



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 05:33 PM UTC

PDB ID : 7QGU / pdb_00007qgu
EMDB ID : EMD-13959
Title : Structure of the B. subtilis disome - stalled 70S ribosome
Authors : Kratzat, H.; Buschauer, R.; Berninghausen, O.; Beckmann, R.
Deposited on : 2021-12-10
Resolution : 4.75 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
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

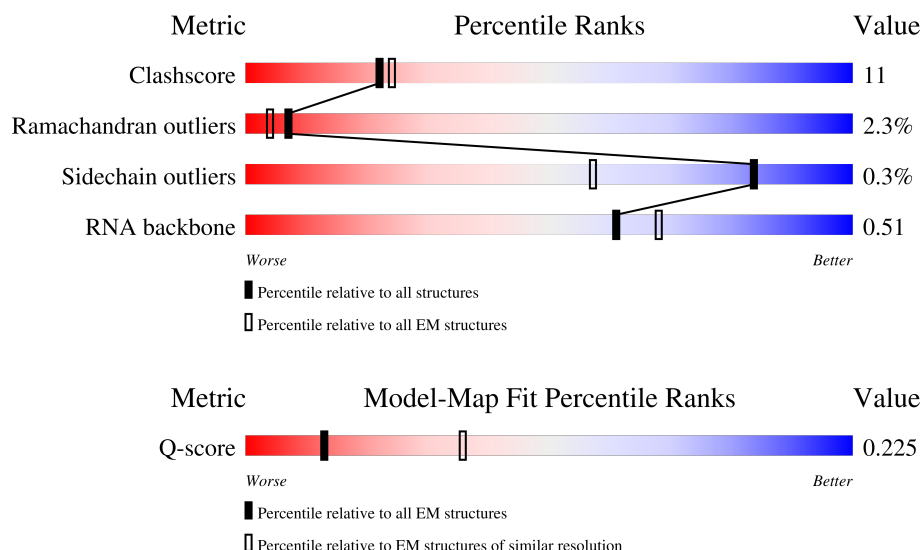
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.75 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	1613 (4.25 - 5.25)

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

Mol	Chain	Length	Quality of chain
1	A	2928	
2	B	119	
3	C	277	

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Mol	Chain	Length	Quality of chain
4	D	208	
5	E	207	
6	F	179	
7	G	179	
8	H	166	
9	I	141	
10	J	145	
11	K	122	
12	L	146	
13	M	144	
14	N	120	
15	O	120	
16	P	115	
17	Q	119	
18	R	102	
19	S	113	
20	T	95	
21	U	103	
22	V	94	
23	X	149	
24	Y	62	
25	Z	66	
26	a	59	
27	b	59	
28	c	49	

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Mol	Chain	Length	Quality of chain
29	d	44	
30	e	66	
31	f	37	
32	W	1555	
33	g	246	
34	h	218	
35	i	200	
36	j	166	
37	k	95	
38	l	156	
39	m	132	
40	n	130	
41	o	102	
42	p	131	
43	q	138	
44	r	121	
45	s	61	
46	t	89	
47	u	90	
48	v	87	
49	w	79	
50	x	92	
51	y	88	
52	z	77	
53	2	95	

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Mol	Chain	Length	Quality of chain
54	3	66	9% 50% 17% • 32%

2 Entry composition [i](#)

There are 54 unique types of molecules in this entry. The entry contains 135606 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	A	2923	Total	C	N	O	P	0	0
			62767	28002	11589	20253	2923		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1558	C	G	conflict	GB 1864548803

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	112	Total	C	N	O	P	0	0
			2395	1068	435	780	112		

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	275	Total	C	N	O	S	0	0
			2111	1312	416	377	6		

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	207	Total	C	N	O	S	0	0
			1575	988	290	292	5		

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	205	Total	C	N	O	S	0	0
			1561	980	289	290	2		

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	178	Total	C	N	O	S	0	0
			1404	893	245	259	7		

- Molecule 7 is a protein called Ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	175	Total	C	N	O	S	0	0
			1342	835	248	257	2		

- Molecule 8 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	123	Total	C	N	O	S	0	0
			955	602	163	189	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	154	THR	ALA	variant	UNP A0A063X7V1

- Molecule 9 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	133	Total	C	N	O	S	0	0
			981	617	173	185	6		

- Molecule 10 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	142	Total	C	N	O	S	0	0
			1123	710	206	202	5		

- Molecule 11 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	122	Total	C	N	O	S	0	0
			920	571	173	172	4		

- Molecule 12 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	146	Total	C	N	O	S	0	0
			1081	671	207	201	2		

- Molecule 13 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	138	Total	C	N	O	S	0	0
			1097	703	208	181	5		

- Molecule 14 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	119	Total	C	N	O	S	0	0
			953	583	186	180	4		

- Molecule 15 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	120	Total	C	N	O	S	0	0
			912	564	176	171	1		

- Molecule 16 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	P	114	Total	C	N	O	0	0
			936	595	184	157		

- Molecule 17 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	117	Total	C	N	O	S	0	0
			940	591	189	156	4		

- Molecule 18 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	R	101	Total	C	N	O	0	0
			786	501	139	146		

- Molecule 19 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	109	Total	C	N	O	S	0	0
			842	525	164	150	3		

- Molecule 20 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	93	Total	C	N	O	S	0	0
			752	472	137	139	4		

- Molecule 21 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	100	Total	C	N	O	S	0	0
			754	473	141	137	3		

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	82	Total	C	N	O		0	0
			630	390	123	117			

- Molecule 23 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	149	Total	C	N	O		0	0
			733	435	149	149			

- Molecule 24 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	58	Total	C	N	O	S	0	0
			444	275	92	75	2		

- Molecule 25 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	65	Total	C	N	O	S	0	0
			530	328	102	98	2		

- Molecule 26 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	a	58	Total	C	N	O	S	0	0
			455	281	89	84	1		

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	54	Total	C	N	O	S	0	0
			426	262	86	71	7		

- Molecule 28 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	c	48	Total	C	N	O	S	0	0
			401	244	80	73	4		

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	44	Total	C	N	O	S	0	0
			367	222	89	54	2		

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	64	Total	C	N	O	S	0	0
			512	321	107	82	2		

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	36	Total	C	N	O	S	0	0
			288	181	59	44	4		

- Molecule 32 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	W	1544	Total	C	N	O	P	0	0
			33115	14768	6067	10736	1544		

- Molecule 33 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	g	224	Total	C	N	O	0	0
			896	448	224	224		

- Molecule 34 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	h	210	Total	C	N	O	0	0
			840	420	210	210		

- Molecule 35 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	i	199	Total	C	N	O	0	0
			797	398	199	200		

- Molecule 36 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	j	165	Total	C	N	O	0	0
			661	330	165	166		

- Molecule 37 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	k	95	Total	C	N	O	0	0
			381	190	95	96		

- Molecule 38 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	l	153	Total	C	N	O	0	0
			613	306	153	154		

- Molecule 39 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	m	131	Total	C	N	O	0	0
			525	262	131	132		

- Molecule 40 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	n	130	Total	C	N	O	0	0
			521	260	130	131		

- Molecule 41 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	o	102	Total	C	N	O	0	0
			409	204	102	103		

- Molecule 42 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	p	118	Total	C	N	O	0	0
			472	236	118	118		

- Molecule 43 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	q	137	Total	C	N	O	0	0
			549	274	137	138		

- Molecule 44 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	r	119	Total	C	N	O	0	0
			476	238	119	119		

- Molecule 45 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	s	60	Total	C	N	O	0	0
			241	120	60	61		

- Molecule 46 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	t	88	Total	C	N	O	0	0
			353	176	88	89		

- Molecule 47 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	u	89	Total	C	N	O	0	0
			357	178	89	90		

- Molecule 48 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	v	86	Total	C	N	O	0	0
			345	172	86	87		

- Molecule 49 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	w	71	Total	C	N	O	0	0
			285	142	71	72		

- Molecule 50 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	x	84	Total	C	N	O	0	0
			336	168	84	84		

- Molecule 51 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	y	86	Total	C	N	O	0	0
			345	172	86	87		

- Molecule 52 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	z	77	Total	C	N	O	P	0	0
			1643	731	290	545	77		

- Molecule 53 is a protein called YqzJ.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	2	24	Total	C	N	O	S	0	0
			107	64	28	14	1		

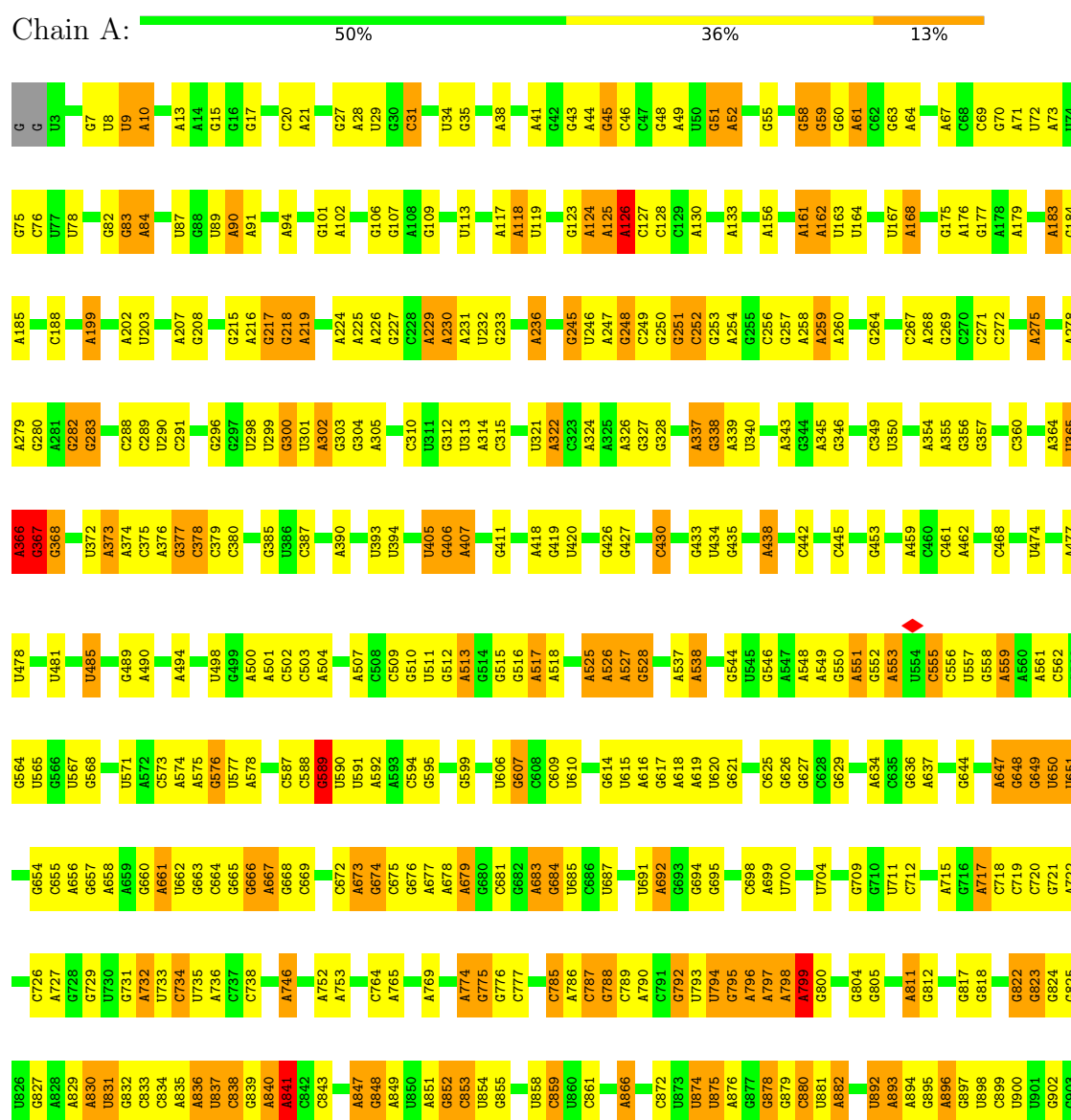
- Molecule 54 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	3	45	Total	C	N	O	S	0	0
			366	227	66	71	2		

