



wwPDB EM Validation Summary Report ⓘ

Jun 23, 2026 – 12:52 PM JST

PDB ID : 7D80 / pdb_00007d80
EMDB ID : EMD-30611
Title : Molecular model of the cryo-EM structure of 70S ribosome in complex with peptide deformylase, trigger factor, and methionine aminopeptidase
Authors : Akbar, S.; Bhakta, S.; Sengupta, J.
Deposited on : 2020-10-06
Resolution : 4.10 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:

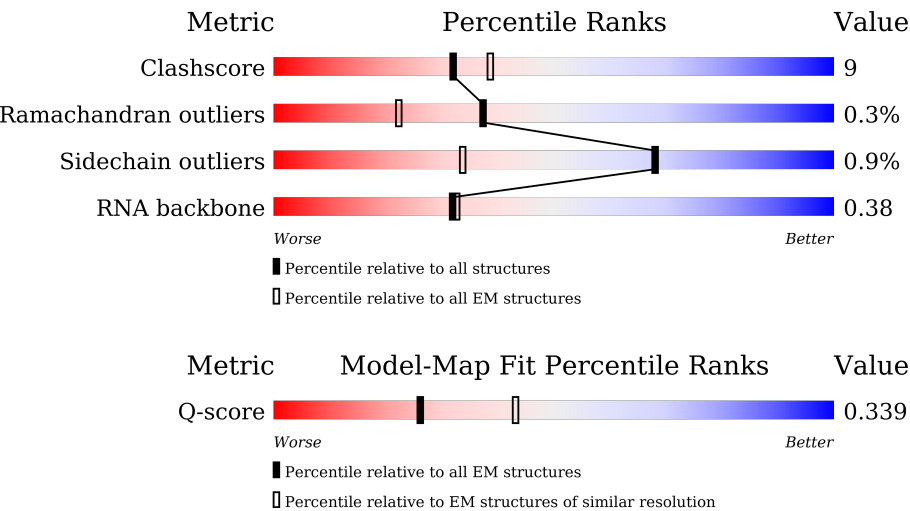
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.10 Å.

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



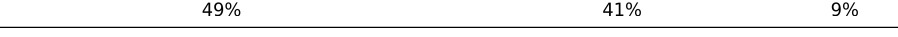
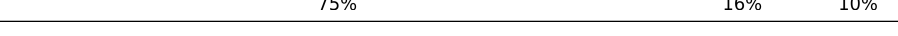
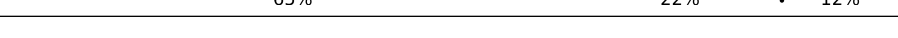
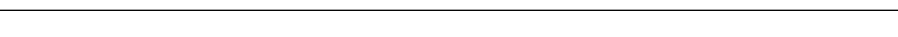
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	6458 (3.60 - 4.60)

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

Mol	Chain	Length	Quality of chain
1	0	46	78% 22%
2	1	65	75% 18% ...
3	2	38	61% 37% .

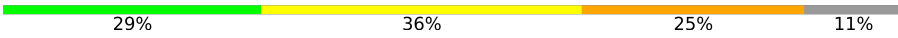
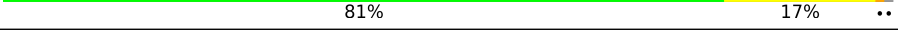
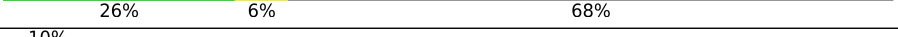
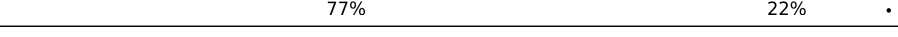
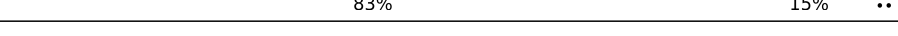
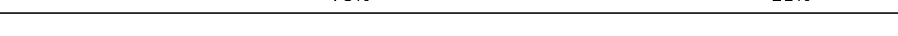
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Mol	Chain	Length	Quality of chain
4	3	169	
5	5	432	
6	6	57	
7	A	2903	
8	B	1539	
9	C	241	
10	D	233	
11	E	206	
12	F	167	
13	G	135	
14	H	179	
15	I	130	
16	J	130	
17	K	103	
18	L	129	
19	M	124	
20	N	118	
21	O	101	
22	P	89	
23	Q	82	
24	R	84	
25	S	75	
26	T	92	
27	U	87	
28	V	71	

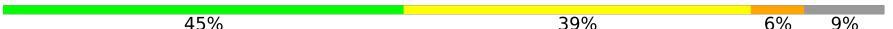
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Mol	Chain	Length	Quality of chain
29	W	100	
30	X	73	
31	Z	76	
32	a	118	
33	b	273	
34	c	209	
35	d	201	
36	e	179	
37	f	177	
38	g	149	
39	h	142	
40	i	142	
41	j	123	
42	k	144	
43	l	136	
44	m	127	
45	n	117	
46	o	115	
47	p	118	
48	q	103	
49	r	110	
50	s	104	
51	t	94	
52	u	85	
53	v	78	

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Mol	Chain	Length	Quality of chain
54	w	63	 78% 22%
55	x	59	 85% 14% .
56	y	77	 45% 39% 6% 9%
57	z	55	 73% 18% 9%

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 150808 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 2 is a protein called 50S ribosomal protein L35.

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

- Molecule 3 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 4 is a protein called Peptide deformylase.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	168	Total	C	N	O	S	0	0
			1346	844	241	255	6		

- Molecule 5 is a protein called Trigger factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	432	Total	C	N	O	S	0	0
			3386	2119	582	674	11		

- Molecule 6 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 7 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	2903	Total	C	N	O	P	0	0
			62317	27801	11467	20147	2902		

- Molecule 8 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	1539	Total	C	N	O	P	0	0
			33015	14725	6052	10699	1539		

- Molecule 9 is a protein called 30S ribosomal protein S2.

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

- Molecule 10 is a protein called 30S ribosomal protein S3.

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

- Molecule 11 is a protein called 30S ribosomal protein S4.

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

- Molecule 12 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	150	Total	C	N	O	S	0	0
			1105	687	211	201	6		

- Molecule 13 is a protein called 30S ribosomal protein S6, fully modified isoform.

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

- Molecule 14 is a protein called 30S ribosomal protein S7.

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

- Molecule 15 is a protein called 30S ribosomal protein S8.

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

- Molecule 16 is a protein called 30S ribosomal protein S9.

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

- Molecule 17 is a protein called 30S ribosomal protein S10.

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

- Molecule 18 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	L	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 19 is a protein called 30S ribosomal protein S12.

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

- Molecule 20 is a protein called 30S ribosomal protein S13.

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

- Molecule 21 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	O	96	Total	C	N	O	S	0	0
			774	483	160	128	3		

- Molecule 22 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	P	88	Total	C	N	O	S	0	0
			710	437	143	129	1		

- Molecule 23 is a protein called 30S ribosomal protein S16.

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

- Molecule 24 is a protein called 30S ribosomal protein S17.

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

- Molecule 25 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	S	55	Total	C	N	O	0	0
			455	288	86	81		

- Molecule 26 is a protein called 30S ribosomal protein S19.

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

- Molecule 27 is a protein called 30S ribosomal protein S20.

