



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 05:08 PM UTC

PDB ID : 7NHL / pdb_00007nhl
EMDB ID : EMD-12332
Title : VgaA-LC, an antibiotic resistance ABCF, in complex with 70S ribosome from *Staphylococcus aureus*
Authors : Crowe-McAuliffe, C.; Murina, V.; Hauryliuk, V.; Wilson, D.N.
Deposited on : 2021-02-10
Resolution : 3.10 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

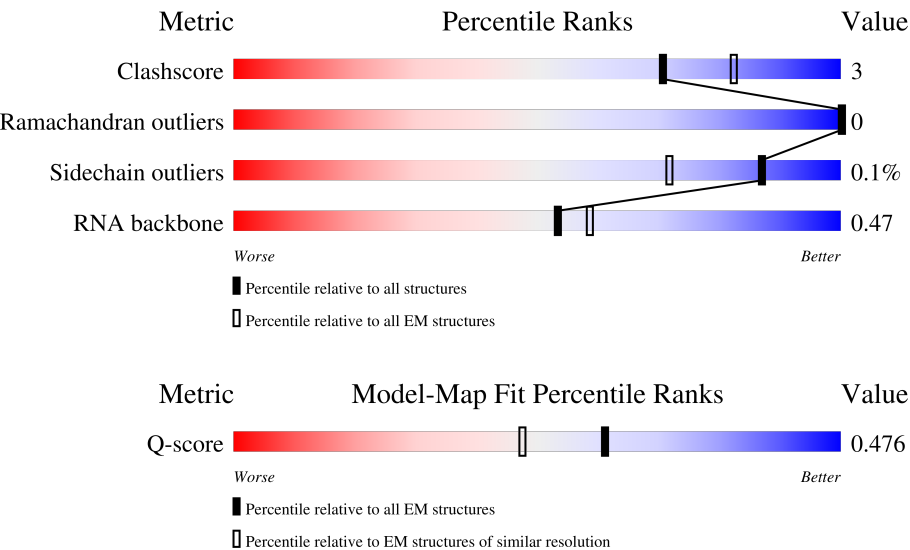
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 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	546	
2	D	76	
3	Z	94	

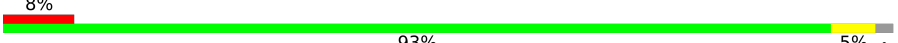
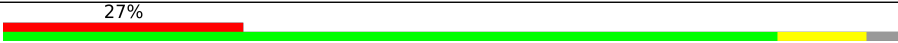
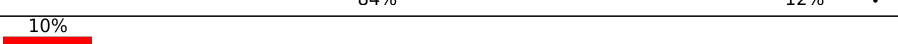
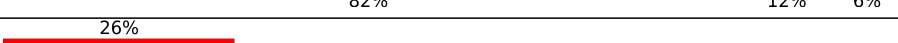
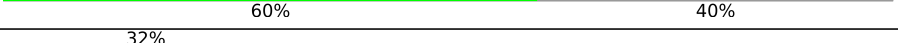
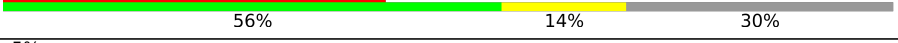
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Mol	Chain	Length	Quality of chain
4	P	144	
5	A	2923	
6	a	1551	
7	B	115	
8	G	277	
9	H	220	
10	I	207	
11	J	179	
12	K	178	
13	M	145	
14	N	122	
15	O	146	
16	Q	122	
17	R	119	
18	S	116	
19	T	118	
20	U	102	
21	V	117	
22	W	91	
23	X	105	
24	Y	217	
25	1	62	
26	2	69	
27	3	59	
28	6	49	

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Mol	Chain	Length	Quality of chain
29	8	66	
30	7	45	
31	d	217	
32	e	200	
33	h	156	
34	k	102	
35	l	129	
36	o	60	
37	p	89	
38	q	91	
39	u	83	
40	9	37	
41	t	92	
42	n	121	
43	j	132	
44	f	166	
45	i	132	
46	s	80	
47	g	98	
48	b	15	
49	m	137	
50	r	87	
51	c	255	
52	4	84	
53	5	57	

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 145969 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 Lincosamide-streptogramin A resistance protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	465	Total	C	N	O	S	0	0
			3770	2397	659	707	7		

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	105	GLN	GLU	engineered mutation	UNP A0SNL9
0	410	GLN	GLU	engineered mutation	UNP A0SNL9
0	523	GLY	-	expression tag	UNP A0SNL9
0	524	GLY	-	expression tag	UNP A0SNL9
0	525	ASP	-	expression tag	UNP A0SNL9
0	526	TYR	-	expression tag	UNP A0SNL9
0	527	LYS	-	expression tag	UNP A0SNL9
0	528	ASP	-	expression tag	UNP A0SNL9
0	529	HIS	-	expression tag	UNP A0SNL9
0	530	ASP	-	expression tag	UNP A0SNL9
0	531	GLY	-	expression tag	UNP A0SNL9
0	532	ASP	-	expression tag	UNP A0SNL9
0	533	TYR	-	expression tag	UNP A0SNL9
0	534	LYS	-	expression tag	UNP A0SNL9
0	535	ASP	-	expression tag	UNP A0SNL9
0	536	HIS	-	expression tag	UNP A0SNL9
0	537	ASP	-	expression tag	UNP A0SNL9
0	538	ILE	-	expression tag	UNP A0SNL9
0	539	ASP	-	expression tag	UNP A0SNL9
0	540	TYR	-	expression tag	UNP A0SNL9
0	541	LYS	-	expression tag	UNP A0SNL9
0	542	ASP	-	expression tag	UNP A0SNL9
0	543	ASP	-	expression tag	UNP A0SNL9
0	544	ASP	-	expression tag	UNP A0SNL9
0	545	ASP	-	expression tag	UNP A0SNL9
0	546	LYS	-	expression tag	UNP A0SNL9

- Molecule 2 is a RNA chain called P-tRNA fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	73	Total	C	N	O	P	0	0
			1562	696	284	509	73		

- Molecule 3 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Z	76	Total	C	N	O		0	0
			585	361	114	110			

- Molecule 4 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	P	135	Total	C	N	O	S	0	0
			1081	693	205	180	3		

- Molecule 5 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A	2914	Total	C	N	O	P	0	0
			62482	27895	11429	20244	2914		

- Molecule 6 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	a	1538	Total	C	N	O	P	0	0
			32937	14706	6006	10687	1538		

- Molecule 7 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	113	Total	C	N	O	P	0	0
			2408	1076	431	788	113		

- Molecule 8 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	273	Total	C	N	O	S	0	0
			2085	1297	413	370	5		

- Molecule 9 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	216	Total	C	N	O	S	0	0
			1637	1024	301	307	5		

- Molecule 10 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	204	Total	C	N	O	S	0	0
			1564	981	286	295	2		

- Molecule 11 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	175	Total	C	N	O	S	0	0
			1381	876	237	261	7		

- Molecule 12 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	164	Total	C	N	O	S	0	0
			1284	799	232	250	3		

- Molecule 13 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	142	Total	C	N	O	S	0	0
			1127	704	205	216	2		

- Molecule 14 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	122	Total	C	N	O	S	0	0
			920	572	174	170	4		

- Molecule 15 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	145	Total	C	N	O	S	0	0
			1090	674	214	201	1		

- Molecule 16 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	120	Total	C	N	O	S	0	0
			952	584	182	185	1		

- Molecule 17 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	118	Total	C	N	O		0	0
			914	569	173	172			

- Molecule 18 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	114	Total	C	N	O		0	0
			922	580	185	157			

- Molecule 19 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	116	Total	C	N	O	S	0	0
			943	593	189	157	4		

- Molecule 20 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	101	Total	C	N	O	S	0	0
			793	503	141	148	1		

- Molecule 21 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	111	Total	C	N	O	S	0	0
			853	532	163	155	3		

- Molecule 22 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	89	Total	C	N	O	S	0	0
			725	457	130	134	4		

- Molecule 23 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	99	Total	C	N	O	S	0	0
			761	480	140	139	2		

- Molecule 24 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	94	Total	C	N	O	S	0	0
			738	471	131	134	2		

- Molecule 25 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	1	60	Total	C	N	O	S	0	0
			474	293	103	77	1		

- Molecule 26 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	2	64	Total	C	N	O		0	0
			527	324	99	104			

- Molecule 27 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	3	56	Total	C	N	O		0	0
			436	271	82	83			

- Molecule 28 is a protein called 50S ribosomal protein L33 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	6	47	Total	C	N	O	S	0	0
			389	232	79	74	4		

- Molecule 29 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	8	64	Total	C	N	O	S	0	0
			521	324	113	82	2		

- Molecule 30 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	7	42	Total	C	N	O	S	0	0
			360	220	88	51	1		

- Molecule 31 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	208	Total	C	N	O	S	0	0
			1638	1032	306	298	2		

- Molecule 32 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	199	Total	C	N	O	S	0	0
			1617	1020	302	293	2		

- Molecule 33 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	h	138	Total	C	N	O	S	0	0
			1101	686	208	203	4		

- Molecule 34 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	k	100	Total	C	N	O	S	0	0
			801	505	147	148	1		

- Molecule 35 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	l	118	Total	C	N	O	S	0	0
			876	542	166	165	3		

- Molecule 36 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	o	59	Total	C	N	O	S	0	0
			496	314	99	78	5		

- Molecule 37 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	p	87	Total	C	N	O	S	0	0
			733	451	152	129	1		

- Molecule 38 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	q	90	Total	C	N	O	S	0	0
			712	448	132	131	1		

- Molecule 39 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	u	80	Total	C	N	O	S	0	0
			606	367	119	118	2		

- Molecule 40 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	9	36	Total	C	N	O	S	0	0
			292	184	59	44	5		

- Molecule 41 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	t	79	Total	C	N	O	S	0	0
			646	416	116	112	2		

- Molecule 42 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	n	116	Total	C	N	O	S	0	0
			922	566	183	172	1		

- Molecule 43 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	j	127	Total	C	N	O	S	0	0
			1008	624	201	182	1		

- Molecule 44 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	f	156	Total	C	N	O	S	0	0
			1160	730	213	215	2		

- Molecule 45 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	i	131	Total	C	N	O	S	0	0
			1032	652	183	193	4		

- Molecule 46 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	s	63	Total	C	N	O	S	0	0
			516	330	96	87	3		

- Molecule 47 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	g	93	Total	C	N	O	S	0	0
			773	489	136	146	2		

- Molecule 48 is a RNA chain called RNA (5'-R(P*GP*GP*AP*GP*GP*UP*AP*UP*G)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
48	b	9	Total	C	N	O	P	0	0
			199	88	39	63	9		

- Molecule 49 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	m	135	Total	C	N	O	S	0	0
			1058	658	214	184	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	r	79	Total	C	N	O	S	0	0
			651	413	116	121	1		

- Molecule 51 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	c	221	Total	C	N	O	S	0	0
			1781	1136	310	328	7		

- Molecule 52 is a protein called 50S ribosomal protein L31 type B.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	4	59	Total	C	N	O	S	0	0
			486	310	88	87	1		

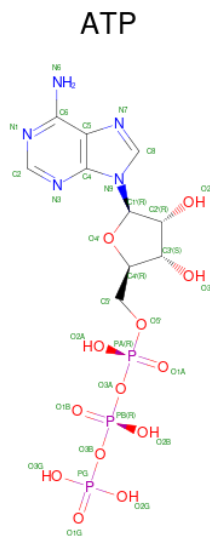
- Molecule 53 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	5	53	Total	C	N	O	S	0	0
			422	256	86	75	5		

- Molecule 54 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
54	0	2	Total	Mg	0
			2	2	
54	A	115	Total	Mg	0
			115	115	
54	a	19	Total	Mg	0
			19	19	
54	G	1	Total	Mg	0
			1	1	
54	O	1	Total	Mg	0
			1	1	

- Molecule 55 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



Mol	Chain	Residues	Atoms					AltConf
55	0	1	Total 31	C 10	N 5	O 13	P 3	0
55	0	1	Total 31	C 10	N 5	O 13	P 3	0

- Molecule 56 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
56	P	1	Total 1	K 1	0
56	A	15	Total 15	K 15	0
56	a	2	Total 2	K 2	0

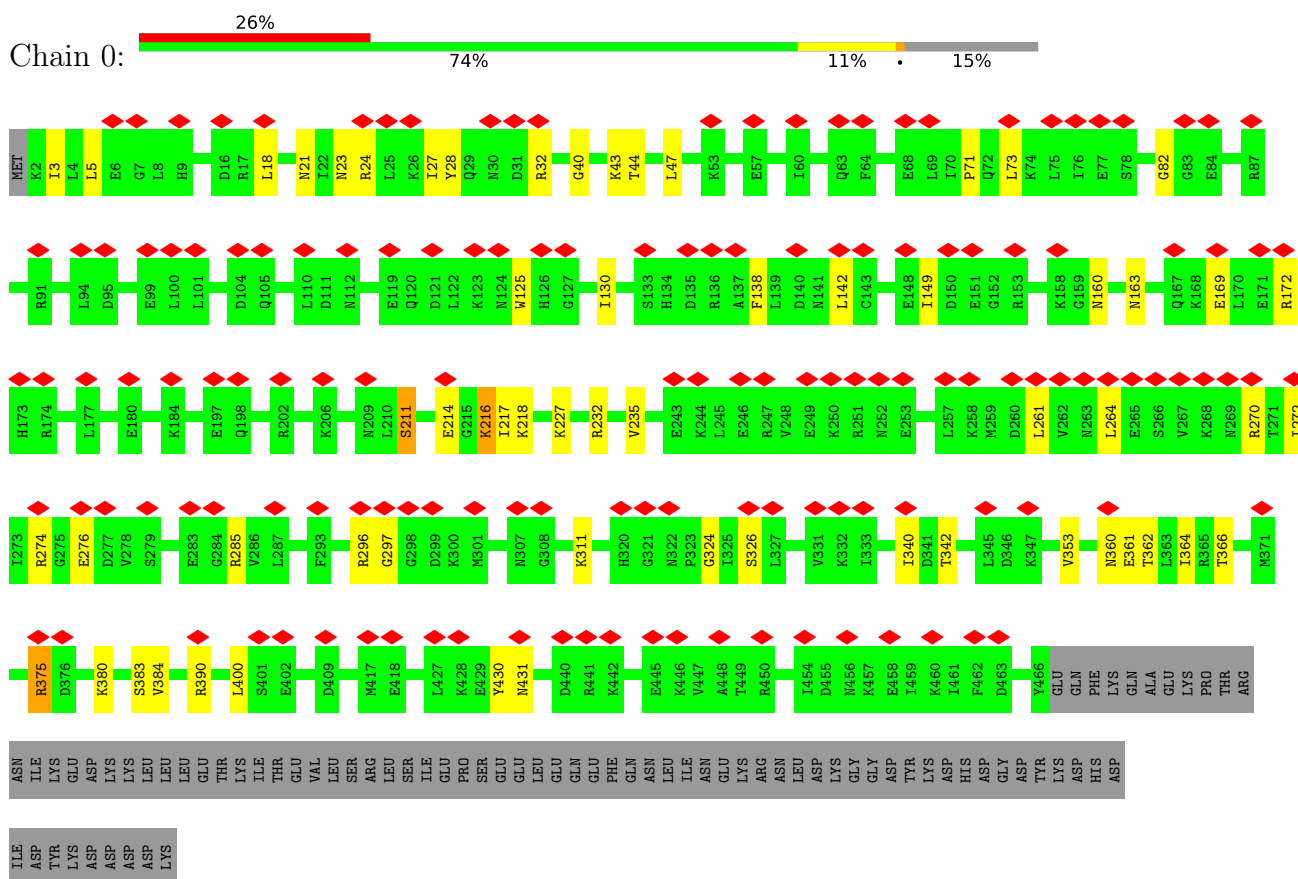
- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
57	6	1	Total Zn 1 1	0
57	o	1	Total Zn 1 1	0
57	9	1	Total Zn 1 1	0
57	5	1	Total Zn 1 1	0

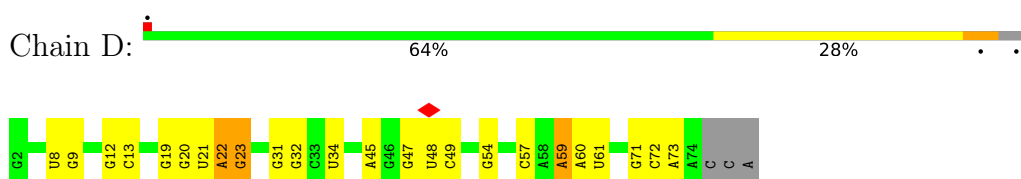
3 Residue-property plots

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: Lincosamide-streptogramin A resistance protein