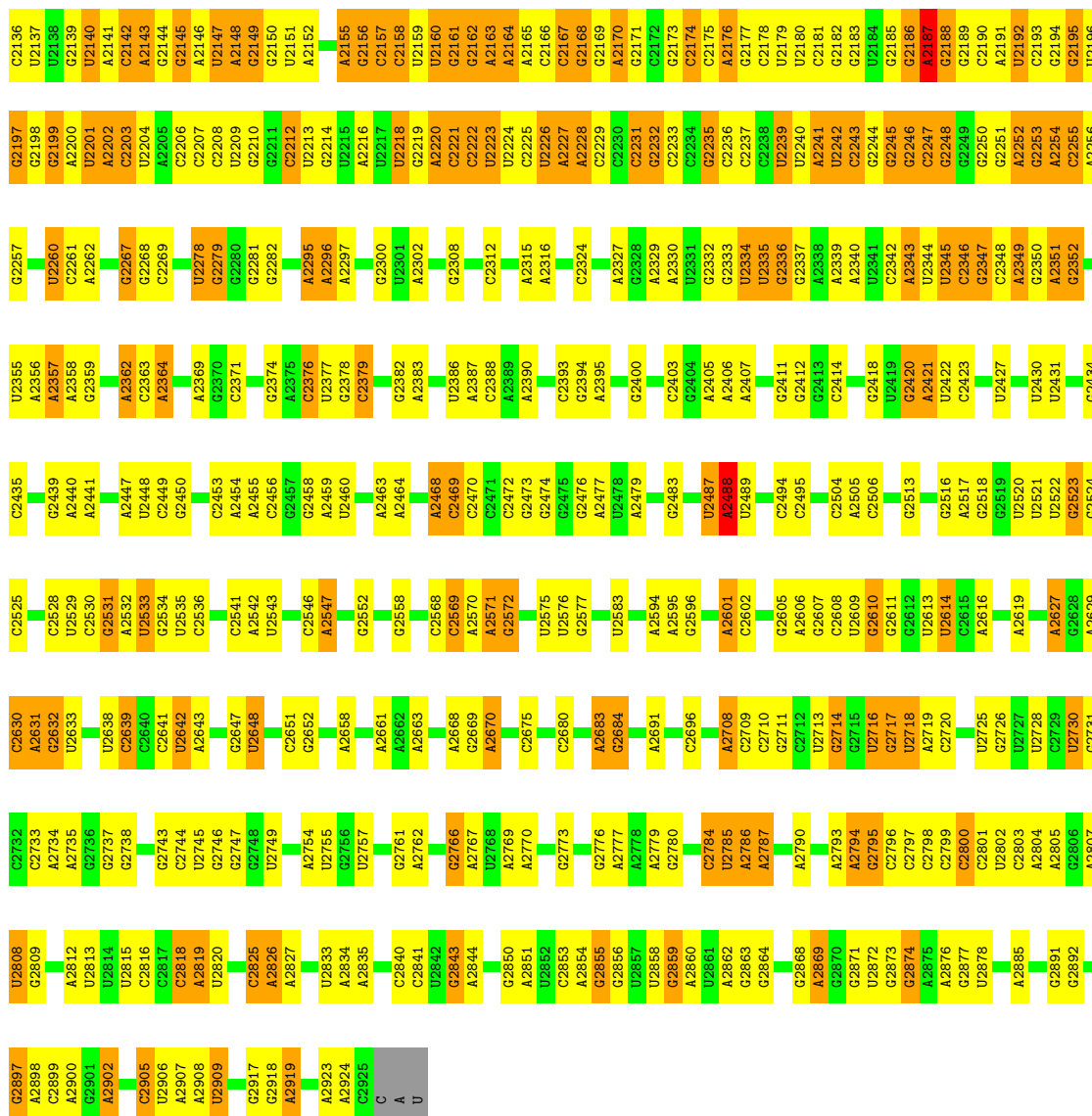
3 Residue-property plots [i](#)

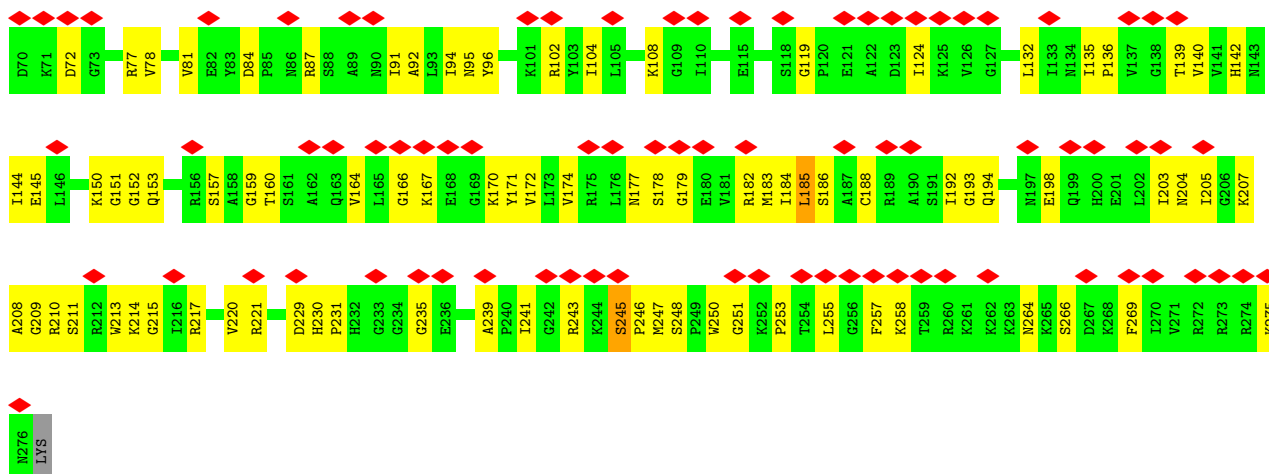
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 23S rRNA

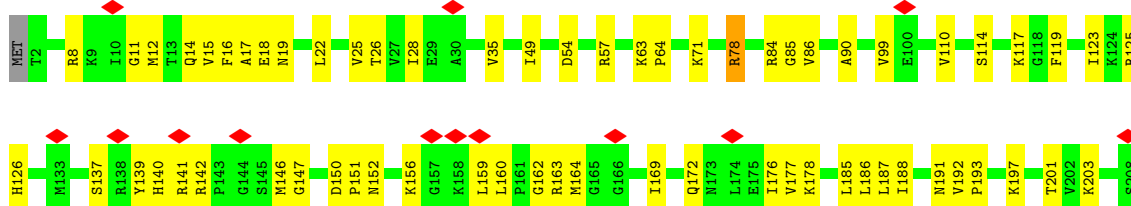


A2052	A1957	G1872	A1789	U1692	C1598	U1501	G1394	G1309	A1222	A1131	U1064	A978	A904
A2059	G1958	U1873	U1790	C1693	U1599	A1504	A1398	A1312	C1223	A1132	U1065	C981	A908
A2060	U1960	A1876	A1791	G1694	A1601	U1507	C1403	A1313	G1225	G1133	A1066	U982	G909
G2061	A1877	A1793	G1792	G1695	A1607	U1513	G1402	A1314	U1226	U1136	U1068	U983	G911
A2062	C1796	A1882	C1796	A1608	A1608	U1513	A1404	G1315	G1227	G1137	G1070	G985	C912
A2066	G1799	A1883	U1706	C1613	C1613	A1516	G1407	A1316	G1231	C1138	A1072	A913	A914
G2067	U1969	G1886	U1708	A1614	A1614	A1517	G1408	G1317	G1236	G1139	A1073	U915	U916
U2070	A1802	G1887	A1802	A1615	A1615	G1518	U1411	G1319	U1242	U1141	A1074	G992	G916
A2071	U1808	A1888	G1710	G1616	G1616	C1519	U1411	G1322	U1243	G1145	A1075	C997	A917
C2072	A1809	U1889	G1711	A1617	A1617	A1520	U1417	A1325	A1244	C1148	G1076	G998	U918
A2078	C1810	U1894	G1712	A1618	A1618	G1521	U1418	A1326	G1245	C1149	A1078	G921	G921
G2082	C1811	U1894	A1713	A1620	A1620	U1522	U1423	U1327	G1246	A1149	U1079	A1003	U924
A2083	A1812	C1897	C1715	A1621	A1621	A1524	A1424	G1344	G1247	U1151	A1005	U1004	A925
A2088	A1813	U1900	G1719	U1626	U1626	G1525	G1425	A1345	U1249	G1152	A1006	A1006	U925
A2090	A1814	A1901	C1739	A1627	A1627	G1527	A1426	U1346	G1250	C1155	U1087	G1007	G928
A2091	A1815	G1902	G1744	G1628	G1628	U1528	G1431	A1347	U1251	G1156	G1088	U1013	G929
C2092	A1816	A1902	A1745	G1630	G1630	G1529	A1432	U1348	G1252	A1157	A1092	U1013	C930
A2096	C1817	G1903	A1727	A1631	A1631	G1530	U1433	G1348	A1253	G1158	A1093	A1014	C931
G2098	A1818	C1904	C1728	G1632	G1632	U1535	A1434	U1349	A1254	G1171	A1094	G1015	C932
G2099	C1819	A1905	C1739	A1638	A1638	U1536	U1435	U1349	G1255	A1172	A1095	U1016	C933
A2100	A1820	A1906	G1752	G1639	G1639	G1537	U1436	A1347	C1257	A1173	A1096	G1017	U934
G2101	G1827	U1915	C1753	U1647	U1647	U1543	A1440	U1351	G1261	A1174	A1100	G1023	A942
U2105	G1828	U1916	U1754	A1648	A1648	A1553	U1441	U1352	G1263	G1177	G1101	G1024	A943
G2109	C1829	U1917	G1755	U1651	U1651	U1554	A1442	C1353	A1265	U1178	G1102	A1025	C944
G2110	A1830	A1918	U1756	G1652	G1652	U1555	U1443	U1354	G1267	C1180	U1103	A1026	C945
A2111	A1831	U1919	G1757	A1653	A1653	C1558	U1451	U1355	G1268	G1182	U1105	A1027	C946
G2116	C1832	A1925	U1758	A1654	A1654	U1561	U1452	A1360	A1269	G1183	U1107	G1028	A947
A2117	G1833	U1928	U1759	A1655	A1655	G1562	A1453	G1361	G1278	G1184	G1108	G1030	A948
U2120	A1834	A1929	A1767	C1656	C1656	A1562	C1454	G1362	G1285	U1187	C1110	A1034	A952
G2122	G1835	U1930	G1768	C1657	C1657	G1563	A1455	G1363	G1286	A1188	U1111	G1035	G953
A2123	A1839	A1931	U1769	G1658	G1658	G1563	A1456	U1364	G1289	A1189	G1112	A1036	A956
A2124	G1840	C1932	G1770	C1659	C1659	G1568	U1459	U1365	U1289	A1194	G1113	G1037	A957
U2125	U1841	G1933	C1771	A1661	A1661	G1572	G1460	G1371	G1290	A1197	G1114	A1038	C959
G2126	U1847	U1934	A1774	G1664	G1664	C1573	A1464	C1374	A1291	C1198	A1115	G1039	A964
U2127	U1848	U1940	G1775	A1667	A1667	G1578	C1474	A1375	G1292	C1199	G1117	A1042	A965
G2128	A1850	U1941	G1776	G1674	G1674	U1581	U1477	G1376	A1293	G1200	C1118	U1058	A966
G2129	C1855	A1942	G1777	U1679	U1679	U1582	G1478	U1377	U1294	G1201	C1119	U1059	A970
U2130	A1858	C1943	A1778	A1680	A1680	U1583	G1479	G1378	G1295	A1202	G1120	G972	A971
A2043	C1862	U1944	C1783	A1686	A1686	U1584	C1495	U1379	G1296	G1209	C1121	U1060	U972
U2044	U1784	A1948	A1784	G1687	G1687	U1587	G1496	U1380	C1297	U1218	C1122	G973	A973
A2045	G1785	C1954	G1785	G1688	G1688	U1595	G1497	U1381	G1298	C1219	A1126	U1060	A974
U2046	U1786	U1948	U1786	A1691	A1691	U1596	U1498	A1382	G1299	G1220	U1127	C1061	C975
A2047	A1788	C1954	A1788			C1597	U1500	A1388	U1303	C1221	U1128	U1061	U976
U2048								A1393	G1306		A1130	G1063	U977

