



wwPDB EM Validation Summary Report ⓘ

Jun 21, 2026 – 09:18 am BST

PDB ID : 5NP6 / pdb_00005np6
EMDB ID : EMD-3618
Title : 70S structure prior to bypassing
Authors : Agirrezabala, X.; Samatova, E.; Klimova, M.; Zamora, M.; Gil-Carton, D.;
Rodnina, M.; Valle, M.
Deposited on : 2017-04-13
Resolution : 3.60 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:

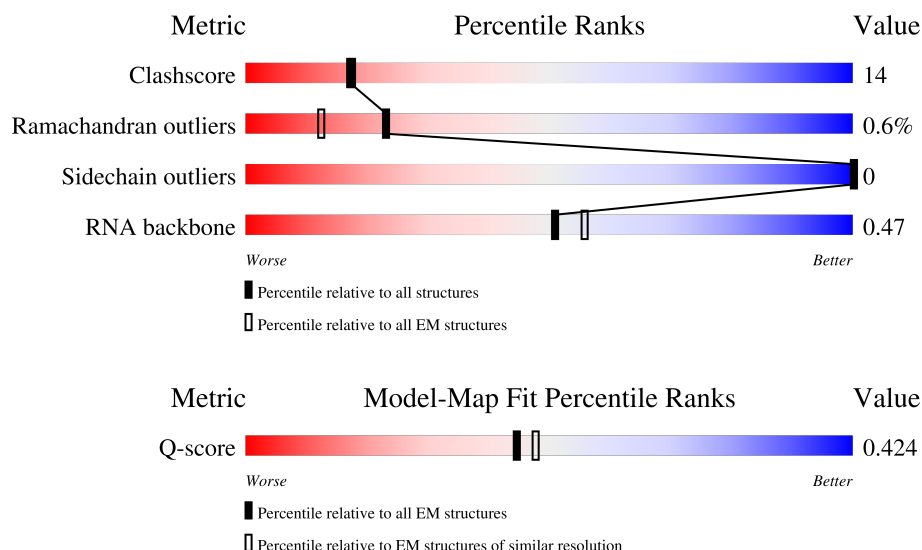
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.60 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	12797 (3.10 - 4.10)

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	29	
2	B	76	
3	C	46	

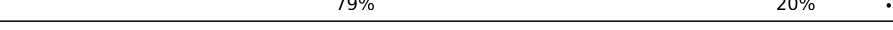
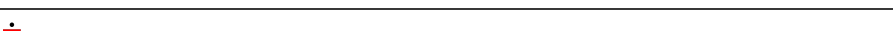
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Mol	Chain	Length	Quality of chain
4	D	1539	
5	E	218	
6	F	206	
7	G	205	
8	H	157	
9	I	100	
10	J	151	
11	K	129	
12	L	127	
13	M	98	
14	N	116	
15	O	123	
16	P	114	
17	Q	101	
18	R	88	
19	S	82	
20	T	80	
21	U	65	
22	V	79	
23	W	85	
24	X	65	
25	Y	2903	
26	Z	120	
27	a	271	
28	b	209	

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Mol	Chain	Length	Quality of chain
29	c	201	
30	d	177	
31	e	176	
32	f	149	
33	g	141	
34	h	142	
35	i	122	
36	j	143	
37	k	136	
38	l	120	
39	m	116	
40	n	114	
41	o	117	
42	p	103	
43	q	110	
44	r	93	
45	s	102	
46	t	94	
47	u	75	
48	v	77	
49	w	63	
50	x	58	
51	y	56	
52	z	50	
53	0	46	

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Mol	Chain	Length	Quality of chain
54	1	64	 77% 23%
55	2	38	 82% 18%
56	3	131	 49% 40% 57% .
57	4	66	 62% 38%

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 146883 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 mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	29	Total	C	N	O	P	0	0
			621	277	111	204	29		

- Molecule 2 is a RNA chain called P-site tRNA-Gly.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	76	Total	C	N	O	P	0	0
			1623	722	291	534	76		

- Molecule 3 is a protein called DNA topoisomerase small subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	46	Total	C	N	O	S	0	0
			362	222	65	71	4		

- Molecule 4 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	1539	Total	C	N	O	P	0	0
			33028	14738	6052	10699	1539		

- Molecule 5 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 6 is a protein called 30S ribosomal protein S3.

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

- Molecule 7 is a protein called 30S ribosomal protein S4.

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

- Molecule 8 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	157	Total	C	N	O	S	0	0
			1141	709	218	208	6		

- Molecule 9 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 10 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 11 is a protein called 30S ribosomal protein S8.

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

- Molecule 12 is a protein called 30S ribosomal protein S9.

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

- Molecule 13 is a protein called 30S ribosomal protein S10.

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

- Molecule 14 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 15 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 16 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 17 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	101	Total	C	N	O	S	0	0
			799	498	165	133	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	35	ALA	-	insertion	UNP P0AG59

- Molecule 18 is a protein called 30S ribosomal protein S15.

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

- Molecule 19 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 20 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 21 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	65	Total	C	N	O		0	0
			504	317	96	91			

- Molecule 22 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 23 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 24 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	65	Total	C	N	O	S	0	0
			495	307	100	87	1		

- Molecule 25 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	2903	Total	C	N	O	P	0	0
			62338	27816	11471	20148	2903		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Y	747	5MC	U	conflict	GB 802133627
Y	887	A	U	conflict	GB 802133627
Y	1847	G	A	conflict	GB 802133627

- Molecule 26 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	120	Total	C	N	O	P	0	0
			2572	1145	471	836	120		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Z	120	A	U	conflict	GB 1146054517

- Molecule 27 is a protein called 50S ribosomal protein L2.

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

- Molecule 28 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 29 is a protein called 50S ribosomal protein L4.

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

- Molecule 30 is a protein called 50S ribosomal protein L5.

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

- Molecule 31 is a protein called 50S ribosomal protein L6.

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

- Molecule 32 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 33 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 34 is a protein called 50S ribosomal protein L13.

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

- Molecule 35 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	i	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 36 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	j	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 37 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	k	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 38 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	l	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 39 is a protein called 50S ribosomal protein L18.

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

- Molecule 40 is a protein called 50S ribosomal protein L19.

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

- Molecule 41 is a protein called 50S ribosomal protein L20.

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

- Molecule 42 is a protein called 50S ribosomal protein L21.

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

- Molecule 43 is a protein called 50S ribosomal protein L22.

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

- Molecule 44 is a protein called 50S ribosomal protein L23.

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

- Molecule 45 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	s	102	Total	C	N	O	0	0
			779	492	146	141		

- Molecule 46 is a protein called 50S ribosomal protein L25.

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

- Molecule 47 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	u	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 48 is a protein called 50S ribosomal protein L28.

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

- Molecule 49 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	w	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

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

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

- Molecule 51 is a protein called 50S ribosomal protein L32.

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

- Molecule 52 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	z	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 53 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	0	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 54 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	1	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 55 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	2	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 56 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	3	131	Total	C	N	O	S	0	0
			988	625	175	183	5		

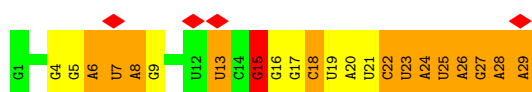
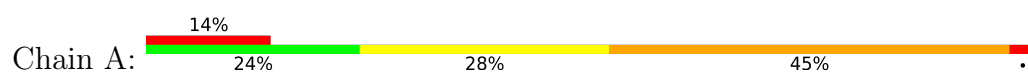
- Molecule 57 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	4	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

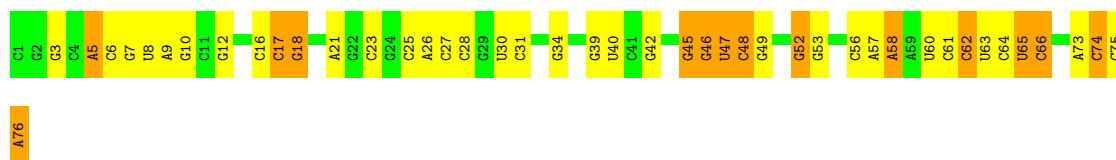
3 Residue-property plots

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.