- Molecule 2: P-tRNA fMet

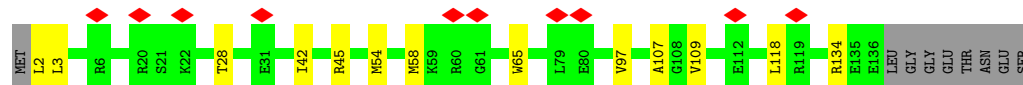
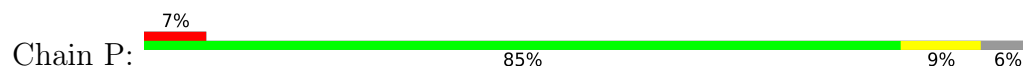


- Molecule 3: 50S ribosomal protein L27

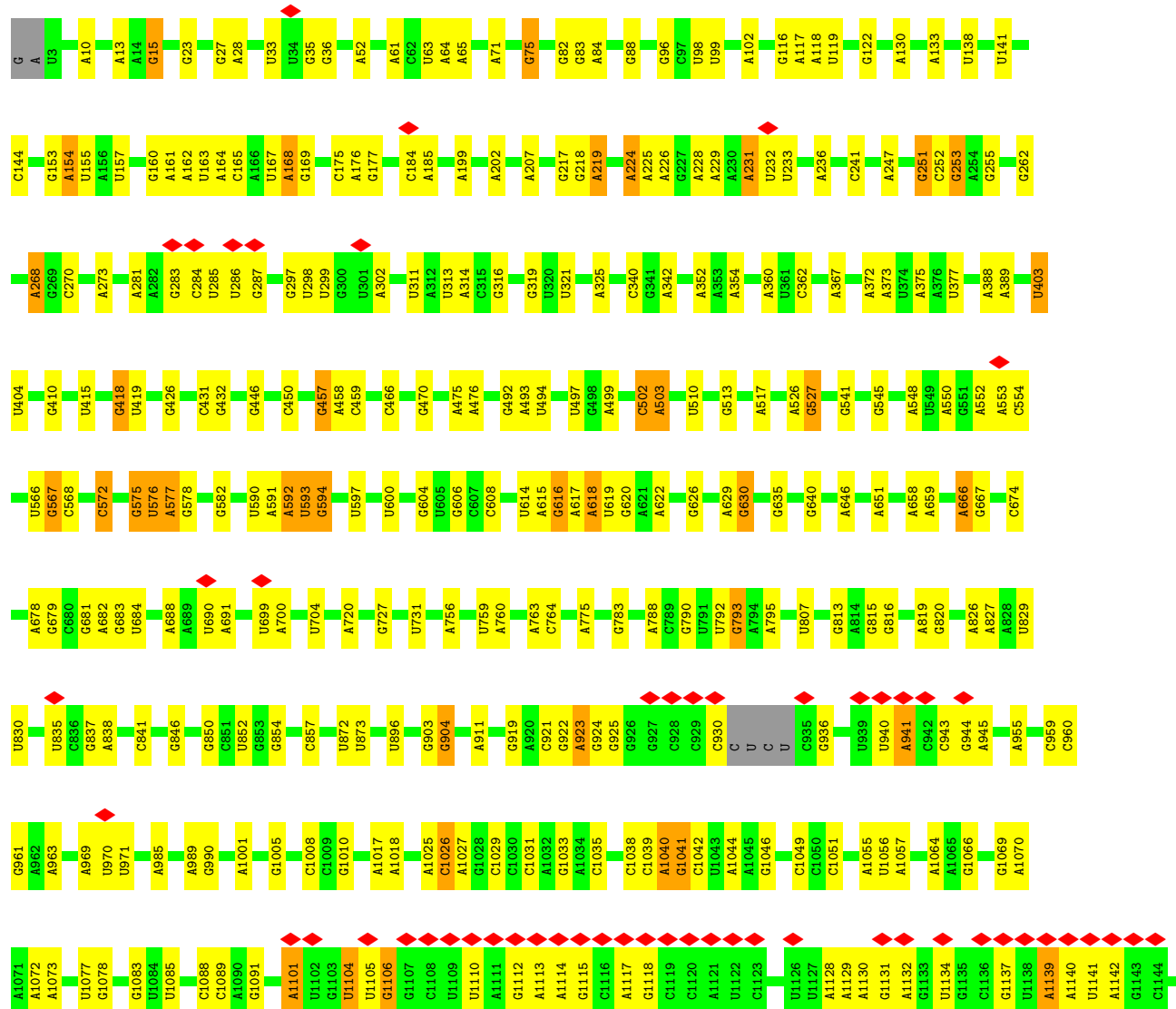




- Molecule 4: 50S ribosomal protein L16



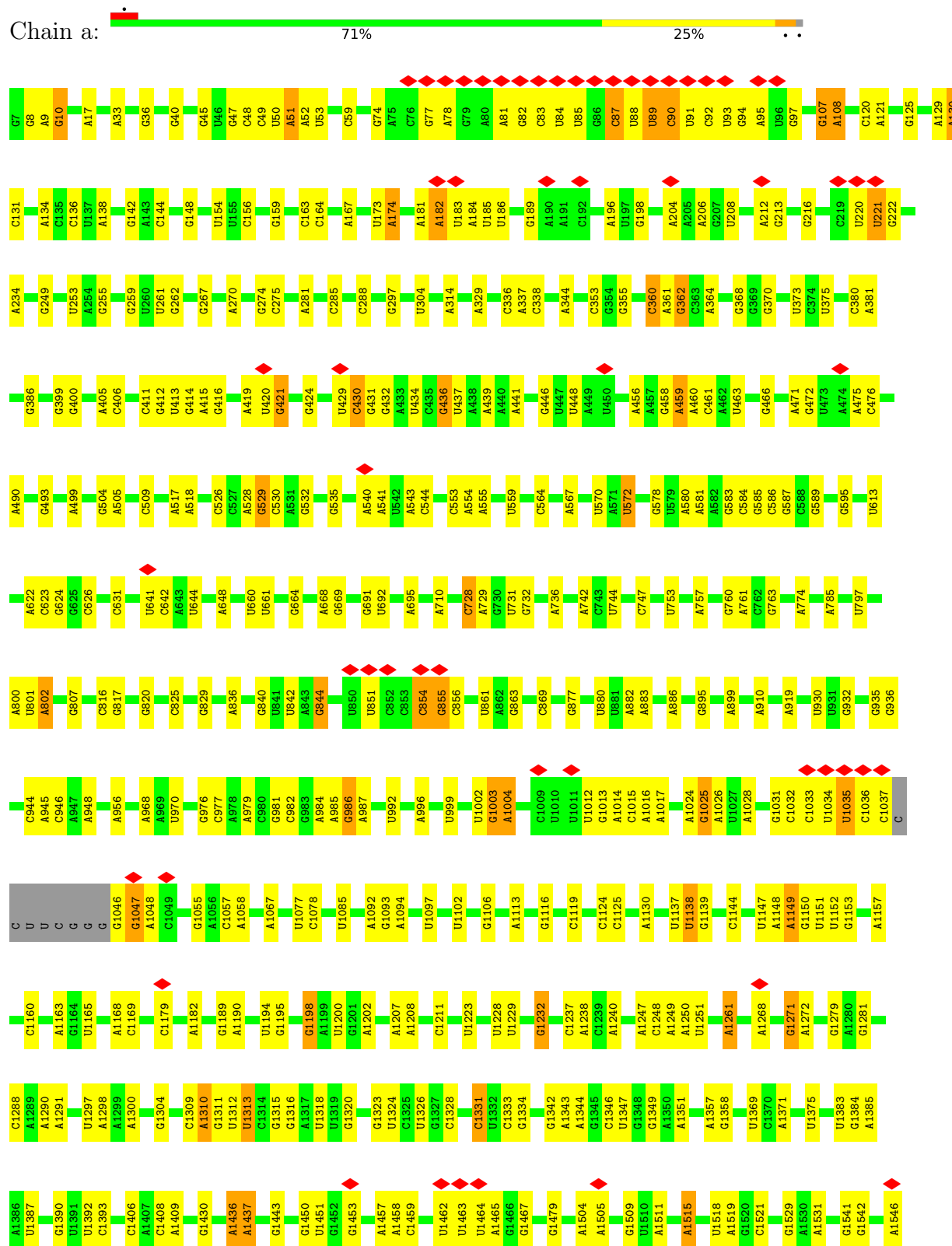
- Molecule 5: 23S rRNA

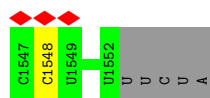


C	A2805	U2855	G2508	U2390	G2251	U2159	G2007	A1886	A1764	A1617	A1481	A1337	A1147
A	U2806	A2856	G2509	A2396	A2252	G2160	A2008	U1891	A1765	A1618	A1488	U1338	C1148
	U2820	G2857	G2511	A2403	A2254	G2161	U2019	U1892	C1768	U1625	A1490	U1339	U1149
	U2821	A2858	G2514	G2410	G2265	C2164	G2018	A1893	G1772	A1631	G1494	C1342	C1153
	C2822	A2859	U2520	A2411	G2266	G2167	U2020	U1896	G1781	A1632	C1495	G1155	G1154
	G2823	U2663	G2521	C2412	G2273	A2168	C2021	U1897	C1782	A1633	C1496	G1357	A1155
	G2824	A2666	G2522	A2415	G2277	A2169	C2023	C1898	G1783	A1634	A1497	A1358	G1160
	A2827	A2684	C2523	G2418	C2285	C2170	A2040	U1899	G1789	G1641	G1500	U1361	U1163
	G2831	G2685	C2524	U2429	C2290	C2171	U2046	U1907	G1790	C1651	G1504	C1362	G1166
	C2835	G2686	C2526	C2430	G2291	C2172	A2047	A1908	G1791	A1652	U1504	U1363	G1169
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	C2838	U2530	A2530	C2432	A2294	A2174	A2057	A1926	A1800	A1654	C1511	C1367	
	A2840	U2531	A2531	C2433	A2295	C2176	A2058	G1930	U1808	A1658	G1526	U1378	A1173
	G2842	C2542	G2542	G2437	A2300	U2177	C2059	G1930	C1809	C1659	A1527	U1379	U1174
	A2843	A2545	A2545	A2438	A2301	U2178	A2060	C1933	C1810	A1660	U1532	G1380	G1175
	U2844	U2546	U2546	U2446	A2305	A2179	G2062	G1934	A1811	A1670	U1533	U1381	A1177
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	A2848	G2558	A2558	U2450	A2314	G2183	G2075	A1940	U1823	A1679	C1536	U1402	U1185
	G2849	C2559	C2559	C2451	C2320	A2185	A2076	C1941	C1824	U1683	A1537	G1405	A1186
	U2850	U2562	U2562	A2452	G2326	A2186	C2077	A1943	U1825	C1690	U1540	U1416	A1195
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	G2882	A2641	A2641	G2497	A2385	U2237	U2139	A1997	A1874	G1747	G1613	C1472	A1310
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	U2884	G2649	G2649	A2504	A2388	A2239	A2153	G1999	A1875	G1759	A1616	G1473	
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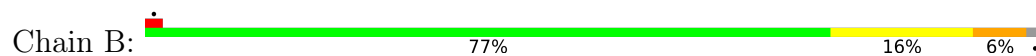
● Molecule 6: 16S rRNA

Chain a:

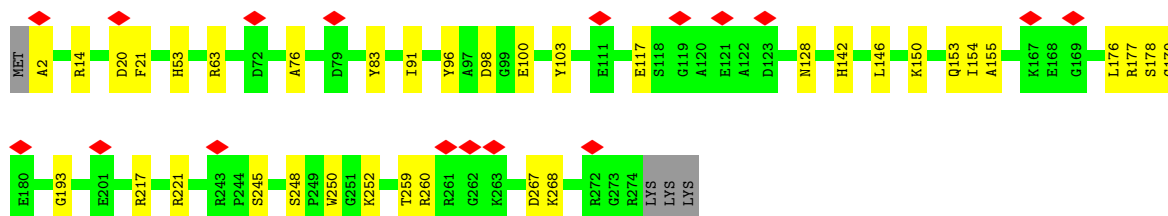
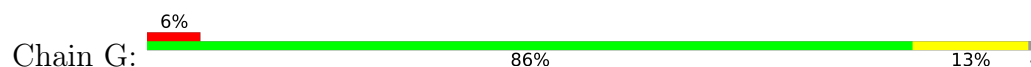




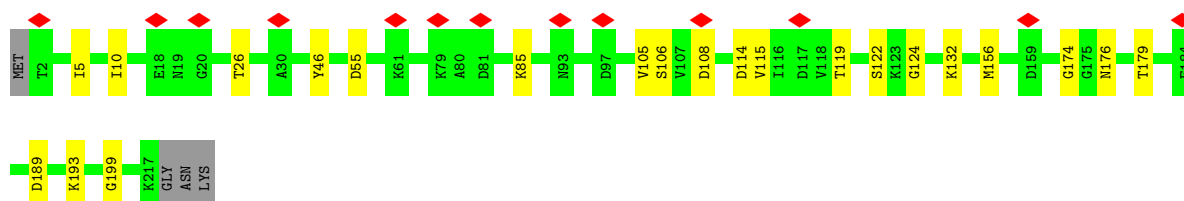
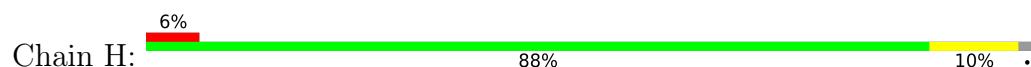
• Molecule 7: 5S rRNA



• Molecule 8: 50S ribosomal protein L2



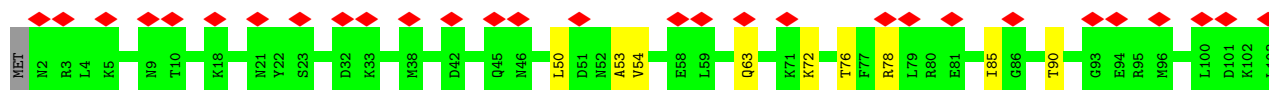
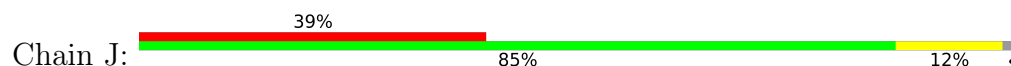
• Molecule 9: 50S ribosomal protein L3

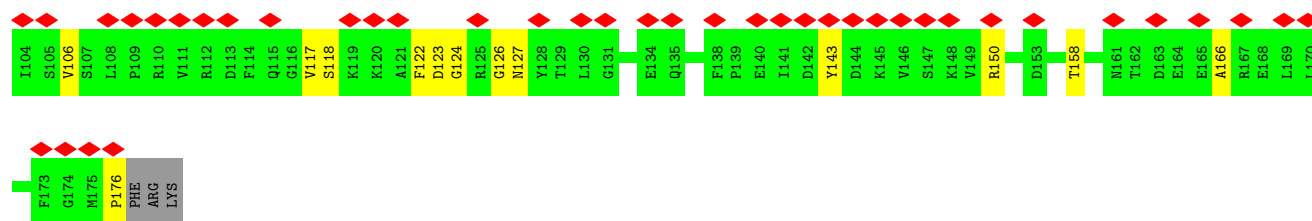


• Molecule 10: 50S ribosomal protein L4

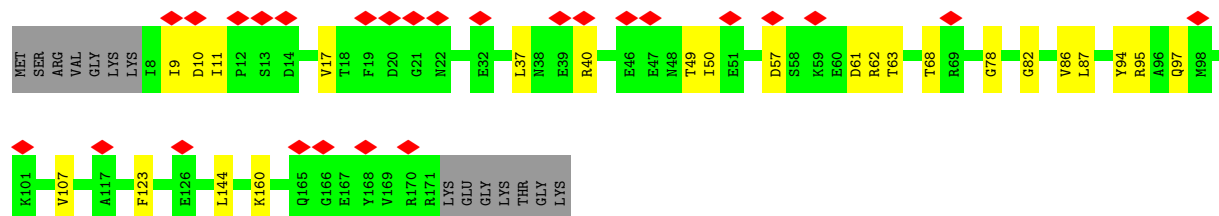
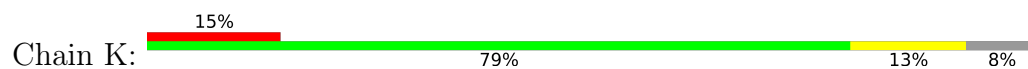