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

- Molecule 28 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	V	51	Total	C	N	O	S	0	0
			425	265	86	73	1		

- Molecule 29 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	W	96	Total	C	N	O	S	0	0
			764	484	142	136	2		

- Molecule 30 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	X	65	Total	C	N	O	P	0	0
			1392	621	258	449	64		

- Molecule 31 is a RNA chain called A-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Z	66	Total	C	N	O	P	0	0
			1406	629	255	457	65		

- Molecule 32 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	a	118	Total	C	N	O	P	0	0
			2529	1126	464	821	118		

- Molecule 33 is a protein called 50S ribosomal protein L2.

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

- Molecule 34 is a protein called 50S ribosomal protein L3.

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

- Molecule 35 is a protein called 50S ribosomal protein L4.

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

- Molecule 36 is a protein called 50S ribosomal protein L5.

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

- Molecule 37 is a protein called 50S ribosomal protein L6.

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

- Molecule 38 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	g	47	Total	C	N	O	S	0	0
			359	233	62	63	1		

- Molecule 39 is a protein called 50S ribosomal protein L11.

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

- Molecule 40 is a protein called 50S ribosomal protein L13.

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

- Molecule 41 is a protein called 50S ribosomal protein L14.

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

- Molecule 42 is a protein called 50S ribosomal protein L15.

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

- Molecule 43 is a protein called 50S ribosomal protein L16.

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

- Molecule 44 is a protein called 50S ribosomal protein L17.

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

- Molecule 45 is a protein called 50S ribosomal protein L18.

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

- Molecule 46 is a protein called 50S ribosomal protein L19.

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

- Molecule 47 is a protein called 50S ribosomal protein L20.

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

- Molecule 48 is a protein called 50S ribosomal protein L21.

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

- Molecule 49 is a protein called 50S ribosomal protein L22.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L25.

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

- Molecule 52 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	u	75	Total	C	N	O	S	0	0
			569	353	113	102	1		

- Molecule 53 is a protein called 50S ribosomal protein L28.

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

- Molecule 54 is a protein called 50S ribosomal protein L29.

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

- Molecule 55 is a protein called 50S ribosomal protein L30.

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

- Molecule 56 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	y	70	Total	C	N	O	P	0	0
			1496	665	267	494	70		

- Molecule 57 is a protein called 50S ribosomal protein L33.

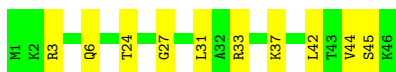
Mol	Chain	Residues	Atoms				AltConf	Trace
57	z	50	Total	C	N	O	0	0
			409	263	75	71		

3 Residue-property plots [i](#)

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

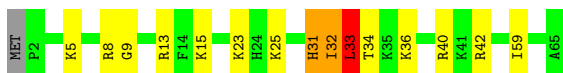
- Molecule 1: 50S ribosomal protein L34

Chain 0:  78% 22%



- Molecule 2: 50S ribosomal protein L35

Chain 1:  75% 18% . . .



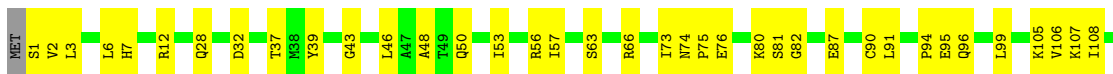
- Molecule 3: 50S ribosomal protein L36

Chain 2:  61% 37% .



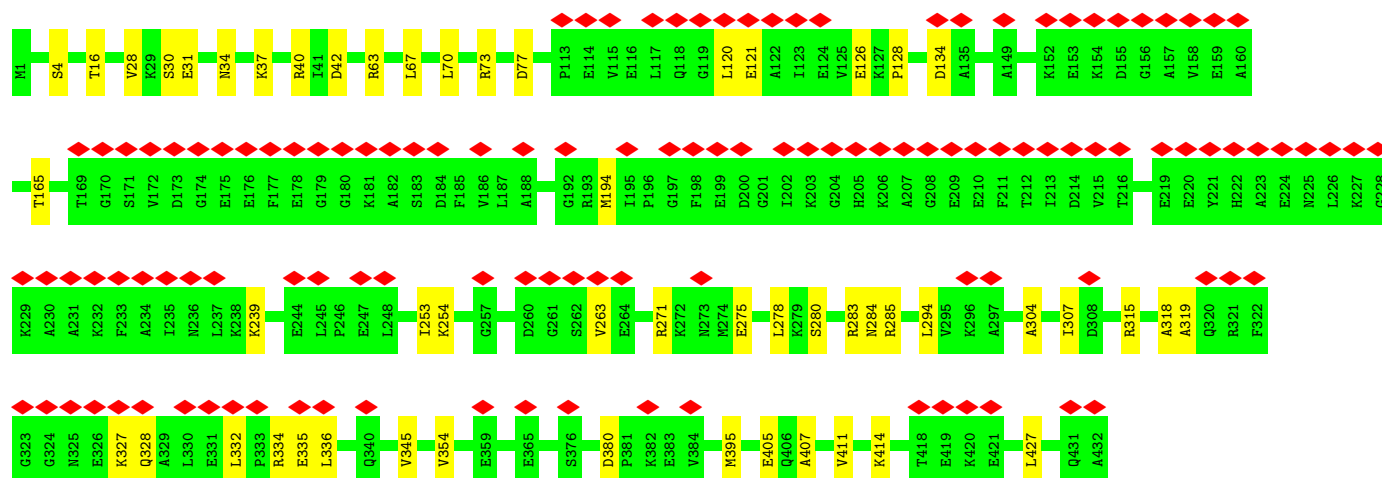
- Molecule 4: Peptide deformylase

Chain 3:  71% 28% .