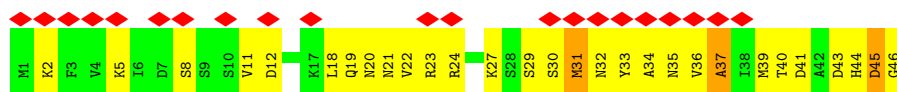
• Molecule 1: mRNA



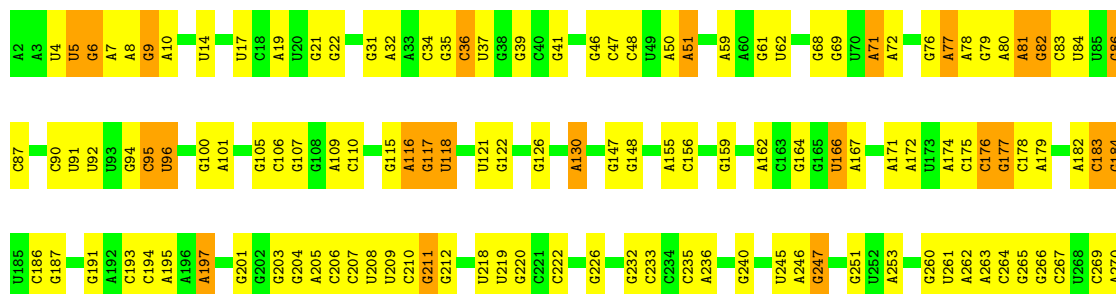
• Molecule 2: P-site tRNA-Gly

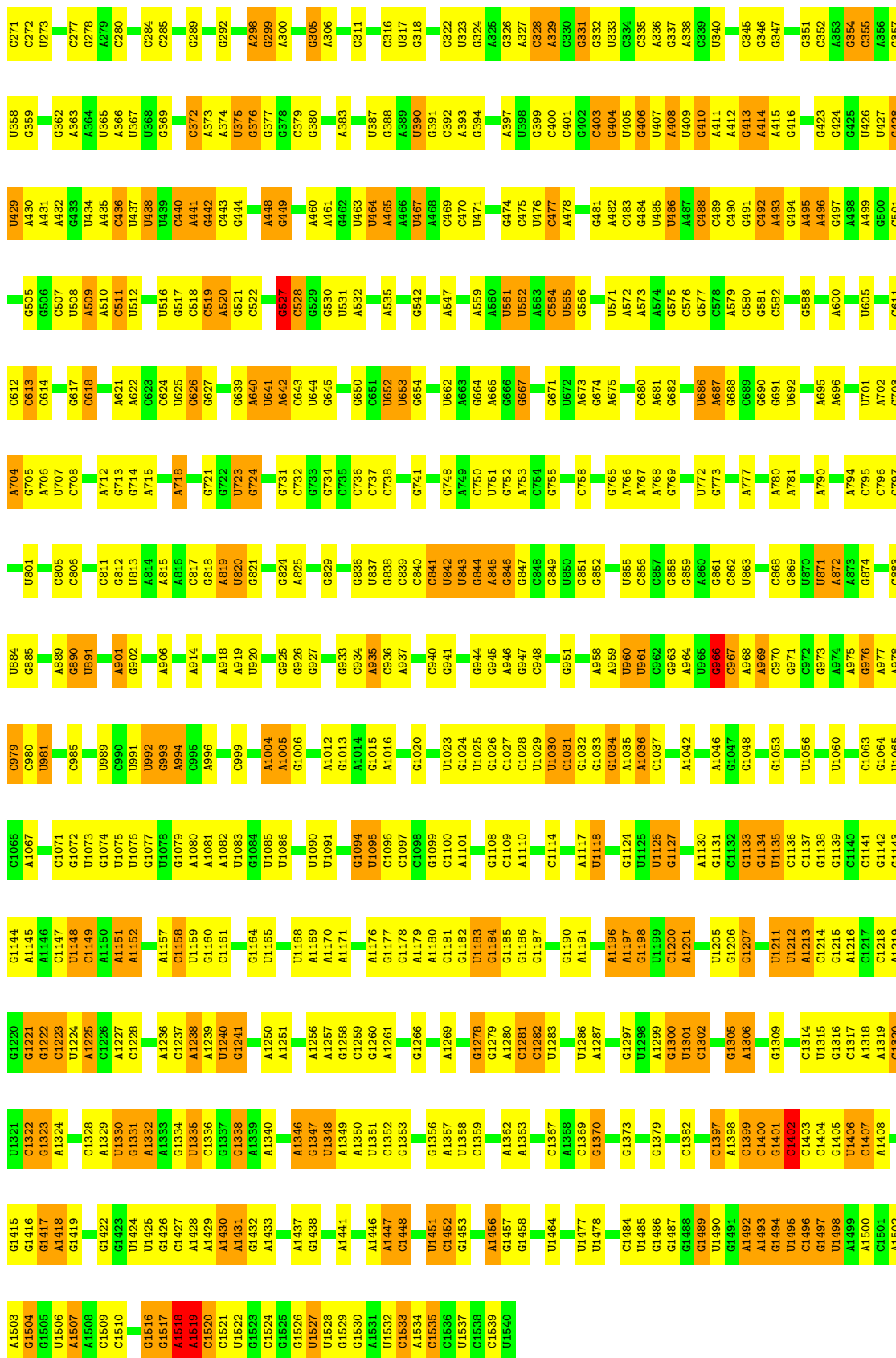


• Molecule 3: DNA topoisomerase small subunit



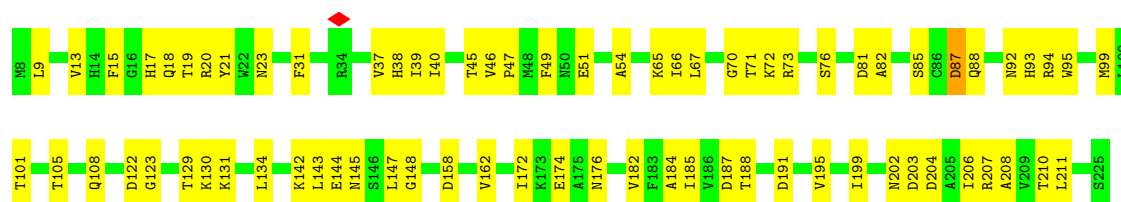
• Molecule 4: 16S ribosomal RNA





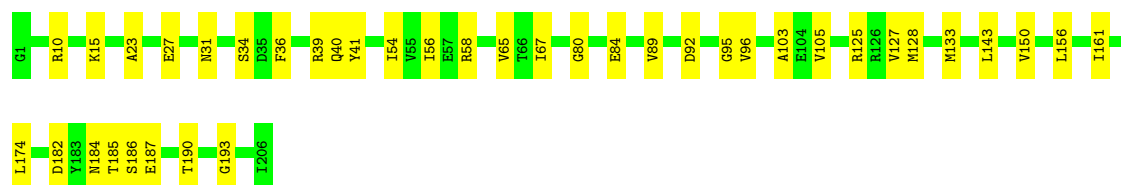
- Molecule 5: 30S ribosomal protein S2

Chain E:  66% 33%



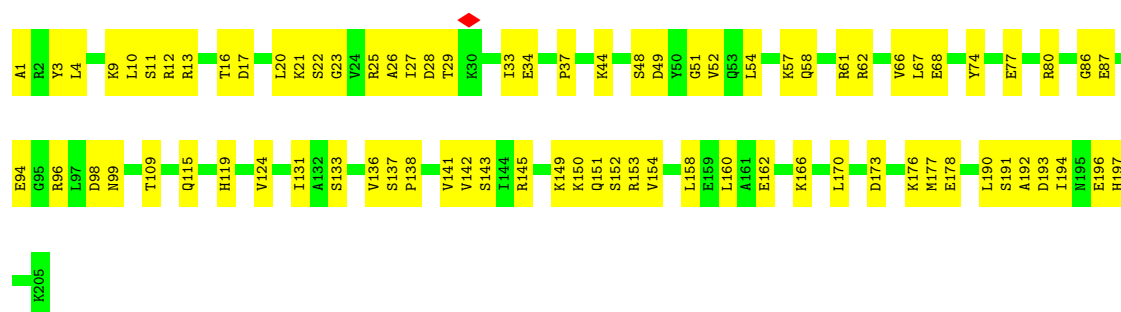
- Molecule 6: 30S ribosomal protein S3

Chain F:  81% 19%



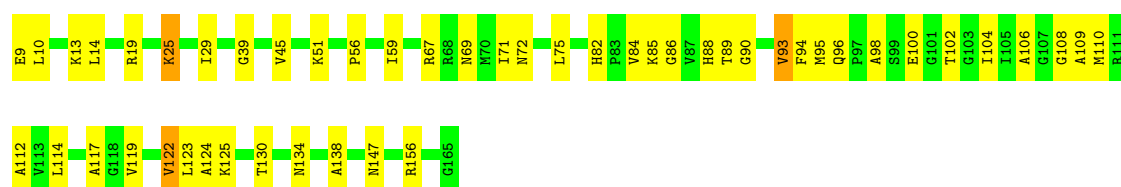
- Molecule 7: 30S ribosomal protein S4

Chain G:  61% 39%



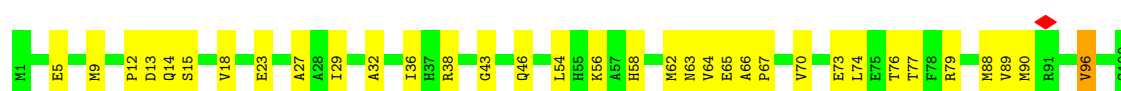
- Molecule 8: 30S ribosomal protein S5

Chain H:  69% 29%

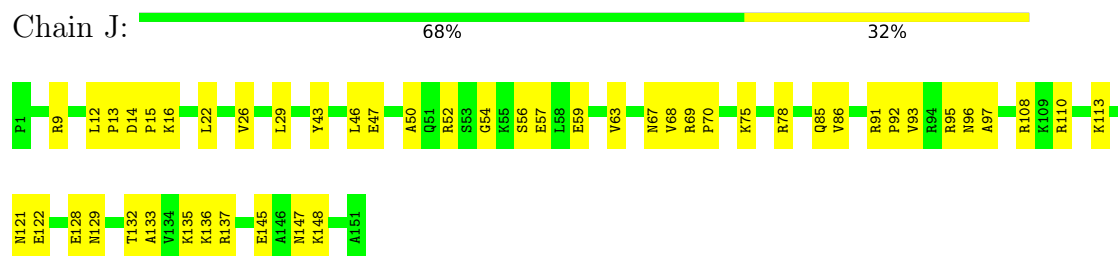


- Molecule 9: 30S ribosomal protein S6

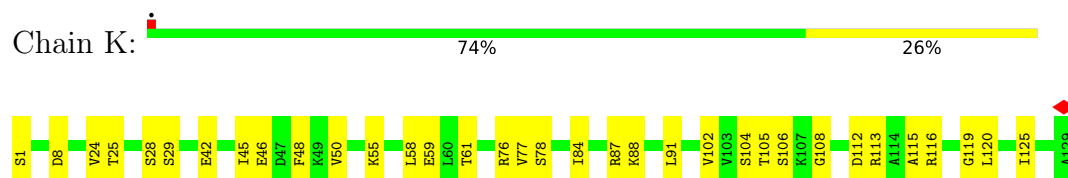
Chain I:  66% 33%



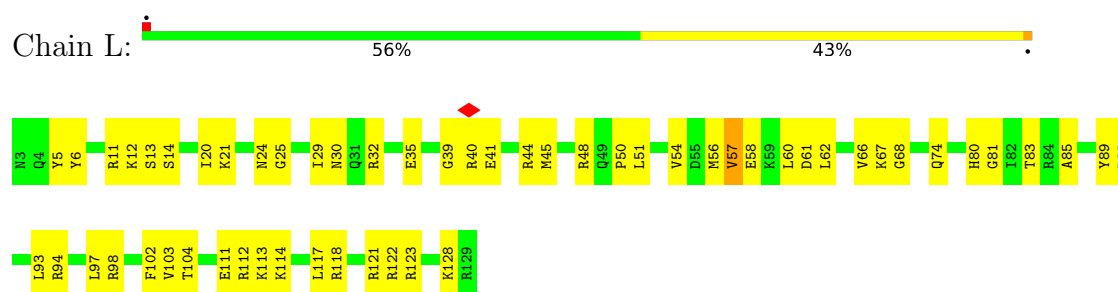
- Molecule 10: 30S ribosomal protein S7



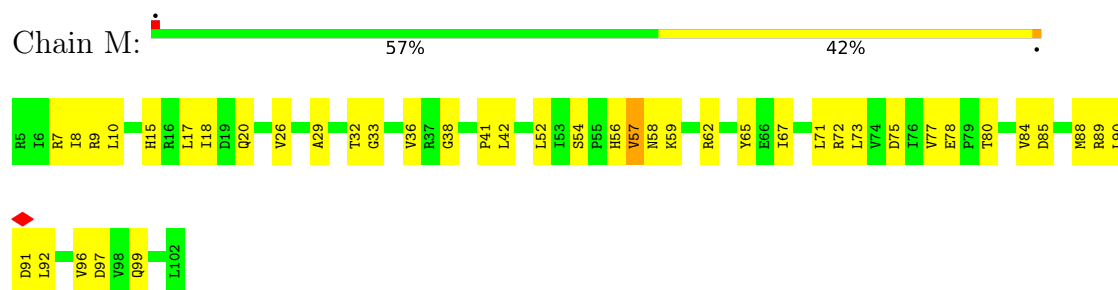
- Molecule 11: 30S ribosomal protein S8



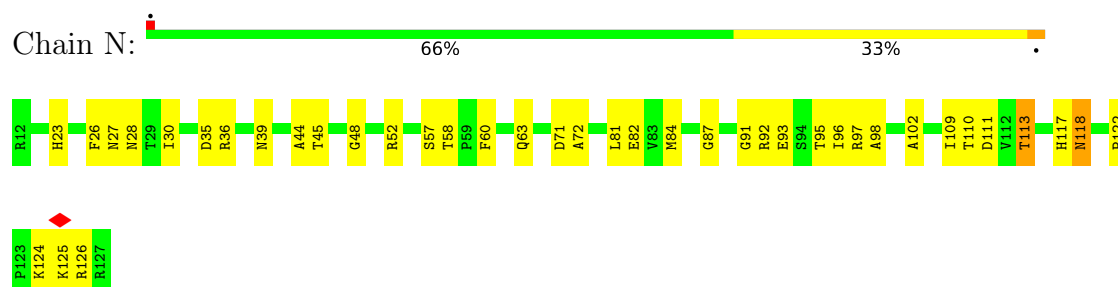
- Molecule 12: 30S ribosomal protein S9



- Molecule 13: 30S ribosomal protein S10



- Molecule 14: 30S ribosomal protein S11



- Molecule 15: 30S ribosomal protein S12

Chain O:  77% 23%



- Molecule 16: 30S ribosomal protein S13

Chain P:  74% 26%



- Molecule 17: 30S ribosomal protein S14

Chain Q:  69% 31%



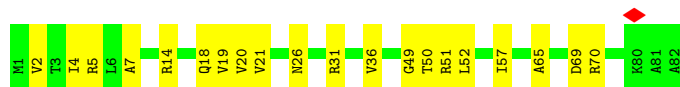
- Molecule 18: 30S ribosomal protein S15

Chain R:  82% 18%



- Molecule 19: 30S ribosomal protein S16

Chain S:  76% 24%



- Molecule 20: 30S ribosomal protein S17

Chain T:  76% 24%



- Molecule 21: 30S ribosomal protein S18

Chain U:  69% 29%



- Molecule 22: 30S ribosomal protein S19

Chain V:  73% 27%



- Molecule 23: 30S ribosomal protein S20

Chain W:  59% 40%

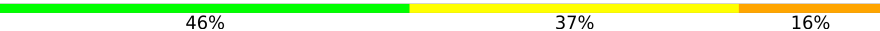


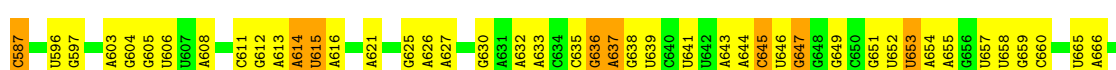
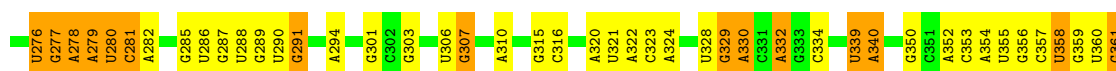
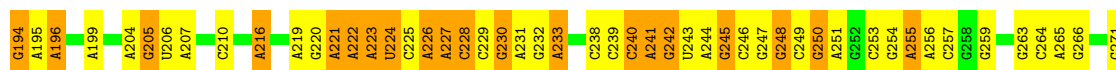
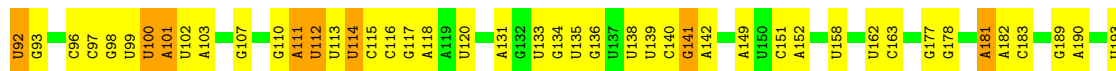
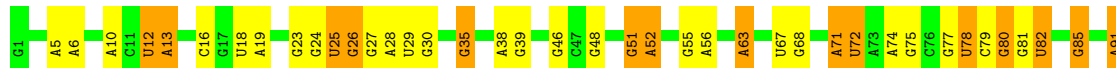
- Molecule 24: 30S ribosomal protein S21