• Molecule 11: 50S ribosomal protein L5

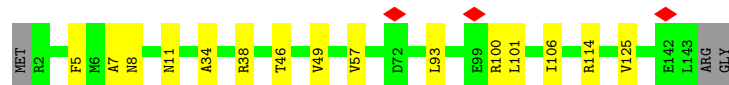
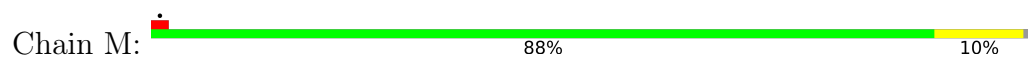




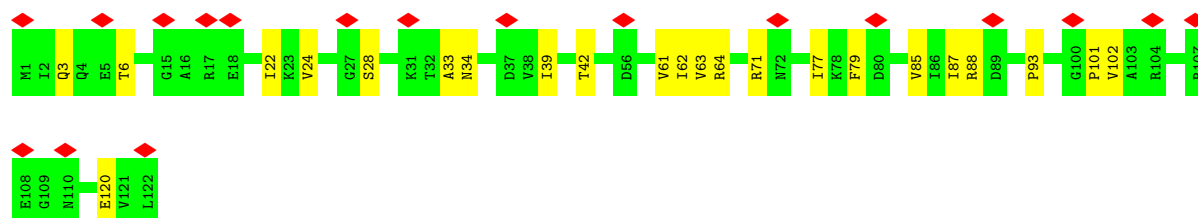
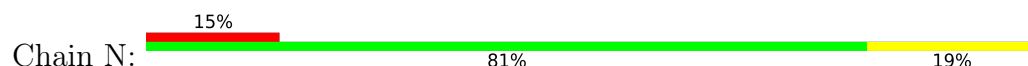
• Molecule 12: 50S ribosomal protein L6



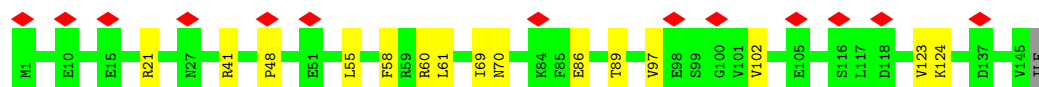
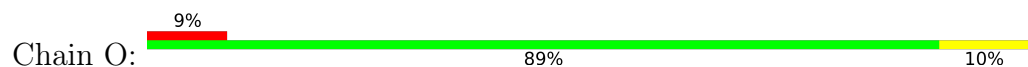
• Molecule 13: 50S ribosomal protein L13



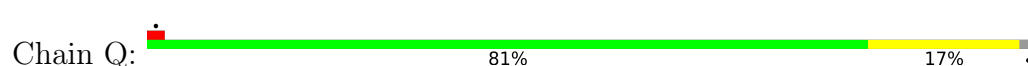
• Molecule 14: 50S ribosomal protein L14



• Molecule 15: 50S ribosomal protein L15

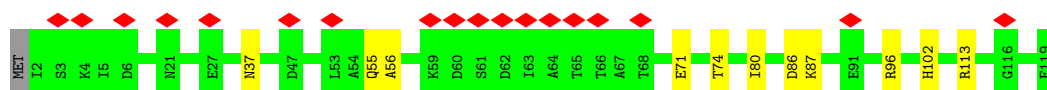
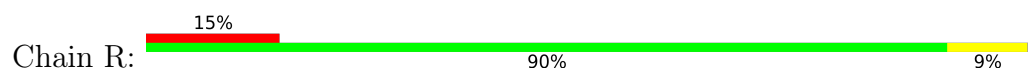


• Molecule 16: 50S ribosomal protein L17

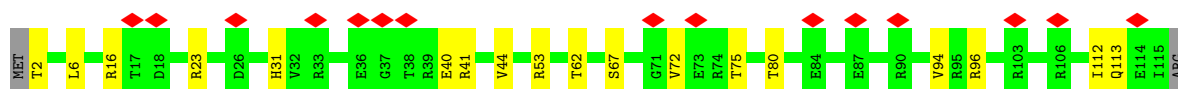
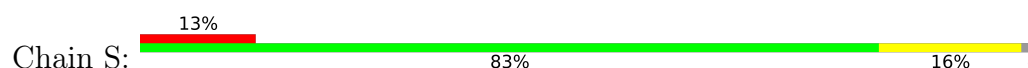




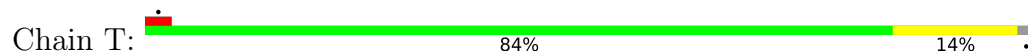
- Molecule 17: 50S ribosomal protein L18



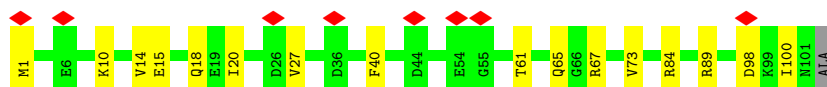
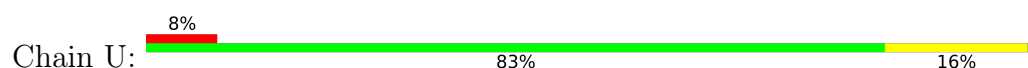
- Molecule 18: 50S ribosomal protein L19



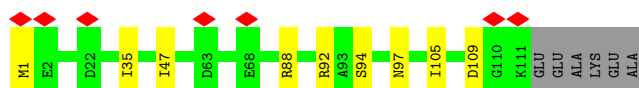
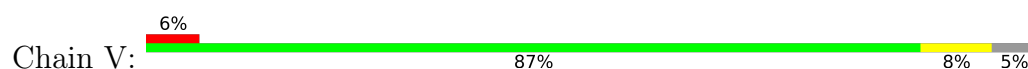
- Molecule 19: 50S ribosomal protein L20



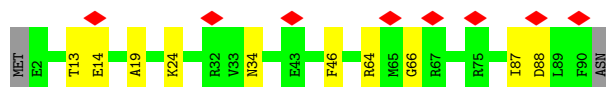
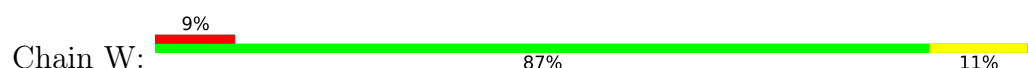
- Molecule 20: 50S ribosomal protein L21



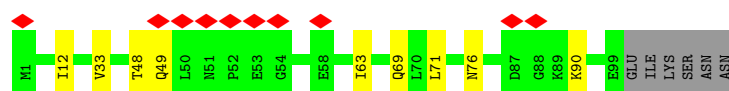
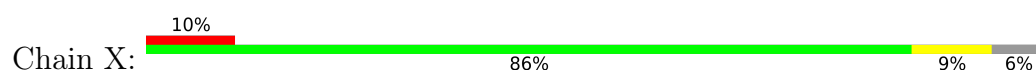
- Molecule 21: 50S ribosomal protein L22



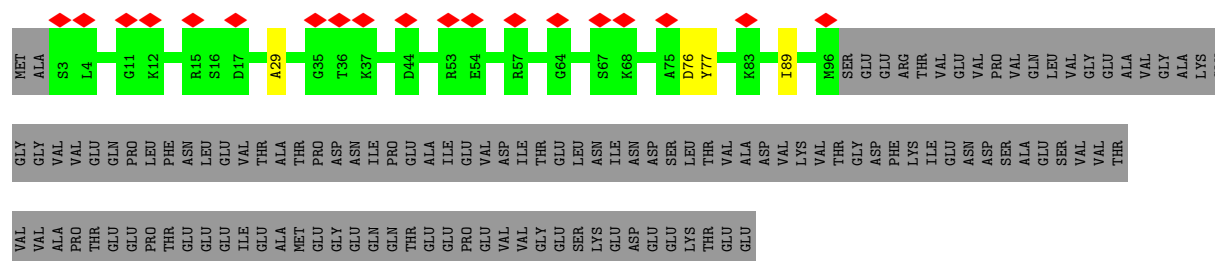
- Molecule 22: 50S ribosomal protein L23



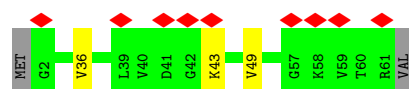
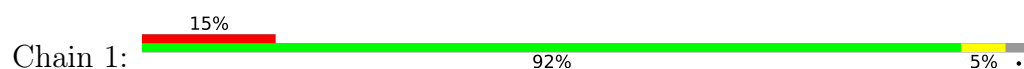
- Molecule 23: 50S ribosomal protein L24



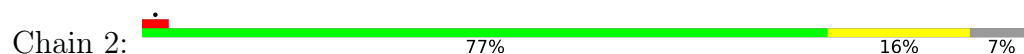
- Molecule 24: 50S ribosomal protein L25



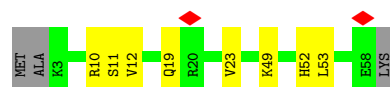
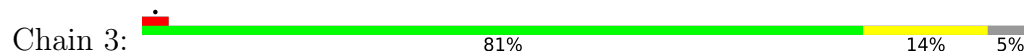
- Molecule 25: 50S ribosomal protein L28



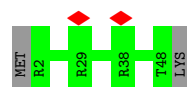
- Molecule 26: 50S ribosomal protein L29



- Molecule 27: 50S ribosomal protein L30



- Molecule 28: 50S ribosomal protein L33 2



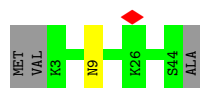
- Molecule 29: 50S ribosomal protein L35

Chain 8:  74% 23% .



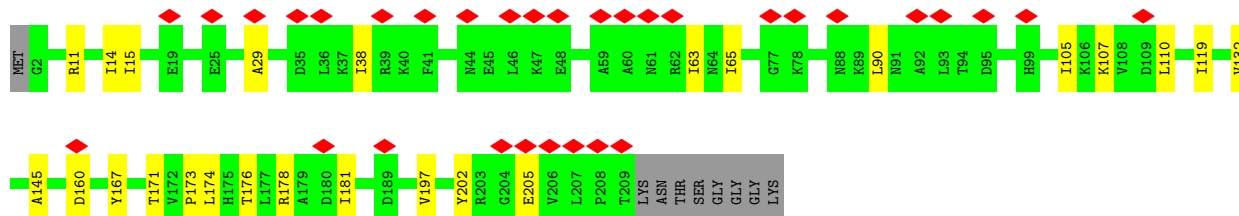
- Molecule 30: 50S ribosomal protein L34

Chain 7:  91% 7% .



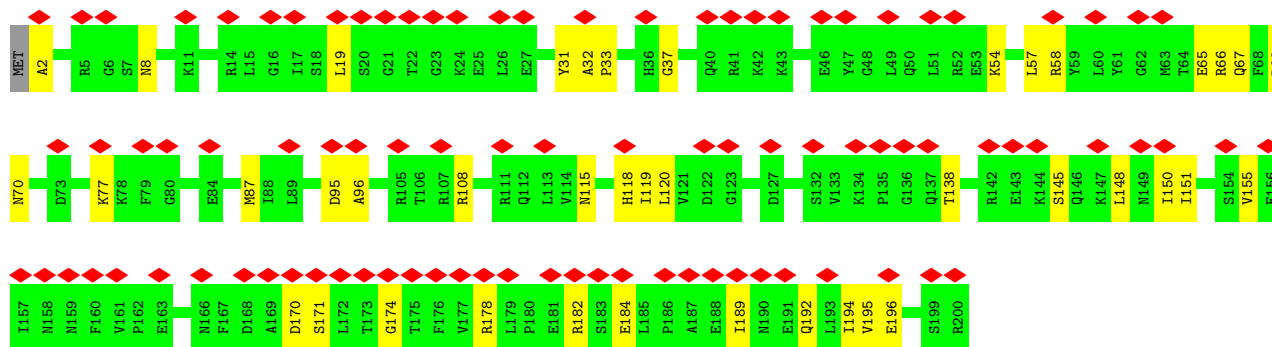
- Molecule 31: 30S ribosomal protein S3

Chain d:  15% 84% 12% .



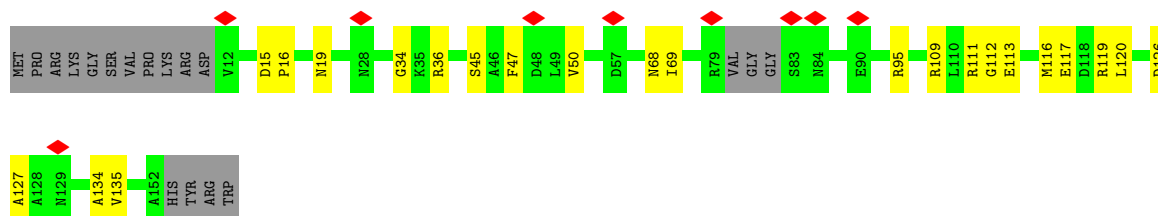
- Molecule 32: 30S ribosomal protein S4

Chain e:  46% 79% 20%

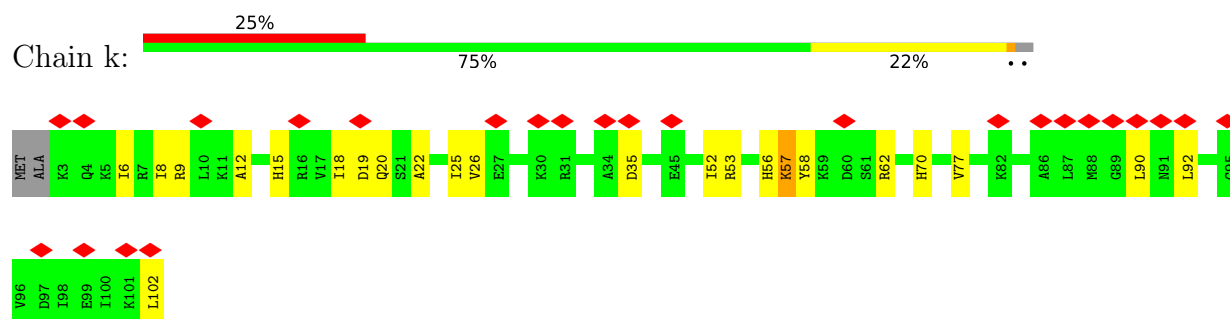


- Molecule 33: 30S ribosomal protein S7

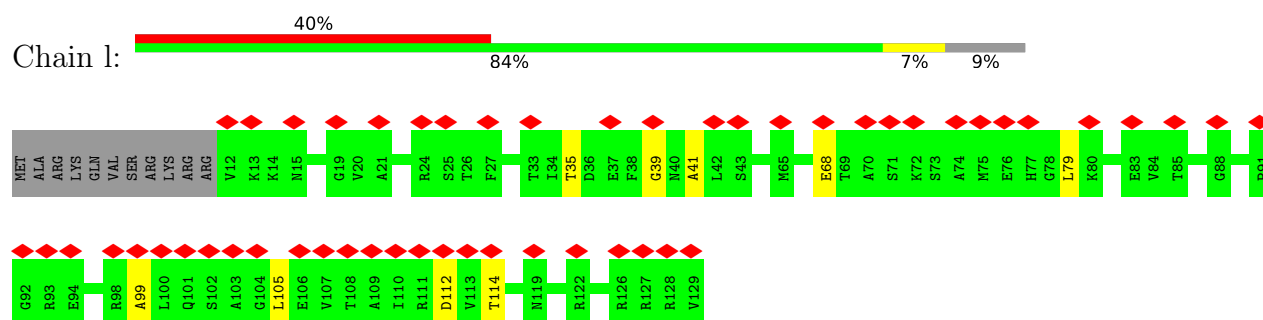
Chain h:  6% 74% 15% 12%



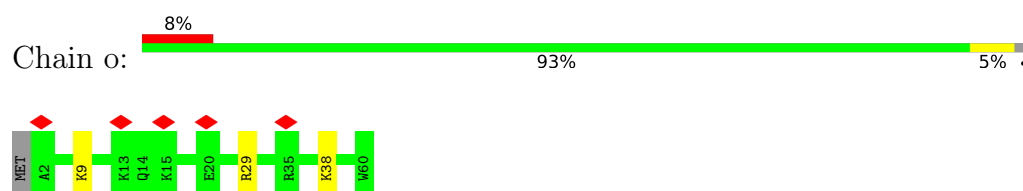
- Molecule 34: 30S ribosomal protein S10



