



wwPDB EM Validation Summary Report ⓘ

Dec 18, 2022 – 08:58 am GMT

PDB ID : 7ASP
EMDB ID : EMD-11903
Title : Staphylococcus aureus 70S after 50 minutes incubation at 37C
Authors : Camicata, G.; Bashan, A.; Yonath, A.
Deposited on : 2020-10-27
Resolution : 2.86 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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

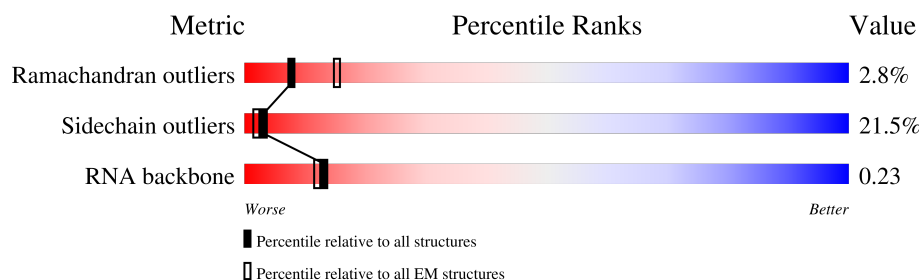
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.86 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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	Y	2923	
2	X	1552	
3	3	114	
4	1	105	
4	A	105	
5	B	43	
6	2	64	
7	4	37	

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Mol	Chain	Length	Quality of chain
8	a	80	
9	b	114	
10	c	136	
11	C	274	
12	d	113	
13	D	215	
14	E	206	
15	e	60	
16	f	88	
17	g	83	
18	G	175	
19	H	145	
20	h	80	
21	I	122	
22	i	56	
23	j	78	
24	J	146	
25	k	202	
26	K	137	
27	L	120	
28	l	198	
29	m	156	
30	M	119	
31	n	95	
32	N	114	

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Mol	Chain	Length	Quality of chain
33	o	130	 5% 76% 22% .
34	O	116	 88% 12%
35	p	155	 26% 78% 21% ..
36	P	102	 78% 21% .
37	q	127	 26% 75% 24% .
38	Q	112	 90% 10%
39	R	89	 81% 18% .
40	S	103	 83% 17%
41	T	94	 82% 18%
42	U	79	 82% 16% .
43	V	49	 82% 16% .
44	W	67	 78% 22%
45	Z	47	 83% 17%
46	F	158	 92% 6% .

2 Entry composition [i](#)

There are 46 unique types of molecules in this entry. The entry contains 128828 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 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Y	2723	Total	C	N	O	P	0	0
			58376	26062	10687	18904	2723		

- Molecule 2 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	X	1447	Total	C	N	O	P	0	0
			31009	13847	5680	10037	1445		

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	114	Total	C	N	O	P	0	0
			2430	1086	436	794	114		

- Molecule 4 is a protein called 50S ribosomal protein L33,50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	47	Total	C	N	O	S	0	0
			390	238	78	70	4		
4	1	58	Total	C	N	O		0	0
			449	280	85	84			

- Molecule 5 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	43	Total	C	N	O	S	0	0
			367	225	89	52	1		

- Molecule 6 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	2	64	Total	C	N	O	S	0	0
			521	324	113	82	2		

- Molecule 7 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	4	37	Total	C	N	O	S	0	0
			295	186	60	44	5		

- Molecule 8 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	a	80	Total	C	N	O	S	0	0
			626	394	116	116			

- Molecule 9 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	b	114	Total	C	N	O	S	0	0
			826	507	158	159	2		

- Molecule 10 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	c	136	Total	C	N	O	S	0	0
			976	611	190	173	2		

- Molecule 11 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	274	Total	C	N	O	S	0	0
			2094	1303	415	371	5		

- Molecule 12 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	d	113	Total	C	N	O	S	0	0
			828	510	168	149	1		

- Molecule 13 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	D	215	Total	C	N	O	S	0	0
			1627	1018	299	305	5		

- Molecule 14 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	E	206	Total	C	N	O	S	0	0
			1572	986	288	296	2		

- Molecule 15 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	e	60	Total	C	N	O	S	0	0
			497	314	99	79	5		

- Molecule 16 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	f	88	Total	C	N	O	S	0	0
			713	441	148	123	1		

- Molecule 17 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	g	83	Total	C	N	O	S	0	0
			537	335	105	96	1		

- Molecule 18 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	G	165	Total	C	N	O	S	0	0
			1184	739	226	216	3		

- Molecule 19 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	H	145	Total	C	N	O	S	0	0
			1143	714	208	218	3		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
20	h	80	Total	C	N	O	0	0
			520	327	97	96		

- Molecule 21 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	I	122	Total	C	N	O	S	0	0
			918	572	174	168	4		

- Molecule 22 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	i	56	Total	C	N	O	S	0	0
			458	292	88	76	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	j	77	Total	C	N	O	S	0	0
			498	300	99	98	1		

- Molecule 24 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	J	146	Total	C	N	O	S	0	0
			1086	674	214	197	1		

- Molecule 25 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	k	202	Total	C	N	O	S	0	0
			1551	979	293	278	1		

- Molecule 26 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	K	137	Total	C	N	O	S	0	0
			1071	689	203	175	4		

- Molecule 27 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	L	120	Total	C	N	O	S	0	0
			932	576	182	173	1		

- Molecule 28 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	l	198	Total	C	N	O		0	0
			1058	634	211	213			

- Molecule 29 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	m	156	Total	C	N	O	S	0	0
			1153	727	211	213	2		

- Molecule 30 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	M	119	Total	C	N	O		0	0
			882	549	174	159			

- Molecule 31 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	n	95	Total	C	N	O	S	0	0
			785	496	138	149	2		

- Molecule 32 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	N	114	Total	C	N	O		0	0
			889	563	175	151			

- Molecule 33 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	o	130	Total	C	N	O	S	0	0
			1007	639	180	184	4		

- Molecule 34 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	O	116	Total	C	N	O	S	0	0
			942	593	189	156	4		

- Molecule 35 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	p	154	Total	C	N	O	S	0	0
			1155	719	219	214	3		

- Molecule 36 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	P	102	Total	C	N	O	S	0	0
			790	503	142	144	1		

- Molecule 37 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	q	127	Total	C	N	O	S	0	0
			975	605	194	175	1		

- Molecule 38 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Q	112	Total	C	N	O	S	0	0
			854	534	164	153	3		

- Molecule 39 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	R	89	Total	C	N	O	S	0	0
			715	453	127	131	4		

- Molecule 40 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	S	103	Total	C	N	O	S	0	0
			770	486	142	141	1		

- Molecule 41 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	T	94	Total	C	N	O	0	0
			722	463	130	129		

- Molecule 42 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	U	79	Total	C	N	O	0	0
			597	369	117	111		

- Molecule 43 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	V	49	Total	C	N	O	0	0
			379	234	82	63		

- Molecule 44 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	W	67	Total	C	N	O	0	0
			541	333	102	106		

- Molecule 45 is a protein called 50S ribosomalprotein L32p.

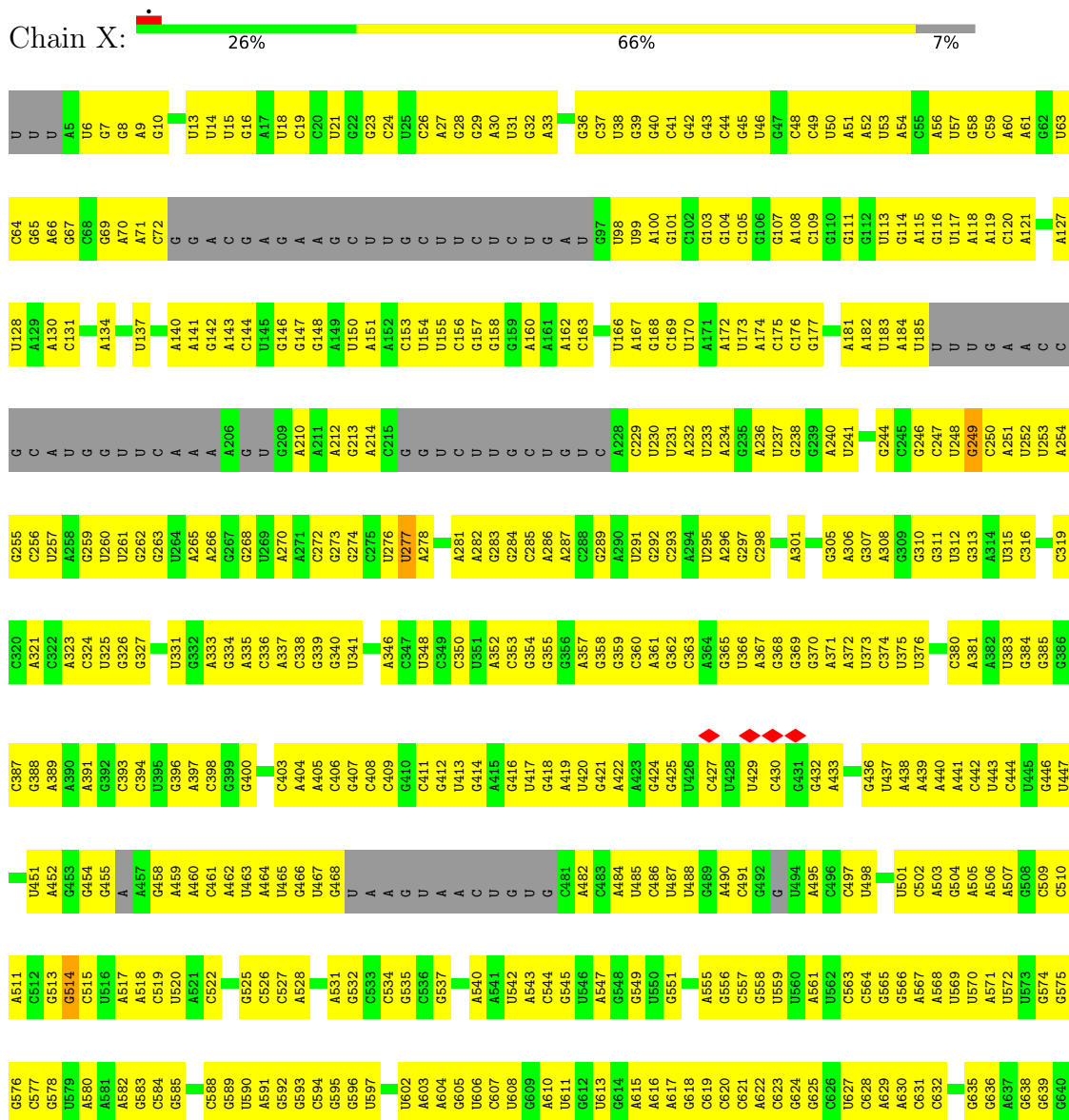
Mol	Chain	Residues	Atoms					AltConf	Trace
45	Z	47	Total	C	N	O	S	0	0
			355	219	76	58	2		