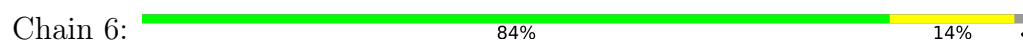


- Molecule 5: Trigger factor

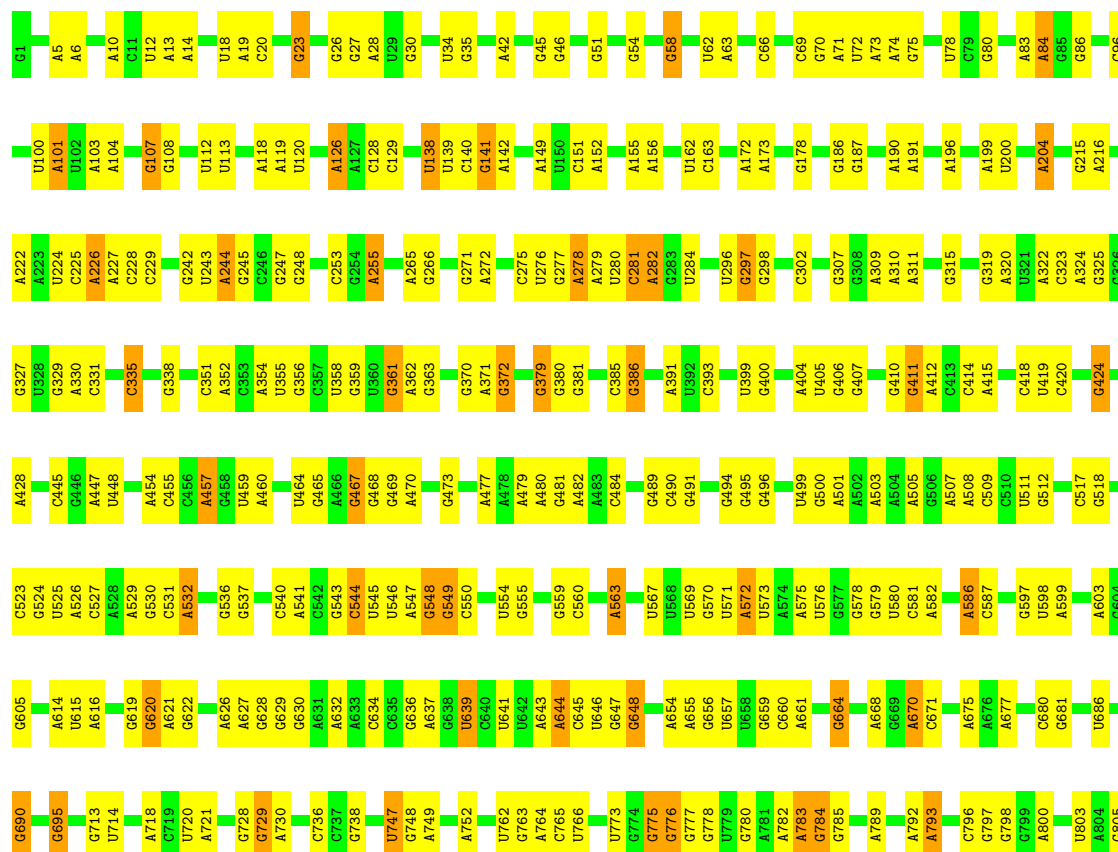
Chain 5:  28% 88% 12%



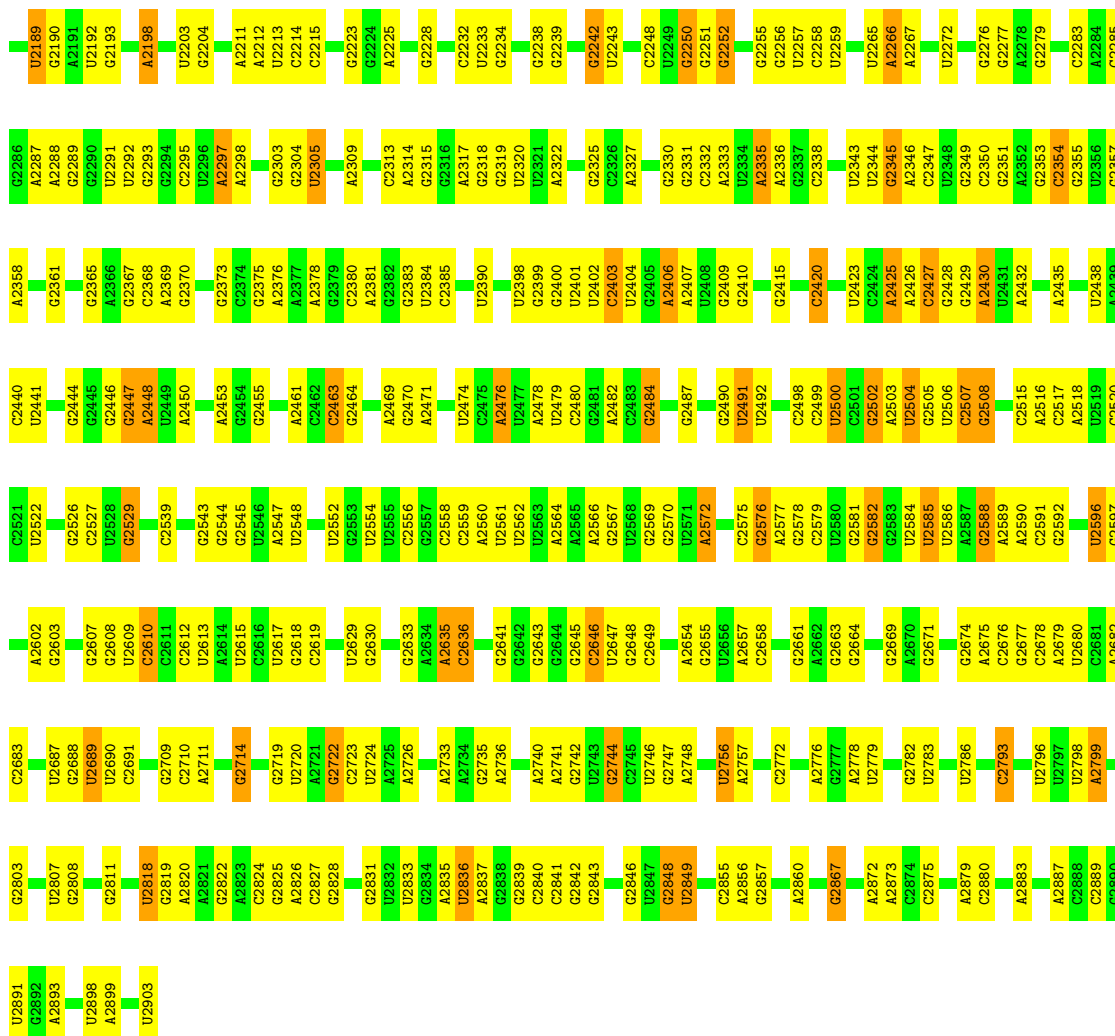
- Molecule 6: 50S ribosomal protein L32



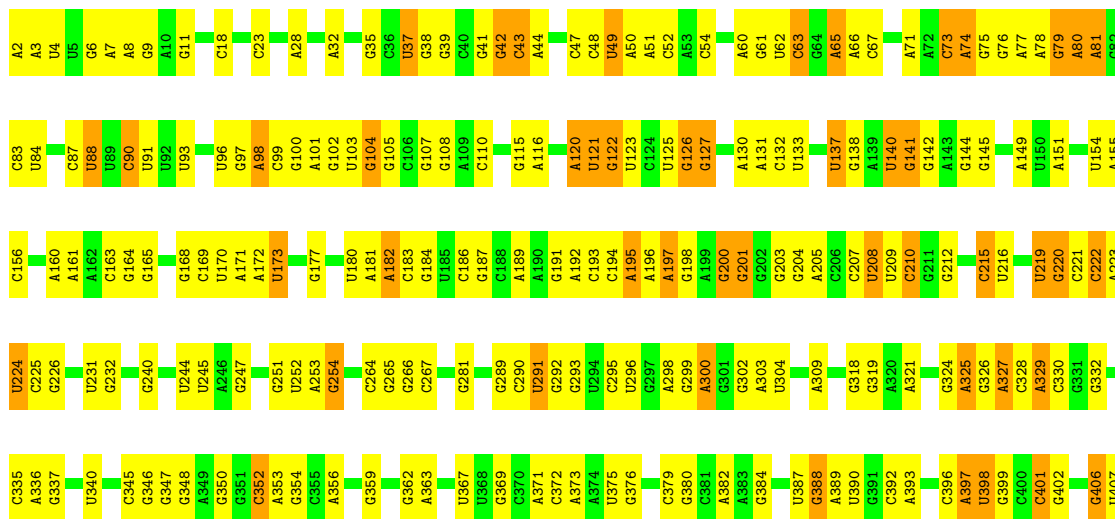
- Molecule 7: 23S ribosomal RNA

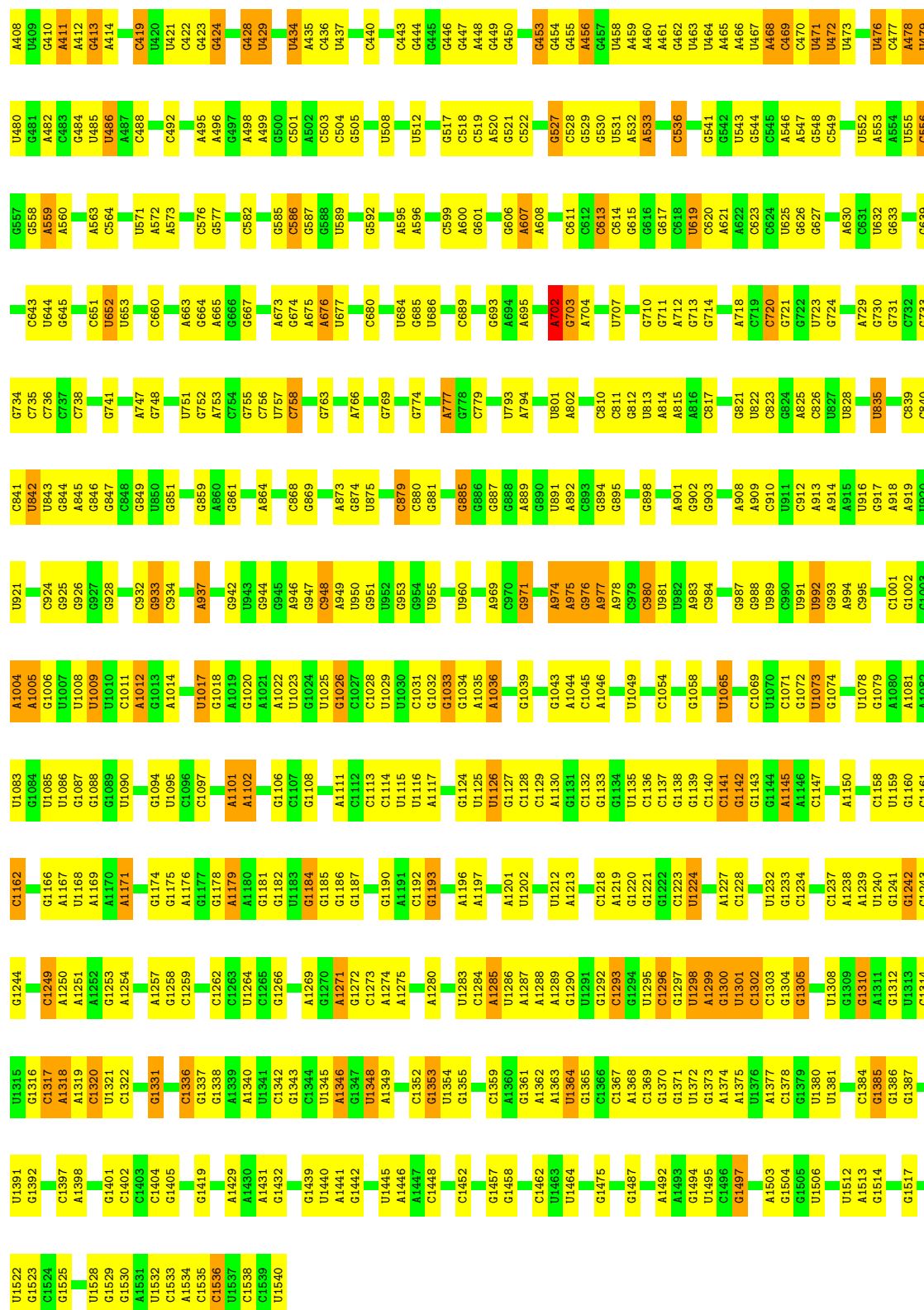


A2114	A2033	A1953	G1817	G1730	A1632	G1537	A1433	G1349	G1256	C1161	A1077	G989	G907	C806
G2115	U2034	G1954	U1818	G1731	A1635	G1540	A1434	C1349	C1257	G1162	U1078	A990	C908	U807
G2116	G2035	U1955	A1819	U1636	U1636	G1541	C1437	U1352	U1258	G1163	A1080	C991	A909	U811
A2117	C2036	U1956	C1822	A1637	A1637	G1542	C1437	U1352	U1258	C1164	U1081	G993	A910	C812
U2118						G1543	C1451	G1355	U1263	G1165	G1087	C994	A911	C912
A2119	U2039	A1960	U1825	G1738	A1641	G1544	C1452	G1356	A1264	C1167	A1088	C995	U913	A819
G2120	G2040	U1963	G1826	G1743	G1642	A1544	A1453	G1357	A1265	G1168	A1089	A996	G914	A820
U2121	A2041	G1964	U1827				C1454	C1358	G1266	A1169	U1091	U999	A917	U827
G2122	A2042	U1965	G1828	G1748	C1646	G1545	G1455	G1359	C1270	C1170	A1090	U999	A917	U828
G2123	C2043	C1965	A1829	A1749	U1647	C1561	G1456	A1359	A1272	G1171	G1002	G1003	C921	A829
G2124	A1966	U1966	C1830	G1750	U1648	U1562	G1457	G1360	A1273	C1172	U1097	U1004	C922	G830
G2125	G2049	C1967	G1831		G1649		U1458	C1362	U1273	U1173	A1098	C1005	G923	G831
A2126				G1753	A1650	A1566	C1459	C1363		U1174	U1098		G924	G832
G2127	A2052	U1970	C1832		G1651	G1567	U1460	G1364	C1278	U1175	A1099	C1009	U929	A833
G2128	G2053	U1971	U1833	G1756	A1652	G1568	C1461	G1365	G1279	U1176	U1101			A834
C2129	A2054	G1972	G1835	U1757	G1653	A1569	U1466	A1366	G1283	C1177	G1102	U1012	U832	G841
U2130	C2055			U1758					A1284	U1179	A1103	U1012	U832	G841
U2131	G2056	G1980	G1845		C1658	C1577	U1471	G1369	A1285	U1180	C1104	C1013	C935	A845
U2132		A1981	G1846	G1781		U1578		G1370	A1286	U1181	U1105	A1021	A941	U846
G2133	A2059	U1982	A1847		G1666	G1581	G1478	G1370	A1287	U1182	G1106	U1022	U847	U847
A2134	A2060	G1983	U1848	C1764	G1667	C1582	G1479	G1371	U1294	U1183	G1110	G942	A943	G858
A2135	G2061	G1984	G1849	U1777	A1668	U1583	C1480	U1372	U1295	U1184	G1111	U1023		G859
G2136	A2062	C1985	G1850	U1778	A1669	U1584	U1481	U1375	G1296	G1185	G1112	G1026		
U2137	C2063			G1770		C1585	G1482	C1376	C1297	G1187				
G2140	C2064	G1989	U1855		G1674				C1298	U1188	G1115	G1031	C946	A863