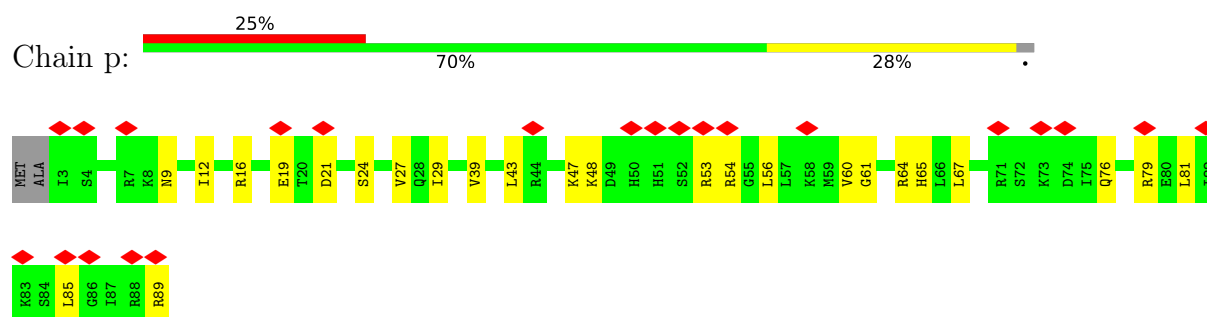
- Molecule 35: 30S ribosomal protein S11



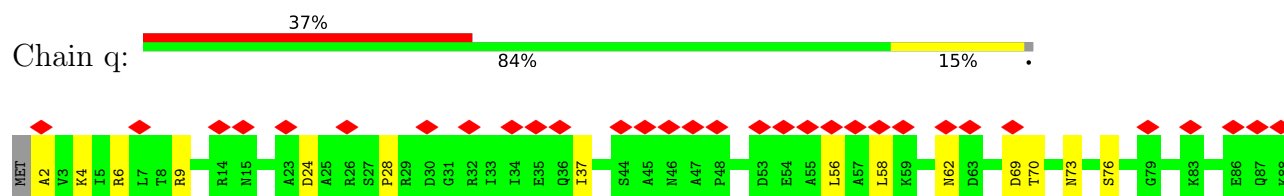
- Molecule 36: 30S ribosomal protein S14 type Z



- Molecule 37: 30S ribosomal protein S15

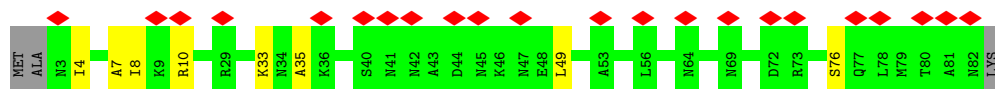
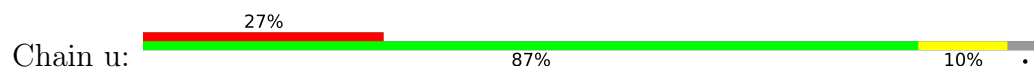


- Molecule 38: 30S ribosomal protein S16

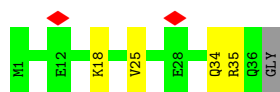
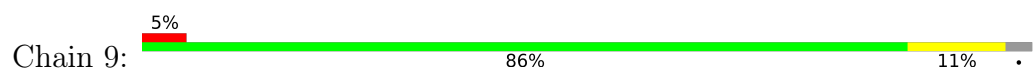




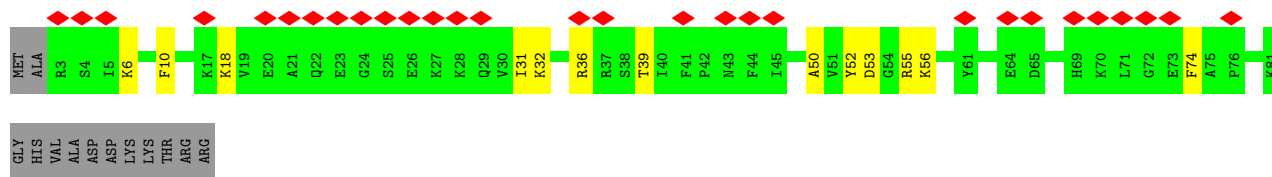
- Molecule 39: 30S ribosomal protein S20



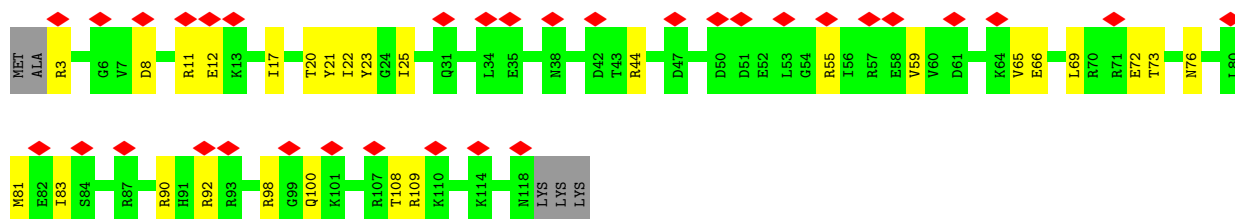
- Molecule 40: 50S ribosomal protein L36



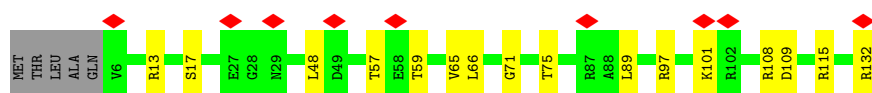
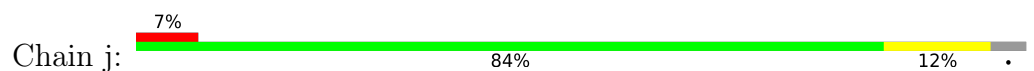
- Molecule 41: 30S ribosomal protein S19



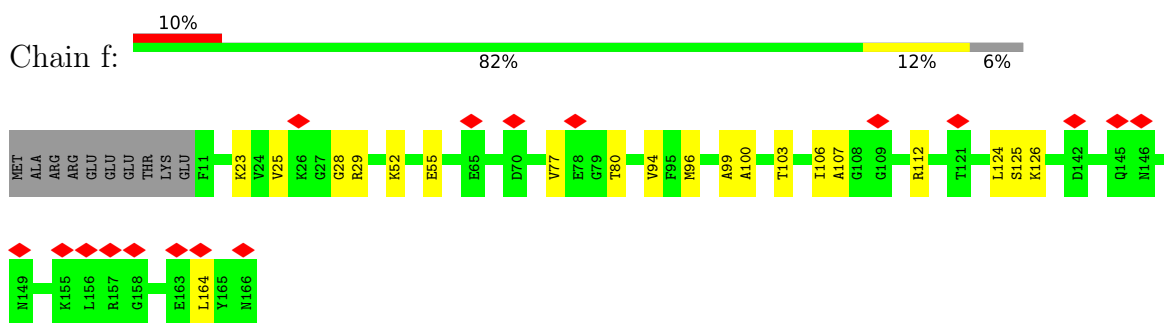
- Molecule 42: 30S ribosomal protein S13



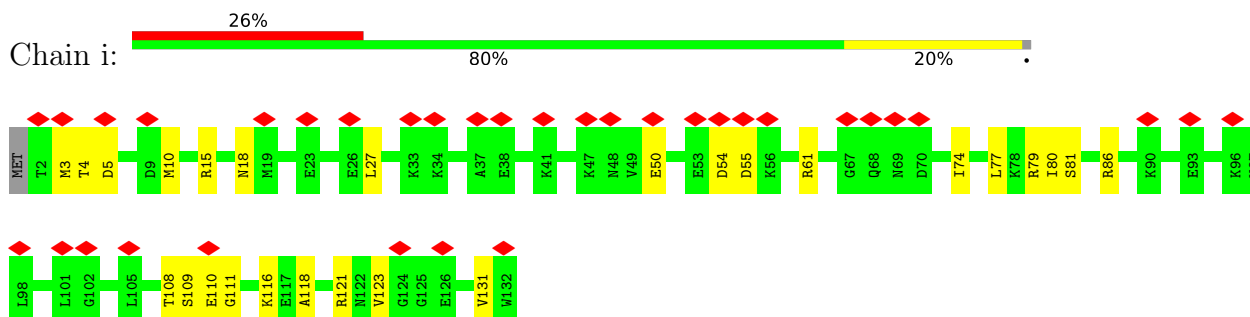
- Molecule 43: 30S ribosomal protein S9



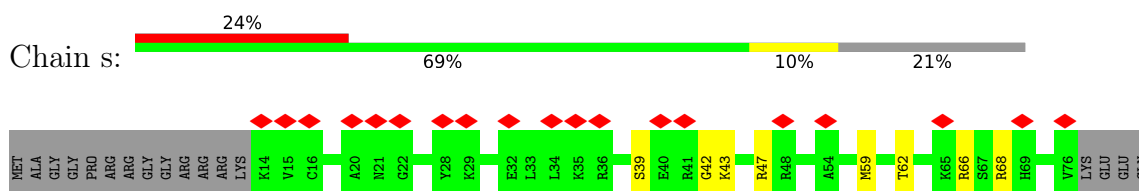
- Molecule 44: 30S ribosomal protein S5



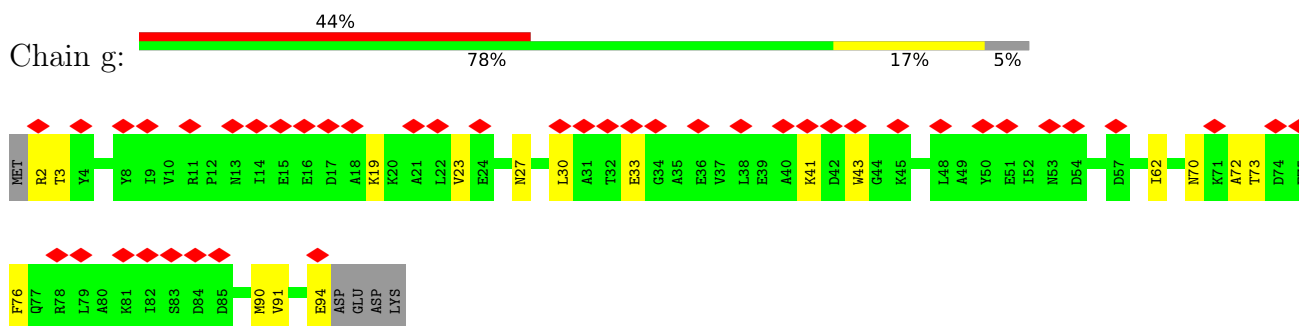
- Molecule 45: 30S ribosomal protein S8



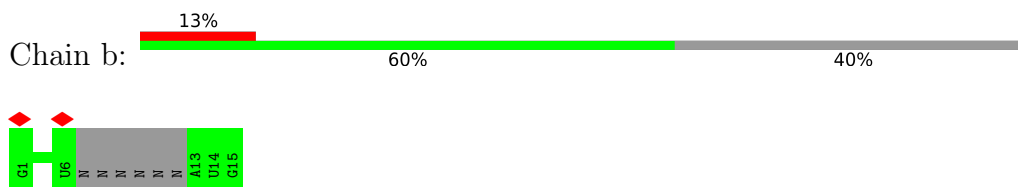
- Molecule 46: 30S ribosomal protein S18



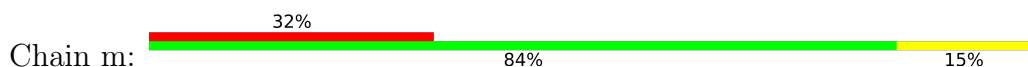
- Molecule 47: 30S ribosomal protein S6



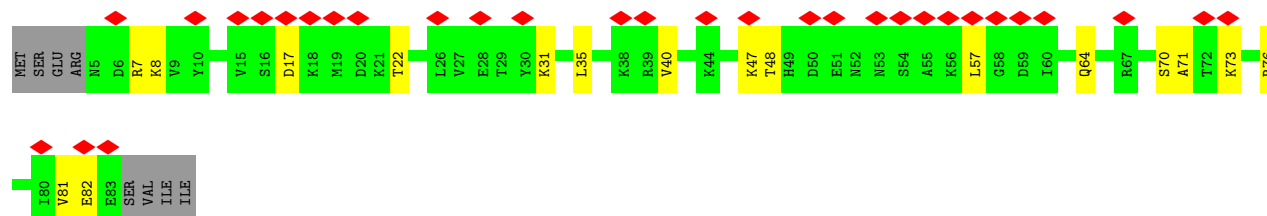
- Molecule 48: RNA (5'-R(P*GP*GP*AP*GP*GP*UP*AP*UP*G)-3')



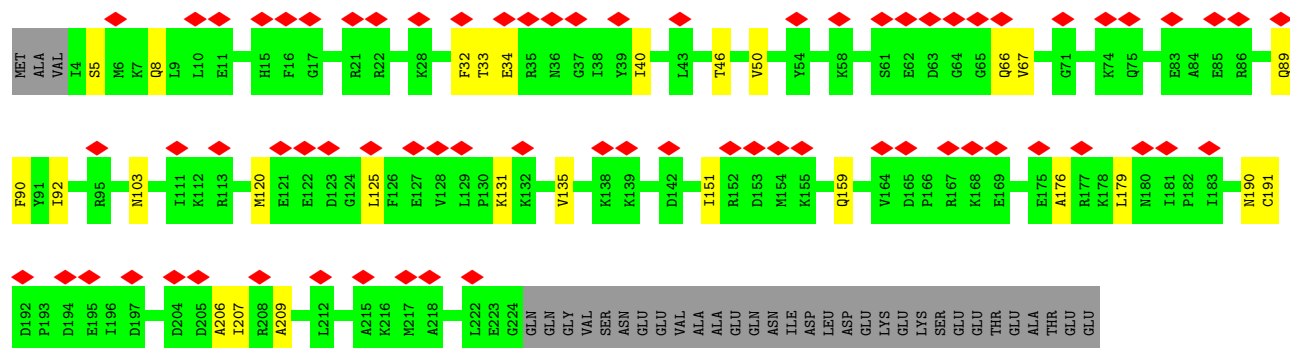
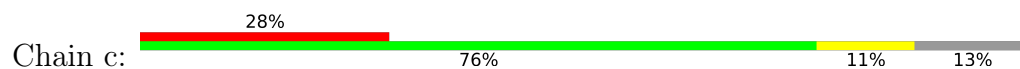
- Molecule 49: 30S ribosomal protein S12



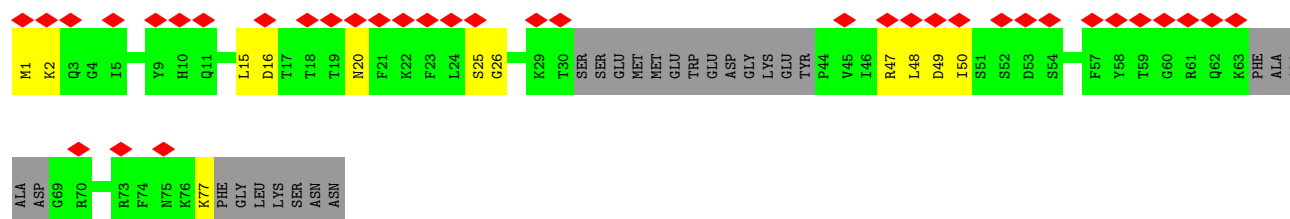
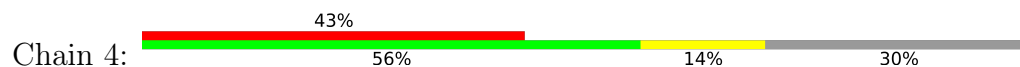
- Molecule 50: 30S ribosomal protein S17



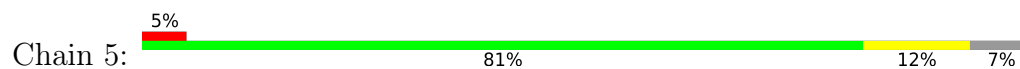
- Molecule 51: 30S ribosomal protein S2

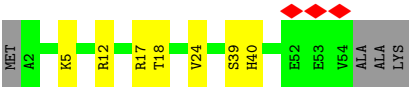


- Molecule 52: 50S ribosomal protein L31 type B



- Molecule 53: 50S ribosomal protein L32





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	61910	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 ($e^-/\text{\AA}^2$)	26.3	Depositor
Minimum defocus (nm)	-700	Depositor
Maximum defocus (nm)	-1900	Depositor
Magnification	165000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.031	Depositor
Minimum map value	-0.012	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.008	Depositor
Map size (Å)	366.432, 366.432, 366.432	wwPDB
Map dimensions	352, 352, 352	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.041, 1.041, 1.041	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: K, ZN, ATP, MG

