



wwPDB EM Validation Summary Report ⓘ

Jun 18, 2026 – 11:14 am BST

PDB ID : 6YSR / pdb_00006ysr
EMDB ID : EMD-10905
Title : Structure of the P+9 stalled ribosome complex
Authors : Chan, K.-H.; Petrychenko, V.; Mueller, C.; Maracci, C.; Holtkamp, W.; Wilson, D.N.; Fischer, N.; Rodnina, M.V.
Deposited on : 2020-04-23
Resolution : 3.10 Å (reported)
Based on initial models : 5AFI, 4RB7

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:

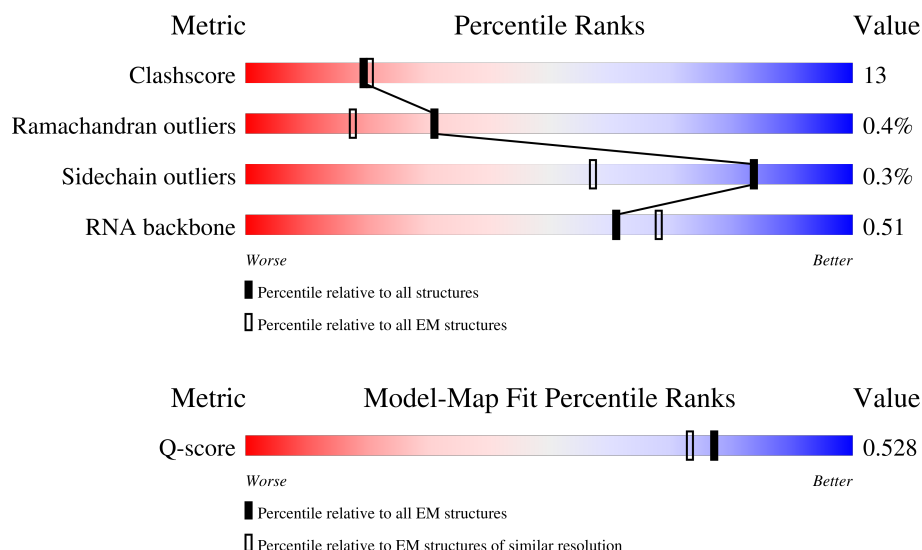
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal 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 3.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



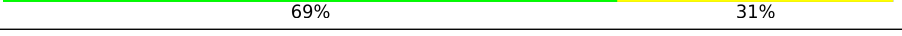
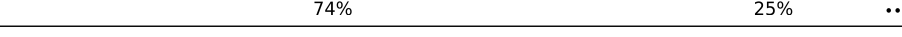
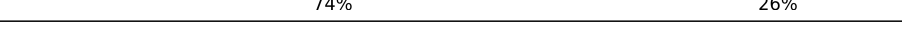
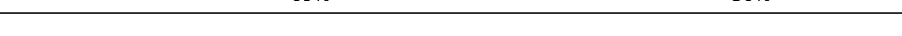
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	57	
2	1	55	
3	2	46	

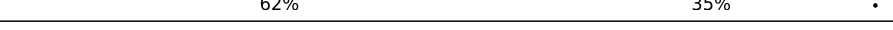
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Mol	Chain	Length	Quality of chain
4	3	65	
5	4	38	
6	5	165	
7	6	70	
8	A	2903	
9	B	120	
10	C	273	
11	D	209	
12	E	201	
13	F	179	
14	G	177	
15	H	149	
16	I	142	
17	J	142	
18	K	123	
19	L	144	
20	M	136	
21	N	127	
22	O	117	
23	P	115	
24	Q	118	
25	R	103	
26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

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Mol	Chain	Length	Quality of chain
29	V	94	 76% 24%
30	W	85	 64% 25% 12%
31	X	78	 59% 40% .
32	Y	63	 57% 40% . .
33	Z	59	 81% 17% .
34	a	1542	 45% 45% 10%
35	b	240	 61% 28% . 9%
36	c	233	 56% 33% 12%
37	d	206	 56% 37% 5% .
38	e	167	 69% 25% 6%
39	f	135	 46% 28% 26%
40	g	179	 51% 34% 16%
41	h	130	 69% 30% .
42	i	130	 62% 35% .
43	j	103	 60% 33% . . 5%
44	k	129	 65% 25% 10%
45	l	124	 76% 23% .
46	m	118	 67% 28% . .
47	n	102	 61% 38% .
48	o	89	 85% 13% .
49	p	82	 61% 39%
50	q	84	 67% 25% . 5%
51	r	75	 63% 24% 13%
52	s	92	 59% 30% 11%
53	t	87	 67% 29% . . .

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Mol	Chain	Length	Quality of chain
54	u	71	65% 25% 8%
55	v	2	50% 50%
56	w	76	42% 46% 8%
57	x	15	20% 47% 33%

2 Entry composition

There are 62 unique types of molecules in this entry. The entry contains 145959 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L32.

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 3 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 4 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 5 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 6 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	5	131	Total	C	N	O	0	0
			647	385	131	131		

- Molecule 7 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 8 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A	2903	Total	C	N	O	P	0	0
			62336	27815	11468	20150	2903		

- Molecule 9 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	B	120	Total	C	N	O	P	0	0
			2570	1144	468	838	120		

- Molecule 10 is a protein called 50S ribosomal protein L2.

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

- Molecule 11 is a protein called 50S ribosomal protein L3.

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

- Molecule 12 is a protein called 50S ribosomal protein L4.

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

- Molecule 13 is a protein called 50S ribosomal protein L5.

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

- Molecule 14 is a protein called 50S ribosomal protein L6.

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

- Molecule 15 is a protein called 50S ribosomal protein L9.

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

- Molecule 16 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	I	141	Total	C	N	O	S	0	0
			693	411	141	141			

- Molecule 17 is a protein called 50S ribosomal protein L13.

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

- Molecule 18 is a protein called 50S ribosomal protein L14.

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

- Molecule 19 is a protein called 50S ribosomal protein L15.

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

- Molecule 20 is a protein called 50S ribosomal protein L16.

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

- Molecule 21 is a protein called 50S ribosomal protein L17.

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

- Molecule 22 is a protein called 50S ribosomal protein L18.

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

- Molecule 23 is a protein called 50S ribosomal protein L19.

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

- Molecule 24 is a protein called 50S ribosomal protein L20.

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

- Molecule 25 is a protein called 50S ribosomal protein L21.

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

- Molecule 26 is a protein called 50S ribosomal protein L22.

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

- Molecule 27 is a protein called 50S ribosomal protein L23.

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

- Molecule 28 is a protein called 50S ribosomal protein L24.

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

- Molecule 29 is a protein called 50S ribosomal protein L25.

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

- Molecule 30 is a protein called 50S ribosomal protein L27.

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

- Molecule 31 is a protein called 50S ribosomal protein L28.

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

- Molecule 32 is a protein called 50S ribosomal protein L29.

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

- Molecule 33 is a protein called 50S ribosomal protein L30.

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

- Molecule 34 is a RNA chain called 16S ribosomal RNA.

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

- Molecule 35 is a protein called 30S ribosomal protein S2.

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

- Molecule 36 is a protein called 30S ribosomal protein S3.

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

- Molecule 37 is a protein called 30S ribosomal protein S4.

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

- Molecule 38 is a protein called 30S ribosomal protein S5.

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

- Molecule 39 is a protein called 30S ribosomal protein S6.

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

- Molecule 40 is a protein called 30S ribosomal protein S7.

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

- Molecule 41 is a protein called 30S ribosomal protein S8.

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

- Molecule 42 is a protein called 30S ribosomal protein S9.

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

- Molecule 43 is a protein called 30S ribosomal protein S10.

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

- Molecule 44 is a protein called 30S ribosomal protein S11.

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

- Molecule 45 is a protein called 30S ribosomal protein S12.

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

- Molecule 46 is a protein called 30S ribosomal protein S13.

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

- Molecule 47 is a protein called 30S ribosomal protein S14.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	35	ALA	-	insertion	UNP C3SR07

- Molecule 48 is a protein called 30S ribosomal protein S15.

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

- Molecule 49 is a protein called 30S ribosomal protein S16.

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

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

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

- Molecule 51 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	r	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 52 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	s	82	Total	C	N	O	S	0	0
			658	421	125	110	2		

- Molecule 53 is a protein called 30S ribosomal protein S20.

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

- Molecule 54 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	u	65	Total	C	N	O	S	0	0
			506	313	105	87	1		

- Molecule 55 is a protein called P-site fMet-Phe-tRNA(Phe).

Mol	Chain	Residues	Atoms					AltConf	Trace
55	v	2	Total	C	N	O	S	0	0
			19	14	2	2	1		

- Molecule 56 is a RNA chain called P-site fMet-Phe-tRNA(Phe).

Mol	Chain	Residues	Atoms						AltConf	Trace
56	w	76	Total	C	N	O	P	S	0	0
			1631	731	291	531	76	2		

- Molecule 57 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	x	15	Total	C	N	O	P	0	0
			314	141	49	109	15		

- Molecule 58 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
58	0	1	Total	Mg	0
			1	1	
58	6	1	Total	Mg	0
			1	1	
58	A	236	Total	Mg	0
			236	236	
58	B	5	Total	Mg	0
			5	5	
58	O	1	Total	Mg	0
			1	1	
58	Q	1	Total	Mg	0
			1	1	
58	T	1	Total	Mg	0
			1	1	
58	a	82	Total	Mg	0
			82	82	
58	g	1	Total	Mg	0
			1	1	
58	w	3	Total	Mg	0
			3	3	

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

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

- Molecule 60 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		AltConf
60	A	1	Total 1	Cl 1	0

- Molecule 61 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		AltConf
61	A	1	Total 1	Na 1	0
61	V	1	Total 1	Na 1	0

- Molecule 62 is water.

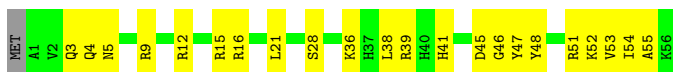
Mol	Chain	Residues	Atoms		AltConf
62	A	1	Total 1	O 1	0
62	a	1	Total 1	O 1	0

3 Residue-property plots [i](#)

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

- Molecule 1: 50S ribosomal protein L32

Chain 0: 



- Molecule 2: 50S ribosomal protein L33

Chain 1: 



- Molecule 3: 50S ribosomal protein L34

Chain 2: 



- Molecule 4: 50S ribosomal protein L35

Chain 3: 

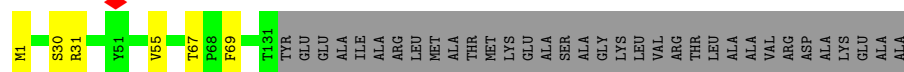
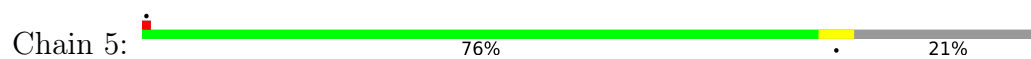


- Molecule 5: 50S ribosomal protein L36

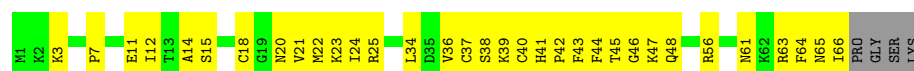
Chain 4: 



