



wwPDB EM Validation Summary Report ⓘ

Sep 19, 2026 – 11:43 AM JST

PDB ID : 8ZFF / pdb_00008zff
EMDB ID : EMD-60059
Title : Structure of the Bacterial Ribosome without hypoxia-induced rRNA modifications
Authors : Ishiguro, K.; Yokoyama, T.; Shirouzu, M.; Ito, T.; Suzuki, T.
Deposited on : 2024-05-07
Resolution : 2.59 Å(reported)
Based on initial model : 7K00

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.dev133
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
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) : 2.50

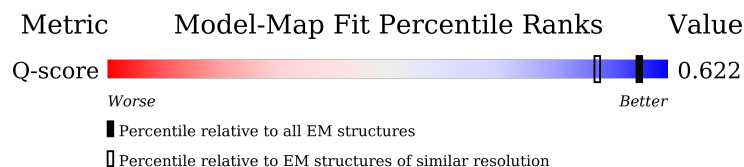
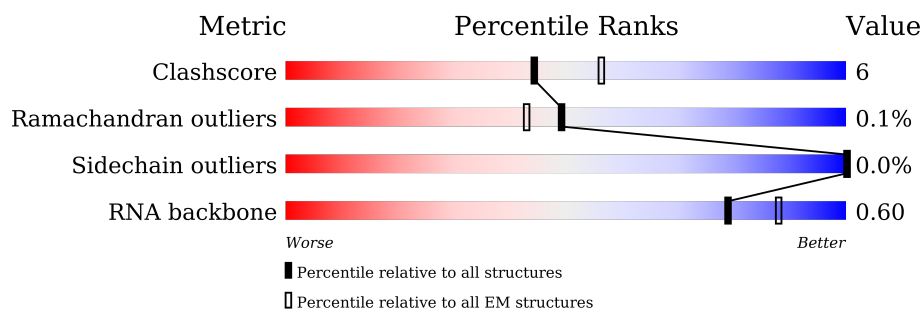
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.59 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	7741 (2.09 - 3.09)

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	A	1542	 61% 33% 6%
2	B	241	 38% 80% 12% 7%
3	C	233	 6% 73% 15% 12%

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Mol	Chain	Length	Quality of chain
4	D	206	
5	E	167	
6	F	135	
7	G	179	
8	H	130	
9	I	130	
10	J	103	
11	K	129	
12	L	124	
13	M	118	
14	N	101	
15	O	89	
16	P	82	
17	Q	84	
18	R	75	
19	S	92	
20	T	87	
21	U	71	
22	a	2904	
23	b	120	
24	c	273	
25	d	209	
26	e	201	
27	f	179	
28	g	177	

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Mol	Chain	Length	Quality of chain
29	h	149	
30	i	142	
31	j	123	
32	k	144	
33	l	136	
34	m	127	
35	n	117	
36	o	115	
37	p	118	
38	q	103	
39	r	110	
40	s	100	
41	t	104	
42	u	94	
43	v	85	
44	w	78	
45	x	63	
46	y	59	
47	z	57	
48	0	55	
49	1	46	
50	2	65	
51	3	38	
52	4	70	
53	X	66	

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Mol	Chain	Length	Quality of chain
54	Z	77	8% 56% 35% 8%

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 140322 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 RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1512	Total	C	N	O	P	0	0
			32466	14487	5964	10503	1512		

- Molecule 2 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	224	Total	C	N	O	S	0	0
			1753	1109	315	321	8		

- Molecule 3 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 4 is a protein called Small ribosomal subunit protein uS4.

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

- Molecule 5 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	156	Total	C	N	O	S	0	0
			1152	717	217	212	6		

- Molecule 6 is a protein called Small ribosomal subunit protein bS6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	103	Total	C	N	O	S	0	0
			839	530	151	151	7		

- Molecule 7 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	153	Total	C	N	O	S	0	0
			1203	750	231	218	4		

- Molecule 8 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 9 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 10 is a protein called Small ribosomal subunit protein uS10.

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

- Molecule 11 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	117	Total	C	N	O	S	0	0
			877	540	173	161	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	119	IAS	ASN	conflict	UNP P0A7R9

- Molecule 12 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 13 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	115	Total	C	N	O	S	0	0
			891	552	179	157	3		

- Molecule 14 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 15 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 16 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	81	Total	C	N	O	S	0	0
			643	403	127	112	1		

- Molecule 17 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	79	Total	C	N	O	S	0	0
			641	406	120	112	3		

- Molecule 18 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	66	Total	C	N	O	S	0	0
			544	345	102	96	1		

- Molecule 19 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	84	Total	C	N	O	S	0	0
			668	427	127	112	2		

- Molecule 20 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 21 is a protein called Small ribosomal subunit protein bS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 22 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	a	2761	Total	C	N	O	P	0	0
			59301	26460	10925	19155	2761		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	b	119	Total	C	N	O	P	0	0
			2549	1135	466	829	119		

- Molecule 24 is a protein called Large ribosomal subunit protein uL2.

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

- Molecule 25 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	d	209	Total	C	N	O	S	0	0
			1566	980	288	294	4		

- Molecule 26 is a protein called Large ribosomal subunit protein uL4.

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

- Molecule 27 is a protein called Large ribosomal subunit protein uL5.

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

- Molecule 28 is a protein called Large ribosomal subunit protein uL6.

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

- Molecule 29 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	h	41	Total	C	N	O	S	0	0
			303	194	54	54	1		

- Molecule 30 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 31 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	j	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 32 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	k	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 33 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	l	136	Total	C	N	O	S	0	0
			1075	686	205	177	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	82	MS6	MET	conflict	UNP P0ADY7

- Molecule 34 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	m	118	Total	C	N	O	S	0	0
			945	585	194	161	5		

- Molecule 35 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 36 is a protein called Large ribosomal subunit protein bL19.

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

- Molecule 37 is a protein called Large ribosomal subunit protein bL20.

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

- Molecule 38 is a protein called Large ribosomal subunit protein bL21.

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

- Molecule 39 is a protein called Large ribosomal subunit protein uL22.

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

- Molecule 40 is a protein called Large ribosomal subunit protein uL23.

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

- Molecule 41 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	t	102	Total	C	N	O	S	0	0
			779	492	146	141			

- Molecule 42 is a protein called Large ribosomal subunit protein bL25.

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

- Molecule 43 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	v	78	Total	C	N	O	S	0	0
			592	365	119	107	1		

- Molecule 44 is a protein called Large ribosomal subunit protein bL28.

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

- Molecule 45 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	x	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 46 is a protein called Large ribosomal subunit protein uL30.

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

- Molecule 47 is a protein called Large ribosomal subunit protein bL32.

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

- Molecule 48 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	0	51	Total	C	N	O		0	0
			417	269	76	72			

- Molecule 49 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	1	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 50 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	2	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 51 is a protein called Large ribosomal subunit protein bL36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	3	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 52 is a protein called Large ribosomal subunit protein bL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	4	60	Total	C	N	O	S	0	0
			480	299	90	85	6		

- Molecule 53 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	X	6	Total	C	N	O	P	0	0
			130	58	25	41	6		

- Molecule 54 is a RNA chain called P-site tRNA-fMet.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	Z	77	Total	C	N	O	P	S	0	0
			1645	734	297	536	77	1		

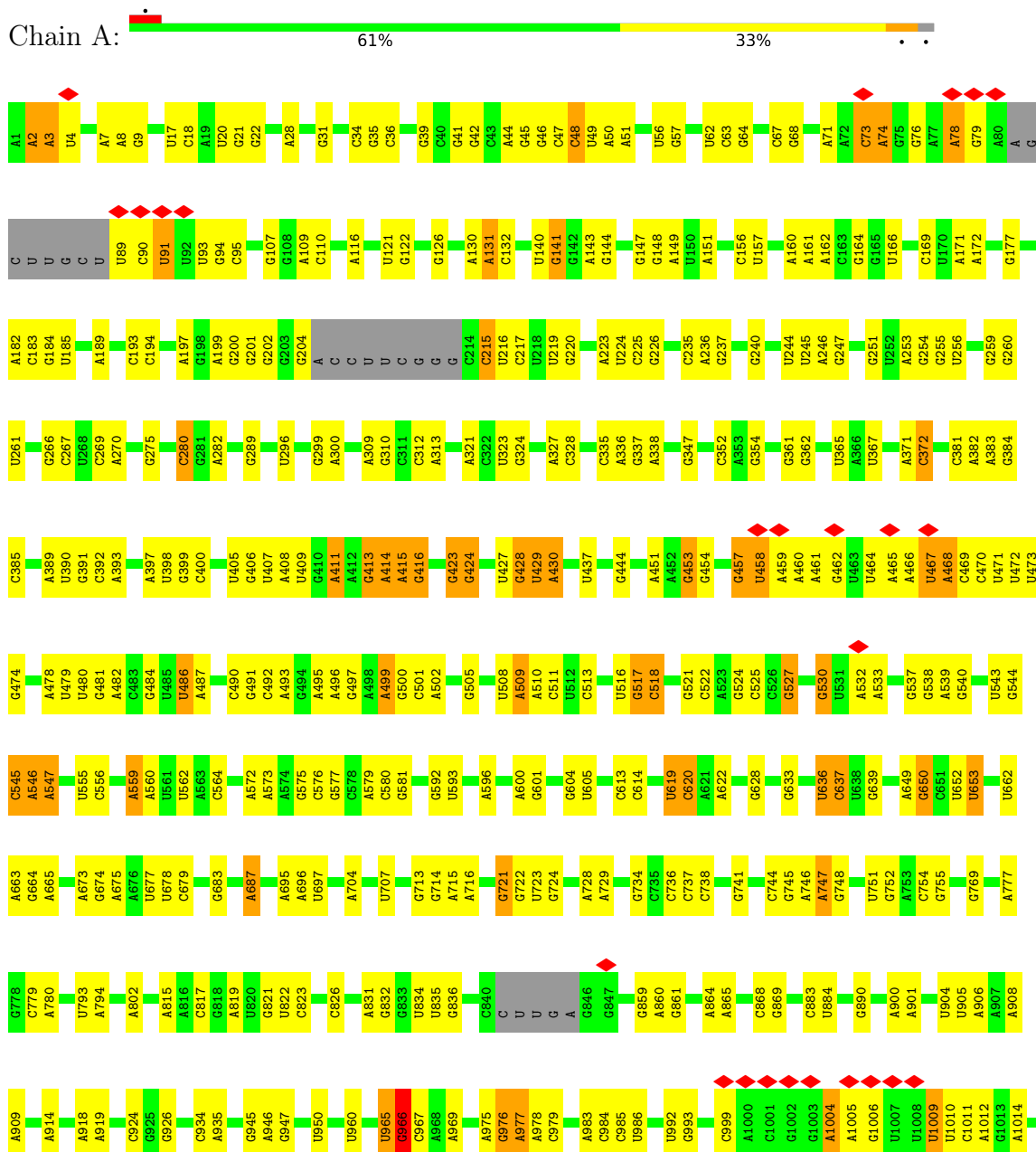
- Molecule 55 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

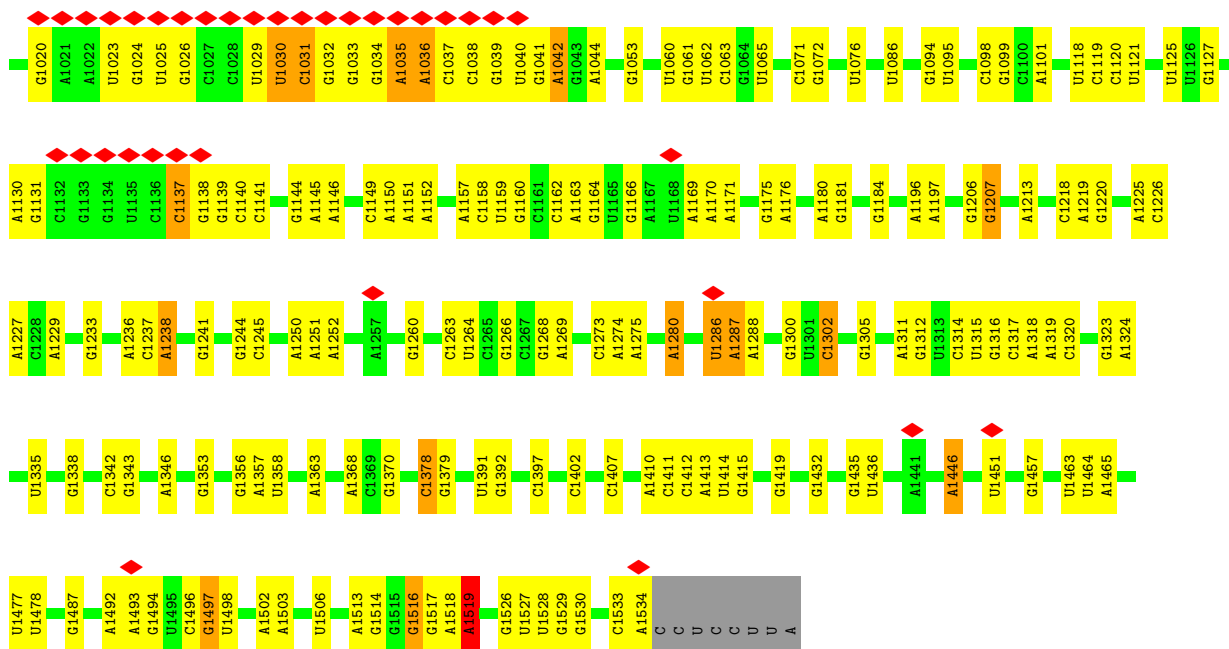
Mol	Chain	Residues	Atoms		AltConf
55	A	119	Total	Mg	0
			119	119	
55	a	328	Total	Mg	0
			328	328	
55	b	6	Total	Mg	0
			6	6	
55	c	1	Total	Mg	0
			1	1	
55	d	1	Total	Mg	0
			1	1	
55	z	1	Total	Mg	0
			1	1	
55	Z	1	Total	Mg	0
			1	1	

3 Residue-property plots

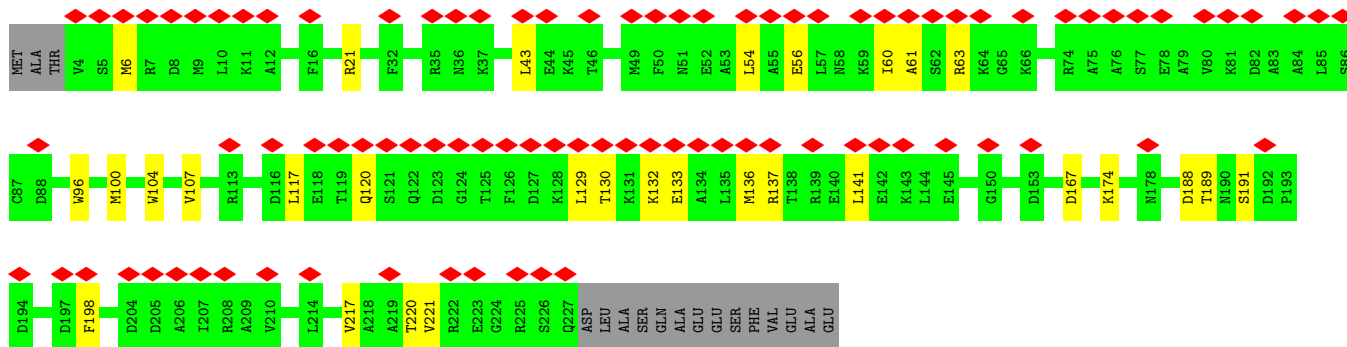
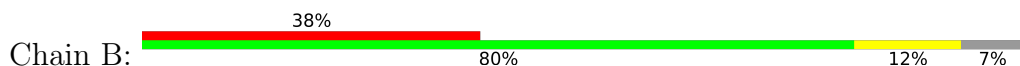
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 16S rRNA