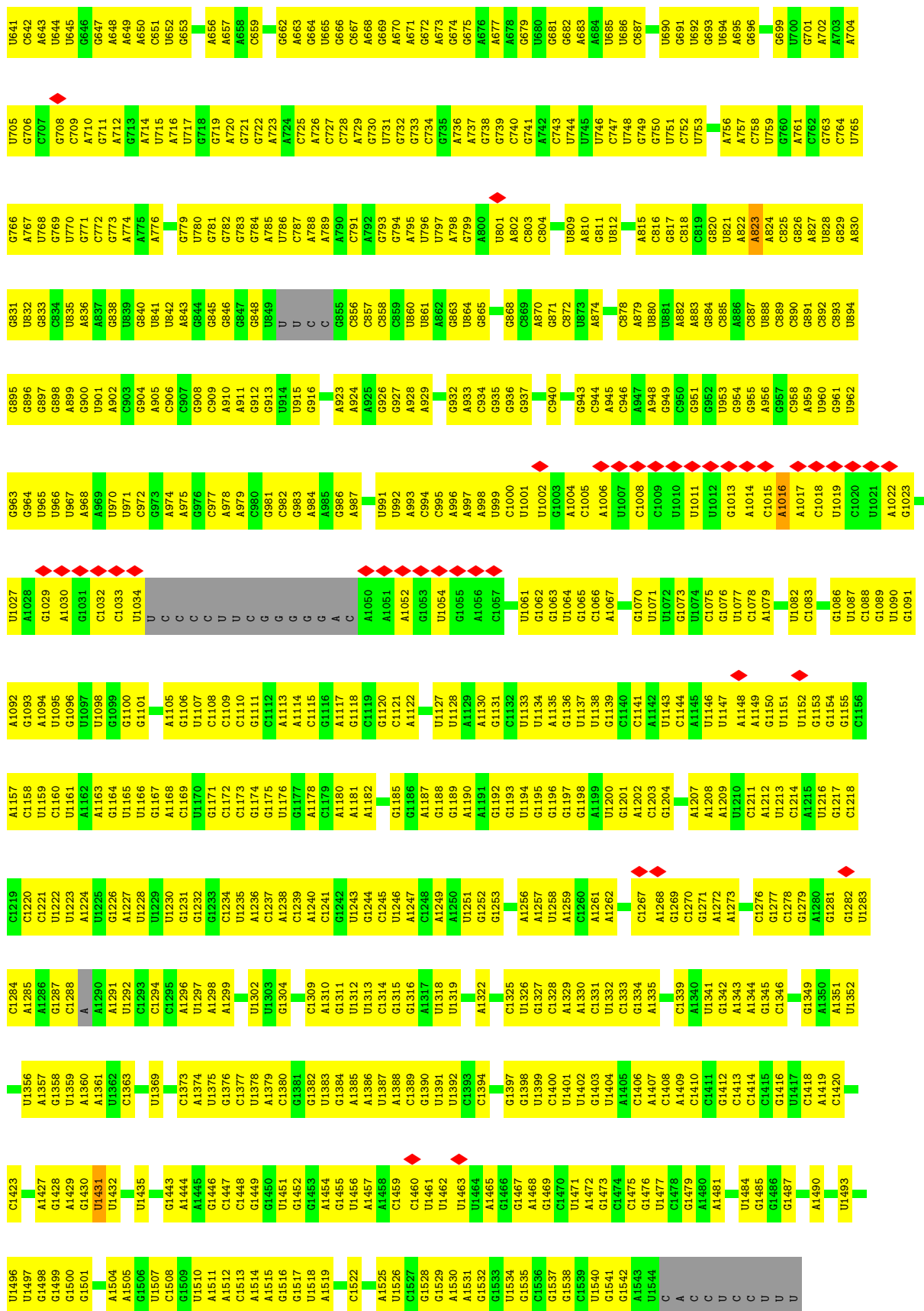
- Molecule 46 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	F	155	Total	C	N	O	0	0
			765	455	155	155		

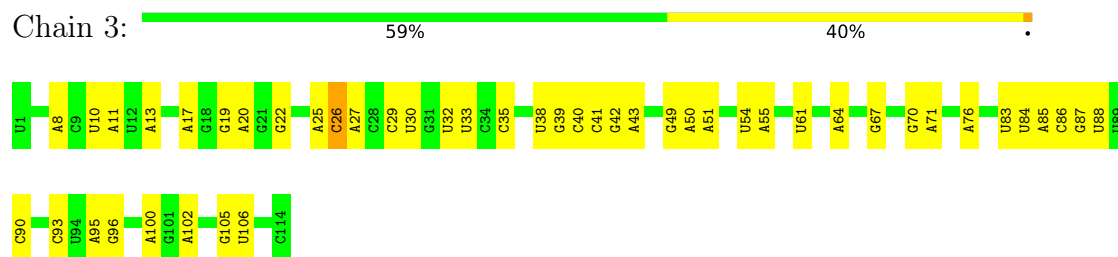
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G2326	U2003	A1814	C1662	A	G1518	U	A1337	A1177	A1027
U2329	A2004	A1917	A1917	U	U1519	U	U1338	C1178	C1029
G2330	A	A1814	A1677	U	A1520	A	U1339	C1179	C1030
G2331	U2011	A1918	A1678	G	A1521	A	U1342	G1180	G1031
U2332	G2012	A1818	U1683	U1586	G1522	U1460	C1342	G1181	A1032
U2333	G2013	C1827	U1683	C1587	G1523	C1461	U1343	U1185	G1033
A2208	C2015	U1828	A1690	U1588	U1524	G1463	G1357	A1186	A1034
G2209	A2016	A1829	G1691	U1589	U1525	U1464	A1358	U1194	C1035
G2334	C2017	G1839	G1692	C1590	A1527	G1465	A1359	A1195	A1040
A2335	G1924	U1939	G1693	A1592	U1528	G1468	G1360	U1198	U1043
A2337	A1928	A1842	U1709	U1593	U1529	A1471	G1361	G1201	A1052
A2338	G1933	U1843	G1718	U1594	A1530	C1472	U1362	G1205	A1053
U2339	G1934	G1844	A1721	U	U	G1473	U1363	U1206	A1054
C2340	C1936	A1856	G1738	U	A	C1474	U1366	G	U1055
A2345	C1937	G1866	G1739	G	G	U1477	C1367	U1207	U1056
U2346	G1937	U1870	A1800	U1597	G	A1478	G1369	A1208	A1057
G2348	U1938	U1871	G1740	U1598	C	G1479	C1370	U1214	U1060
U2352	C1941	A1874	G1748	G1599	A	G1481	U1373	G1217	G1061
G2353	U1942	A1875	U1755	A1600	A	U1482	G1374	G1218	U1062
U2354	A1943	G1876	U1756	U1601	A	A1483	U1374	G1219	G1066
A2360	U1944	U1877	U1757	U1602	C	G1484	U1389	G1220	U1067
U2361	A1946	U1878	A1758	U1603	C	G1485	A1396	C1221	G1068
A2362	C1947	U1879	G1759	U1604	G	U1487	U1396	G1222	G1069
U2363	A1948	U1880	U1760	C1604	U	A1488	C1399	G1229	A1070
C2374	G1949	A1881	G1765	U1607	G	A1489	C1400	G1245	U1077
U2377	U1950	G1882	A1766	C1608	C	G1490	G1401	A1263	U1078
U2378	C1951	U1883	G1767	U1609	U	C1491	A1402	U1267	C1082
U2379	C1952	G1884	C1768	G1610	U	G1492	G1405	G1086	G1083
A2381	U1953	U1885	G1769	U1611	A	U1493	U1416	U1275	U1089
G2242	A1954	G1886	U1770	A1614	G	C1494	G1417	C1276	A1090
U2244	A1955	U1887	G1775	U1615	U	G1495	A1421	C1277	G1091
G2245	G1956	G1888	G1785	A1616	U	G1496	A1422	C1278	A1092
U2246	U1957	U1889	U1788	U1626	A	U1497	A1423	U1280	C1093
G2395	U1958	G1890	A1789	A1627	G	U1498	G1425	A1285	A1094
U2398	A1959	U1891	U1790	G1627	A	U1499	A1430	A1291	A1095
G2399	G1960	G1892	G1791	A1628	G	U1500	A1440	U1292	C1096
U2400	A1965	U1893	A1796	U1629	U	G1501	U1446	G1309	U1097
C2401	U1966	G1894	A1800	A1630	G	U1502	U1447	A1448	A1098
G2410	U1967	C1895	U1806	G1631	U	U1503	U1448	A1310	G
A2411	U1978	U1896	A1807	A1635	G	U1504	A1449	A1312	U
C2412	U1982	G1897	U1907	U1636	U	G1505	A1450	G1314	G
U2413	U1989	U1898	A1908	A1637	G	C1506	U1451	A1171	U
U2417	C1990	U1899	U1907	G1638	U	C1507	U1452	A1172	G
G2418	G1991	U1900	A1908	U1639	G	A1507	G1453		
A2419	C1992	C1901	A1908	U1640	U	C1508	G1453		
U2425	A1993	G1902	A1908	G1641	G	G1509	G1453		
C2433	C1994	A1903	A1908	C1642	U	U1510	G1453		
A2434	U1997	U1907	A1908	C1643	G	G1511	G1453		
G2437	A1998	A1907	A1908	C1651	U	U1512	G1453		
	G1999	A1908	A1908	G1652	G	A1513	G1453		
				A1653	U	A1514	G1453		
				A1654	G	G1515	G1453		
				A1807	U	G1516	G1453		
					G	G1517	G1453		
					U	G1573	G1453		
					G	G1574	G1453		
					U	A1578	G1453		