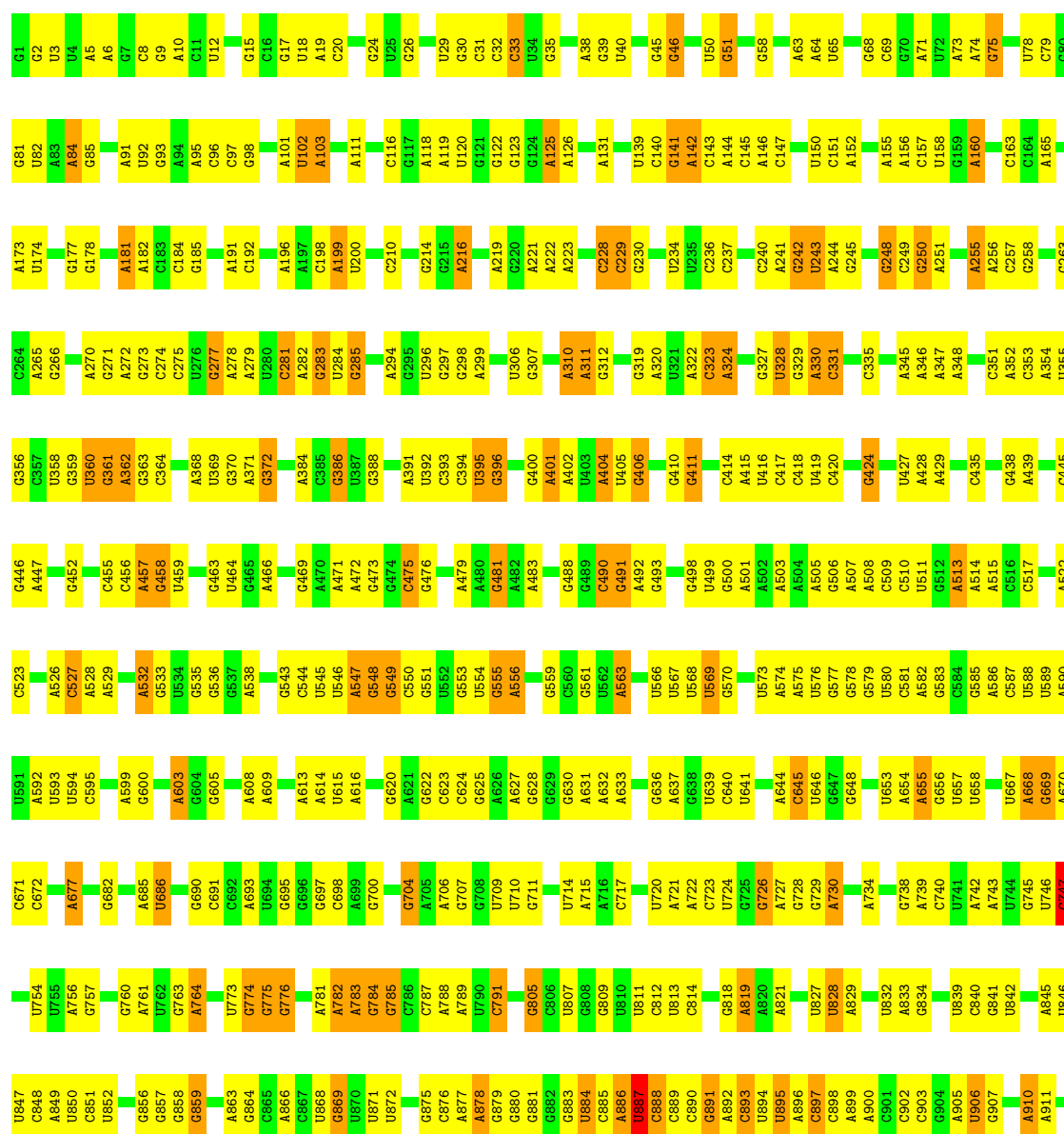
- Molecule 6: 50S ribosomal protein L10



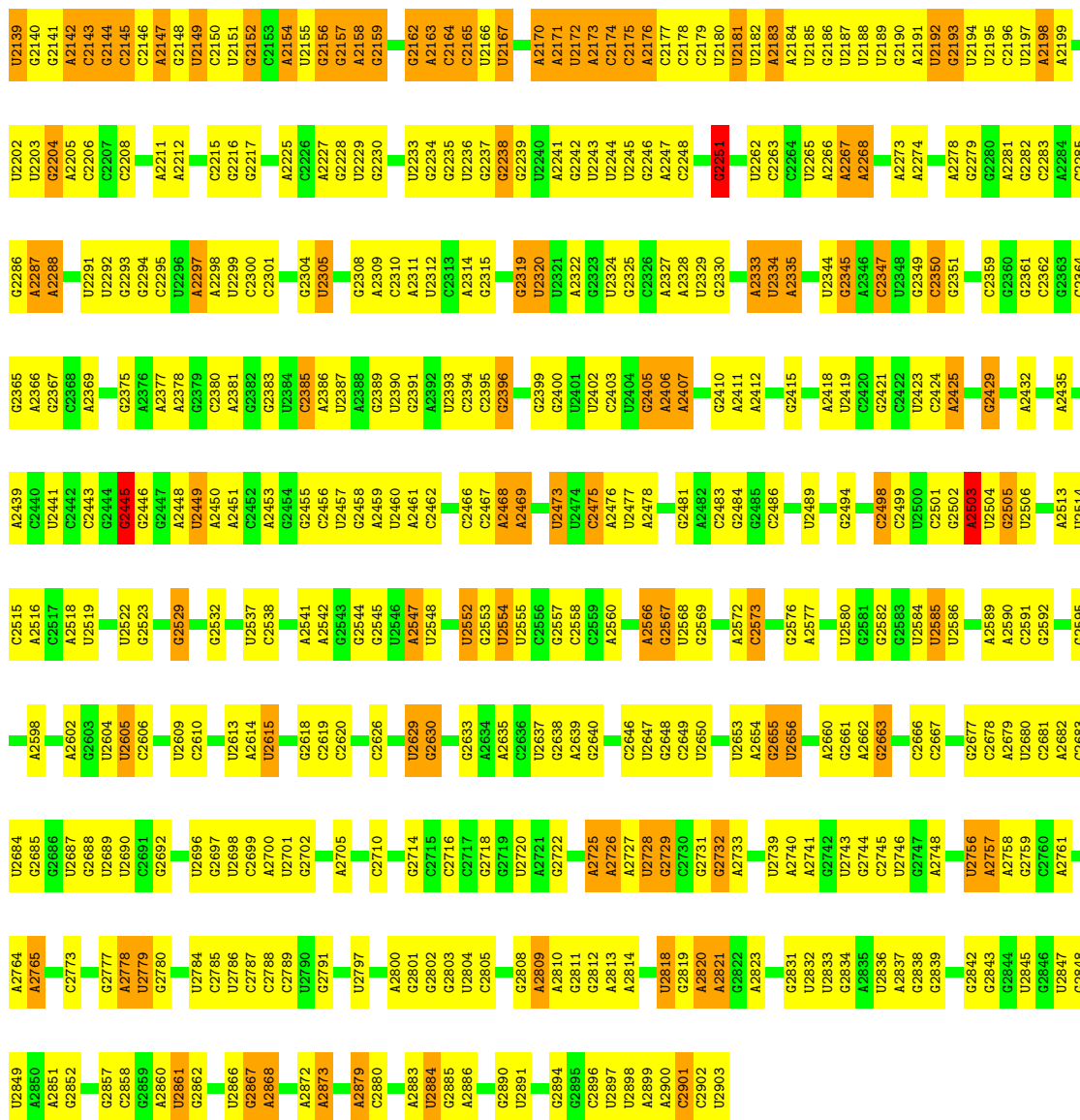
- Molecule 7: 50S ribosomal protein L31



- Molecule 8: 23S ribosomal RNA

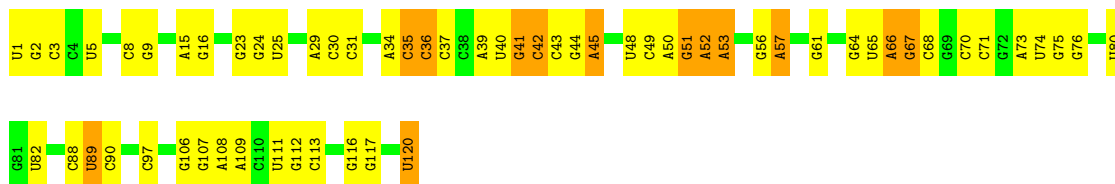


G2069	U1971	G1884	C1795	U1720	A1632	A1548	G1478	U1397	G1317	U1141	C1072	A1000	G916
A2070	G1972	A1885	U1796	G1721	G1633	A1548	G1482	C1398	U1318	A1142	A1073	A1001	A917
A2071	U1982	A1889	G1797	A1722	A1634	A1549	A1482	C1399	G1319	A1143	G1074	U1004	A918
C2073	U1982	A1890	U1798	G1723	A1635	C1550	G1483	U1406	C1320	G1149	C1075	C1005	A925
U2075	U1991	G1890	C1800	G1726	U1636	A1551	U1485	U1405	A1321	C1150	C1076	A1009	G926
U2076	G1992	G1891	A1801	C1727	U1637	U1554	U1486	G1407	A1322	C1153	A1077	A1010	A927
	C1996	A1900	A1802	C1728	G1645	C1558	U1487	G1408	G1324	G1154	C1079	A1011	G930
U2079	C1997	A1901	A1803	U1729	G1646	U1563	A1490	U1410	U1325	A1155	A1080	G1012	U931
A2080	U1997	G1902		G1730	U1647	G1563	G1491	U1411	U1326	A1156	U1081	C1013	U932
U2081	U2011	G1903	A1808	G1731	U1648	U1564	G1492	U1412	A1327	U1159	U1082	U1019	U933
G2082	G2012	G1904	A1809	G1732	G1649	C1565	C1493	U1413	G1331	G1160	U1083	U1019	U934
G2087	A2013	G1905		G1733	A1650	A1566	A1494	C1414	G1332	G1250	A1084	A1020	C935
A2088	A2014	G1906	U1812	G1734	G1651	A1566	A1495	U1415			A1085	A1021	A936
	A2015	U1911	G1813	U1735	A1652		A1496	U1416	G1338	A1169	A1086	A1022	C937
G2093	A2016	A1912	A1814	U1736	G1653	A1569	U1497	C1417	U1339	C1170	G1087	G1022	
U2096	U2017	A1913	A1815	G1737	A1654	A1570	U1498	U1417	G1340	G1171	A1088	U1023	A941
C2097	A2020	A1914	A1816	G1738	A1655	A1571	C1498	G1429	U1341	G1172	A1089	G1024	G942
U2098	C2021	C201915	U1817	G1739	C1656	A1572	A1499	A1420	G1341	U1173	A1090	G1025	
U2099	U2022	A1916	U1818	G1740	U1657		G1500	G1421	C1349	U1174	G1091	G1026	A945
G2100	U2023	A1917	G1824	G1741	C1658	C1577	G1501	A1427	C1350	U1175	C1092	A1027	C946
A2101	C2024	A1918	U1825	G1742	G1659	A1578	A1502	C1428	G1351	U1176	G1093	A1028	A947
G2102	A1919	G1914	A1826	G1743		A1579	A1503	G1429	C1351	G1177	U1094	A1029	C948
	U1923	U1923	U1827	A1744	G1667	A1580	A1504	G1430	A1352	C1178	A1095	A1032	
U2105	C1924	C1924	G1828	A1745		G1581	U1505	G1431	A1353	U1179	A1096	U1033	G953
U2106	U1927	A1927	A1829	A1746	A1672	C1582	U1506	A1432	A1354	U1180	A1097	U1033	G954
G2107	A1928	A1928	G1830	U1747	G1673	A1583	C1507	A1433	G1358	U1181	A1098	G1036	U955
A2108	A2030	A2030	A1831	G1753	C1675	U1584	A1508	A1434	A1359	G1182	G1099	G1037	A959
U2109	G2032	G1929	G1835	G1754	A1678	A1586	G1510	G1435	G1360	U1183	U1101	G1038	A960
G2110	A2033	G1930	G1836	G1755	A1679	G1587	G1511	G1436	G1361	G1186	C1102	A1039	C961
U2111	U2034	U1931	G1842	G1756	U1679	U1588	C1512	C1437	C1362	U1187	A1103	A1040	
G2112	A1932	A1932	C1843	C1760	G1682	U1589	U1513	G1441	G1363	U1188	C1104	A1043	G966
A2114	G1933	G1933	G1847	G1763	U1683	A1590	G1514	U1442	A1365	A1189	U1105	C1044	U967
G2115	A1936	A1936	A1848	G1764	G1684	U1594	G1516	U1443	A1366	G1190	G1106		C968
G2116	A1937	A1937			C1685	C1595	G1519	G1444	A1367	G1195	C1109	G1047	G969
A2117	U1939	U1939	A1853	C1771	A1689	U1599	A1522	C1447	G1368	C1196	G1110	A1048	U970
A2119	C2042	C2042	A1854	A1772	A1690	C1600	U1523	G1448	G1369	G1197	A1111		G971
G2120	A2043	A2043	U1855	A1773	C1691	C1604	U1524		C1289	U1198	G1112	G1051	A972
G2121	G2046	C1942	U1856	G1774	U1692	C1607	G1524	C1451	C1290	U1199	U1113	C1052	A973
U2122	C2047	U1943	A1857	U1775	U1693	C1608	G1527	A1452	C1291	C1200	C1114	C1053	G974
G2123	G2048	G1946	G1858	G1776	C1694	C1607	G1527	A1453	G1292	U1201	G1115	A1054	A975
G2124	C2050	C1947	U1859			A1608	A1528	C1454	U1293	G1202	G1117	G1055	G976
A2126	A2051	A1952	G1860	U1779	G1699	A1609	A1529		U1294	A1205	C1118	G1056	
G2127	A2052	A1953	U1864	A1780	A1700	A1610	C1533	U1458	A1384	G1206	U1119	A1057	A983
G2128	C2055	U1955	U1865	U1781	A1701	C1611	U1534	G1459	A1385	U1209	C1123	G1059	C957
C2129	G2056	C1961	G1866	U1782	G1702	C1612	A1535	U1460	A1386	G1210	G1124	U1060	A988
U2130	A2060	U1963	G1867	A1783	G1703	G1613	C1536	C1461	A1387	C1211	A1125	U1061	G989
G2133	G2061	A1872	G1869	U1784	C1704	A1614	G1537	A1469	G1388	A1302	G1126	C1063	A990
C2134	A2062	A1873	U1870	A1786	A1711	A1618	G1537	A1470	U1389	C1305	U1130	C1064	C991
A2135	C2063	C1965	G1872	C1788	G1715	G1622	G1540	G1471	U1390	G1216	U1131	U1066	G993
G2136	A1968	A1874	U1873	U1789	U1716	A1626	C1541	G1472	A1391	U1219	U1132	U1067	C994
U2137	C1967	C1874	G1874	C1790	A1717	G1627	U1542	U1474	A1392	G1220	A1133	G1068	C995
G2138	A1970	G1878		A1791	G1718	A1627	G1543	U1475	A1393			A1069	A996
				A1794	G1719	G1631	A1544	U1476	U1394	A1226	C1135	A1070	U999



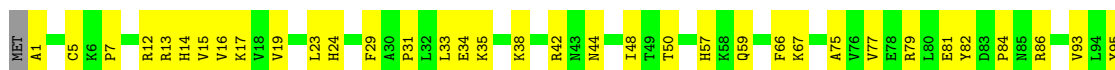
• Molecule 9: 5S ribosomal RNA

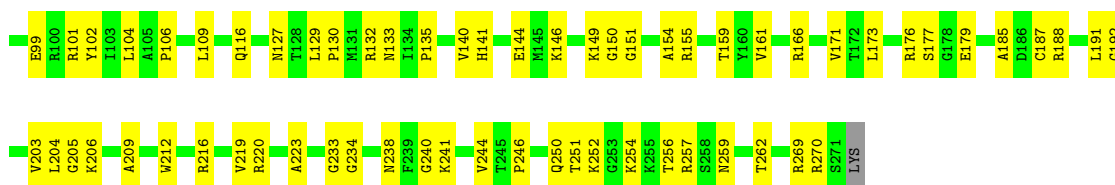
Chain B: 49% 40% 11%



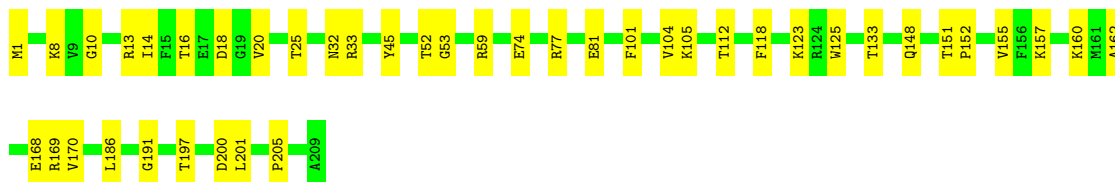
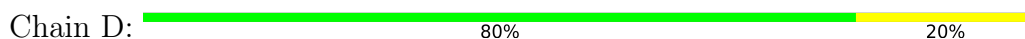
• Molecule 10: 50S ribosomal protein L2

Chain C: 64% 36%

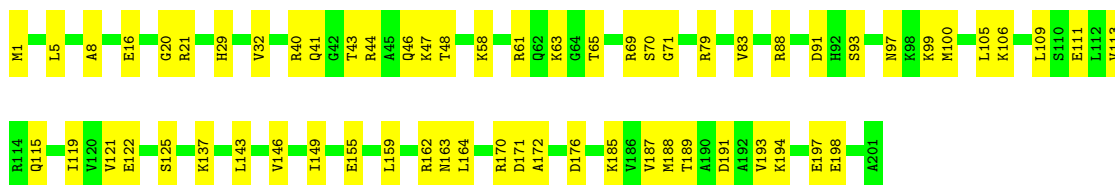




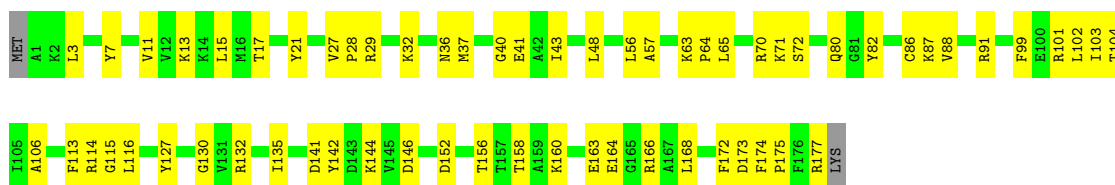
• Molecule 11: 50S ribosomal protein L3



• Molecule 12: 50S ribosomal protein L4



• Molecule 13: 50S ribosomal protein L5

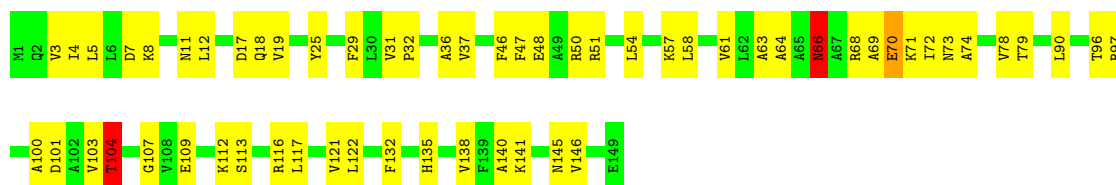


• Molecule 14: 50S ribosomal protein L6

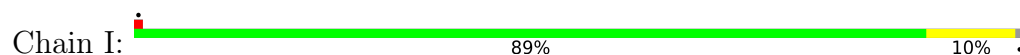


• Molecule 15: 50S ribosomal protein L9

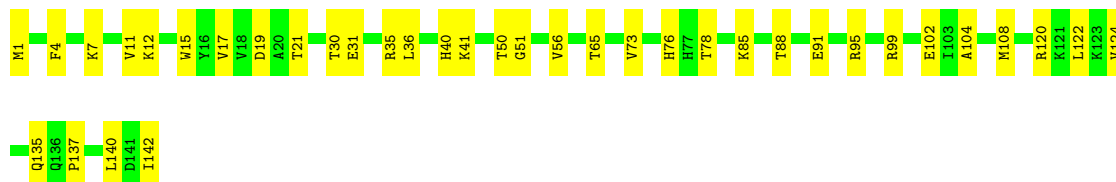




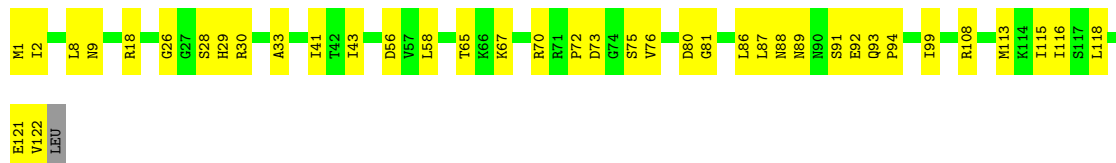
- Molecule 16: 50S ribosomal protein L11