G2141	C2065	U1991	U1856	A1773	C1675	A1590	A1490	U1379	G1299	U1189	G1116	A1032	A947	G864
G2144	U2068	G1992	G1864	G1774	A1676	A1591	G1491	G1380	G1300	G1190	U1119	G1037	G953	C873
C2145	A2070	U1993	U1865	U1775	A1677	A1591	G1492	G1380	G1301	G1191	C1120	G1038	G954	A877
C2146	A2071	U1995	G1869	U1777	A1678	C1592	G1493	A1383	A1302	G1195	C1121	G1039	U955	G878
A2147	C2072	C1996	C1870	U1778	A1679	G1595	A1494	A1383	A1303	G1195	C1122	A1039	G956	G880
	U2075	C1997	A1871	U1779	U1683	A1596	U1495	C1386	A1304	G1195	U1130	G1040	C962	G881
G2152		A1998	A1872	U1780	G1684	A1597	A1496	G1388	A1305	A1204	U1131	G1045	C963	G882
G2156	U2079	C2000	G1873	U1781	A1690	A1598	G1500	G1389	G1309	C1208	G1125	G1046	C964	G883
G2157			U1882	A1783	U1693	U1602	A1501	A1392	G1310	U1209	A1126	A1047	C965	G884
A2158	G2087	G2002		A1784	C1694	A1603	A1502	A1392	G1311	G1210		C1047	C965	C885
G2159	A2088	C2001	G1904	A1791	U1698	A1604	A1503	A1395	U1316	G1212	A1129	G1056	C968	A886
C2160	C2089	A2009	C1905	G1792	A1698	C1607	A1508	U1396	U1316	G1212	U1130	U1061	G969	U887
G2162	A2090	G2010	G1907			A1608	A1509	U1397	G1325	G1211	U1131	G1062	U970	C888
A2163	G2093	U2011	A1913	U1796	A1701	A1609	G1510	C1398	U1326	G1223	U1132	C1064	G971	C889
C2165	A2095	A2013	C1914	U1798	G1702	G1610	G1511	G1401	U1327	G1218	U1133	U1065	A972	C890
U2166	C2096	A2012	G1919	G1799	G1703	C1611	G1512	U1402	A1328	A1237	G1138	U1066	A973	G891
U2167	A2097	U2016	A1919	C1800	A1705	A1616	G1513	A1403	G1329	G1238	G1139	U1067	A974	A892
G2168	U2098	U2017		A1801	A1705	C1617	G1514	A1403	U1329	G1238		U1067	A975	C893
A2169	U2099	U2021	U1926	A1802	C1708	A1618	U1523	U1411	G1337	C1243	A1142	G1068	G976	U894
A2170	G2100	C2022	G1929	C1806	U1709	G1619	G1524	U1412	G1337		A1143	G1069	A980	U895
A2171	A2101	U2023	G1930	G1807	A1711	G1622	G1527	A1413	G1338	A1247	A1144	A1070	A981	C897
A2173	G2107	G2024	A1936	A1809			C1625	G1416	U1339	G1248	C1145	C1072	C982	C898
C2174	C2025	C2025	U1944	G1811	U1714	A1626	G1529	G1421	U1340		C1146	A1073	A883	A899
C2175	U2109	U2026	U1944	G1811	U1715	G1627	G1533	C1428	G1341	G1252	A1147	G1074	A984	
G2110	G2110	G2027	G1945		A1717	G1628	U1535	U1428	G1341	A1253		C1075	C985	G904
U2111	U2111	A2030	U1946	G1814	G1718	U1629	U1535	A1431	G1343	A1254	G1157			
G2112	G2112	A2031	U1946	G1815	U1718	U1629	U1535	A1431	G1343	A1254				
A2183	U2113	G2032	A1952	C1816	U1729	G1631	C1536	G1432	U1344	U1255				



