



wwPDB EM Validation Summary Report ⓘ

Jun 26, 2026 – 02:00 AM EDT

PDB ID : 7UVW / pdb_00007uvw
EMDB ID : EMD-26818
Title : A. baumannii ribosome: 70S with E-site tRNA
Authors : Morgan, C.E.; Yu, E.W.
Deposited on : 2022-05-02
Resolution : 2.37 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:

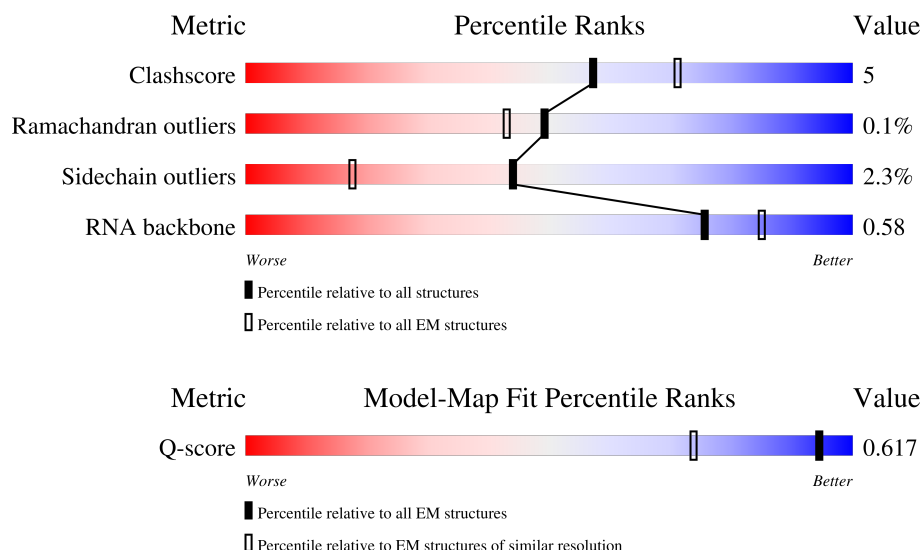
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.37 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	4742 (1.87 - 2.87)

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	51	
2	1	44	
3	2	64	

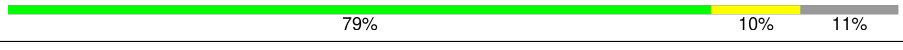
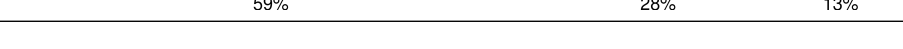
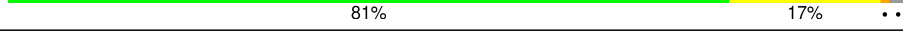
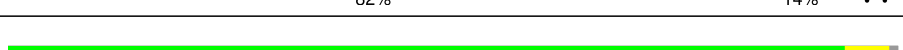
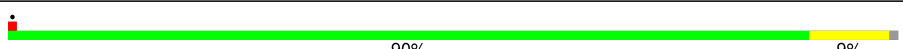
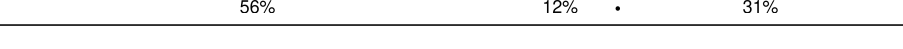
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Mol	Chain	Length	Quality of chain
4	3	38	
5	A	2918	
6	B	115	
7	C	274	
8	D	212	
9	E	200	
10	F	178	
11	G	177	
12	H	148	
13	I	142	
14	J	122	
15	K	146	
16	L	137	
17	M	125	
18	N	116	
19	O	122	
20	P	119	
21	Q	103	
22	R	109	
23	S	106	
24	T	105	
25	U	98	
26	V	85	
27	W	78	
28	X	65	

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Mol	Chain	Length	Quality of chain
29	Y	58	
30	Z	61	
31	a	1544	
32	b	250	
33	c	250	
34	d	208	
35	e	165	
36	f	127	
37	g	156	
38	h	131	
39	i	128	
40	j	103	
41	k	128	
42	l	124	
43	m	118	
44	n	101	
45	o	89	
46	p	101	
47	q	85	
48	r	75	
49	s	91	
50	t	88	
51	u	71	
52	v	77	
53	w	3	

2 Entry composition

There are 54 unique types of molecules in this entry. The entry contains 138233 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	51	Total	C	N	O	S	0	0
			427	274	77	73	3		

- Molecule 2 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	44	Total	C	N	O	S	0	0
			363	222	85	54	2		

- Molecule 3 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	63	Total	C	N	O	S	0	0
			509	319	110	76	4		

- Molecule 4 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	38	Total	C	N	O	S	0	0
			295	179	64	48	4		

- Molecule 5 is a RNA chain called 23s ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A	2719	Total	C	N	O	P	0	0
			58332	26037	10679	18897	2719		

- Molecule 6 is a RNA chain called 5s ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B	115	Total	C	N	O	P	0	0
			2450	1095	440	800	115		

- Molecule 7 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C	272	Total	C	N	O	S	0	0
			2111	1302	436	365	8		

- Molecule 8 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D	211	Total	C	N	O	S	0	0
			1572	972	297	300	3		

- Molecule 9 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	E	200	Total	C	N	O	S	0	0
			1516	952	281	278	5		

- Molecule 10 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	174	Total	C	N	O	S	0	0
			1370	871	243	248	8		

- Molecule 11 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	G	174	Total	C	N	O	S	0	0
			1318	832	236	249	1		

- Molecule 12 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	H	60	Total	C	N	O	S	0	0
			458	287	84	86	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	I	142	Total	C	N	O	S	0	0
			1125	718	200	203	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	J	122	Total	C	N	O	S	0	0
			946	592	180	169	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	K	144	Total	C	N	O		0	0
			1071	663	213	195			

- Molecule 16 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L	137	Total	C	N	O	S	0	0
			1087	687	210	185	5		

- Molecule 17 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	M	119	Total	C	N	O	S	0	0
			942	590	186	163	3		

- Molecule 18 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	N	116	Total	C	N	O	S	0	0
			873	537	176	158	2		

- Molecule 19 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	O	117	Total	C	N	O		0	0
			919	578	177	164			

- Molecule 20 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	P	117	Total	C	N	O	S	0	0
			934	589	197	146	2		

- Molecule 21 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Q	103	Total	C	N	O	S	0	0
			807	506	155	143	3		

- Molecule 22 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	R	109	Total	C	N	O	S	0	0
			826	514	158	150	4		

- Molecule 23 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	91	Total	C	N	O	S	0	0
			710	452	128	129	1		

- Molecule 24 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	T	103	Total	C	N	O		0	0
			766	476	142	148			

- Molecule 25 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	U	97	Total	C	N	O	S	0	0
			760	477	143	139	1		

- Molecule 26 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	V	76	Total	C	N	O	S	0	0
			577	358	111	106	2		

- Molecule 27 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	W	77	Total	C	N	O	S	0	0
			632	395	130	105	2		

- Molecule 28 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	X	60	Total	C	N	O	S	0	0
			486	302	93	90	1		

- Molecule 29 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y	57	Total	C	N	O	S	0	0
			455	281	87	84	3		

- Molecule 30 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Z	54	Total	C	N	O	S	0	0
			447	265	100	81	1		

- Molecule 31 is a RNA chain called 16s Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	a	1528	Total	C	N	O	P	0	0
			32782	14631	5994	10630	1527		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	1007	U	C	conflict	GB 1211343212
a	1034	C	U	conflict	GB 1211343212

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	b	225	Total	C	N	O	S	0	0
			1769	1110	328	325	6		

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	c	215	Total	C	N	O	S	0	0
			1690	1065	318	299	8		

- Molecule 34 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d	207	Total	C	N	O	S	0	0
			1631	1017	313	299	2		

- Molecule 35 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	155	Total	C	N	O	S	0	0
			1129	700	217	207	5		

- Molecule 36 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	f	104	Total	C	N	O	S	0	0
			867	546	158	159	4		

- Molecule 37 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g	136	Total	C	N	O	S	0	0
			1073	671	201	194	7		

- Molecule 38 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	130	Total	C	N	O	S	0	0
			985	615	177	187	6		

- Molecule 39 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	126	Total	C	N	O	S	0	0
			991	618	197	175	1		

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	100	Total	C	N	O	S	0	0
			801	500	150	148	3		

- Molecule 41 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k	117	Total	C	N	O	S	0	0
			862	535	167	159	1		

- Molecule 42 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	l	122	Total	C	N	O	S	0	0
			945	580	193	167	5		

- Molecule 43 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	m	115	Total	C	N	O	S	0	0
			903	558	184	158	3		

- Molecule 44 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	n	100	Total	C	N	O	S	0	0
			792	493	158	137	4		

- Molecule 45 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o	88	Total	C	N	O	S	0	0
			705	434	144	126	1		

- Molecule 46 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	p	82	Total	C	N	O	S	0	0
			644	403	128	112	1		

- Molecule 47 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	q	79	Total	C	N	O	S	0	0
			621	390	116	114	1		

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	r	52	Total	C	N	O	0	0
			426	273	74	79		

- Molecule 49 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	s	82	Total	C	N	O	S	0	0
			646	412	125	107	2		

- Molecule 50 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	t	86	Total	C	N	O	S	0	0
			663	409	139	113	2		

- Molecule 51 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	u	63	Total	C	N	O	S	0	0
			522	327	105	89	1		

- Molecule 52 is a RNA chain called tRNA-met.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	v	77	Total	C	N	O	P	S	0	0
			1636	733	291	535	76	1		

- Molecule 53 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	w	3	Total	C	N	O	P	0	0
			65	29	12	21	3		

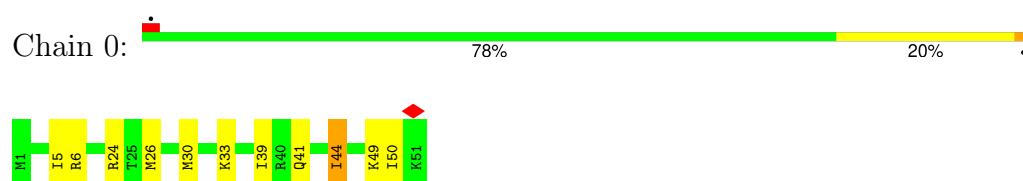
- Molecule 54 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
54	3	1	Total	Zn	0
			1	1	

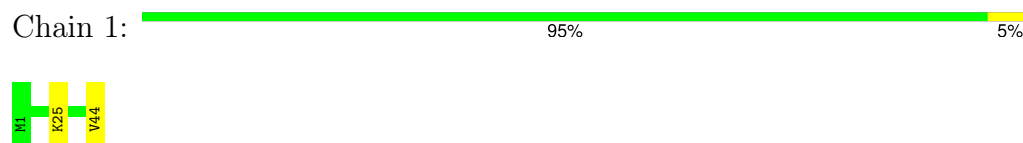
3 Residue-property plots [i](#)