- Molecule 2: 16S rRNA

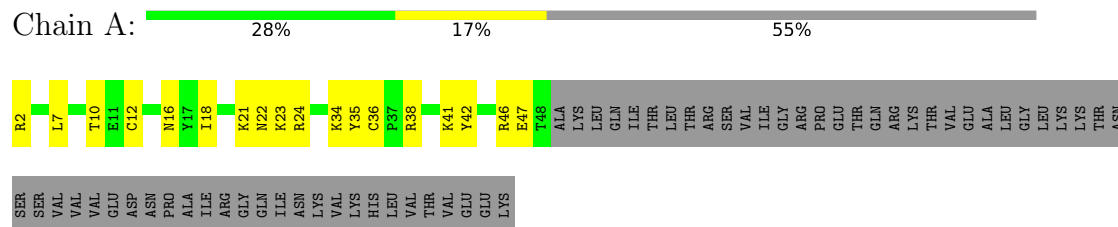




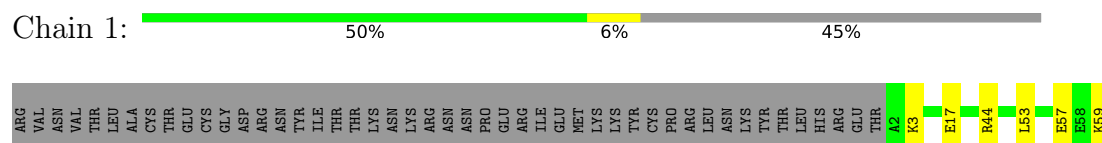
- Molecule 3: 5S rRNA



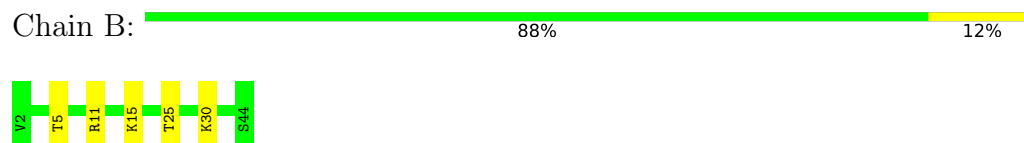
- Molecule 4: 50S ribosomal protein L33, 50S ribosomal protein L30



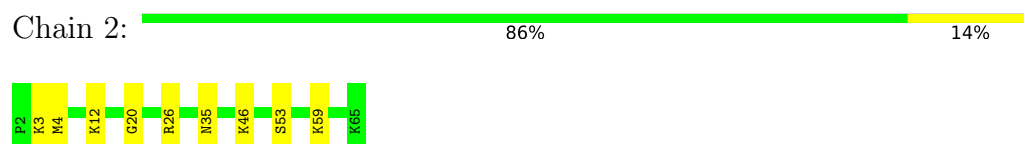
- Molecule 4: 50S ribosomal protein L33, 50S ribosomal protein L30



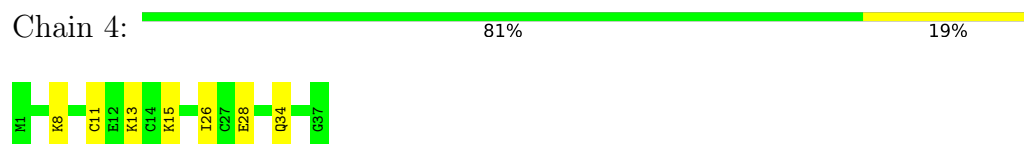
- Molecule 5: 50S ribosomal protein L34



- Molecule 6: 50S ribosomal protein L35

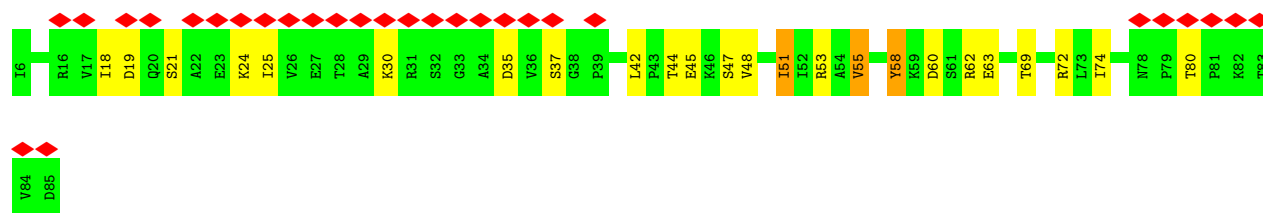


- Molecule 7: 50S ribosomal protein L36

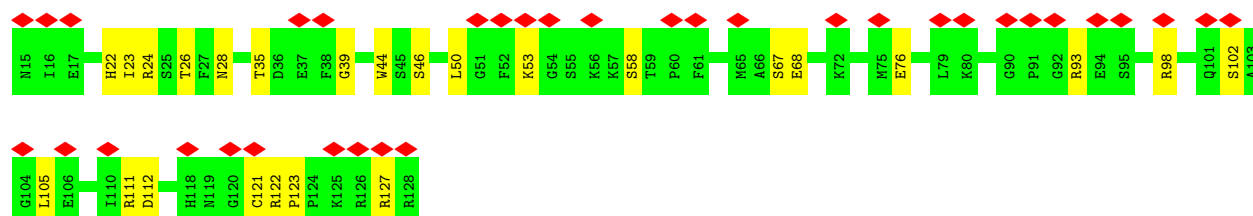
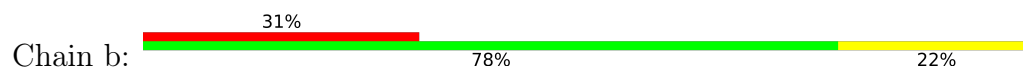


- Molecule 8: 30S ribosomal protein S10

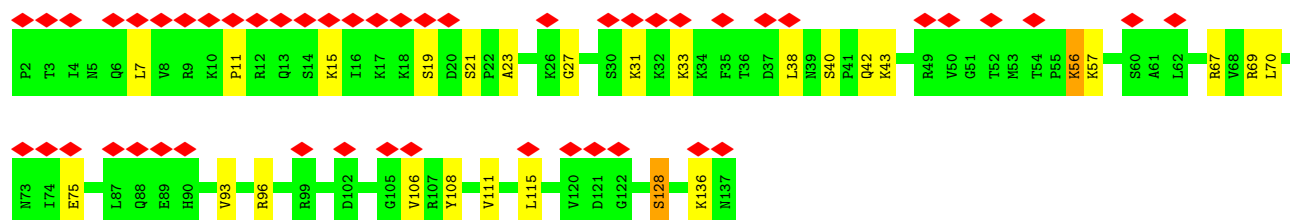
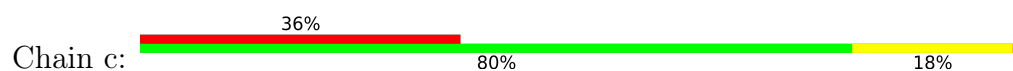




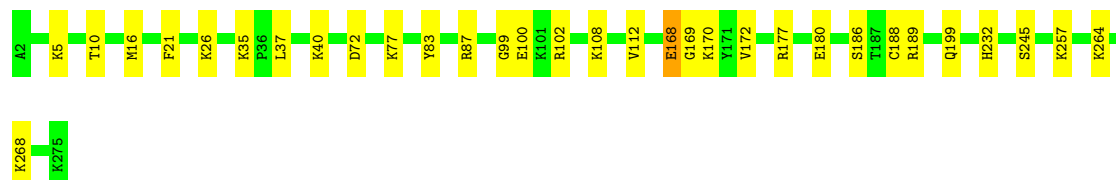
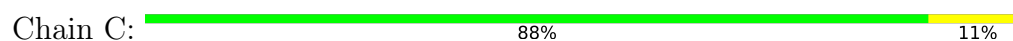
• Molecule 9: 30S ribosomal protein S11



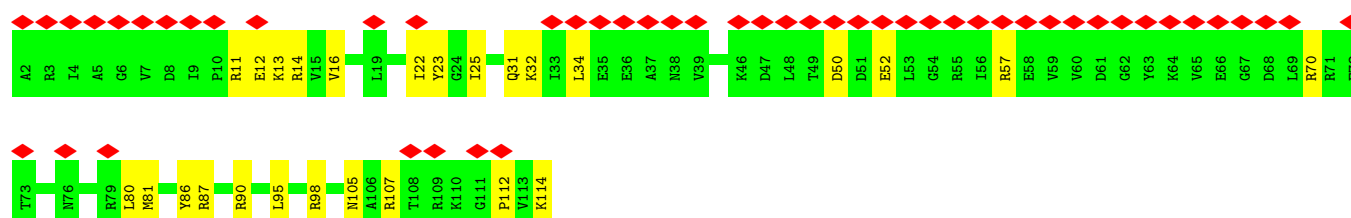
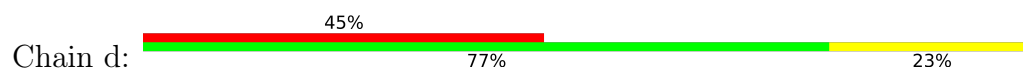
• Molecule 10: 30S ribosomal protein S12



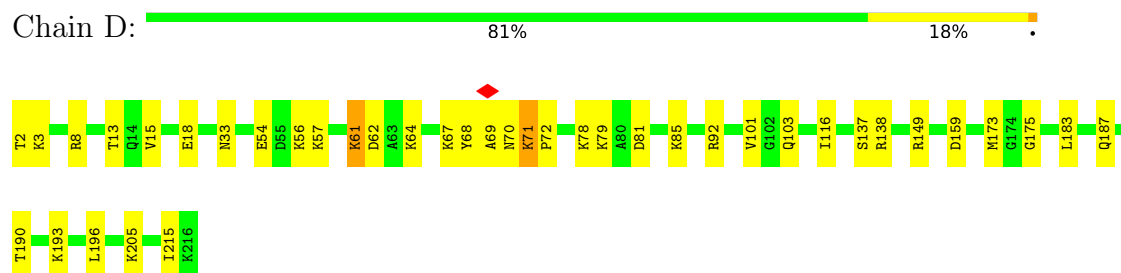
• Molecule 11: 50S ribosomal protein L2



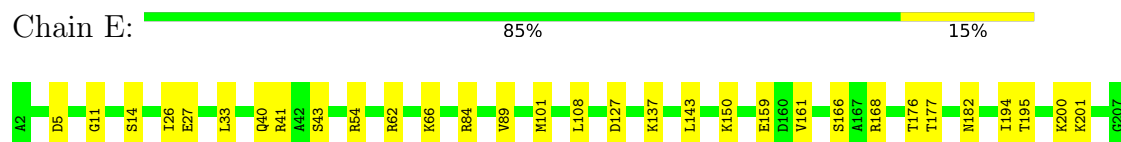
• Molecule 12: 30S ribosomal protein S13