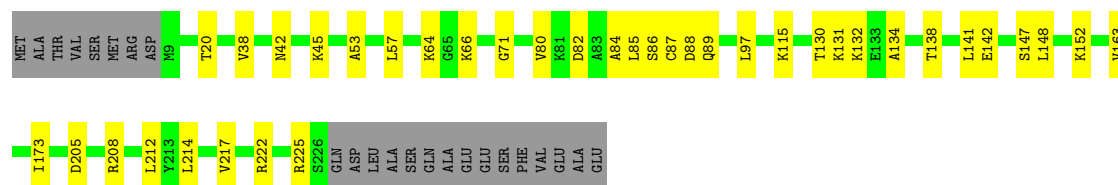
- Molecule 8: 16S ribosomal RNA





● Molecule 9: 30S ribosomal protein S2

Chain C: 75% 16% 10%



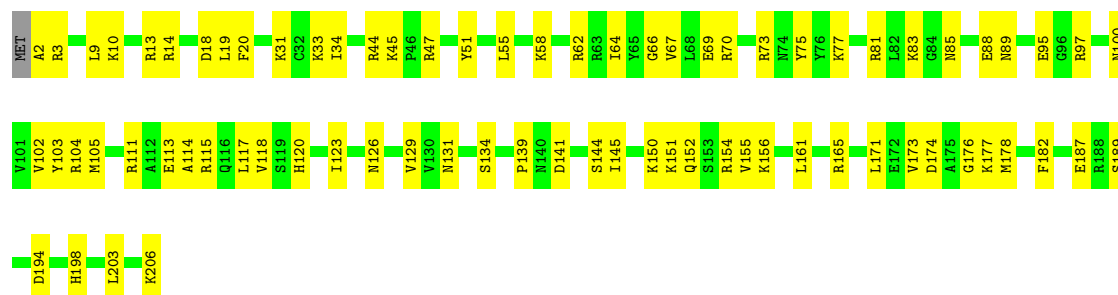
- Molecule 10: 30S ribosomal protein S3

Chain D: 65% 22% 12%



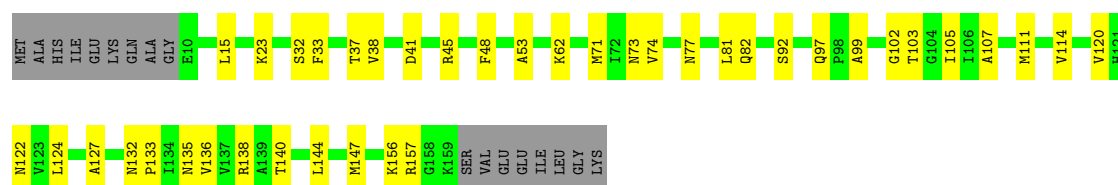
- Molecule 11: 30S ribosomal protein S4

Chain E: 63% 37%



- Molecule 12: 30S ribosomal protein S5

Chain F: 66% 24% 10%



- Molecule 13: 30S ribosomal protein S6, fully modified isoform

Chain G: 54% 20% 26%



ASP
ASP
PHE
ALA
ASN
GLU
THR
ALA
ASP
ASP
ALA
GLU
ALA
GLY
ASP
SER
SER
GLU
GLU
GLU
GLU
GLU

• Molecule 14: 30S ribosomal protein S7

Chain H: 60% 24% 16%

MET P2 R3 R4 R5 V6 I7 P16 E21 A24 K25 F26 N28 K31 K35 V43 L47 A51 S57 E58 A65 M68 V69 R70 P71 K76 R79 V89 R96 N97 A108 R111 G112 D113 K114 S115 M116 A117 L118 R119 L120 A121

N122 E123 D126 A127 A128 E129 N130 D140 R143 A152 HIS TYR ARG TRP LEU SER LEU ARG SER PHE SER HIS GLN ALA GLY ALA SER SER LYS GLN PRO ALA LEU GLY TYR LEU ASN

• Molecule 15: 30S ribosomal protein S8

Chain I: 66% 33% .