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

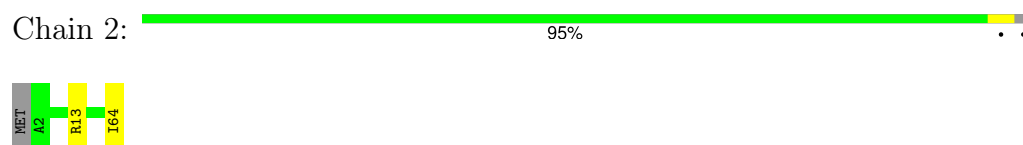
- Molecule 1: 50S ribosomal protein L33



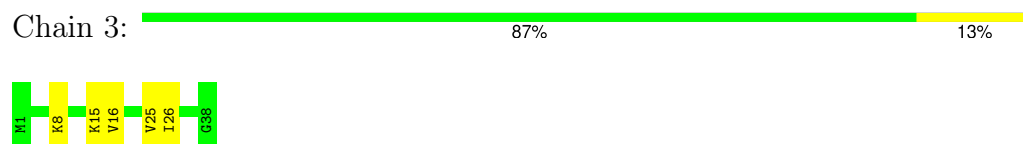
- Molecule 2: 50S ribosomal protein L34



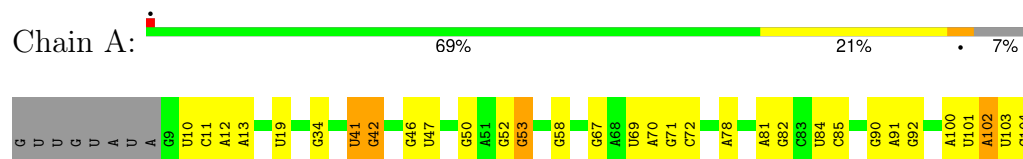
- Molecule 3: 50S ribosomal protein L35



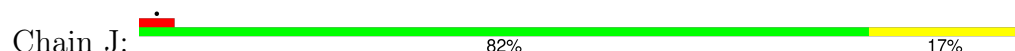
- Molecule 4: 50S ribosomal protein L36

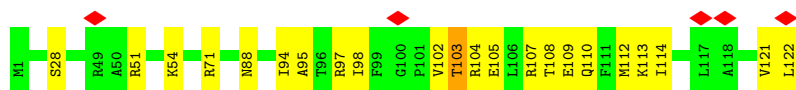


- Molecule 5: 23s ribosomal RNA

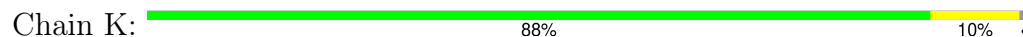


G1960	G1807	C1642	G1525	A1414	A1242	U	G1023	G	G727	U591	G410	U278	G117
C1963	C1812	U1645	C1526	U1415	G1245	A	A1024	G	A728	U592	C416	U279	A118
U1966	A1825	U1646	U1527	G1416	G1246	C	A1025	U	G740	C593	U418	A280	U119
G1968	U1967	G1647	G1528	C1422	A1248	U	A1026	C	U741	C417	C419	A281	G120
U1987	A1844	U1657	U1529	C1423	G1251	A	U1030	U	U745	U596	U284	A125	A125
U1989	G1845	U1672	C1531	A1428	G1261	C	G1033	C	G758	A597	A285	U127	U127
G2008	A1854	G1675	U1532	A1429	G1266	U	A1043	C	A759	A601	U286	A138	A138
A2017	G1865	U1680	U1533	C1432	A1267	U	G1044	A	A762	U605	G291	U141	U141
U2018	A1868	U1681	G1534	G1447	A1286	U	A1047	U	G773	A607	U292	A142	A142
C2019	G1869	U1687	U1535	U1448	G1306	U	G1048	U	G774	U611	U293	C143	C143
G2020	A1872	A1688	A1538	G1463	C1310	A	C1049	A	A781	A612	U294	A147	A147
C2021	U1876	U1716	G1539	A1464	A1311	C	U1050	C	G782	U613	U295	A148	A148
U2022	C1877	G1717	C1540	A1465	G1312	A	A1051	A	G783	G618	A296	G149	G149
A2026	G1547	U1471	G1547	U1471	A1316	G	G	A899	A625	A625	U306	U157	U157
A2027	U1548	A1472	U1548	A1472	A1324	A	G	C900	G826	G826	C307	U158	U158
G2028	G1550	U1477	U1549	U1477	U1324	G	U	G905	A630	A630	U308	A161	A161
A2029	G1557	G1478	U1558	G1478	U1347	U	A908	A908	A631	A631	G309	A162	A162
G2034	G1558	U1479	G1558	U1479	A1348	U	A909	A909	U502	A502	G310	A170	A170
U2035	U1565	A1480	U1565	A1480	A1349	G	C913	C913	U503	U503	G311	A312	A312
C2039	G1566	U1481	G1566	U1481	G1356	U	U	U	G832	G832	A313	A313	A313
G2051	G1567	U1482	G1567	U1482	C1357	U	C	C	U811	G834	A326	U177	U177
G2052	A1567	U1483	G1568	U1483	C1358	U	U	U	C812	G835	A326	U178	U178
A2056	A1568	U1484	U1568	U1484	G1359	A	U	U	A817	U507	G331	A188	A188
G2057	U1569	A1485	U1569	A1485	A1360	G	A	A	U825	C508	A332	G193	G193
A2058	U1576	C1488	U1576	C1488	G1363	A	A	A	U826	G511	U336	A198	A198
C2059	U1577	A1489	U1577	A1489	A1373	C	C	C	U830	G529	A347	A199	A199
C2061	G1579	U1492	C1580	U1492	U1374	G	G	G	A831	C530	A348	A203	A203
G2062	U1581	C1493	C1580	C1493	A1378	C	C	C	G843	G532	A349	A206	A206
G2063	U1582	C1494	C1581	C1494	U1382	A	A	A	A844	U544	G357	G222	G222
U2064	C1583	G1498	C1582	G1498	A1381	C	C	C	A845	C545	A358	A223	A223
G2065	G1584	U1499	C1583	U1499	U1390	C	C	C	U846	U547	U359	A228	A228
A2066	U1585	C1501	C1584	C1501	A1400	U	U	U	A847	G548	A360	A236	A236
G2067	U1586	G1502	C1585	G1502	U1401	A	A	A	G854	A554	A364	A240	A240
C2068	U1587	U1503	C1586	U1503	C1402	G	G	G	G855	U701	U365	U235	U235
G2069	U1588	U1504	C1587	U1504	U1403	A	A	A	G856	A561	A366	U236	U236
U2070	A1588	U1505	C1588	U1505	G1404	A	A	A	G857	G568	A367	A240	A240
U2071	A1589	U1506	C1589	U1506	U1405	A	A	A	A714	U571	U368	A240	A240
U2082	U1590	G1605	C1590	G1605	U1406	A	A	A	C715	A572	A369	A246	A246
G2083	A1606	U1507	C1591	U1507	G1407	G	G	G	A716	A573	G371	G255	G255
U2092	U1607	U1508	C1592	U1508	U1407	C	C	C	C874	U578	G385	C256	C256
U2093	A1616	U1509	C1593	U1509	G1411	U	U	U	U	C579	A369	G257	G257
U2094	U1632	U1518	C1594	U1518	G1412	C	C	C	A	A580	A403	A282	A282
U2095	A1633	A1519	C1595	A1519	U1193	U	U	U	G	G581			
G2096	G1634	A1520	C1596	A1520	U1194	A	A	A					
A2097	A1635	G1521	C1597	G1521	C1195	A	A	A					
		A1524		A1524									





- Molecule 15: 50S ribosomal protein L15



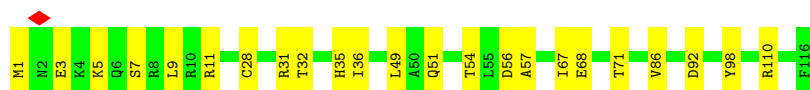
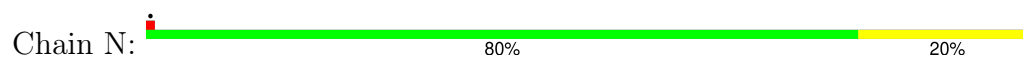
- Molecule 16: 50S ribosomal protein L16



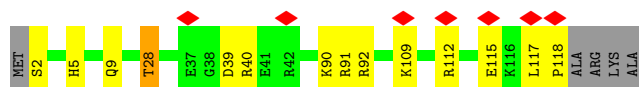
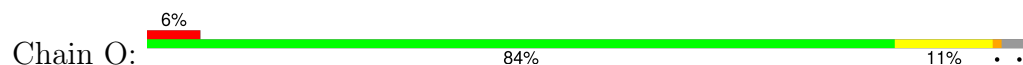
- Molecule 17: 50S ribosomal protein L17



- Molecule 18: 50S ribosomal protein L18



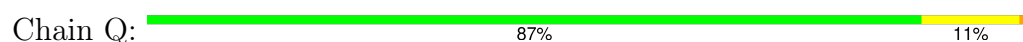
- Molecule 19: 50S ribosomal protein L19

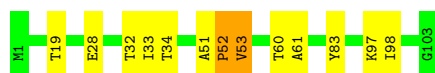


- Molecule 20: 50S ribosomal protein L20



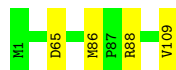
- Molecule 21: 50S ribosomal protein L21





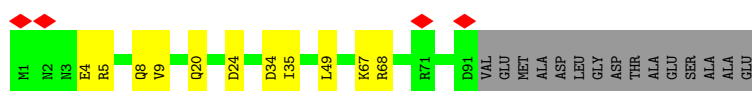
- Molecule 22: 50S ribosomal protein L22

Chain R: 96% .



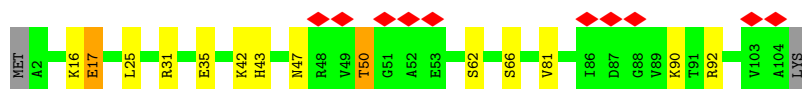
- Molecule 23: 50S ribosomal protein L23

Chain S: 75% 10% 14%



- Molecule 24: 50S ribosomal protein L24

Chain T: 10% 85% 11% . .



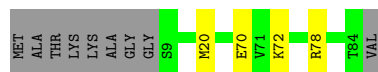
- Molecule 25: 50S ribosomal protein L25

Chain U: 86% 13% .



- Molecule 26: 50S ribosomal protein L27

Chain V: 85% 5% 11%



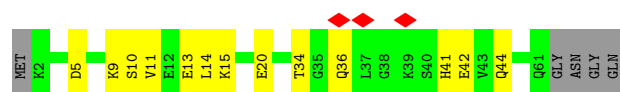
- Molecule 27: 50S ribosomal protein L28

Chain W: 88% 10% .



