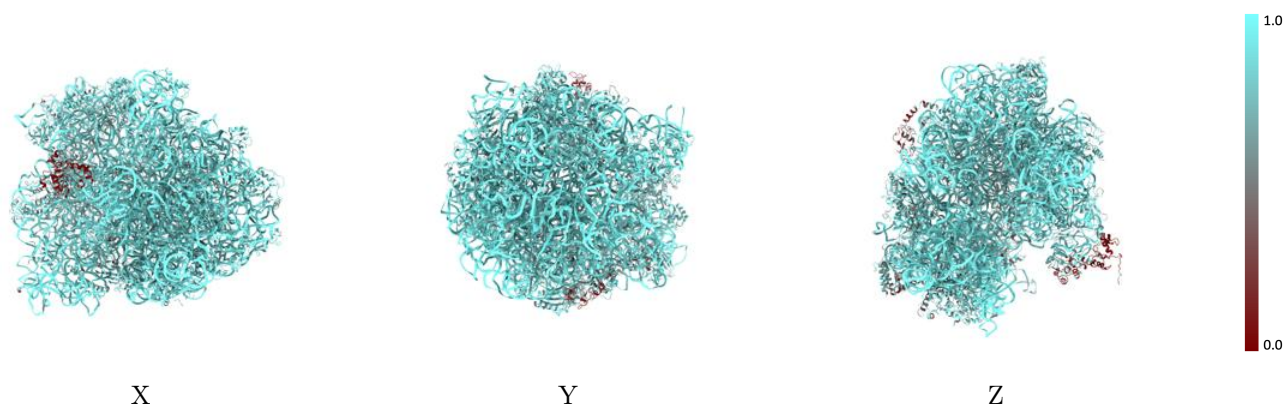
The images above show the 3D surface view of the map at the recommended contour level 1.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