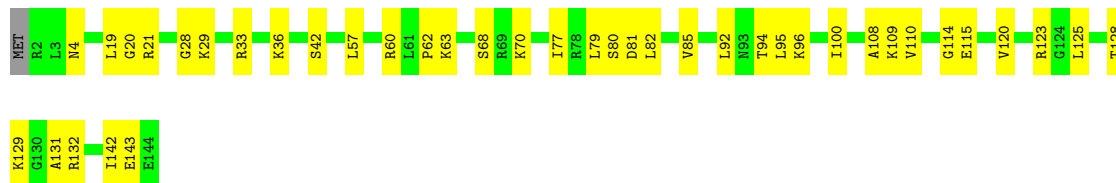
- Molecule 17: 50S ribosomal protein L13



- Molecule 18: 50S ribosomal protein L14

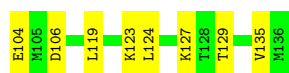


- Molecule 19: 50S ribosomal protein L15



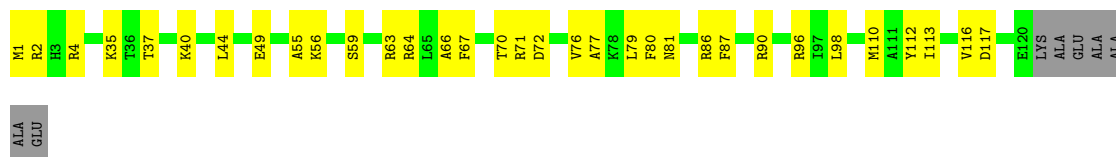
- Molecule 20: 50S ribosomal protein L16





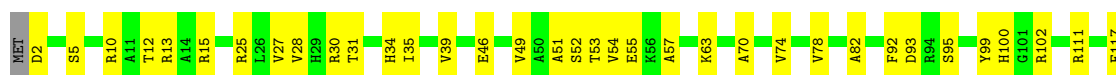
- Molecule 21: 50S ribosomal protein L17

Chain N: 69% 26% 6%



- Molecule 22: 50S ribosomal protein L18

Chain O: 69% 30% .



- Molecule 23: 50S ribosomal protein L19

Chain P: 69% 30% .



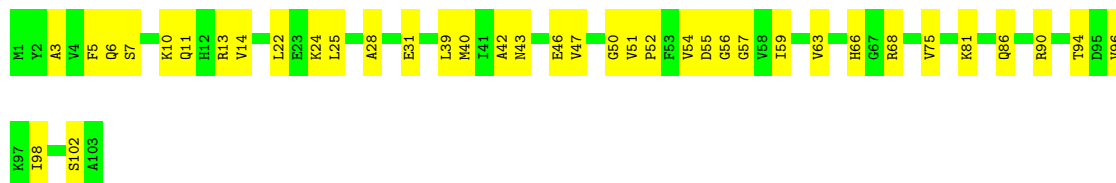
- Molecule 24: 50S ribosomal protein L20

Chain Q: 78% 21% .



- Molecule 25: 50S ribosomal protein L21

Chain R: 63% 37%



- Molecule 26: 50S ribosomal protein L22

Chain S: 81% 19%



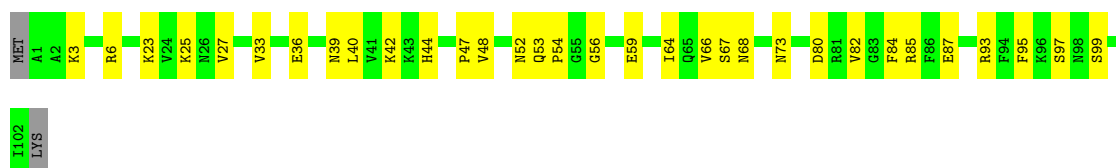
- Molecule 27: 50S ribosomal protein L23

Chain T: 70% 23% 7%



- Molecule 28: 50S ribosomal protein L24

Chain U: 67% 31% .



- Molecule 29: 50S ribosomal protein L25

Chain V: 76% 24%



- Molecule 30: 50S ribosomal protein L27

Chain W: 64% 25% 12%



- Molecule 31: 50S ribosomal protein L28

Chain X: 59% 40% .



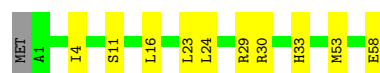
- Molecule 32: 50S ribosomal protein L29

Chain Y: 57% 40% . .

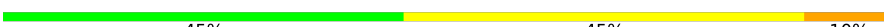


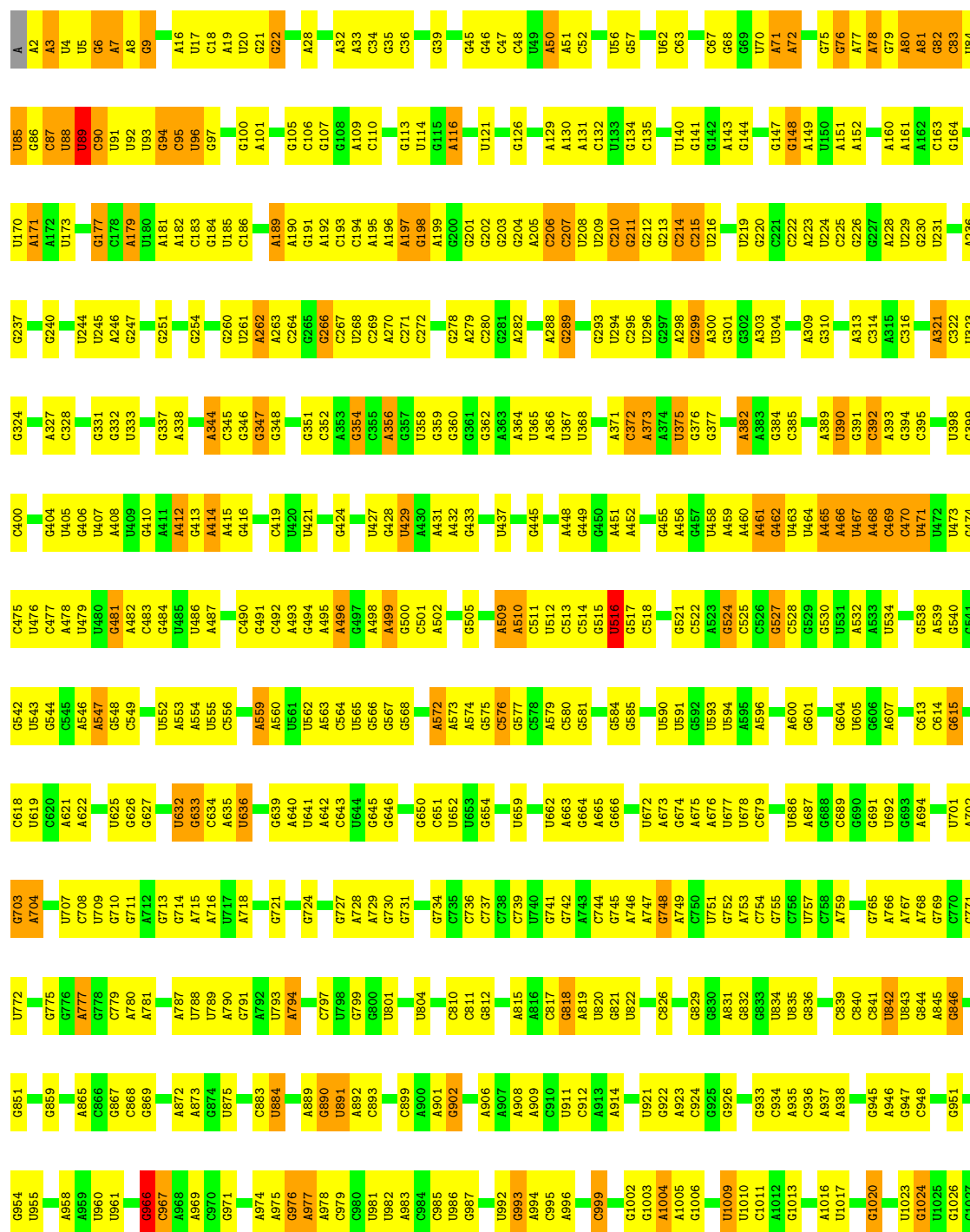
- Molecule 33: 50S ribosomal protein L30

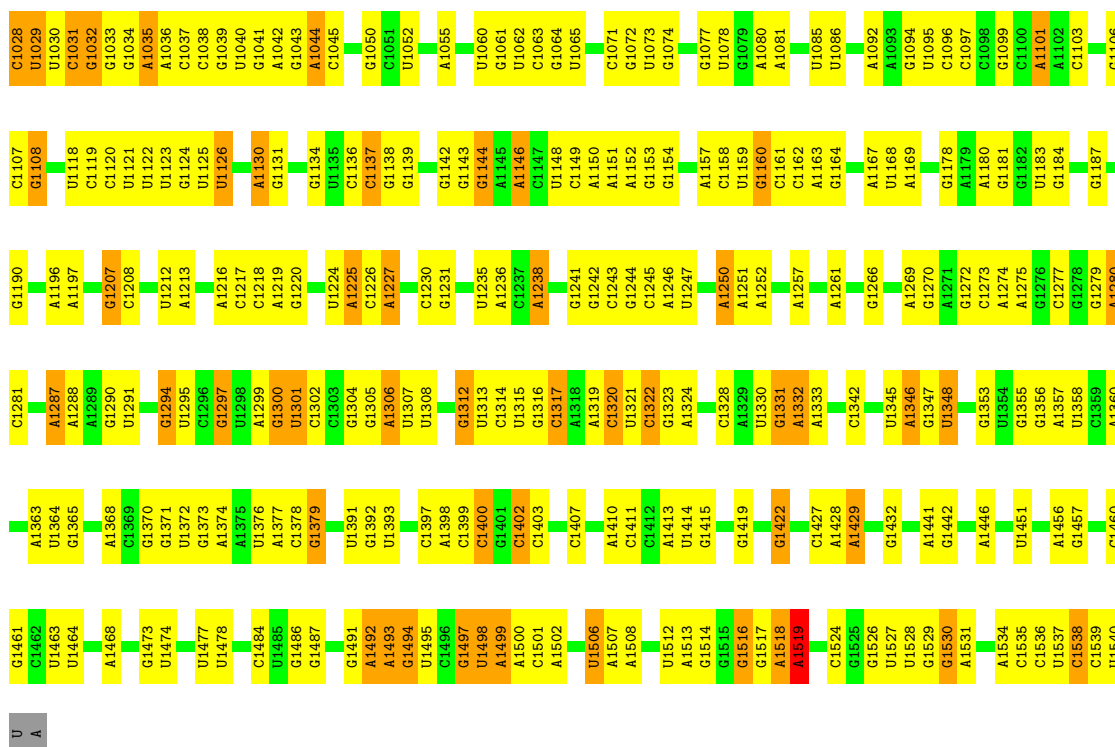
Chain Z:  81% 17%



• Molecule 34: 16S ribosomal RNA

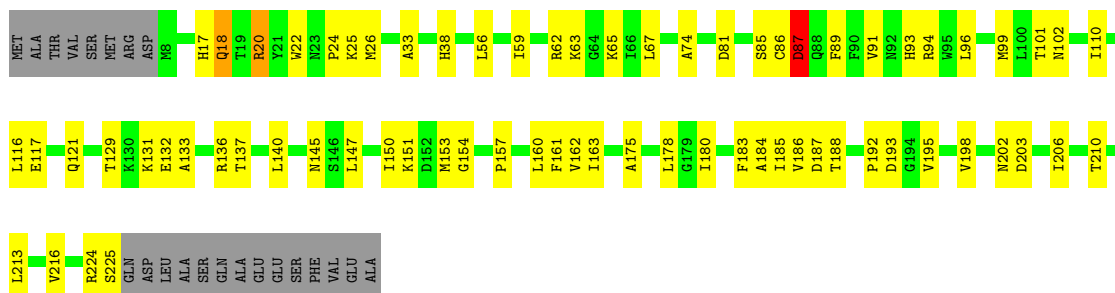
Chain a:  45% 45% 10%





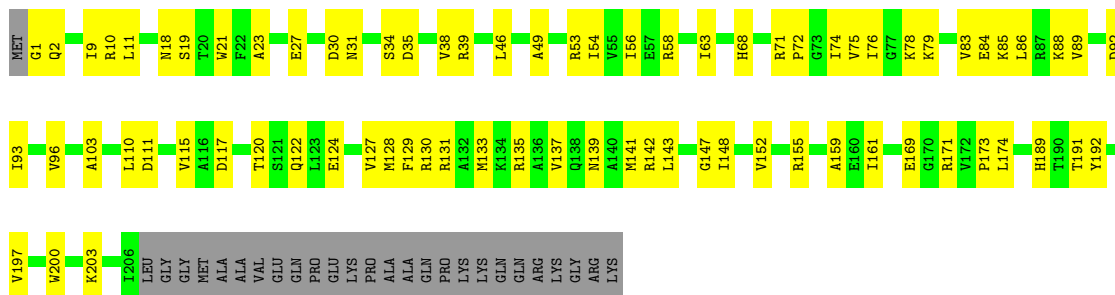
• Molecule 35: 30S ribosomal protein S2

Chain b: 61% 28% 9%



• Molecule 36: 30S ribosomal protein S3

Chain c: 56% 33% 12%



• Molecule 37: 30S ribosomal protein S4

K176	T86	MET
M177	G86	A1
E178	N88	L4
F181	L93	G5
P185	E94	P6
E186	G95	K7
L187	R96	L8
A192	L97	
D193	D98	R12
I194	N99	R13
N195	V100	E14
E196	R103	G15
I199	G105	T16
K205	F106	D17
	G107	
	R110	S22
	A111	G23
	E112	V24
	L116	R25
	H119	A26
	M123	I27
	V124	D28
	N125	T29
	N130	R30
	Y134	C31
	P138	K32
	D140	I33
	V141	E34
	S143	Q35
	I144	A36
	E146	P37
	K149	G38
	Q150	
	Q151	G41
	S152	R46
	V154	L47
	K155	R55
	E159	F56
		K57
		Q58
		K59
		V60
		R61
		R62
		E68
		R69
		Q70
		F71
		R72
		N73
		Y74
		A78
		A79
		N84

M10	M11	A112	V113	M121	K125	A126	I133	M134	V135	V136	R137	A138	T139	M151	V152	K155	G165	Lys																										
Met	Ala	His	Ile	Glu	Lys	Gln	Ala	Gly	E9	I16	K22	T23	V24	G27	F32	L35	T36	V37	G43	R44	V45	G46	F47	K51	E54	V55	P56	I59	M63	I71	F72	V73	A74	L75	G78	T79	H88	V93	I104	I105	A106	G107	G108	A109

[illegible]

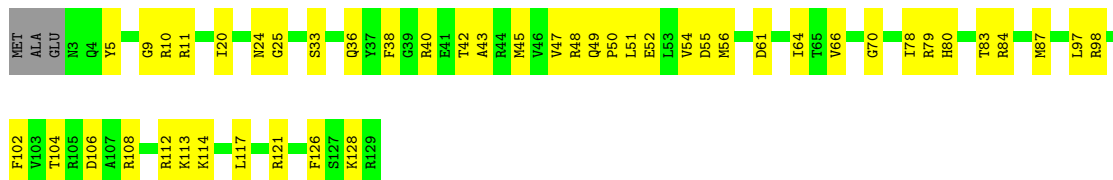
LEU	ASN	R110	P1	MET
		G111	R2	
		D112	R3	
		K113	R4	
		S114	V5	
			I6	
		R118	G7	
		L119	Q8	
			R9	
		E122	P13	
		L123	D14	
		S124	P15	
		D125		
		E128	K24	
		M129	F25	
		K130	V26	
			I27	
		V134	I28	
		K135		
		E138	K35	
		D139	S36	
		V140	E39	
		H141		
		R142	V42	
		M143	Y43	
		A144		
		E145	L46	
		A146	E47	
		N147	T48	
		K148	L49	
			A50	
		A151		
		HIS	E57	
		TYR		
		ARG	A60	
		TRP	F61	
		LEU	E62	
		SER	V63	
		LEU	A64	
		ARG	L65	
		SER	E66	
		PHE		
		SER	T71	
		HIS		
		GLN	V74	
		ALA		
		GLY	R78	
		ALA		
		SER	T83	
		SER	Y84	
		LYS	Q85	
		GLN		
		PRO	R91	
		ALA		
		LEU	R95	
		GLY		
		TRP	T102	

Met	S1	S2	I6	A7	D8	M9	L10	T11	R12	L13	R14	M15	K21	P27	S28	S29	K32	V38	L39	K40	E41	L45	E46	D47	L58	E59	L60	T61	Y64	I74	R75	R76	V77	S78	R79	R82	R83	I84	R87	L91	M95	L98	S106
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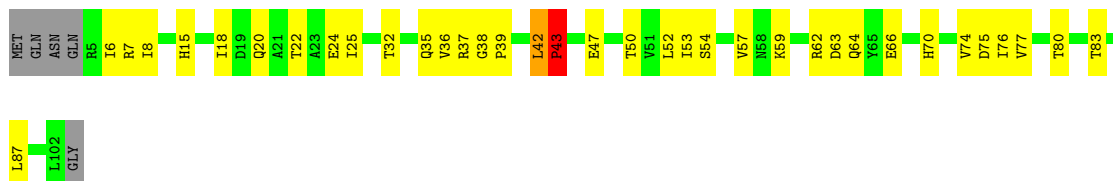
- Molecule 42: 30S ribosomal protein S9

Chain i:  62% 35% .