- Molecule 28: 50S ribosomal protein L29

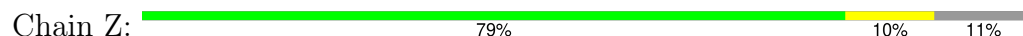
Chain X: 5% 72% 20% 8%



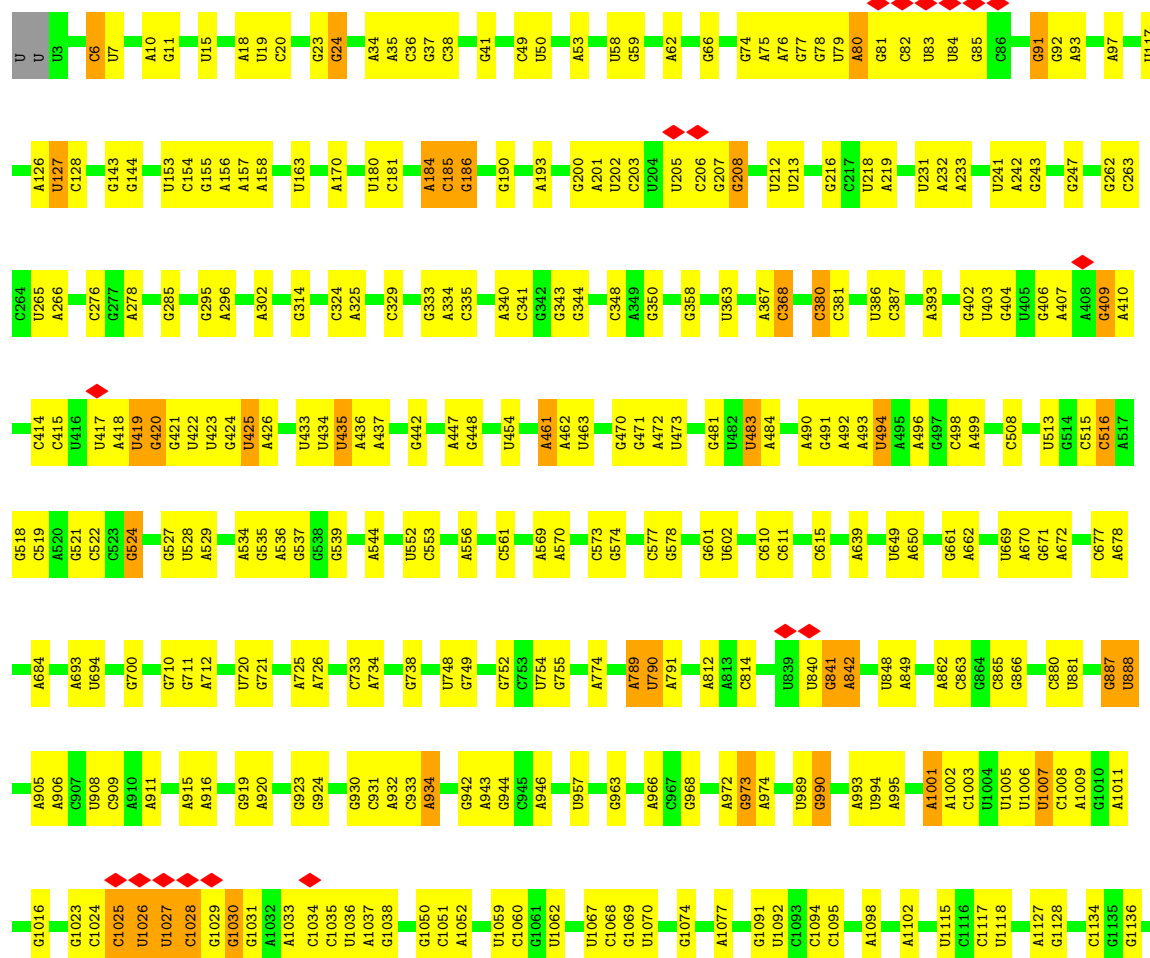
- Molecule 29: 50S ribosomal protein L30

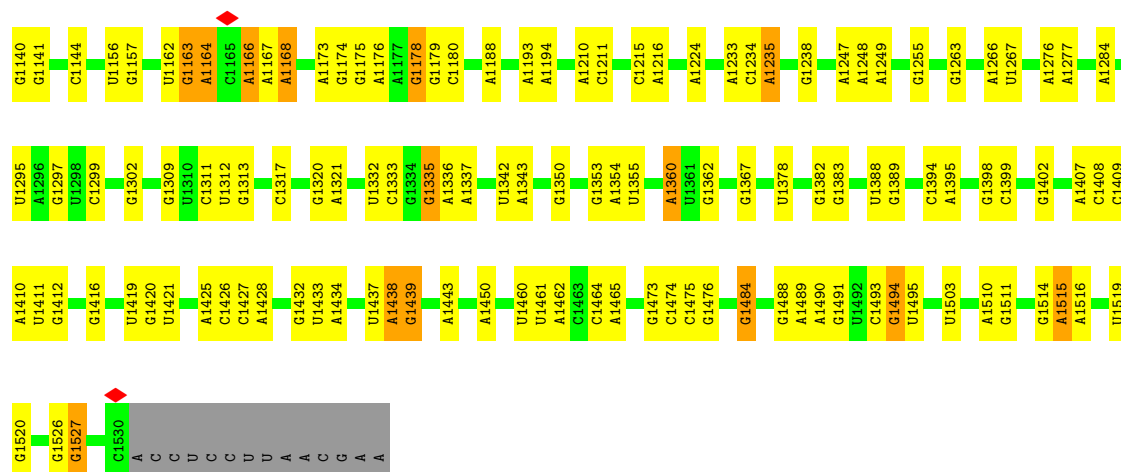


- Molecule 30: 50S ribosomal protein L32

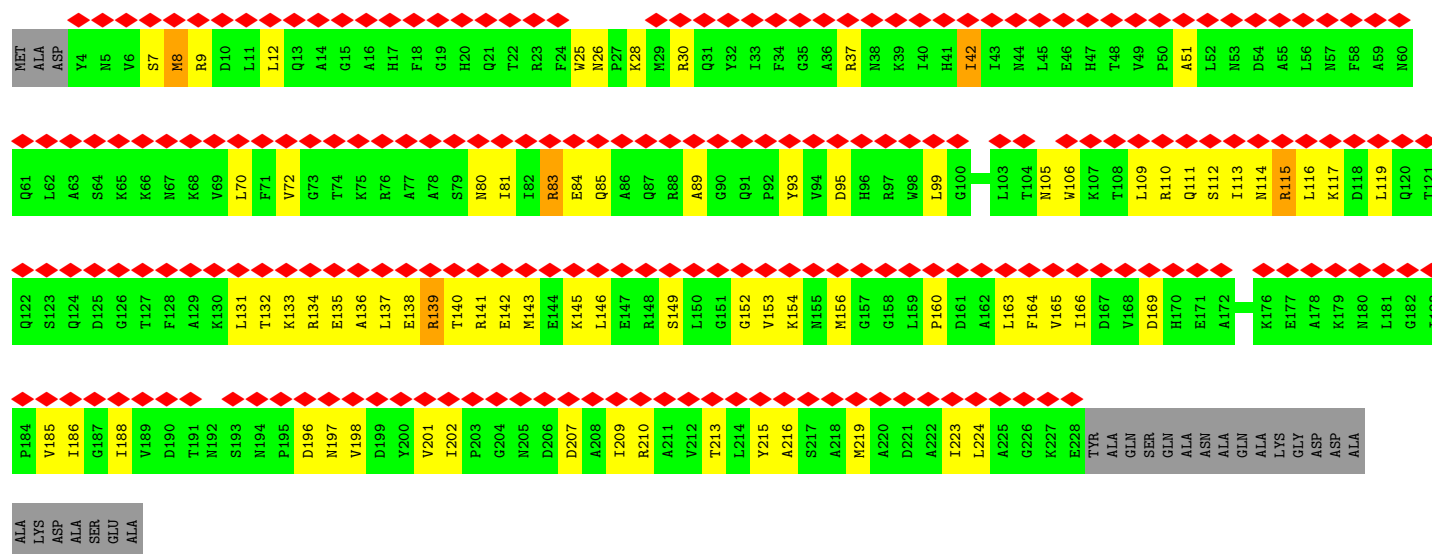
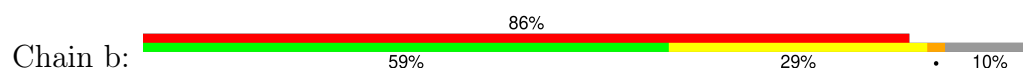


- Molecule 31: 16s Ribosomal RNA

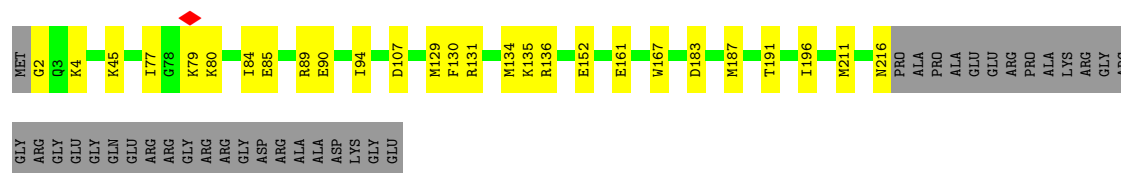




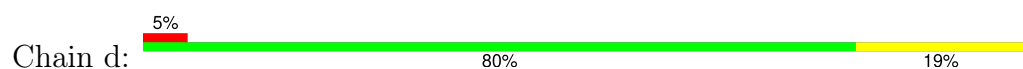
• Molecule 32: 30S ribosomal protein S2

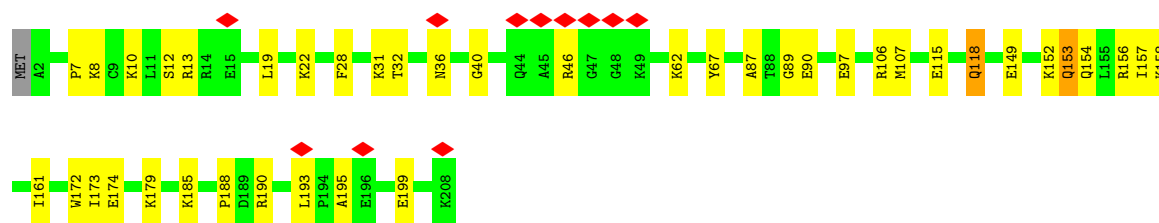


• Molecule 33: 30S ribosomal protein S3



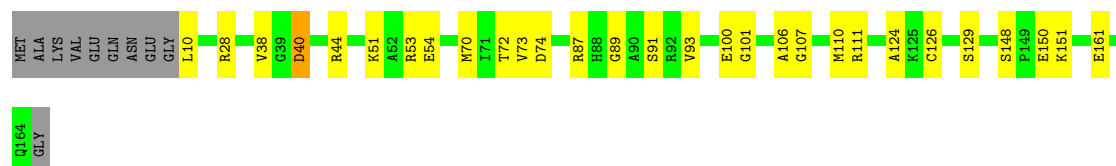
• Molecule 34: 30S ribosomal protein S4





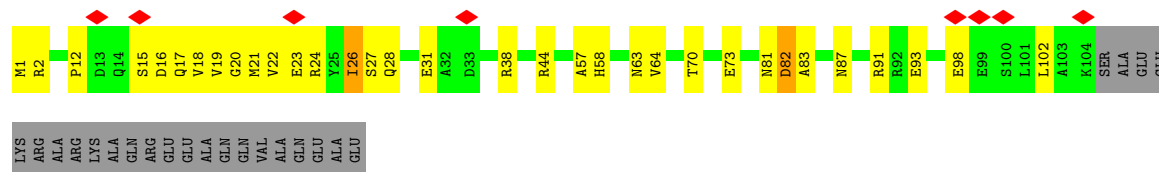
- Molecule 35: 30S ribosomal protein S5

Chain e: 76% 17% • 6%



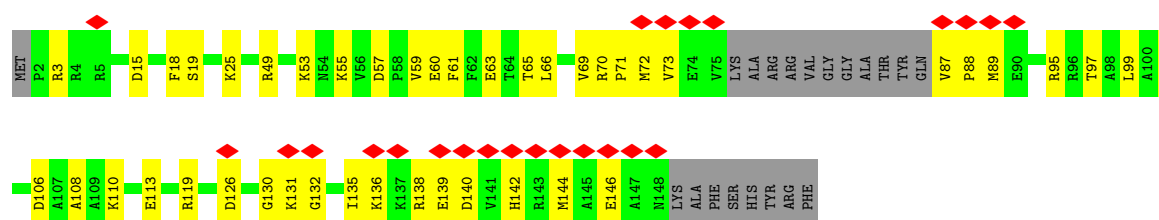
- Molecule 36: 30S ribosomal protein S6

Chain f: 6% 56% 24% • 18%



- Molecule 37: 30S ribosomal protein S7

Chain g: 15% 59% 28% 13%



- Molecule 38: 30S ribosomal protein S8

Chain h: 92% 8% •

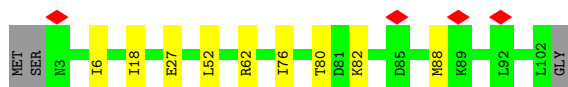
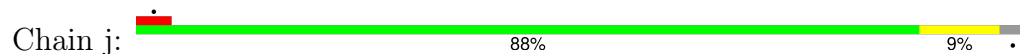