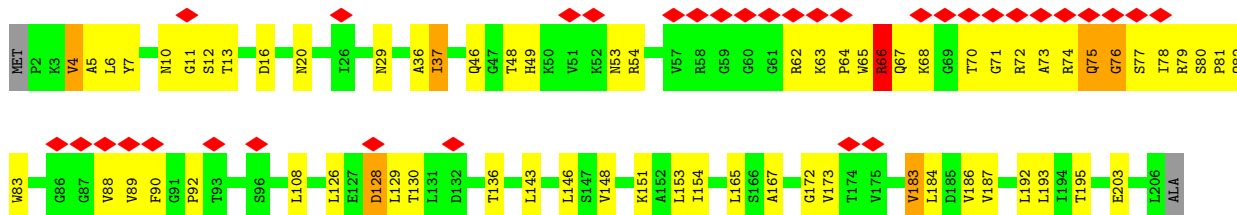




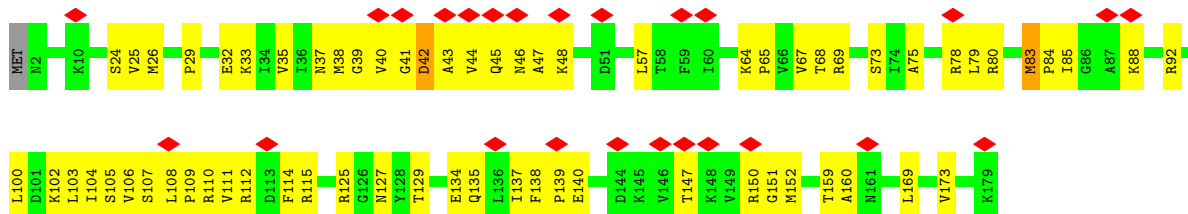
• Molecule 4: 50S ribosomal protein L3



• Molecule 5: 50S ribosomal protein L4

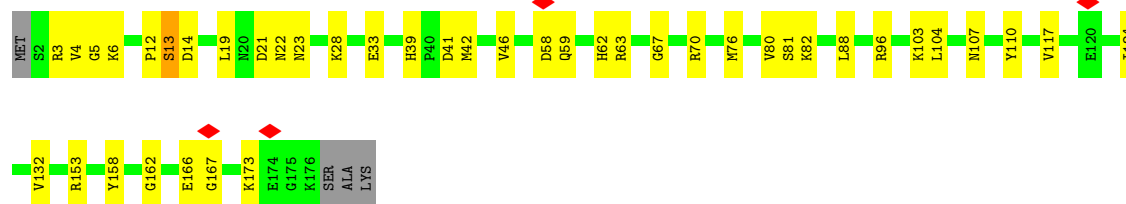


• Molecule 6: 50S ribosomal protein L5



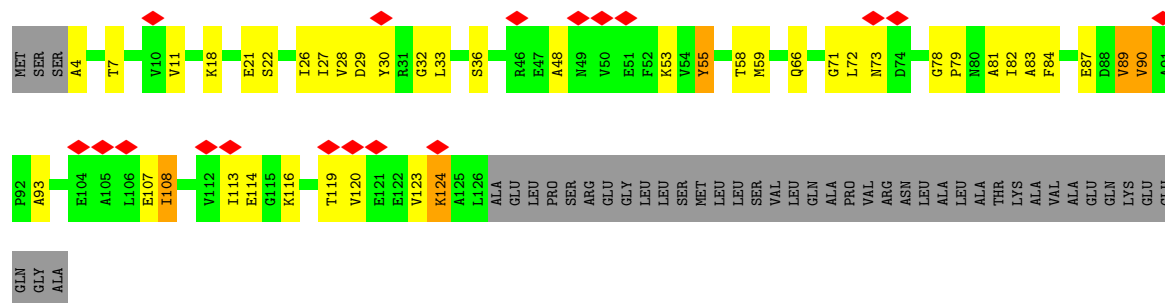
• Molecule 7: Ribosomal protein L6

Chain G:  74% 23% ..



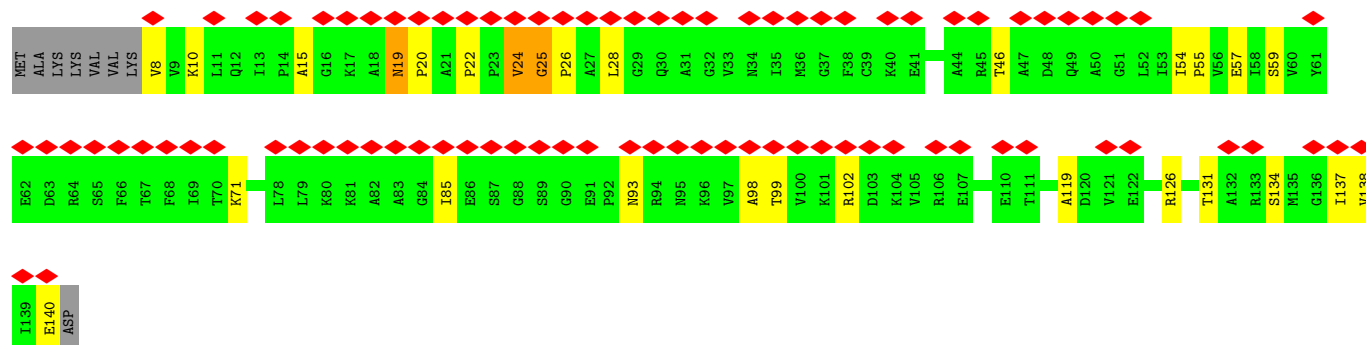
• Molecule 8: 50S ribosomal protein L10

Chain H:  11% 49% 22% • 26%



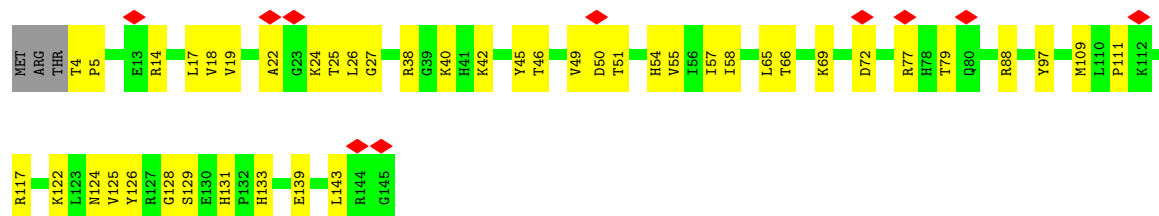
• Molecule 9: 50S ribosomal protein L11

Chain I:  60% 74% 18% • 6%

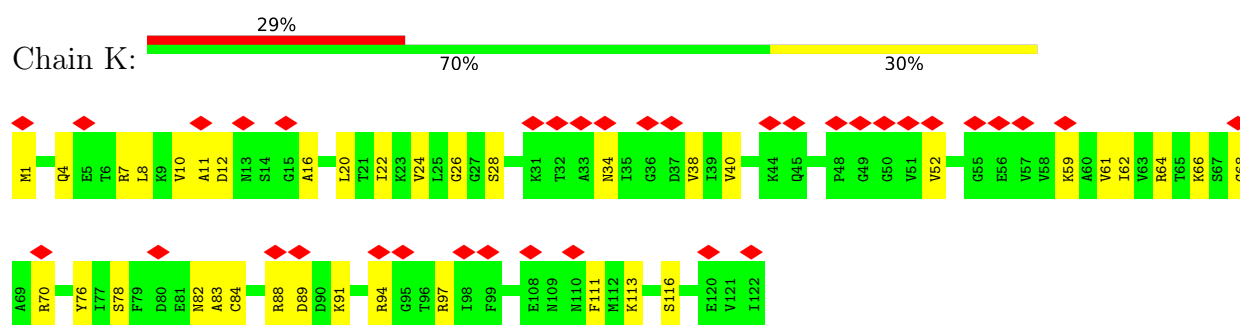


• Molecule 10: 50S ribosomal protein L13

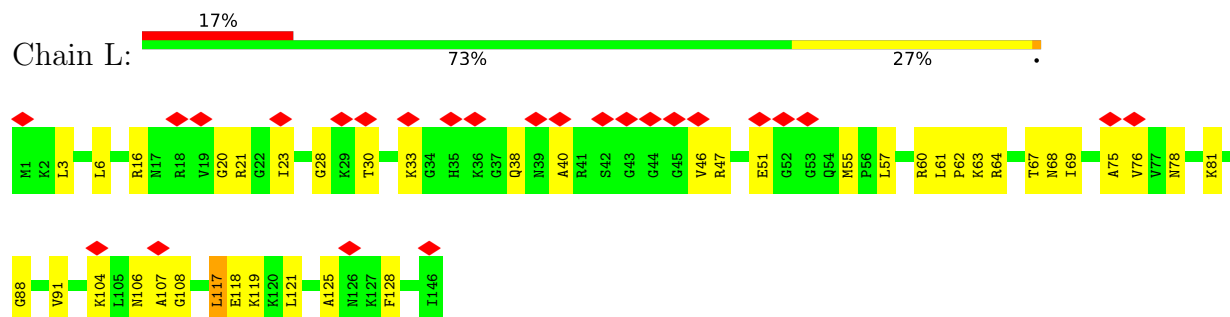
Chain J:  7% 68% 30% •



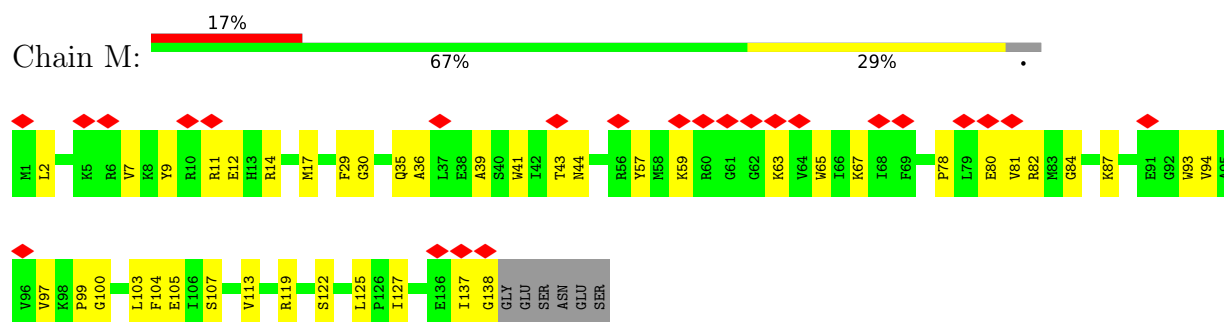
• Molecule 11: 50S ribosomal protein L14



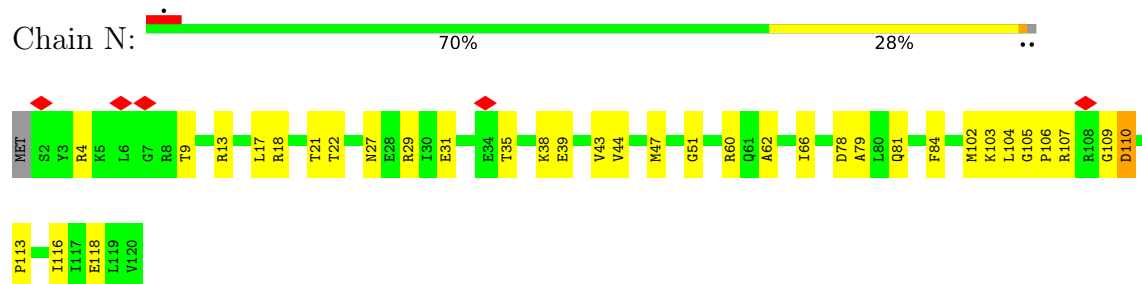
• Molecule 12: 50S ribosomal protein L15



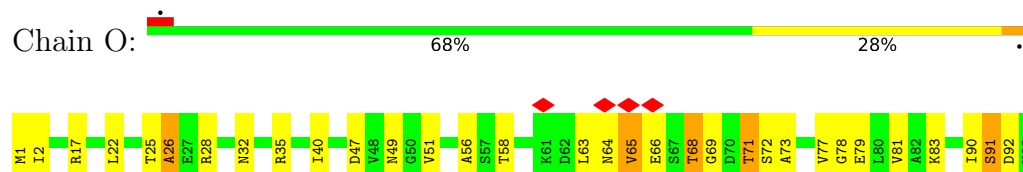
• Molecule 13: 50S ribosomal protein L16



• Molecule 14: 50S ribosomal protein L17

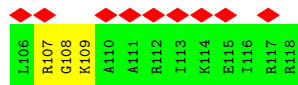


• Molecule 15: 50S ribosomal protein L18

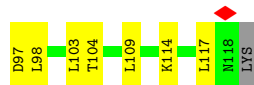




- Molecule 16: 50S ribosomal protein L19



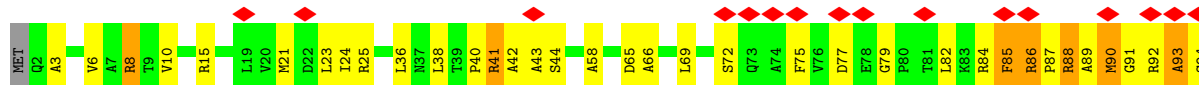
- Molecule 17: 50S ribosomal protein L20