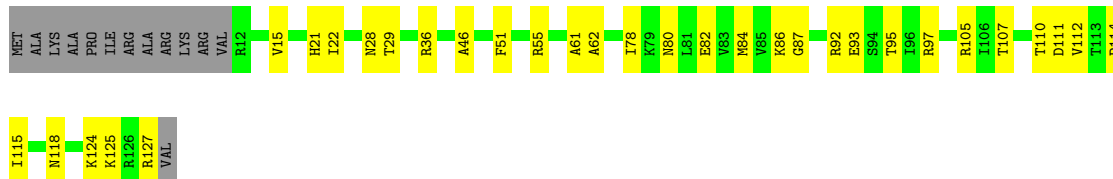
- Molecule 43: 30S ribosomal protein S10

Chain j:  60% 33% .. 5%



- Molecule 44: 30S ribosomal protein S11

Chain k:  65% 25% 10%



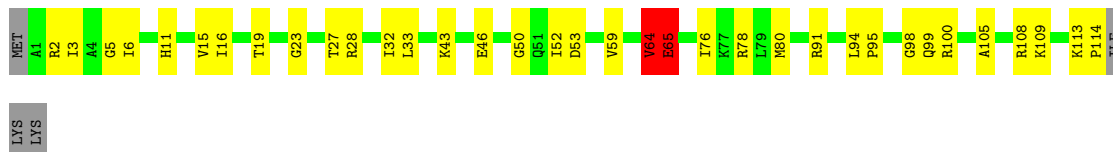
- Molecule 45: 30S ribosomal protein S12

Chain l:  76% 23% .

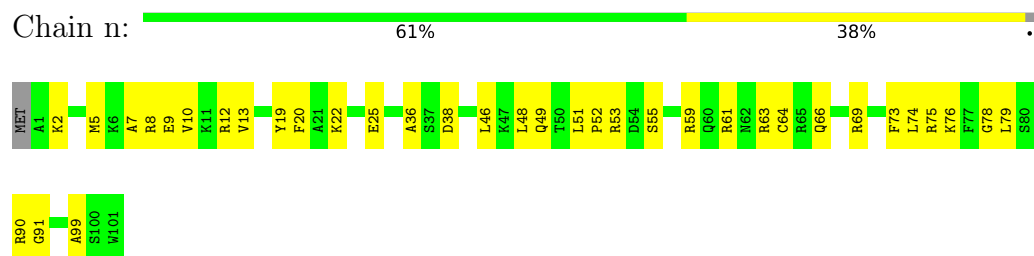


- Molecule 46: 30S ribosomal protein S13

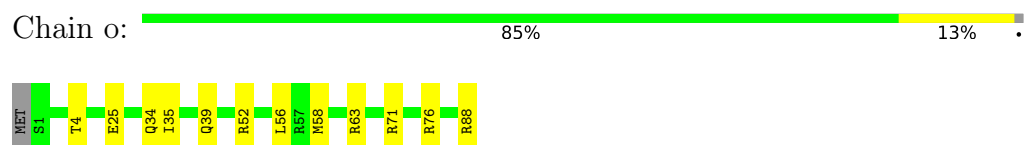
Chain m:  67% 28% . .



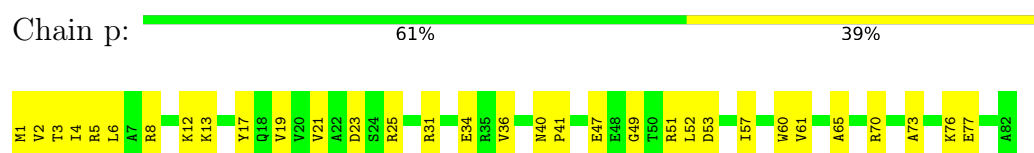
- Molecule 47: 30S ribosomal protein S14



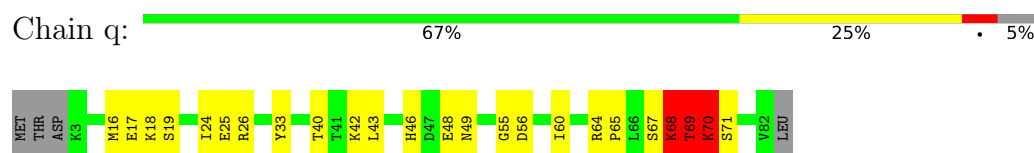
- Molecule 48: 30S ribosomal protein S15



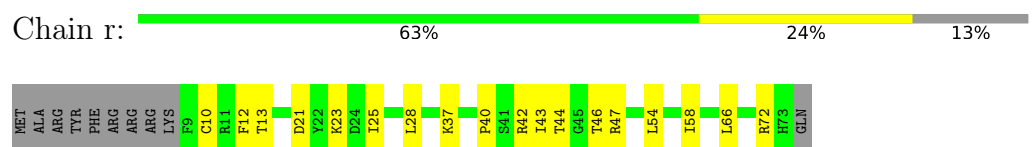
- Molecule 49: 30S ribosomal protein S16



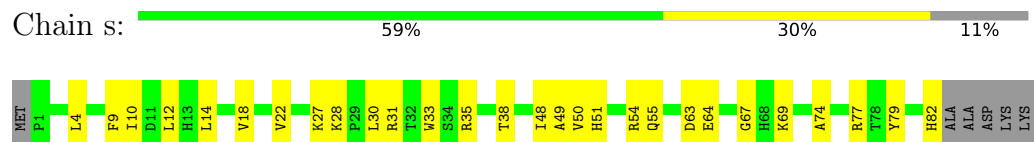
- Molecule 50: 30S ribosomal protein S17



- Molecule 51: 30S ribosomal protein S18



- Molecule 52: 30S ribosomal protein S19



- Molecule 53: 30S ribosomal protein S20





- Molecule 54: 30S ribosomal protein S21

Chain u: 65% 25% 8%



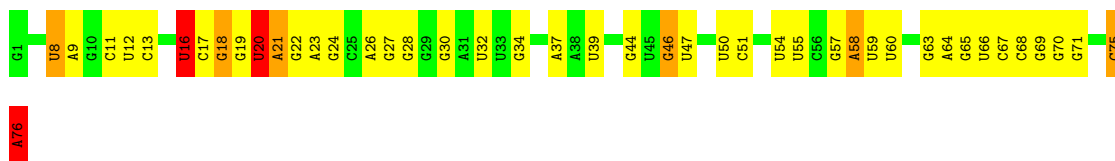
- Molecule 55: P-site fMet-Phe-tRNA(Phe)

Chain v: 50% 50%



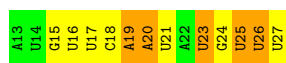
- Molecule 56: P-site fMet-Phe-tRNA(Phe)

Chain w: 42% 46% 8%



- Molecule 57: mRNA

Chain x: 20% 47% 33%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	25347	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	15.609	Depositor
Minimum map value	-7.539	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	0.035	Depositor
Map size (Å)	334.08, 334.08, 334.08	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.6525, 0.6525, 0.6525	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: OMG, 2MG, 5MU, 3TD, 6MZ, MA6, MIA, 1MG, PSU, 4SU, 4OC, ZN, 5MC, CL, NA, OMC, 2MA, UR3, G7M, OMU, MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.29	0/450	0.46	0/599
2	1	0.25	0/416	0.42	0/554
3	2	0.33	0/380	0.43	0/498
4	3	0.39	0/513	0.53	0/676
5	4	0.31	0/303	0.47	0/397
6	5	0.23	0/646	0.55	0/898
7	6	0.21	0/531	0.47	0/709
8	A	0.33	3/69263 (0.0%)	0.34	0/108050
9	B	0.29	1/2873 (0.0%)	0.31	0/4478
10	C	0.34	0/2121	0.47	0/2852
11	D	0.32	0/1586	0.45	0/2134
12	E	0.30	0/1571	0.42	0/2113
13	F	0.27	0/1434	0.52	2/1926 (0.1%)
14	G	0.24	0/1343	0.42	0/1816
15	H	0.30	0/1122	0.58	1/1515 (0.1%)
16	I	0.19	0/692	0.50	0/960
17	J	0.31	0/1152	0.38	0/1551
18	K	0.32	0/947	0.44	0/1268
19	L	0.31	0/1054	0.52	0/1403
20	M	0.30	0/1093	0.42	0/1460
21	N	0.31	0/973	0.50	0/1301
22	O	0.25	0/902	0.47	0/1209
23	P	0.30	0/929	0.43	0/1242
24	Q	0.36	0/960	0.42	0/1278
25	R	0.31	0/829	0.44	0/1107
26	S	0.30	0/864	0.43	0/1156
27	T	0.26	0/744	0.46	0/994
28	U	0.25	0/787	0.44	0/1051
29	V	0.28	0/766	0.42	0/1025
30	W	0.31	0/582	0.40	0/769
31	X	0.32	0/635	0.47	0/848

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Y	0.28	0/510	0.75	5/677 (0.7%)
33	Z	0.29	0/453	0.41	0/605
34	a	0.29	0/36700	0.34	5/57246 (0.0%)
35	b	0.25	0/1735	0.55	3/2338 (0.1%)
36	c	0.27	0/1651	0.43	0/2225
37	d	1.18	11/1665 (0.7%)	0.99	21/2227 (0.9%)
38	e	0.28	0/1154	0.48	0/1554
39	f	0.27	0/835	0.50	0/1128
40	g	0.23	0/1195	0.48	0/1602
41	h	0.27	0/989	0.42	0/1326
42	i	0.25	0/1034	0.52	0/1375
43	j	1.09	4/796 (0.5%)	0.86	9/1077 (0.8%)
44	k	0.25	0/885	0.42	0/1195
45	l	0.28	0/969	0.48	0/1300
46	m	1.07	4/892 (0.4%)	0.73	4/1193 (0.3%)
47	n	0.26	0/811	0.45	0/1081
48	o	0.25	0/722	0.40	0/964
49	p	0.31	0/659	0.49	0/884
50	q	1.10	5/657 (0.8%)	1.14	8/881 (0.9%)
51	r	0.27	0/544	0.49	0/731
52	s	0.24	0/675	0.36	0/908
53	t	1.04	3/671 (0.4%)	0.88	6/888 (0.7%)
54	u	0.45	1/512 (0.2%)	1.17	5/683 (0.7%)
55	v	5.90	4/19 (21.1%)	2.15	2/23 (8.7%)
56	w	0.82	10/1650 (0.6%)	0.52	5/2569 (0.2%)
57	x	0.22	0/349	0.30	0/540
All	All	0.37	46/157193 (0.0%)	0.41	76/235057 (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
43	j	0	1
46	m	0	1
50	q	0	2
53	t	0	2
56	w	0	1
All	All	0	7

The worst 5 of 46 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
37	d	35	GLN	C-O	-26.77	0.95	1.23
43	j	42	LEU	C-O	-21.75	0.96	1.24
53	t	7	LYS	C-O	-21.38	0.92	1.24
46	m	64	VAL	C-O	-21.33	0.98	1.24
50	q	70	LYS	C-O	-17.47	1.01	1.24

The worst 5 of 76 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	u	13	VAL	N-CA-C	-17.13	96.74	113.53
53	t	7	LYS	N-CA-C	-15.64	91.03	112.30
37	d	37	PRO	N-CA-CB	-15.21	87.28	103.25
56	w	76	A	C1'-C2'-O2'	13.25	131.67	111.80
50	q	70	LYS	CA-C-N	-12.19	102.71	122.95

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
43	j	42	LEU	Mainchain
46	m	64	VAL	Mainchain
50	q	69	THR	Mainchain
50	q	70	LYS	Mainchain
53	t	5	SER	Mainchain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	444	0	461	21	0
2	1	409	0	440	16	0
3	2	377	0	418	9	0
4	3	504	0	574	25	0
5	4	302	0	340	13	0
6	5	647	0	336	10	0
7	6	522	0	521	30	0
8	A	62336	0	31365	1177	0
9	B	2570	0	1301	48	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	C	2082	0	2157	80	0
11	D	1565	0	1616	34	0
12	E	1552	0	1619	45	0
13	F	1410	0	1447	48	0
14	G	1323	0	1374	32	0
15	H	1111	0	1147	44	0
16	I	693	0	347	13	0
17	J	1129	0	1162	27	0
18	K	938	0	1012	30	0
19	L	1045	0	1117	36	0
20	M	1074	0	1157	33	0
21	N	960	0	1000	25	0
22	O	892	0	923	30	0
23	P	917	0	965	29	0
24	Q	947	0	1022	24	0
25	R	816	0	839	25	0
26	S	857	0	920	16	0
27	T	738	0	807	15	0
28	U	779	0	834	28	0
29	V	753	0	780	19	0
30	W	575	0	592	18	0
31	X	625	0	655	26	0
32	Y	509	0	543	18	0
33	Z	449	0	491	7	0
34	a	33028	0	16640	701	0
35	b	1704	0	1732	51	0
36	c	1624	0	1699	58	0
37	d	1643	0	1710	70	0
38	e	1141	0	1170	32	0
39	f	817	0	808	33	0
40	g	1181	0	1240	49	0
41	h	979	0	1034	30	0
42	i	1022	0	1070	43	0
43	j	786	0	828	25	0
44	k	869	0	878	25	0
45	l	955	0	1019	22	0
46	m	883	0	944	26	0
47	n	799	0	841	32	0
48	o	714	0	737	11	0
49	p	649	0	666	31	0
50	q	648	0	688	22	0
51	r	535	0	552	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	s	658	0	685	29	0
53	t	665	0	714	21	0
54	u	506	0	502	14	0
55	v	19	0	17	8	0
56	w	1631	0	834	28	0
57	x	314	0	158	11	0
58	0	1	0	0	0	0
58	6	1	0	0	0	0
58	A	236	0	0	0	0
58	B	5	0	0	0	0
58	O	1	0	0	0	0
58	Q	1	0	0	0	0
58	T	1	0	0	0	0
58	a	82	0	0	0	0
58	g	1	0	0	0	0
58	w	3	0	0	0	0
59	4	1	0	0	0	0
59	6	1	0	0	0	0
60	A	1	0	0	0	0
61	A	1	0	0	0	0
61	V	1	0	0	0	0
62	A	1	0	0	0	0
62	a	1	0	0	0	0
All	All	145959	0	97448	2988	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 13.