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	0.55	0/3827	0.72	4/5139 (0.1%)
2	D	0.45	0/1746	0.44	0/2721
3	Z	0.75	0/591	0.64	0/785
4	P	0.74	0/1105	0.61	0/1483
5	A	0.60	0/69977	0.50	0/109141
6	a	0.43	0/36875	0.46	2/57502 (0.0%)
7	B	0.44	0/2692	0.48	0/4193
8	G	0.82	0/2120	0.68	0/2847
9	H	0.77	0/1661	0.61	0/2227
10	I	0.75	0/1587	0.64	0/2143
11	J	0.45	0/1398	0.62	0/1877
12	K	0.44	0/1302	0.52	0/1757
13	M	0.72	0/1149	0.62	0/1549
14	N	0.71	0/927	0.69	0/1243
15	O	0.75	0/1104	0.64	0/1471
16	Q	0.69	0/956	0.66	0/1277
17	R	0.48	0/923	0.61	0/1234
18	S	0.69	0/934	0.68	0/1249
19	T	0.81	0/955	0.66	0/1265
20	U	0.73	0/803	0.60	0/1073
21	V	0.80	0/861	0.68	0/1159
22	W	0.68	0/733	0.62	0/978
23	X	0.54	0/770	0.60	0/1029
24	Y	0.49	0/746	0.61	0/1000
25	1	0.63	0/480	0.73	0/639
26	2	0.56	0/528	0.68	0/703
27	3	0.72	0/438	0.65	0/590
28	6	0.61	0/392	0.60	0/523
29	8	0.82	0/526	0.72	0/690
30	7	0.91	0/364	0.62	0/474
31	d	0.53	0/1661	0.59	0/2233
32	e	0.43	0/1647	0.57	0/2211

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h	0.48	0/1114	0.56	0/1498
34	k	0.51	0/813	0.67	0/1094
35	l	0.40	0/891	0.49	0/1203
36	o	0.58	0/506	0.63	0/671
37	p	0.48	0/742	0.58	0/989
38	q	0.41	0/723	0.59	0/971
39	u	0.42	0/606	0.61	0/810
40	9	0.74	0/295	0.66	0/388
41	t	0.40	0/663	0.52	0/889
42	n	0.44	0/929	0.64	0/1246
43	j	0.53	0/1024	0.66	0/1374
44	f	0.58	0/1174	0.57	0/1583
45	i	0.47	0/1044	0.62	0/1401
46	s	0.48	0/525	0.54	0/704
47	g	0.37	0/784	0.60	0/1052
48	b	0.40	0/222	0.47	0/343
49	m	0.50	0/1075	0.60	0/1439
50	r	0.43	0/659	0.59	0/881
51	c	0.39	0/1808	0.59	0/2426
52	4	0.35	0/496	0.52	0/661
53	5	0.80	0/429	0.70	0/571
All	All	0.56	0/158300	0.52	6/236599 (0.0%)

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	71	PRO	N-CA-C	6.89	121.40	111.13
6	a	475	A	C2'-C3'-O3'	6.54	119.31	109.50
1	0	216	LYS	CA-C-N	-5.46	113.36	120.63
1	0	216	LYS	C-N-CA	-5.46	113.36	120.63
6	a	1046	G	C4'-C3'-O3'	5.37	117.45	109.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	3770	0	3913	48	0
2	D	1562	0	791	8	0
3	Z	585	0	597	8	0
4	P	1081	0	1143	7	0
5	A	62482	0	31401	235	0
6	a	32937	0	16584	138	0
7	B	2408	0	1218	14	0
8	G	2085	0	2192	27	0
9	H	1637	0	1680	14	0
10	I	1564	0	1611	9	0
11	J	1381	0	1435	17	0
12	K	1284	0	1301	14	0
13	M	1127	0	1117	11	0
14	N	920	0	981	20	0
15	O	1090	0	1131	11	0
16	Q	952	0	999	14	0
17	R	914	0	956	8	0
18	S	922	0	994	13	0
19	T	943	0	1014	12	0
20	U	793	0	831	10	0
21	V	853	0	914	7	0
22	W	725	0	761	7	0
23	X	761	0	823	6	0
24	Y	738	0	787	2	0
25	1	474	0	514	2	0
26	2	527	0	554	7	0
27	3	436	0	473	5	0
28	6	389	0	389	0	0
29	8	521	0	586	13	0
30	7	360	0	406	1	0
31	d	1638	0	1702	17	0
32	e	1617	0	1646	29	0
33	h	1101	0	1133	16	0
34	k	801	0	846	22	0
35	l	876	0	895	6	0
36	o	496	0	518	3	0
37	p	733	0	764	18	0
38	q	712	0	744	8	0
39	u	606	0	650	6	0
40	9	292	0	336	3	0
41	t	646	0	653	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	n	922	0	970	19	0
43	j	1008	0	1031	14	0
44	f	1160	0	1223	14	0
45	i	1032	0	1082	16	0
46	s	516	0	548	5	0
47	g	773	0	772	12	0
48	b	199	0	99	0	0
49	m	1058	0	1130	15	0
50	r	651	0	689	11	0
51	c	1781	0	1844	16	0
52	4	486	0	488	9	0
53	5	422	0	426	7	0
54	0	2	0	0	0	0
54	A	115	0	0	0	0
54	G	1	0	0	0	0
54	O	1	0	0	0	0
54	a	19	0	0	0	0
55	0	62	0	24	11	0
56	A	15	0	0	0	0
56	P	1	0	0	0	0
56	a	2	0	0	0	0
57	5	1	0	0	0	0
57	6	1	0	0	0	0
57	9	1	0	0	0	0
57	o	1	0	0	0	0
All	All	145969	0	98309	783	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 3.

The worst 5 of 783 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)
1:0:311:LYS:NZ	55:0:604:ATP:O1B	1.96	0.97
1:0:380:LYS:NZ	55:0:603:ATP:N3	2.16	0.94
6:a:1200:U:OP1	34:k:53:ARG:NH2	2.11	0.84
4:P:42:ILE:HD12	4:P:97:VAL:HG21	1.59	0.84
5:A:1137:G:H21	5:A:1142:A:H62	1.23	0.84

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	463/546 (85%)	420 (91%)	43 (9%)	0	100	100
3	Z	74/94 (79%)	68 (92%)	6 (8%)	0	100	100
4	P	133/144 (92%)	120 (90%)	13 (10%)	0	100	100
8	G	271/277 (98%)	245 (90%)	26 (10%)	0	100	100
9	H	214/220 (97%)	193 (90%)	21 (10%)	0	100	100
10	I	202/207 (98%)	180 (89%)	22 (11%)	0	100	100
11	J	173/179 (97%)	150 (87%)	23 (13%)	0	100	100
12	K	162/178 (91%)	155 (96%)	7 (4%)	0	100	100
13	M	140/145 (97%)	131 (94%)	9 (6%)	0	100	100
14	N	120/122 (98%)	107 (89%)	13 (11%)	0	100	100
15	O	143/146 (98%)	131 (92%)	12 (8%)	0	100	100
16	Q	118/122 (97%)	112 (95%)	6 (5%)	0	100	100
17	R	116/119 (98%)	105 (90%)	11 (10%)	0	100	100
18	S	112/116 (97%)	96 (86%)	16 (14%)	0	100	100
19	T	114/118 (97%)	107 (94%)	7 (6%)	0	100	100
20	U	99/102 (97%)	89 (90%)	10 (10%)	0	100	100
21	V	109/117 (93%)	106 (97%)	3 (3%)	0	100	100
22	W	87/91 (96%)	78 (90%)	9 (10%)	0	100	100
23	X	97/105 (92%)	92 (95%)	5 (5%)	0	100	100
24	Y	92/217 (42%)	81 (88%)	11 (12%)	0	100	100
25	1	58/62 (94%)	51 (88%)	7 (12%)	0	100	100
26	2	62/69 (90%)	57 (92%)	5 (8%)	0	100	100
27	3	54/59 (92%)	51 (94%)	3 (6%)	0	100	100
28	6	45/49 (92%)	38 (84%)	7 (16%)	0	100	100
29	8	62/66 (94%)	56 (90%)	6 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	7	40/45 (89%)	39 (98%)	1 (2%)	0	100	100
31	d	206/217 (95%)	185 (90%)	21 (10%)	0	100	100
32	e	197/200 (98%)	173 (88%)	24 (12%)	0	100	100
33	h	134/156 (86%)	121 (90%)	13 (10%)	0	100	100
34	k	98/102 (96%)	85 (87%)	13 (13%)	0	100	100
35	l	116/129 (90%)	107 (92%)	9 (8%)	0	100	100
36	o	57/60 (95%)	54 (95%)	3 (5%)	0	100	100
37	p	85/89 (96%)	80 (94%)	5 (6%)	0	100	100
38	q	88/91 (97%)	79 (90%)	9 (10%)	0	100	100
39	u	78/83 (94%)	73 (94%)	5 (6%)	0	100	100
40	9	34/37 (92%)	30 (88%)	4 (12%)	0	100	100
41	t	77/92 (84%)	69 (90%)	8 (10%)	0	100	100
42	n	114/121 (94%)	96 (84%)	18 (16%)	0	100	100
43	j	125/132 (95%)	118 (94%)	7 (6%)	0	100	100
44	f	154/166 (93%)	142 (92%)	12 (8%)	0	100	100
45	i	129/132 (98%)	117 (91%)	12 (9%)	0	100	100
46	s	61/80 (76%)	54 (88%)	7 (12%)	0	100	100
47	g	91/98 (93%)	79 (87%)	12 (13%)	0	100	100
49	m	133/137 (97%)	111 (84%)	22 (16%)	0	100	100
50	r	77/87 (88%)	67 (87%)	10 (13%)	0	100	100
51	c	219/255 (86%)	199 (91%)	20 (9%)	0	100	100
52	4	53/84 (63%)	47 (89%)	6 (11%)	0	100	100
53	5	51/57 (90%)	46 (90%)	5 (10%)	0	100	100
All	All	5737/6320 (91%)	5190 (90%)	547 (10%)	0	100	100

There are no Ramachandran outliers to report.

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	423/500 (85%)	421 (100%)	2 (0%)	81	85
3	Z	59/75 (79%)	59 (100%)	0	100	100
4	P	112/119 (94%)	112 (100%)	0	100	100
8	G	220/224 (98%)	219 (100%)	1 (0%)	81	85
9	H	174/177 (98%)	174 (100%)	0	100	100
10	I	168/169 (99%)	168 (100%)	0	100	100
11	J	154/158 (98%)	154 (100%)	0	100	100
12	K	144/155 (93%)	144 (100%)	0	100	100
13	M	121/123 (98%)	121 (100%)	0	100	100
14	N	100/100 (100%)	100 (100%)	0	100	100
15	O	111/112 (99%)	111 (100%)	0	100	100
16	Q	101/102 (99%)	101 (100%)	0	100	100
17	R	94/95 (99%)	94 (100%)	0	100	100
18	S	100/102 (98%)	100 (100%)	0	100	100
19	T	96/98 (98%)	95 (99%)	1 (1%)	68	79
20	U	86/86 (100%)	86 (100%)	0	100	100
21	V	90/94 (96%)	90 (100%)	0	100	100
22	W	80/82 (98%)	80 (100%)	0	100	100
23	X	84/90 (93%)	84 (100%)	0	100	100
24	Y	83/190 (44%)	83 (100%)	0	100	100
25	1	50/52 (96%)	50 (100%)	0	100	100
26	2	58/62 (94%)	58 (100%)	0	100	100
27	3	51/53 (96%)	51 (100%)	0	100	100
28	6	45/47 (96%)	45 (100%)	0	100	100
29	8	55/57 (96%)	55 (100%)	0	100	100
30	7	38/40 (95%)	38 (100%)	0	100	100
31	d	169/175 (97%)	169 (100%)	0	100	100
32	e	174/175 (99%)	174 (100%)	0	100	100
33	h	117/132 (89%)	117 (100%)	0	100	100
34	k	90/91 (99%)	89 (99%)	1 (1%)	65	78
35	l	94/104 (90%)	94 (100%)	0	100	100
36	o	52/53 (98%)	52 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	p	80/81 (99%)	80 (100%)	0	100	100
38	q	76/77 (99%)	76 (100%)	0	100	100
39	u	67/69 (97%)	67 (100%)	0	100	100
40	9	35/35 (100%)	35 (100%)	0	100	100
41	t	70/80 (88%)	70 (100%)	0	100	100
42	n	100/104 (96%)	100 (100%)	0	100	100
43	j	105/109 (96%)	105 (100%)	0	100	100
44	f	122/131 (93%)	122 (100%)	0	100	100
45	i	112/113 (99%)	112 (100%)	0	100	100
46	s	56/68 (82%)	56 (100%)	0	100	100
47	g	81/86 (94%)	81 (100%)	0	100	100
49	m	117/119 (98%)	117 (100%)	0	100	100
50	r	74/82 (90%)	74 (100%)	0	100	100
51	c	192/221 (87%)	192 (100%)	0	100	100
52	4	55/75 (73%)	55 (100%)	0	100	100
53	5	48/50 (96%)	48 (100%)	0	100	100
All	All	4983/5392 (92%)	4978 (100%)	5 (0%)	87	90

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	0	73	LEU
1	0	375	ARG
8	G	14	ARG
19	T	92	ARG
34	k	57	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
31	d	88	ASN
53	5	14	ASN
34	k	56	HIS
49	m	77	ASN
33	h	18	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	D	72/76 (94%)	19 (26%)	1 (1%)
48	b	7/15 (46%)	0	0
5	A	2912/2923 (99%)	532 (18%)	15 (0%)
6	a	1536/1551 (99%)	288 (18%)	0
7	B	112/115 (97%)	16 (14%)	0
All	All	4639/4680 (99%)	855 (18%)	16 (0%)

5 of 855 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	D	8	U
2	D	9	G
2	D	13	C
2	D	19	G
2	D	20	G

5 of 16 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	A	2239	A
5	A	2135	U
5	A	1457	U
5	A	1938	U
5	A	1310	A

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 162 ligands modelled in this entry, 160 are monoatomic - leaving 2 for Mogul analysis.

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
55	ATP	0	603	54	32,33,33	0.65	1 (3%)	48,52,52	0.75	2 (4%)
55	ATP	0	604	54	32,33,33	0.52	0	48,52,52	0.71	0

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
55	ATP	0	603	54	-	5/22/38/38	0/3/3/3
55	ATP	0	604	54	-	8/22/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	0	603	ATP	PA-O3A	-2.24	1.57	1.59

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	0	603	ATP	O2'-C2'-C3'	-2.25	104.61	111.82
55	0	603	ATP	O3'-C3'-C2'	-2.04	105.29	111.82

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

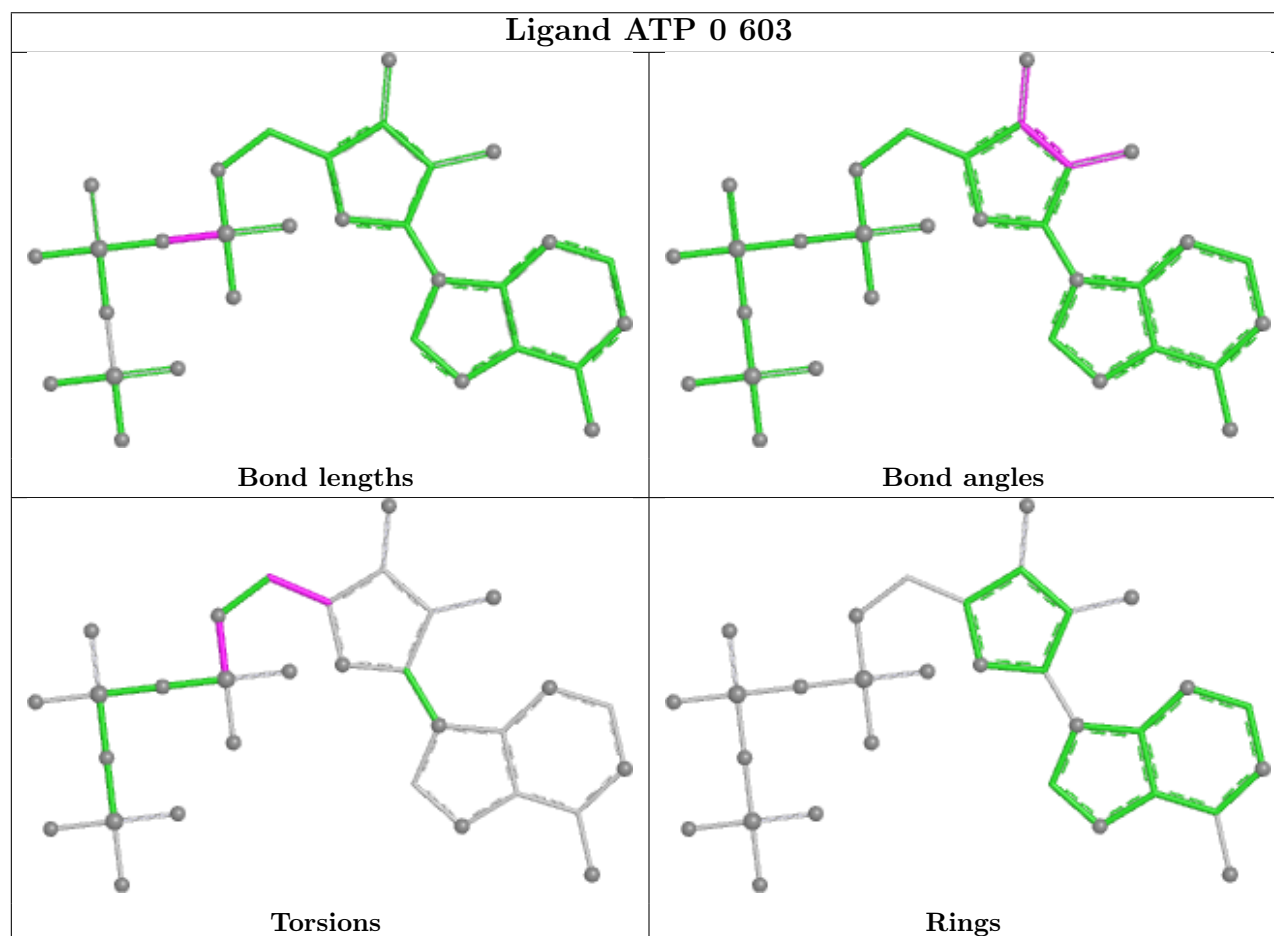
Mol	Chain	Res	Type	Atoms
55	0	603	ATP	C5'-O5'-PA-O1A
55	0	603	ATP	C5'-O5'-PA-O3A
55	0	604	ATP	PB-O3B-PG-O2G
55	0	604	ATP	C5'-O5'-PA-O3A
55	0	603	ATP	O4'-C4'-C5'-O5'