- Molecule 39: 30S ribosomal protein S9

Chain i: 83% 16% •



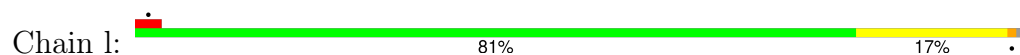
- Molecule 40: 30S ribosomal protein S10



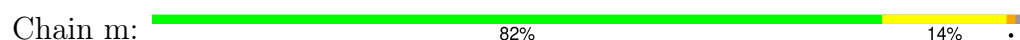
- Molecule 41: 30S ribosomal protein S11



- Molecule 42: 30S ribosomal protein S12



- Molecule 43: 30S ribosomal protein S13



- Molecule 44: 30S ribosomal protein S14

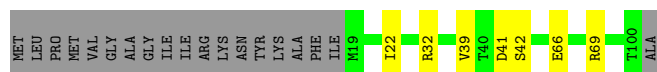


- Molecule 45: 30S ribosomal protein S15

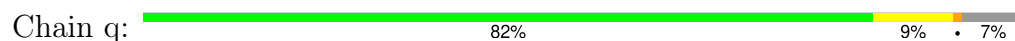




- Molecule 46: 30S ribosomal protein S16



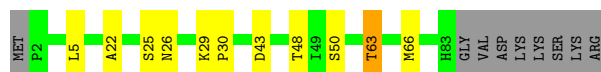
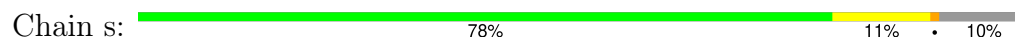
- Molecule 47: 30S ribosomal protein S17



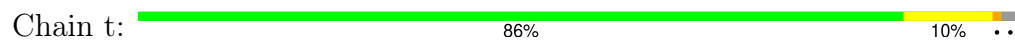
- Molecule 48: 30S ribosomal protein S18



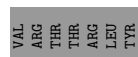
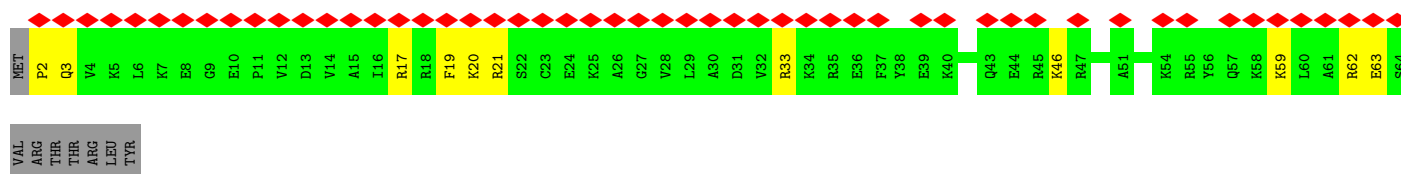
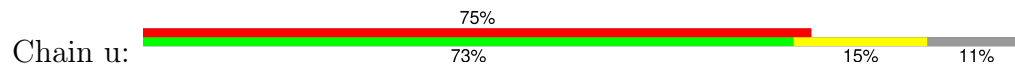
- Molecule 49: 30S ribosomal protein S19



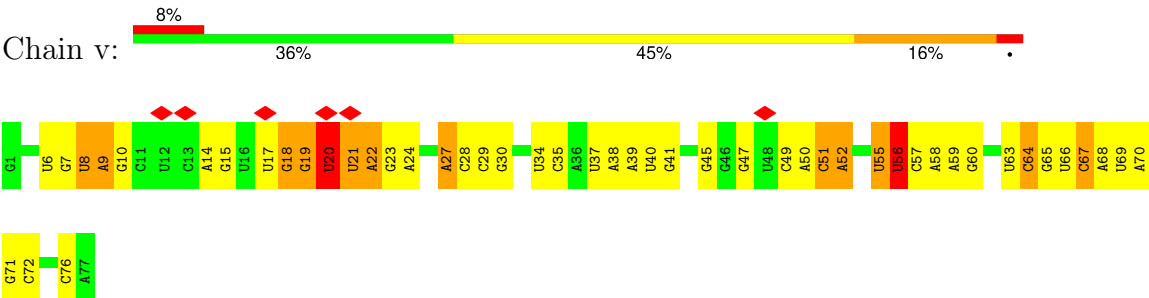
- Molecule 50: 30S ribosomal protein S20



- Molecule 51: 30S ribosomal protein S21



• Molecule 52: tRNA-met



• Molecule 53: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	109944	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)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.362	Depositor
Minimum map value	0.000	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.036	Depositor
Recommended contour level	0.12	Depositor
Map size (Å)	434.176, 434.176, 434.176	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.848, 0.848, 0.848	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PSU, ZN, H2U, 4OC, 7MG, 6MZ, 2MA, 2MG, OMU, UR3, OMG, 4SU, 5MU, MA6, 5MC

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	0.19	0/434	0.38	0/573
2	1	0.19	0/367	0.37	0/481
3	2	0.20	0/515	0.40	0/678
4	3	0.22	0/296	0.42	0/389
5	A	0.22	0/65034	0.32	0/101432
6	B	0.17	0/2739	0.30	0/4266
7	C	0.21	0/2152	0.46	0/2891
8	D	0.20	0/1590	0.37	0/2142
9	E	0.18	0/1537	0.36	0/2073
10	F	0.22	0/1390	0.63	5/1863 (0.3%)
11	G	0.17	0/1337	0.41	0/1807
12	H	0.15	0/461	0.43	0/616
13	I	0.21	0/1151	0.42	0/1551
14	J	0.21	0/956	0.49	0/1286
15	K	0.19	0/1079	0.39	0/1439
16	L	0.19	0/1104	0.39	0/1475
17	M	0.20	0/956	0.40	0/1282
18	N	0.18	0/881	0.46	0/1177
19	O	0.20	0/931	0.44	0/1249
20	P	0.21	0/947	0.37	0/1262
21	Q	0.19	0/818	0.37	0/1094
22	R	0.19	0/831	0.34	0/1113
23	S	0.16	0/716	0.32	0/957
24	T	0.15	0/770	0.33	0/1034
25	U	0.18	0/770	0.38	0/1036
26	V	0.21	0/585	0.36	0/783
27	W	0.20	0/642	0.39	0/856
28	X	0.14	0/487	0.31	0/646
29	Y	0.20	0/460	0.35	0/614
30	Z	0.19	0/453	0.45	0/604
31	a	0.19	0/36476	0.29	0/56895
32	b	0.21	0/1799	0.58	3/2429 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	c	0.18	0/1714	0.42	0/2304
34	d	0.16	0/1653	0.39	0/2213
35	e	0.17	0/1141	0.38	0/1537
36	f	0.17	0/882	0.46	0/1189
37	g	0.22	0/1087	0.59	0/1456
38	h	0.19	0/993	0.36	0/1331
39	i	0.19	0/1002	0.41	0/1339
40	j	0.20	0/811	0.42	0/1096
41	k	0.16	0/878	0.39	0/1189
42	l	0.19	0/958	0.48	0/1284
43	m	0.18	0/913	0.44	0/1226
44	n	0.19	0/803	0.37	0/1071
45	o	0.18	0/715	0.32	0/958
46	p	0.18	0/655	0.37	0/879
47	q	0.19	0/628	0.39	0/847
48	r	0.17	0/432	0.39	0/583
49	s	0.20	0/664	0.41	0/897
50	t	0.22	0/669	0.31	0/892
51	u	0.10	0/528	0.24	0/697
52	v	0.19	0/1739	0.31	0/2709
53	w	0.14	0/72	0.20	0/110
All	All	0.21	0/149601	0.34	8/223800 (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
10	F	0	1
21	Q	0	1
All	All	0	2

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	b	115	ARG	CA-CB-CG	5.84	125.77	114.10
32	b	83	ARG	CG-CD-NE	-5.61	99.67	112.00
32	b	139	ARG	CB-CG-CD	5.53	124.02	111.30
10	F	115	ARG	CA-CB-CG	5.35	124.81	114.10
10	F	79	ILE	CA-C-N	5.32	130.60	121.87

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	F	80	ARG	Peptide
21	Q	51	ALA	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	427	0	462	7	0
2	1	363	0	401	1	0
3	2	509	0	566	1	0
4	3	295	0	326	2	0
5	A	58332	0	29333	298	0
6	B	2450	0	1241	21	0
7	C	2111	0	2176	23	0
8	D	1572	0	1610	7	0
9	E	1516	0	1569	11	0
10	F	1370	0	1420	63	0
11	G	1318	0	1373	20	0
12	H	458	0	480	7	0
13	I	1125	0	1148	8	0
14	J	946	0	1007	24	0
15	K	1071	0	1141	9	0
16	L	1087	0	1162	7	0
17	M	942	0	987	2	0
18	N	873	0	917	15	0
19	O	919	0	973	12	0
20	P	934	0	997	4	0
21	Q	807	0	842	7	0
22	R	826	0	894	2	0
23	S	710	0	768	8	0
24	T	766	0	816	7	0
25	U	760	0	783	6	0
26	V	577	0	580	3	0
27	W	632	0	667	4	0
28	X	486	0	528	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	Y	455	0	476	5	0
30	Z	447	0	435	4	0
31	a	32782	0	16508	221	0
32	b	1769	0	1787	67	0
33	c	1690	0	1774	17	0
34	d	1631	0	1691	27	0
35	e	1129	0	1174	18	0
36	f	867	0	868	24	0
37	g	1073	0	1118	36	0
38	h	985	0	1047	4	0
39	i	991	0	1048	12	0
40	j	801	0	832	6	0
41	k	862	0	877	21	0
42	l	945	0	998	13	0
43	m	903	0	962	9	0
44	n	792	0	833	3	0
45	o	705	0	712	5	0
46	p	644	0	655	5	0
47	q	621	0	665	5	0
48	r	426	0	447	6	0
49	s	646	0	663	8	0
50	t	663	0	715	6	0
51	u	522	0	565	8	0
52	v	1636	0	835	32	0
53	w	65	0	33	4	0
54	3	1	0	0	0	0
All	All	138233	0	92885	1089	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 5.