The worst 5 of 2988 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)
15:H:63:ALA:C	15:H:66:ASN:OD1	1.71	1.32
8:A:2165:C:N4	8:A:2171:A:H62	1.41	1.16
8:A:2165:C:H42	8:A:2171:A:N6	1.41	1.15
34:a:615:G:N2	34:a:626:G:C4	2.21	1.08
15:H:63:ALA:O	15:H:66:ASN:OD1	1.72	1.07

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	54/57 (95%)	49 (91%)	5 (9%)	0	100	100
2	1	48/55 (87%)	46 (96%)	2 (4%)	0	100	100
3	2	44/46 (96%)	44 (100%)	0	0	100	100
4	3	62/65 (95%)	55 (89%)	7 (11%)	0	100	100
5	4	36/38 (95%)	32 (89%)	4 (11%)	0	100	100
6	5	129/165 (78%)	108 (84%)	21 (16%)	0	100	100
7	6	64/70 (91%)	50 (78%)	14 (22%)	0	100	100
10	C	269/273 (98%)	248 (92%)	20 (7%)	1 (0%)	30	61
11	D	207/209 (99%)	191 (92%)	16 (8%)	0	100	100
12	E	199/201 (99%)	187 (94%)	12 (6%)	0	100	100
13	F	175/179 (98%)	153 (87%)	22 (13%)	0	100	100
14	G	174/177 (98%)	154 (88%)	19 (11%)	1 (1%)	21	52
15	H	147/149 (99%)	111 (76%)	33 (22%)	3 (2%)	6	25
16	I	139/142 (98%)	109 (78%)	30 (22%)	0	100	100
17	J	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
18	K	120/123 (98%)	113 (94%)	7 (6%)	0	100	100
19	L	141/144 (98%)	124 (88%)	17 (12%)	0	100	100
20	M	134/136 (98%)	125 (93%)	9 (7%)	0	100	100
21	N	118/127 (93%)	112 (95%)	6 (5%)	0	100	100
22	O	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
23	P	112/115 (97%)	102 (91%)	10 (9%)	0	100	100
24	Q	115/118 (98%)	113 (98%)	2 (2%)	0	100	100
25	R	101/103 (98%)	89 (88%)	12 (12%)	0	100	100
26	S	108/110 (98%)	100 (93%)	8 (7%)	0	100	100
27	T	91/100 (91%)	81 (89%)	10 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	U	100/104 (96%)	90 (90%)	10 (10%)	0	100	100
29	V	92/94 (98%)	86 (94%)	6 (6%)	0	100	100
30	W	73/85 (86%)	66 (90%)	7 (10%)	0	100	100
31	X	75/78 (96%)	71 (95%)	4 (5%)	0	100	100
32	Y	61/63 (97%)	57 (93%)	3 (5%)	1 (2%)	7	30
33	Z	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
35	b	216/240 (90%)	188 (87%)	25 (12%)	3 (1%)	9	34
36	c	204/233 (88%)	195 (96%)	9 (4%)	0	100	100
37	d	203/206 (98%)	167 (82%)	29 (14%)	7 (3%)	3	16
38	e	155/167 (93%)	138 (89%)	17 (11%)	0	100	100
39	f	98/135 (73%)	88 (90%)	10 (10%)	0	100	100
40	g	149/179 (83%)	142 (95%)	7 (5%)	0	100	100
41	h	127/130 (98%)	116 (91%)	11 (9%)	0	100	100
42	i	125/130 (96%)	105 (84%)	20 (16%)	0	100	100
43	j	96/103 (93%)	78 (81%)	16 (17%)	2 (2%)	5	25
44	k	114/129 (88%)	107 (94%)	7 (6%)	0	100	100
45	l	121/124 (98%)	105 (87%)	16 (13%)	0	100	100
46	m	112/118 (95%)	101 (90%)	10 (9%)	1 (1%)	14	44
47	n	99/102 (97%)	86 (87%)	13 (13%)	0	100	100
48	o	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
49	p	80/82 (98%)	68 (85%)	12 (15%)	0	100	100
50	q	78/84 (93%)	63 (81%)	13 (17%)	2 (3%)	4	21
51	r	63/75 (84%)	53 (84%)	10 (16%)	0	100	100
52	s	80/92 (87%)	73 (91%)	7 (9%)	0	100	100
53	t	83/87 (95%)	82 (99%)	1 (1%)	0	100	100
54	u	63/71 (89%)	51 (81%)	11 (18%)	1 (2%)	7	30
All	All	5850/6220 (94%)	5250 (90%)	578 (10%)	22 (0%)	31	61

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
35	b	87	ASP
37	d	34	GLU

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Mol	Chain	Res	Type
37	d	37	PRO
37	d	150	LYS
43	j	43	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	47/48 (98%)	47 (100%)	0	100	100
2	1	45/49 (92%)	45 (100%)	0	100	100
3	2	38/38 (100%)	38 (100%)	0	100	100
4	3	51/52 (98%)	50 (98%)	1 (2%)	48	72
5	4	34/34 (100%)	34 (100%)	0	100	100
7	6	59/62 (95%)	59 (100%)	0	100	100
10	C	216/218 (99%)	216 (100%)	0	100	100
11	D	164/164 (100%)	164 (100%)	0	100	100
12	E	165/165 (100%)	165 (100%)	0	100	100
13	F	148/150 (99%)	148 (100%)	0	100	100
14	G	137/138 (99%)	137 (100%)	0	100	100
15	H	114/114 (100%)	112 (98%)	2 (2%)	51	73
17	J	116/116 (100%)	116 (100%)	0	100	100
18	K	103/104 (99%)	103 (100%)	0	100	100
19	L	102/103 (99%)	102 (100%)	0	100	100
20	M	109/109 (100%)	109 (100%)	0	100	100
21	N	100/103 (97%)	100 (100%)	0	100	100
22	O	86/87 (99%)	86 (100%)	0	100	100
23	P	99/100 (99%)	99 (100%)	0	100	100
24	Q	89/90 (99%)	89 (100%)	0	100	100
25	R	84/84 (100%)	84 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	S	93/93 (100%)	93 (100%)	0	100	100
27	T	80/84 (95%)	79 (99%)	1 (1%)	61	77
28	U	83/85 (98%)	83 (100%)	0	100	100
29	V	78/78 (100%)	78 (100%)	0	100	100
30	W	57/63 (90%)	57 (100%)	0	100	100
31	X	67/68 (98%)	67 (100%)	0	100	100
32	Y	55/55 (100%)	55 (100%)	0	100	100
33	Z	48/49 (98%)	48 (100%)	0	100	100
35	b	180/198 (91%)	180 (100%)	0	100	100
36	c	170/190 (90%)	170 (100%)	0	100	100
37	d	172/173 (99%)	168 (98%)	4 (2%)	44	70
38	e	114/126 (90%)	114 (100%)	0	100	100
39	f	87/116 (75%)	87 (100%)	0	100	100
40	g	124/147 (84%)	124 (100%)	0	100	100
41	h	104/105 (99%)	104 (100%)	0	100	100
42	i	105/107 (98%)	105 (100%)	0	100	100
43	j	86/90 (96%)	85 (99%)	1 (1%)	63	78
44	k	89/99 (90%)	89 (100%)	0	100	100
45	l	103/104 (99%)	103 (100%)	0	100	100
46	m	92/96 (96%)	92 (100%)	0	100	100
47	n	79/84 (94%)	79 (100%)	0	100	100
48	o	76/77 (99%)	76 (100%)	0	100	100
49	p	65/65 (100%)	65 (100%)	0	100	100
50	q	74/78 (95%)	71 (96%)	3 (4%)	27	59
51	r	56/65 (86%)	56 (100%)	0	100	100
52	s	72/79 (91%)	72 (100%)	0	100	100
53	t	65/66 (98%)	65 (100%)	0	100	100
54	u	46/61 (75%)	46 (100%)	0	100	100
55	v	2/2 (100%)	1 (50%)	1 (50%)	0	0
All	All	4628/4831 (96%)	4615 (100%)	13 (0%)	84	87

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
37	d	150	LYS
43	j	43	PRO
55	v	101	MET
50	q	68	LYS
50	q	70	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 54 such sidechains are listed below:

Mol	Chain	Res	Type
28	U	52	ASN
37	d	88	ASN
49	p	59	HIS
28	U	53	GLN
35	b	18	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	a	1538/1542 (99%)	285 (18%)	0
56	w	75/76 (98%)	13 (17%)	0
57	x	14/15 (93%)	8 (57%)	0
8	A	2902/2903 (99%)	579 (19%)	56 (1%)
9	B	119/120 (99%)	18 (15%)	3 (2%)
All	All	4648/4656 (99%)	903 (19%)	59 (1%)

5 of 903 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	A	10	A
8	A	15	G
8	A	33	C
8	A	35	G
8	A	46	G

5 of 59 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	A	1458	U
8	A	2832	U
8	A	1847	G
8	A	2820	A

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Mol	Chain	Res	Type
8	A	2655	G

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

41 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	G7M	A	2069	8	23,26,27	3.45	10 (43%)	35,39,42	1.63	8 (22%)
8	PSU	A	955	58,8	18,21,22	1.09	1 (5%)	22,30,33	1.85	5 (22%)
34	MA6	a	1519	34	23,26,27	1.46	5 (21%)	34,38,41	2.87	12 (35%)
8	2MG	A	2445	8	23,26,27	2.87	8 (34%)	32,38,41	2.29	12 (37%)
56	5MU	w	54	56	19,22,23	4.80	7 (36%)	28,32,35	3.65	9 (32%)
8	PSU	A	1917	8	18,21,22	1.03	1 (5%)	22,30,33	1.78	4 (18%)
8	PSU	A	2580	8	18,21,22	1.08	2 (11%)	22,30,33	1.92	5 (22%)
8	6MZ	A	1618	8	22,25,26	2.96	5 (22%)	30,36,39	4.33	14 (46%)
8	3TD	A	1915	58,8	18,22,23	4.33	5 (27%)	22,32,35	1.65	3 (13%)
34	2MG	a	1516	34	23,26,27	2.91	9 (39%)	32,38,41	2.27	12 (37%)
8	OMU	A	2552	8	19,22,23	2.92	8 (42%)	26,31,34	1.79	5 (19%)
34	PSU	a	516	34,58	18,21,22	0.93	2 (11%)	22,30,33	1.76	5 (22%)
8	5MC	A	747	8	18,22,23	3.62	7 (38%)	26,32,35	1.13	2 (7%)
56	PSU	w	32	56	18,21,22	1.00	1 (5%)	22,30,33	1.64	5 (22%)
34	G7M	a	527	34	23,26,27	3.57	10 (43%)	35,39,42	1.65	7 (20%)
34	2MG	a	1207	34	23,26,27	2.89	8 (34%)	32,38,41	2.22	11 (34%)
8	PSU	A	2457	8	18,21,22	1.01	2 (11%)	22,30,33	1.95	6 (27%)
8	5MU	A	1939	8	19,22,23	4.67	7 (36%)	28,32,35	3.75	10 (35%)
8	1MG	A	745	8	22,26,27	2.64	5 (22%)	33,39,42	2.01	8 (24%)
34	MA6	a	1518	34	23,26,27	1.47	5 (21%)	34,38,41	2.77	12 (35%)
8	PSU	A	2605	8	18,21,22	1.33	2 (11%)	22,30,33	1.89	4 (18%)
34	UR3	a	1498	34	19,22,23	2.63	6 (31%)	26,32,35	1.49	3 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	PSU	A	746	58,8	18,21,22	1.09	2 (11%)	22,30,33	1.78	4 (18%)
56	4SU	w	8	56	18,21,22	3.61	7 (38%)	26,30,33	2.22	4 (15%)
8	5MC	A	1962	8	18,22,23	3.63	7 (38%)	26,32,35	1.03	2 (7%)
56	PSU	w	39	56	18,21,22	1.01	1 (5%)	22,30,33	1.75	3 (13%)
34	5MC	a	1407	34	18,22,23	3.65	7 (38%)	26,32,35	0.99	1 (3%)
8	PSU	A	2604	8	18,21,22	1.33	2 (11%)	22,30,33	1.98	5 (22%)
8	OMG	A	2251	56,8	23,26,27	2.35	9 (39%)	33,38,41	1.76	7 (21%)
8	2MA	A	2503	58,8	22,25,26	3.71	8 (36%)	33,37,40	2.25	8 (24%)
8	PSU	A	1911	8	18,21,22	1.08	2 (11%)	22,30,33	1.77	4 (18%)
8	2MG	A	1835	8	23,26,27	2.88	8 (34%)	32,38,41	2.30	11 (34%)
34	2MG	a	966	34	23,26,27	2.90	8 (34%)	32,38,41	2.29	12 (37%)
34	5MC	a	967	34	18,22,23	3.69	7 (38%)	26,32,35	1.00	2 (7%)
8	OMC	A	2498	58,8	19,22,23	2.86	7 (36%)	26,31,34	0.82	0
8	PSU	A	2504	8	18,21,22	1.02	1 (5%)	22,30,33	1.90	5 (22%)
34	4OC	a	1402	34	20,23,24	2.97	8 (40%)	26,32,35	0.92	2 (7%)
56	PSU	w	55	56	18,21,22	1.04	1 (5%)	22,30,33	1.84	5 (22%)
8	6MZ	A	2030	8	22,25,26	2.94	5 (22%)	30,36,39	4.38	14 (46%)
56	G7M	w	46	56	23,26,27	2.62	8 (34%)	35,39,42	2.20	10 (28%)
56	MIA	w	37	56	28,31,32	2.51	6 (21%)	40,44,47	2.91	17 (42%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	G7M	A	2069	8	-	1/7/25/26	0/3/3/3
8	PSU	A	955	58,8	-	0/7/25/26	0/2/2/2
34	MA6	a	1519	34	-	1/11/29/30	0/3/3/3
8	2MG	A	2445	8	-	2/9/27/28	0/3/3/3
56	5MU	w	54	56	-	2/7/25/26	0/2/2/2
8	PSU	A	1917	8	-	0/7/25/26	0/2/2/2
8	PSU	A	2580	8	-	0/7/25/26	0/2/2/2
8	6MZ	A	1618	8	-	1/9/27/28	0/3/3/3
8	3TD	A	1915	58,8	-	3/7/25/26	0/2/2/2
34	2MG	a	1516	34	-	0/9/27/28	0/3/3/3
8	OMU	A	2552	8	-	2/9/27/28	0/2/2/2

Continued on next page...