MET S2 M3 Q4 D5 P6 I7 A8 D9 M10 L11 I14 A15 M16 M27 P28 S29 S30 K31 L32 K33 V34 K41 F45 F49 L59 K64 K67 G68 K69 A70 V71 S74 I75 Q76 R77 R84 K87 R88 A102 V103 V104 S105 D113 R117

E124 I125 I126 C127 Y128 V129 A130

• Molecule 16: 30S ribosomal protein S9

Chain J: 65% 32% ..

MET ALA GLU M4 Q5 Y6 T9 R12 K13 R18 V19 K22 P23 G24 P25 G26 K27 L28 V29 I30 R45 R49 L52 E53 L54 D56 V57 V58 E59 K60 L61 D62 L63 L64 I65 T66 G74 T83 T84 R85 E89 Y90 D91 R95 L98 G102

R106 D107 K120 A121 R122 R123 P125 Q126 F127 S128 K129 R130

• Molecule 17: 30S ribosomal protein S10

Chain K: 68% 26% . 5%

MET GLN ASN GLN R5 I6 R7 A12 F13 L14 H15 I18 P41 L42 P43 T44 R45 K46 E47 S54 P55 H56 V57 N58 R62 D63 Q64 Y65 E66 T69 H70 L71 L72 T80 T83 V84 D85 M88 R89 L102 GLY

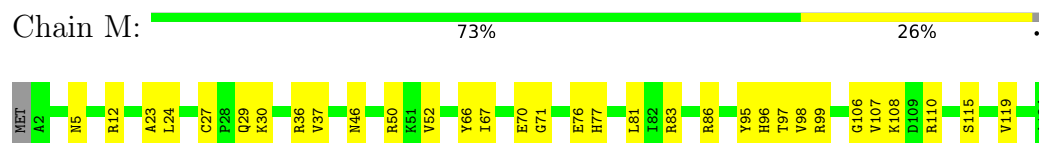
• Molecule 18: 30S ribosomal protein S11

Chain L: 69% 22% 9%

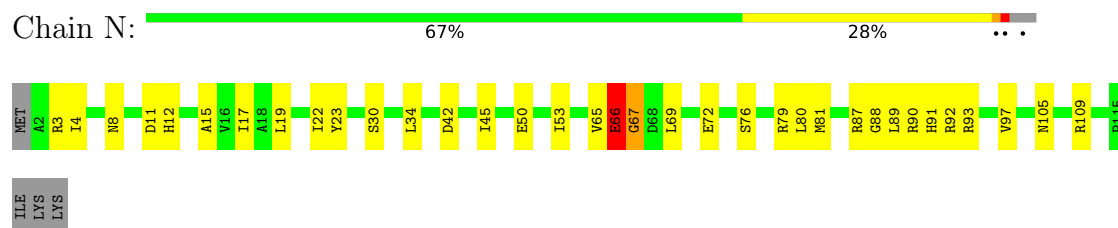
MET ALA LYS ALA PRO ILE ARG ARG ARG LYS ARG VAL R13 S17 V20 A21 H22 I23 V32 T33 N40 W44 R53 G54 S55 S58 E76 I79 E83 W84 W85 V86 K87 R93 N101 R106 I107 D112 V113 P117 R122 K126 R127

R128 V129

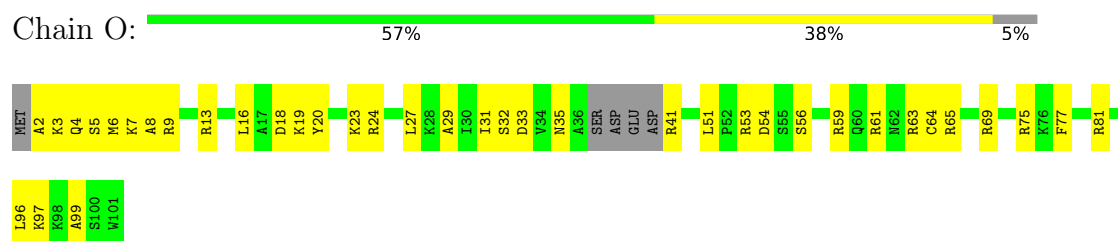
• Molecule 19: 30S ribosomal protein S12



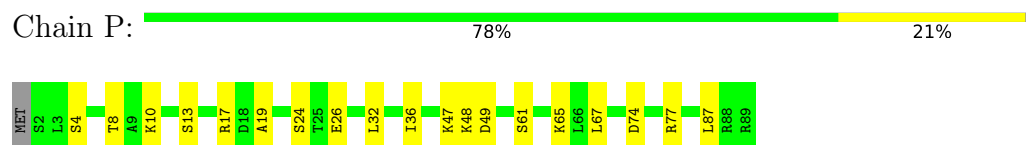
- Molecule 20: 30S ribosomal protein S13



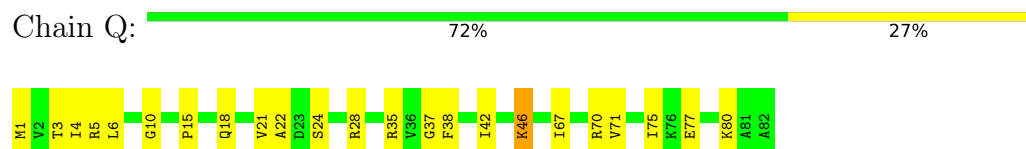
- Molecule 21: 30S ribosomal protein S14



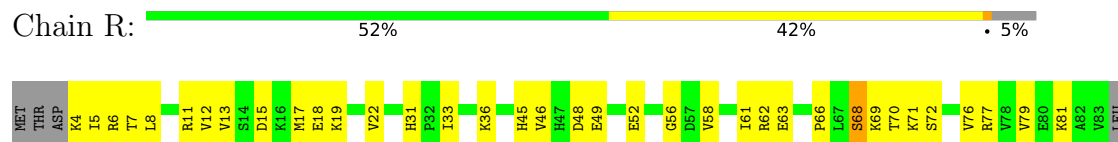
- Molecule 22: 30S ribosomal protein S15



- Molecule 23: 30S ribosomal protein S16

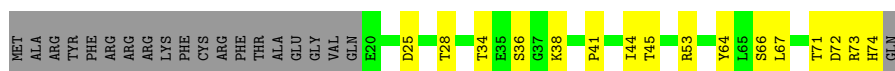


- Molecule 24: 30S ribosomal protein S17

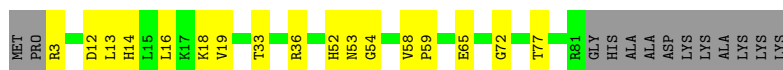


- Molecule 25: 30S ribosomal protein S18





- Molecule 26: 30S ribosomal protein S19



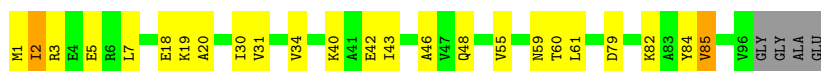
- Molecule 27: 30S ribosomal protein S20