Chain X:  68% 31%

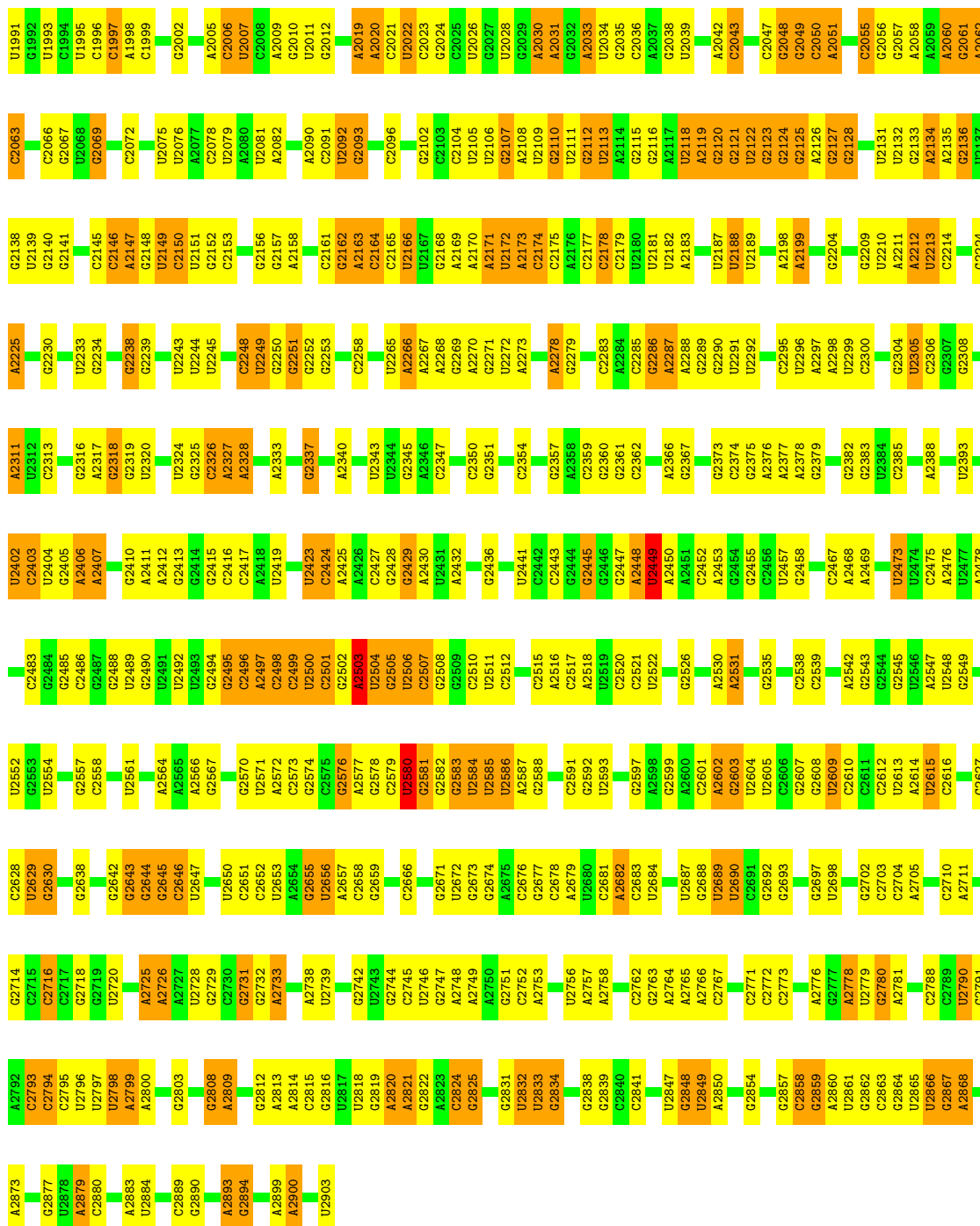


- Molecule 25: 23S ribosomal RNA

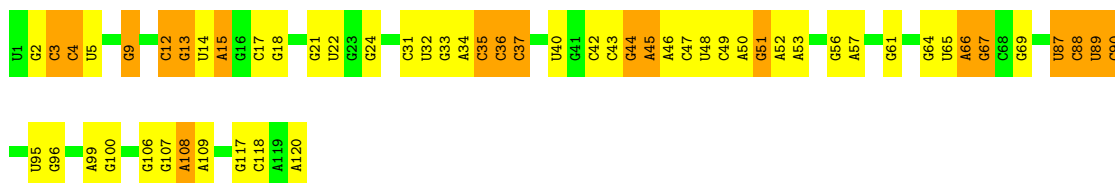
Chain Y:  46% 37% 16%



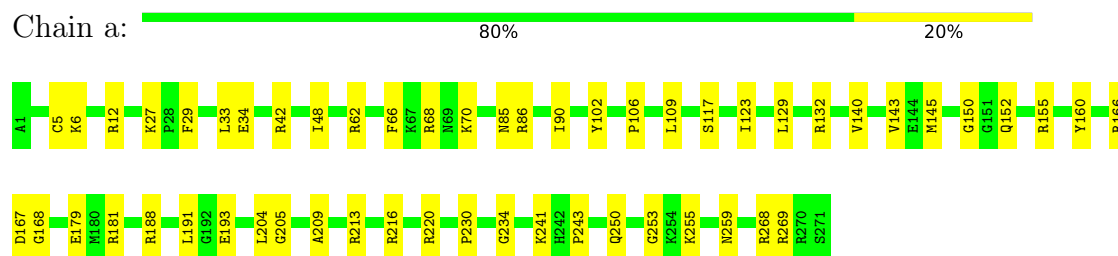
G1905	A1808	U1629	G1538	C1451	C1350	C1270	G1182	A1095	G1025	C851	C765	G669
G1906	A1809	A1630	U1639	G1452	C1351	G1271	G1187	A1096	G1026	U852	G770	A670
G1910	G1814	G1631	G1540	A1453	U1352	U1272	U1188	A1097	A1027	C853	G771	C671
U1911	A1815	A1632	G1543	C1454	C1357	A1273	A1189	U1098	A1028	C854	G772	C672
A1912	C1816	G1634	G1544	U1458	G1358	G1280	G1195	G1100	A1029	G855	U773	A675
A1913	G1817	A1635	A1545	G1459	A1359	G1281	C1196	U1101	G1030	G856	G774	A676
C1914	U1818	U1636	G1546	U1460	A1359	G1282	C1197	C1102	U1033	G857	G775	A677
3TD1915	A1819	A1637	U1559	G1461	C1363	G1283	U1198	A1103	G1034	G858	G776	U686
A1916	U1827	G1640	G1560	U1466	A1365	A1284	G1202	U1105	C1043	U860	U779	U686
U1917	G1828	A1641	U1568	U1467	G1368	A1285	G1208	G1106	C1044	U861	G780	U687
A1918	A1829	U1648	A1569	U1468	G1369	A1286	U1209	G1107	C1045	G862	A781	G890
C1920	C1833	G1649	C1574	A1469	U1370	G1287	U1220	U1108	A1046	C865	A782	U703
U1926	U1834	A1650	U1578	U1488	C1371	G1288	G1221	C1109	G1051	A866	A783	U704
A1927	G1835	G1651	G1579	G1475	A1372	A1289	U1222	G1110	C1052	C867	G784	G704
A1928	A1745	A1652	U1579	U1481	A1373	C1291	G1212	U1111	A1053	U868	G785	A705
G1929	G1836	G1653	U1579	G1482	A1374	G1292	A1213	G1112	C1054	G869	G786	A706
G1930	C1838	G1656	C1582	G1483	G1374	U1294	G1215	U1119	A1054	U870	C787	U710
U1931	G1839	U1657	U1583	U1484	A1378	C1295	G1218	G1124	C1055	A878	A788	G711
U1936	U1841	A1664	U1584	G1491	A1378	G1296	G1218	G1125	A1056	C964	A789	U711
A1937	G1842	A1665	U1584	G1492	U1379	C1297	G1221	U1126	C1057	C965	A793	A715
A1938	C1843	G1666	U1584	G1493	G1380	C1297	U1224	A1127	A1058	C966	U967	A716
U1939	G1845	G1667	C1585	G1494	A1383	G1299	G1223	G1128	C1059	C967	C796	C717
U1940	A1757	G1668	G1587	U1495	C1386	A1301	U1224	G1129	U1060	C968	A800	G726
C1941	G1846	A1669	U1587	A1496	A1392	A1306	A1226	U1130	C1062	A971	G801	A727
C1942	G1847	C1670	A1596	A1496	A1392	C1306	A1226	G1131	G1063	A972	A802	G728
U1943	A1848	U1671	A1596	U1497	A1395	G1310	G1230	U1132	C1064	A973	G805	G729
U1946	G1849	A1672	A1597	C1498	U1396	G1311	A1231	A1134	U1065	A983	C806	A730
C1947	A1858	G1673	A1598	C1498	U1397	C1315	G1231	C1135	A1066	A984	U807	C731
U1948	U1864	A1674	U1599	A1504	C1398	U1316	C1232	G1136	C1067	A985	G808	C732
G1949	U1865	C1600	C1600	A1505	G1398	G1317	C1233	G1137	A1068	A986	G808	G733
U1955	A1866	A1678	G1601	U1506	G1407	U1318	U1234	G1138	A1069	A987	G809	G734
C1961	G1867	U1679	U1602	C1507	U1415	C1319	G1235	G1139	A1070	A988	U811	A735
U1963	C1868	G1681	A1603	A1508	U1416	C1320	G1236	C1140	G1071	A989	C812	C736
C1962	G1869	U1682	C1604	A1509	G1416	A1321	A1237	U1141	C1072	C903	C813	C737
G1964	C1870	U1683	C1605	U1515	U1417	A1322	G1238	A1142	A1073	G904	C814	G738
U1967	A1871	G1684	C1606	G1516	G1418	G1324	U1240	C1152	C1075	A905	G818	U744
C1967	G1872	C1685	C1607	U1516	G1419	C1324	A1244	G1153	C1076	A906	G818	G745
G1968	C1874	U1687	A1608	G1521	A1420	U1325	G1245	G1154	C1077	A907	A819	U746
A1969	U1875	G1688	A1609	A1522	G1424	U1326	A1246	A1155	U1078	A910	U826	G748
A1970	A1876	U1689	A1610	U1523	G1425	A1327	U1247	C1167	C1079	A911	U827	A749
U1971	G1884	A1698	A1614	U1524	G1426	A1328	G1248	C1168	A1080	G914	U828	A750
G1972	U1889	G1699	C1615	U1525	A1427	U1329	U1249	A1169	U1081	C915	A829	A751
G1975	A1890	A1700	C1616	A1526	G1428	C1330	G1250	C1170	U1082	U1010	U832	A752
U1976	U1891	G1702	A1617	G1527	G1429	G1334	C1251	C1171	A1084	A1009	A833	U753
G1980	C1895	C1703	A1618	G1530	G1430	U1340	G1252	G1172	A1085	A1010	G834	U754
U1981	U1896	G1704	A1619	C1531	A1431	G1341	A1253	C1175	A1086	G1011	U832	G757
U1982	C1900	A1705	G1622	G1532	A1432	A1342	U1255	A1176	G1087	U1012	A844	C758
G1983	A1801	C1706	U1624	C1533	G1433	G1342	G1256	A1177	A1088	A927	A845	G759
G1984	A1901	C1706	C1625	U1534	G1435	C1345	C1257	C1178	A1089	A928	U846	G760
C1990	G1904	U1716	A1626	U1535	G1436	G1346	G1265	C1179	A1090	U929	U847	A761
			G1627	C1536	C1437	C1347	A1266	U1180	G1091	G930	C848	U762
			G1628	G1537	C1447	C1349	G1266	U1181	C1092	U931	A849	A764
									G1093	U932	U850	



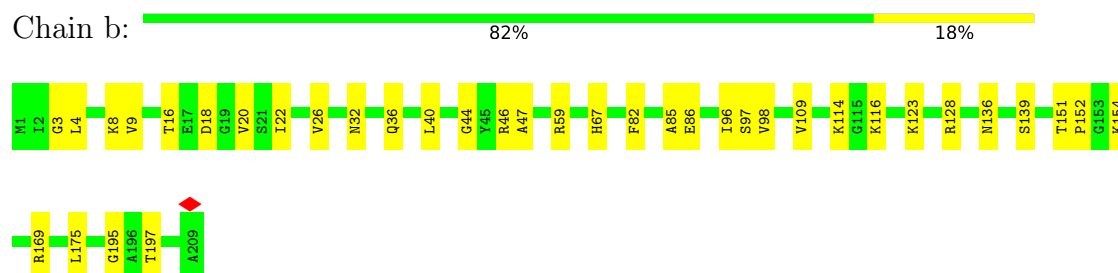
- Molecule 26: 5S ribosomal RNA



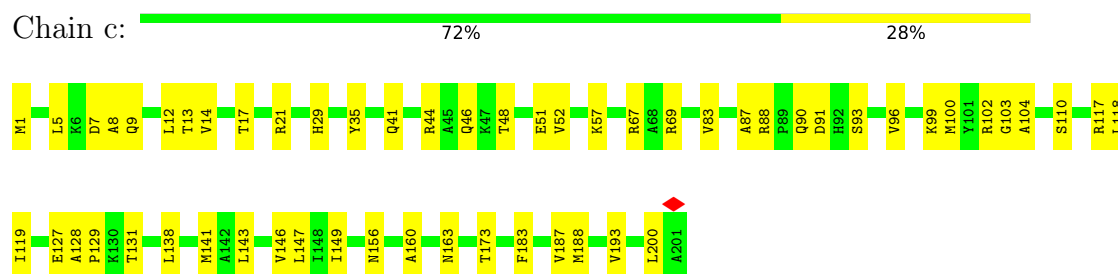
- Molecule 27: 50S ribosomal protein L2



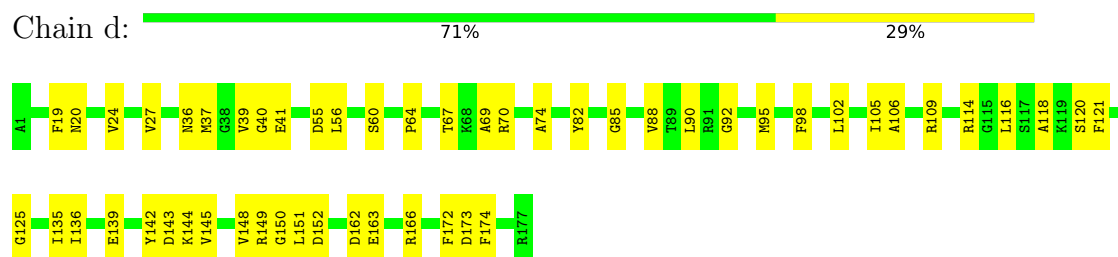
- Molecule 28: 50S ribosomal protein L3



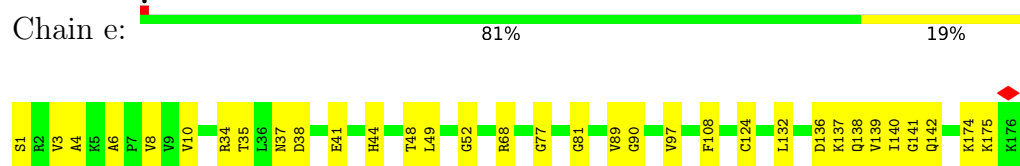
- Molecule 29: 50S ribosomal protein L4



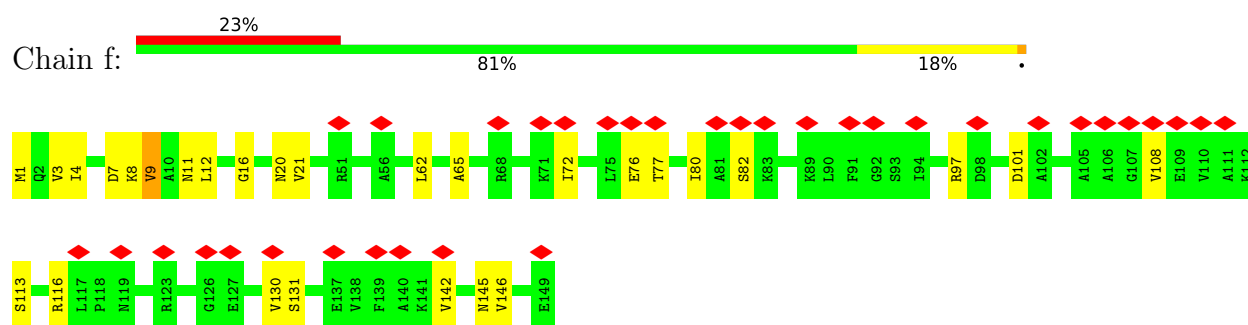
- Molecule 30: 50S ribosomal protein L5



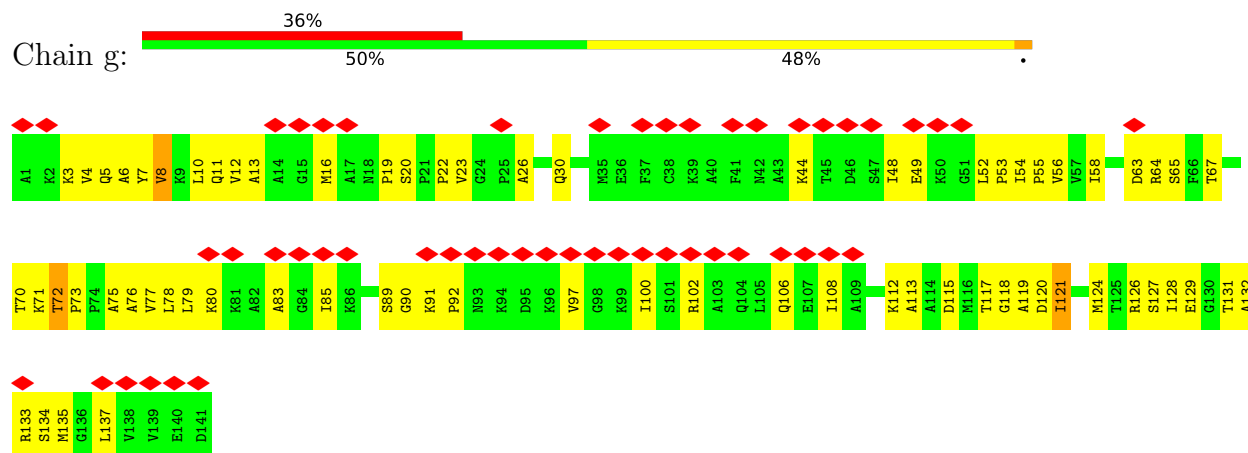
- Molecule 31: 50S ribosomal protein L6



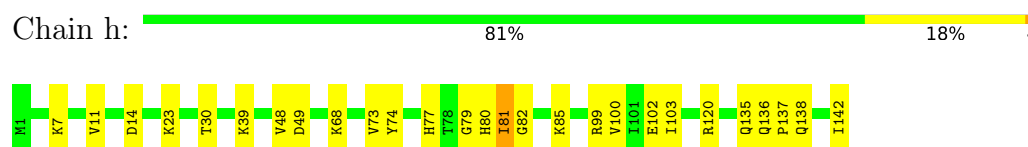
- Molecule 32: 50S ribosomal protein L9



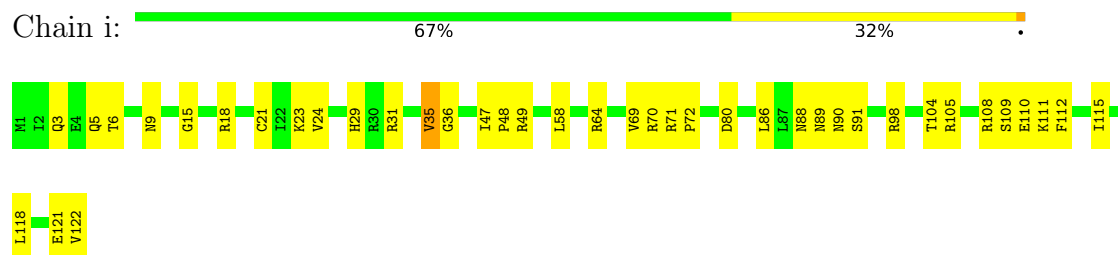
• Molecule 33: 50S ribosomal protein L11