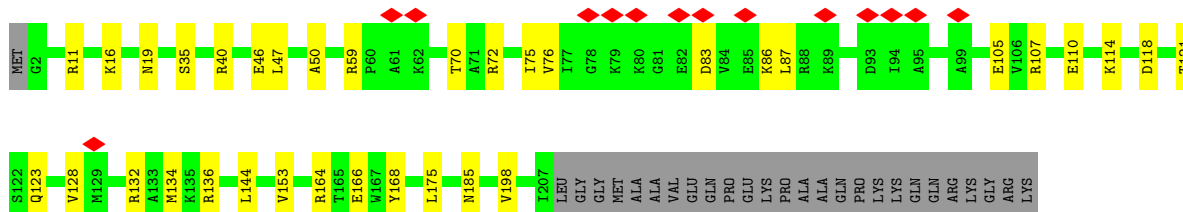
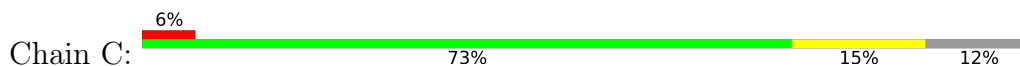




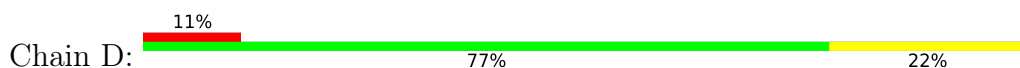
• Molecule 2: Small ribosomal subunit protein uS2

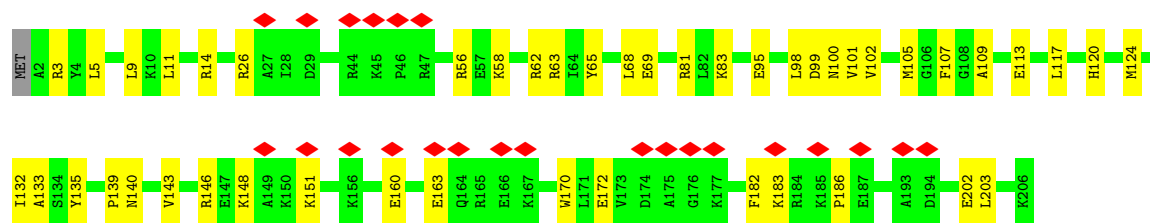


• Molecule 3: Small ribosomal subunit protein uS3

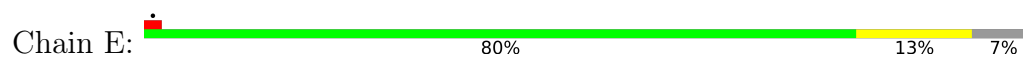


• Molecule 4: Small ribosomal subunit protein uS4

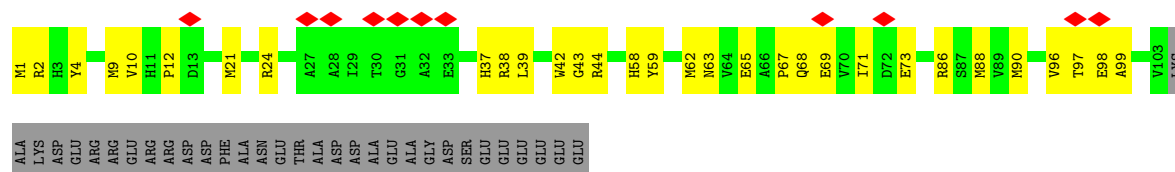




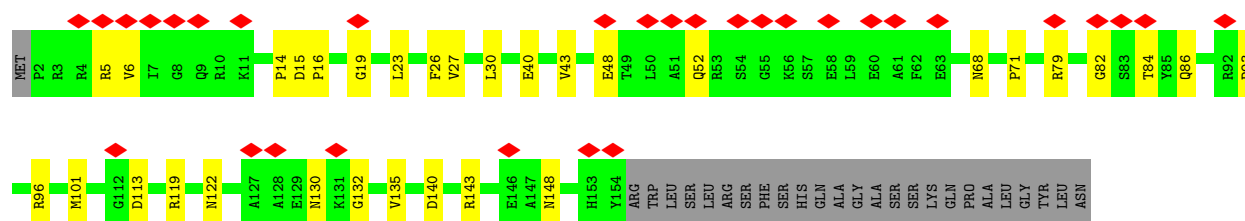
- Molecule 5: Small ribosomal subunit protein uS5



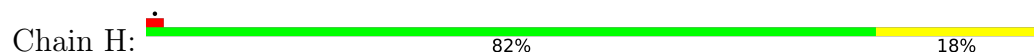
- Molecule 6: Small ribosomal subunit protein bS6, fully modified isoform



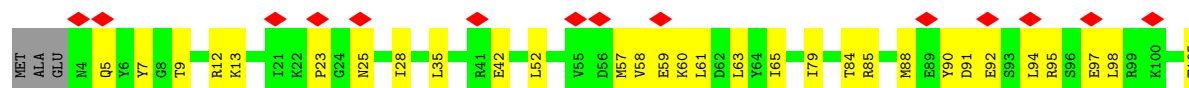
- Molecule 7: Small ribosomal subunit protein uS7



- Molecule 8: Small ribosomal subunit protein uS8

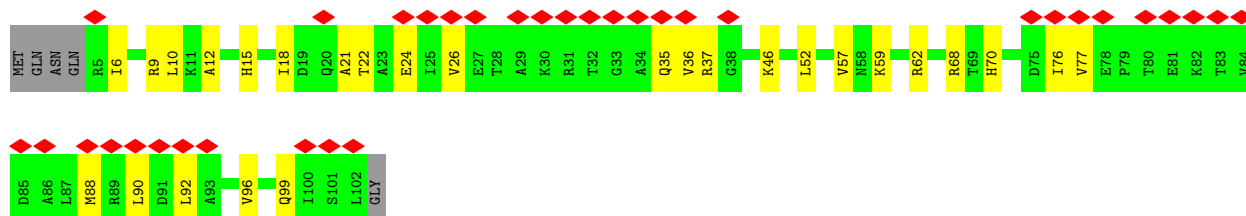


- Molecule 9: Small ribosomal subunit protein uS9





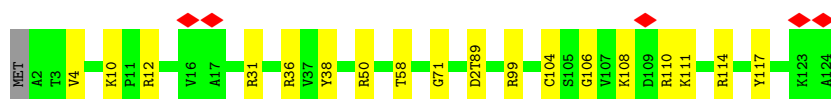
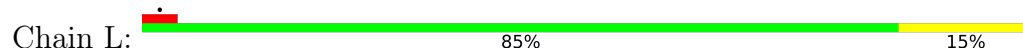
- Molecule 10: Small ribosomal subunit protein uS10



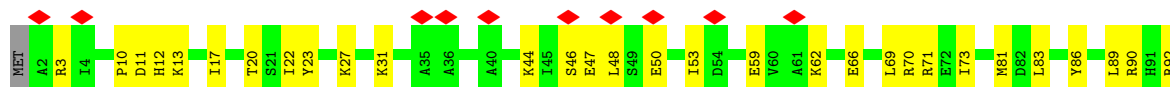
- Molecule 11: Small ribosomal subunit protein uS11



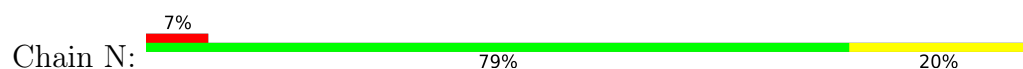
- Molecule 12: Small ribosomal subunit protein uS12

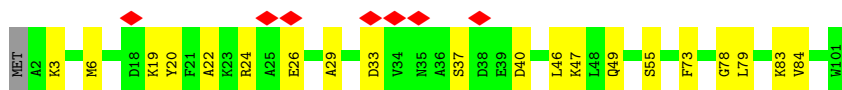


- Molecule 13: Small ribosomal subunit protein uS13

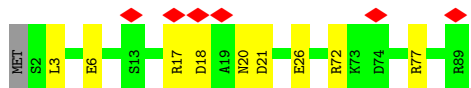
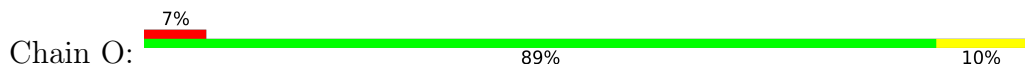


- Molecule 14: Small ribosomal subunit protein uS14

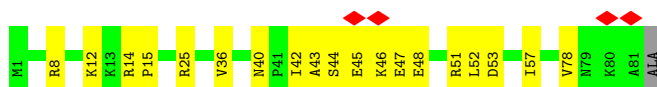




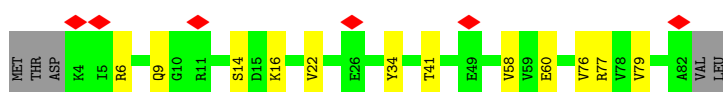
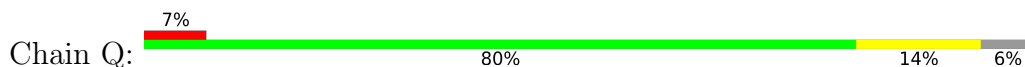
- Molecule 15: Small ribosomal subunit protein uS15



- Molecule 16: Small ribosomal subunit protein bS16



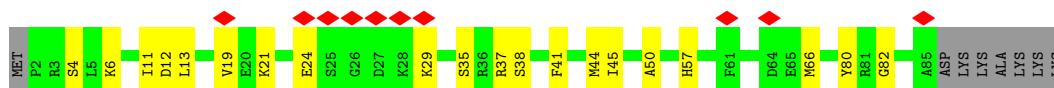
- Molecule 17: Small ribosomal subunit protein uS17



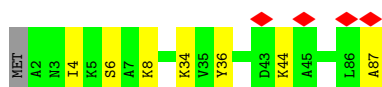
- Molecule 18: Small ribosomal subunit protein bS18



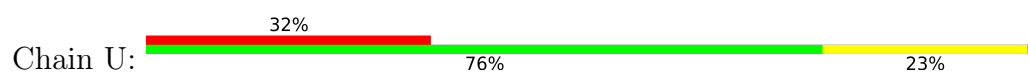
- Molecule 19: Small ribosomal subunit protein uS19



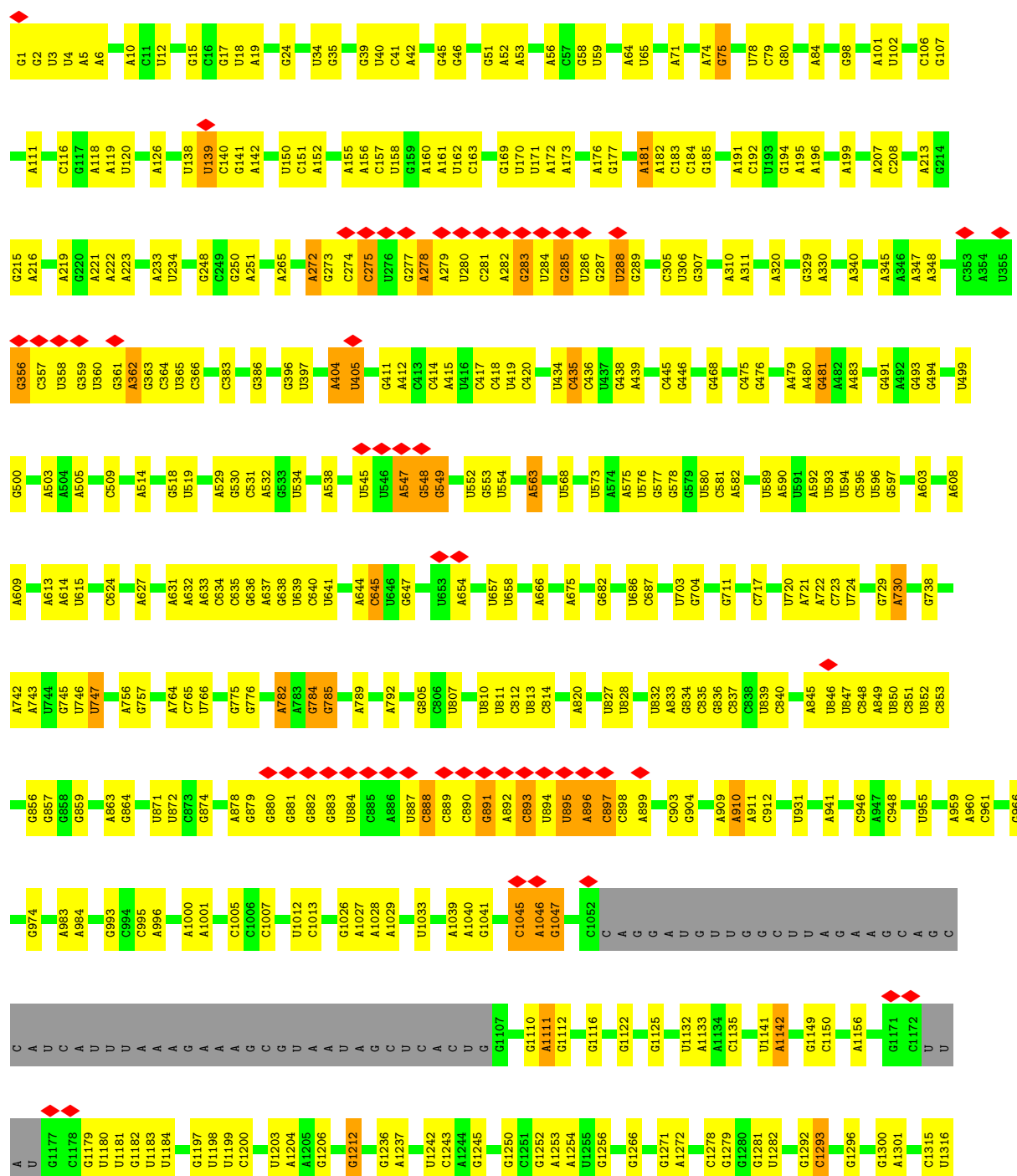
- Molecule 20: Small ribosomal subunit protein bS20



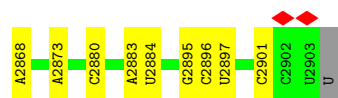
- Molecule 21: Small ribosomal subunit protein bS21