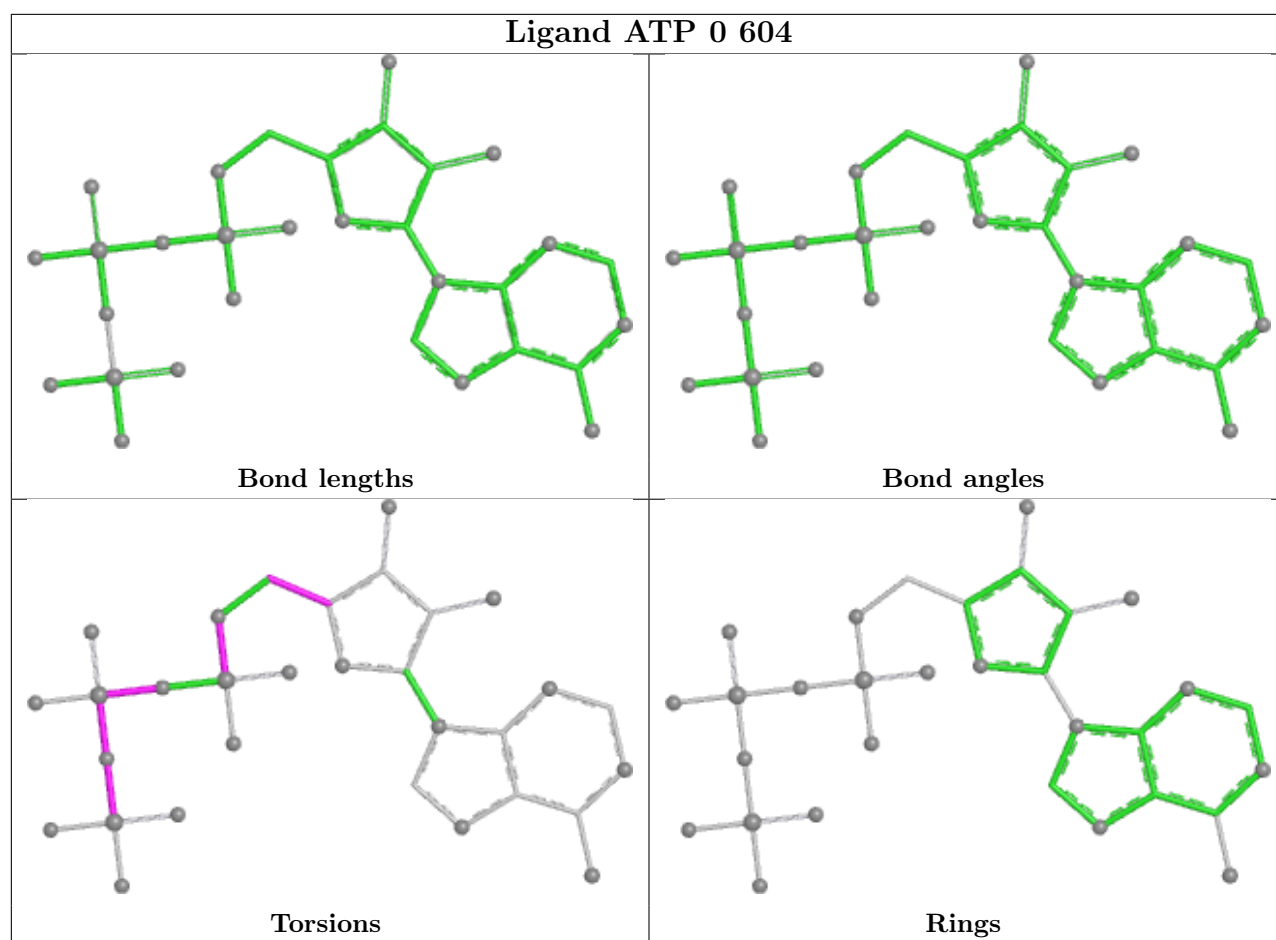
There are no ring outliers.

2 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
55	0	603	ATP	7	0
55	0	604	ATP	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.

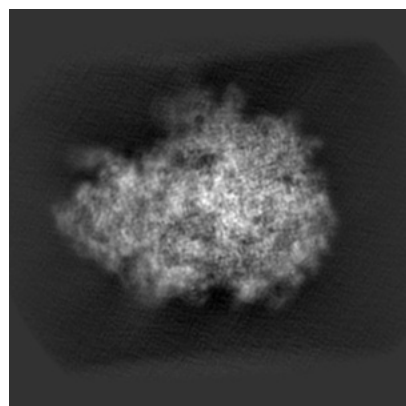
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12332. These allow visual inspection of the internal detail of the map and identification of artifacts.

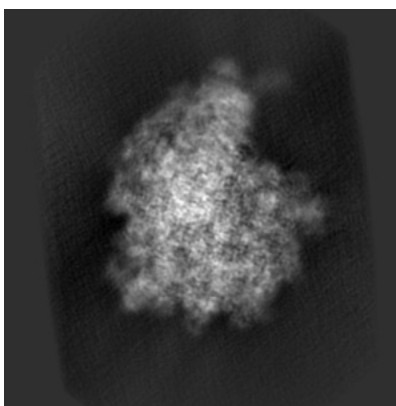
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

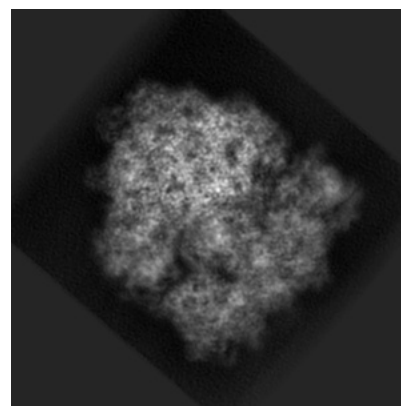
6.1.1 Primary map



X

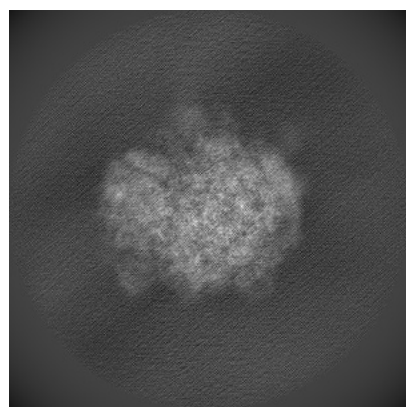


Y

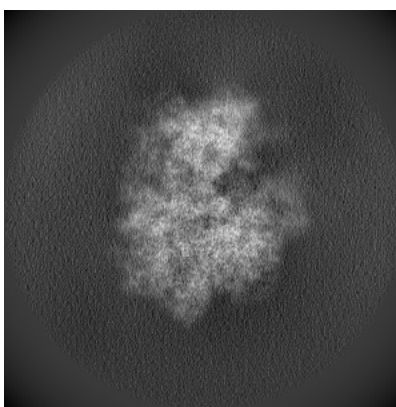


Z

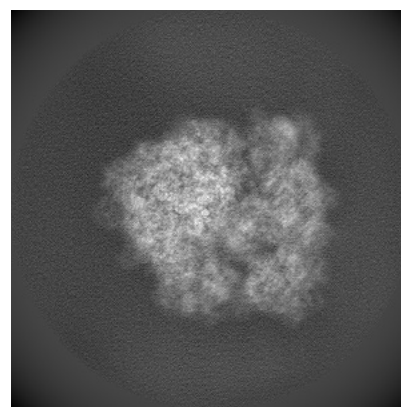
6.1.2 Raw map



X



Y

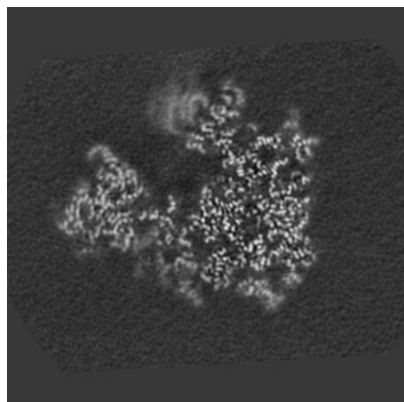


Z

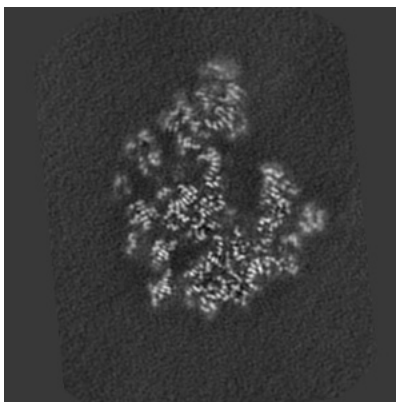
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

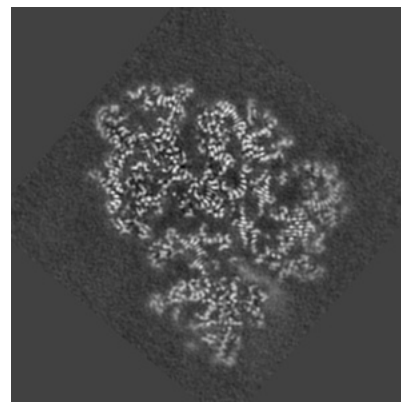
6.2.1 Primary map



X Index: 176

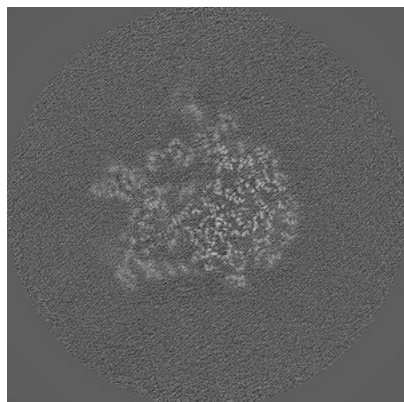


Y Index: 176

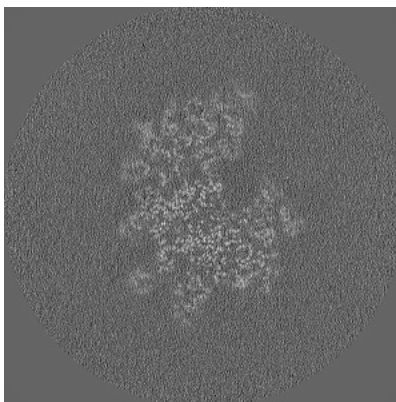


Z Index: 176

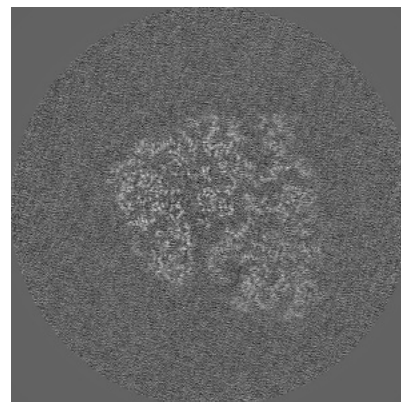
6.2.2 Raw map



X Index: 255



Y Index: 255

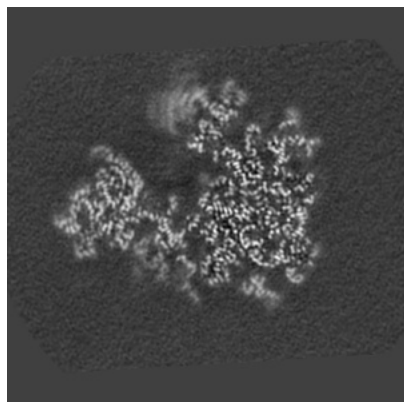


Z Index: 255

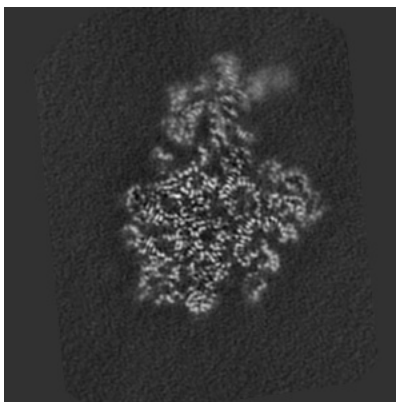
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

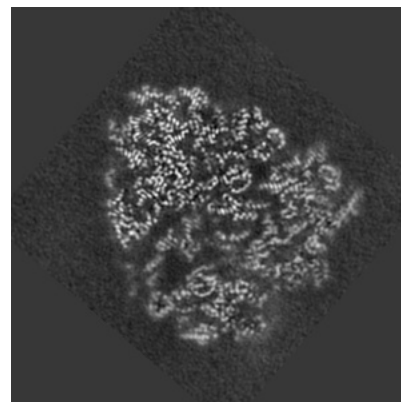
6.3.1 Primary map



X Index: 173

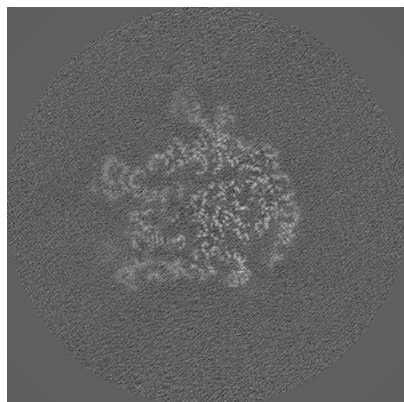


Y Index: 189

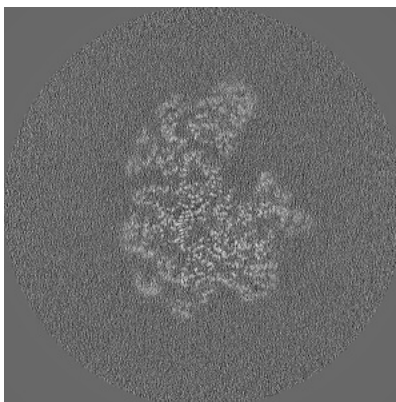


Z Index: 186

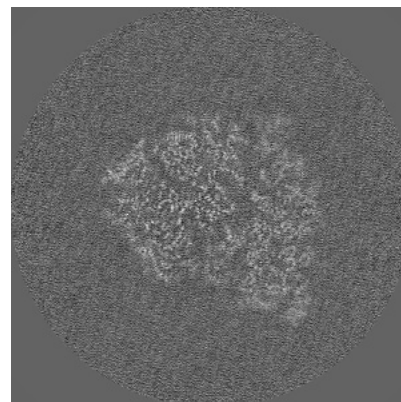
6.3.2 Raw map



X Index: 249



Y Index: 268

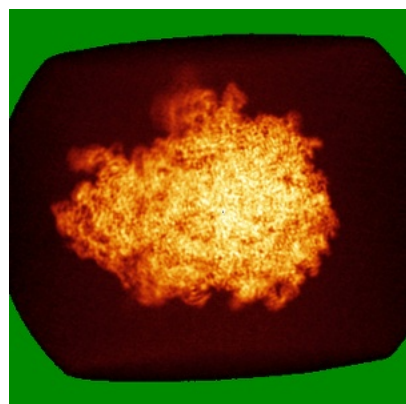


Z Index: 249

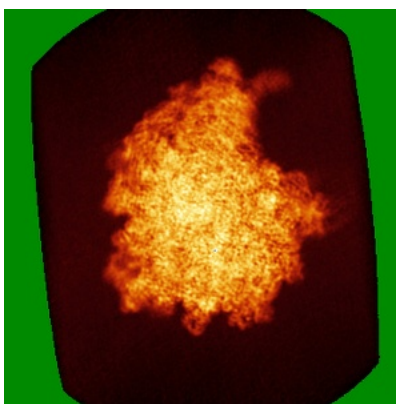
The images above show the largest variance slices of the map in three orthogonal directions.