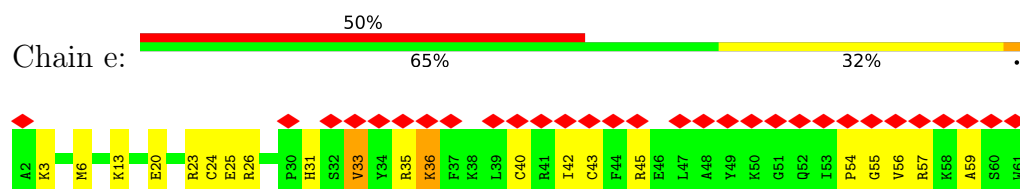
- Molecule 13: 50S ribosomal protein L3



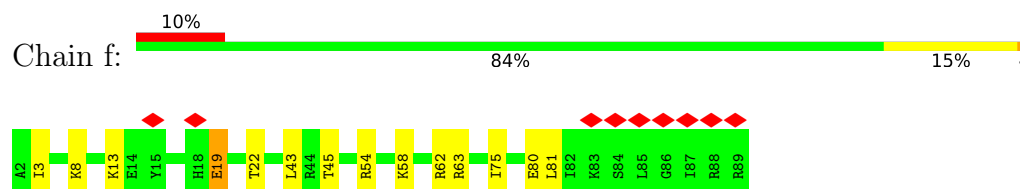
- Molecule 14: 50S ribosomal protein L4



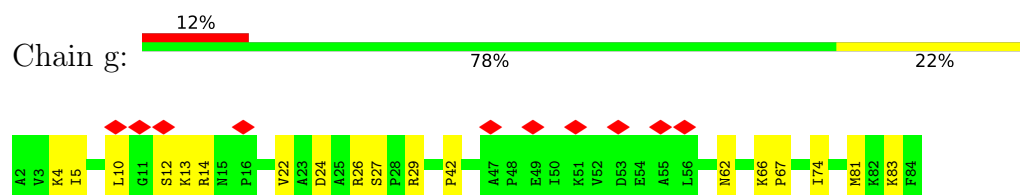
- Molecule 15: 30S ribosomal protein S14 type Z



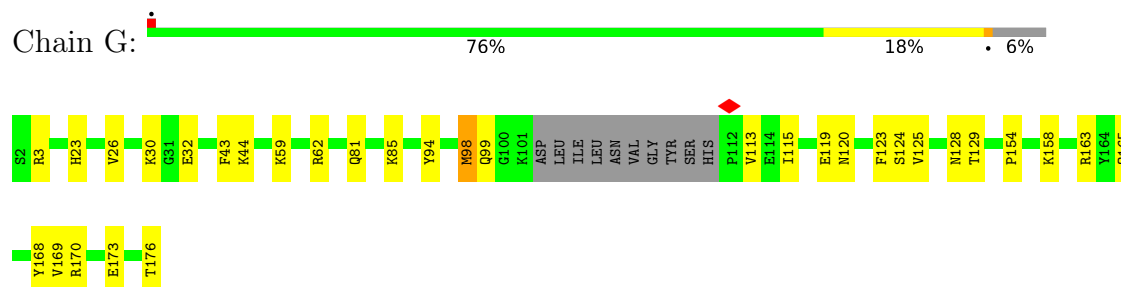
- Molecule 16: 30S ribosomal protein S15



- Molecule 17: 30S ribosomal protein S16

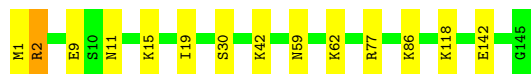


- Molecule 18: 50S ribosomal protein L6




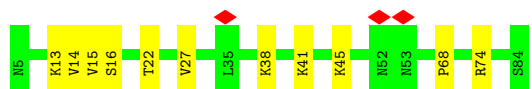
- Molecule 19: 50S ribosomal protein L13

Chain H:  90% 9%




- Molecule 20: 30S ribosomal protein S17

Chain h:  86% 14%



- Molecule 21: 50S ribosomal protein L14

Chain I:  86% 13%



- Molecule 22: 30S ribosomal protein S18

Chain i:  7% 64% 36%




- Molecule 23: 30S ribosomal protein S20

Chain j:  74% 23%




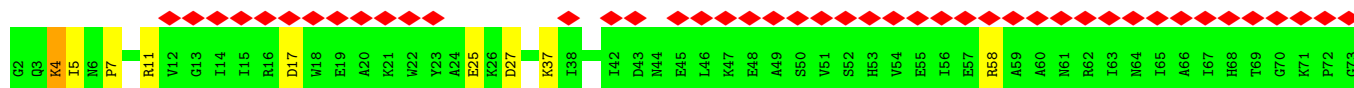
- Molecule 24: 50S ribosomal protein L15

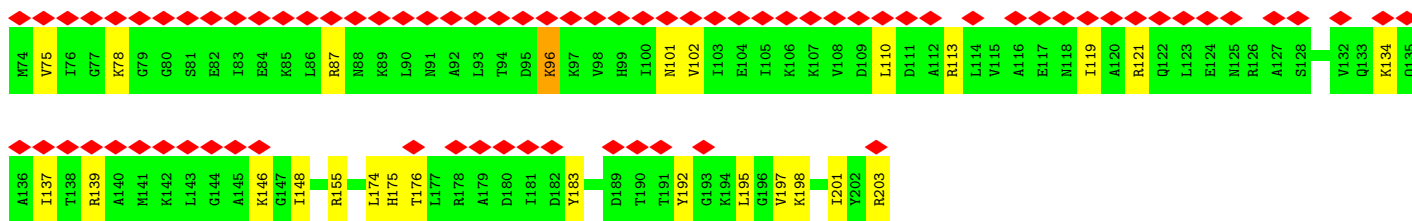
Chain J:  85% 14%



- Molecule 25: 30S ribosomal protein S3

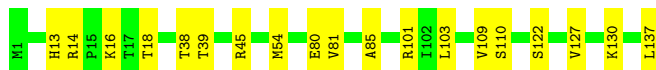
Chain k:  60% 83% 16%





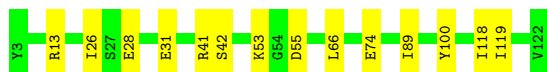
- Molecule 26: 50S ribosomal protein L16

Chain K: 86% 14%



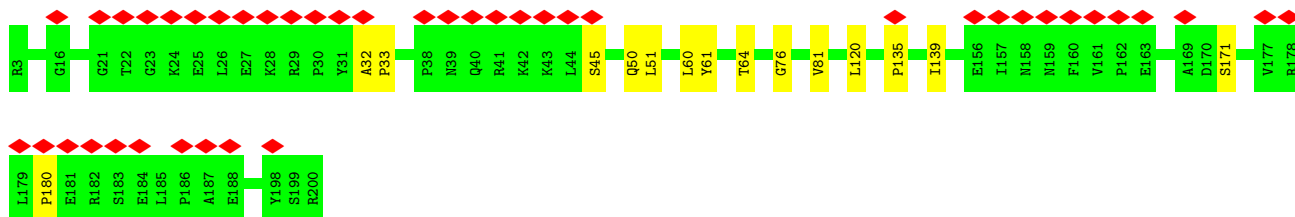
- Molecule 27: 50S ribosomal protein L17

Chain L: 88% 12%



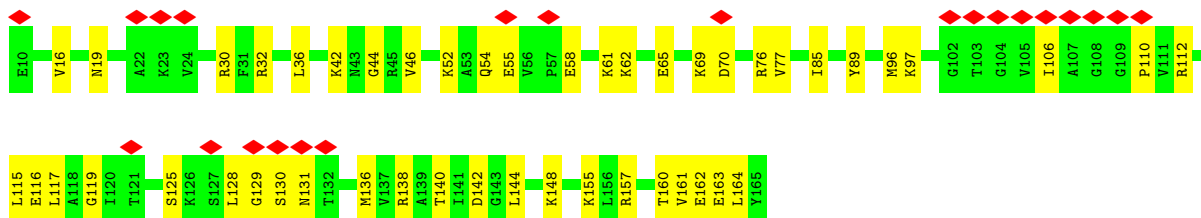
- Molecule 28: 30S ribosomal protein S4

Chain l: 22% 92% 8%



- Molecule 29: 30S ribosomal protein S5

Chain m: 14% 69% 31%

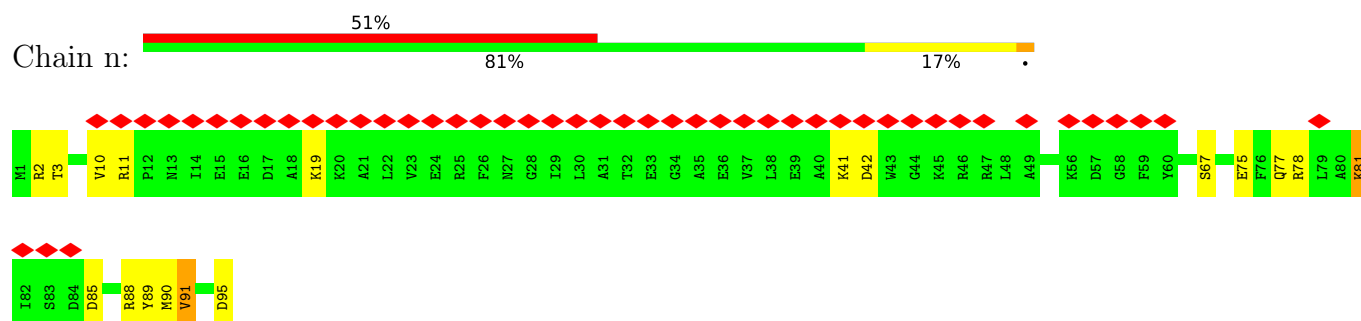


- Molecule 30: 50S ribosomal protein L18

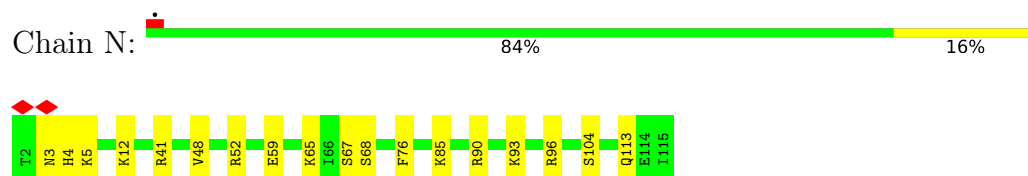
Chain M: 74% 25%



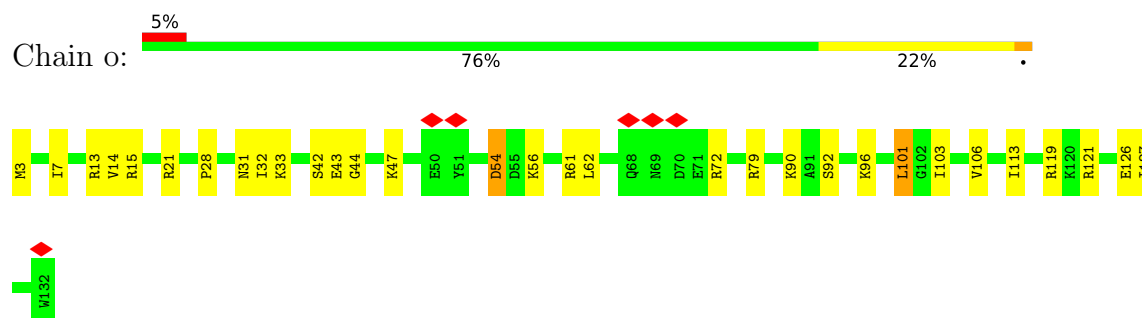
- Molecule 31: 30S ribosomal protein S6



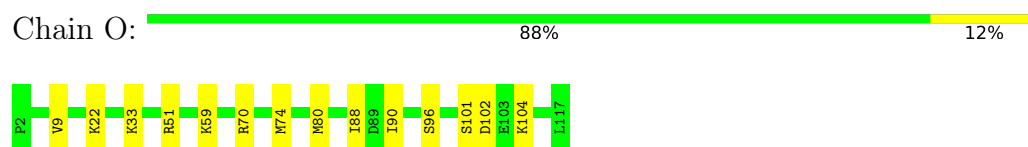
- Molecule 32: 50S ribosomal protein L19