The worst 5 of 1089 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)
32:b:131:LEU:HD21	32:b:135:GLU:HG2	1.46	0.97
31:a:74:G:H1	31:a:93:A:H61	0.97	0.96
5:A:2093:U:H3	5:A:2188:G:H1	0.97	0.96
31:a:1007:U:H3	31:a:1016:G:H1	1.01	0.92
31:a:74:G:H1	31:a:93:A:N6	1.69	0.89

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	49/51 (96%)	49 (100%)	0	0	100	100
2	1	42/44 (96%)	42 (100%)	0	0	100	100
3	2	61/64 (95%)	59 (97%)	2 (3%)	0	100	100
4	3	36/38 (95%)	36 (100%)	0	0	100	100
7	C	270/274 (98%)	262 (97%)	7 (3%)	1 (0%)	30	40
8	D	209/212 (99%)	201 (96%)	8 (4%)	0	100	100
9	E	198/200 (99%)	198 (100%)	0	0	100	100
10	F	172/178 (97%)	159 (92%)	11 (6%)	2 (1%)	10	14
11	G	172/177 (97%)	164 (95%)	7 (4%)	1 (1%)	21	30
12	H	58/148 (39%)	55 (95%)	3 (5%)	0	100	100
13	I	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
14	J	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
15	K	142/146 (97%)	139 (98%)	3 (2%)	0	100	100
16	L	135/137 (98%)	132 (98%)	2 (2%)	1 (1%)	18	26
17	M	117/125 (94%)	115 (98%)	2 (2%)	0	100	100
18	N	114/116 (98%)	111 (97%)	3 (3%)	0	100	100
19	O	115/122 (94%)	113 (98%)	2 (2%)	0	100	100
20	P	115/119 (97%)	115 (100%)	0	0	100	100
21	Q	101/103 (98%)	97 (96%)	3 (3%)	1 (1%)	12	17
22	R	107/109 (98%)	106 (99%)	1 (1%)	0	100	100
23	S	89/106 (84%)	88 (99%)	1 (1%)	0	100	100
24	T	101/105 (96%)	98 (97%)	3 (3%)	0	100	100
25	U	95/98 (97%)	94 (99%)	1 (1%)	0	100	100
26	V	74/85 (87%)	73 (99%)	1 (1%)	0	100	100
27	W	75/78 (96%)	75 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	X	58/65 (89%)	58 (100%)	0	0	100	100
29	Y	55/58 (95%)	53 (96%)	2 (4%)	0	100	100
30	Z	52/61 (85%)	50 (96%)	2 (4%)	0	100	100
32	b	223/250 (89%)	209 (94%)	13 (6%)	1 (0%)	30	40
33	c	213/250 (85%)	206 (97%)	7 (3%)	0	100	100
34	d	205/208 (99%)	200 (98%)	5 (2%)	0	100	100
35	e	153/165 (93%)	152 (99%)	1 (1%)	0	100	100
36	f	102/127 (80%)	97 (95%)	5 (5%)	0	100	100
37	g	132/156 (85%)	127 (96%)	5 (4%)	0	100	100
38	h	128/131 (98%)	123 (96%)	5 (4%)	0	100	100
39	i	124/128 (97%)	121 (98%)	3 (2%)	0	100	100
40	j	98/103 (95%)	95 (97%)	3 (3%)	0	100	100
41	k	115/128 (90%)	111 (96%)	4 (4%)	0	100	100
42	l	120/124 (97%)	114 (95%)	6 (5%)	0	100	100
43	m	113/118 (96%)	109 (96%)	4 (4%)	0	100	100
44	n	98/101 (97%)	95 (97%)	3 (3%)	0	100	100
45	o	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
46	p	80/101 (79%)	80 (100%)	0	0	100	100
47	q	77/85 (91%)	77 (100%)	0	0	100	100
48	r	50/75 (67%)	50 (100%)	0	0	100	100
49	s	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
50	t	84/88 (96%)	84 (100%)	0	0	100	100
51	u	61/71 (86%)	59 (97%)	2 (3%)	0	100	100
All	All	5414/5872 (92%)	5264 (97%)	143 (3%)	7 (0%)	49	62

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	F	137	VAL
32	b	8	MET
10	F	5	LYS
11	G	13	ASN
16	L	79	LEU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	47/47 (100%)	45 (96%)	2 (4%)	26	41
2	1	36/36 (100%)	35 (97%)	1 (3%)	38	58
3	2	52/53 (98%)	51 (98%)	1 (2%)	50	69
4	3	33/33 (100%)	31 (94%)	2 (6%)	17	27
7	C	218/220 (99%)	217 (100%)	1 (0%)	81	90
8	D	166/167 (99%)	163 (98%)	3 (2%)	51	71
9	E	155/155 (100%)	150 (97%)	5 (3%)	34	53
10	F	144/147 (98%)	136 (94%)	8 (6%)	19	30
11	G	139/142 (98%)	132 (95%)	7 (5%)	22	35
12	H	45/112 (40%)	44 (98%)	1 (2%)	45	65
13	I	118/118 (100%)	117 (99%)	1 (1%)	73	85
14	J	103/103 (100%)	102 (99%)	1 (1%)	68	82
15	K	106/108 (98%)	104 (98%)	2 (2%)	50	69
16	L	113/113 (100%)	112 (99%)	1 (1%)	70	84
17	M	96/101 (95%)	95 (99%)	1 (1%)	68	82
18	N	85/85 (100%)	84 (99%)	1 (1%)	63	79
19	O	99/102 (97%)	98 (99%)	1 (1%)	68	82
20	P	85/86 (99%)	85 (100%)	0	100	100
21	Q	84/84 (100%)	83 (99%)	1 (1%)	63	79
22	R	88/88 (100%)	87 (99%)	1 (1%)	65	81
23	S	77/87 (88%)	76 (99%)	1 (1%)	61	78
24	T	83/85 (98%)	79 (95%)	4 (5%)	23	37
25	U	79/80 (99%)	75 (95%)	4 (5%)	21	34
26	V	59/64 (92%)	59 (100%)	0	100	100
27	W	69/70 (99%)	67 (97%)	2 (3%)	37	57
28	X	53/56 (95%)	52 (98%)	1 (2%)	50	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	Y	53/54 (98%)	52 (98%)	1 (2%)	50	69
30	Z	46/50 (92%)	45 (98%)	1 (2%)	45	65
32	b	185/200 (92%)	180 (97%)	5 (3%)	39	59
33	c	175/198 (88%)	174 (99%)	1 (1%)	78	88
34	d	170/171 (99%)	167 (98%)	3 (2%)	51	71
35	e	113/120 (94%)	110 (97%)	3 (3%)	39	59
36	f	94/111 (85%)	89 (95%)	5 (5%)	20	33
37	g	113/128 (88%)	113 (100%)	0	100	100
38	h	108/109 (99%)	105 (97%)	3 (3%)	38	58
39	i	99/100 (99%)	96 (97%)	3 (3%)	36	56
40	j	89/91 (98%)	88 (99%)	1 (1%)	65	81
41	k	88/98 (90%)	85 (97%)	3 (3%)	32	51
42	l	104/106 (98%)	96 (92%)	8 (8%)	12	18
43	m	95/98 (97%)	92 (97%)	3 (3%)	34	53
44	n	81/82 (99%)	80 (99%)	1 (1%)	63	79
45	o	71/72 (99%)	71 (100%)	0	100	100
46	p	63/77 (82%)	63 (100%)	0	100	100
47	q	71/76 (93%)	70 (99%)	1 (1%)	59	77
48	r	46/66 (70%)	45 (98%)	1 (2%)	45	65
49	s	70/78 (90%)	68 (97%)	2 (3%)	37	57
50	t	65/67 (97%)	62 (95%)	3 (5%)	24	38
51	u	54/62 (87%)	53 (98%)	1 (2%)	50	69
All	All	4485/4756 (94%)	4383 (98%)	102 (2%)	44	64

5 of 102 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	b	109	LEU
36	f	102	LEU
50	t	48	THR
32	b	169	ASP
35	e	40	ASP

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

Mol	Chain	Res	Type
29	Y	8	GLN
50	t	3	ASN
33	c	139	GLN
41	k	118	ASN
32	b	114	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
31	a	1527/1544 (98%)	195 (12%)	0
5	A	2714/2918 (93%)	369 (13%)	20 (0%)
52	v	76/77 (98%)	23 (30%)	0
53	w	2/3 (66%)	0	0
6	B	114/115 (99%)	15 (13%)	2 (1%)
All	All	4433/4657 (95%)	602 (13%)	22 (0%)

5 of 602 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	A	41	U
5	A	42	G
5	A	50	G
5	A	53	G
5	A	58	G

5 of 22 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	A	1564	A
5	A	2443	G
5	A	2419	U
5	A	2502	U
5	A	478	A

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

25 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
5	OMU	A	2548	5	19,22,23	2.95	8 (42%)	25,31,34	1.85	5 (20%)
5	PSU	A	2500	5	18,21,22	1.08	1 (5%)	21,30,33	1.90	4 (19%)
31	2MG	a	963	31	23,26,27	0.50	0	33,38,41	0.50	0
31	MA6	a	1515	31	23,26,27	1.41	4 (17%)	33,38,41	3.21	11 (33%)
5	2MA	A	2499	5	22,25,26	3.91	9 (40%)	32,37,40	2.67	10 (31%)
52	4SU	v	8	52	18,21,22	4.45	8 (44%)	25,30,33	2.28	5 (20%)
5	PSU	A	2453	5	18,21,22	1.08	1 (5%)	21,30,33	1.97	5 (23%)
5	2MG	A	2441	5	23,26,27	0.55	0	33,38,41	0.48	0
31	7MG	a	524	31	23,26,27	1.09	1 (4%)	27,39,42	0.89	2 (7%)
52	PSU	v	56	52	18,21,22	1.06	1 (5%)	21,30,33	1.90	5 (23%)
5	OMG	A	2247	5	23,26,27	0.52	0	32,38,41	0.47	0
5	7MG	A	2065	5	23,26,27	1.00	1 (4%)	27,39,42	0.92	2 (7%)
31	MA6	a	1516	31	23,26,27	1.43	4 (17%)	33,38,41	3.31	12 (36%)
31	UR3	a	1495	31	19,22,23	2.87	7 (36%)	26,32,35	1.61	3 (11%)
5	PSU	A	2576	5	18,21,22	1.11	2 (11%)	21,30,33	2.02	5 (23%)
31	PSU	a	513	31	18,21,22	1.10	1 (5%)	21,30,33	1.96	5 (23%)
5	6MZ	A	2026	5	22,25,26	2.49	4 (18%)	29,36,39	3.36	10 (34%)
52	5MU	v	55	52	19,22,23	0.41	0	27,32,35	0.59	0
31	4OC	a	1399	31	20,23,24	3.12	8 (40%)	25,32,35	0.90	1 (4%)
31	2MG	a	1204	31	23,26,27	0.49	0	33,38,41	0.52	0
31	5MC	a	964	31	19,22,23	0.60	0	26,32,35	0.58	0
5	PSU	A	2601	5	18,21,22	1.06	1 (5%)	21,30,33	1.97	5 (23%)
5	5MU	A	1935	5	19,22,23	0.50	0	27,32,35	0.48	0
5	PSU	A	952	5	18,21,22	1.05	1 (5%)	21,30,33	1.97	4 (19%)
52	H2U	v	20	52	18,21,22	0.50	0	19,30,33	1.46	3 (15%)