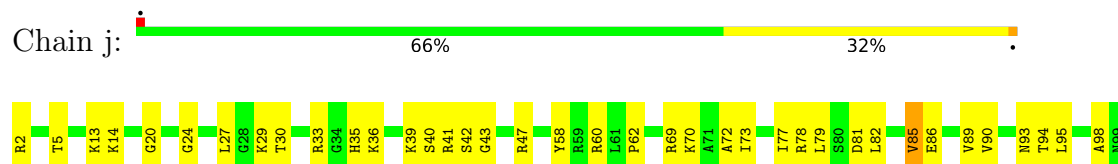
• Molecule 34: 50S ribosomal protein L13



• Molecule 35: 50S ribosomal protein L14



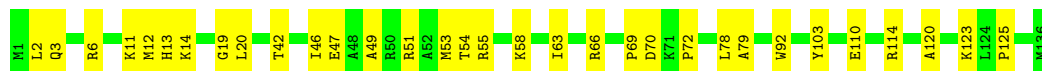
• Molecule 36: 50S ribosomal protein L15





- Molecule 37: 50S ribosomal protein L16

Chain k: 76% 24%



- Molecule 38: 50S ribosomal protein L17

Chain l: 69% 30%



- Molecule 39: 50S ribosomal protein L18

Chain m: 74% 26%



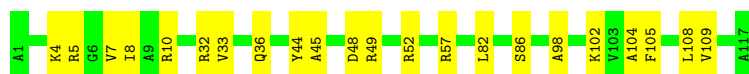
- Molecule 40: 50S ribosomal protein L19

Chain n: 79% 21%



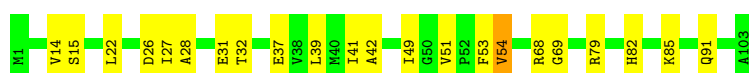
- Molecule 41: 50S ribosomal protein L20

Chain o: 81% 19%



- Molecule 42: 50S ribosomal protein L21

Chain p: 79% 20%



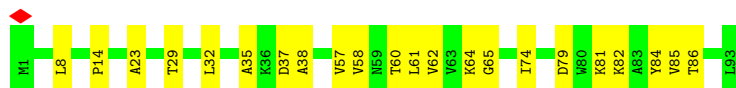
- Molecule 43: 50S ribosomal protein L22

Chain q:  68% 32%



- Molecule 44: 50S ribosomal protein L23

Chain r:  76% 24%



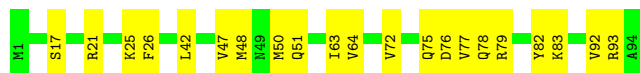
- Molecule 45: 50S ribosomal protein L24

Chain s:  78% 22%



- Molecule 46: 50S ribosomal protein L25

Chain t:  78% 22%



- Molecule 47: 50S ribosomal protein L27

Chain u:  89% 11%



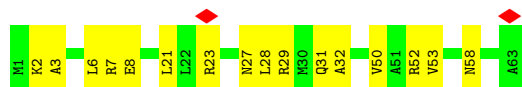
- Molecule 48: 50S ribosomal protein L28

Chain v:  78% 22%

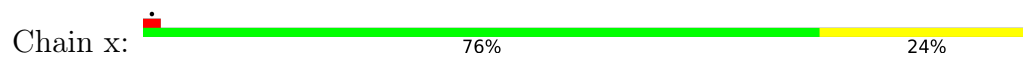


- Molecule 49: 50S ribosomal protein L29

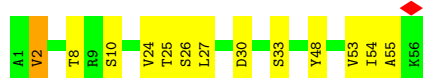
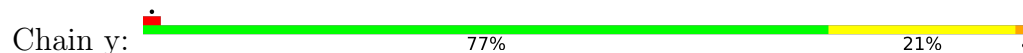
Chain w:  75% 25%



- Molecule 50: 50S ribosomal protein L30



- Molecule 51: 50S ribosomal protein L32



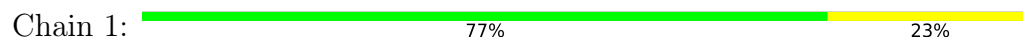
- Molecule 52: 50S ribosomal protein L33



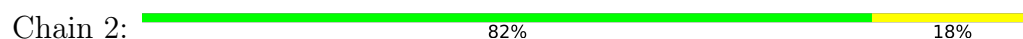
- Molecule 53: 50S ribosomal protein L34



- Molecule 54: 50S ribosomal protein L35

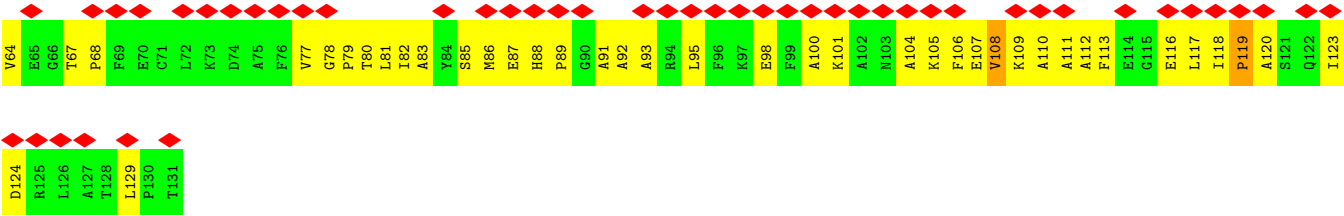


- Molecule 55: 50S ribosomal protein L36

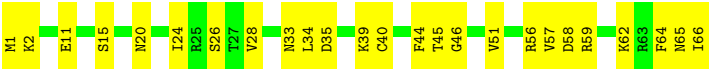


- Molecule 56: 50S ribosomal protein L10





• Molecule 57: 50S ribosomal protein L31



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	36983	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE; CTF correction inside Relion	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.66	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	47170	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.033	Depositor
Minimum map value	-0.014	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0045	Depositor
Map size ($\text{\AA}$)	360.4, 360.4, 360.4	wwPDB
Map dimensions	340, 340, 340	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.06, 1.06, 1.06	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 5MC, 7MG, 3TD, 2MG, UR3, OMG, 2MA, 6MZ, 1MG, OMU, MA6, PSU, 5MU, 4OC, OMC, H2U

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	0.58	0/694	1.01	2/1078 (0.2%)
2	B	0.16	0/1812	0.38	0/2822
3	C	0.37	0/365	0.99	4/485 (0.8%)
4	D	0.14	1/36700 (0.0%)	0.30	0/57246
5	E	0.23	1/1735 (0.1%)	0.42	0/2338
6	F	0.21	0/1651	0.40	0/2225
7	G	0.25	1/1665 (0.1%)	0.44	0/2227
8	H	0.18	0/1154	0.44	0/1554
9	I	0.18	0/835	0.44	0/1128
10	J	0.16	0/1195	0.40	0/1602
11	K	0.27	1/989 (0.1%)	0.43	0/1326
12	L	0.31	1/1034 (0.1%)	0.54	2/1375 (0.1%)
13	M	0.28	1/796 (0.1%)	0.37	0/1077
14	N	0.26	1/885 (0.1%)	0.45	0/1195
15	O	0.21	0/969	0.43	0/1300
16	P	0.18	0/892	0.41	0/1193
17	Q	0.20	0/811	0.41	0/1081
18	R	0.34	1/722 (0.1%)	0.50	2/964 (0.2%)
19	S	0.21	0/659	0.41	0/884
20	T	0.19	0/657	0.44	0/881
21	U	0.18	0/511	0.42	0/689
22	V	0.17	0/652	0.40	0/877
23	W	0.35	1/671 (0.1%)	0.49	2/888 (0.2%)
24	X	0.21	0/500	0.52	0/668
25	Y	0.14	1/69244 (0.0%)	0.31	0/108021
26	Z	0.12	0/2876	0.28	0/4483
27	a	0.32	0/2121	0.43	0/2852
28	b	0.17	0/1586	0.35	0/2134
29	c	0.32	1/1571 (0.1%)	0.39	0/2113
30	d	0.17	0/1434	0.39	0/1926
31	e	0.15	0/1343	0.39	0/1816

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	f	0.24	0/1122	0.43	0/1515
33	g	0.18	0/1046	0.45	0/1410
34	h	0.16	0/1152	0.35	0/1551
35	i	0.19	0/947	0.40	0/1268
36	j	0.36	1/1054 (0.1%)	0.55	2/1403 (0.1%)
37	k	0.19	0/1093	0.42	0/1460
38	l	0.19	0/973	0.46	0/1301
39	m	0.15	0/902	0.41	0/1209
40	n	0.29	1/929 (0.1%)	0.40	0/1242
41	o	0.29	0/960	0.42	0/1278
42	p	0.17	0/829	0.41	0/1107
43	q	0.19	0/864	0.43	0/1156
44	r	0.17	0/744	0.34	0/994
45	s	0.21	0/787	0.41	0/1051
46	t	0.16	0/766	0.33	0/1025
47	u	0.18	0/582	0.36	0/769
48	v	0.19	0/635	0.37	0/848
49	w	0.34	1/510 (0.2%)	0.42	0/677
50	x	0.17	0/453	0.35	0/605
51	y	0.17	0/450	0.38	0/599
52	z	0.17	0/416	0.39	0/554
53	0	0.19	0/380	0.45	0/498
54	1	0.17	0/513	0.53	0/676
55	2	0.21	0/303	0.45	0/397
56	3	0.21	0/1001	0.49	0/1350
57	4	0.16	0/531	0.45	0/709
All	All	0.18	14/158671 (0.0%)	0.35	14/237100 (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
1	A	3	3
5	E	0	1
23	W	0	1
40	n	0	1
56	3	0	2
All	All	3	8

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
29	c	128	ALA	C-N	8.49	1.53	1.33
4	D	1489	G	O3'-P	-7.76	1.49	1.61
11	K	55	LYS	C-N	6.50	1.49	1.33
13	M	78	GLU	C-N	6.20	1.48	1.33
18	R	41	HIS	ND1-CE1	5.25	1.37	1.32

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	43	ASP	N-CA-C	11.03	123.30	111.28
1	A	15	G	C4'-C3'-O3'	6.62	122.94	113.00
23	W	19	HIS	CB-CG-CD2	-6.62	122.59	131.20
12	L	80	HIS	CB-CG-CD2	-6.56	122.67	131.20
36	j	35	HIS	CB-CG-CD2	-6.52	122.72	131.20

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	15	G	C2',C4',C3'

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	13	U	Sidechain
1	A	17	G	Sidechain
1	A	18	C	Sidechain
5	E	87	ASP	Peptide
23	W	68	LYS	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	621	0	310	111	0
2	B	1623	0	822	75	0
3	C	362	0	368	86	0
4	D	33028	0	16644	614	0
5	E	1704	0	1732	50	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	F	1624	0	1699	29	0
7	G	1643	0	1708	68	0
8	H	1141	0	1170	62	0
9	I	817	0	808	29	0
10	J	1181	0	1240	33	0
11	K	979	0	1034	22	0
12	L	1022	0	1070	45	0
13	M	786	0	828	32	0
14	N	869	0	878	38	0
15	O	955	0	1019	20	0
16	P	883	0	944	25	0
17	Q	799	0	841	28	0
18	R	714	0	737	11	0
19	S	649	0	666	14	0
20	T	648	0	691	16	0
21	U	504	0	502	13	0
22	V	637	0	665	16	0
23	W	665	0	714	36	0
24	X	495	0	486	22	0
25	Y	62338	0	31376	1346	0
26	Z	2572	0	1302	45	0
27	a	2082	0	2157	45	0
28	b	1565	0	1616	26	0
29	c	1552	0	1619	37	0
30	d	1410	0	1447	38	0
31	e	1323	0	1374	22	0
32	f	1111	0	1148	18	0
33	g	1032	0	1088	91	0
34	h	1129	0	1162	16	0
35	i	938	0	1012	29	0
36	j	1045	0	1117	40	0
37	k	1074	0	1157	24	0
38	l	960	0	1000	27	0
39	m	892	0	923	19	0
40	n	917	0	965	18	0
41	o	947	0	1022	16	0
42	p	816	0	839	17	0
43	q	857	0	922	35	0
44	r	738	0	807	21	0
45	s	779	0	834	15	0
46	t	753	0	780	13	0
47	u	575	0	592	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
48	v	625	0	655	15	0
49	w	509	0	543	12	0
50	x	449	0	491	9	0
51	y	444	0	461	13	0
52	z	409	0	440	9	0
53	0	377	0	418	14	0
54	1	504	0	574	16	0
55	2	302	0	343	7	0
56	3	988	0	1025	82	0
57	4	522	0	522	22	0
All	All	146883	0	99307	3257	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 14.