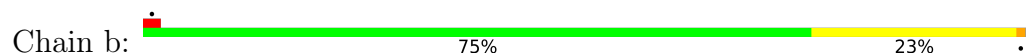
• Molecule 22: 23S rRNA



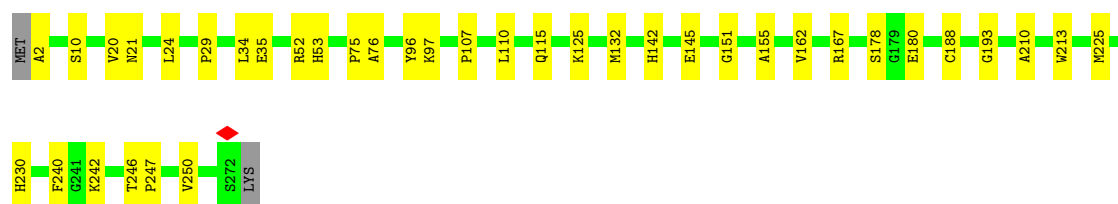
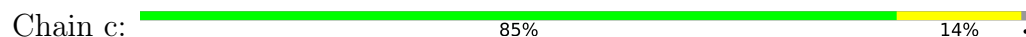
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G2626	C2626	G2502	U2384	A2288	C	G	G2024	C1874	A1773	A1618	A1528	G1432	C1320
G2627	G2627	A2503	C2385	U2291	C	A	U2026	G1875	C1774	A1618	G1529	A1433	A1434
G2630	G2630	U2504	C	U2292	C	U	G2027	A1889	U1782	G1622	C1531	G1436	U1329
A2635	A2635	G2505	U2392	G2293	C	A	A2030	A1890	A1786	A1626	A1532	U1340	U1340
G2636	G2636	U2514	C2394	G2294	U	G	A2031	C1902	A1786	A1626	G1533	G1341	G1341
U2637	U2637	C2515	G2395	A2298	U	U	G2032	C1905	C1790	U1636	U1534	A1342	A1342
G2638	G2638	A2516	G2396	U2299	A	G	A2033	G1906	A1791	A1637	A1535	G1343	G1343
C2646	C2646	U2518	U2402	C2301	A	G	G2038	U1911	U1794	C1646	C1536	U1442	U1442
U2647	U2647	U2522	C2403	U2302	U	A	U2039	A1912	C1795	U1647	U1537	U1443	C1349
G2648	G2648	U2529	A2406	U2305	G	G	C2043	A1913	U1796	G1648	G1538	G1444	C1350
U2650	U2650	G2532	G2410	G2308	U	U	A2052	C1914	U1797	G1649	U1539	G1445	U1351
A2657	A2657	U2532	U2187	U2312	U	U	C2055	U1915	U1798	A1654	G1540	C1447	C1447
G2661	G2661	U2537	U2188	C2313	U	U	G2056	A1916	G1799	G1667	C1541	G1448	A1354
G2663	G2663	U2537	U2189	U2316	U	U	U2060	U1917	C1800	A1677	A1548	G1469	G1355
U2680	U2680	A2547	U2190	A2317	G	G	A2061	G1929	A1801	G1674	G1547	U1460	G1361
C2681	C2681	U2548	G2193	U2322	A	A	G2062	U1930	A1802	A1678	A1549	A1470	C1362
U2687	U2687	U2552	U2194	G2325	U	U	U2065	U1931	A1803	U1683	U1554	G1473	C1363
G2688	G2688	G2553	A2198	G2326	G	G	A2069	A1932	G1807	G1684	C1569	U1484	G1370
U2689	U2689	U2554	G2204	A2327	C	C	A2070	U1933	A1808	C1685	A1570	U1485	A1383
G2690	G2690	U2555	G2208	U2328	C	U	C2071	U1934	A1809	C1686	A1571	A1494	U1394
U2698	U2698	G2557	U2229	U2329	C	C	C2072	U1935	G1824	C1704	C1575	A1495	U1395
C2699	C2699	C2558	U2233	U2230	C	A	U2074	C1962	A1829	A1705	U1576	A1496	U1396
U2700	U2700	A2566	G2234	U2231	U	U	U2075	C1967	C1830	G1710	C1577	C1498	U1405
G2709	G2709	U2568	G2238	U2232	C	C	U2086	G1968	G1831	A1711	A1566	U1406	U1406
G2714	G2714	C2573	G2239	U2240	C	G	G2087	A1969	G1835	G1715	A1569	U1411	U1411
C2716	C2716	U2580	U2241	U2344	A	A	A2093	U1970	C1842	U1720	A1570	U1412	U1412
U2723	U2723	C2591	U2242	G2345	U	U	A2095	G1971	C1843	G1721	A1571	A1413	A1413
U2724	U2724	G2592	U2243	A2346	G	G	C2096	U1980	A1847	U1725	C1575	G1416	G1416
A2725	A2725	U2602	U2244	G2347	A	A	U2098	A1981	A1848	C1728	U1578	C1417	C1417
G2726	G2726	U2603	U2245	U2350	C	C	U2099	U1982	A1853	U1729	A1583	A1427	A1427
U2728	U2728	U2604	G2246	G2351	C	C	G2100	G1983	A1854	C1730	C1585	C1428	C1428
G2729	G2729	U2605	U2247	U2352	C	U	A2101	U1983	G1857	G1731	A1586	G1524	G1524
U2732	U2732	U2608	G2251	C2364	A	A	G2102	C1987	A1858	U1736	G1587	A1525	A1525
A2733	A2733	U2609	U2266	G2365	C	C	C	C2000	G1862	G1737	A1590	C1500	C1500
U2740	U2740	U2613	A2267	U2373	U	U	U	G2012	U1864	G1738	A1591	G1515	G1515
A2741	A2741	U2614	U2273	C2374	G	G	A	A2013	A1744	A1745	A1591	G1519	G1519
G2744	G2744	U2615	U2274	A2377	A	A	U	A2014	U1746	U1747	A1597	G1524	G1524
U2747	U2747	G2618	G2279	U2378	U	U	G	A2015	G1869	C1760	A1598	A1526	A1526
G2795	G2795	U2796	C2283	C2380	A	A	U	A2020	A1871	A1872	C1600	C1600	C1600
U2796	U2796	U2797											
U2798	U2798	U2799											
A2800	A2800	U2804											
U2804	U2804	C2805											
C2805	C2805	U2809											
A2809	A2809	U2810											
G2810	G2810	G2811											
G2812	G2812	G2813											
U2818	U2818	C2819											
A2820	A2820	U2821											
C2830	C2830	U2835											
A2835	A2835	U2845											
U2845	U2845	G2846											
G2847	G2847	U2848											
U2849	U2849	C2858											
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U2860	U2860	G2861											
G2867	G2867												



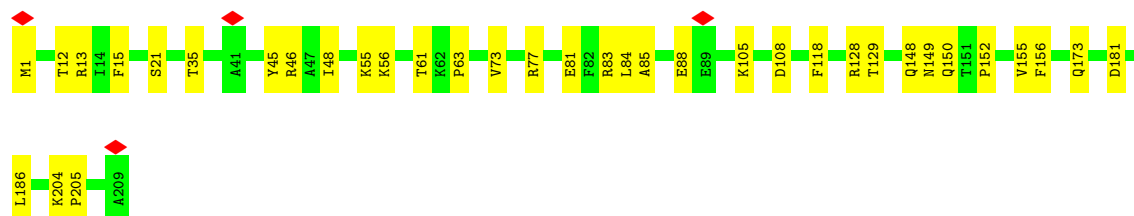
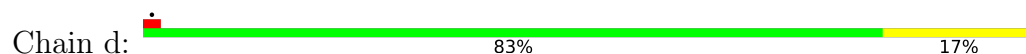
• Molecule 23: 5S rRNA



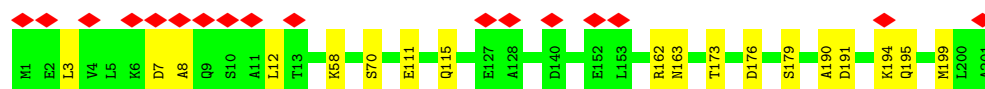
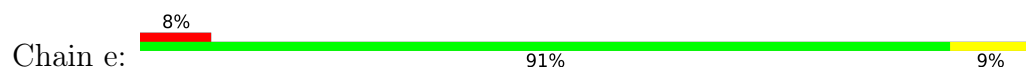
• Molecule 24: Large ribosomal subunit protein uL2



• Molecule 25: Large ribosomal subunit protein uL3

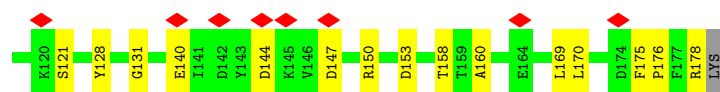


• Molecule 26: Large ribosomal subunit protein uL4

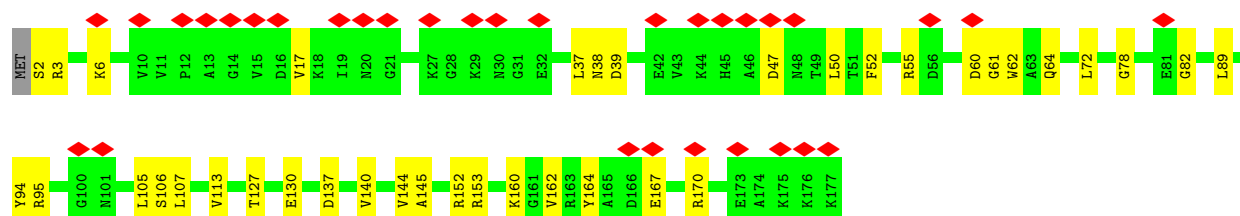
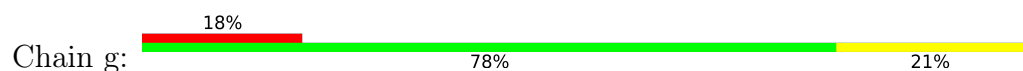


• Molecule 27: Large ribosomal subunit protein uL5

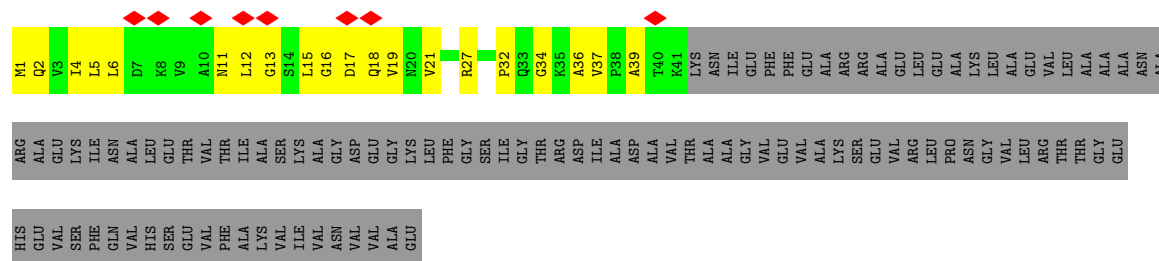




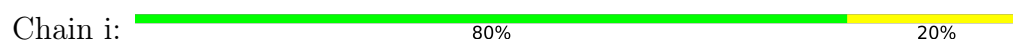
- Molecule 28: Large ribosomal subunit protein uL6



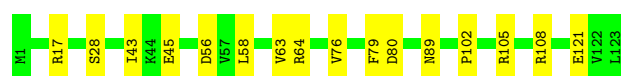
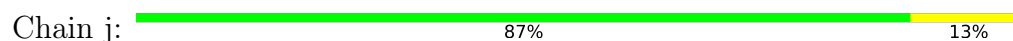
- Molecule 29: Large ribosomal subunit protein bL9



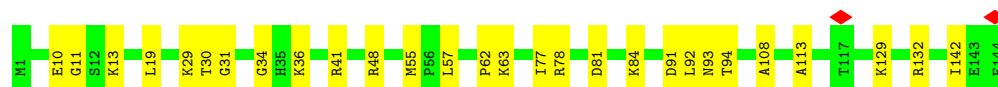
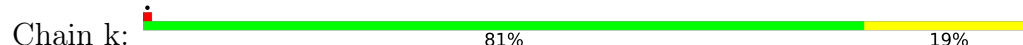
- Molecule 30: Large ribosomal subunit protein uL13



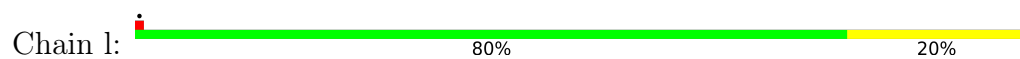
- Molecule 31: Large ribosomal subunit protein uL14



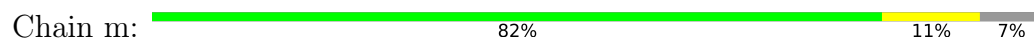
- Molecule 32: Large ribosomal subunit protein uL15



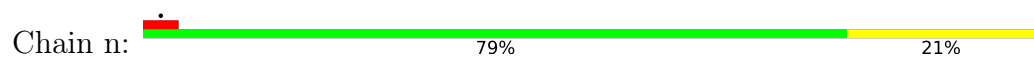
- Molecule 33: Large ribosomal subunit protein uL16



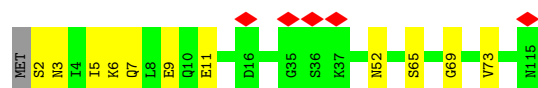
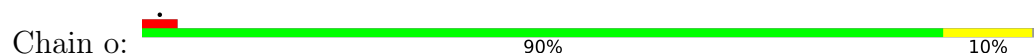
- Molecule 34: Large ribosomal subunit protein bL17



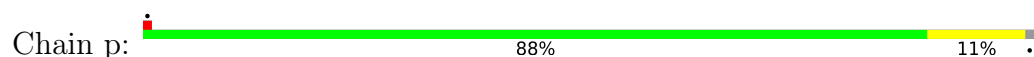
- Molecule 35: Large ribosomal subunit protein uL18



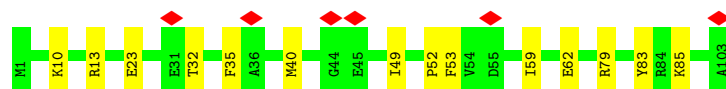
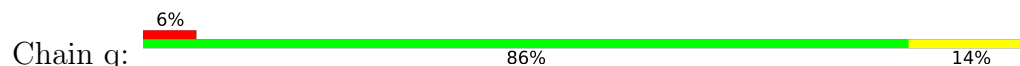
- Molecule 36: Large ribosomal subunit protein bL19



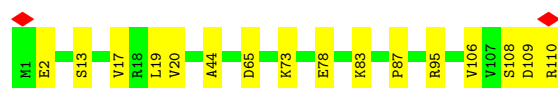
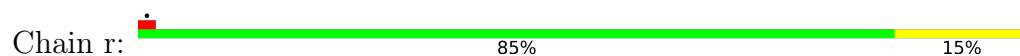
- Molecule 37: Large ribosomal subunit protein bL20