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
5	OMU	A	2548	5	-	0/9/27/28	0/2/2/2
5	PSU	A	2500	5	-	1/7/25/26	0/2/2/2
31	2MG	a	963	31	-	0/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
31	MA6	a	1515	31	-	0/11/29/30	0/3/3/3
5	2MA	A	2499	5	-	2/7/25/26	0/3/3/3
52	4SU	v	8	52	-	3/7/25/26	0/2/2/2
5	PSU	A	2453	5	-	0/7/25/26	0/2/2/2
5	2MG	A	2441	5	-	2/9/27/28	0/3/3/3
31	7MG	a	524	31	-	2/7/37/38	0/3/3/3
52	PSU	v	56	52	-	1/7/25/26	0/2/2/2
5	OMG	A	2247	5	-	1/9/27/28	0/3/3/3
5	7MG	A	2065	5	-	0/7/37/38	0/3/3/3
31	MA6	a	1516	31	-	0/11/29/30	0/3/3/3
31	UR3	a	1495	31	-	0/7/25/26	0/2/2/2
5	PSU	A	2576	5	-	0/7/25/26	0/2/2/2
31	PSU	a	513	31	-	0/7/25/26	0/2/2/2
5	6MZ	A	2026	5	-	2/9/27/28	0/3/3/3
52	5MU	v	55	52	-	7/7/25/26	0/2/2/2
31	4OC	a	1399	31	-	1/9/29/30	0/2/2/2
31	2MG	a	1204	31	-	0/9/27/28	0/3/3/3
31	5MC	a	964	31	-	0/7/25/26	0/2/2/2
5	PSU	A	2601	5	-	0/7/25/26	0/2/2/2
5	5MU	A	1935	5	-	0/7/25/26	0/2/2/2
5	PSU	A	952	5	-	0/7/25/26	0/2/2/2
52	H2U	v	20	52	-	3/7/38/39	0/2/2/2

The worst 5 of 62 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	2499	2MA	C4-N3	11.90	1.49	1.34
5	A	2026	6MZ	C6-N6	9.73	1.45	1.34
52	v	8	4SU	C2-N1	9.72	1.53	1.38
52	v	8	4SU	C4-N3	8.87	1.46	1.37
52	v	8	4SU	C5-C4	7.25	1.51	1.42

The worst 5 of 97 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	a	1516	MA6	N1-C6-N6	-12.14	102.07	116.86
31	a	1515	MA6	N1-C6-N6	-11.67	102.63	116.86
5	A	2026	6MZ	C4-N9-C1'	-9.17	105.19	126.63
5	A	2026	6MZ	C1'-N9-C8	9.00	147.06	127.09
31	a	1516	MA6	C5-C6-N6	8.00	138.00	125.33

There are no chirality outliers.

5 of 25 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
52	v	8	4SU	O4'-C1'-N1-C2
52	v	20	H2U	C2'-C1'-N1-C2
52	v	55	5MU	O4'-C4'-C5'-O5'
5	A	2247	OMG	C1'-C2'-O2'-CM2
5	A	2499	2MA	O4'-C4'-C5'-O5'

There are no ring outliers.

8 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	2548	OMU	1	0
31	a	1515	MA6	2	0
52	v	8	4SU	1	0
52	v	56	PSU	1	0
5	A	2247	OMG	1	0
5	A	2026	6MZ	2	0
52	v	55	5MU	1	0
52	v	20	H2U	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is 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.

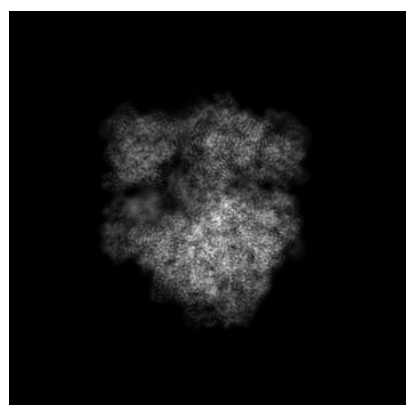
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26818. These allow visual inspection of the internal detail of the map and identification of artifacts.

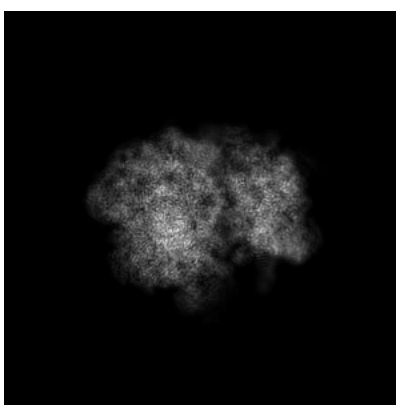
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

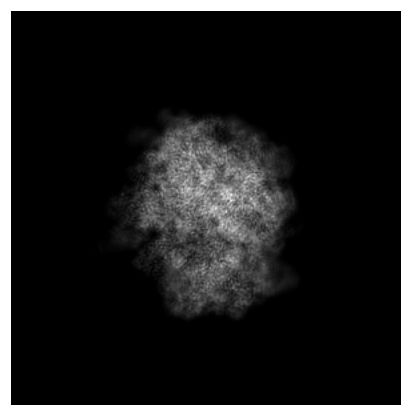
6.1.1 Primary map



X



Y

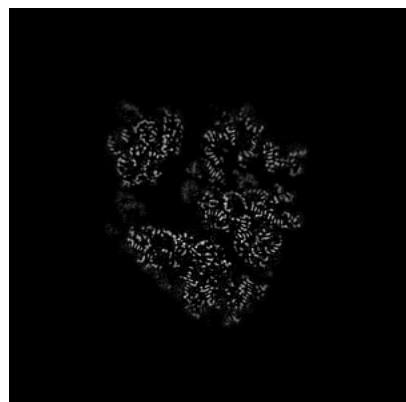


Z

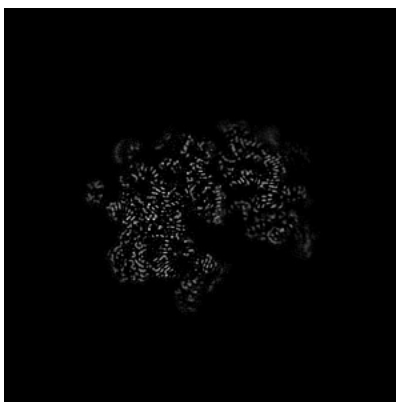
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

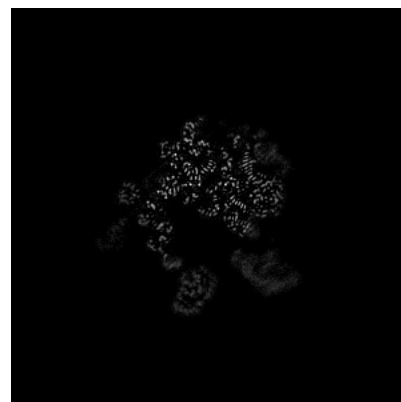
6.2.1 Primary map



X Index: 256



Y Index: 256

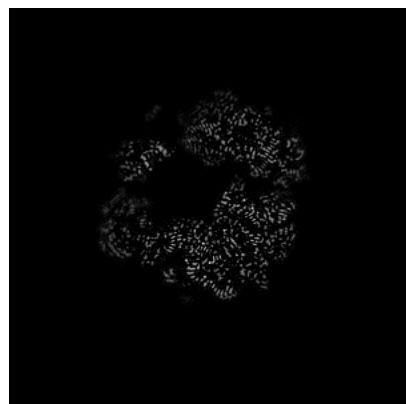


Z Index: 256

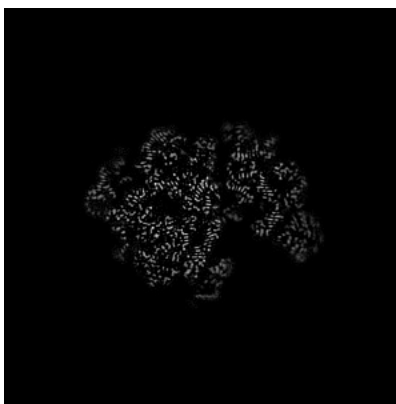
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

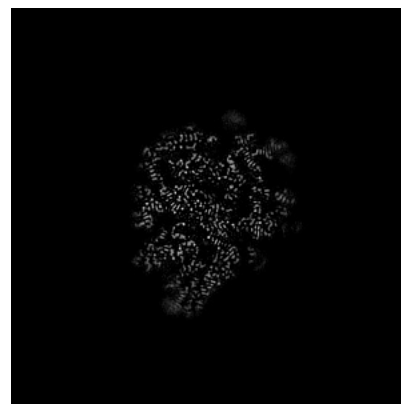
6.3.1 Primary map



X Index: 228



Y Index: 276

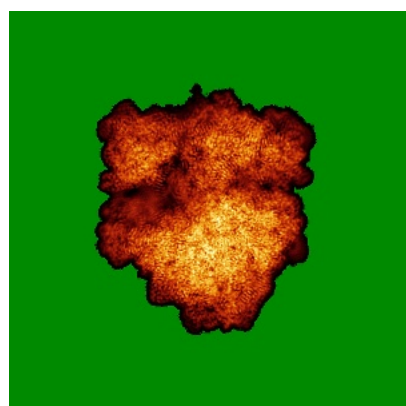


Z Index: 208

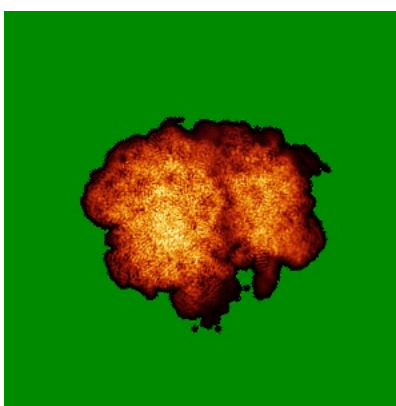
The images above show the largest variance slices of the map in three orthogonal directions.