The worst 5 of 3257 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)
2:B:17:C:H4'	2:B:18:G:C5'	1.44	1.44
1:A:26:A:H62	8:H:19:ARG:NH1	1.15	1.41
1:A:26:A:H62	8:H:19:ARG:CZ	1.32	1.40
2:B:17:C:N3	2:B:61:C:H5'	1.22	1.40
1:A:27:G:H2'	1:A:28:A:C8	1.59	1.38

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	
3	C	44/46 (96%)	37 (84%)	6 (14%)	1 (2%)	5	30
5	E	216/218 (99%)	177 (82%)	39 (18%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	F	204/206 (99%)	178 (87%)	26 (13%)	0	100	100
7	G	203/205 (99%)	162 (80%)	41 (20%)	0	100	100
8	H	155/157 (99%)	128 (83%)	24 (16%)	3 (2%)	6	33
9	I	98/100 (98%)	79 (81%)	18 (18%)	1 (1%)	12	45
10	J	149/151 (99%)	124 (83%)	25 (17%)	0	100	100
11	K	127/129 (98%)	107 (84%)	19 (15%)	1 (1%)	16	49
12	L	125/127 (98%)	95 (76%)	29 (23%)	1 (1%)	16	49
13	M	96/98 (98%)	75 (78%)	20 (21%)	1 (1%)	12	45
14	N	114/116 (98%)	97 (85%)	16 (14%)	1 (1%)	14	46
15	O	121/123 (98%)	101 (84%)	20 (16%)	0	100	100
16	P	112/114 (98%)	91 (81%)	21 (19%)	0	100	100
17	Q	99/101 (98%)	75 (76%)	24 (24%)	0	100	100
18	R	86/88 (98%)	66 (77%)	20 (23%)	0	100	100
19	S	80/82 (98%)	66 (82%)	14 (18%)	0	100	100
20	T	78/80 (98%)	69 (88%)	9 (12%)	0	100	100
21	U	63/65 (97%)	52 (82%)	10 (16%)	1 (2%)	7	36
22	V	77/79 (98%)	66 (86%)	11 (14%)	0	100	100
23	W	83/85 (98%)	66 (80%)	17 (20%)	0	100	100
24	X	63/65 (97%)	41 (65%)	21 (33%)	1 (2%)	7	36
27	a	269/271 (99%)	241 (90%)	28 (10%)	0	100	100
28	b	207/209 (99%)	184 (89%)	23 (11%)	0	100	100
29	c	199/201 (99%)	172 (86%)	26 (13%)	1 (0%)	24	57
30	d	175/177 (99%)	151 (86%)	24 (14%)	0	100	100
31	e	174/176 (99%)	153 (88%)	21 (12%)	0	100	100
32	f	147/149 (99%)	121 (82%)	24 (16%)	2 (1%)	9	38
33	g	139/141 (99%)	114 (82%)	22 (16%)	3 (2%)	5	30
34	h	140/142 (99%)	129 (92%)	7 (5%)	4 (3%)	3	26
35	i	120/122 (98%)	108 (90%)	11 (9%)	1 (1%)	16	49
36	j	141/143 (99%)	121 (86%)	18 (13%)	2 (1%)	9	38
37	k	134/136 (98%)	116 (87%)	18 (13%)	0	100	100
38	l	118/120 (98%)	98 (83%)	19 (16%)	1 (1%)	16	49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	m	114/116 (98%)	92 (81%)	21 (18%)	1 (1%)	14	46
40	n	112/114 (98%)	103 (92%)	9 (8%)	0	100	100
41	o	115/117 (98%)	92 (80%)	23 (20%)	0	100	100
42	p	101/103 (98%)	89 (88%)	11 (11%)	1 (1%)	12	45
43	q	108/110 (98%)	92 (85%)	16 (15%)	0	100	100
44	r	91/93 (98%)	74 (81%)	17 (19%)	0	100	100
45	s	100/102 (98%)	89 (89%)	11 (11%)	0	100	100
46	t	92/94 (98%)	85 (92%)	7 (8%)	0	100	100
47	u	73/75 (97%)	69 (94%)	4 (6%)	0	100	100
48	v	75/77 (97%)	67 (89%)	8 (11%)	0	100	100
49	w	61/63 (97%)	49 (80%)	12 (20%)	0	100	100
50	x	56/58 (97%)	49 (88%)	6 (11%)	1 (2%)	6	34
51	y	54/56 (96%)	49 (91%)	4 (7%)	1 (2%)	6	33
52	z	48/50 (96%)	42 (88%)	5 (10%)	1 (2%)	5	31
53	0	44/46 (96%)	35 (80%)	9 (20%)	0	100	100
54	1	62/64 (97%)	56 (90%)	6 (10%)	0	100	100
55	2	36/38 (95%)	32 (89%)	4 (11%)	0	100	100
56	3	129/131 (98%)	102 (79%)	23 (18%)	4 (3%)	3	25
57	4	64/66 (97%)	53 (83%)	11 (17%)	0	100	100
All	All	5891/5995 (98%)	4979 (84%)	878 (15%)	34 (1%)	23	54

5 of 34 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	45	ASP
34	h	81	ILE
52	z	4	ILE
8	H	122	VAL
39	m	35	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	
3	C	42/42 (100%)	42 (100%)	0	100	100
5	E	180/180 (100%)	180 (100%)	0	100	100
6	F	170/170 (100%)	170 (100%)	0	100	100
7	G	172/172 (100%)	172 (100%)	0	100	100
8	H	114/119 (96%)	114 (100%)	0	100	100
9	I	87/87 (100%)	87 (100%)	0	100	100
10	J	124/124 (100%)	124 (100%)	0	100	100
11	K	104/104 (100%)	104 (100%)	0	100	100
12	L	105/105 (100%)	105 (100%)	0	100	100
13	M	86/86 (100%)	86 (100%)	0	100	100
14	N	89/89 (100%)	89 (100%)	0	100	100
15	O	103/103 (100%)	103 (100%)	0	100	100
16	P	92/92 (100%)	92 (100%)	0	100	100
17	Q	79/83 (95%)	79 (100%)	0	100	100
18	R	76/76 (100%)	76 (100%)	0	100	100
19	S	65/65 (100%)	65 (100%)	0	100	100
20	T	74/74 (100%)	74 (100%)	0	100	100
21	U	48/56 (86%)	48 (100%)	0	100	100
22	V	70/70 (100%)	70 (100%)	0	100	100
23	W	65/65 (100%)	65 (100%)	0	100	100
24	X	44/55 (80%)	44 (100%)	0	100	100
27	a	216/216 (100%)	216 (100%)	0	100	100
28	b	164/164 (100%)	164 (100%)	0	100	100
29	c	165/165 (100%)	165 (100%)	0	100	100
30	d	148/148 (100%)	148 (100%)	0	100	100
31	e	137/137 (100%)	137 (100%)	0	100	100
32	f	114/114 (100%)	114 (100%)	0	100	100
33	g	109/109 (100%)	109 (100%)	0	100	100
34	h	116/116 (100%)	116 (100%)	0	100	100
35	i	103/103 (100%)	103 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	j	102/102 (100%)	102 (100%)	0	100	100
37	k	109/109 (100%)	109 (100%)	0	100	100
38	l	100/100 (100%)	100 (100%)	0	100	100
39	m	86/86 (100%)	86 (100%)	0	100	100
40	n	99/99 (100%)	99 (100%)	0	100	100
41	o	89/89 (100%)	89 (100%)	0	100	100
42	p	84/84 (100%)	84 (100%)	0	100	100
43	q	93/93 (100%)	93 (100%)	0	100	100
44	r	80/80 (100%)	80 (100%)	0	100	100
45	s	83/83 (100%)	83 (100%)	0	100	100
46	t	78/78 (100%)	78 (100%)	0	100	100
47	u	57/57 (100%)	57 (100%)	0	100	100
48	v	67/67 (100%)	67 (100%)	0	100	100
49	w	55/55 (100%)	55 (100%)	0	100	100
50	x	48/48 (100%)	48 (100%)	0	100	100
51	y	47/47 (100%)	47 (100%)	0	100	100
52	z	45/45 (100%)	45 (100%)	0	100	100
53	0	38/38 (100%)	38 (100%)	0	100	100
54	1	51/51 (100%)	51 (100%)	0	100	100
55	2	34/34 (100%)	34 (100%)	0	100	100
56	3	100/100 (100%)	100 (100%)	0	100	100
57	4	59/59 (100%)	59 (100%)	0	100	100
All	All	4865/4893 (99%)	4865 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
32	f	128	HIS
41	o	80	ASN
53	0	29	GLN
37	k	17	ASN
42	p	12	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	28/29 (96%)	14 (50%)	8 (28%)
2	B	75/76 (98%)	18 (24%)	3 (4%)
25	Y	2902/2903 (99%)	676 (23%)	123 (4%)
26	Z	119/120 (99%)	22 (18%)	6 (5%)
4	D	1538/1539 (99%)	329 (21%)	58 (3%)
All	All	4662/4667 (99%)	1059 (22%)	198 (4%)

5 of 1059 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	A
1	A	7	U
1	A	8	A
1	A	15	G
1	A	16	G

5 of 198 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
25	Y	1060	U
25	Y	1728	C
25	Y	1103	A
25	Y	1327	A
25	Y	1941	C

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

35 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
25	5MU	Y	1939	25	19,22,23	4.76	7 (36%)	28,32,35	3.56	9 (32%)
4	2MG	D	966	4	23,26,27	2.96	8 (34%)	32,38,41	2.22	12 (37%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	MA6	D	1519	4	23,26,27	1.40	5 (21%)	34,38,41	2.70	11 (32%)
4	5MC	D	1407	4	18,22,23	3.74	7 (38%)	26,32,35	1.04	1 (3%)
25	PSU	Y	1911	25	18,21,22	1.03	1 (5%)	22,30,33	1.85	5 (22%)
25	5MC	Y	747	25	18,22,23	3.78	7 (38%)	26,32,35	1.05	2 (7%)
25	2MG	Y	1835	25	23,26,27	2.97	8 (34%)	32,38,41	2.19	10 (31%)
4	UR3	D	1498	4	19,22,23	2.74	8 (42%)	26,32,35	1.23	1 (3%)
4	PSU	D	516	4	18,21,22	1.09	1 (5%)	22,30,33	1.84	6 (27%)
25	PSU	Y	2580	25	18,21,22	0.98	1 (5%)	22,30,33	1.84	4 (18%)
25	1MG	Y	745	25	22,26,27	2.71	5 (22%)	33,39,42	1.97	7 (21%)
25	7MG	Y	2069	25	22,26,27	3.74	10 (45%)	29,39,42	1.98	8 (27%)
25	6MZ	Y	1618	25	22,25,26	3.01	4 (18%)	30,36,39	4.00	12 (40%)
25	2MG	Y	2445	25	23,26,27	2.96	8 (34%)	32,38,41	2.17	11 (34%)
25	5MC	Y	1962	25	18,22,23	3.81	7 (38%)	26,32,35	1.08	2 (7%)
4	2MG	D	1207	4	23,26,27	2.97	8 (34%)	32,38,41	2.16	9 (28%)
25	PSU	Y	2604	25	18,21,22	1.05	1 (5%)	22,30,33	1.87	5 (22%)
25	PSU	Y	2605	25	18,21,22	1.04	1 (5%)	22,30,33	1.85	5 (22%)
25	OMC	Y	2498	25	19,22,23	3.01	7 (36%)	26,31,34	0.70	0
4	5MC	D	967	4	18,22,23	3.77	7 (38%)	26,32,35	1.09	2 (7%)
25	3TD	Y	1915	25	18,22,23	4.40	5 (27%)	22,32,35	1.61	3 (13%)
25	H2U	Y	2449	25	18,21,22	3.00	5 (27%)	21,30,33	2.11	5 (23%)
4	4OC	D	1402	4	20,23,24	0.79	0	26,32,35	1.15	2 (7%)
25	6MZ	Y	2030	25	22,25,26	2.97	4 (18%)	30,36,39	4.16	14 (46%)
25	2MA	Y	2503	25	22,25,26	3.75	8 (36%)	33,37,40	2.08	9 (27%)
25	PSU	Y	746	25	18,21,22	1.04	1 (5%)	22,30,33	1.77	4 (18%)
4	2MG	D	1516	4	23,26,27	2.97	8 (34%)	32,38,41	2.14	10 (31%)
25	PSU	Y	2504	25	18,21,22	1.02	2 (11%)	22,30,33	1.94	5 (22%)
4	MA6	D	1518	4	23,26,27	1.43	5 (21%)	34,38,41	2.64	11 (32%)
25	PSU	Y	955	25	18,21,22	1.07	1 (5%)	22,30,33	1.81	5 (22%)
25	PSU	Y	1917	25	18,21,22	1.05	1 (5%)	22,30,33	1.81	5 (22%)
25	OMG	Y	2251	25,2	23,26,27	2.45	8 (34%)	33,38,41	1.95	9 (27%)
25	OMU	Y	2552	25	19,22,23	3.02	8 (42%)	26,31,34	1.66	4 (15%)
25	PSU	Y	2457	25	18,21,22	1.01	1 (5%)	22,30,33	1.84	4 (18%)
4	7MG	D	527	4	22,26,27	3.82	10 (45%)	29,39,42	2.09	9 (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
25	5MU	Y	1939	25	-	2/7/25/26	0/2/2/2
4	2MG	D	966	4	-	2/9/27/28	0/3/3/3
4	MA6	D	1519	4	-	6/11/29/30	0/3/3/3
4	5MC	D	1407	4	-	1/7/25/26	0/2/2/2
25	PSU	Y	1911	25	-	1/7/25/26	0/2/2/2
25	5MC	Y	747	25	-	3/7/25/26	0/2/2/2
25	2MG	Y	1835	25	-	2/9/27/28	0/3/3/3
4	UR3	D	1498	4	-	2/7/25/26	0/2/2/2
4	PSU	D	516	4	-	0/7/25/26	0/2/2/2
25	PSU	Y	2580	25	-	0/7/25/26	0/2/2/2
25	1MG	Y	745	25	-	0/7/25/26	0/3/3/3
25	7MG	Y	2069	25	-	2/7/37/38	0/3/3/3
25	6MZ	Y	1618	25	-	2/9/27/28	0/3/3/3
25	2MG	Y	2445	25	-	2/9/27/28	0/3/3/3
25	5MC	Y	1962	25	-	3/7/25/26	0/2/2/2
4	2MG	D	1207	4	-	2/9/27/28	0/3/3/3
25	PSU	Y	2604	25	-	0/7/25/26	0/2/2/2
25	PSU	Y	2605	25	-	0/7/25/26	0/2/2/2
25	OMC	Y	2498	25	-	2/9/27/28	0/2/2/2
4	5MC	D	967	4	-	0/7/25/26	0/2/2/2
25	3TD	Y	1915	25	-	3/7/25/26	0/2/2/2
25	H2U	Y	2449	25	-	2/7/38/39	0/2/2/2
4	4OC	D	1402	4	-	4/9/29/30	0/2/2/2
25	6MZ	Y	2030	25	-	3/9/27/28	0/3/3/3
25	2MA	Y	2503	25	-	4/7/25/26	0/3/3/3
25	PSU	Y	746	25	-	4/7/25/26	0/2/2/2
4	2MG	D	1516	4	-	2/9/27/28	0/3/3/3
25	PSU	Y	2504	25	-	2/7/25/26	0/2/2/2
4	MA6	D	1518	4	-	6/11/29/30	0/3/3/3
25	PSU	Y	955	25	-	2/7/25/26	0/2/2/2
25	PSU	Y	1917	25	-	0/7/25/26	0/2/2/2
25	OMG	Y	2251	25,2	-	1/9/27/28	0/3/3/3
25	OMU	Y	2552	25	-	5/9/27/28	0/2/2/2
25	PSU	Y	2457	25	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	7MG	D	527	4	-	3/7/37/38	0/3/3/3

The worst 5 of 178 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	Y	1915	3TD	C6-C5	13.21	1.50	1.35
25	Y	1618	6MZ	C6-N6	12.71	1.48	1.34
25	Y	2030	6MZ	C6-N6	12.41	1.47	1.34
25	Y	2503	2MA	C4-N3	11.89	1.49	1.34
25	Y	1939	5MU	C2-N1	11.02	1.56	1.38

The worst 5 of 221 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	Y	2030	6MZ	C4-N9-C8	12.59	119.38	105.73
25	Y	1618	6MZ	C4-N9-C8	12.17	118.92	105.73
25	Y	1939	5MU	C5-C4-N3	12.07	125.62	115.31
25	Y	2030	6MZ	N9-C8-N7	-9.64	100.73	113.91
25	Y	1618	6MZ	N9-C8-N7	-9.39	101.07	113.91

There are no chirality outliers.