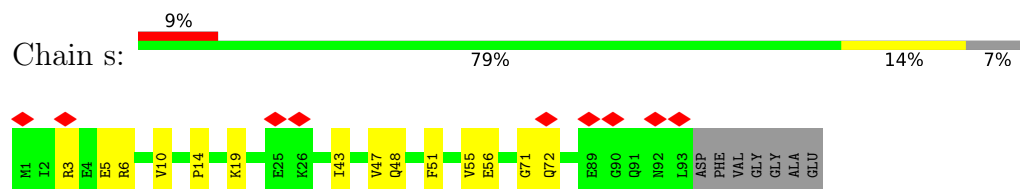
- Molecule 38: Large ribosomal subunit protein bL21



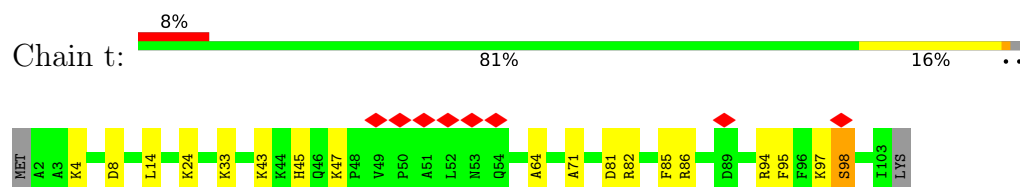
- Molecule 39: Large ribosomal subunit protein uL22



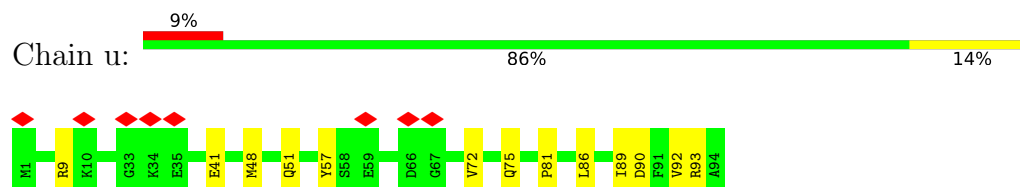
- Molecule 40: Large ribosomal subunit protein uL23



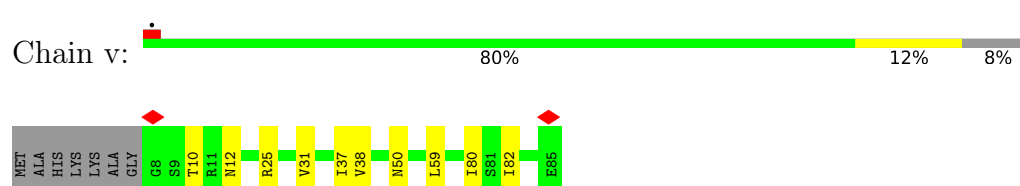
- Molecule 41: Large ribosomal subunit protein uL24



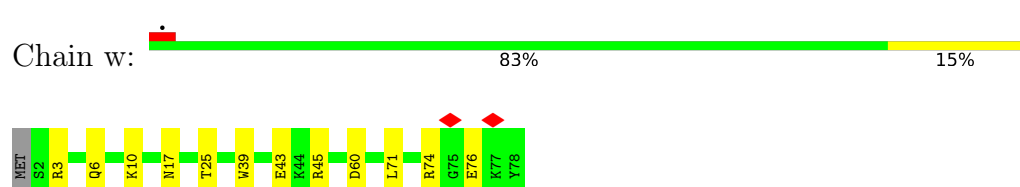
- Molecule 42: Large ribosomal subunit protein bL25



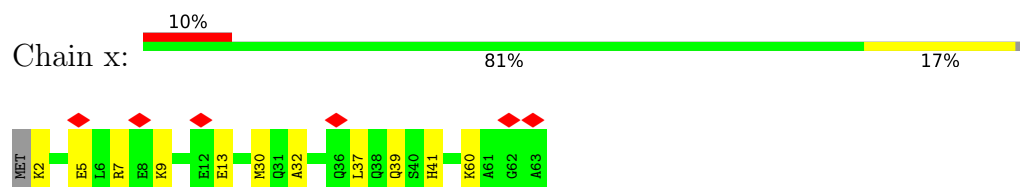
- Molecule 43: Large ribosomal subunit protein bL27



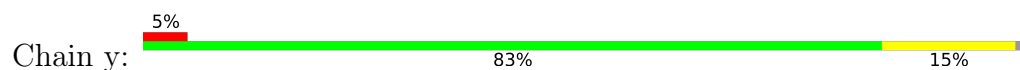
- Molecule 44: Large ribosomal subunit protein bL28



- Molecule 45: Large ribosomal subunit protein uL29

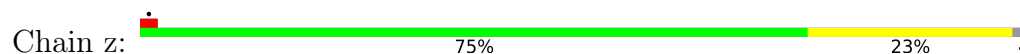


- Molecule 46: Large ribosomal subunit protein uL30





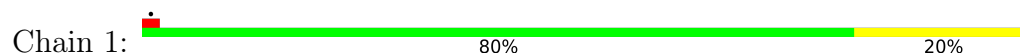
- Molecule 47: Large ribosomal subunit protein bL32



- Molecule 48: Large ribosomal subunit protein bL33



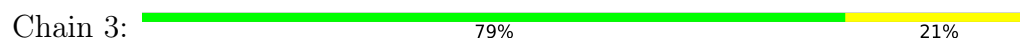
- Molecule 49: Large ribosomal subunit protein bL34



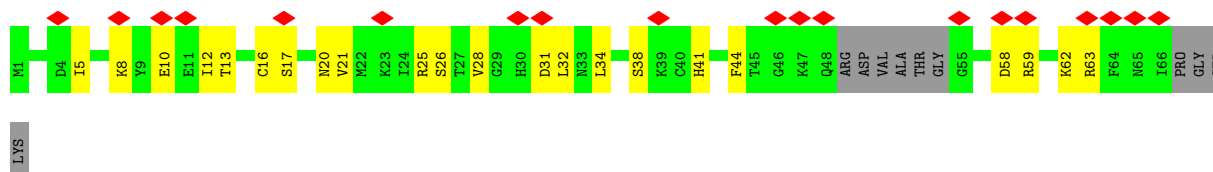
- Molecule 50: Large ribosomal subunit protein bL35



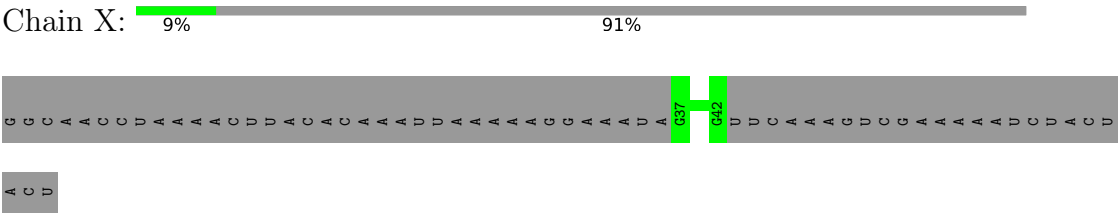
- Molecule 51: Large ribosomal subunit protein bL36A



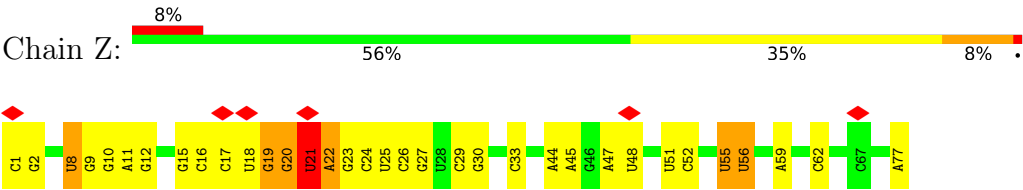
- Molecule 52: Large ribosomal subunit protein bL31



● Molecule 53: mRNA



● Molecule 54: P-site tRNA-fMet



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	244856	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.239	Depositor
Minimum map value	-0.122	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.024	Depositor
Map size ($\text{\AA}$)	439.9, 439.9, 439.9	wwPDB
Map dimensions	530, 530, 530	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.83, 0.83, 0.83	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 6MZ, D2T, IAS, OMG, 4OC, PSU, 4D4, 2MG, H2U, MG, 3TD, 5MU, UR3, MA6, 5MC, MS6, G7M, 4SU, 2MA, OMC, MEQ, OMU, 1MG

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	A	0.35	0/36073	0.30	0/56264
2	B	0.21	0/1784	0.32	0/2403
3	C	0.26	0/1651	0.36	0/2225
4	D	0.27	0/1665	0.37	0/2227
5	E	0.30	0/1165	0.37	0/1568
6	F	0.26	0/858	0.42	0/1160
7	G	0.22	0/1219	0.36	0/1635
8	H	0.31	0/989	0.38	0/1326
9	I	0.27	0/1034	0.42	0/1375
10	J	0.27	0/796	0.43	0/1077
11	K	0.27	0/884	0.35	0/1191
12	L	0.31	0/960	0.40	0/1286
13	M	0.27	0/900	0.45	0/1204
14	N	0.28	0/817	0.43	0/1088
15	O	0.29	0/722	0.38	0/964
16	P	0.31	0/653	0.39	0/877
17	Q	0.28	0/650	0.36	0/871
18	R	0.28	0/553	0.38	0/742
19	S	0.24	0/685	0.39	0/922
20	T	0.29	0/676	0.35	0/895
21	U	0.19	0/597	0.35	0/792
22	a	0.40	0/65842	0.31	0/102711
23	b	0.33	0/2850	0.27	0/4444
24	c	0.36	0/2121	0.39	0/2852
25	d	0.36	0/1576	0.35	0/2119
26	e	0.31	0/1571	0.35	0/2113
27	f	0.27	0/1434	0.36	0/1926
28	g	0.25	0/1343	0.42	0/1816
29	h	0.23	0/306	0.40	0/413
30	i	0.34	0/1152	0.35	0/1551
31	j	0.35	0/955	0.36	0/1279

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	k	0.34	0/1062	0.39	0/1413
33	l	0.34	0/1073	0.37	0/1433
34	m	0.37	0/958	0.42	0/1281
35	n	0.29	0/902	0.39	0/1209
36	o	0.34	0/929	0.34	0/1242
37	p	0.38	0/960	0.37	0/1278
38	q	0.35	0/829	0.38	0/1107
39	r	0.34	0/864	0.39	0/1156
40	s	0.30	0/744	0.45	0/994
41	t	0.28	0/787	0.49	2/1051 (0.2%)
42	u	0.29	0/766	0.36	0/1025
43	v	0.35	0/599	0.36	0/792
44	w	0.34	0/635	0.40	0/848
45	x	0.25	0/502	0.38	0/667
46	y	0.33	0/453	0.36	0/605
47	z	0.34	0/450	0.36	0/599
48	0	0.28	0/424	0.31	0/565
49	1	0.38	0/380	0.43	0/498
50	2	0.37	0/513	0.42	0/676
51	3	0.36	0/303	0.38	0/397
52	4	0.21	0/488	0.41	0/649
53	X	0.29	0/145	0.26	0/224
54	Z	0.28	0/1725	0.26	0/2687
All	All	0.36	0/150972	0.33	2/225712 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
13	M	0	1
50	2	0	1
All	All	0	2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	t	98	SER	CA-C-N	5.71	132.44	121.54
41	t	98	SER	C-N-CA	5.71	132.44	121.54

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
50	2	31	HIS	Peptide
13	M	104	THR	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32466	0	16359	351	0
2	B	1753	0	1780	19	0
3	C	1624	0	1696	19	0
4	D	1643	0	1707	36	0
5	E	1152	0	1196	17	0
6	F	839	0	833	24	0
7	G	1203	0	1254	22	0
8	H	979	0	1031	17	0
9	I	1022	0	1070	30	0
10	J	786	0	828	19	0
11	K	877	0	884	16	0
12	L	957	0	1017	17	0
13	M	891	0	952	31	0
14	N	805	0	844	12	0
15	O	714	0	734	7	0
16	P	643	0	661	11	0
17	Q	641	0	682	9	0
18	R	544	0	565	9	0
19	S	668	0	693	15	0
20	T	670	0	719	5	0
21	U	589	0	629	10	0
22	a	59301	0	29850	524	0
23	b	2549	0	1291	15	0
24	c	2082	0	2154	26	0
25	d	1566	0	1618	26	0
26	e	1552	0	1619	10	0
27	f	1410	0	1444	37	0
28	g	1323	0	1371	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	h	303	0	327	15	0
30	i	1129	0	1162	19	0
31	j	946	0	1023	11	0
32	k	1053	0	1129	21	0
33	l	1075	0	1145	16	0
34	m	945	0	989	9	0
35	n	892	0	923	14	0
36	o	917	0	962	8	0
37	p	947	0	1019	12	0
38	q	816	0	839	10	0
39	r	857	0	922	10	0
40	s	738	0	807	9	0
41	t	779	0	831	14	0
42	u	753	0	780	10	0
43	v	592	0	607	6	0
44	w	625	0	652	8	0
45	x	501	0	531	7	0
46	y	449	0	488	5	0
47	z	444	0	458	9	0
48	0	417	0	451	8	0
49	1	377	0	418	9	0
50	2	504	0	572	7	0
51	3	302	0	343	6	0
52	4	480	0	482	18	0
53	X	130	0	66	0	0
54	Z	1645	0	842	16	0
55	A	119	0	0	0	0
55	Z	1	0	0	0	0
55	a	328	0	0	0	0
55	b	6	0	0	0	0
55	c	1	0	0	0	0
55	d	1	0	0	0	0
55	z	1	0	0	0	0
All	All	140322	0	94249	1465	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 6.