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

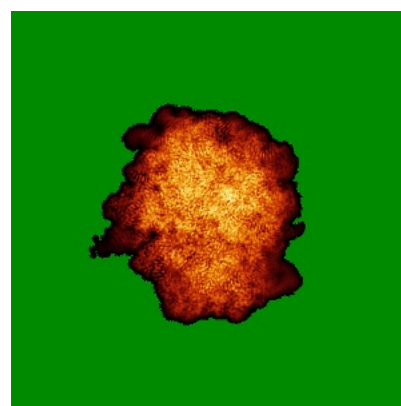
6.4.1 Primary map



X



Y



Z

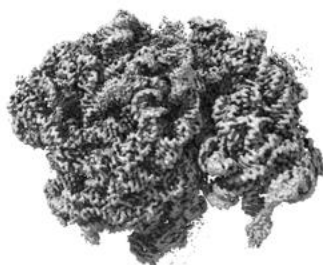
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

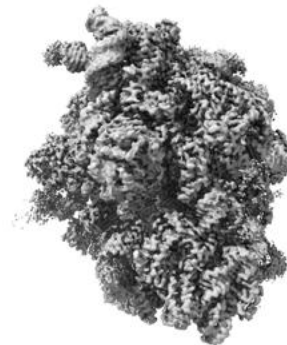
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.12. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

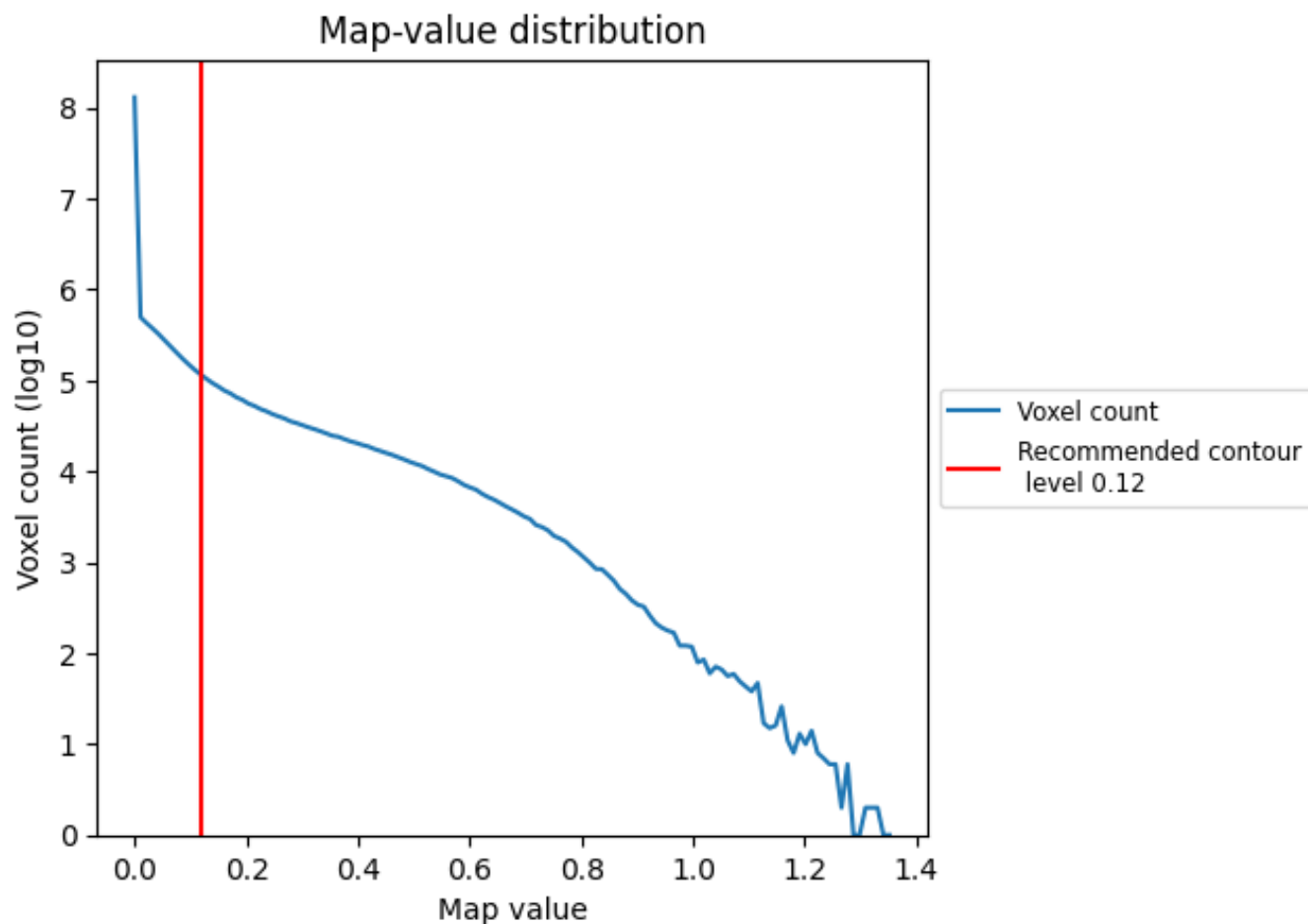
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

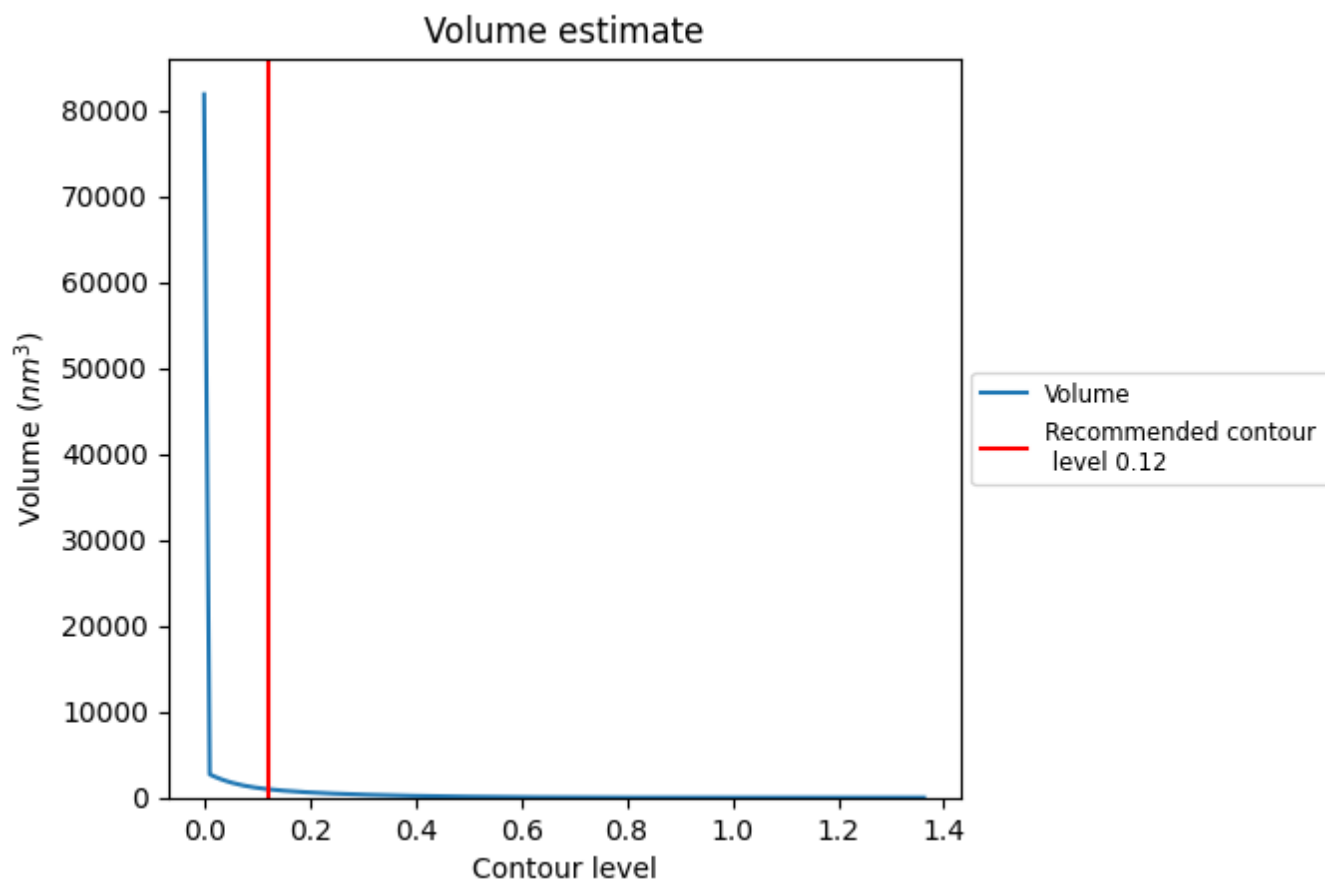
This section contains the results of statistical analysis of the map.

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.

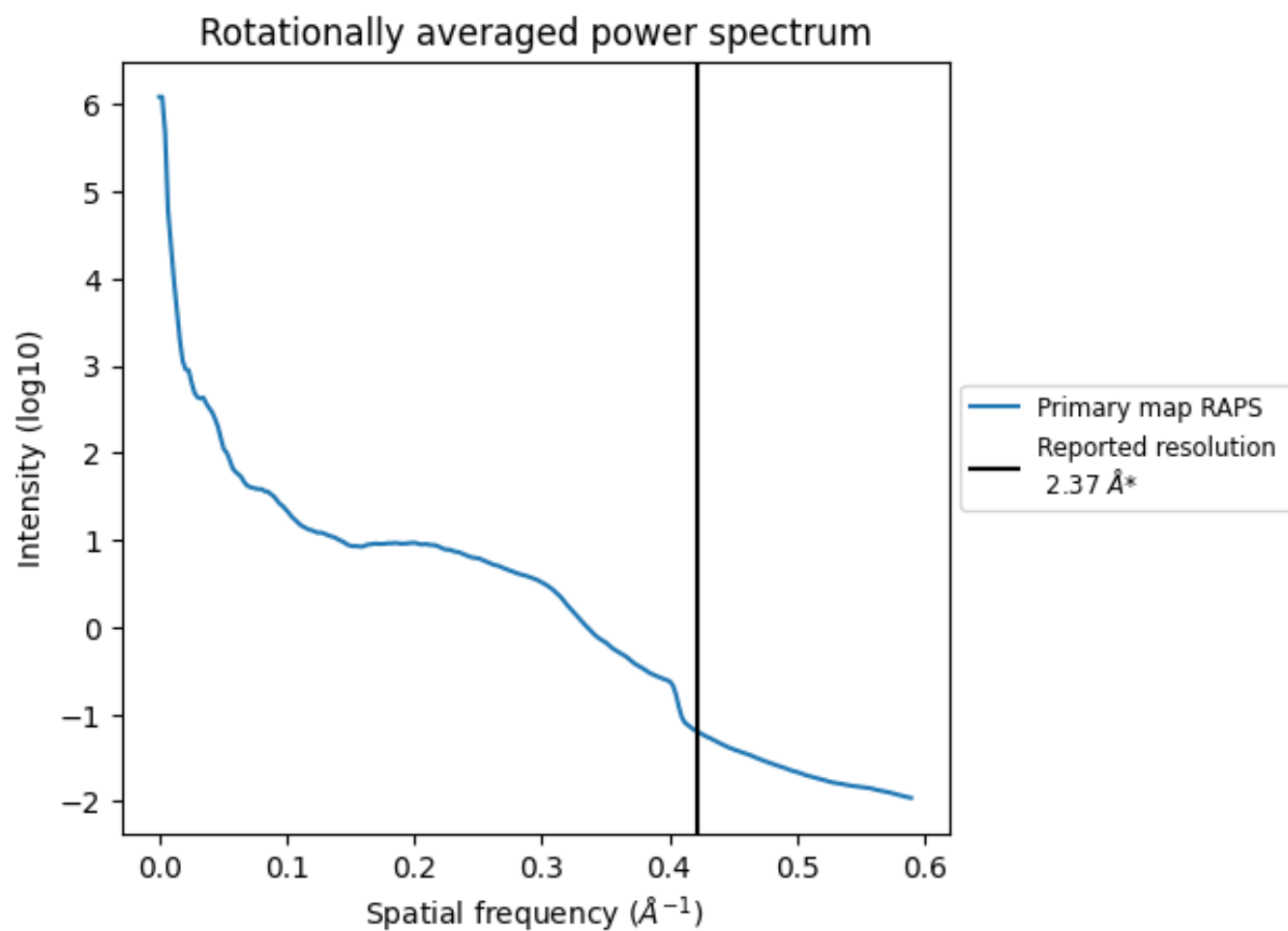
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 982 nm^3 ; this corresponds to an approximate mass of 887 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 0.422 Å⁻¹

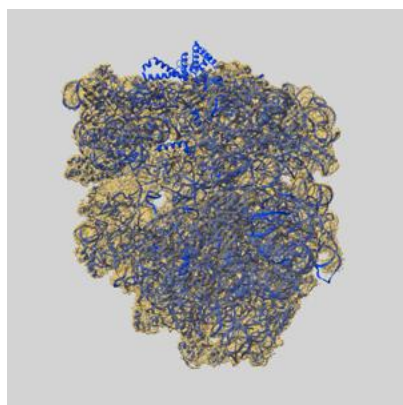
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

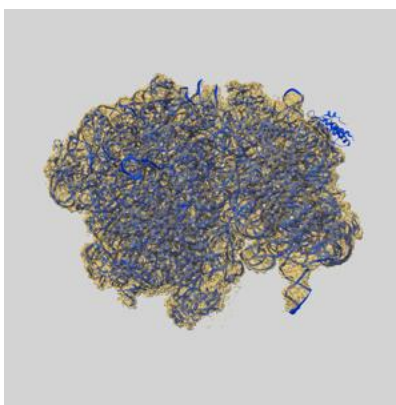
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-26818 and PDB model 7UVW. Per-residue inclusion information can be found in section [3](#) on page [13](#).