5 of 73 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	527	7MG	C3'-C4'-C5'-O5'
4	D	1207	2MG	C3'-C4'-C5'-O5'
4	D	1402	4OC	O4'-C4'-C5'-O5'
4	D	1402	4OC	C1'-C2'-O2'-CM2
4	D	1498	UR3	O4'-C1'-N1-C2

There are no ring outliers.

21 monomers are involved in 48 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
25	Y	1939	5MU	1	0
4	D	966	2MG	2	0
4	D	1519	MA6	2	0
4	D	1407	5MC	4	0
25	Y	1911	PSU	1	0
25	Y	747	5MC	1	0
25	Y	1835	2MG	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	1498	UR3	1	0
25	Y	2580	PSU	6	0
25	Y	745	1MG	4	0
25	Y	1962	5MC	3	0
25	Y	2498	OMC	1	0
4	D	967	5MC	2	0
25	Y	2449	H2U	1	0
4	D	1402	4OC	7	0
25	Y	2503	2MA	1	0
25	Y	746	PSU	2	0
4	D	1518	MA6	4	0
25	Y	955	PSU	2	0
25	Y	2251	OMG	4	0
4	D	527	7MG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

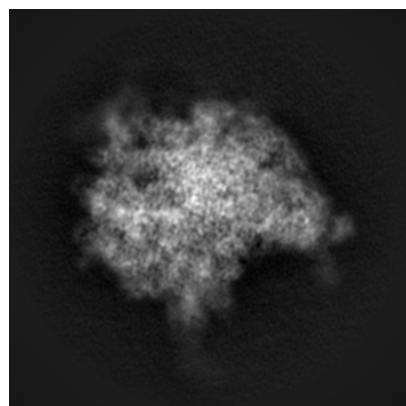
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3618. These allow visual inspection of the internal detail of the map and identification of artifacts.

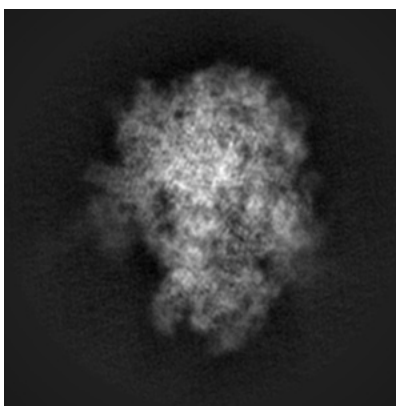
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

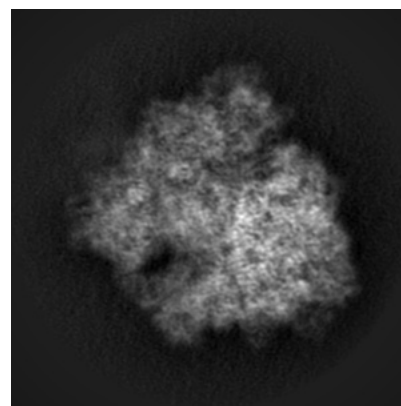
6.1.1 Primary map



X

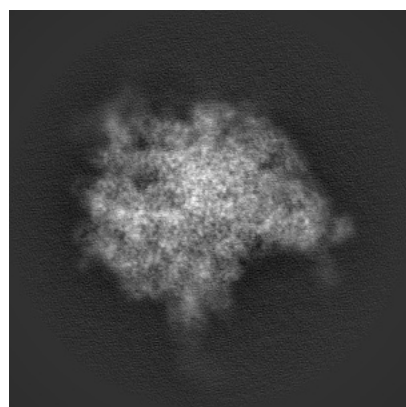


Y

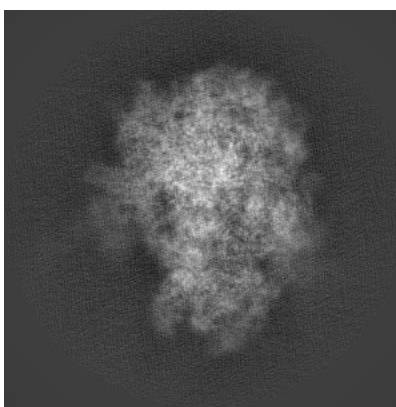


Z

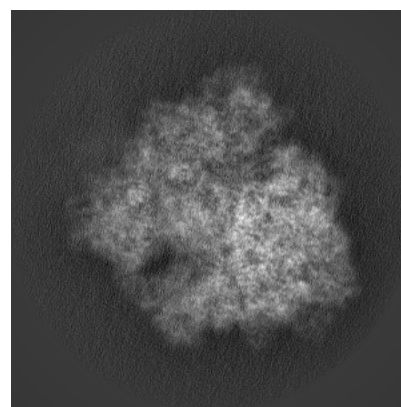
6.1.2 Raw map



X



Y

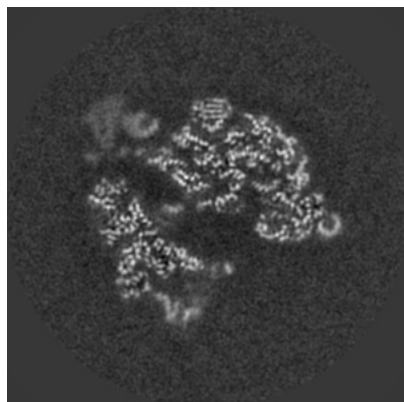


Z

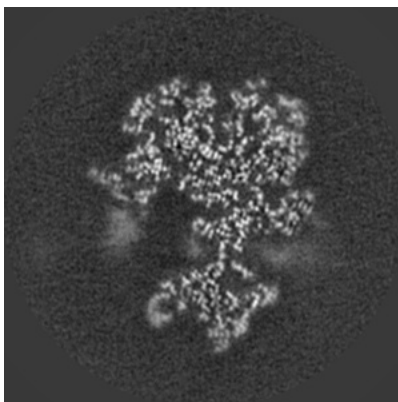
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

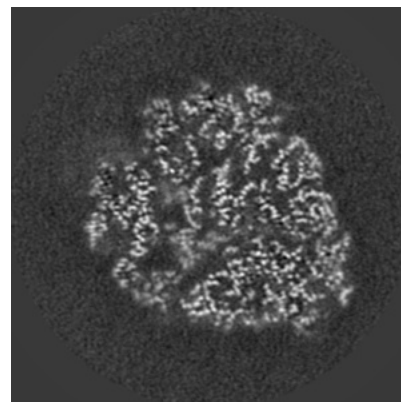
6.2.1 Primary map



X Index: 170

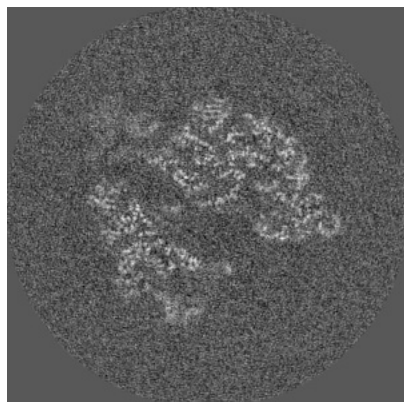


Y Index: 170

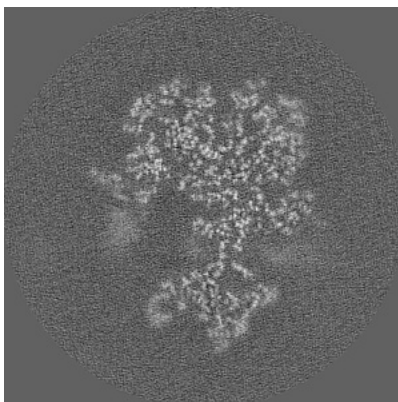


Z Index: 170

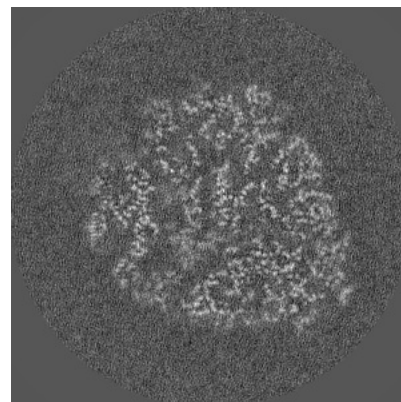
6.2.2 Raw map



X Index: 170



Y Index: 170

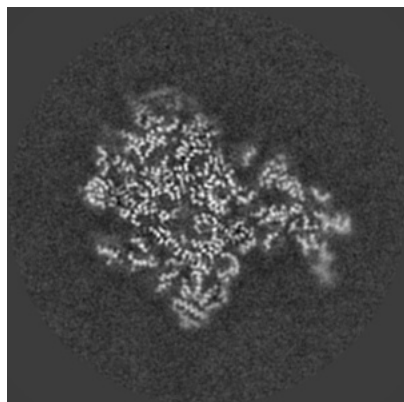


Z Index: 170

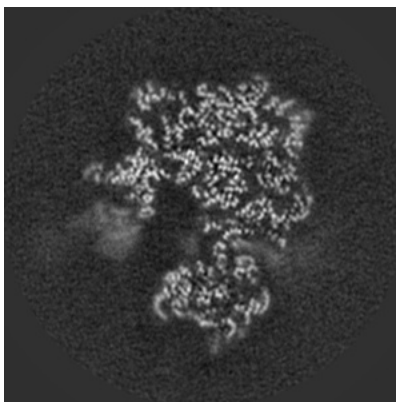
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

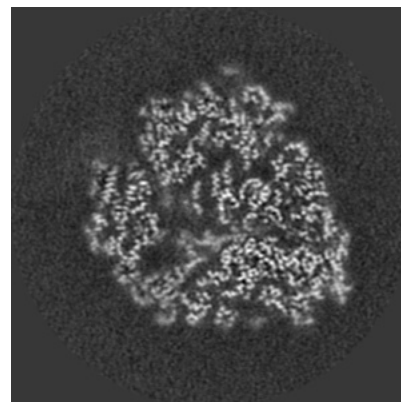
6.3.1 Primary map



X Index: 196

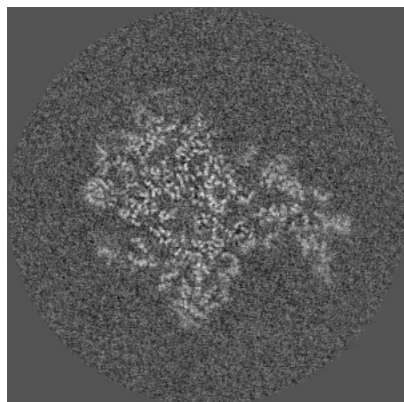


Y Index: 163

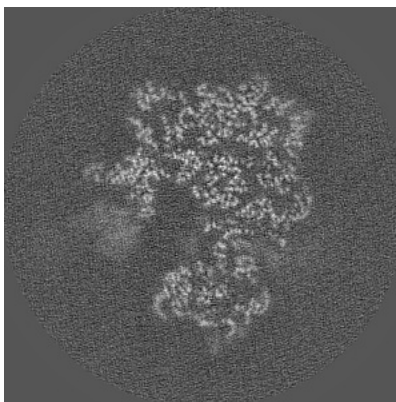


Z Index: 166

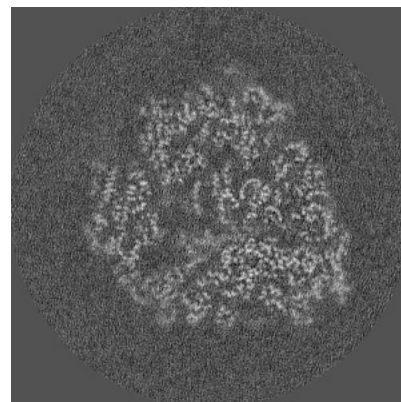
6.3.2 Raw map



X Index: 196



Y Index: 163

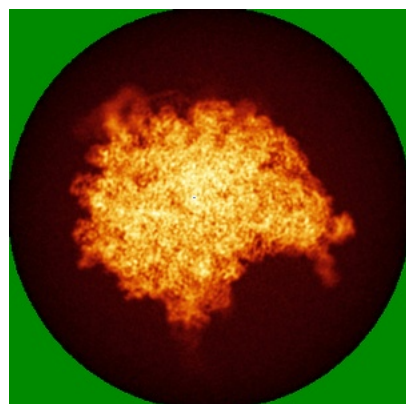


Z Index: 166

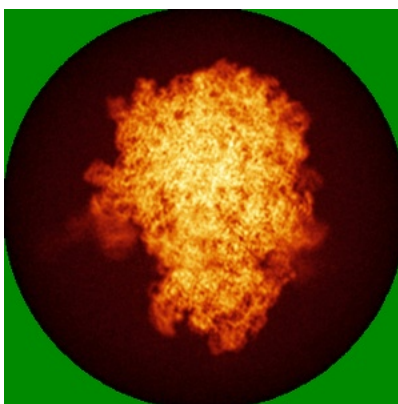
The images above show the largest variance slices of the map in three orthogonal directions.

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

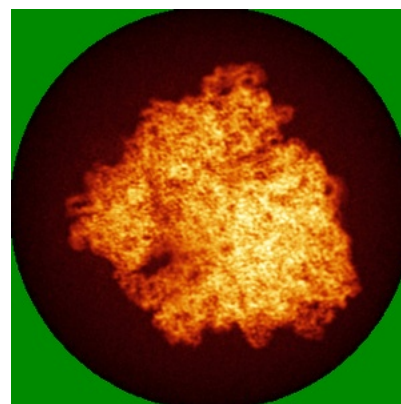
6.4.1 Primary map



X

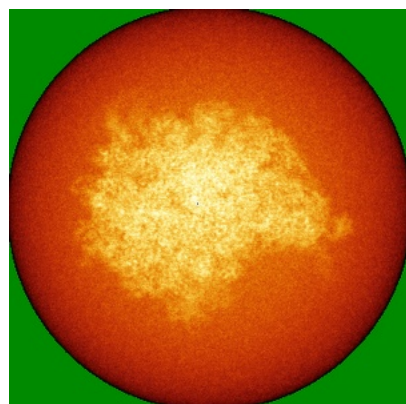


Y

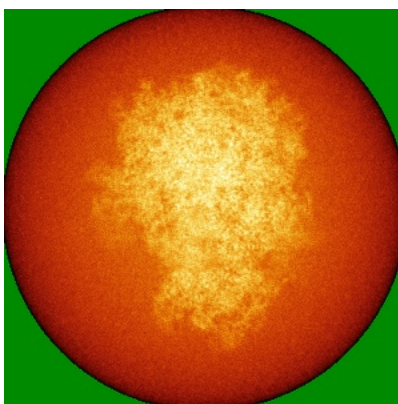


Z

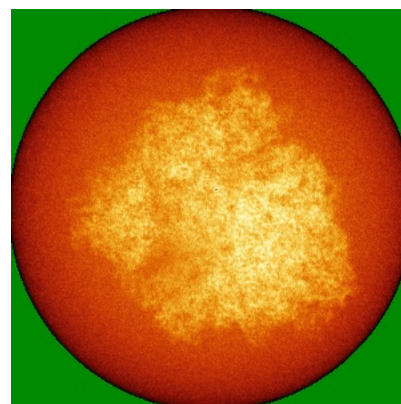
6.4.2 Raw map



X



Y

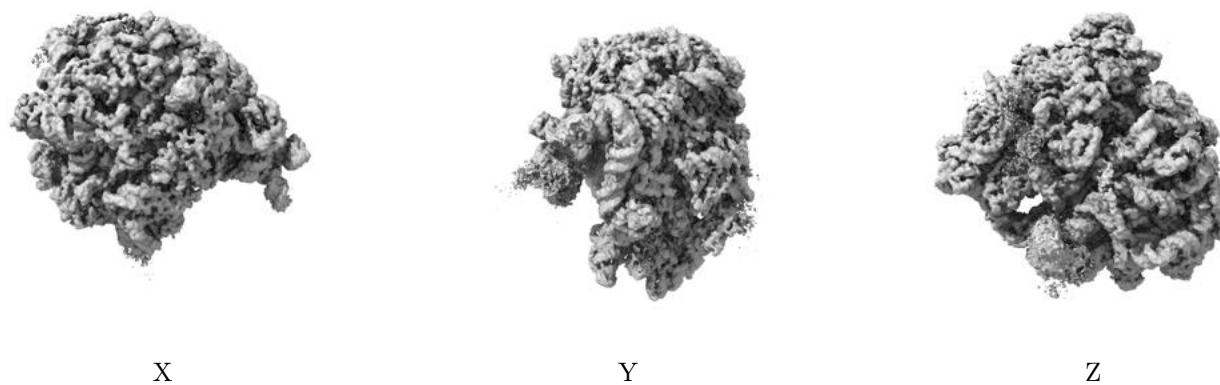


Z

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.