The worst 5 of 1465 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:A:414:A:HO2'	1:A:415:A:H8	0.99	0.97
22:a:1047:G:HO2'	22:a:1110:G:H1	1.13	0.97
1:A:76:G:H1	1:A:93:U:H3	1.11	0.97
22:a:1870:C:HO2'	22:a:1871:A:H8	0.99	0.95
22:a:2100:G:H1	22:a:2189:U:H3	0.95	0.93

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	222/241 (92%)	211 (95%)	11 (5%)	0	100	100
3	C	204/233 (88%)	197 (97%)	7 (3%)	0	100	100
4	D	203/206 (98%)	199 (98%)	4 (2%)	0	100	100
5	E	154/167 (92%)	147 (96%)	7 (4%)	0	100	100
6	F	101/135 (75%)	95 (94%)	6 (6%)	0	100	100
7	G	151/179 (84%)	139 (92%)	12 (8%)	0	100	100
8	H	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
9	I	125/130 (96%)	120 (96%)	5 (4%)	0	100	100
10	J	96/103 (93%)	91 (95%)	4 (4%)	1 (1%)	12	28
11	K	113/129 (88%)	105 (93%)	8 (7%)	0	100	100
12	L	120/124 (97%)	111 (92%)	9 (8%)	0	100	100
13	M	113/118 (96%)	108 (96%)	5 (4%)	0	100	100
14	N	98/101 (97%)	94 (96%)	4 (4%)	0	100	100
15	O	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
16	P	79/82 (96%)	75 (95%)	4 (5%)	0	100	100
17	Q	77/84 (92%)	77 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	R	64/75 (85%)	60 (94%)	4 (6%)	0	100	100
19	S	82/92 (89%)	82 (100%)	0	0	100	100
20	T	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
21	U	68/71 (96%)	67 (98%)	1 (2%)	0	100	100
24	c	269/273 (98%)	261 (97%)	8 (3%)	0	100	100
25	d	206/209 (99%)	202 (98%)	3 (2%)	1 (0%)	24	46
26	e	199/201 (99%)	196 (98%)	3 (2%)	0	100	100
27	f	175/179 (98%)	166 (95%)	9 (5%)	0	100	100
28	g	174/177 (98%)	165 (95%)	9 (5%)	0	100	100
29	h	39/149 (26%)	35 (90%)	4 (10%)	0	100	100
30	i	140/142 (99%)	138 (99%)	2 (1%)	0	100	100
31	j	121/123 (98%)	118 (98%)	3 (2%)	0	100	100
32	k	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
33	l	132/136 (97%)	131 (99%)	1 (1%)	0	100	100
34	m	116/127 (91%)	111 (96%)	5 (4%)	0	100	100
35	n	114/117 (97%)	109 (96%)	5 (4%)	0	100	100
36	o	112/115 (97%)	108 (96%)	4 (4%)	0	100	100
37	p	115/118 (98%)	115 (100%)	0	0	100	100
38	q	101/103 (98%)	95 (94%)	6 (6%)	0	100	100
39	r	108/110 (98%)	108 (100%)	0	0	100	100
40	s	91/100 (91%)	87 (96%)	4 (4%)	0	100	100
41	t	100/104 (96%)	91 (91%)	9 (9%)	0	100	100
42	u	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
43	v	76/85 (89%)	73 (96%)	3 (4%)	0	100	100
44	w	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
45	x	60/63 (95%)	56 (93%)	4 (7%)	0	100	100
46	y	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
47	z	54/57 (95%)	54 (100%)	0	0	100	100
48	0	49/55 (89%)	49 (100%)	0	0	100	100
49	1	44/46 (96%)	44 (100%)	0	0	100	100
50	2	62/65 (95%)	59 (95%)	2 (3%)	1 (2%)	7	16

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	3	36/38 (95%)	36 (100%)	0	0	100	100
52	4	56/70 (80%)	53 (95%)	3 (5%)	0	100	100
All	All	5481/5913 (93%)	5281 (96%)	197 (4%)	3 (0%)	49	70

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
25	d	149	ASN
10	J	57	VAL
50	2	32	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	186/199 (94%)	186 (100%)	0	100	100
3	C	170/190 (90%)	170 (100%)	0	100	100
4	D	172/173 (99%)	172 (100%)	0	100	100
5	E	119/126 (94%)	119 (100%)	0	100	100
6	F	90/116 (78%)	90 (100%)	0	100	100
7	G	126/147 (86%)	126 (100%)	0	100	100
8	H	104/105 (99%)	104 (100%)	0	100	100
9	I	105/107 (98%)	105 (100%)	0	100	100
10	J	86/90 (96%)	86 (100%)	0	100	100
11	K	89/98 (91%)	89 (100%)	0	100	100
12	L	102/103 (99%)	102 (100%)	0	100	100
13	M	93/96 (97%)	93 (100%)	0	100	100
14	N	83/84 (99%)	83 (100%)	0	100	100
15	O	76/77 (99%)	76 (100%)	0	100	100
16	P	65/65 (100%)	65 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	Q	73/78 (94%)	73 (100%)	0	100	100
18	R	57/65 (88%)	57 (100%)	0	100	100
19	S	72/79 (91%)	72 (100%)	0	100	100
20	T	65/66 (98%)	65 (100%)	0	100	100
21	U	60/61 (98%)	60 (100%)	0	100	100
24	c	216/218 (99%)	216 (100%)	0	100	100
25	d	163/163 (100%)	163 (100%)	0	100	100
26	e	165/165 (100%)	165 (100%)	0	100	100
27	f	148/150 (99%)	148 (100%)	0	100	100
28	g	137/138 (99%)	137 (100%)	0	100	100
29	h	32/114 (28%)	32 (100%)	0	100	100
30	i	116/116 (100%)	115 (99%)	1 (1%)	70	87
31	j	104/104 (100%)	104 (100%)	0	100	100
32	k	103/103 (100%)	103 (100%)	0	100	100
33	l	107/107 (100%)	107 (100%)	0	100	100
34	m	98/103 (95%)	98 (100%)	0	100	100
35	n	86/87 (99%)	86 (100%)	0	100	100
36	o	99/100 (99%)	99 (100%)	0	100	100
37	p	89/90 (99%)	89 (100%)	0	100	100
38	q	84/84 (100%)	84 (100%)	0	100	100
39	r	93/93 (100%)	93 (100%)	0	100	100
40	s	80/84 (95%)	80 (100%)	0	100	100
41	t	83/85 (98%)	83 (100%)	0	100	100
42	u	78/78 (100%)	78 (100%)	0	100	100
43	v	59/63 (94%)	59 (100%)	0	100	100
44	w	67/68 (98%)	67 (100%)	0	100	100
45	x	54/55 (98%)	54 (100%)	0	100	100
46	y	48/49 (98%)	48 (100%)	0	100	100
47	z	47/48 (98%)	47 (100%)	0	100	100
48	0	46/49 (94%)	46 (100%)	0	100	100
49	1	38/38 (100%)	38 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
50	2	51/52 (98%)	51 (100%)	0	100	100
51	3	34/34 (100%)	34 (100%)	0	100	100
52	4	55/62 (89%)	55 (100%)	0	100	100
All	All	4573/4825 (95%)	4572 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	i	128	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 46 such sidechains are listed below:

Mol	Chain	Res	Type
28	g	73	ASN
36	o	66	ASN
28	g	88	GLN
33	l	13	HIS
40	s	70	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1508/1542 (97%)	201 (13%)	6 (0%)
22	a	2757/2904 (94%)	301 (10%)	0
23	b	118/120 (98%)	13 (11%)	0
53	X	5/66 (7%)	0	0
54	Z	76/77 (98%)	10 (13%)	0
All	All	4464/4709 (94%)	525 (11%)	6 (0%)

5 of 525 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	2	A
1	A	3	A
1	A	4	U
1	A	7	A
1	A	9	G

5 of 6 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	636	U
1	A	1030	U
1	A	1035	A
1	A	517	G
1	A	429	U

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

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$
22	2MA	a	2503	55,22	22,25,26	3.70	9 (40%)	33,37,40	2.81	8 (24%)
22	6MZ	a	2030	22	22,25,26	2.67	4 (18%)	30,36,39	2.46	12 (40%)
33	4D4	l	81	33	9,11,12	1.51	2 (22%)	8,13,15	2.04	3 (37%)
22	OMG	a	2251	22,54	23,26,27	2.53	10 (43%)	33,38,41	1.93	9 (27%)
22	PSU	a	2580	22	18,21,22	1.11	3 (16%)	22,30,33	2.09	6 (27%)
22	OMC	a	2498	55,22	19,22,23	2.75	8 (42%)	26,31,34	0.86	0
22	5MU	a	747	22	19,22,23	4.54	7 (36%)	28,32,35	3.79	10 (35%)
1	MA6	A	1518	1	23,26,27	1.41	5 (21%)	34,38,41	2.26	12 (35%)
22	PSU	a	2605	22	18,21,22	1.02	2 (11%)	22,30,33	1.89	3 (13%)
22	PSU	a	2504	22	18,21,22	1.04	1 (5%)	22,30,33	1.82	4 (18%)
22	OMU	a	2552	22	19,22,23	2.69	6 (31%)	26,31,34	1.82	5 (19%)
22	6MZ	a	1618	22	22,25,26	2.69	4 (18%)	30,36,39	2.40	11 (36%)
1	4OC	A	1402	1,55	20,23,24	2.93	8 (40%)	26,32,35	1.01	2 (7%)
1	MA6	A	1519	1	23,26,27	1.38	4 (17%)	34,38,41	2.32	12 (35%)
54	4SU	Z	8	54	18,21,22	4.10	8 (44%)	26,30,33	2.27	4 (15%)
22	G7M	a	2069	55,22	23,26,27	2.72	8 (34%)	35,39,42	1.73	9 (25%)
22	PSU	a	746	55,22	18,21,22	1.07	2 (11%)	22,30,33	1.71	3 (13%)
22	PSU	a	1911	22	18,21,22	1.02	1 (5%)	22,30,33	1.84	3 (13%)
54	H2U	Z	21	54	18,21,22	1.05	2 (11%)	21,30,33	0.74	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
12	D2T	L	89	12	7,9,10	1.40	0	6,11,13	2.06	3 (50%)
1	5MC	A	967	1	18,22,23	3.68	8 (44%)	26,32,35	1.02	1 (3%)
22	3TD	a	1915	22	18,22,23	4.06	6 (33%)	22,32,35	1.74	3 (13%)
22	5MC	a	1962	22	18,22,23	3.54	7 (38%)	26,32,35	1.09	2 (7%)
1	2MG	A	1516	1	23,26,27	2.52	7 (30%)	32,38,41	2.17	11 (34%)
54	5MU	Z	55	54	19,22,23	4.64	6 (31%)	28,32,35	3.67	9 (32%)
33	MS6	l	82	33	5,7,8	1.17	1 (20%)	2,7,9	2.05	1 (50%)
22	5MU	a	1939	22	19,22,23	4.51	7 (36%)	28,32,35	3.82	10 (35%)
22	PSU	a	2457	22	18,21,22	1.08	2 (11%)	22,30,33	2.02	6 (27%)
54	PSU	Z	56	54	18,21,22	1.06	1 (5%)	22,30,33	1.86	5 (22%)
22	PSU	a	1917	22	18,21,22	1.01	1 (5%)	22,30,33	1.86	5 (22%)
1	2MG	A	966	1	23,26,27	2.61	7 (30%)	32,38,41	2.21	9 (28%)
22	PSU	a	2604	22	18,21,22	1.03	1 (5%)	22,30,33	1.86	4 (18%)
22	2MG	a	2445	22	23,26,27	2.53	7 (30%)	32,38,41	2.24	10 (31%)
1	PSU	A	516	1,55	18,21,22	1.03	1 (5%)	22,30,33	1.68	5 (22%)
11	IAS	K	119	11	6,7,8	1.02	0	6,8,10	1.26	1 (16%)
1	UR3	A	1498	1	19,22,23	2.60	7 (36%)	26,32,35	1.33	1 (3%)
1	G7M	A	527	1	23,26,27	2.76	8 (34%)	35,39,42	1.72	9 (25%)
54	OMC	Z	33	54	19,22,23	2.84	8 (42%)	26,31,34	0.75	0
25	MEQ	d	150	25	8,9,10	1.10	0	5,10,12	1.50	2 (40%)
22	1MG	a	745	22	22,26,27	2.57	7 (31%)	33,39,42	1.78	8 (24%)
22	2MG	a	1835	22	23,26,27	2.54	7 (30%)	32,38,41	2.25	10 (31%)
22	PSU	a	955	22	18,21,22	1.08	2 (11%)	22,30,33	1.92	5 (22%)
22	H2U	a	2449	22	18,21,22	1.29	3 (16%)	21,30,33	1.03	1 (4%)
1	5MC	A	1407	1	18,22,23	3.54	8 (44%)	26,32,35	1.02	2 (7%)
1	2MG	A	1207	1	23,26,27	2.57	8 (34%)	32,38,41	2.14	10 (31%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
22	2MA	a	2503	55,22	-	1/7/25/26	0/3/3/3
22	6MZ	a	2030	22	-	2/9/27/28	0/3/3/3
33	4D4	l	81	33	-	3/11/12/14	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
22	OMG	a	2251	22,54	-	1/9/27/28	0/3/3/3
22	PSU	a	2580	22	-	0/7/25/26	0/2/2/2
22	OMC	a	2498	55,22	-	0/9/27/28	0/2/2/2
22	5MU	a	747	22	-	0/7/25/26	0/2/2/2
1	MA6	A	1518	1	-	0/11/29/30	0/3/3/3
22	PSU	a	2605	22	-	0/7/25/26	0/2/2/2
22	PSU	a	2504	22	-	2/7/25/26	0/2/2/2
22	OMU	a	2552	22	-	1/9/27/28	0/2/2/2
22	6MZ	a	1618	22	-	0/9/27/28	0/3/3/3
1	4OC	A	1402	1,55	-	1/9/29/30	0/2/2/2
1	MA6	A	1519	1	-	2/11/29/30	0/3/3/3
54	4SU	Z	8	54	-	0/7/25/26	0/2/2/2
22	G7M	a	2069	55,22	-	1/7/25/26	0/3/3/3
22	PSU	a	746	55,22	-	1/7/25/26	0/2/2/2
22	PSU	a	1911	22	-	0/7/25/26	0/2/2/2
54	H2U	Z	21	54	-	7/7/38/39	0/2/2/2
12	D2T	L	89	12	-	3/7/12/14	-
1	5MC	A	967	1	-	0/7/25/26	0/2/2/2
22	3TD	a	1915	22	-	2/7/25/26	0/2/2/2
22	5MC	a	1962	22	-	0/7/25/26	0/2/2/2
1	2MG	A	1516	1	-	0/9/27/28	0/3/3/3
54	5MU	Z	55	54	-	2/7/25/26	0/2/2/2
33	MS6	l	82	33	-	1/4/6/8	-
22	5MU	a	1939	22	-	0/7/25/26	0/2/2/2
22	PSU	a	2457	22	-	0/7/25/26	0/2/2/2
54	PSU	Z	56	54	-	0/7/25/26	0/2/2/2
22	PSU	a	1917	22	-	0/7/25/26	0/2/2/2
1	2MG	A	966	1	-	2/9/27/28	0/3/3/3
22	PSU	a	2604	22	-	0/7/25/26	0/2/2/2
22	2MG	a	2445	22	-	2/9/27/28	0/3/3/3
1	PSU	A	516	1,55	-	2/7/25/26	0/2/2/2
11	IAS	K	119	11	-	0/7/7/8	-
1	UR3	A	1498	1	-	0/7/25/26	0/2/2/2
1	G7M	A	527	1	-	3/7/25/26	0/3/3/3
54	OMC	Z	33	54	-	0/9/27/28	0/2/2/2
25	MEQ	d	150	25	-	2/8/9/11	-
22	1MG	a	745	22	-	0/7/25/26	0/3/3/3
22	2MG	a	1835	22	-	0/9/27/28	0/3/3/3
22	PSU	a	955	22	-	0/7/25/26	0/2/2/2
22	H2U	a	2449	22	-	0/7/38/39	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	5MC	A	1407	1	-	0/7/25/26	0/2/2/2
1	2MG	A	1207	1	-	0/9/27/28	0/3/3/3

The worst 5 of 214 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	a	1915	3TD	C6-C5	12.17	1.49	1.35
22	a	2503	2MA	C4-N3	11.28	1.48	1.34
22	a	1618	6MZ	C6-N6	11.19	1.46	1.34
22	a	2030	6MZ	C6-N6	10.98	1.46	1.34
54	Z	55	5MU	C6-N1	10.58	1.56	1.38

The worst 5 of 249 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	a	747	5MU	C5-C4-N3	12.47	125.95	115.31
22	a	1939	5MU	C5-C4-N3	12.46	125.95	115.31
54	Z	55	5MU	C5-C4-N3	12.28	125.79	115.31
22	a	1939	5MU	C5-C6-N1	-10.87	112.16	123.34
22	a	747	5MU	C5-C6-N1	-10.71	112.33	123.34

There are no chirality outliers.