- Molecule 18: 50S ribosomal protein L21

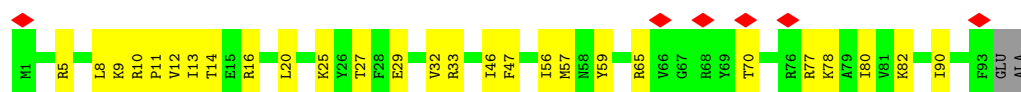


- Molecule 19: 50S ribosomal protein L22

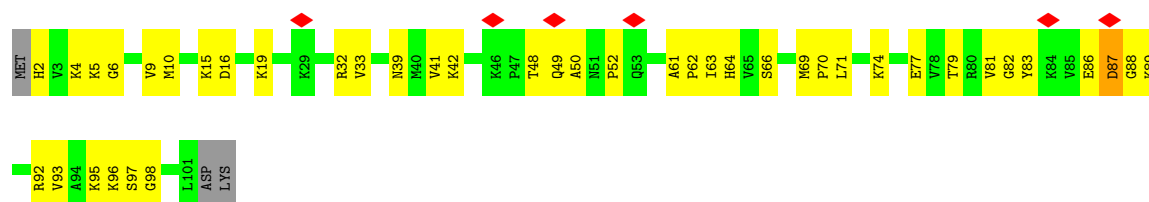


- Molecule 20: 50S ribosomal protein L23

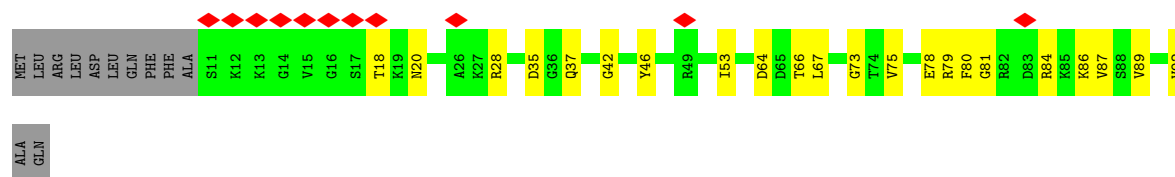




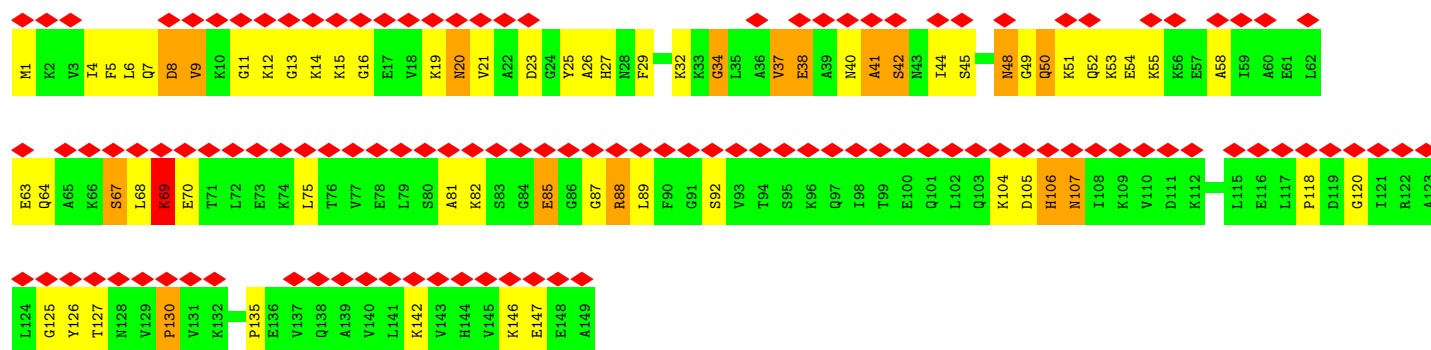
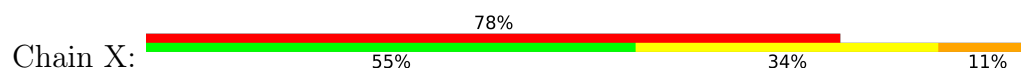
- Molecule 21: 50S ribosomal protein L24



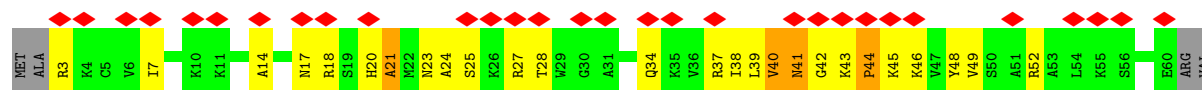
- Molecule 22: 50S ribosomal protein L27



- Molecule 23: 50S ribosomal protein L9



- Molecule 24: 50S ribosomal protein L28

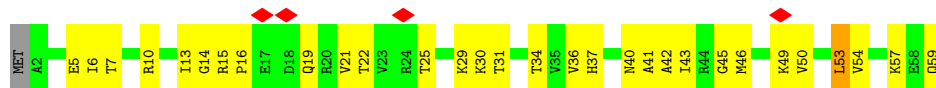


- Molecule 25: 50S ribosomal protein L29

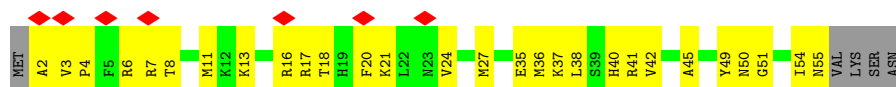
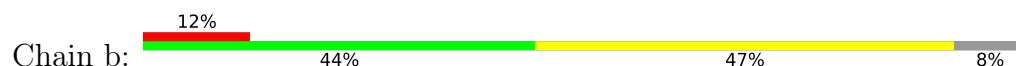




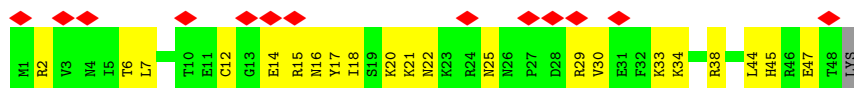
- Molecule 26: 50S ribosomal protein L30



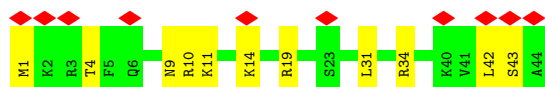
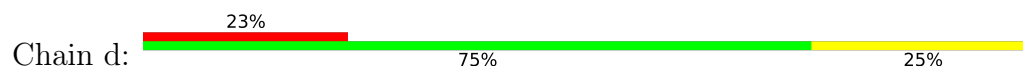
- Molecule 27: 50S ribosomal protein L32



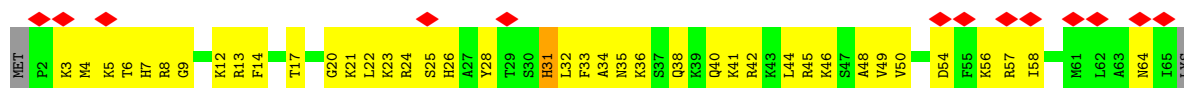
- Molecule 28: 50S ribosomal protein L33



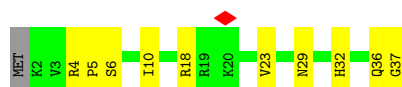
- Molecule 29: 50S ribosomal protein L34



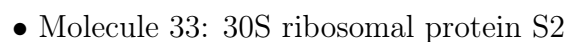
- Molecule 30: 50S ribosomal protein L35

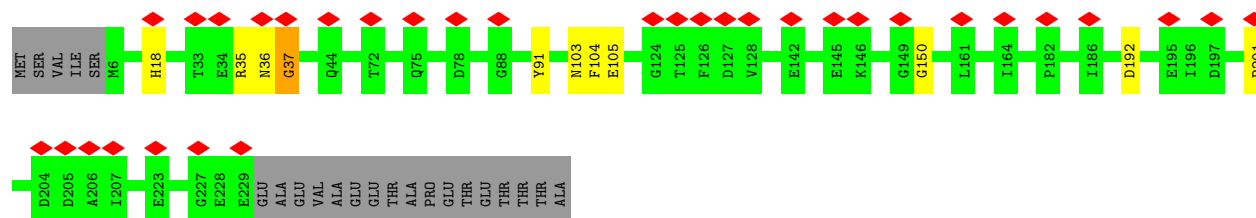
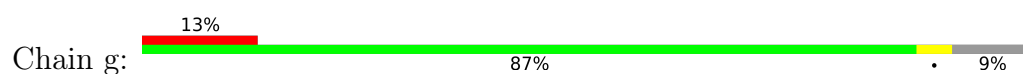


- Molecule 31: 50S ribosomal protein L36

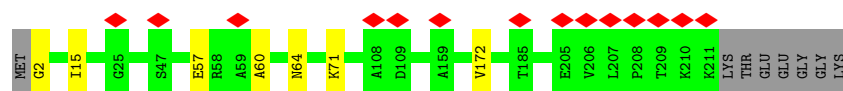
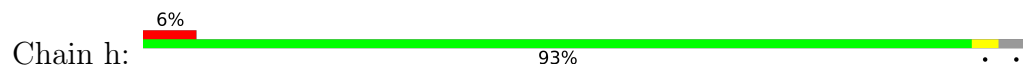


- Molecule 32: 16S rRNA

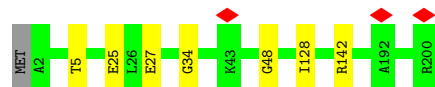




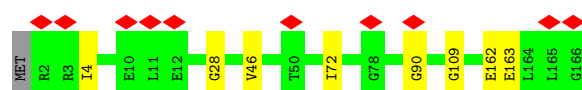
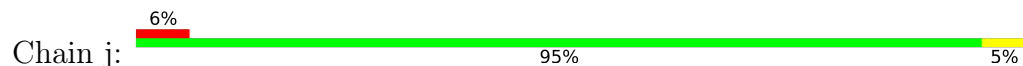
- Molecule 34: 30S ribosomal protein S3



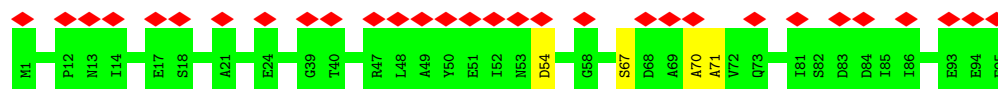
- Molecule 35: 30S ribosomal protein S4



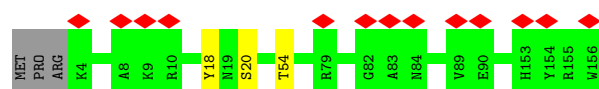
- Molecule 36: 30S ribosomal protein S5



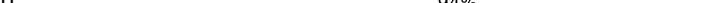
- Molecule 37: 30S ribosomal protein S6

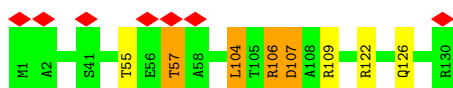


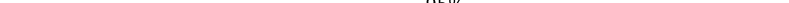
- Molecule 38: 30S ribosomal protein S7

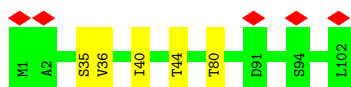


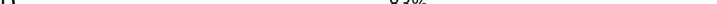
- Molecule 39: 30S ribosomal protein S8

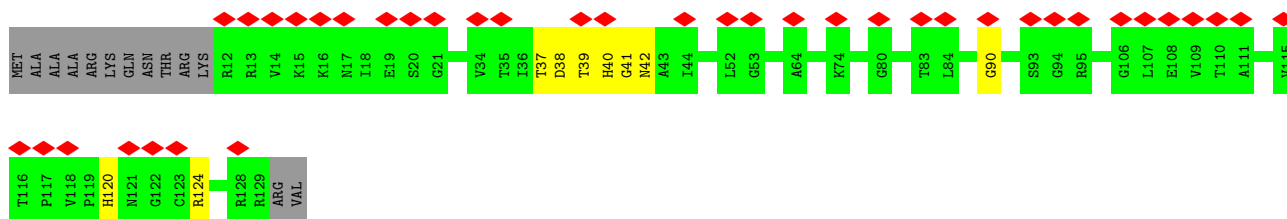
- Chain n:  5% 94%

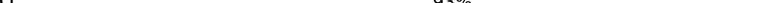


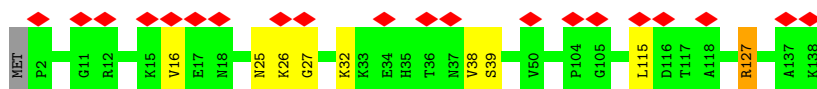
- Chain o:  5% 95% 5%

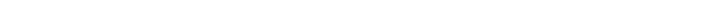


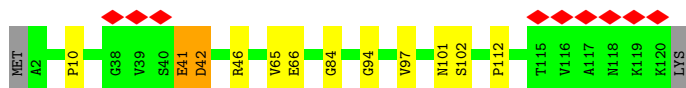
- Chain p: 

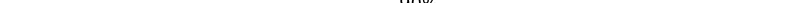


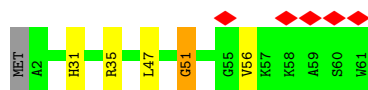
- Chain q:  14% 93% 6% ..