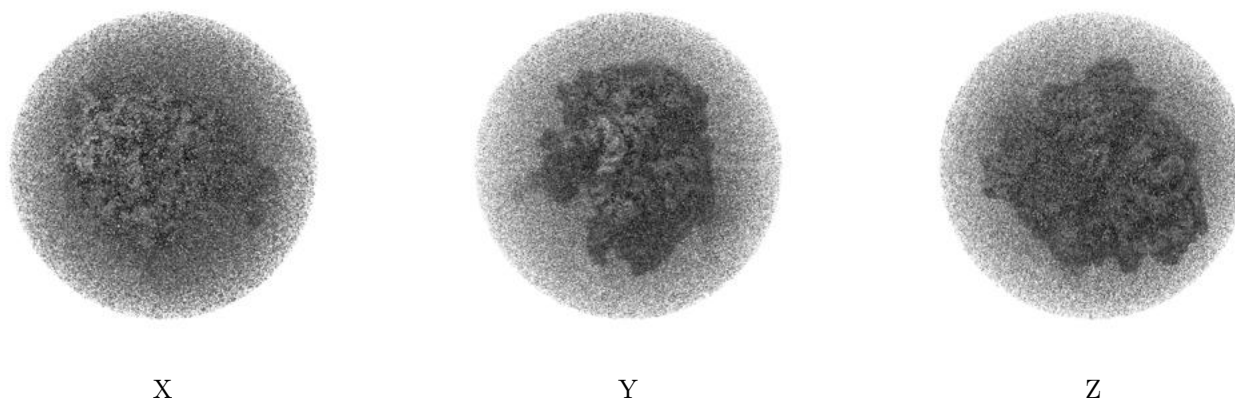
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0045. 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.

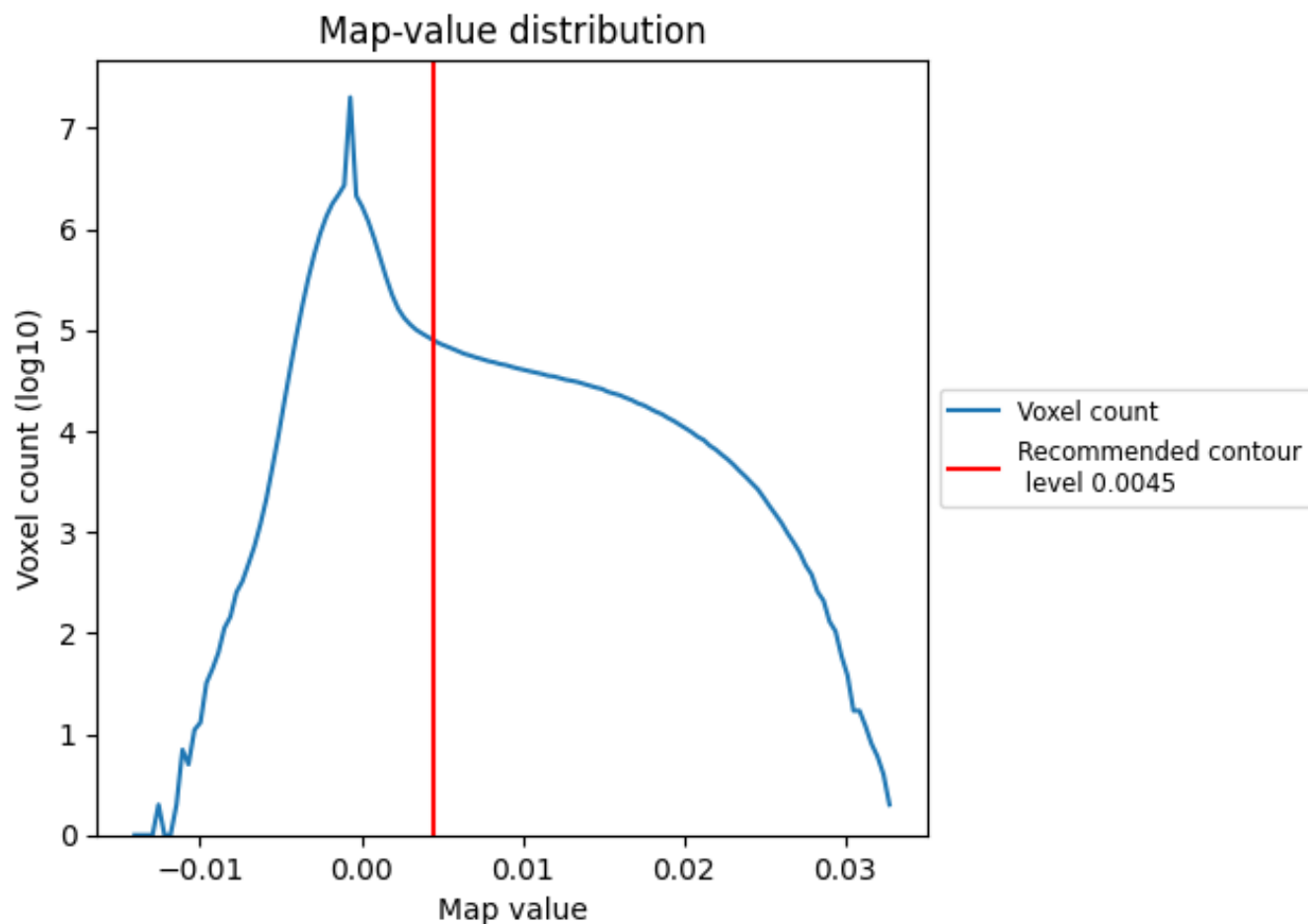
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

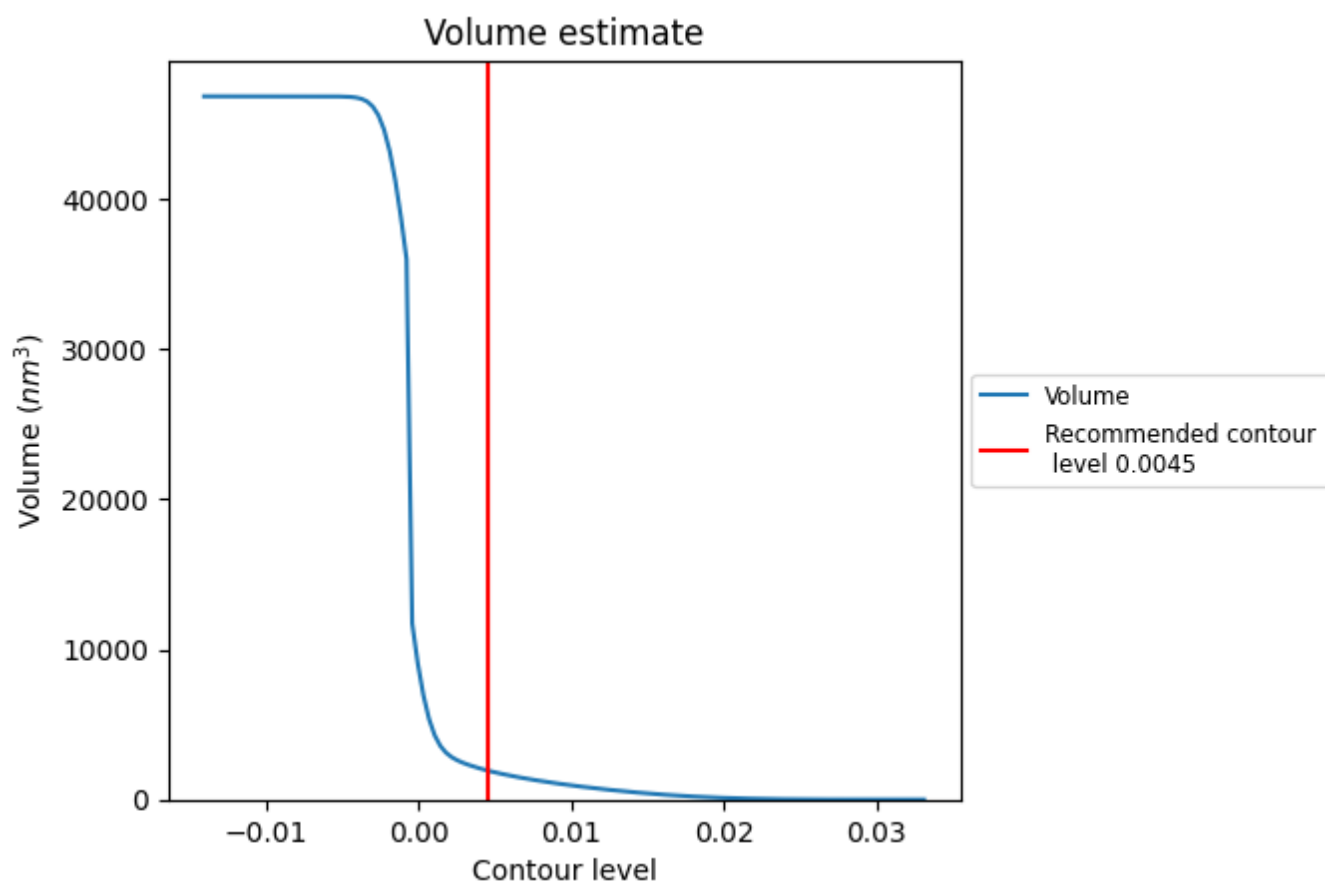
This section contains the results of statistical analysis of the map.

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.

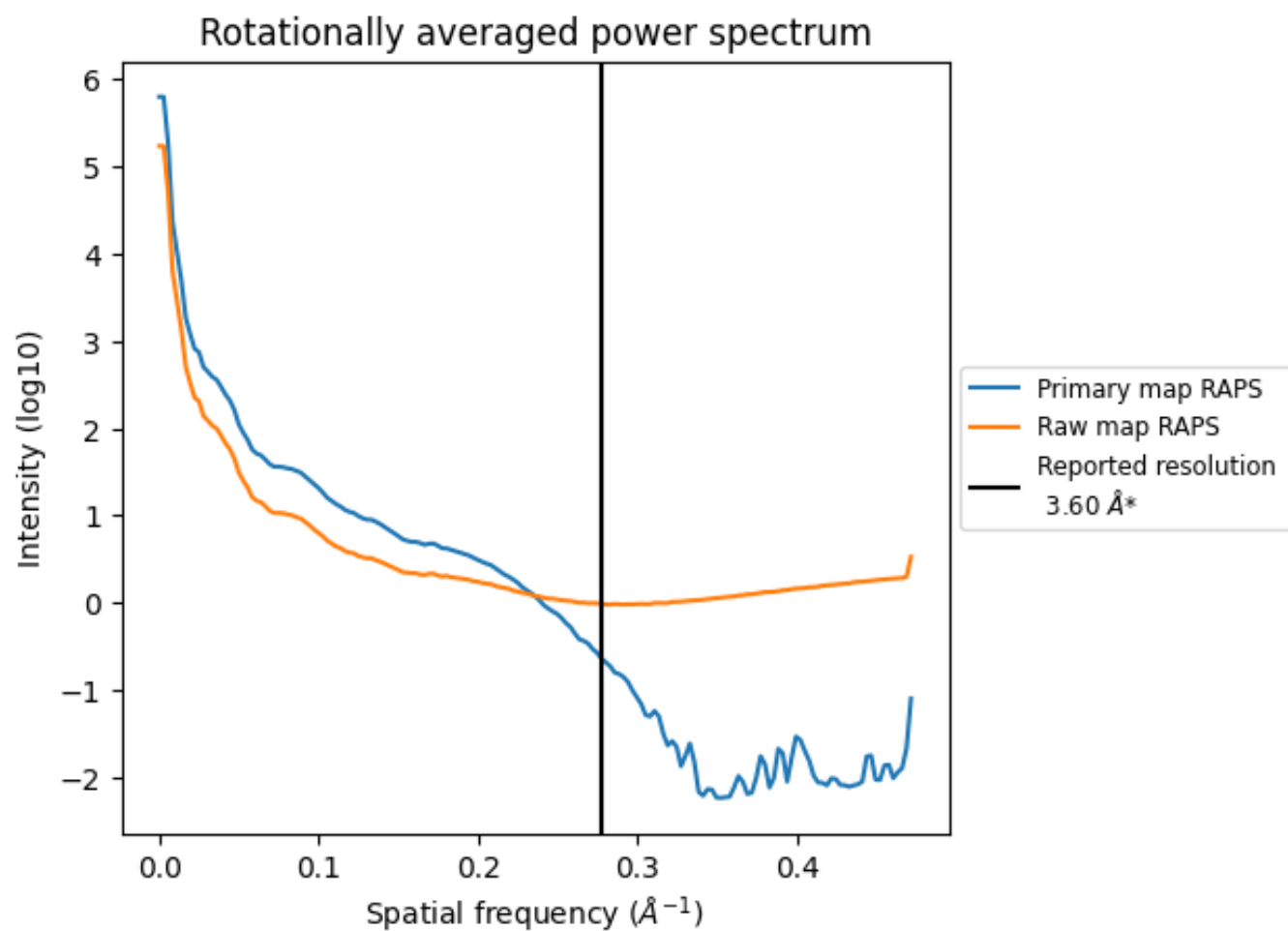
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1939 nm³; this corresponds to an approximate mass of 1751 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 ⓘ