5 of 41 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	966	2MG	O4'-C4'-C5'-O5'
1	A	966	2MG	C3'-C4'-C5'-O5'
54	Z	21	H2U	O4'-C4'-C5'-O5'
54	Z	21	H2U	C3'-C4'-C5'-O5'
54	Z	21	H2U	O4'-C1'-N1-C6

There are no ring outliers.

10 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
22	a	2030	6MZ	2	0
1	A	1519	MA6	1	0
54	Z	21	H2U	1	0
22	a	1915	3TD	1	0
1	A	1516	2MG	1	0
54	Z	55	5MU	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
22	a	1939	5MU	1	0
54	Z	56	PSU	1	0
1	A	966	2MG	1	0
1	A	1207	2MG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 457 ligands modelled in this entry, 457 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

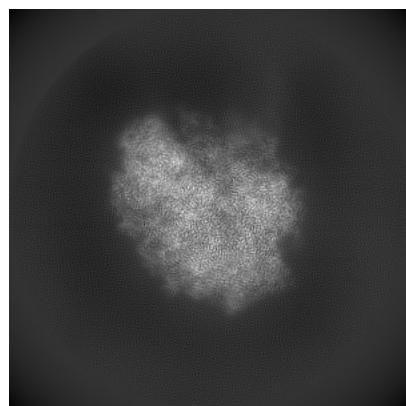
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-60059. These allow visual inspection of the internal detail of the map and identification of artifacts.

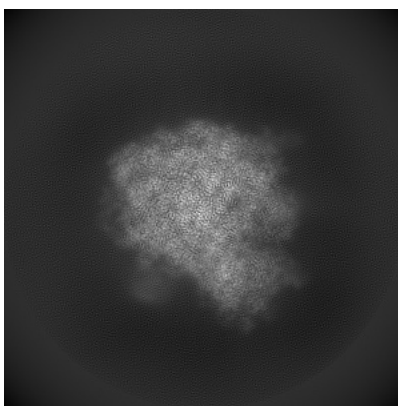
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

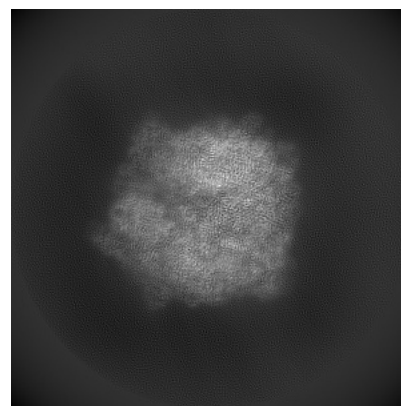
6.1.1 Primary map



X

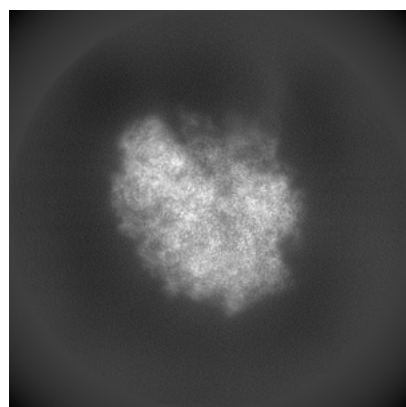


Y

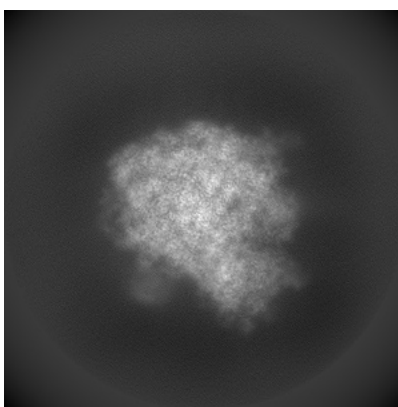


Z

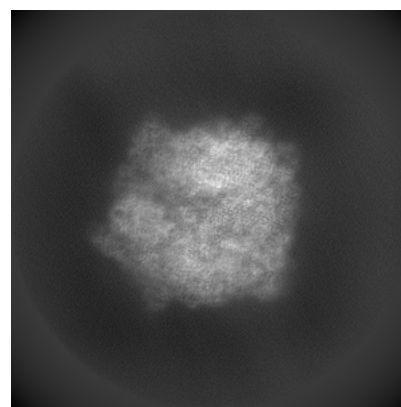
6.1.2 Raw map



X



Y

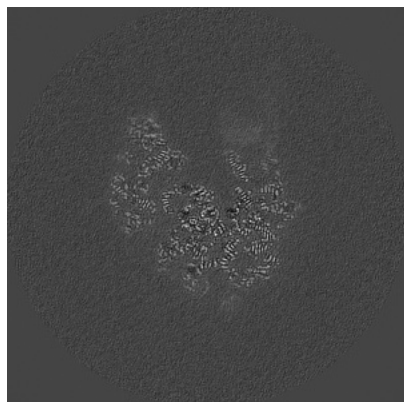


Z

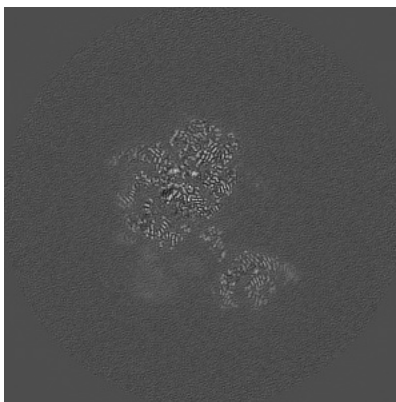
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

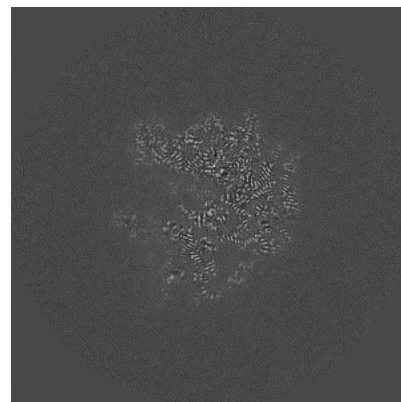
6.2.1 Primary map



X Index: 265

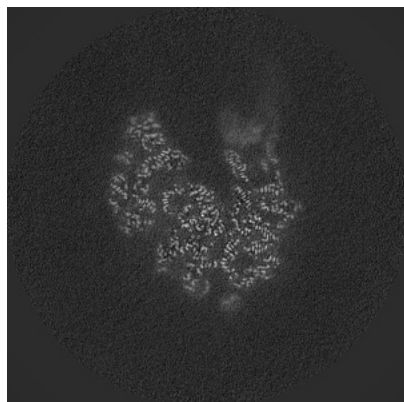


Y Index: 265

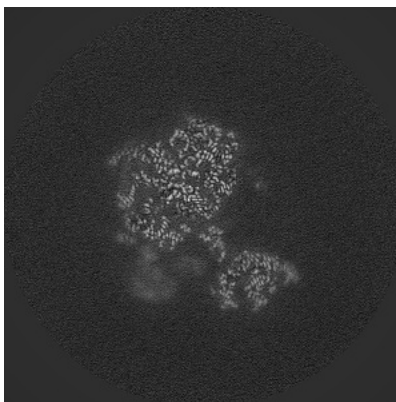


Z Index: 265

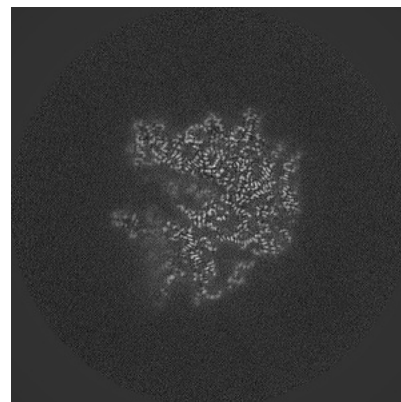
6.2.2 Raw map



X Index: 265



Y Index: 265

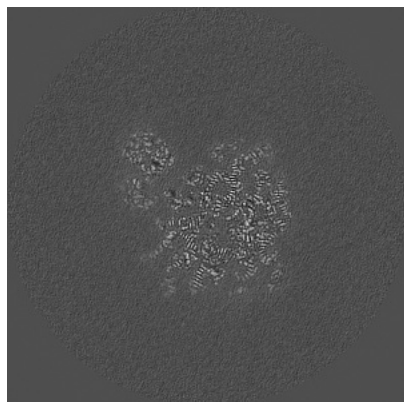


Z Index: 265

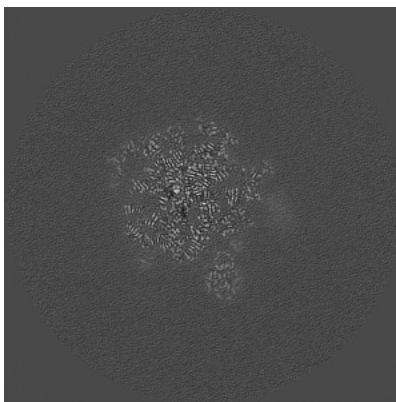
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

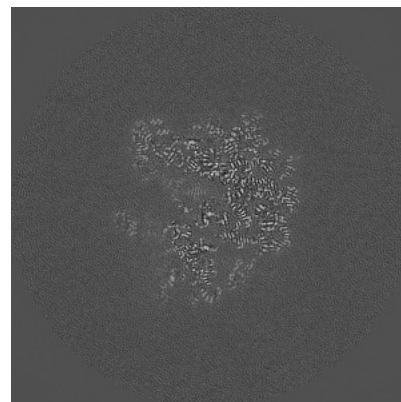
6.3.1 Primary map



X Index: 298

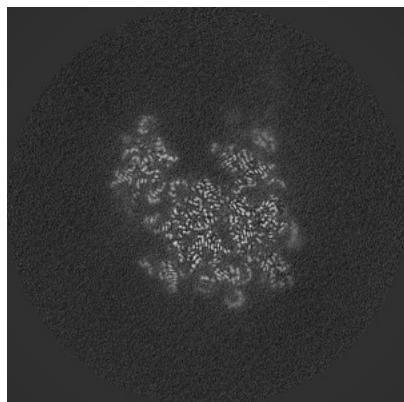


Y Index: 319

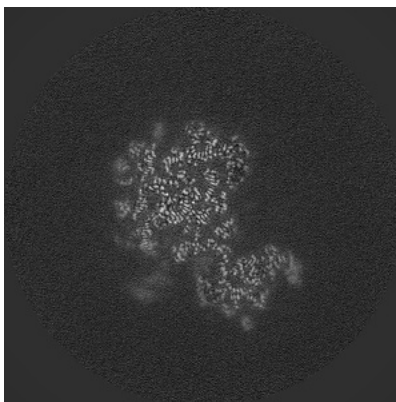


Z Index: 269

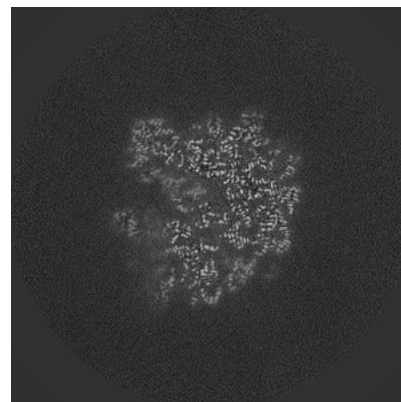
6.3.2 Raw map



X Index: 285



Y Index: 244

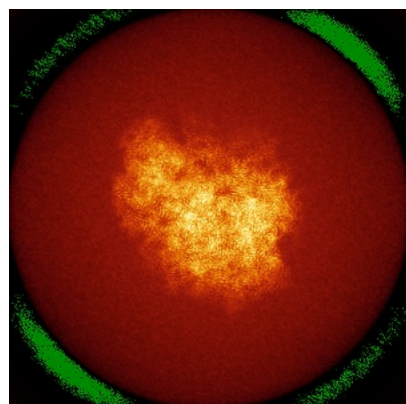


Z Index: 270

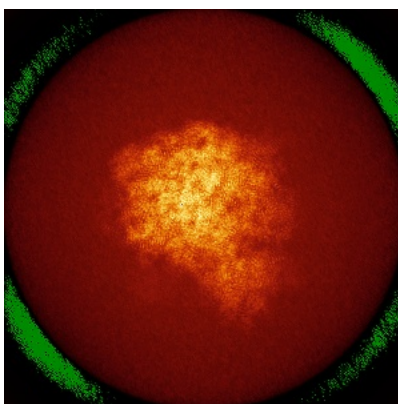
The images above show the largest variance slices of the map in three orthogonal directions.