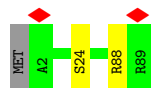
- Chain r:  7% 88% 8% ..



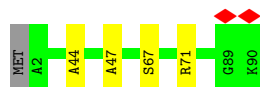
- Chain s:  8% 90% 7%



- Molecule 46: 30S ribosomal protein S15



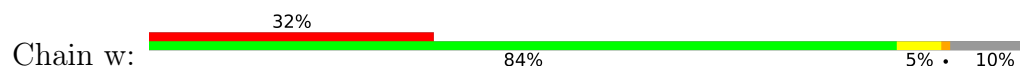
- Molecule 47: 30S ribosomal protein S16



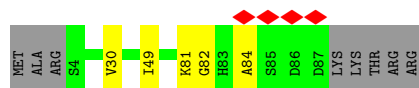
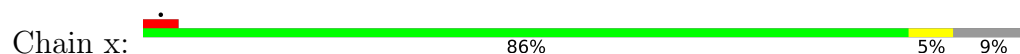
- Molecule 48: 30S ribosomal protein S17



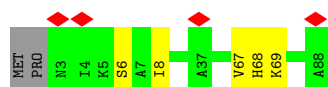
- Molecule 49: 30S ribosomal protein S18



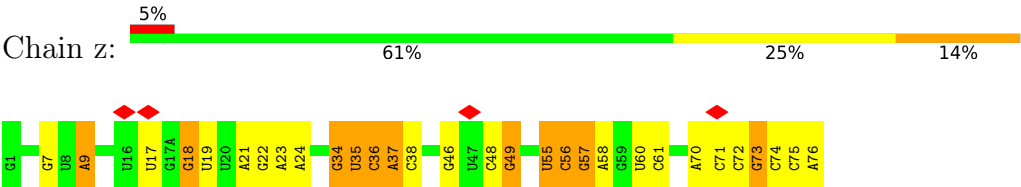
- Molecule 50: 30S ribosomal protein S19



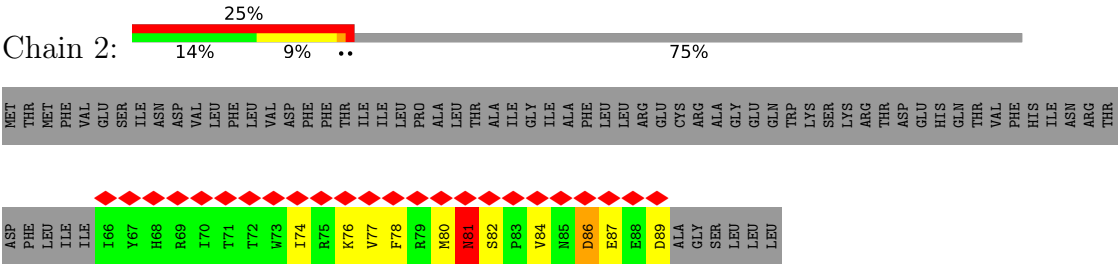
- Molecule 51: 30S ribosomal protein S20



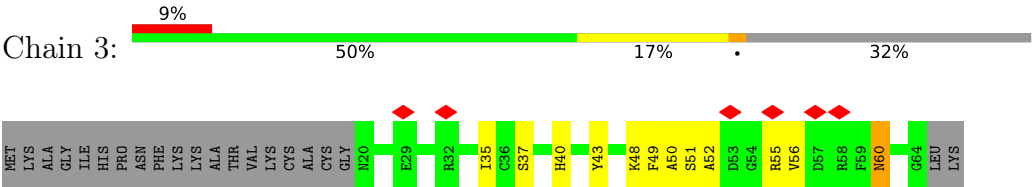
- Molecule 52: P-site tRNA



• Molecule 53: YqzJ



• Molecule 54: 50S ribosomal protein L31



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	12739	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	1.709	Depositor
Minimum map value	-0.823	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.090	Depositor
Recommended contour level	0.3	Depositor
Map size ($\text{\AA}$)	650.4, 650.4, 650.4	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.084, 1.084, 1.084	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	A	0.53	0/70307	0.59	26/109687 (0.0%)
2	B	0.50	0/2678	0.52	0/4174
3	C	0.38	0/2148	0.85	2/2881 (0.1%)
4	D	0.39	0/1597	0.76	2/2140 (0.1%)
5	E	0.37	0/1580	0.80	3/2132 (0.1%)
6	F	0.40	0/1423	0.82	5/1910 (0.3%)
7	G	0.33	0/1360	0.76	0/1832
8	H	0.38	0/963	0.73	0/1298
9	I	0.42	0/995	0.90	5/1346 (0.4%)
10	J	0.36	0/1146	0.77	2/1542 (0.1%)
11	K	0.40	0/927	0.80	1/1245 (0.1%)
12	L	0.30	0/1093	0.78	2/1457 (0.1%)
13	M	0.29	0/1120	0.72	1/1496 (0.1%)
14	N	0.36	0/960	0.69	0/1284
15	O	0.44	0/921	0.84	1/1236 (0.1%)
16	P	0.33	0/949	0.73	0/1269
17	Q	0.34	0/952	0.66	0/1266
18	R	0.39	0/797	0.81	2/1070 (0.2%)
19	S	0.53	1/851 (0.1%)	0.88	2/1146 (0.2%)
20	T	0.40	0/759	0.74	0/1011
21	U	0.37	0/764	0.88	0/1022
22	V	0.40	0/638	0.77	0/847
23	X	1.03	5/732 (0.7%)	1.72	15/1016 (1.5%)
24	Y	0.38	0/448	0.89	2/596 (0.3%)
25	Z	0.30	0/531	0.65	0/707
26	a	0.33	0/457	0.68	0/613
27	b	0.30	0/433	0.75	0/574
28	c	0.34	0/406	0.69	0/540
29	d	0.26	0/370	0.76	1/483 (0.2%)
30	e	0.29	0/519	0.64	0/680
31	f	0.26	0/291	0.76	0/383
32	W	0.52	0/37074	0.53	0/57834
33	g	0.52	0/895	0.95	2/1117 (0.2%)
34	h	0.47	0/839	0.92	3/1047 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	i	0.44	0/796	1.03	4/992 (0.4%)
36	j	0.46	0/660	1.05	1/822 (0.1%)
37	k	0.51	0/380	1.00	2/472 (0.4%)
38	l	0.43	0/612	0.82	0/762
39	m	0.42	0/524	0.96	0/652
40	n	0.44	0/520	0.97	1/647 (0.2%)
41	o	0.50	0/408	1.00	2/507 (0.4%)
42	p	0.44	0/471	1.15	4/587 (0.7%)
43	q	0.42	0/548	1.12	0/682
44	r	0.49	0/475	1.00	1/592 (0.2%)
45	s	0.39	0/240	1.03	0/297
46	t	0.42	0/352	0.84	0/437
47	u	0.46	0/356	0.95	0/442
48	v	0.44	0/344	0.90	0/427
49	w	0.47	0/284	0.96	2/352 (0.6%)
50	x	0.53	0/335	0.98	1/417 (0.2%)
51	y	0.43	0/344	0.75	0/427
52	z	0.41	0/1834	0.47	0/2858
53	2	0.79	0/106	1.66	3/122 (2.5%)
54	3	0.40	0/373	0.76	0/497
All	All	0.50	6/147885 (0.0%)	0.64	98/221872 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	79
2	B	0	2
5	E	0	1
19	S	0	2
23	X	0	2
32	W	0	33
52	z	0	2
All	All	0	121

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	X	69	LYS	C-O	-11.68	1.09	1.24
23	X	63	GLU	C-O	-7.11	1.14	1.24

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Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	S	95	GLN	CA-C	-6.18	1.45	1.52
23	X	54	GLU	C-O	-5.90	1.15	1.23
23	X	48	ASN	CA-C	-5.52	1.45	1.52

The worst 5 of 98 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	589	G	C4'-C3'-O3'	20.92	140.78	109.40
1	A	83	G	C4'-C3'-O3'	-17.73	82.81	109.40
23	X	69	LYS	CA-C-N	17.05	154.11	121.54
23	X	69	LYS	C-N-CA	17.05	154.11	121.54
23	X	51	LYS	N-CA-C	-16.80	93.10	111.07

There are no chirality outliers.

5 of 121 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	126	A	Sidechain
1	A	168	A	Sidechain
1	A	52	A	Sidechain
1	A	64	A	Sidechain
1	A	67	A	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	62767	0	31581	1262	0
2	B	2395	0	1212	21	0
3	C	2111	0	2200	90	0
4	D	1575	0	1642	47	0
5	E	1561	0	1647	88	0
6	F	1404	0	1467	67	0
7	G	1342	0	1388	29	0
8	H	955	0	990	26	0
9	I	981	0	1020	28	0
10	J	1123	0	1162	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	K	920	0	977	22	0
12	L	1081	0	1132	78	0
13	M	1097	0	1165	27	0
14	N	953	0	983	39	0
15	O	912	0	947	35	0
16	P	936	0	1008	36	0
17	Q	940	0	1005	43	0
18	R	786	0	826	39	0
19	S	842	0	899	53	0
20	T	752	0	802	65	0
21	U	754	0	809	33	0
22	V	630	0	644	17	0
23	X	733	0	345	49	0
24	Y	444	0	486	86	0
25	Z	530	0	568	65	0
26	a	455	0	491	70	0
27	b	426	0	445	60	0
28	c	401	0	413	20	0
29	d	367	0	409	36	0
30	e	512	0	563	152	0
31	f	288	0	330	24	0
32	W	33115	0	16676	245	0
33	g	896	0	244	3	0
34	h	840	0	241	3	0
35	i	797	0	224	2	0
36	j	661	0	197	2	0
37	k	381	0	104	0	0
38	l	613	0	164	1	0
39	m	525	0	146	0	0
40	n	521	0	155	3	0
41	o	409	0	104	0	0
42	p	472	0	135	7	0
43	q	549	0	157	2	0
44	r	476	0	137	2	0
45	s	241	0	62	2	0
46	t	353	0	94	0	0
47	u	357	0	95	1	0
48	v	345	0	90	1	0
49	w	285	0	76	1	0
50	x	336	0	93	2	0
51	y	345	0	89	2	0
52	z	1643	0	830	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	2	107	0	58	20	0
54	3	366	0	343	20	0
All	All	135606	0	80070	2447	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 11.