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	PSU	a	516	34,58	-	3/7/25/26	0/2/2/2
8	5MC	A	747	8	-	4/7/25/26	0/2/2/2
56	PSU	w	32	56	-	2/7/25/26	0/2/2/2
34	G7M	a	527	34	-	3/7/25/26	0/3/3/3
34	2MG	a	1207	34	-	0/9/27/28	0/3/3/3
8	PSU	A	2457	8	-	0/7/25/26	0/2/2/2
8	5MU	A	1939	8	-	0/7/25/26	0/2/2/2
8	1MG	A	745	8	-	0/7/25/26	0/3/3/3
34	MA6	a	1518	34	-	0/11/29/30	0/3/3/3
8	PSU	A	2605	8	-	1/7/25/26	0/2/2/2
34	UR3	a	1498	34	-	2/7/25/26	0/2/2/2
8	PSU	A	746	58,8	-	1/7/25/26	0/2/2/2
56	4SU	w	8	56	-	0/7/25/26	0/2/2/2
8	5MC	A	1962	8	-	0/7/25/26	0/2/2/2
56	PSU	w	39	56	-	3/7/25/26	0/2/2/2
34	5MC	a	1407	34	-	0/7/25/26	0/2/2/2
8	PSU	A	2604	8	-	1/7/25/26	0/2/2/2
8	OMG	A	2251	56,8	-	3/9/27/28	0/3/3/3
8	2MA	A	2503	58,8	-	2/7/25/26	0/3/3/3
8	PSU	A	1911	8	-	0/7/25/26	0/2/2/2
8	2MG	A	1835	8	-	2/9/27/28	0/3/3/3
34	2MG	a	966	34	-	0/9/27/28	0/3/3/3
34	5MC	a	967	34	-	0/7/25/26	0/2/2/2
8	OMC	A	2498	58,8	-	0/9/27/28	0/2/2/2
8	PSU	A	2504	8	-	0/7/25/26	0/2/2/2
34	4OC	a	1402	34	-	2/9/29/30	0/2/2/2
56	PSU	w	55	56	-	1/7/25/26	0/2/2/2
8	6MZ	A	2030	8	-	2/9/27/28	0/3/3/3
56	G7M	w	46	56	-	3/7/25/26	0/3/3/3
56	MIA	w	37	56	-	3/15/33/34	0/3/3/3

The worst 5 of 220 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1915	3TD	C6-C5	13.20	1.50	1.35
8	A	1618	6MZ	C6-N6	12.23	1.47	1.34
8	A	2030	6MZ	C6-N6	11.94	1.47	1.34
8	A	2503	2MA	C4-N3	11.66	1.49	1.34
56	w	54	5MU	C2-N1	10.85	1.55	1.38

The worst 5 of 278 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	2030	6MZ	C4-N9-C8	13.40	120.25	105.73
8	A	1618	6MZ	C4-N9-C8	13.24	120.08	105.73
8	A	1939	5MU	C5-C4-N3	12.36	125.86	115.31
56	w	54	5MU	C5-C4-N3	12.15	125.69	115.31
8	A	2030	6MZ	N9-C8-N7	-10.77	99.18	113.91

There are no chirality outliers.

5 of 50 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	1618	6MZ	N1-C6-N6-C9
8	A	1915	3TD	C2'-C1'-C5-C4
8	A	1915	3TD	O4'-C1'-C5-C4
8	A	1915	3TD	O4'-C1'-C5-C6
8	A	2030	6MZ	O4'-C4'-C5'-O5'

There are no ring outliers.

18 monomers are involved in 33 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
34	a	1519	MA6	1	0
8	A	2445	2MG	3	0
8	A	1915	3TD	2	0
34	a	1516	2MG	1	0
8	A	2552	OMU	1	0
34	a	516	PSU	3	0
8	A	747	5MC	1	0
34	a	1207	2MG	1	0
34	a	1518	MA6	2	0
8	A	2605	PSU	3	0
34	a	1498	UR3	2	0
56	w	8	4SU	1	0
8	A	2251	OMG	2	0
8	A	2503	2MA	1	0
34	a	966	2MG	4	0
8	A	2498	OMC	1	0
34	a	1402	4OC	1	0
8	A	2030	6MZ	4	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 337 ligands modelled in this entry, 337 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

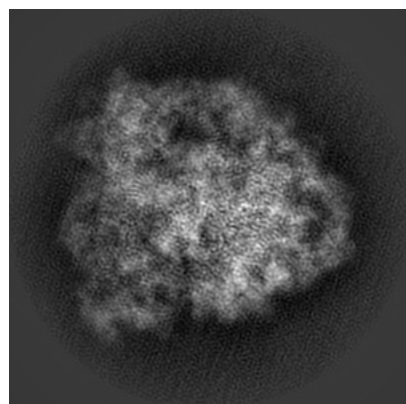
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10905. These allow visual inspection of the internal detail of the map and identification of artifacts.

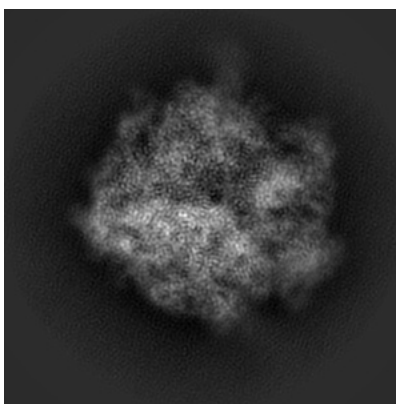
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

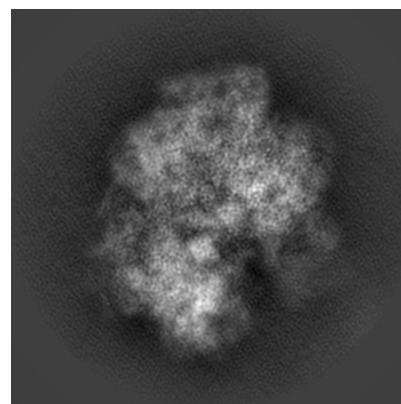
6.1.1 Primary map



X

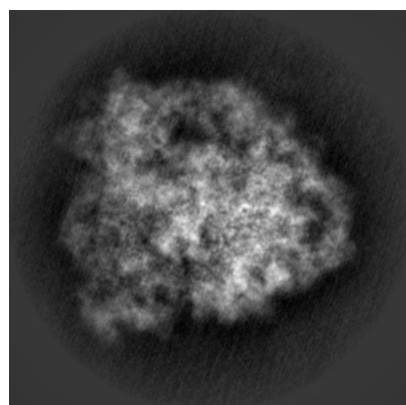


Y

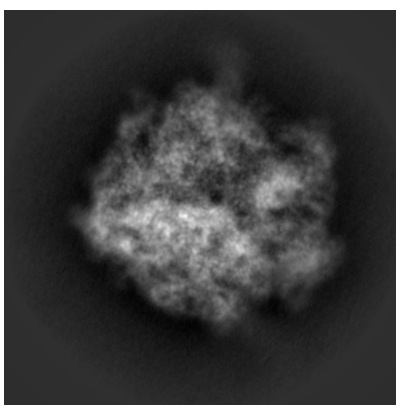


Z

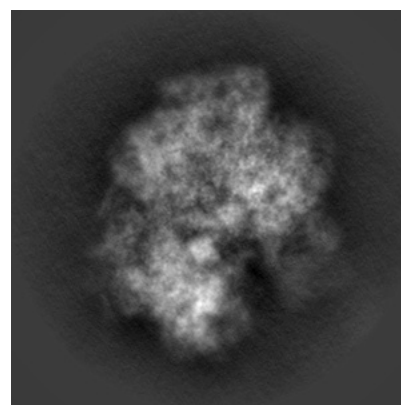
6.1.2 Raw map



X



Y

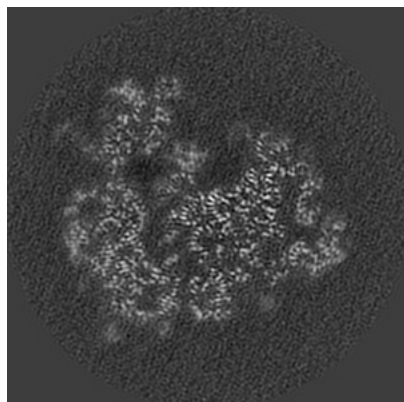


Z

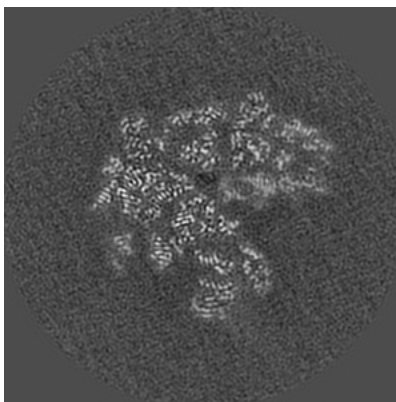
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

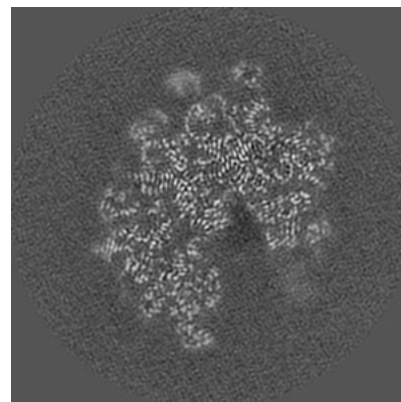
6.2.1 Primary map



X Index: 256

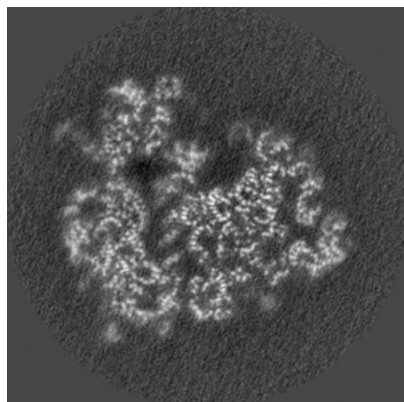


Y Index: 256

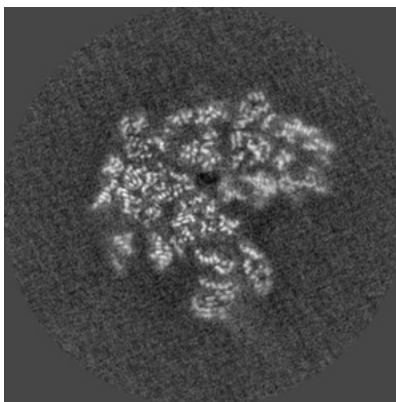


Z Index: 256

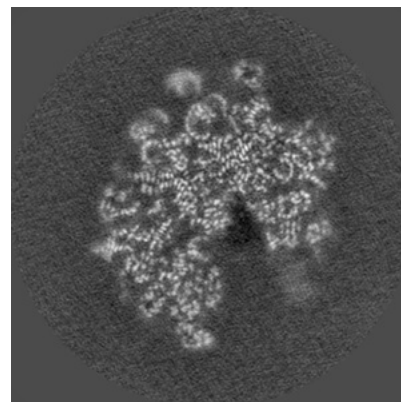
6.2.2 Raw map



X Index: 144



Y Index: 144

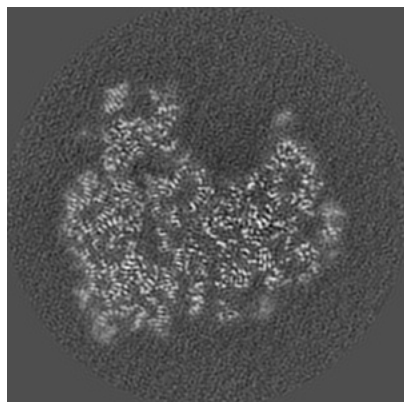


Z Index: 144

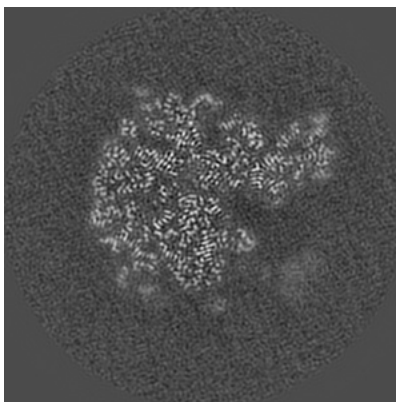
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

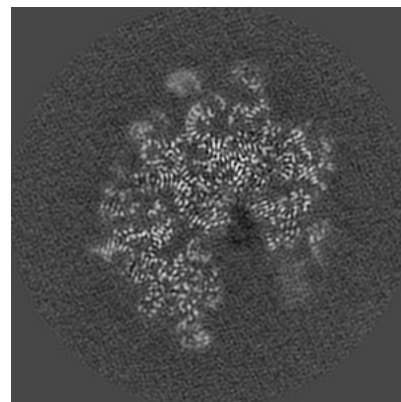
6.3.1 Primary map



X Index: 241

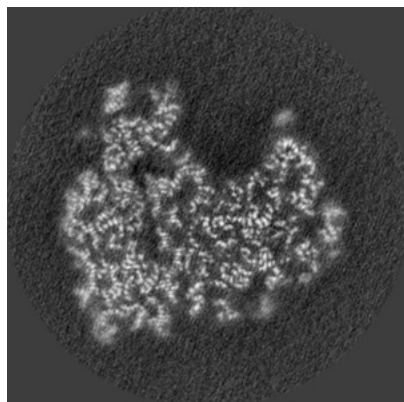


Y Index: 285

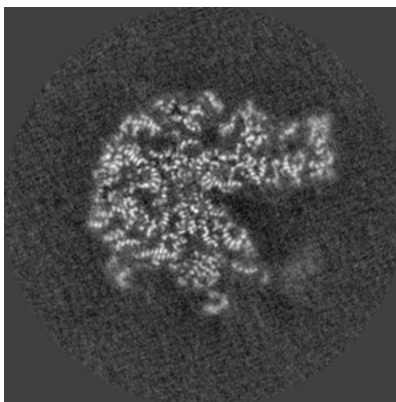


Z Index: 258

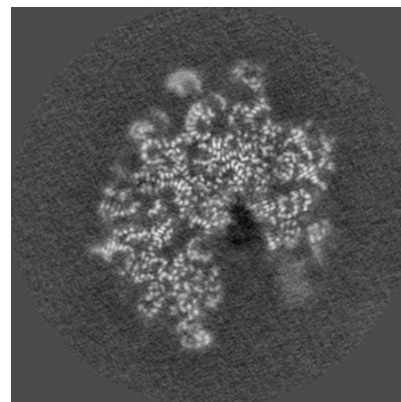
6.3.2 Raw map



X Index: 136



Y Index: 157

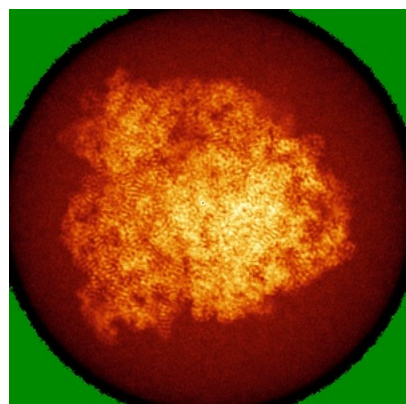


Z Index: 145

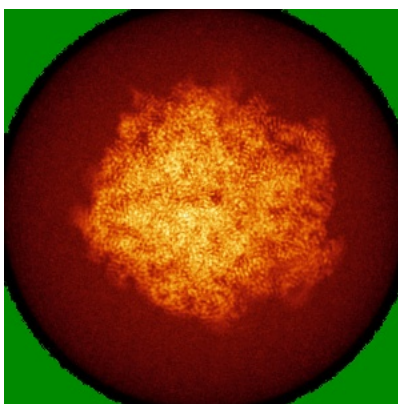
The images above show the largest variance slices of the map in three orthogonal directions.