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

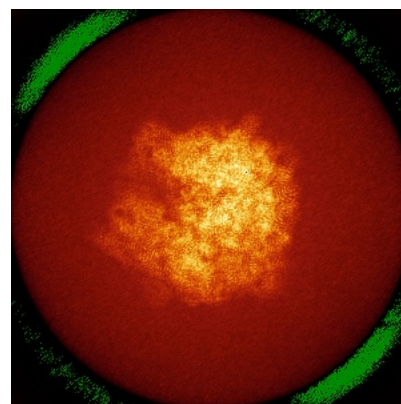
6.4.1 Primary map



X

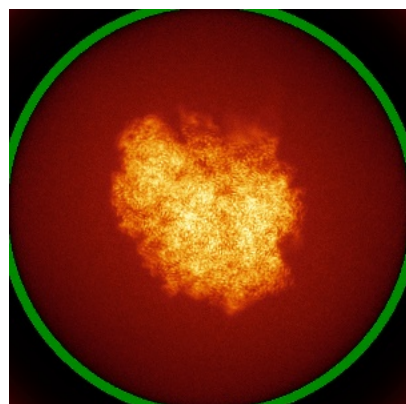


Y

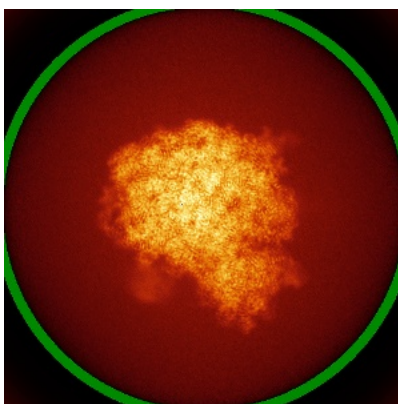


Z

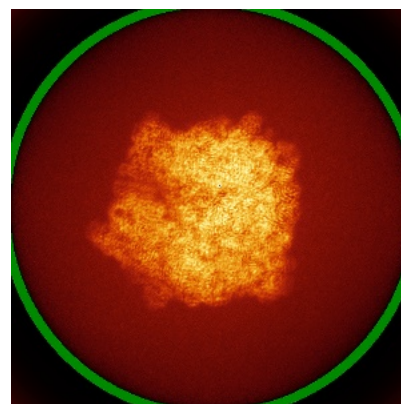
6.4.2 Raw map



X



Y

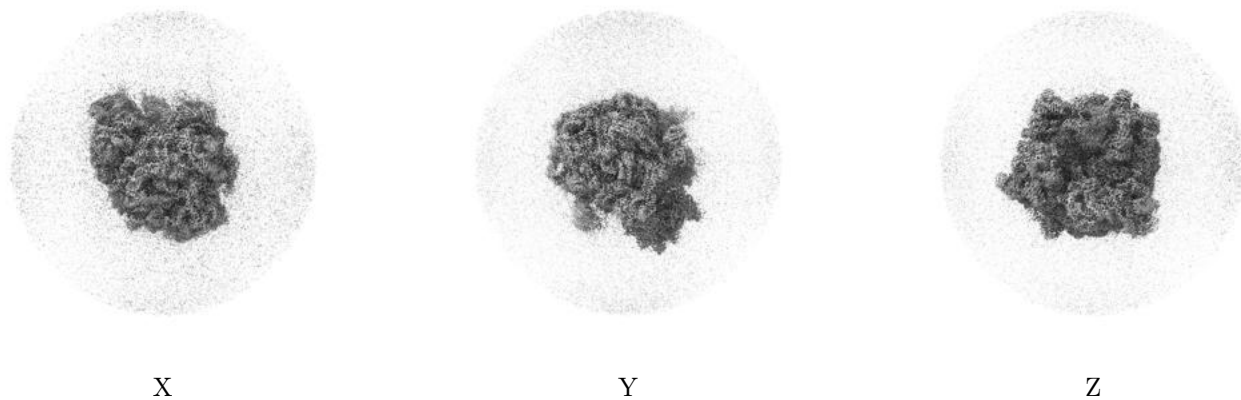


Z

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.

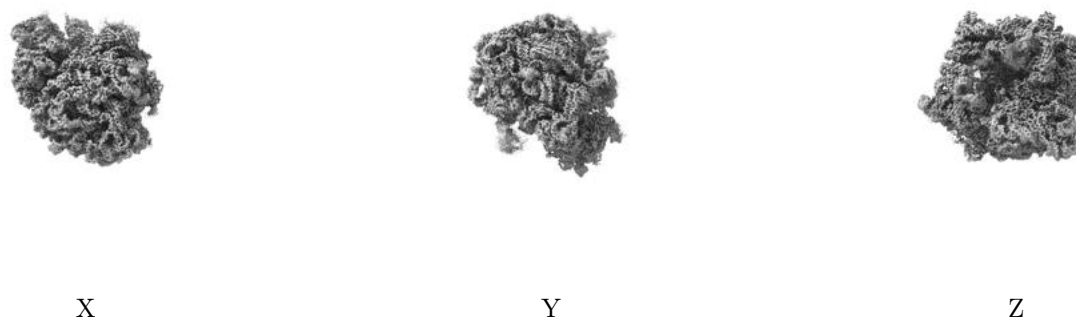
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.024. 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.

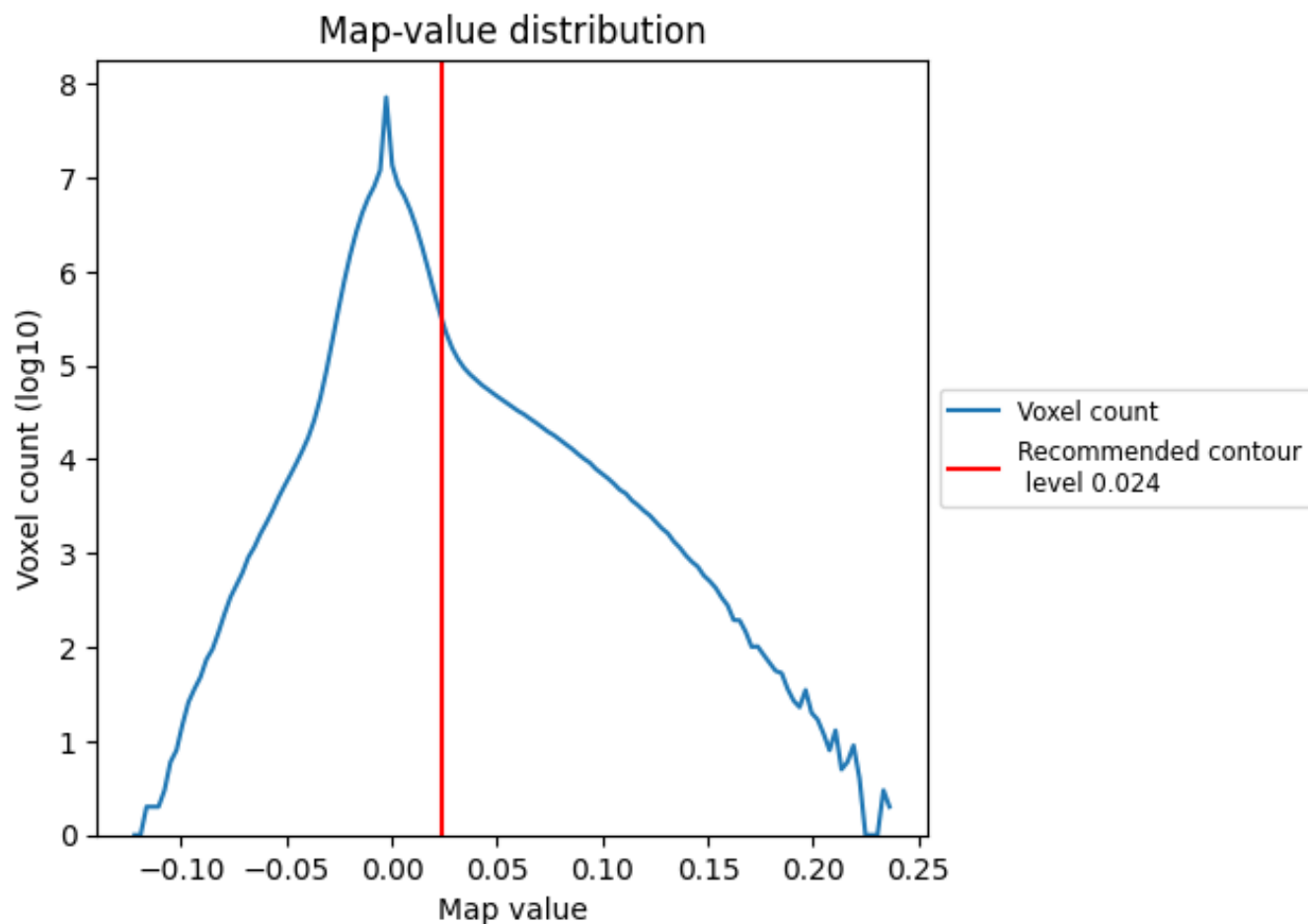
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

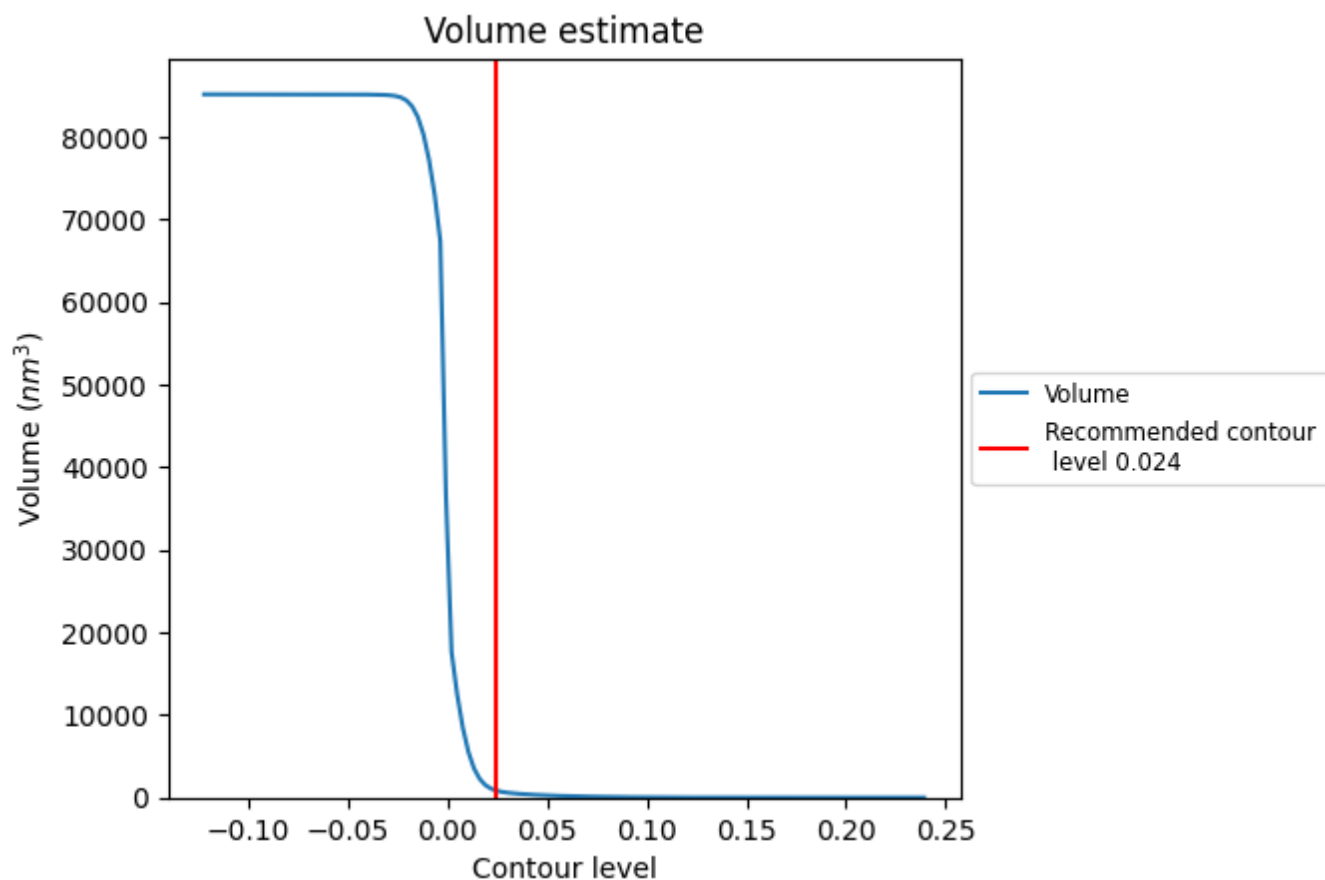
This section contains the results of statistical analysis of the map.

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.

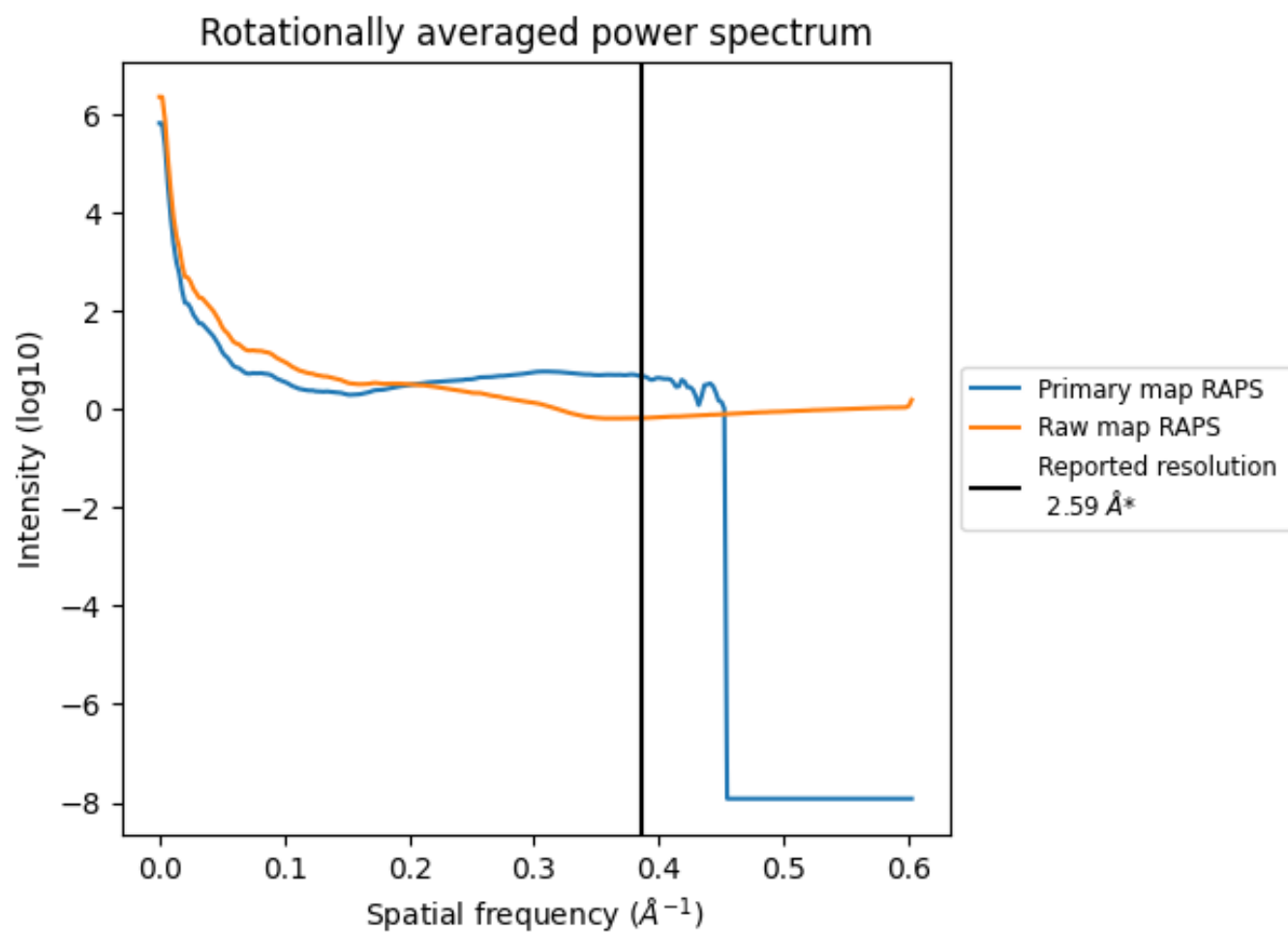
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 892 nm^3 ; this corresponds to an approximate mass of 806 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 ⓘ