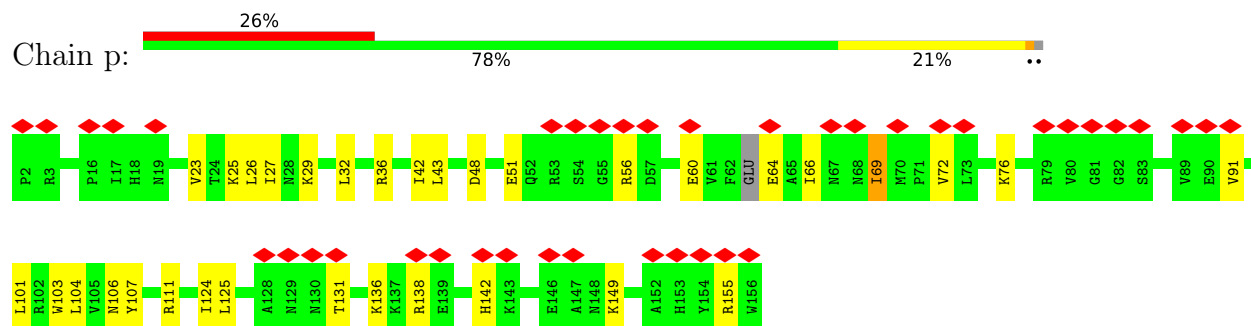
- Molecule 33: 30S ribosomal protein S8




- Molecule 34: 50S ribosomal protein L20

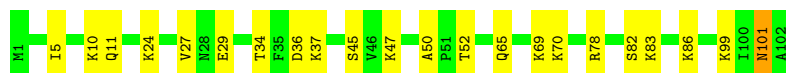


- Molecule 35: 30S ribosomal protein S7




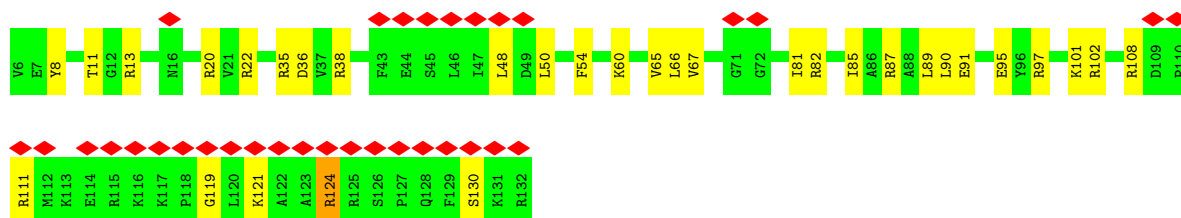
- Molecule 36: 50S ribosomal protein L21

Chain P:  78% 21% .




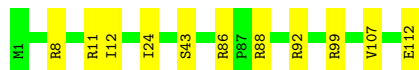
- Molecule 37: 30S ribosomal protein S9

Chain q:  26% 75% 24% .




- Molecule 38: 50S ribosomal protein L22

Chain Q:  90% 10% .




- Molecule 39: 50S ribosomal protein L23

Chain R:  81% 18% .




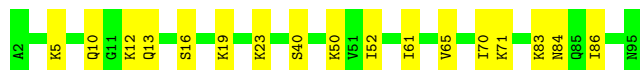
- Molecule 40: 50S ribosomal protein L24

Chain S:  83% 17% .




- Molecule 41: 50S ribosomal protein L25

Chain T:  82% 18% .



- Molecule 42: 50S ribosomal protein L27

Chain U:  82% 16% .



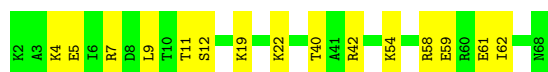
- Molecule 43: 50S ribosomal protein L28

Chain V: 82% 16% •



- Molecule 44: 50S ribosomal protein L29

Chain W: 78% 22%



- Molecule 45: 50S ribosomal protein L32p

Chain Z: 83% 17%



- Molecule 46: 50S ribosomal protein L5

Chain F: 92% 6% •



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	192105	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	47	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.076	Depositor
Minimum map value	-0.028	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0045	Depositor
Map size (\AA)	408.0, 408.0, 408.0	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.85, 0.85, 0.85	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	Y	0.21	0/65368	0.63	2/101922 (0.0%)
2	X	0.20	0/34716	0.64	6/54120 (0.0%)
3	3	0.21	0/2717	0.64	1/4232 (0.0%)
4	1	0.65	0/451	0.57	0/606
4	A	0.62	0/395	0.57	0/530
5	B	0.61	0/371	0.56	0/484
6	2	0.62	0/526	0.57	0/690
7	4	0.64	0/298	0.57	0/392
8	a	0.67	0/637	0.62	0/865
9	b	0.67	0/840	0.60	0/1137
10	c	0.68	0/991	0.60	0/1337
11	C	0.64	0/2129	0.60	0/2858
12	d	0.68	0/835	0.59	0/1123
13	D	0.65	0/1651	0.59	0/2215
14	E	0.64	0/1595	0.57	0/2154
15	e	0.63	0/507	0.58	0/674
16	f	0.65	0/721	0.56	0/964
17	g	0.71	0/541	0.62	0/733
18	G	0.69	0/1199	0.62	0/1621
19	H	0.64	0/1165	0.57	0/1570
20	h	0.72	0/527	0.60	0/721
21	I	0.65	0/925	0.58	0/1242
22	i	0.64	0/465	0.56	0/620
23	j	0.72	0/496	0.71	0/669
24	J	0.65	0/1100	0.59	0/1467
25	k	0.66	0/1573	0.59	0/2121
26	K	0.64	0/1095	0.58	0/1472
27	L	0.65	0/936	0.57	0/1253
28	l	0.78	0/1062	0.64	0/1465
29	m	0.67	0/1167	0.61	0/1576
30	M	0.66	0/891	0.59	0/1194
31	n	0.64	0/796	0.56	0/1069
32	N	0.64	0/901	0.56	0/1209
33	o	0.66	0/1019	0.59	0/1371

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
34	O	0.62	0/954	0.55	0/1264
35	p	0.67	0/1170	0.65	0/1580
36	P	0.64	0/800	0.57	0/1070
37	q	0.65	0/990	0.60	0/1332
38	Q	0.64	0/862	0.57	0/1161
39	R	0.64	0/723	0.56	0/966
40	S	0.66	0/779	0.59	0/1043
41	T	0.67	0/730	0.59	0/981
42	U	0.65	0/603	0.58	0/802
43	V	0.65	0/384	0.58	0/515
44	W	0.65	0/542	0.55	0/722
45	Z	0.65	0/361	0.59	0/482
46	F	0.84	0/763	0.83	0/1059
All	All	0.39	0/140267	0.62	9/210653 (0.0%)

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Y	2591	A	C2'-C3'-O3'	7.59	126.20	109.50
3	3	26	C	C2'-C3'-O3'	7.59	126.20	109.50
2	X	1431	U	C2'-C3'-O3'	7.43	125.85	109.50
2	X	514	G	C2'-C3'-O3'	6.51	124.11	113.70
2	X	277	U	C2'-C3'-O3'	6.34	123.84	113.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	
4	1	56/105 (53%)	51 (91%)	5 (9%)	0	100	100
4	A	45/105 (43%)	41 (91%)	3 (7%)	1 (2%)	6	21
5	B	41/43 (95%)	38 (93%)	3 (7%)	0	100	100
6	2	62/64 (97%)	48 (77%)	13 (21%)	1 (2%)	9	28
7	4	35/37 (95%)	32 (91%)	2 (6%)	1 (3%)	4	15
8	a	78/80 (98%)	51 (65%)	22 (28%)	5 (6%)	1	3
9	b	112/114 (98%)	85 (76%)	22 (20%)	5 (4%)	2	7
10	c	134/136 (98%)	101 (75%)	26 (19%)	7 (5%)	2	5
11	C	272/274 (99%)	230 (85%)	38 (14%)	4 (2%)	10	30
12	d	111/113 (98%)	88 (79%)	20 (18%)	3 (3%)	5	16
13	D	213/215 (99%)	179 (84%)	27 (13%)	7 (3%)	4	13
14	E	204/206 (99%)	181 (89%)	21 (10%)	2 (1%)	15	40
15	e	58/60 (97%)	44 (76%)	9 (16%)	5 (9%)	1	1
16	f	86/88 (98%)	73 (85%)	12 (14%)	1 (1%)	13	35
17	g	81/83 (98%)	54 (67%)	22 (27%)	5 (6%)	1	3
18	G	161/175 (92%)	126 (78%)	31 (19%)	4 (2%)	5	18
19	H	143/145 (99%)	125 (87%)	15 (10%)	3 (2%)	7	22
20	h	78/80 (98%)	60 (77%)	17 (22%)	1 (1%)	12	33
21	I	120/122 (98%)	105 (88%)	14 (12%)	1 (1%)	19	46
22	i	54/56 (96%)	42 (78%)	10 (18%)	2 (4%)	3	11
23	j	73/78 (94%)	56 (77%)	15 (20%)	2 (3%)	5	16
24	J	144/146 (99%)	123 (85%)	18 (12%)	3 (2%)	7	22
25	k	200/202 (99%)	159 (80%)	35 (18%)	6 (3%)	4	14
26	K	135/137 (98%)	119 (88%)	13 (10%)	3 (2%)	6	21
27	L	118/120 (98%)	108 (92%)	9 (8%)	1 (1%)	19	46
28	l	196/198 (99%)	154 (79%)	33 (17%)	9 (5%)	2	7
29	m	154/156 (99%)	116 (75%)	32 (21%)	6 (4%)	3	10
30	M	117/119 (98%)	98 (84%)	15 (13%)	4 (3%)	3	12
31	n	93/95 (98%)	72 (77%)	19 (20%)	2 (2%)	6	21
32	N	112/114 (98%)	100 (89%)	10 (9%)	2 (2%)	8	25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	o	128/130 (98%)	88 (69%)	35 (27%)	5 (4%)	3	10
34	O	114/116 (98%)	108 (95%)	3 (3%)	3 (3%)	5	17
35	p	150/155 (97%)	127 (85%)	20 (13%)	3 (2%)	7	23
36	P	100/102 (98%)	84 (84%)	14 (14%)	2 (2%)	7	23
37	q	125/127 (98%)	98 (78%)	23 (18%)	4 (3%)	4	13
38	Q	110/112 (98%)	96 (87%)	13 (12%)	1 (1%)	17	43
39	R	87/89 (98%)	77 (88%)	8 (9%)	2 (2%)	6	20
40	S	101/103 (98%)	83 (82%)	14 (14%)	4 (4%)	3	9
41	T	92/94 (98%)	82 (89%)	8 (9%)	2 (2%)	6	21
42	U	77/79 (98%)	69 (90%)	6 (8%)	2 (3%)	5	17
43	V	47/49 (96%)	39 (83%)	6 (13%)	2 (4%)	2	8
44	W	65/67 (97%)	58 (89%)	6 (9%)	1 (2%)	10	30
45	Z	45/47 (96%)	38 (84%)	5 (11%)	2 (4%)	2	8
46	F	151/158 (96%)	110 (73%)	32 (21%)	9 (6%)	1	4
All	All	4878/5094 (96%)	4016 (82%)	724 (15%)	138 (3%)	8	16