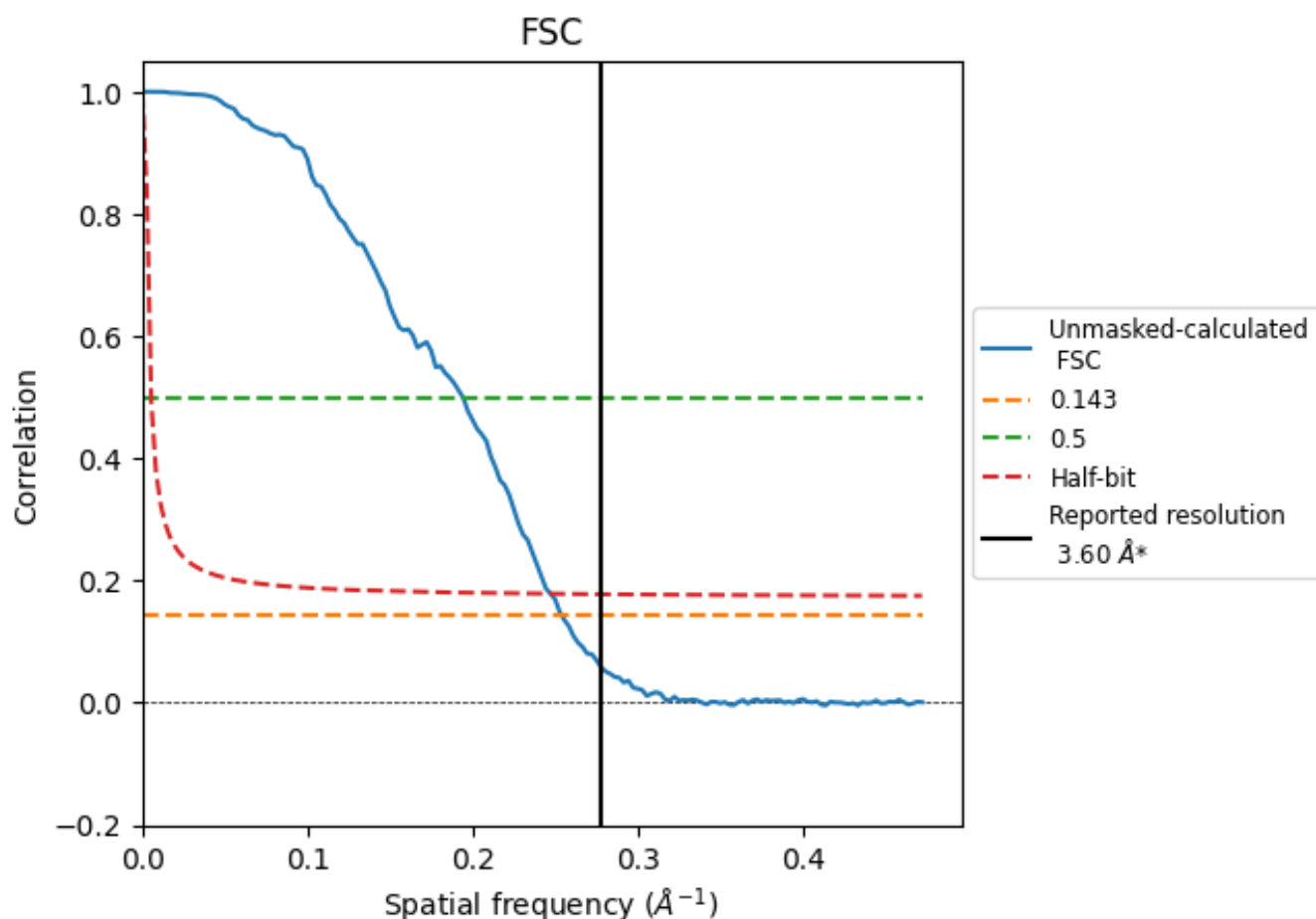


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.278 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

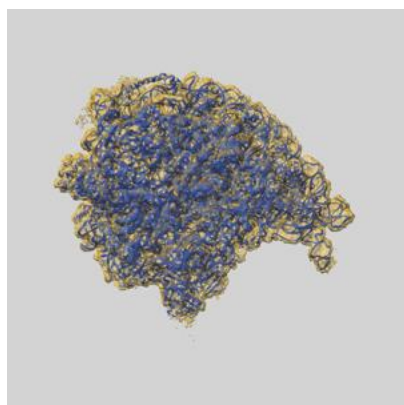
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.94	5.15	4.05

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

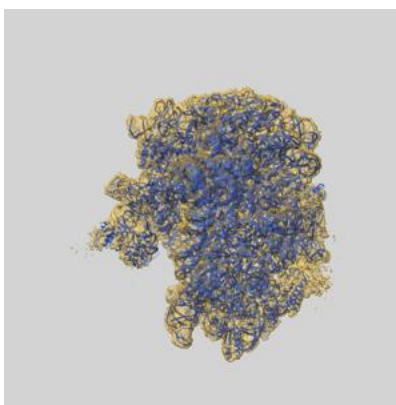
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3618 and PDB model 5NP6. Per-residue inclusion information can be found in section [3](#) on page [15](#).

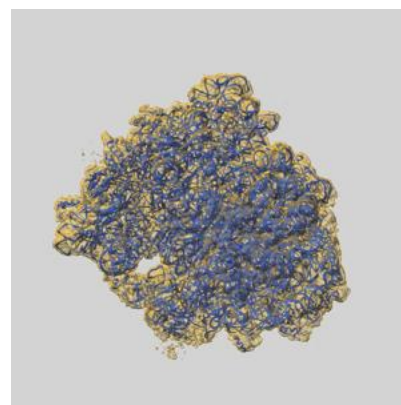
9.1 Map-model overlay [i](#)



X



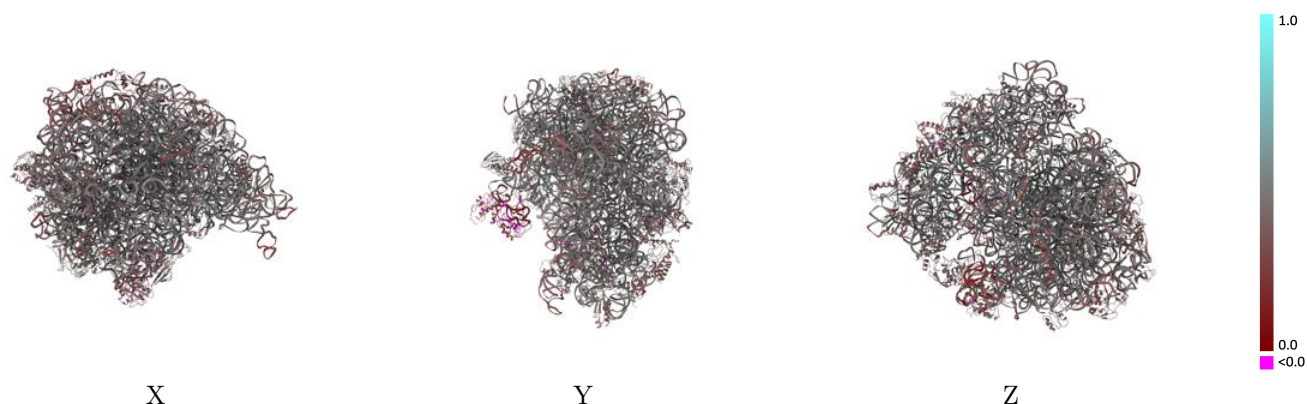
Y



Z

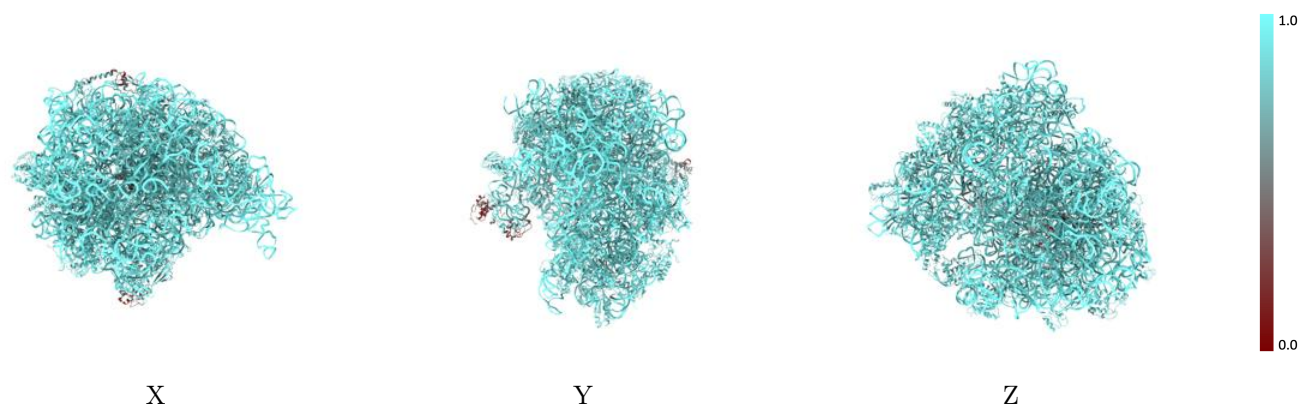
The images above show the 3D surface view of the map at the recommended contour level 0.0045 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



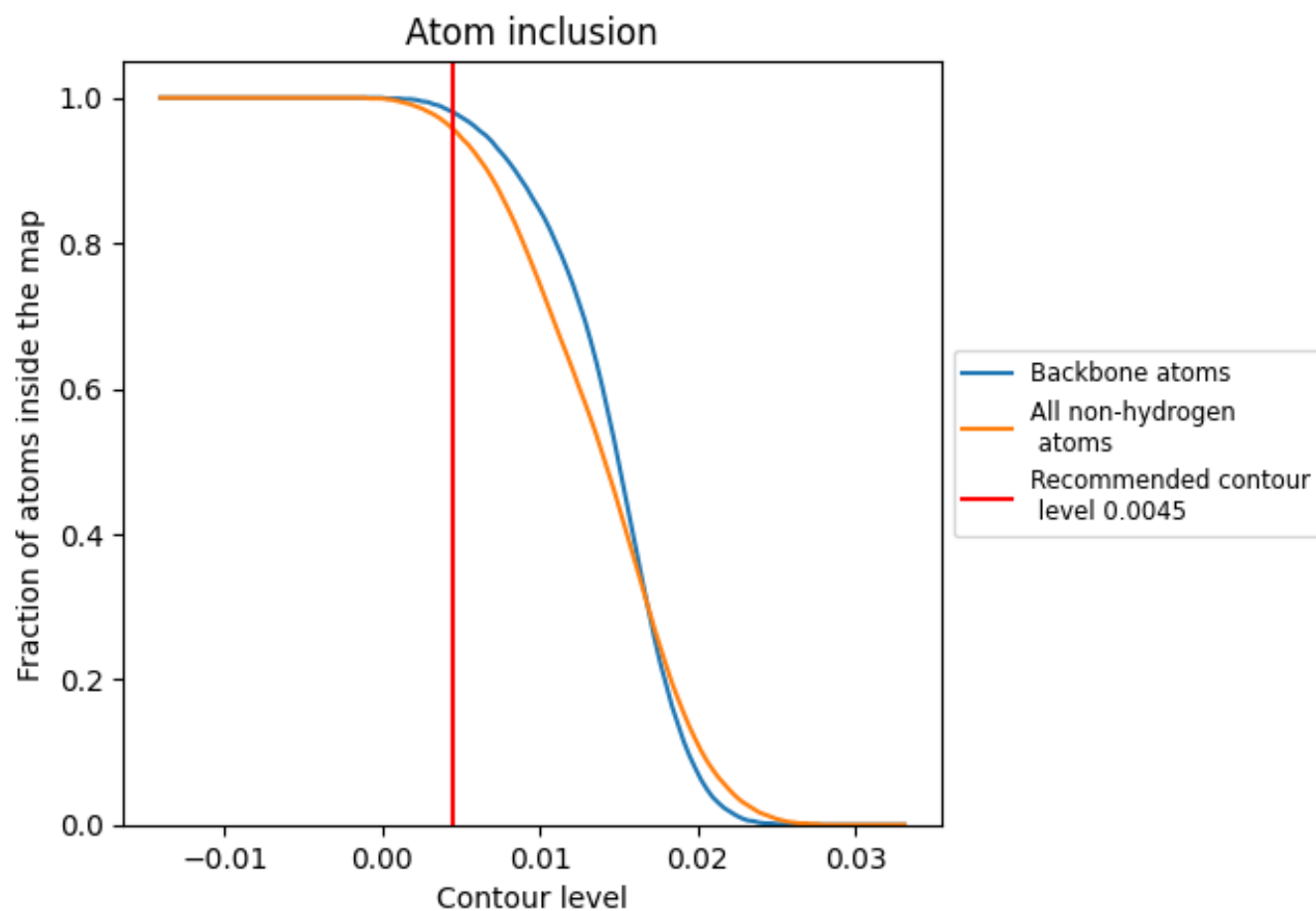
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0045).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 96% 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 (0.0045) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9570	 0.4240
0	 0.9210	 0.4360
1	 0.9330	 0.4710
2	 0.9210	 0.4480
3	 0.4620	 0.1670
4	 0.8920	 0.3630
A	 0.6960	 0.1820
B	 0.9690	 0.4010
C	 0.4410	 0.2550
D	 0.9950	 0.4470
E	 0.8690	 0.3620
F	 0.9000	 0.4290
G	 0.8910	 0.3960
H	 0.9250	 0.4340
I	 0.8930	 0.3920
J	 0.9110	 0.3840
K	 0.9180	 0.4360
L	 0.9120	 0.4000
M	 0.8560	 0.3880
N	 0.9290	 0.4190
O	 0.8960	 0.4470
P	 0.9240	 0.3940
Q	 0.9220	 0.4260
R	 0.9270	 0.4020
S	 0.9230	 0.4250
T	 0.9080	 0.4230
U	 0.9280	 0.4170
V	 0.9310	 0.4080
W	 0.9050	 0.3790
X	 0.8340	 0.3030
Y	 0.9920	 0.4310
Z	 0.9950	 0.4310
a	 0.9310	 0.4600
b	 0.9280	 0.4590
c	 0.9090	 0.4070



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Chain	Atom inclusion	Q-score
d	 0.9070	 0.3880
e	 0.9230	 0.4120
f	 0.6130	 0.3260
g	 0.5800	 0.1280
h	 0.9210	 0.4340
i	 0.8990	 0.4500
j	 0.9240	 0.4270
k	 0.9240	 0.4550
l	 0.9390	 0.4370
m	 0.9430	 0.4070
n	 0.9060	 0.4350
o	 0.9310	 0.4240
p	 0.9110	 0.4360
q	 0.8830	 0.4250
r	 0.9020	 0.4080
s	 0.9280	 0.3940
t	 0.9150	 0.4370
u	 0.9160	 0.4570
v	 0.9100	 0.4260
w	 0.8850	 0.3560
x	 0.9200	 0.4370
y	 0.9160	 0.4270
z	 0.8550	 0.4230