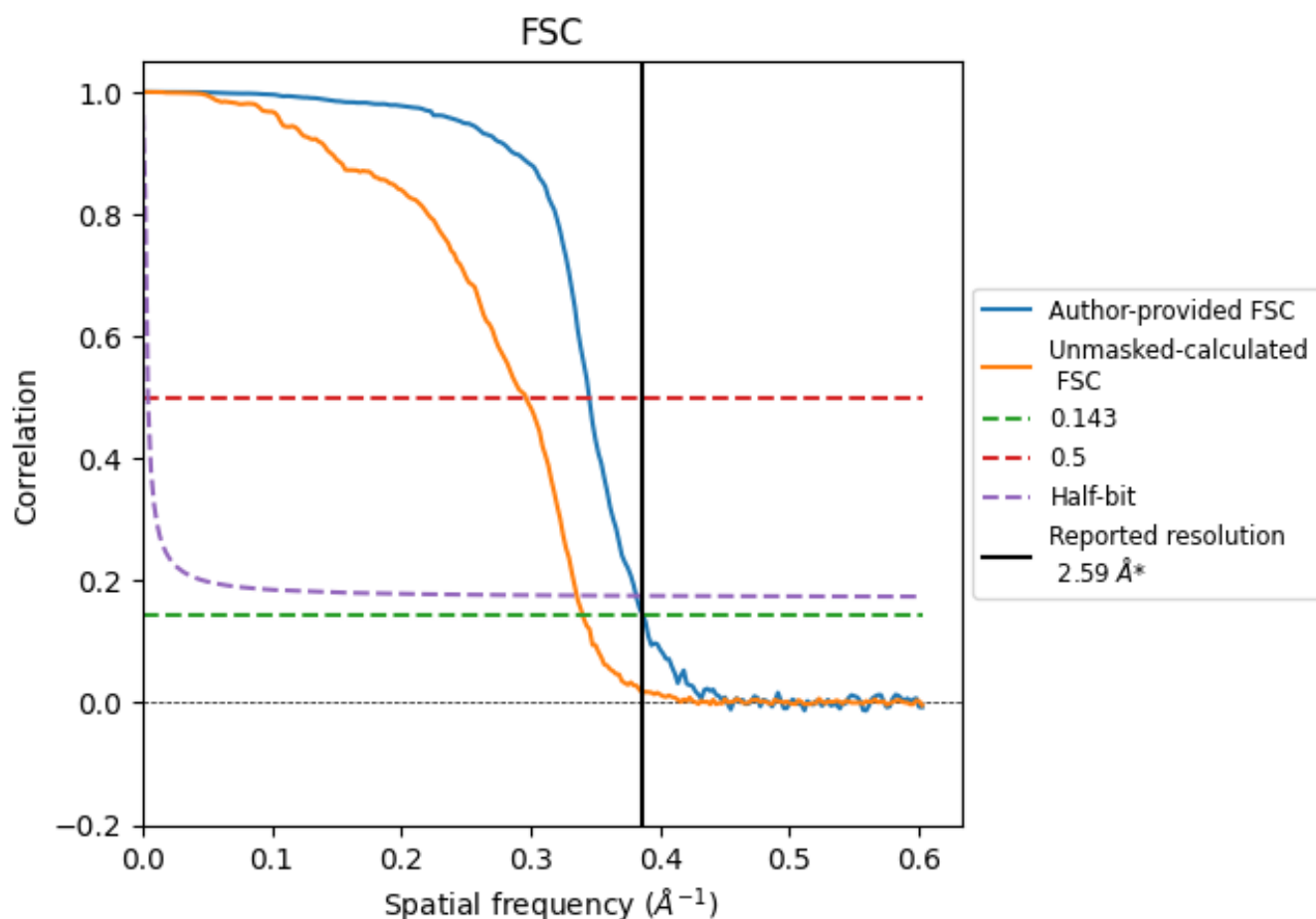


*Reported resolution corresponds to spatial frequency of 0.386 $\text{\AA}^{-1}$

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 0.386 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

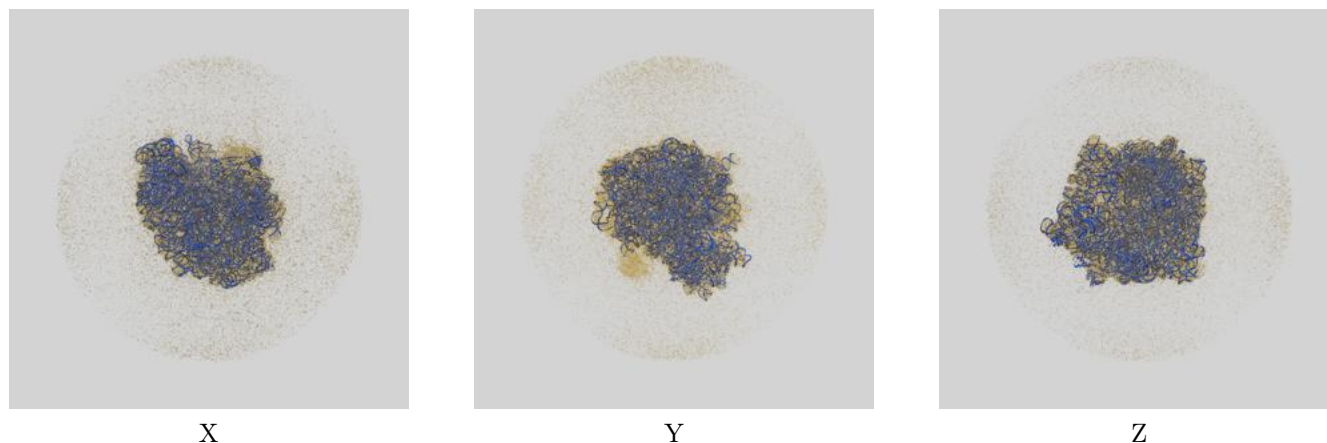
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.59	-	-
Author-provided FSC curve	2.59	2.90	2.62
Unmasked-calculated*	2.94	3.37	2.98

*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 2.94 differs from the reported value 2.59 by more than 10 %

9 Map-model fit [i](#)

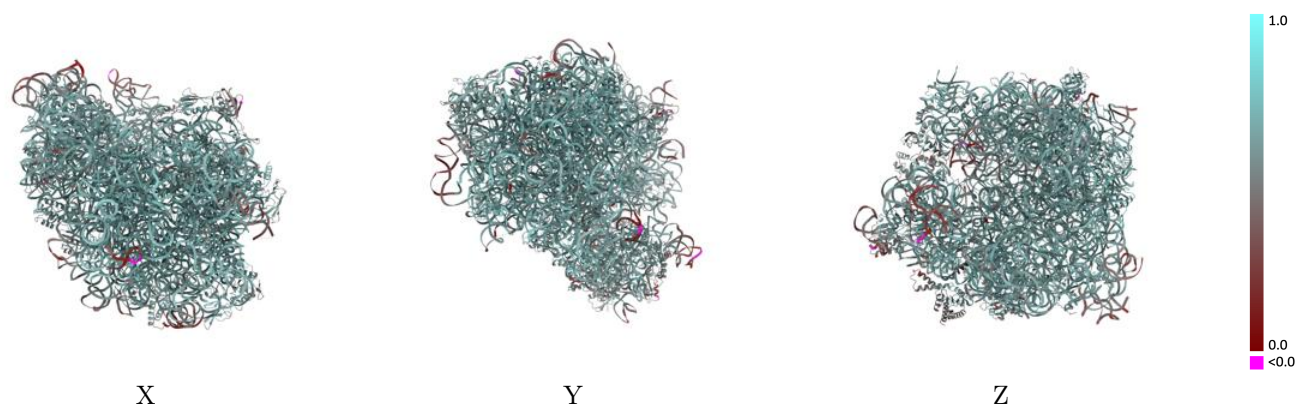
This section contains information regarding the fit between EMDB map EMD-60059 and PDB model 8ZFF. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



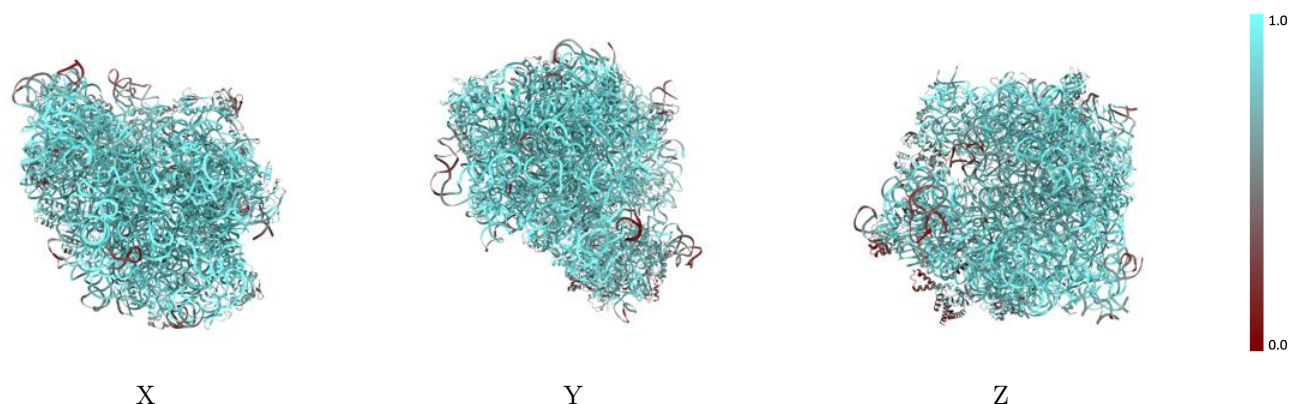
The images above show the 3D surface view of the map at the recommended contour level 0.024 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



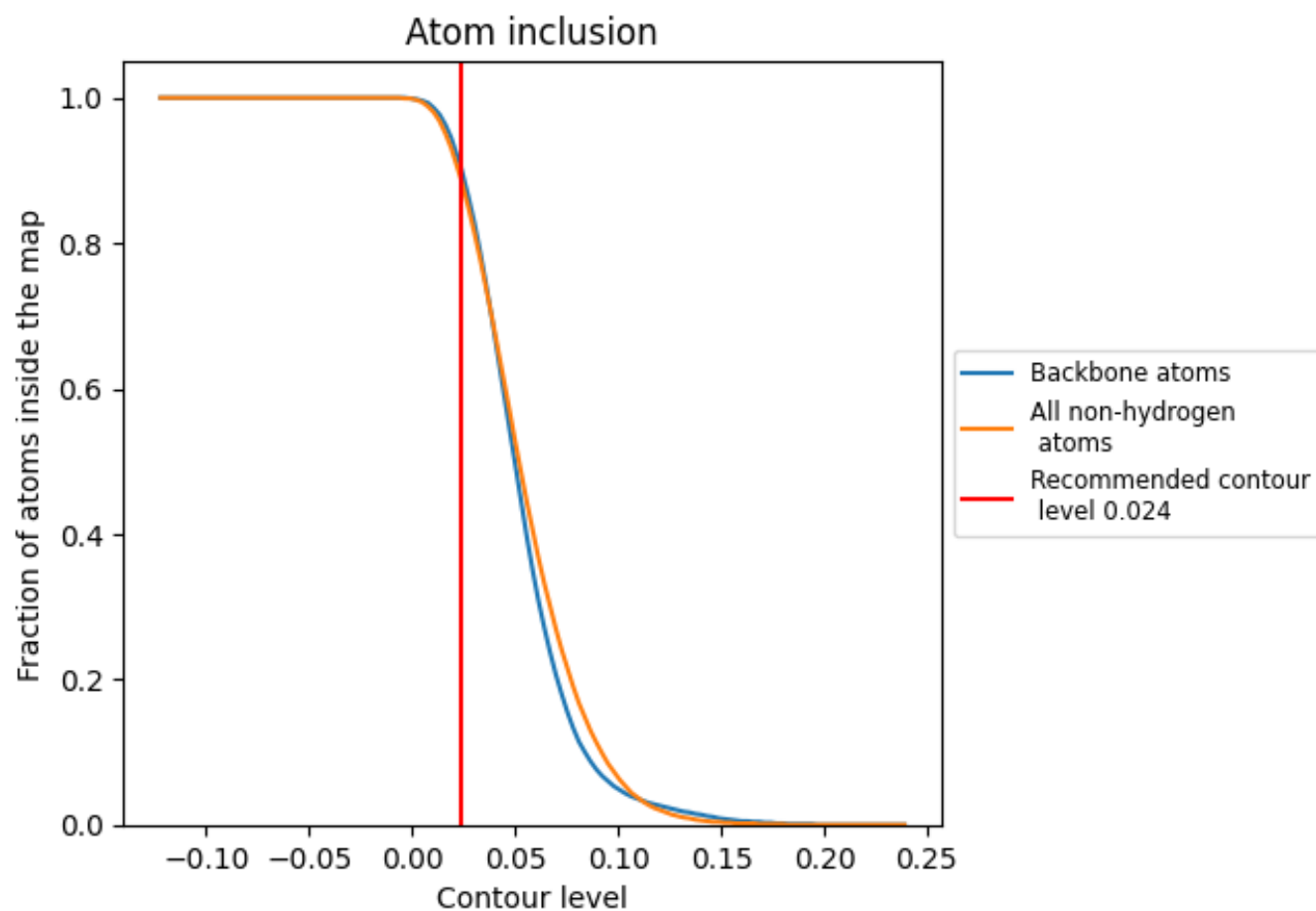
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.024).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 89% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.024) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8860	 0.6220
0	 0.8510	 0.6340
1	 0.9610	 0.6730
2	 0.9550	 0.6740
3	 0.9250	 0.6440
4	 0.5500	 0.5030
A	 0.9030	 0.6210
B	 0.4960	 0.4960
C	 0.7730	 0.6030
D	 0.7530	 0.5780
E	 0.8720	 0.6420
F	 0.7160	 0.5480
G	 0.6400	 0.5330
H	 0.8810	 0.6420
I	 0.7500	 0.5660
J	 0.5810	 0.4960
K	 0.8070	 0.5880
L	 0.8750	 0.6240
M	 0.7440	 0.5640
N	 0.8140	 0.6060
O	 0.8360	 0.6150
P	 0.8650	 0.6070
Q	 0.8030	 0.5880
R	 0.7670	 0.5740
S	 0.7270	 0.5600
T	 0.8570	 0.6080
U	 0.5190	 0.4790
X	 0.7390	 0.5210
Z	 0.7720	 0.5410
a	 0.9330	 0.6390
b	 0.9080	 0.6140
c	 0.9640	 0.6810
d	 0.9170	 0.6600
e	 0.8070	 0.6060
f	 0.7360	 0.5660



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Chain	Atom inclusion	Q-score
g	 0.6550	 0.5210
h	 0.6830	 0.4990
i	 0.9260	 0.6570
j	 0.9160	 0.6570
k	 0.8950	 0.6410
l	 0.9220	 0.6580
m	 0.9640	 0.6730
n	 0.8600	 0.6170
o	 0.9020	 0.6570
p	 0.9540	 0.6700
q	 0.8410	 0.6110
r	 0.8930	 0.6340
s	 0.8260	 0.5920
t	 0.7450	 0.5630
u	 0.7980	 0.6070
v	 0.9220	 0.6640
w	 0.8980	 0.6440
x	 0.7180	 0.5310
y	 0.8900	 0.6250
z	 0.8810	 0.6400