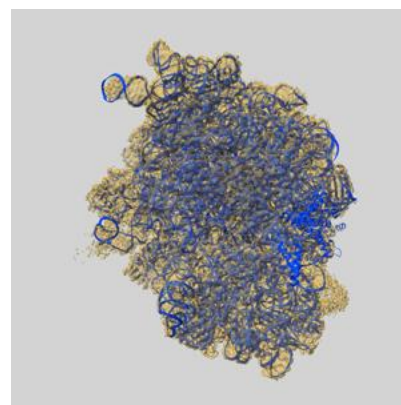
9.1 Map-model overlay [i](#)



X



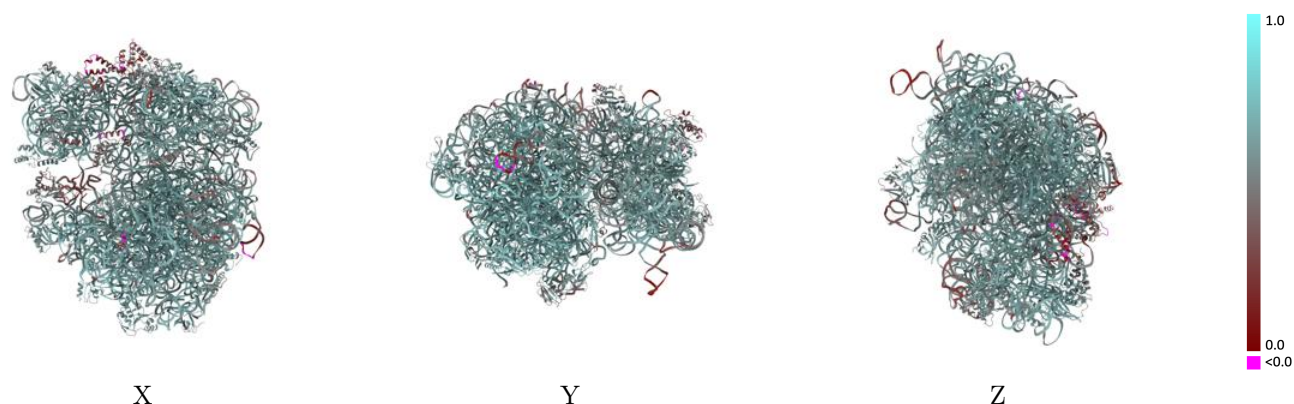
Y



Z

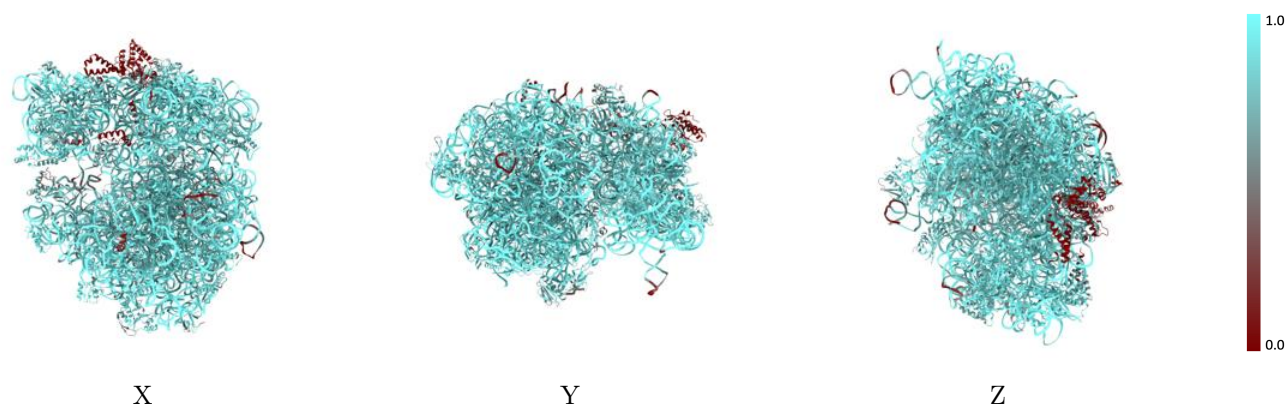
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



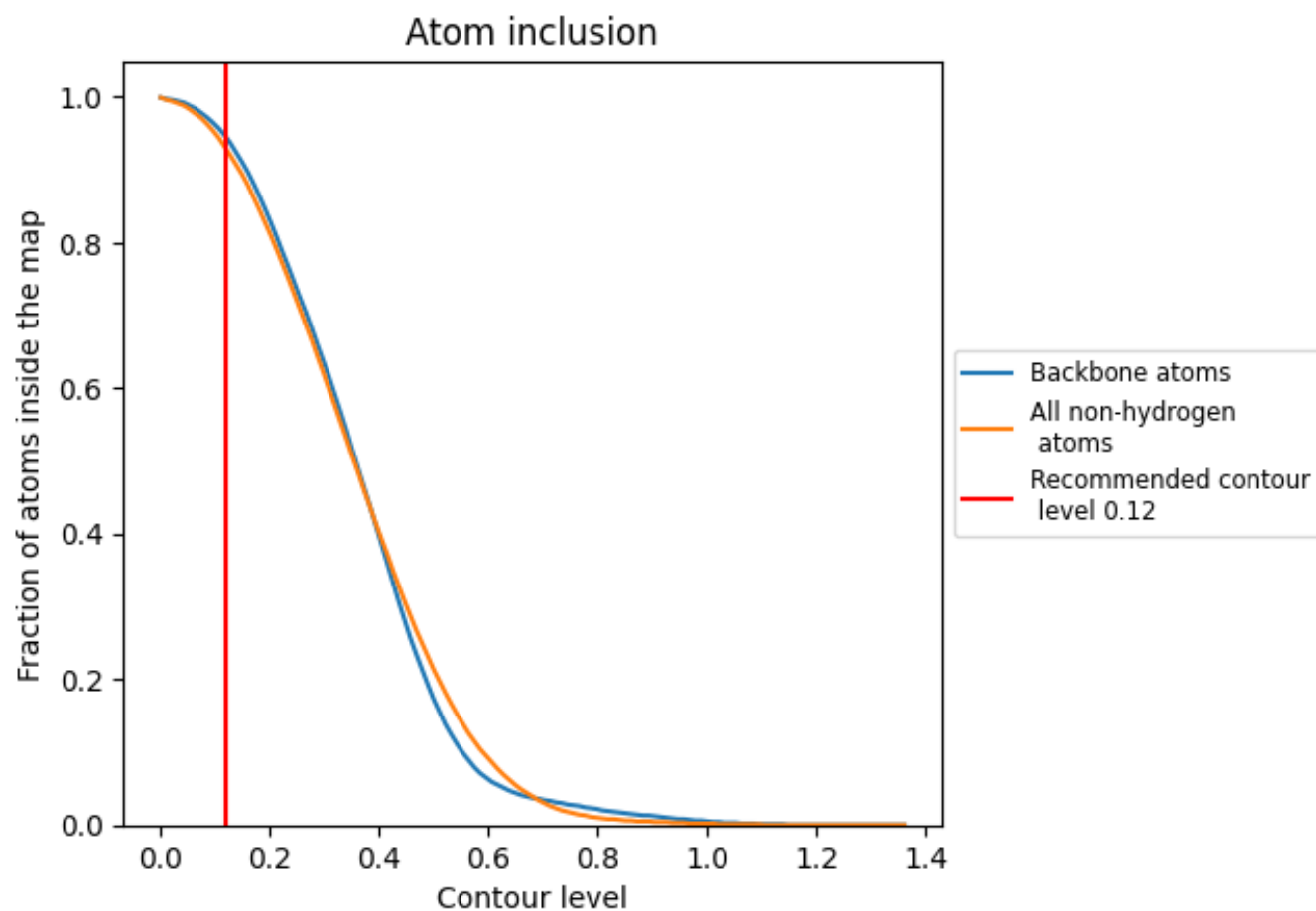
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.12).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 93% 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 (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9290	 0.6170
0	 0.9180	 0.6600
1	 0.9650	 0.6970
2	 0.9920	 0.7050
3	 0.9550	 0.6580
A	 0.9710	 0.6430
B	 0.9840	 0.5890
C	 0.9420	 0.6660
D	 0.9570	 0.6770
E	 0.9090	 0.6500
F	 0.6660	 0.4320
G	 0.8390	 0.5580
H	 0.4230	 0.4090
I	 0.9590	 0.6750
J	 0.8600	 0.6230
K	 0.9640	 0.6730
L	 0.9440	 0.6630
M	 0.9810	 0.6900
N	 0.9360	 0.5950
O	 0.8870	 0.6340
P	 0.9880	 0.6910
Q	 0.9620	 0.6660
R	 0.9530	 0.6750
S	 0.8800	 0.6230
T	 0.8310	 0.5960
U	 0.9290	 0.6310
V	 0.9770	 0.6900
W	 0.9450	 0.6690
X	 0.8170	 0.5540
Y	 0.9570	 0.6740
Z	 0.9460	 0.6700
a	 0.9660	 0.6020
b	 0.0830	 0.3320
c	 0.8990	 0.6040
d	 0.7790	 0.5230



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Chain	Atom inclusion	Q-score
e	 0.9240	 0.6150
f	 0.7280	 0.5100
g	 0.6780	 0.5050
h	 0.9380	 0.6280
i	 0.9370	 0.6290
j	 0.8600	 0.5900
k	 0.7100	 0.4990
l	 0.8380	 0.6070
m	 0.9270	 0.6160
n	 0.9330	 0.6320
o	 0.9310	 0.6200
p	 0.9530	 0.6390
q	 0.8880	 0.6000
r	 0.8690	 0.5880
s	 0.9430	 0.6230
t	 0.9500	 0.6170
u	 0.1710	 0.3520
v	 0.7730	 0.4380
w	 0.8770	 0.5180