The worst 5 of 2447 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)
23:X:49:GLY:CA	23:X:52:GLN:CB	1.78	1.59
23:X:49:GLY:HA2	23:X:52:GLN:CB	1.31	1.56
1:A:2198:G:H3'	1:A:2198:G:N3	1.20	1.52
1:A:2157:C:C3'	1:A:2158:C:C6	1.92	1.50
1:A:2156:G:H21	1:A:2202:A:C1'	1.27	1.46

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	273/277 (99%)	264 (97%)	8 (3%)	1 (0%)	30	67
4	D	205/208 (99%)	189 (92%)	11 (5%)	5 (2%)	4	27
5	E	203/207 (98%)	185 (91%)	15 (7%)	3 (2%)	8	38
6	F	176/179 (98%)	154 (88%)	18 (10%)	4 (2%)	5	28
7	G	173/179 (97%)	164 (95%)	8 (5%)	1 (1%)	21	58
8	H	121/166 (73%)	97 (80%)	14 (12%)	10 (8%)	0	9
9	I	131/141 (93%)	122 (93%)	7 (5%)	2 (2%)	8	38
10	J	140/145 (97%)	130 (93%)	9 (6%)	1 (1%)	18	55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	K	120/122 (98%)	112 (93%)	6 (5%)	2 (2%)	7	35
12	L	144/146 (99%)	132 (92%)	10 (7%)	2 (1%)	9	39
13	M	136/144 (94%)	129 (95%)	7 (5%)	0	100	100
14	N	117/120 (98%)	109 (93%)	7 (6%)	1 (1%)	14	49
15	O	118/120 (98%)	106 (90%)	7 (6%)	5 (4%)	2	17
16	P	112/115 (97%)	100 (89%)	12 (11%)	0	100	100
17	Q	115/119 (97%)	112 (97%)	3 (3%)	0	100	100
18	R	99/102 (97%)	82 (83%)	15 (15%)	2 (2%)	6	31
19	S	107/113 (95%)	96 (90%)	8 (8%)	3 (3%)	4	24
20	T	91/95 (96%)	86 (94%)	5 (6%)	0	100	100
21	U	98/103 (95%)	87 (89%)	8 (8%)	3 (3%)	3	21
22	V	80/94 (85%)	77 (96%)	3 (4%)	0	100	100
23	X	147/149 (99%)	83 (56%)	42 (29%)	22 (15%)	0	3
24	Y	56/62 (90%)	53 (95%)	1 (2%)	2 (4%)	2	20
25	Z	63/66 (96%)	60 (95%)	3 (5%)	0	100	100
26	a	56/59 (95%)	54 (96%)	1 (2%)	1 (2%)	6	33
27	b	52/59 (88%)	47 (90%)	4 (8%)	1 (2%)	6	32
28	c	46/49 (94%)	44 (96%)	2 (4%)	0	100	100
29	d	42/44 (96%)	41 (98%)	1 (2%)	0	100	100
30	e	62/66 (94%)	56 (90%)	5 (8%)	1 (2%)	7	37
31	f	34/37 (92%)	33 (97%)	1 (3%)	0	100	100
33	g	222/246 (90%)	204 (92%)	13 (6%)	5 (2%)	5	28
34	h	208/218 (95%)	193 (93%)	14 (7%)	1 (0%)	24	63
35	i	197/200 (98%)	191 (97%)	4 (2%)	2 (1%)	12	47
36	j	163/166 (98%)	150 (92%)	9 (6%)	4 (2%)	4	26
37	k	93/95 (98%)	88 (95%)	3 (3%)	2 (2%)	5	28
38	l	151/156 (97%)	144 (95%)	6 (4%)	1 (1%)	18	55
39	m	129/132 (98%)	123 (95%)	5 (4%)	1 (1%)	16	52
40	n	128/130 (98%)	113 (88%)	10 (8%)	5 (4%)	2	18
41	o	100/102 (98%)	88 (88%)	8 (8%)	4 (4%)	2	18
42	p	116/131 (88%)	106 (91%)	9 (8%)	1 (1%)	14	49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	q	135/138 (98%)	119 (88%)	9 (7%)	7 (5%)	1	15
44	r	117/121 (97%)	94 (80%)	13 (11%)	10 (8%)	0	9
45	s	58/61 (95%)	51 (88%)	4 (7%)	3 (5%)	1	15
46	t	86/89 (97%)	82 (95%)	2 (2%)	2 (2%)	5	28
47	u	87/90 (97%)	82 (94%)	3 (3%)	2 (2%)	5	28
48	v	84/87 (97%)	78 (93%)	6 (7%)	0	100	100
49	w	69/79 (87%)	64 (93%)	2 (3%)	3 (4%)	2	17
50	x	82/92 (89%)	75 (92%)	5 (6%)	2 (2%)	4	27
51	y	84/88 (96%)	77 (92%)	6 (7%)	1 (1%)	10	43
53	2	22/95 (23%)	17 (77%)	2 (9%)	3 (14%)	0	3
54	3	43/66 (65%)	37 (86%)	4 (9%)	2 (5%)	2	16
All	All	5691/6068 (94%)	5180 (91%)	378 (7%)	133 (2%)	7	28

5 of 133 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	H	93	ALA
9	I	19	ASN
15	O	26	ALA
21	U	87	ASP
23	X	29	PHE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	223/225 (99%)	222 (100%)	1 (0%)	84	83
4	D	168/169 (99%)	168 (100%)	0	100	100
5	E	169/170 (99%)	167 (99%)	2 (1%)	63	73
6	F	153/154 (99%)	153 (100%)	0	100	100
7	G	148/151 (98%)	148 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	H	105/139 (76%)	105 (100%)	0	100	100
9	I	103/110 (94%)	103 (100%)	0	100	100
10	J	120/123 (98%)	120 (100%)	0	100	100
11	K	101/101 (100%)	101 (100%)	0	100	100
12	L	110/110 (100%)	110 (100%)	0	100	100
13	M	111/116 (96%)	111 (100%)	0	100	100
14	N	99/100 (99%)	99 (100%)	0	100	100
15	O	93/93 (100%)	93 (100%)	0	100	100
16	P	99/100 (99%)	99 (100%)	0	100	100
17	Q	96/98 (98%)	96 (100%)	0	100	100
18	R	83/84 (99%)	83 (100%)	0	100	100
19	S	90/93 (97%)	89 (99%)	1 (1%)	65	74
20	T	84/85 (99%)	84 (100%)	0	100	100
21	U	84/87 (97%)	84 (100%)	0	100	100
22	V	64/74 (86%)	64 (100%)	0	100	100
24	Y	47/50 (94%)	47 (100%)	0	100	100
25	Z	56/57 (98%)	56 (100%)	0	100	100
26	a	52/53 (98%)	51 (98%)	1 (2%)	50	66
27	b	48/53 (91%)	48 (100%)	0	100	100
28	c	46/47 (98%)	46 (100%)	0	100	100
29	d	39/39 (100%)	39 (100%)	0	100	100
30	e	54/56 (96%)	54 (100%)	0	100	100
31	f	34/35 (97%)	34 (100%)	0	100	100
53	2	6/87 (7%)	4 (67%)	2 (33%)	0	2
54	3	39/55 (71%)	39 (100%)	0	100	100
All	All	2724/2914 (94%)	2717 (100%)	7 (0%)	84	84

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
19	S	90	MET
26	a	53	LEU
53	2	86	ASP

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Mol	Chain	Res	Type
53	2	81	ASN
5	E	66	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 47 such sidechains are listed below:

Mol	Chain	Res	Type
19	S	102	HIS
26	a	37	HIS
21	U	2	HIS
22	V	37	GLN
27	b	40	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2922/2928 (99%)	829 (28%)	85 (2%)
2	B	111/119 (93%)	32 (28%)	4 (3%)
32	W	1543/1555 (99%)	235 (15%)	17 (1%)
52	z	76/77 (98%)	15 (19%)	0
All	All	4652/4679 (99%)	1111 (23%)	106 (2%)

5 of 1111 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	8	U
1	A	9	U
1	A	10	A
1	A	13	A
1	A	27	G

5 of 106 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1965	A
1	A	2351	A
32	W	873	U
1	A	2139	G
1	A	2254	A

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

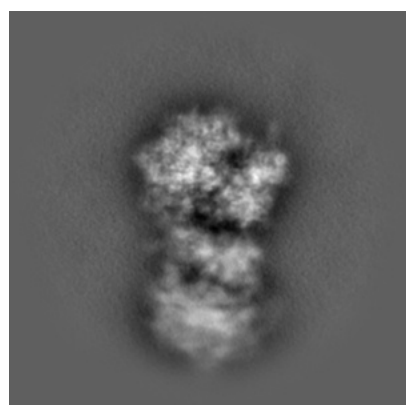
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13959. These allow visual inspection of the internal detail of the map and identification of artifacts.

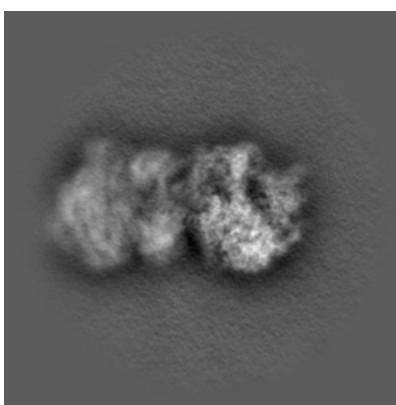
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

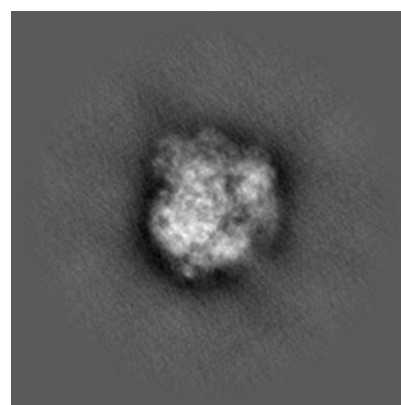
6.1.1 Primary map



X



Y

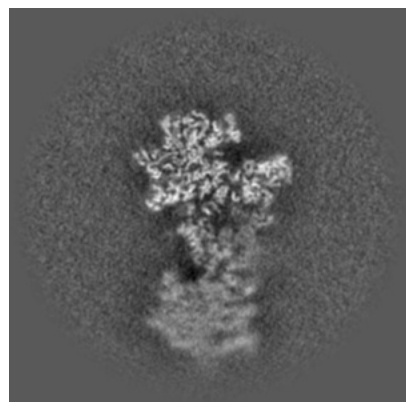


Z

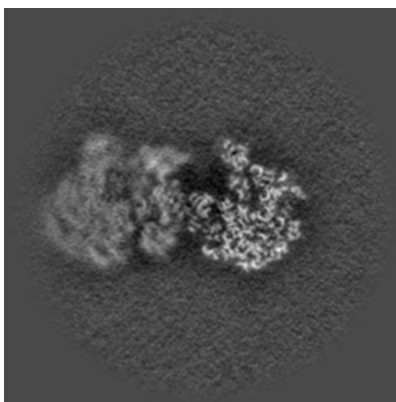
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

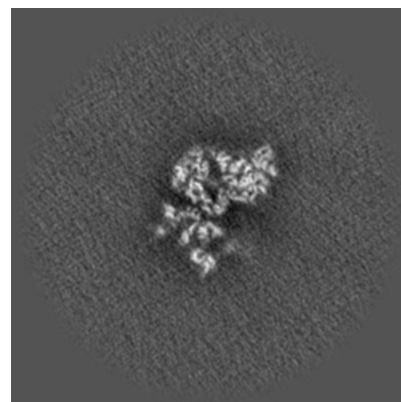
6.2.1 Primary map



X Index: 300



Y Index: 300

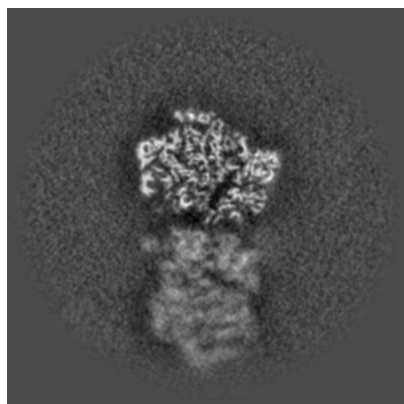


Z Index: 300

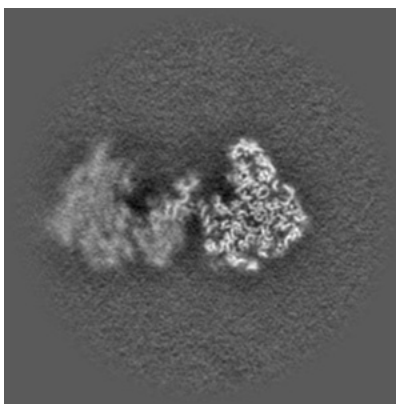
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

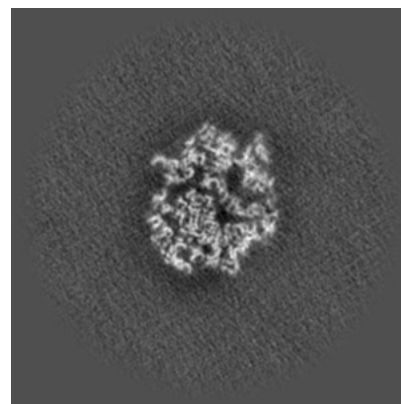
6.3.1 Primary map



X Index: 267



Y Index: 275

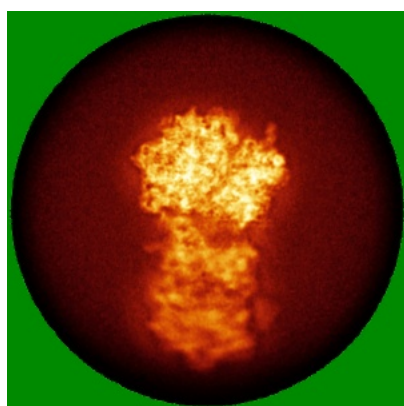


Z Index: 349

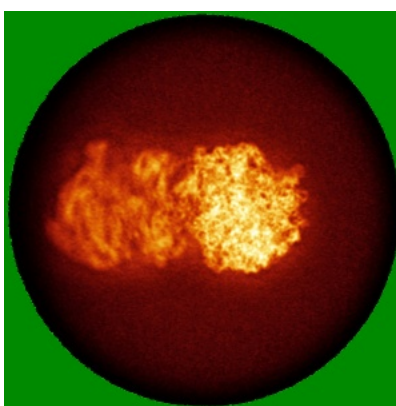
The images above show the largest variance slices of the map in three orthogonal directions.