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

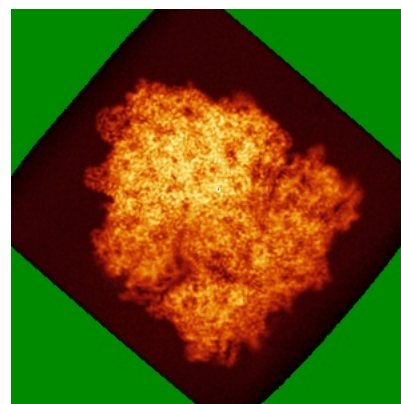
6.4.1 Primary map



X

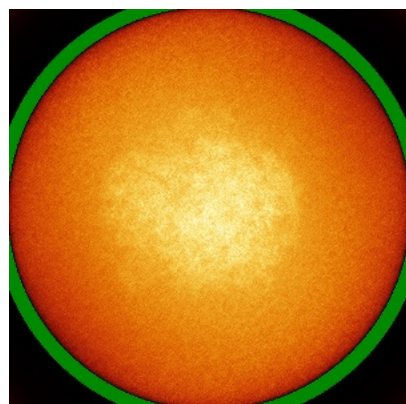


Y

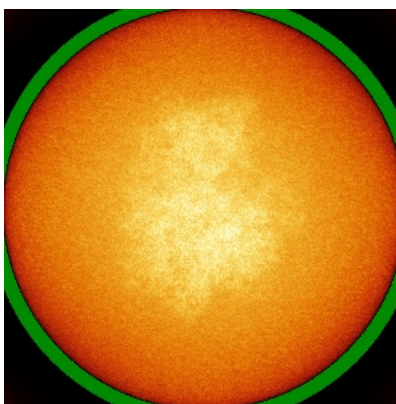


Z

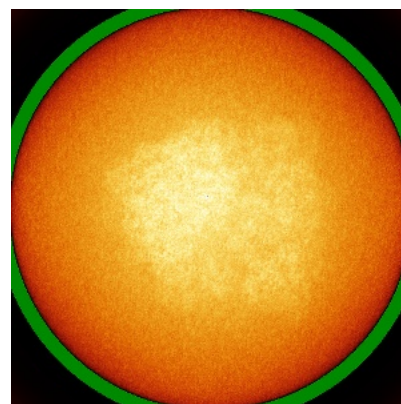
6.4.2 Raw map



X



Y

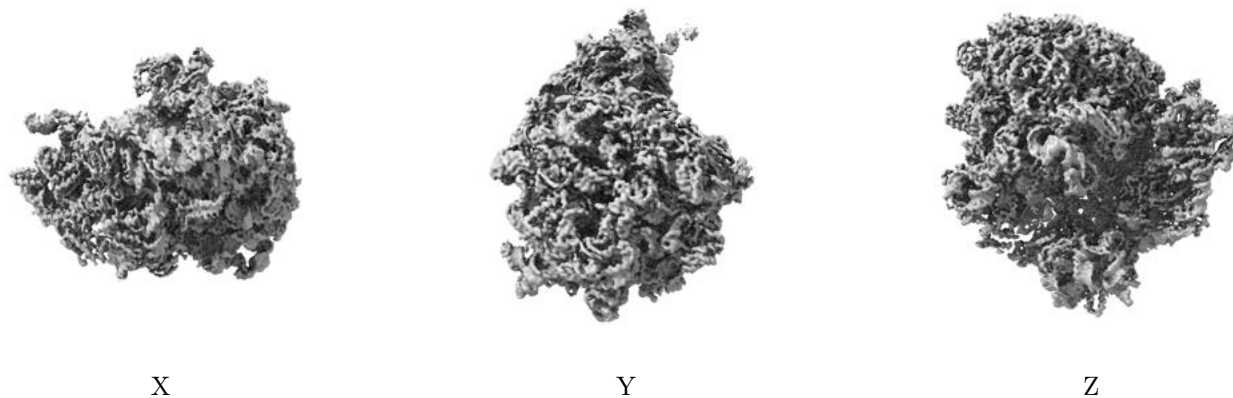


Z

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.

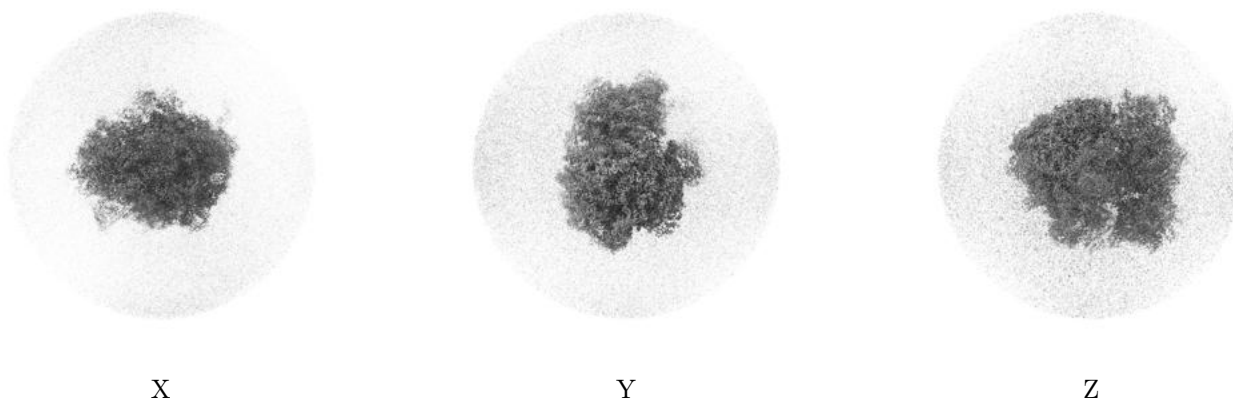
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.008. 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.

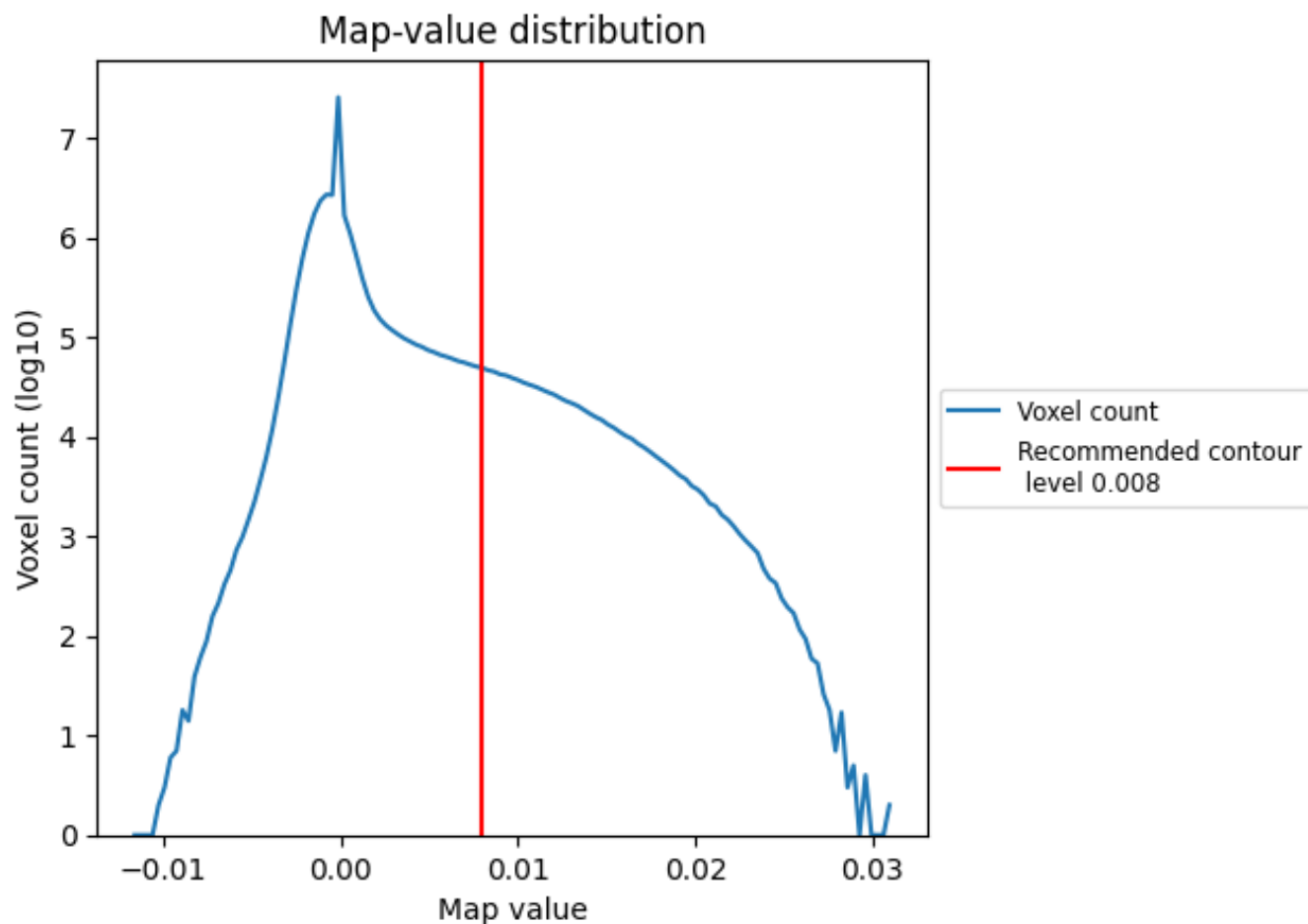
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

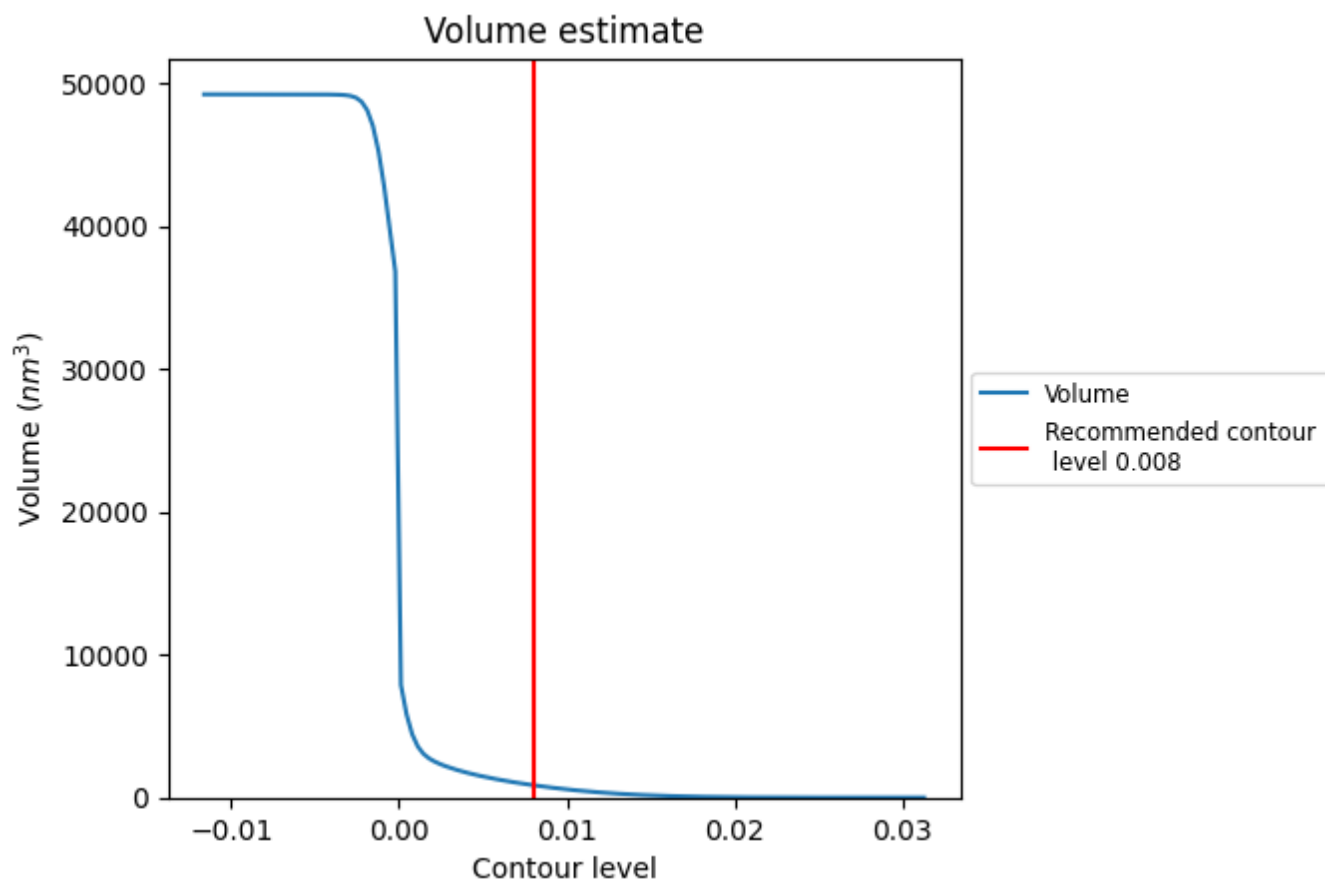
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

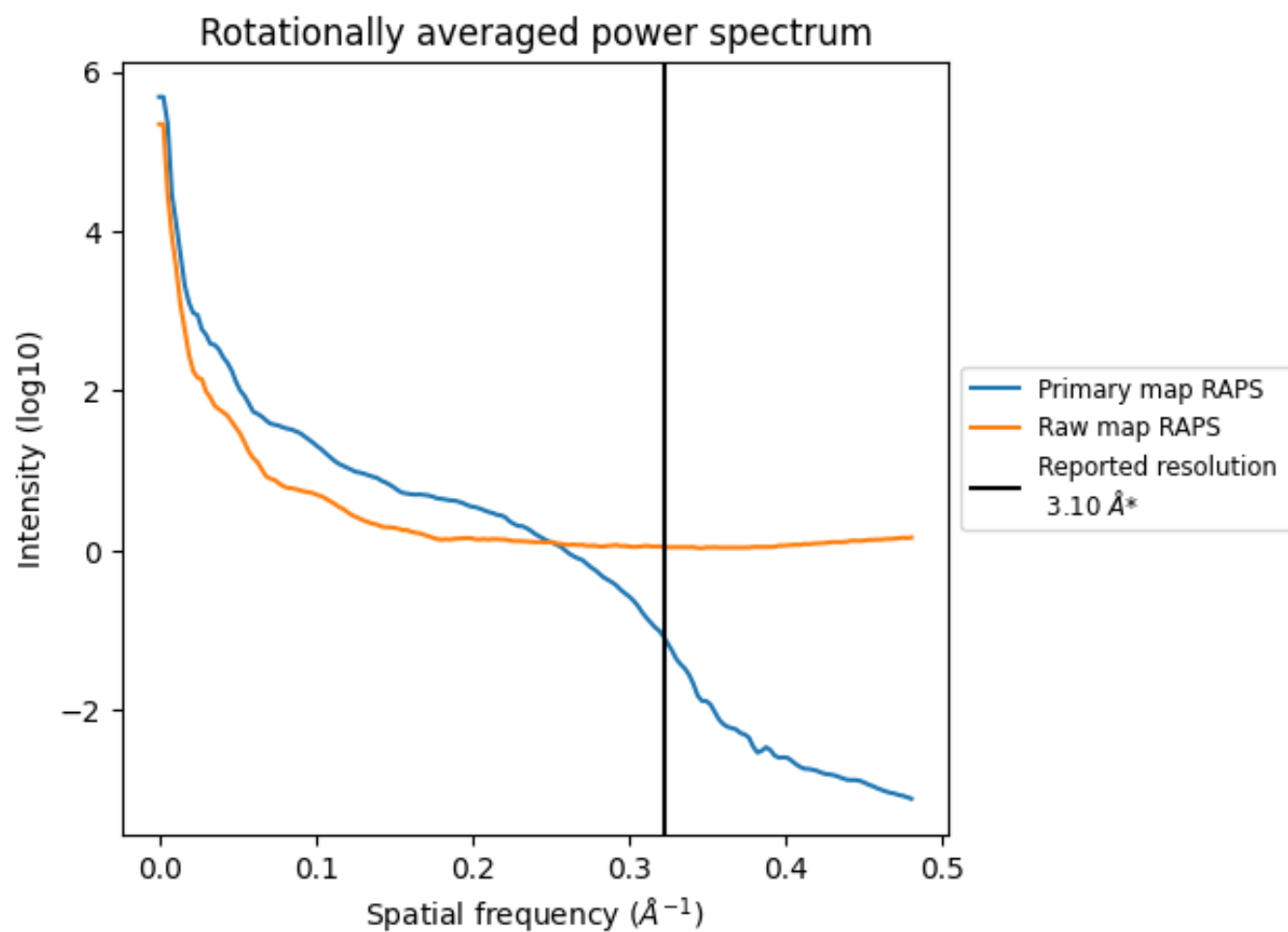
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 865 nm³; this corresponds to an approximate mass of 782 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 ⓘ