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

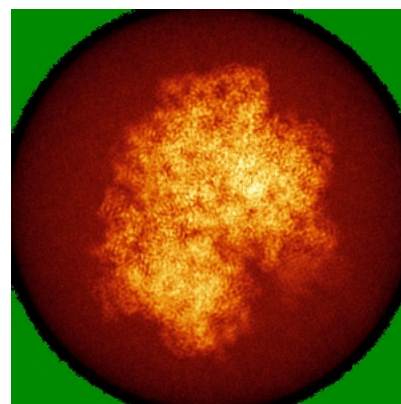
6.4.1 Primary map



X

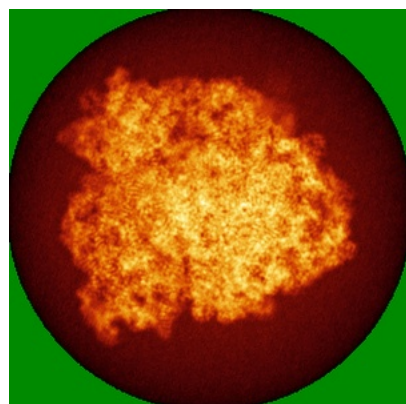


Y

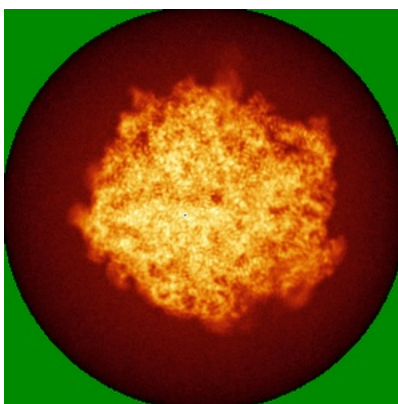


Z

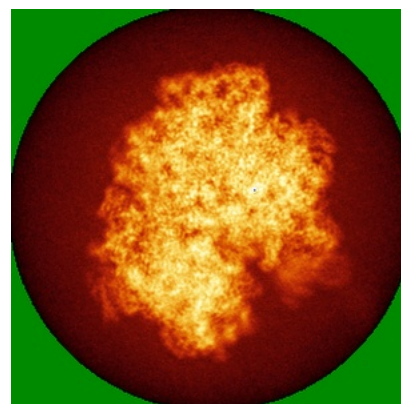
6.4.2 Raw map



X



Y

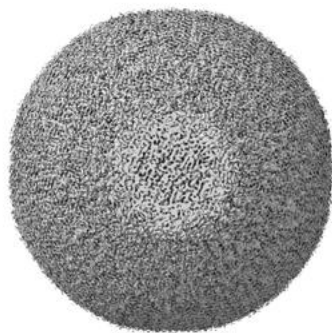


Z

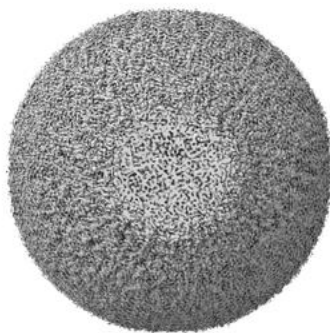
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

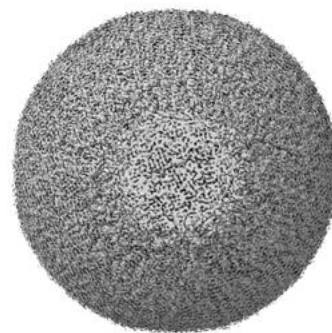
6.5.1 Primary map



X



Y



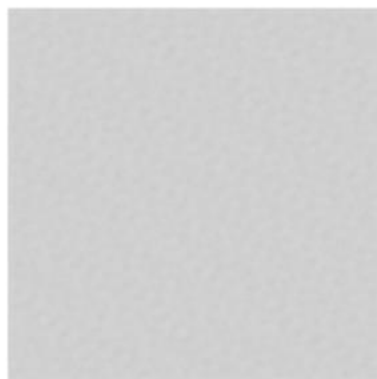
Z

The images above show the 3D surface view of the map at the recommended contour level 0.035. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

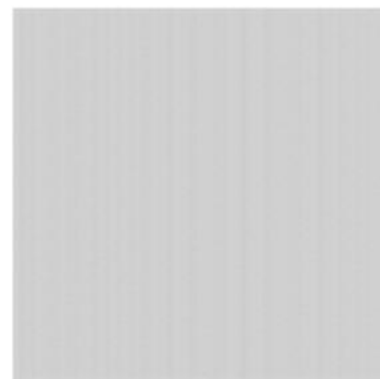
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

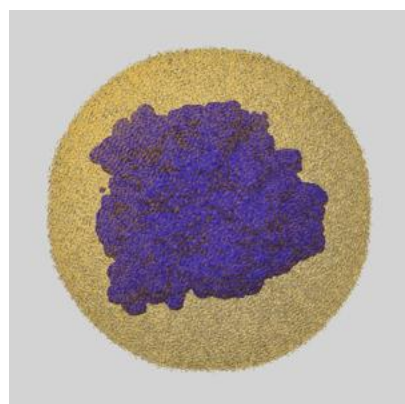
6.6 Mask visualisation [i](#)

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

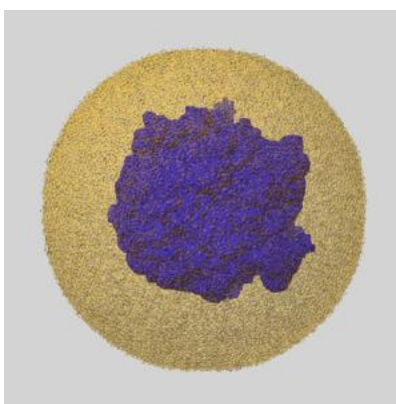
A mask typically either:

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

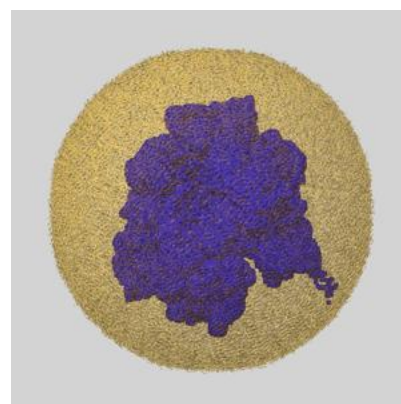
6.6.1 emd_10905_msk_1.map [i](#)



X



Y

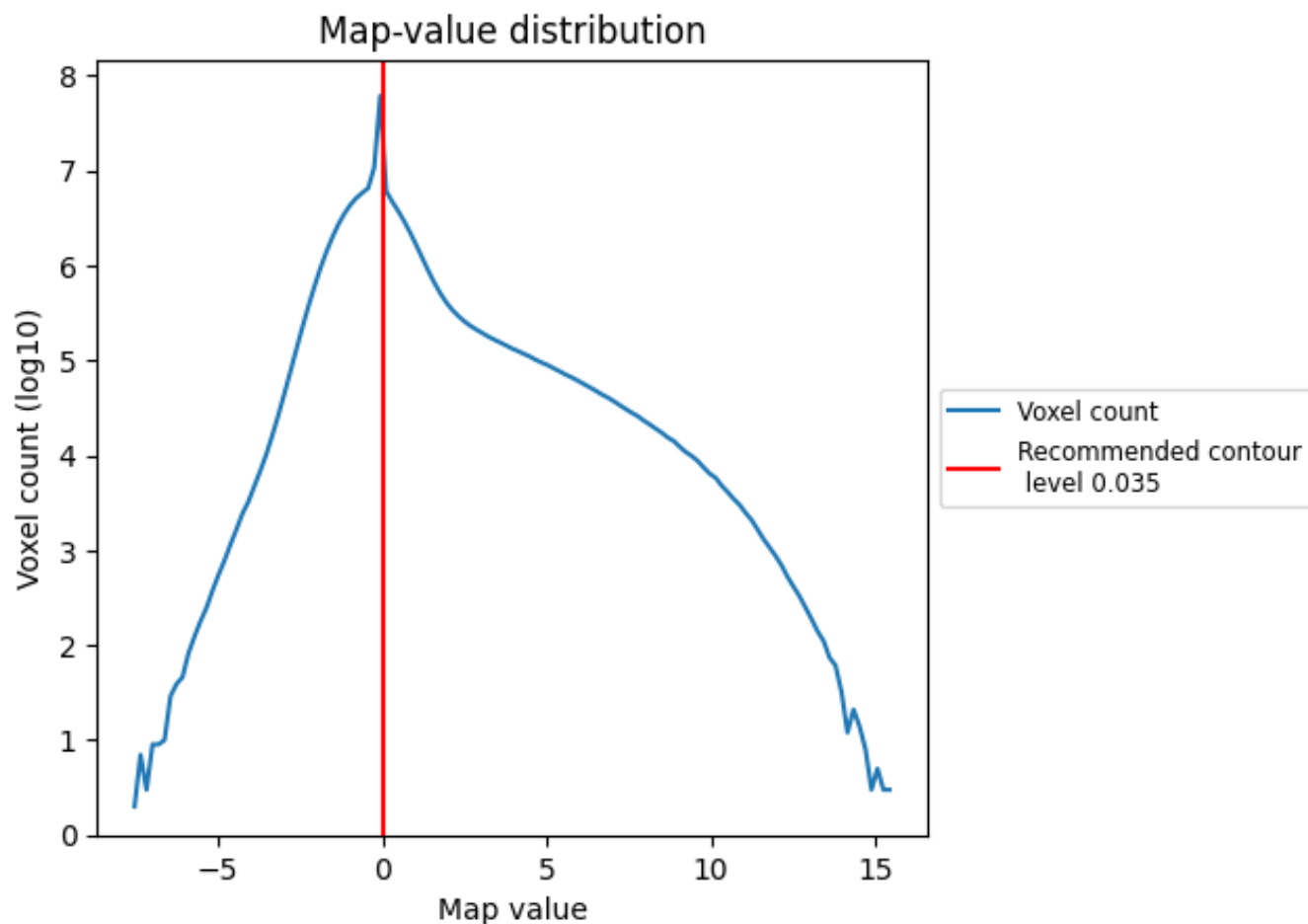


Z

7 Map analysis [i](#)

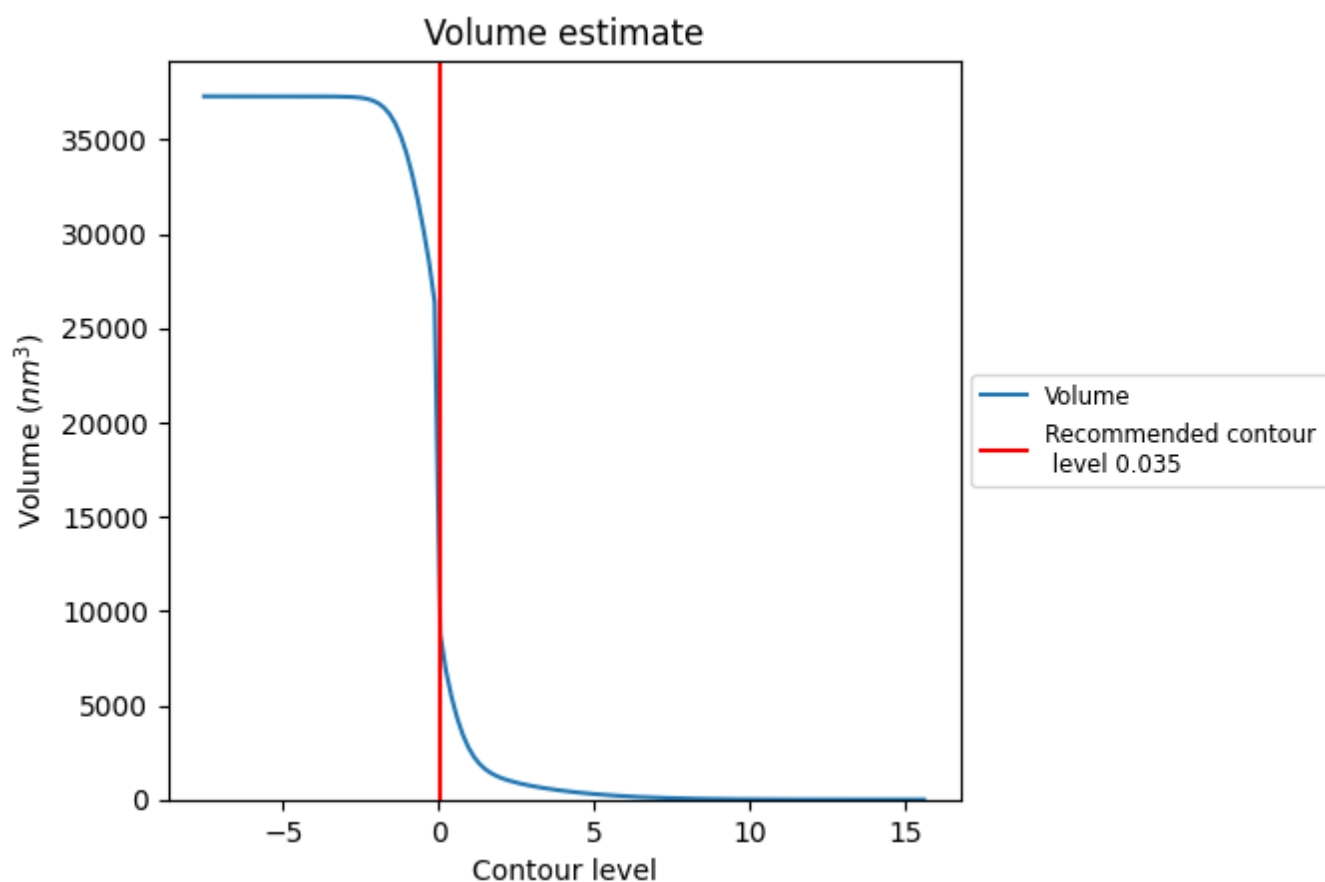
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

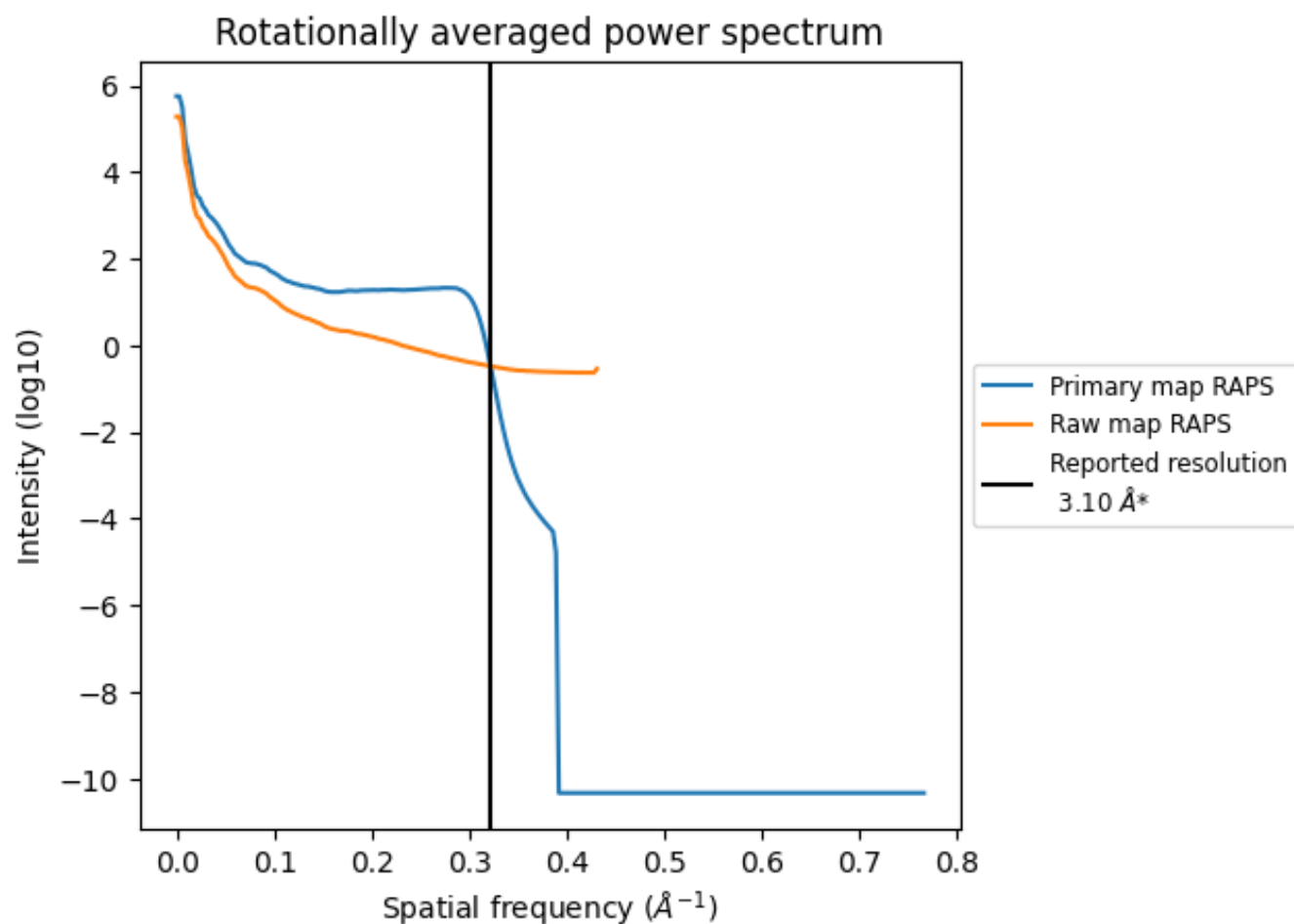
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 10850 nm^3 ; this corresponds to an approximate mass of 9801 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