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

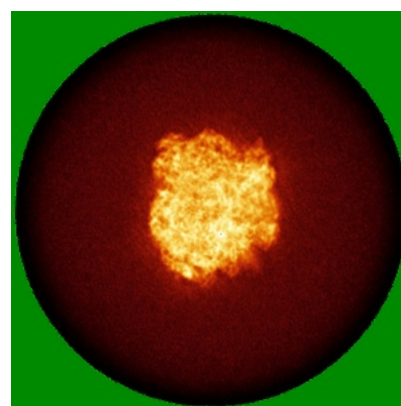
6.4.1 Primary map



X



Y

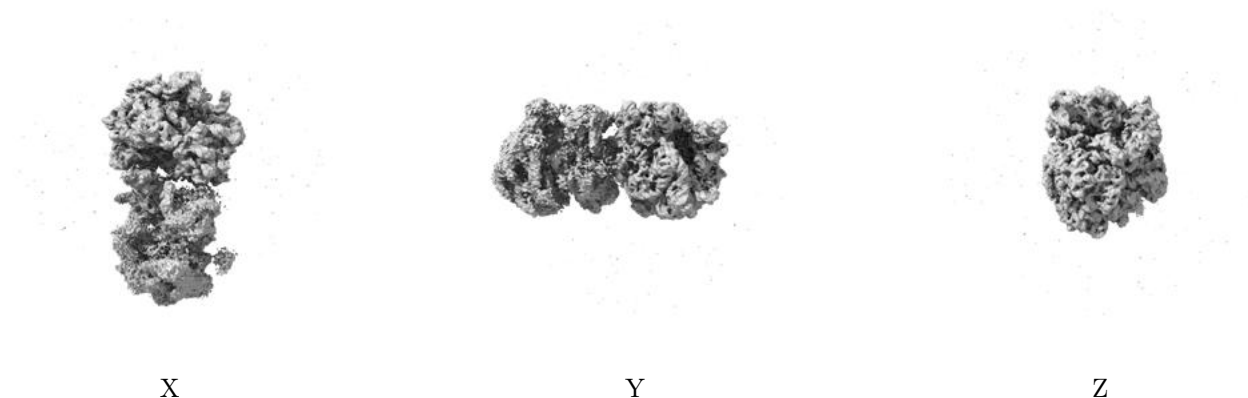


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

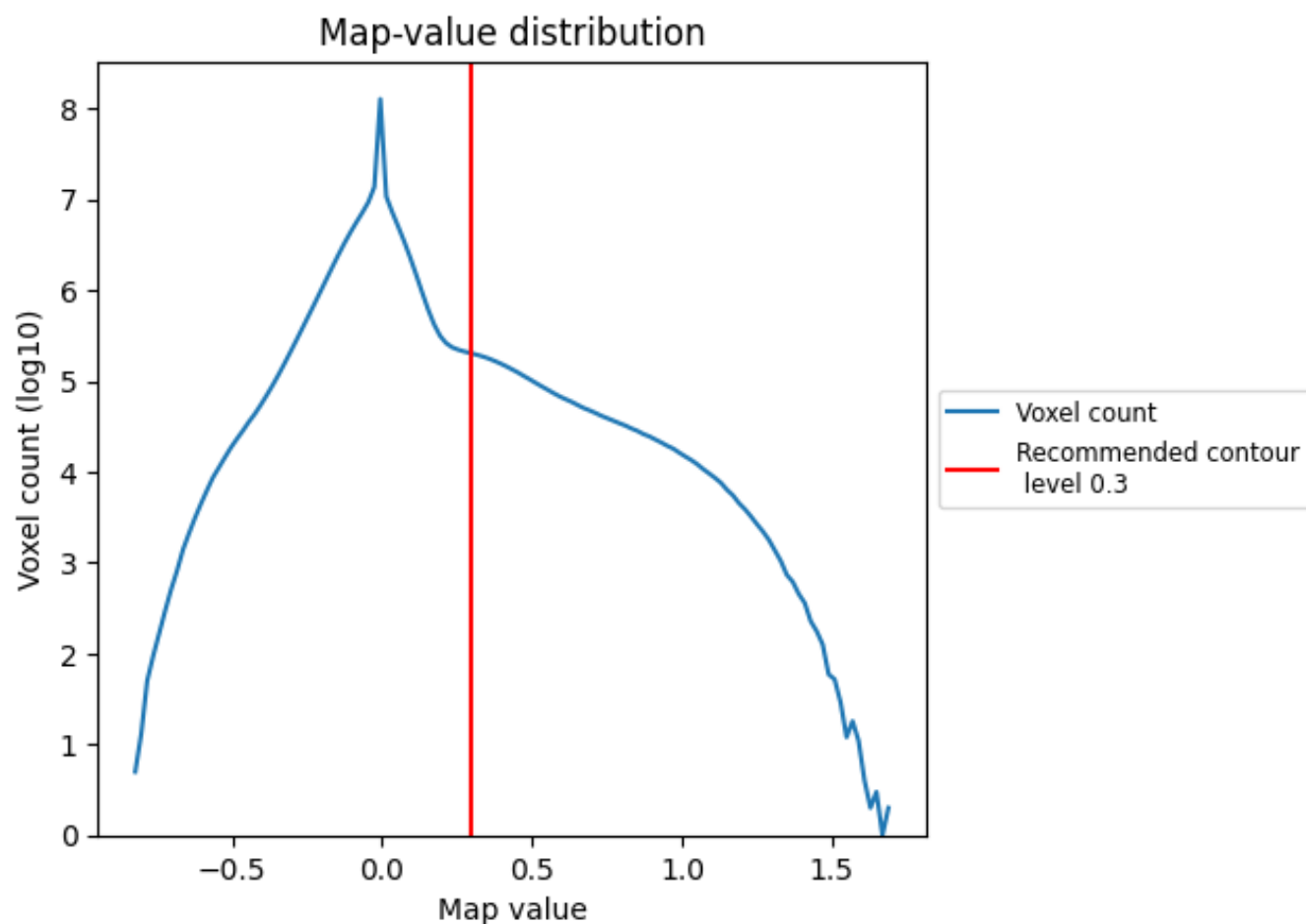
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

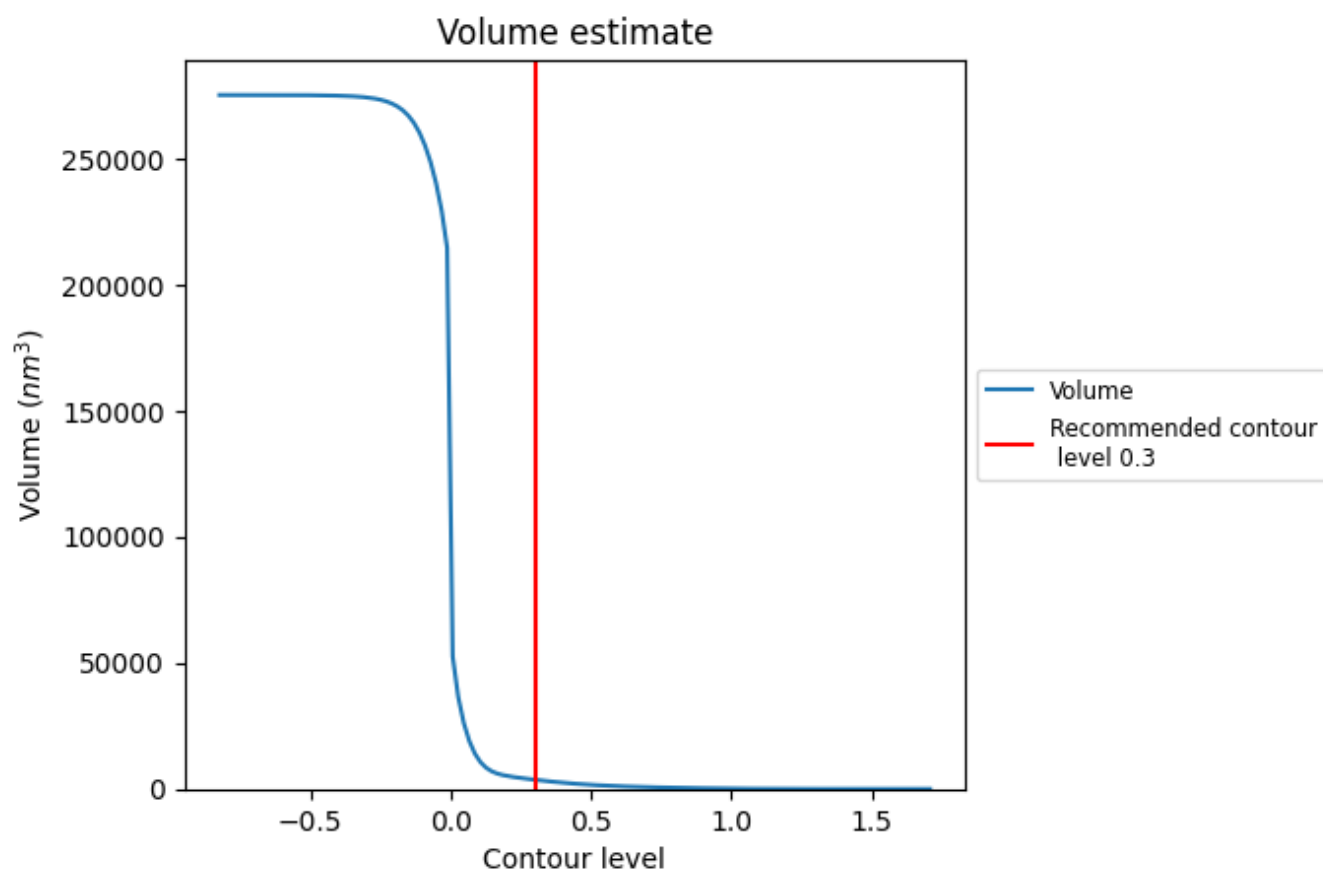
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

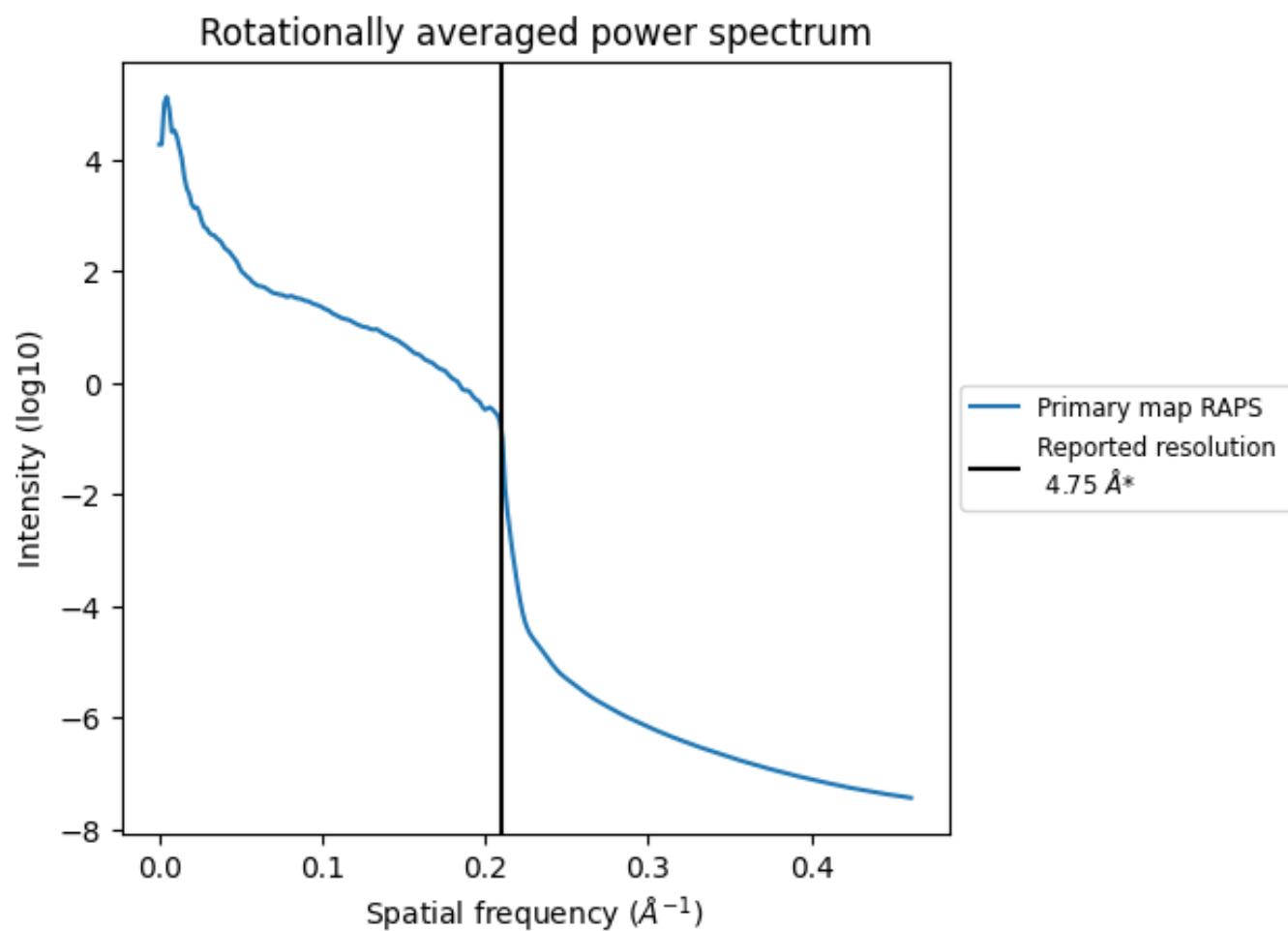
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3652 nm³; this corresponds to an approximate mass of 3299 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 0.211 Å⁻¹