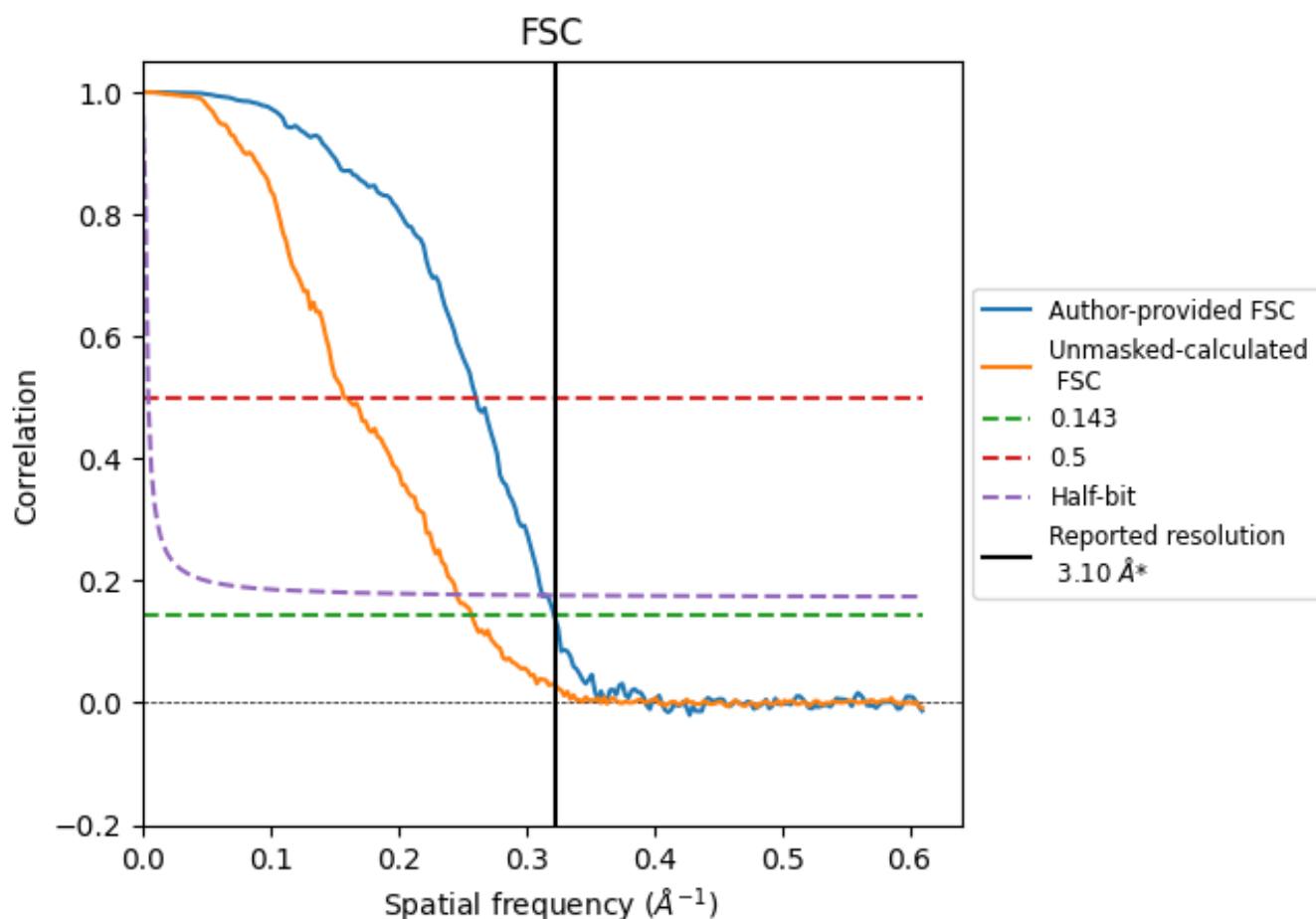


*Reported resolution corresponds to spatial frequency of 0.323 $\text{\AA}^{-1}$

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 0.323 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

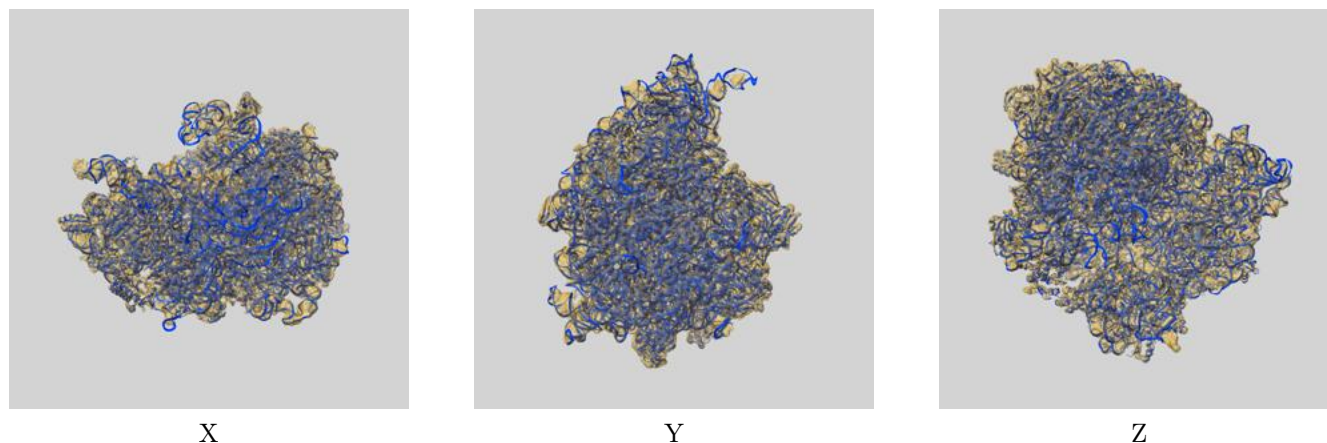
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.10	3.83	3.20
Unmasked-calculated*	3.88	6.34	4.07

*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 3.88 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

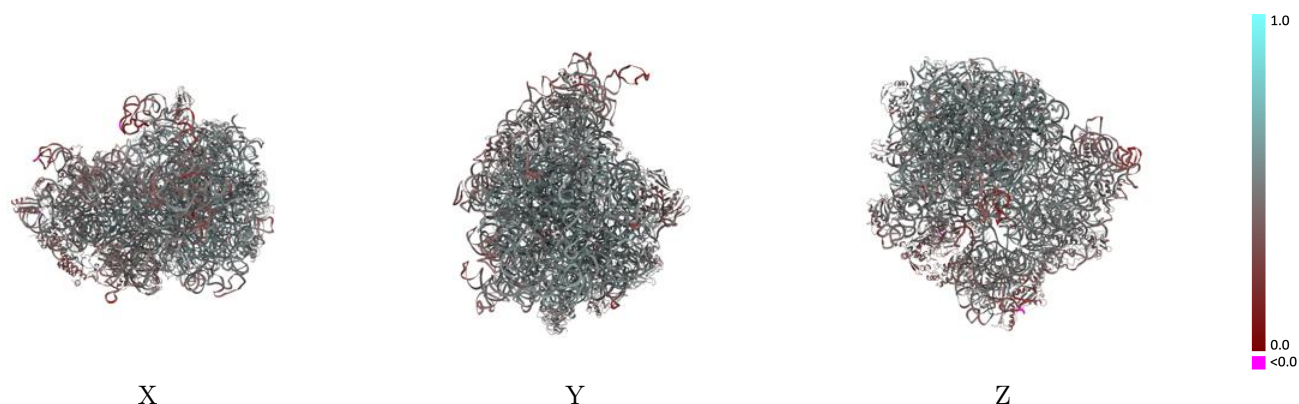
This section contains information regarding the fit between EMDB map EMD-12332 and PDB model 7NHL. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)



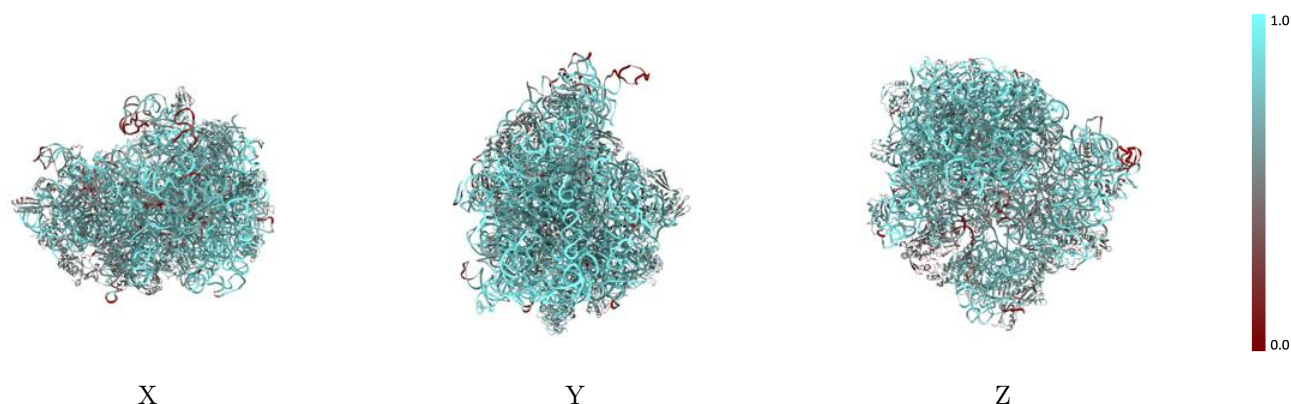
The images above show the 3D surface view of the map at the recommended contour level 0.008 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



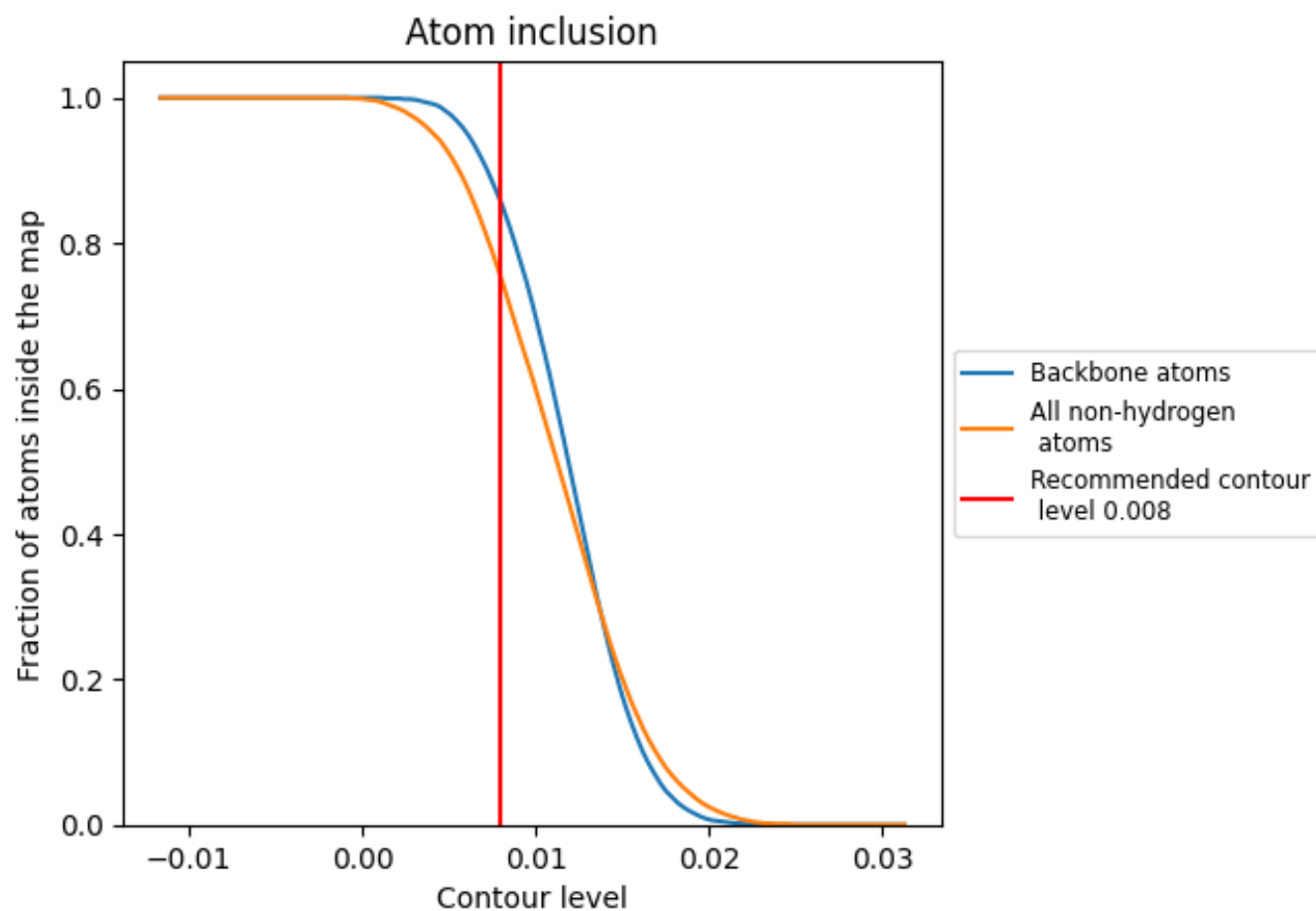
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.008).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 75% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.008) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7530	 0.4760
0	 0.4910	 0.4250
1	 0.5720	 0.4960
2	 0.6480	 0.4410
3	 0.6350	 0.4720
4	 0.3360	 0.3180
5	 0.6920	 0.5010
6	 0.6680	 0.4730
7	 0.7080	 0.5400
8	 0.6690	 0.5280
9	 0.6720	 0.5070
A	 0.8530	 0.5040
B	 0.8400	 0.4520
D	 0.7730	 0.4950
G	 0.6530	 0.5140
H	 0.6600	 0.5050
I	 0.6530	 0.4850
J	 0.4500	 0.3630
K	 0.5590	 0.4100
M	 0.6580	 0.4900
N	 0.5690	 0.5020
O	 0.6550	 0.5010
P	 0.6330	 0.4980
Q	 0.6570	 0.4820
R	 0.5860	 0.4210
S	 0.5900	 0.4790
T	 0.6860	 0.4860
U	 0.6540	 0.4980
V	 0.6640	 0.5110
W	 0.6380	 0.4950
X	 0.5800	 0.4610
Y	 0.5520	 0.4350
Z	 0.6520	 0.5060
a	 0.8090	 0.4640
b	 0.6480	 0.4650



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Chain	Atom inclusion	Q-score
c	 0.4800	 0.3840
d	 0.5820	 0.4200
e	 0.4530	 0.4120
f	 0.5940	 0.4640
g	 0.4340	 0.3820
h	 0.6230	 0.4040
i	 0.5150	 0.4280
j	 0.6290	 0.4420
k	 0.5310	 0.4020
l	 0.4120	 0.3920
m	 0.5010	 0.4560
n	 0.5100	 0.3990
o	 0.6240	 0.4510
p	 0.5210	 0.3910
q	 0.4730	 0.4030
r	 0.4700	 0.4350
s	 0.4900	 0.4130
t	 0.4690	 0.4020
u	 0.5050	 0.3850