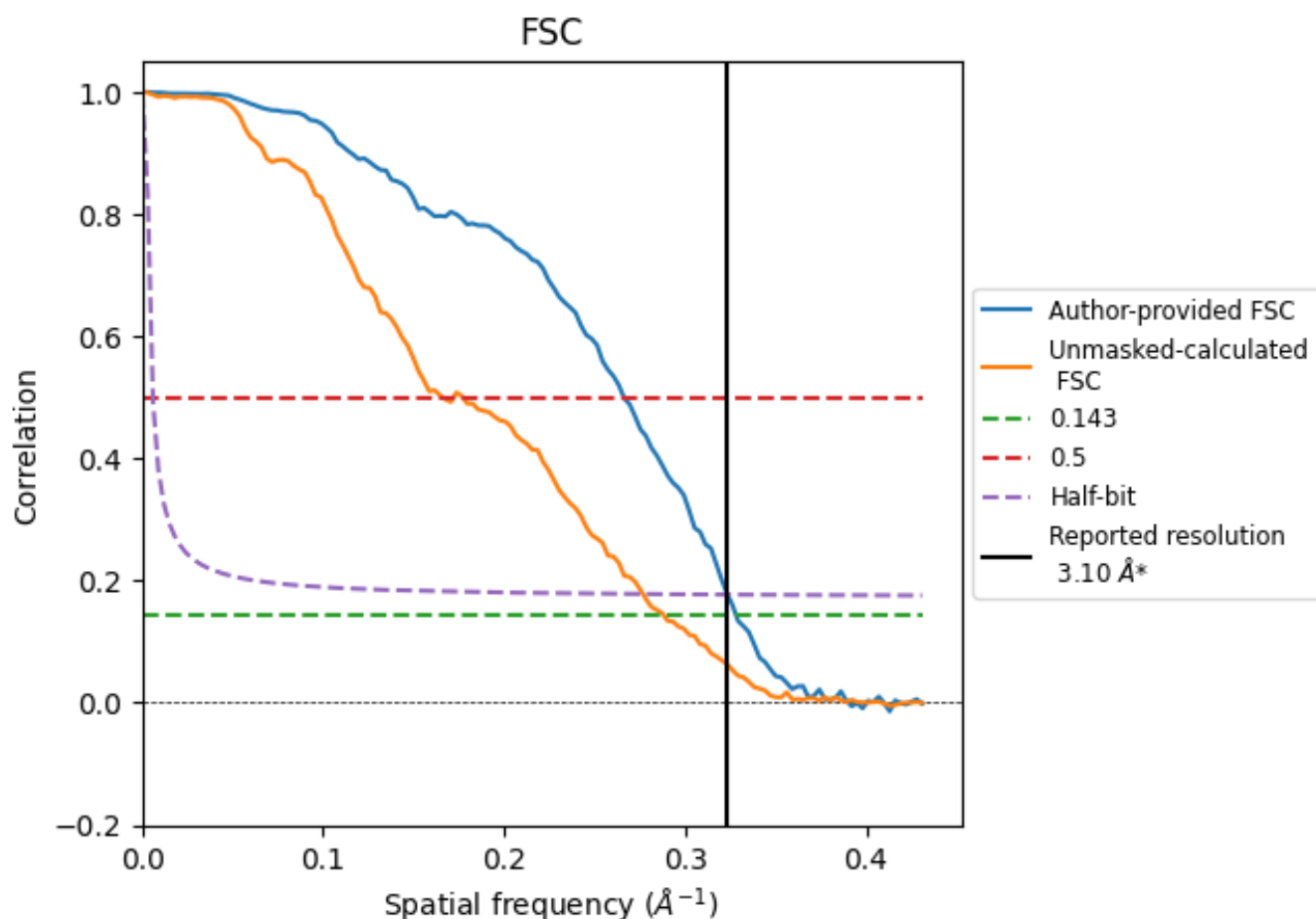


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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

8.2 Resolution estimates [i](#)

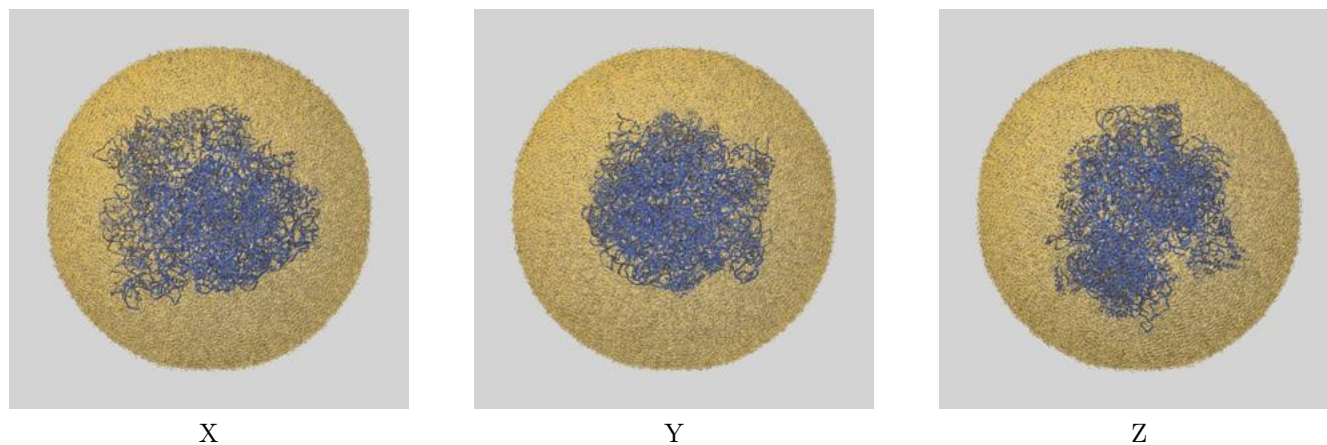
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.05	3.76	3.09
Unmasked-calculated*	3.47	6.02	3.61

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.47 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

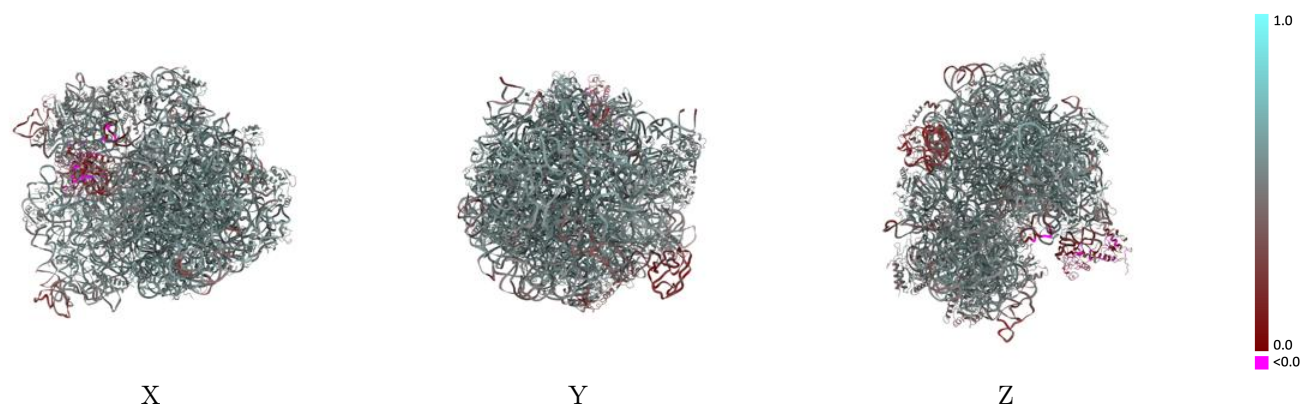
This section contains information regarding the fit between EMDB map EMD-10905 and PDB model 6YSR. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



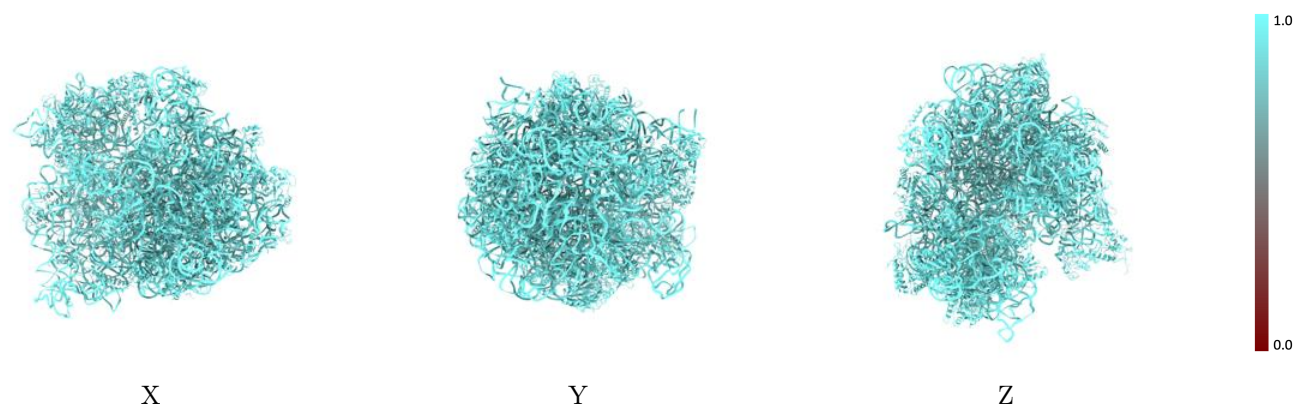
The images above show the 3D surface view of the map at the recommended contour level 0.035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



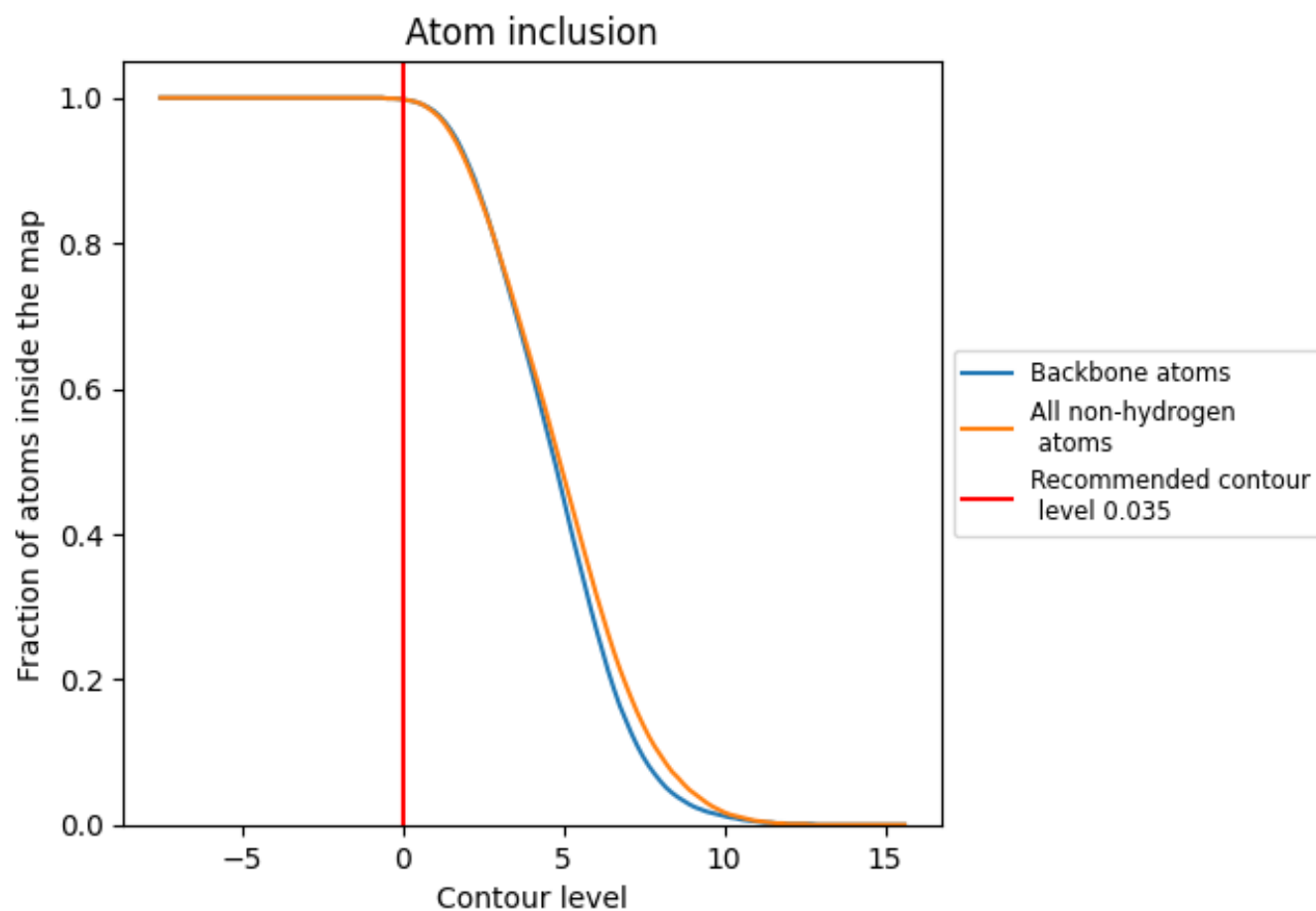
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.035).

9.4 Atom inclusion ⓘ



At the recommended contour level, 100% of all backbone atoms, 100% 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 (0.035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9980	 0.5280
0	 0.9980	 0.5690
1	 1.0000	 0.5540
2	 0.9940	 0.5880
3	 0.9960	 0.5880
4	 0.9930	 0.5740
5	 0.9710	 0.1920
6	 0.9920	 0.4440
A	 0.9980	 0.5340
B	 1.0000	 0.5360
C	 0.9980	 0.5750
D	 0.9970	 0.5730
E	 0.9990	 0.5390
F	 0.9960	 0.5020
G	 0.9970	 0.5040
H	 0.9750	 0.4040
I	 0.9670	 0.1730
J	 1.0000	 0.5740
K	 0.9970	 0.5640
L	 0.9960	 0.5580
M	 0.9990	 0.5600
N	 1.0000	 0.5730
O	 0.9990	 0.5330
P	 0.9990	 0.5700
Q	 0.9970	 0.5690
R	 1.0000	 0.5650
S	 0.9950	 0.5640
T	 1.0000	 0.5370
U	 0.9990	 0.5170
V	 0.9970	 0.5380
W	 0.9930	 0.5800
X	 0.9970	 0.5650
Y	 0.9980	 0.5010
Z	 1.0000	 0.5580
a	 1.0000	 0.5300



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Chain	Atom inclusion	Q-score
b	 0.9920	 0.4770
c	 0.9980	 0.5190
d	 0.9970	 0.5090
e	 0.9990	 0.5460
f	 0.9960	 0.4930
g	 0.9970	 0.4810
h	 0.9960	 0.5560
i	 1.0000	 0.5020
j	 0.9970	 0.4820
k	 0.9950	 0.5300
l	 0.9910	 0.5430
m	 0.9990	 0.5160
n	 1.0000	 0.5260
o	 0.9970	 0.5360
p	 0.9980	 0.5260
q	 0.9980	 0.5230
r	 0.9960	 0.5210
s	 0.9980	 0.5260
t	 0.9950	 0.5250
u	 0.9960	 0.4620
v	 0.8420	 0.4770
w	 1.0000	 0.4820
x	 0.9780	 0.4350