5 of 138 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	a	63	GLU
10	c	57	LYS
12	d	95	LEU
13	D	71	LYS
17	g	66	LYS

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	
4	1	52/97 (54%)	46 (88%)	6 (12%)	5	15
4	A	44/97 (45%)	27 (61%)	17 (39%)	0	0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	B	39/39 (100%)	34 (87%)	5 (13%)	4	11
6	2	55/55 (100%)	47 (86%)	8 (14%)	3	8
7	4	35/35 (100%)	29 (83%)	6 (17%)	2	5
8	a	67/73 (92%)	45 (67%)	22 (33%)	0	0
9	b	85/90 (94%)	65 (76%)	20 (24%)	1	1
10	c	95/118 (80%)	73 (77%)	22 (23%)	1	1
11	C	221/221 (100%)	192 (87%)	29 (13%)	4	10
12	d	75/97 (77%)	52 (69%)	23 (31%)	0	0
13	D	173/173 (100%)	138 (80%)	35 (20%)	1	3
14	E	168/168 (100%)	139 (83%)	29 (17%)	2	5
15	e	51/52 (98%)	33 (65%)	18 (35%)	0	0
16	f	74/80 (92%)	60 (81%)	14 (19%)	1	3
17	g	36/70 (51%)	23 (64%)	13 (36%)	0	0
18	G	115/153 (75%)	86 (75%)	29 (25%)	0	1
19	H	122/123 (99%)	110 (90%)	12 (10%)	8	21
20	h	35/75 (47%)	25 (71%)	10 (29%)	0	1
21	I	100/100 (100%)	83 (83%)	17 (17%)	2	5
22	i	49/50 (98%)	31 (63%)	18 (37%)	0	0
23	j	37/65 (57%)	19 (51%)	18 (49%)	0	0
24	J	109/112 (97%)	89 (82%)	20 (18%)	1	4
25	k	151/164 (92%)	120 (80%)	31 (20%)	1	2
26	K	108/114 (95%)	92 (85%)	16 (15%)	3	8
27	L	96/101 (95%)	83 (86%)	13 (14%)	4	9
28	l	23/174 (13%)	17 (74%)	6 (26%)	0	1
29	m	120/122 (98%)	78 (65%)	42 (35%)	0	0
30	M	83/95 (87%)	55 (66%)	28 (34%)	0	0
31	n	82/83 (99%)	64 (78%)	18 (22%)	1	2
32	N	93/100 (93%)	77 (83%)	16 (17%)	2	5
33	o	107/111 (96%)	79 (74%)	28 (26%)	0	1
34	O	96/96 (100%)	85 (88%)	11 (12%)	5	15
35	p	114/131 (87%)	83 (73%)	31 (27%)	0	1

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	P	84/86 (98%)	63 (75%)	21 (25%)	0	1
37	q	96/105 (91%)	67 (70%)	29 (30%)	0	0
38	Q	89/91 (98%)	79 (89%)	10 (11%)	6	16
39	R	78/80 (98%)	62 (80%)	16 (20%)	1	2
40	S	81/88 (92%)	67 (83%)	14 (17%)	2	5
41	T	78/82 (95%)	63 (81%)	15 (19%)	1	3
42	U	59/62 (95%)	46 (78%)	13 (22%)	1	2
43	V	39/41 (95%)	31 (80%)	8 (20%)	1	2
44	W	58/60 (97%)	44 (76%)	14 (24%)	0	1
45	Z	35/43 (81%)	29 (83%)	6 (17%)	2	5
All	All	3607/4172 (86%)	2830 (78%)	777 (22%)	3	2

5 of 777 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	m	62	LYS
33	o	92	SER
29	m	117	LEU
29	m	61	LYS
30	M	119	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
32	N	14	GLN
41	T	13	GLN
32	N	31	HIS
34	O	91	ASN
41	T	84	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	Y	2709/2923 (92%)	1004 (37%)	48 (1%)
2	X	1436/1552 (92%)	1029 (71%)	56 (3%)
3	3	113/114 (99%)	47 (41%)	2 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	4258/4589 (92%)	2080 (48%)	106 (2%)

5 of 2080 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	Y	10	A
1	Y	11	U
1	Y	12	U
1	Y	14	A
1	Y	34	U

5 of 106 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	X	334	G
2	X	730	G
2	X	1431	U
2	X	384	G
2	X	589	G

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides 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.

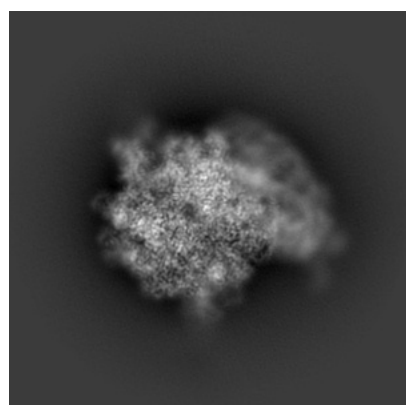
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11903. These allow visual inspection of the internal detail of the map and identification of artifacts.

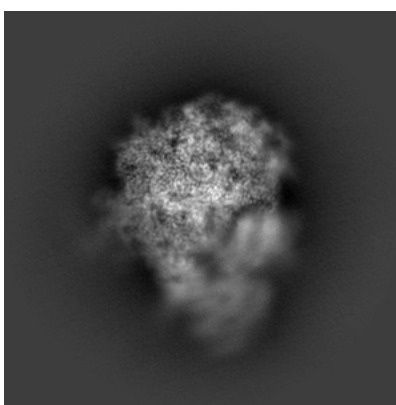
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

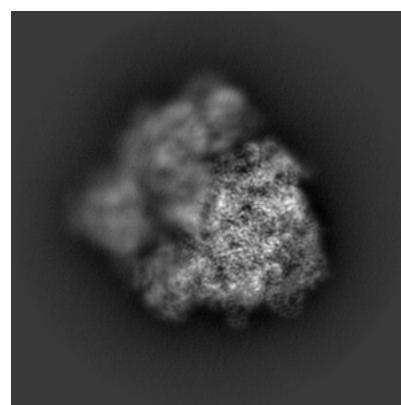
6.1.1 Primary map



X



Y

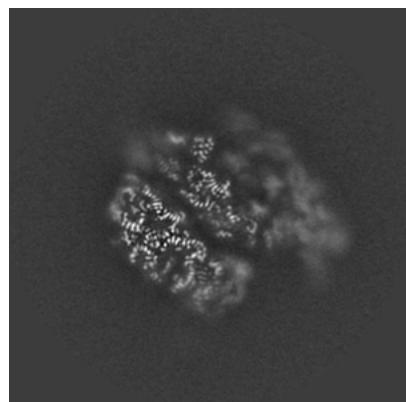


Z

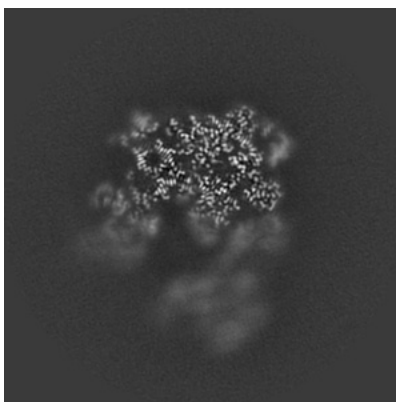
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

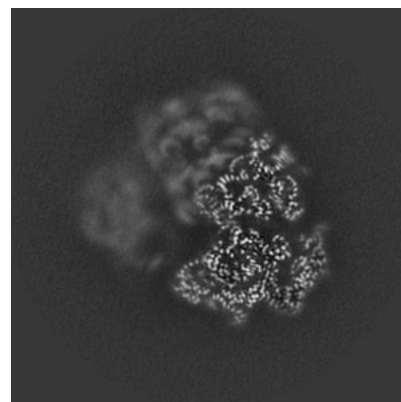
6.2.1 Primary map



X Index: 240



Y Index: 240

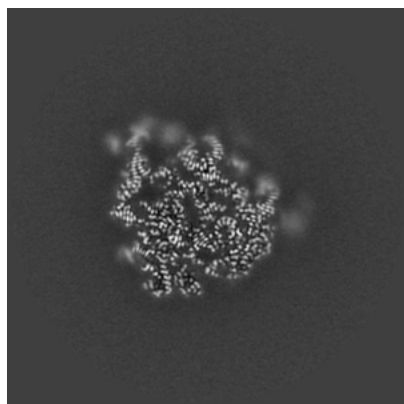


Z Index: 240

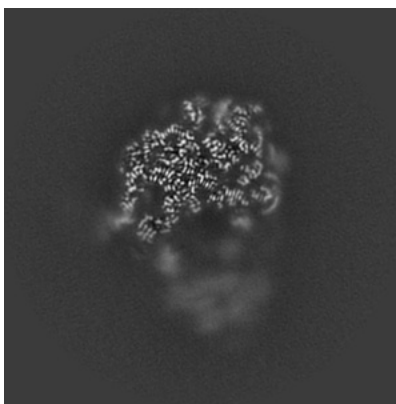
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

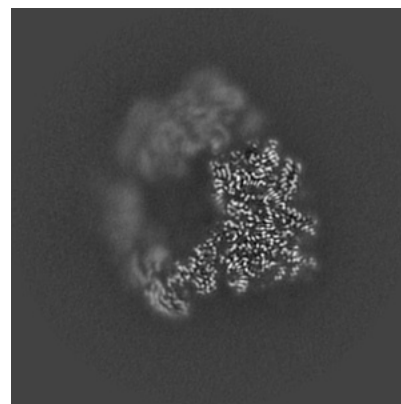
6.3.1 Primary map



X Index: 294



Y Index: 206



Z Index: 213

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

6.4 Orthogonal surface views [i](#)

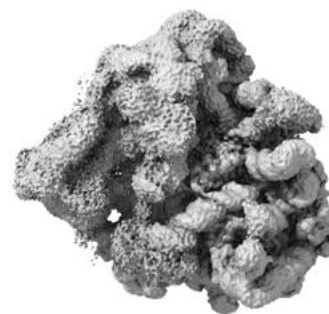
6.4.1 Primary map



X



Y



Z

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.