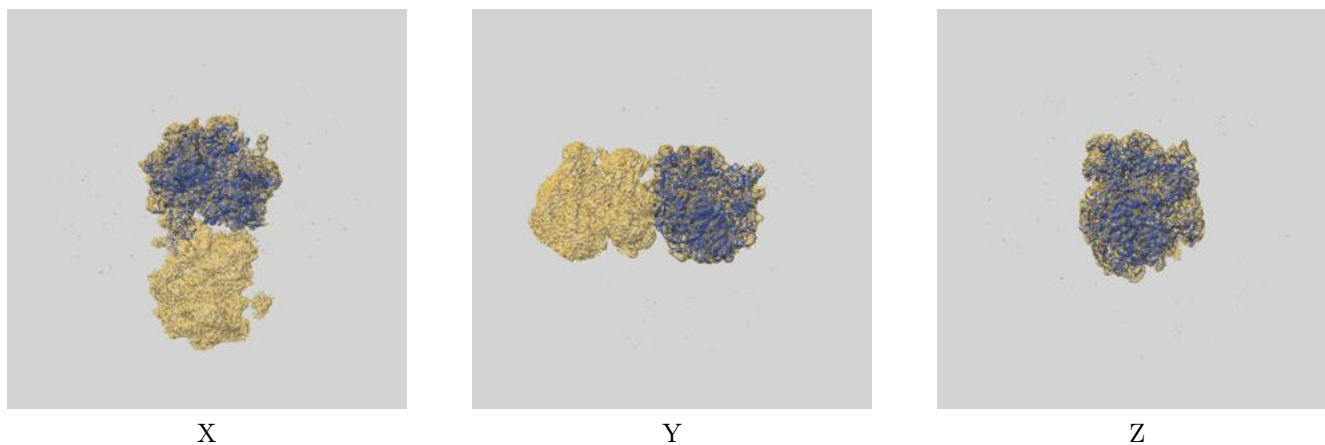
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

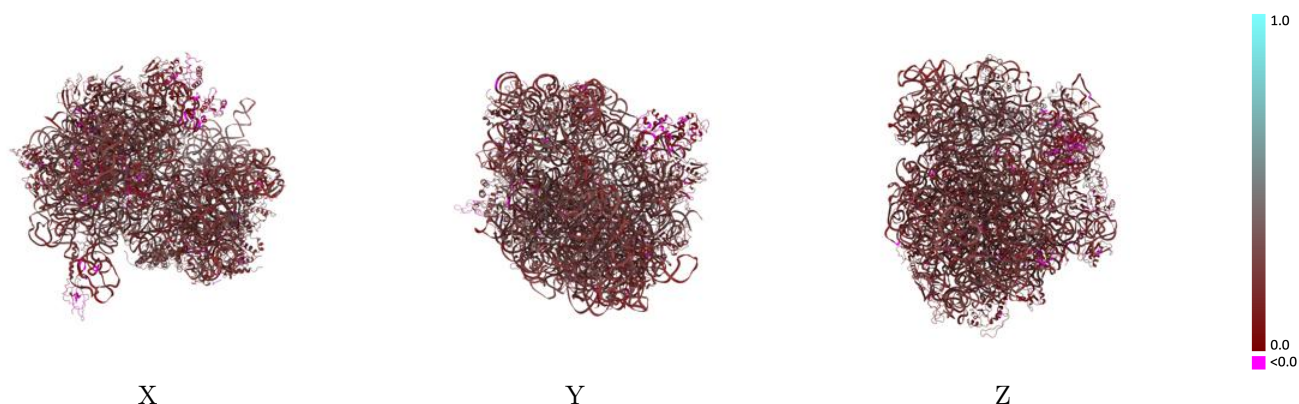
This section contains information regarding the fit between EMDB map EMD-13959 and PDB model 7QGU. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

9.1 Map-model overlay [i](#)



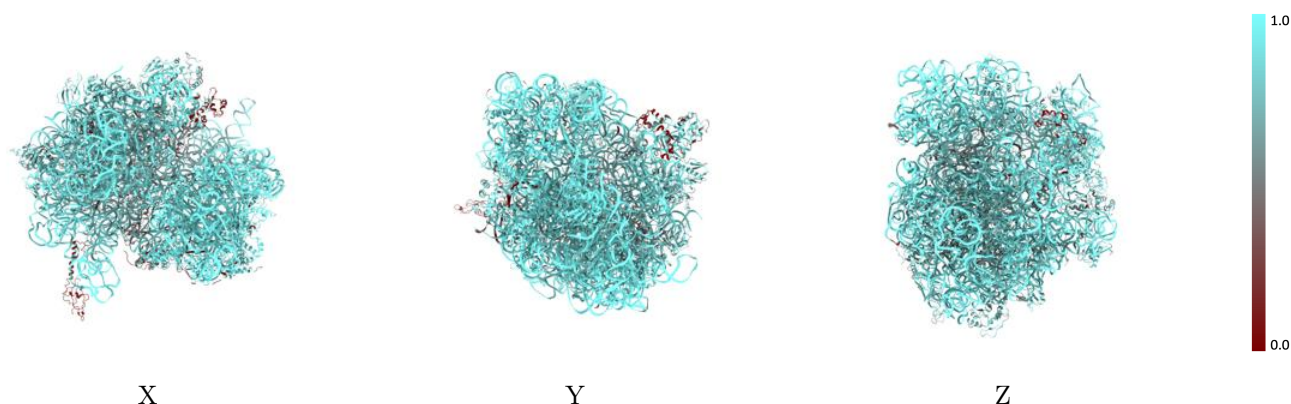
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



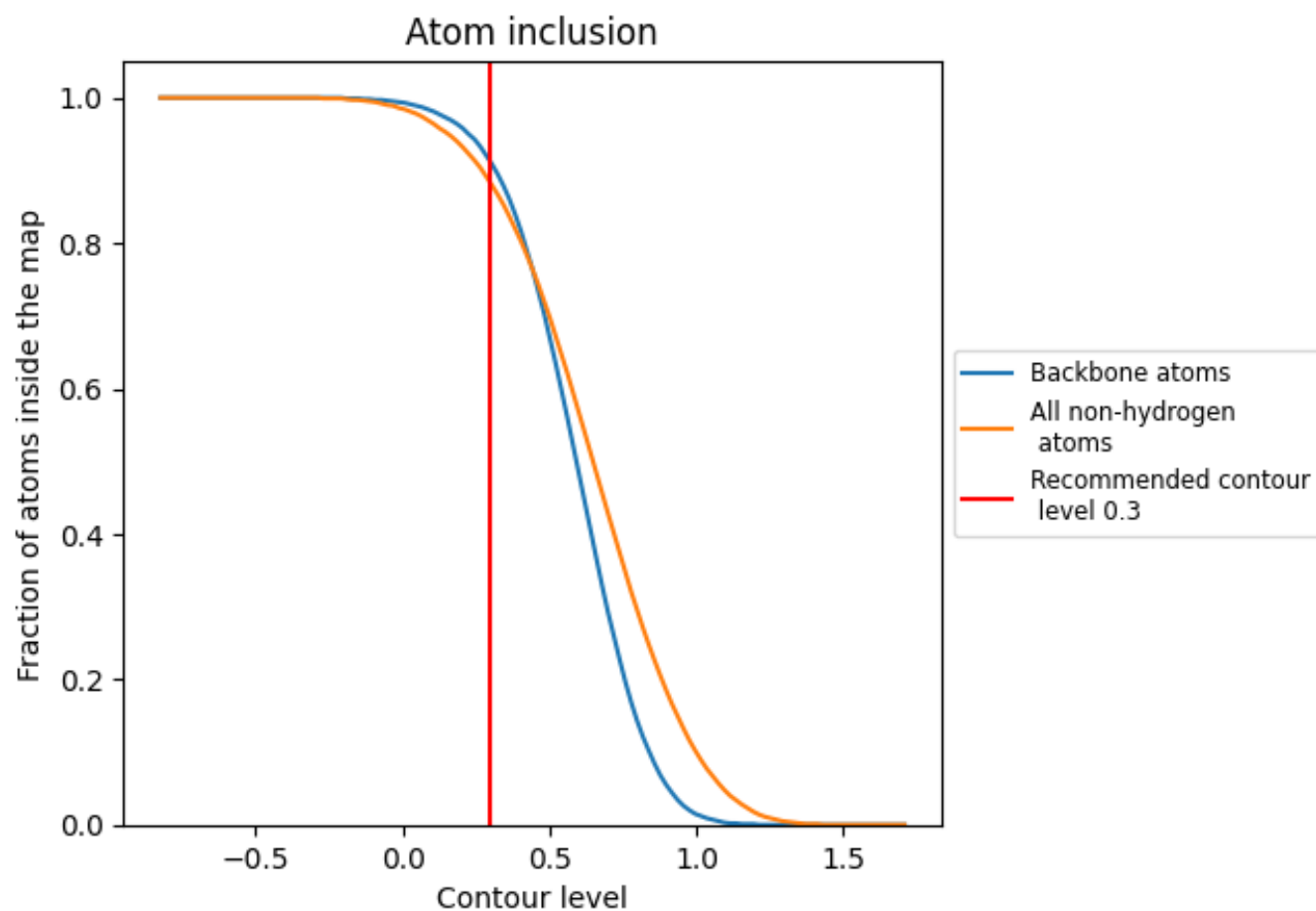
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 88% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8830	 0.2250
2	 0.0380	 0.1920
3	 0.7720	 0.1350
A	 0.9460	 0.2410
B	 0.9770	 0.2340
C	 0.4580	 0.1710
D	 0.7070	 0.1810
E	 0.6430	 0.1760
F	 0.6920	 0.1480
G	 0.8030	 0.1800
H	 0.7230	 0.0760
I	 0.3210	 0.0580
J	 0.7190	 0.1850
K	 0.5130	 0.1810
L	 0.6860	 0.1560
M	 0.6150	 0.1930
N	 0.7360	 0.1580
O	 0.8300	 0.1530
P	 0.6890	 0.1770
Q	 0.7420	 0.1400
R	 0.7680	 0.1870
S	 0.6120	 0.1770
T	 0.7160	 0.1760
U	 0.7340	 0.1640
V	 0.7110	 0.1570
W	 0.9520	 0.2320
X	 0.2320	 0.0990
Y	 0.4280	 0.1200
Z	 0.7020	 0.1510
a	 0.7660	 0.1420
b	 0.6800	 0.1730
c	 0.6180	 0.1400
d	 0.5590	 0.1310
e	 0.6110	 0.1430
f	 0.7380	 0.1730



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Chain	Atom inclusion	Q-score
g	 0.8040	 0.2740
h	 0.9000	 0.2780
i	 0.9650	 0.2740
j	 0.9210	 0.2940
k	 0.6270	 0.2930
l	 0.8790	 0.2850
m	 0.9790	 0.2960
n	 0.9170	 0.2620
o	 0.9270	 0.2700
p	 0.5930	 0.2830
q	 0.8110	 0.2800
r	 0.9120	 0.2550
s	 0.9090	 0.2540
t	 0.9520	 0.2970
u	 0.9610	 0.2840
v	 0.8440	 0.2900
w	 0.5510	 0.2780
x	 0.9520	 0.2850
y	 0.9270	 0.2630
z	 0.8210	 0.2190