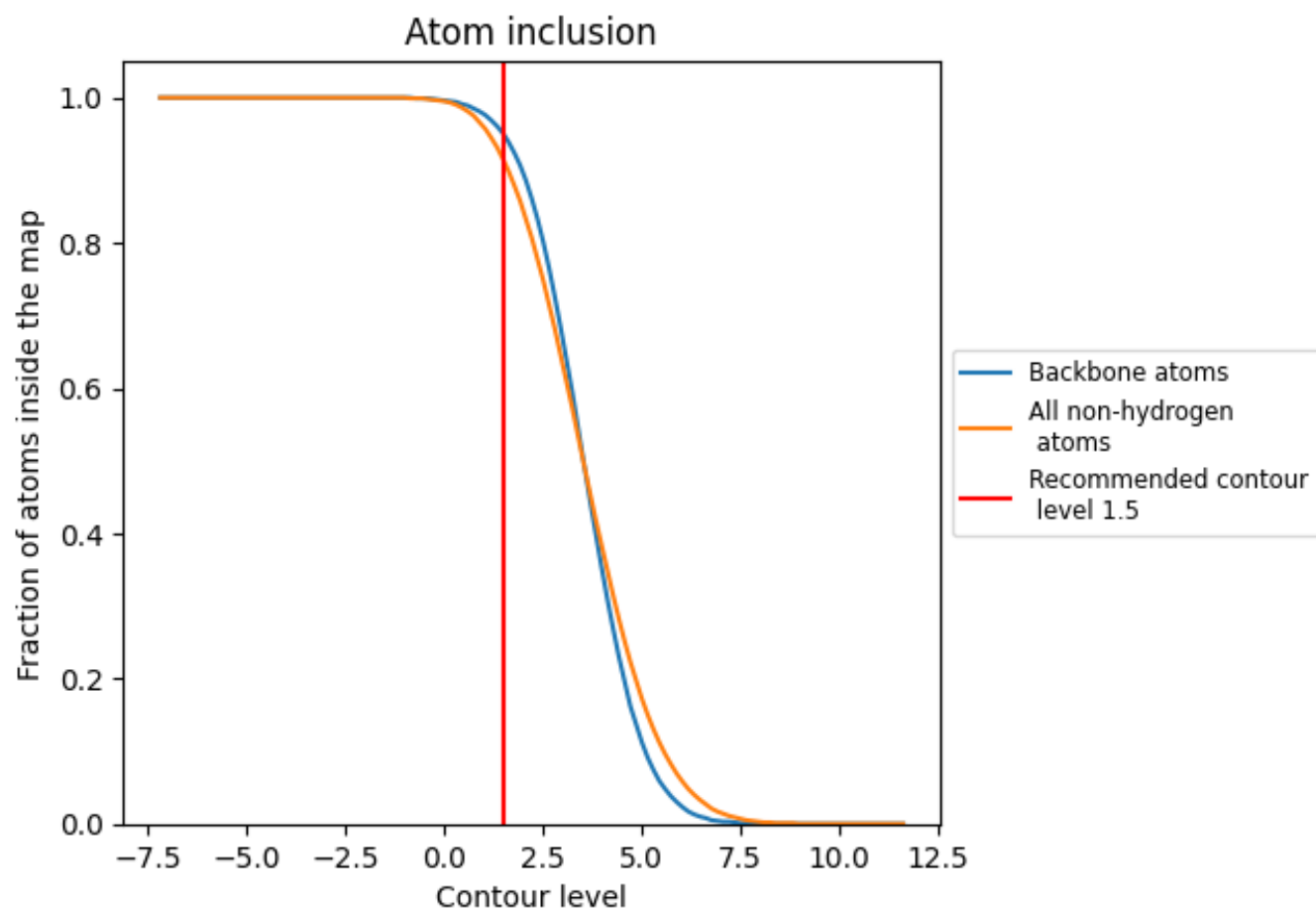
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 95% of all backbone atoms, 91% 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	 0.9140	 0.2680
0	 0.8740	 0.2860
1	 0.8000	 0.2510
2	 0.8170	 0.2680
3	 0.7980	 0.2530
4	 0.8840	 0.2660
5	 0.1980	 0.1440
6	 0.7810	 0.2320
A	 0.9690	 0.2830
B	 0.9860	 0.2740
C	 0.8060	 0.2680
D	 0.8400	 0.2660
E	 0.8160	 0.2690
F	 0.8410	 0.2300
G	 0.8920	 0.2470
H	 0.4410	 0.2090
I	 0.4360	 0.1290
J	 0.8560	 0.2750
K	 0.7630	 0.2690
L	 0.8400	 0.2730
M	 0.8390	 0.2830
N	 0.8670	 0.2420
O	 0.9190	 0.2380
P	 0.8020	 0.2660
Q	 0.8260	 0.2350
R	 0.8520	 0.2590
S	 0.8170	 0.2470
T	 0.8620	 0.2700
U	 0.8970	 0.2540
V	 0.8580	 0.2520
W	 0.8960	 0.2540
X	 0.8450	 0.2770
Y	 0.8590	 0.2100
Z	 0.8510	 0.2590
a	 0.9670	 0.2710



Continued on next page...

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Chain	Atom inclusion	Q-score
b	 0.6200	 0.2350
c	 0.8220	 0.2430
d	 0.8110	 0.2370
e	 0.7900	 0.2570
f	 0.8480	 0.2490
g	 0.6680	 0.2310
h	 0.8290	 0.2480
i	 0.8430	 0.2380
j	 0.7540	 0.2210
k	 0.8320	 0.2510
l	 0.8210	 0.2770
m	 0.7720	 0.2140
n	 0.8670	 0.2230
o	 0.8800	 0.2490
p	 0.8520	 0.2560
q	 0.8420	 0.2350
r	 0.8600	 0.2450
s	 0.8380	 0.2070
t	 0.8420	 0.2290
u	 0.8060	 0.2540
v	 0.9090	 0.2550
w	 0.8710	 0.2180
y	 0.8090	 0.2520
z	 0.8960	 0.2650