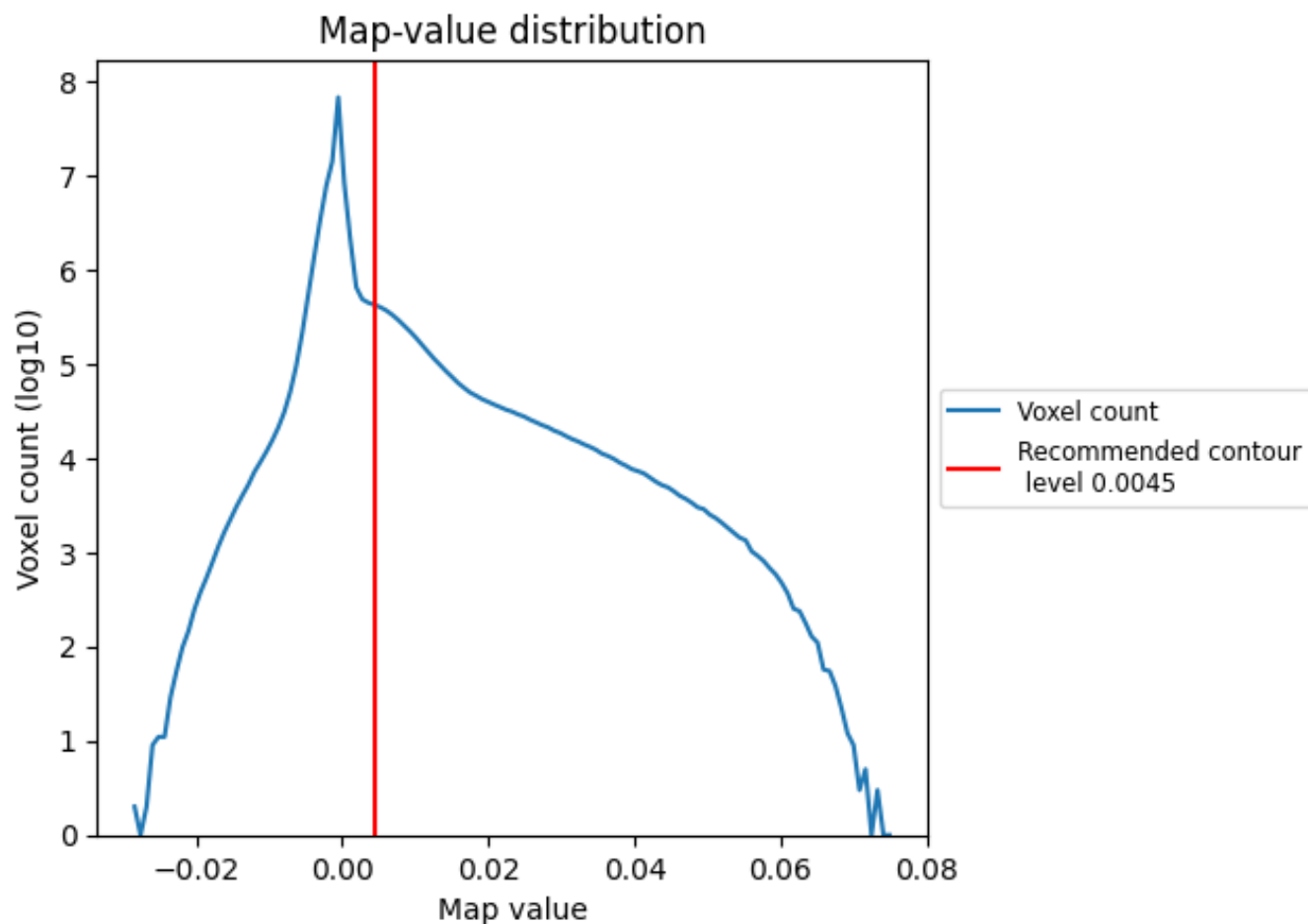
6.5 Mask visualisation

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

7 Map analysis [i](#)

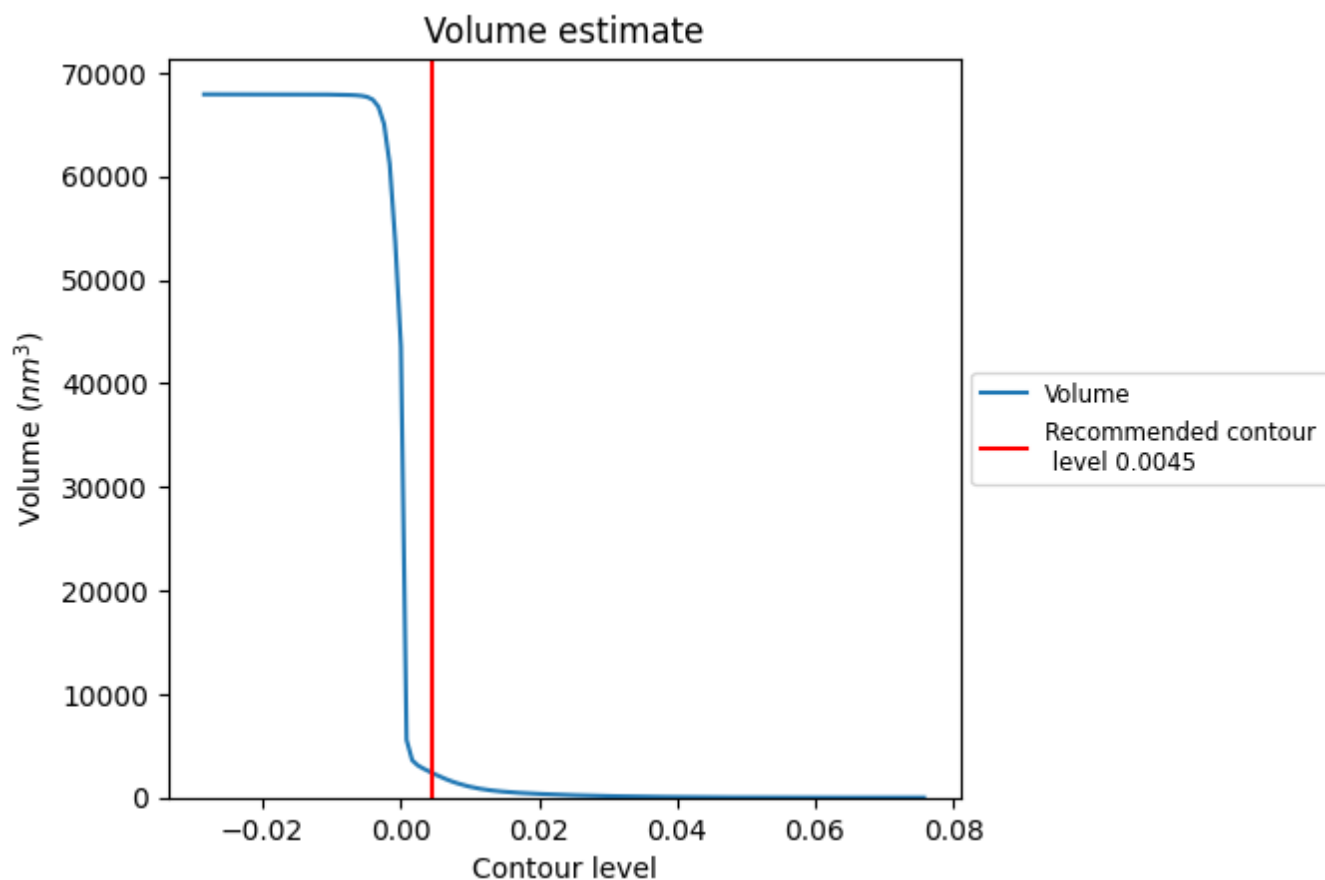
This section contains the results of statistical analysis of the map.

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.

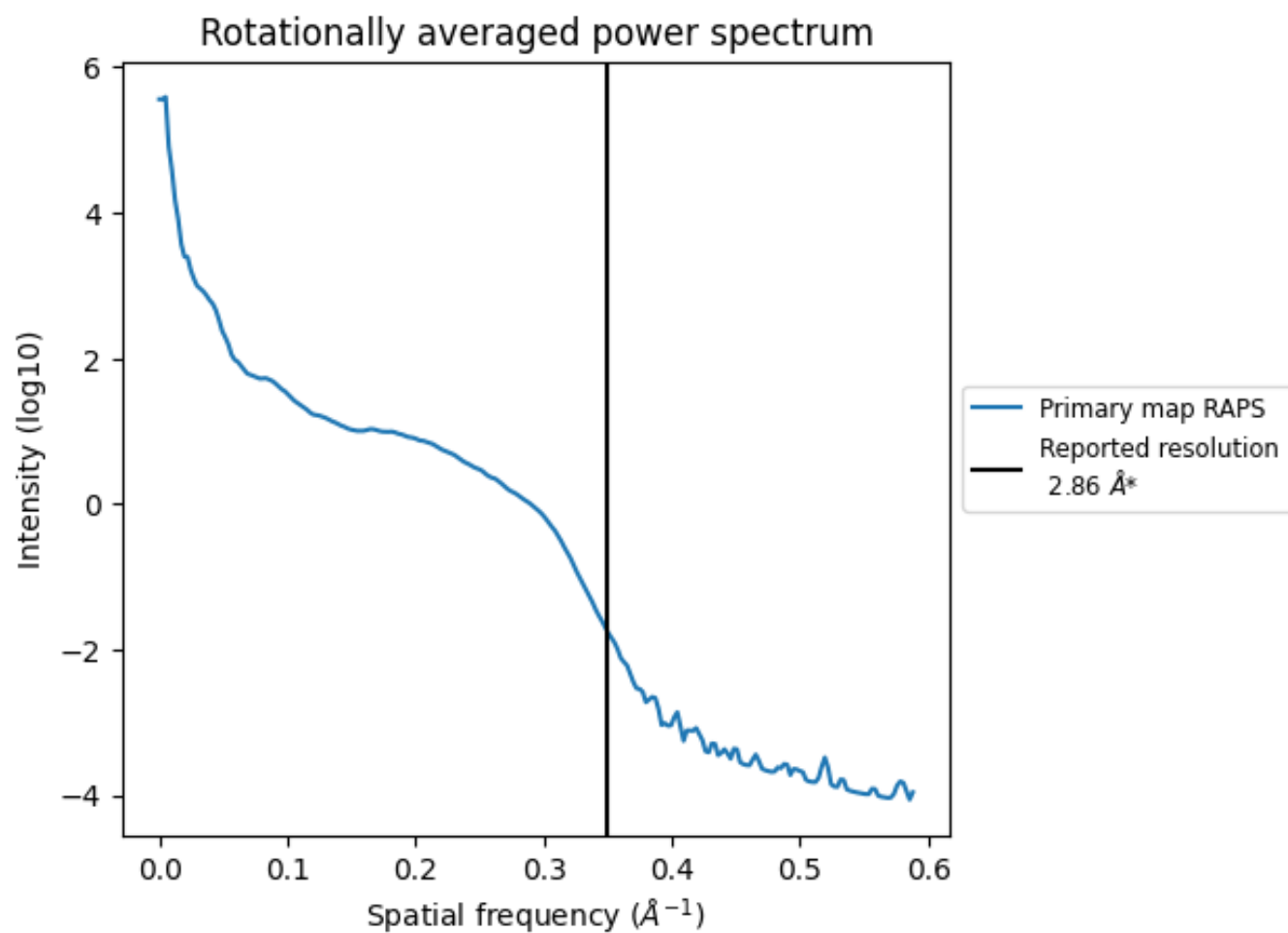
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2394 nm^3 ; this corresponds to an approximate mass of 2163 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 0.350 Å⁻¹