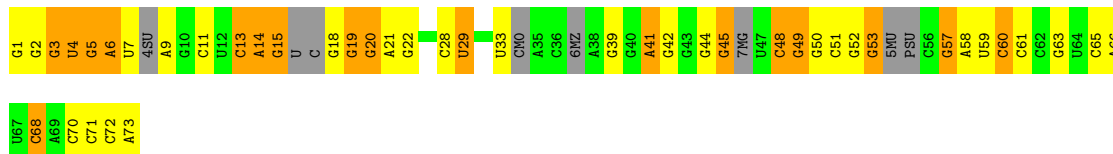
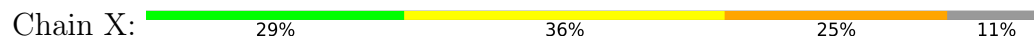
- Molecule 28: 30S ribosomal protein S21



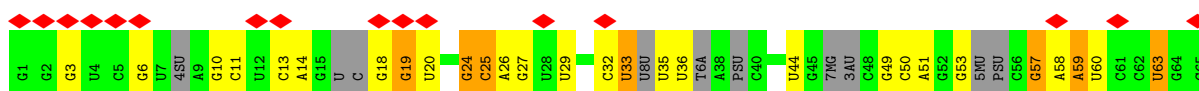
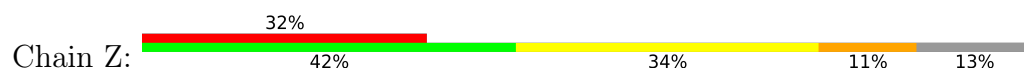
- Molecule 29: 50S ribosomal protein L23

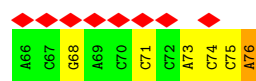


- Molecule 30: E-site tRNA



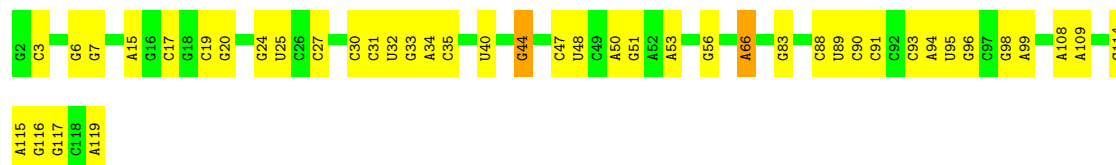
- Molecule 31: A-site tRNA





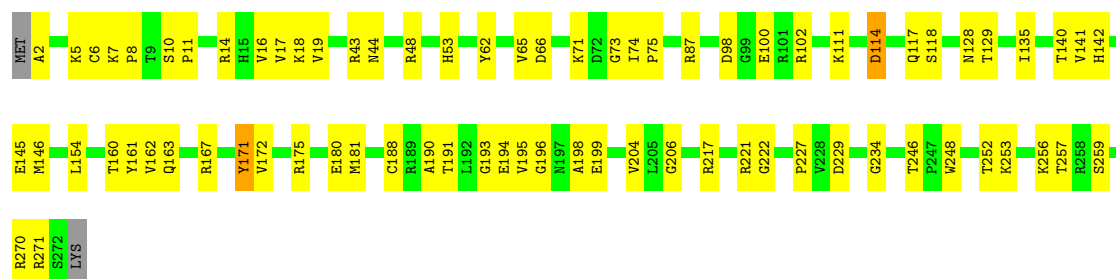
• Molecule 32: 5S ribosomal RNA

Chain a: 64% 35%



• Molecule 33: 50S ribosomal protein L2

Chain b: 71% 27%



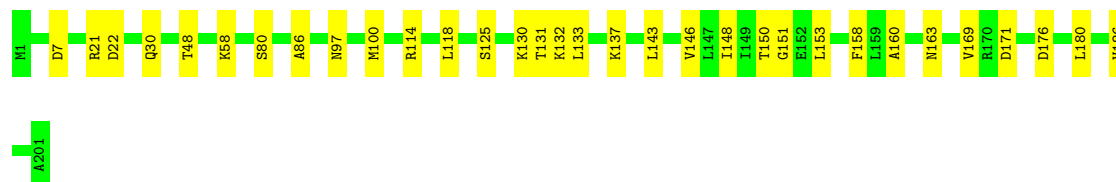
• Molecule 34: 50S ribosomal protein L3

Chain c: 78% 21%



• Molecule 35: 50S ribosomal protein L4

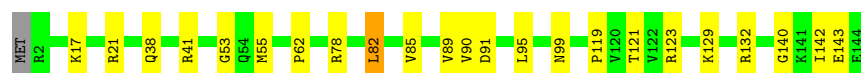
Chain d: 84% 16%



• Molecule 36: 50S ribosomal protein L5

Chain e: 63% 36%

Chain k:  83% 15% ..



- Molecule 43: 50S ribosomal protein L16

Chain l:  81% 18% .



- Molecule 44: 50S ribosomal protein L17

Chain m:  76% 19% 6%



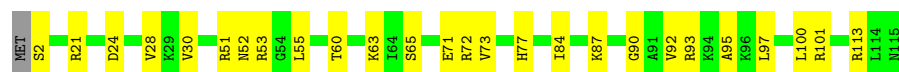
- Molecule 45: 50S ribosomal protein L18

Chain n:  83% 16% .



- Molecule 46: 50S ribosomal protein L19

Chain o:  77% 23% .



- Molecule 47: 50S ribosomal protein L20

Chain p:  78% 21% .



- Molecule 48: 50S ribosomal protein L21

Chain q:  83% 17%



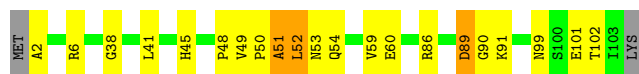
- Molecule 49: 50S ribosomal protein L22

Chain r:  81% 18%



- Molecule 50: 50S ribosomal protein L24

Chain s:  78% 17%



- Molecule 51: 50S ribosomal protein L25

Chain t:  86% 13%



- Molecule 52: 50S ribosomal protein L27

Chain u:  81% 7% 12%



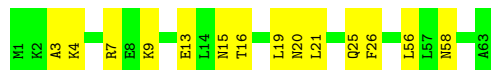
- Molecule 53: 50S ribosomal protein L28

Chain v:  74% 24%



- Molecule 54: 50S ribosomal protein L29

Chain w:  78% 22%



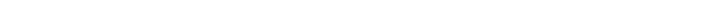
- Molecule 55: 50S ribosomal protein L30

Chain x:  85% 14%



- Molecule 56: P-site tRNA

G1	G2	A3	G7	A5U	A9	G10	G13	U16	G17	G17A	G18	U19	U20	A21	G22	A26	U29	G30	U30	U33	G35	G36	2NA	G38	G39	G45	7MG	U47	G48	G49	C50	C51	G52	G53	SKU	PSU	C56	G57	G64	PSU	C66	C67	G68	U69	U70	C71	C72	G73	C74	C75	A76
----	----	----	----	-----	----	-----	-----	-----	-----	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Chain z:  73% 18% 9%