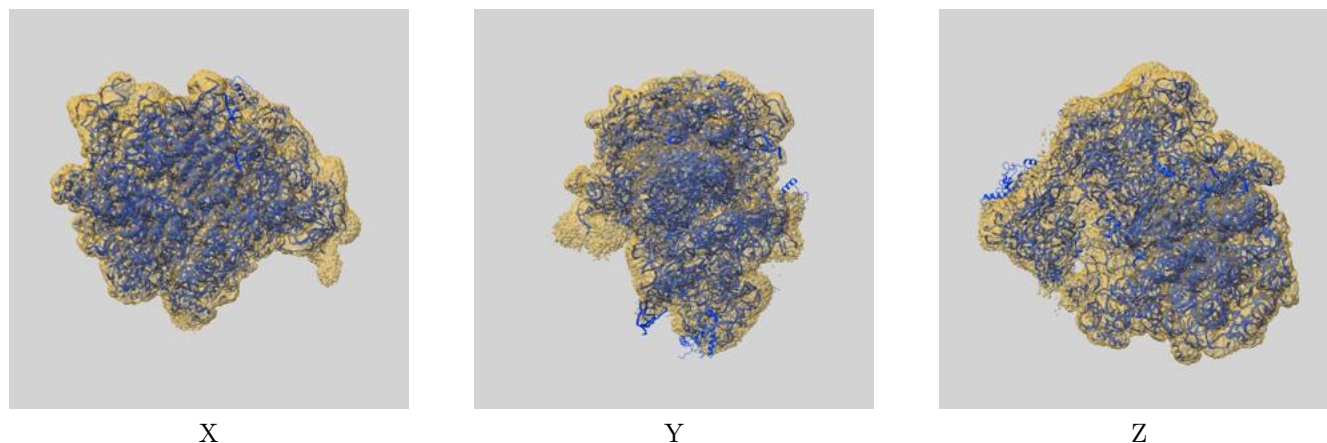
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11903 and PDB model 7ASP. Per-residue inclusion information can be found in section [3](#) on page [12](#).

9.1 Map-model overlay [i](#)



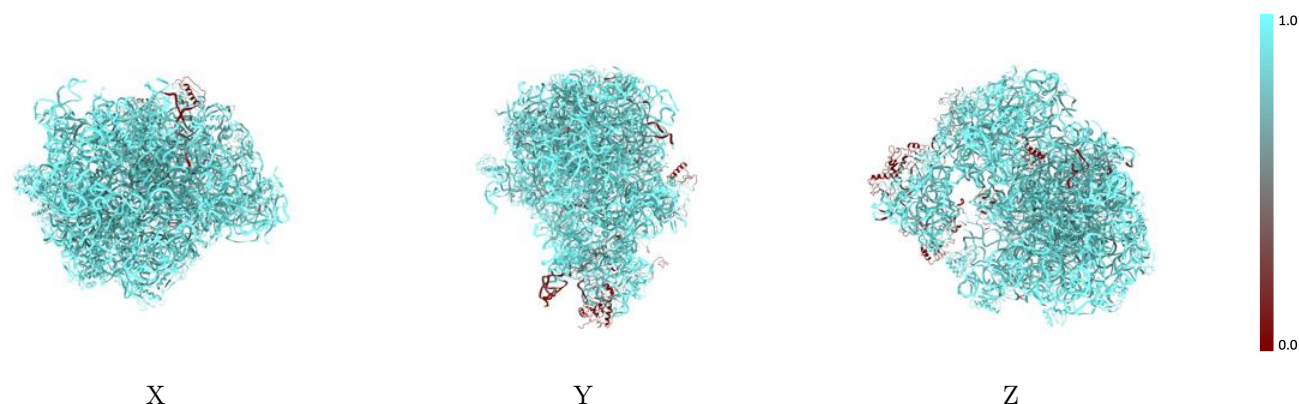
The images above show the 3D surface view of the map at the recommended contour level 0.0045 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



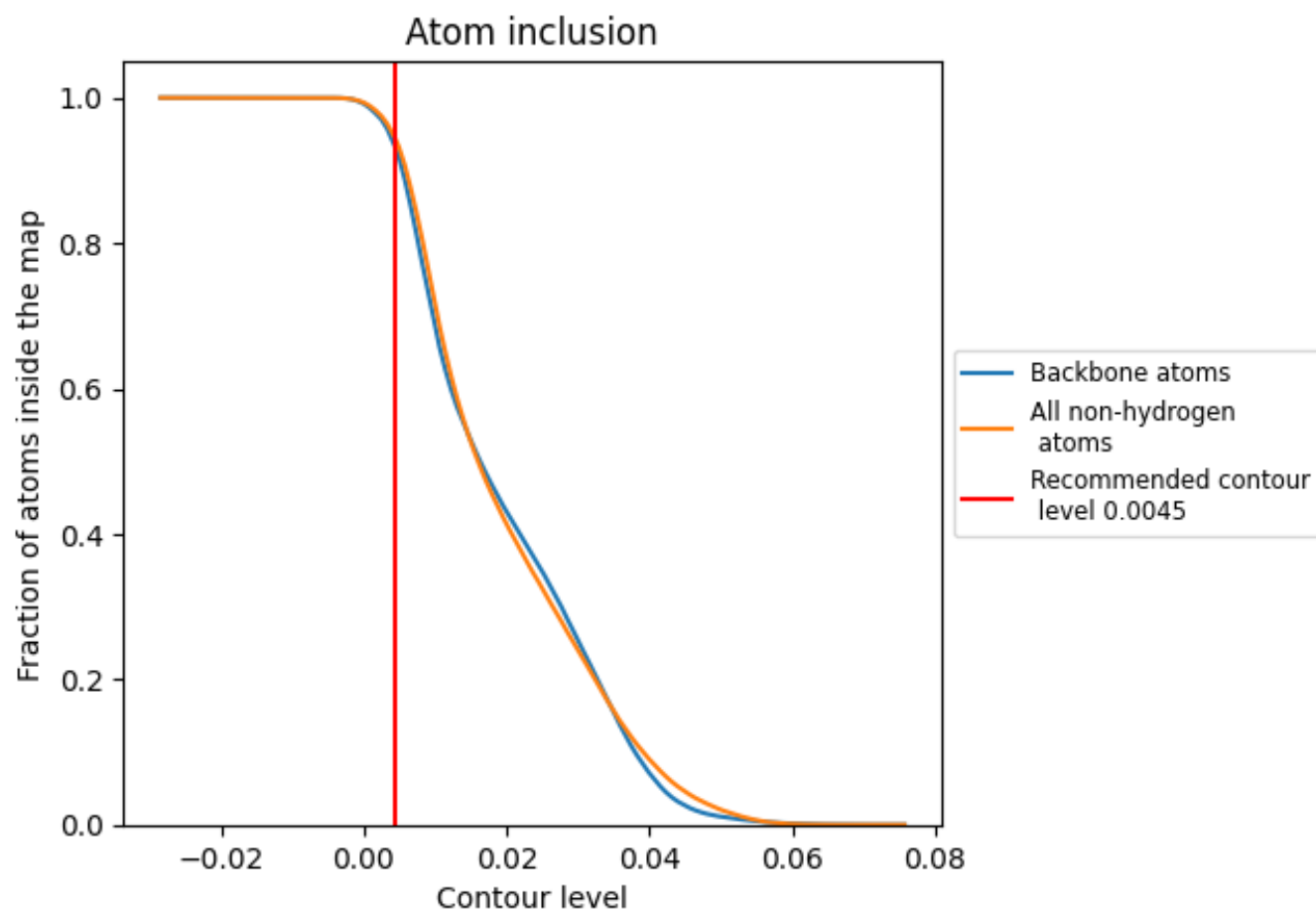
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 93% of all backbone atoms, 94% 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	 0.9422	 0.3760
1	 0.9819	 0.5540
2	 0.9761	 0.5590
3	 0.9975	 0.4340
4	 0.9343	 0.5020
A	 0.8800	 0.4910
B	 0.9827	 0.5810
C	 0.9666	 0.5420
D	 0.9769	 0.5480
E	 0.9812	 0.5310
F	 0.9908	 0.3300
G	 0.9663	 0.2980
H	 0.9812	 0.5560
I	 0.9743	 0.5610
J	 0.9878	 0.5380
K	 0.9798	 0.5410
L	 0.9811	 0.5530
M	 0.9919	 0.4440
N	 0.9616	 0.5490
O	 0.9857	 0.5680
P	 0.9884	 0.5600
Q	 0.9712	 0.5490
R	 0.9828	 0.5250
S	 0.9803	 0.4750
T	 0.9450	 0.4880
U	 0.9671	 0.5580
V	 0.9781	 0.5240
W	 0.9886	 0.4400
X	 0.9558	 0.1800
Y	 0.9806	 0.4900
Z	 0.9854	 0.5060
a	 0.6289	 0.0890
b	 0.6156	 0.0970
c	 0.5692	 0.1800
d	 0.5126	 0.0780



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Chain	Atom inclusion	Q-score
e	 0.4832	 0.0600
f	 0.9009	 0.1860
g	 0.8346	 0.0730
h	 0.9061	 0.1110
i	 0.8730	 0.1350
j	 0.9776	 0.1810
k	 0.4019	 0.0840
l	 0.7633	 0.0860
m	 0.7945	 0.0820
n	 0.4665	 0.0870
o	 0.8882	 0.1140
p	 0.7240	 0.0840
q	 0.7205	 0.1070