MET
ALA
LYS
G4
I5
R6
K10
T17
G18
T22
K33
L34
R44
E51
A52
K53
ILE
LYS

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	54875	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 ($e^-/\text{\AA}^2$)	32.57	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.093	Depositor
Minimum map value	-0.024	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.005	Depositor
Map size (Å)	441.6, 441.6, 441.6	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.38, 1.38, 1.38	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	0	0.79	0/380	0.76	0/498
2	1	0.66	0/513	0.86	1/676 (0.1%)
3	2	0.57	0/303	0.66	0/397
4	3	0.25	0/1361	0.58	0/1830
5	5	0.21	0/3426	0.52	0/4605
6	6	0.66	0/450	0.76	0/599
7	A	0.72	0/69796	0.52	0/108888
8	B	0.36	0/36966	0.40	1/57666 (0.0%)
9	C	0.32	0/1735	0.57	0/2338
10	D	0.27	0/1651	0.57	0/2225
11	E	0.27	0/1665	0.61	0/2227
12	F	0.36	0/1118	0.71	2/1504 (0.1%)
13	G	0.29	0/835	0.66	0/1128
14	H	0.24	0/1195	0.54	0/1602
15	I	0.33	0/989	0.55	0/1326
16	J	0.24	0/1034	0.60	0/1375
17	K	0.26	0/796	0.64	0/1077
18	L	0.31	0/893	0.60	0/1205
19	M	0.35	0/969	0.65	0/1300
20	N	0.25	0/892	0.62	1/1193 (0.1%)
21	O	0.25	0/785	0.58	0/1043
22	P	0.34	0/718	0.61	0/959
23	Q	0.30	0/659	0.59	0/884
24	R	0.33	0/657	0.66	0/881
25	S	0.30	0/462	0.64	2/621 (0.3%)
26	T	0.23	0/652	0.50	0/877
27	U	0.31	0/671	0.61	0/888
28	V	0.35	0/430	0.87	0/570
29	W	0.63	0/771	0.76	0/1031
30	X	0.20	0/1551	0.38	0/2404
31	Z	0.23	0/1565	0.37	0/2421
32	a	0.51	0/2828	0.40	0/4410
33	b	0.70	0/2121	0.72	0/2852
34	c	0.67	0/1586	0.69	0/2134

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	d	0.69	0/1571	0.65	0/2113
36	e	0.31	0/1434	0.56	0/1926
37	f	0.43	0/1343	0.56	0/1816
38	g	0.41	0/364	0.74	0/490
39	h	0.28	0/1046	0.65	1/1410 (0.1%)
40	i	0.71	0/1152	0.68	2/1551 (0.1%)
41	j	0.65	0/947	0.77	0/1268
42	k	0.66	0/1054	0.82	0/1403
43	l	0.63	0/1093	0.73	0/1460
44	m	0.71	0/973	0.86	0/1301
45	n	0.45	0/902	0.58	0/1209
46	o	0.61	0/929	0.69	0/1242
47	p	0.78	0/960	0.71	0/1278
48	q	0.64	0/829	0.68	0/1107
49	r	0.71	0/864	0.70	0/1156
50	s	0.56	0/787	0.69	0/1051
51	t	0.53	0/766	0.54	0/1025
52	u	0.63	0/576	0.61	0/762
53	v	0.67	0/635	0.66	0/848
54	w	0.56	0/510	0.65	0/677
55	x	0.65	0/453	0.71	0/605
56	y	0.21	0/1664	0.35	0/2577
57	z	0.41	0/416	0.57	0/554
All	All	0.57	0/163691	0.53	10/244463 (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
2	1	0	1
3	2	0	1
9	C	0	1
11	E	0	2
12	F	0	2
13	G	0	1
16	J	0	2
17	K	0	1
19	M	0	1
20	N	0	1
23	Q	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
24	R	0	2
28	V	0	2
29	W	0	1
34	c	0	1
37	f	0	2
41	j	0	1
42	k	0	1
43	l	0	1
50	s	0	3
All	All	0	28

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	S	67	LEU	CA-C-N	7.08	138.87	122.31
25	S	67	LEU	C-N-CA	7.08	138.87	122.31
39	h	109	ILE	N-CA-C	-6.89	105.78	111.91
2	1	32	ILE	N-CA-C	6.32	122.49	109.34
12	F	77	ASN	CA-C-N	5.89	132.78	121.54

There are no chirality outliers.

5 of 28 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	1	31	HIS	Peptide
3	2	20	ASP	Peptide
9	C	84	ALA	Peptide
11	E	173	VAL	Peptide
11	E	20	PHE	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	377	0	418	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	1	504	0	572	13	0
3	2	302	0	343	13	0
4	3	1346	0	1394	31	0
5	5	3386	0	3403	34	0
6	6	444	0	458	7	0
7	A	62317	0	31343	644	0
8	B	33015	0	16617	383	0
9	C	1704	0	1732	26	0
10	D	1624	0	1696	34	0
11	E	1643	0	1707	59	0
12	F	1105	0	1148	29	0
13	G	817	0	808	18	0
14	H	1181	0	1238	34	0
15	I	979	0	1031	33	0
16	J	1022	0	1070	33	0
17	K	786	0	828	22	0
18	L	877	0	887	22	0
19	M	955	0	1016	23	0
20	N	883	0	941	26	0
21	O	774	0	824	33	0
22	P	710	0	728	13	0
23	Q	649	0	666	18	0
24	R	648	0	691	25	0
25	S	455	0	478	15	0
26	T	637	0	665	13	0
27	U	665	0	714	17	0
28	V	425	0	449	9	0
29	W	764	0	829	19	0
30	X	1392	0	714	24	0
31	Z	1406	0	722	25	0
32	a	2529	0	1281	17	0
33	b	2082	0	2154	50	0
34	c	1565	0	1616	33	0
35	d	1552	0	1619	21	0
36	e	1410	0	1444	47	0
37	f	1323	0	1371	18	0
38	g	359	0	381	6	0
39	h	1032	0	1085	22	0
40	i	1129	0	1162	18	0
41	j	938	0	1012	22	0
42	k	1045	0	1117	18	0
43	l	1074	0	1157	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	m	960	0	1000	18	0
45	n	892	0	923	16	0
46	o	917	0	962	21	0
47	p	947	0	1019	19	0
48	q	816	0	839	14	0
49	r	857	0	922	14	0
50	s	779	0	831	12	0
51	t	753	0	780	10	0
52	u	569	0	581	3	0
53	v	625	0	652	14	0
54	w	509	0	543	13	0
55	x	449	0	488	5	0
56	y	1496	0	764	14	0
57	z	409	0	440	7	0
All	All	150808	0	102273	1872	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 9.

The worst 5 of 1872 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)
7:A:2506:U:O2'	7:A:2507:C:O4'	1.56	1.19
8:B:98:A:H2'	8:B:99:C:C6	1.85	1.11
7:A:2572:A:N6	34:c:150:GLN:OE1	1.93	1.02
7:A:2508:G:OP1	31:Z:76:A:O5'	1.82	0.95
7:A:2507:C:O2'	31:Z:76:A:C1'	2.14	0.95

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	
1	0	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
2	1	62/65 (95%)	51 (82%)	9 (14%)	2 (3%)	3	24
3	2	36/38 (95%)	30 (83%)	5 (14%)	1 (3%)	4	27
4	3	166/169 (98%)	145 (87%)	21 (13%)	0	100	100
5	5	430/432 (100%)	387 (90%)	43 (10%)	0	100	100
6	6	54/57 (95%)	45 (83%)	8 (15%)	1 (2%)	6	34
9	C	216/241 (90%)	178 (82%)	38 (18%)	0	100	100
10	D	204/233 (88%)	176 (86%)	28 (14%)	0	100	100
11	E	203/206 (98%)	179 (88%)	24 (12%)	0	100	100
12	F	148/167 (89%)	114 (77%)	34 (23%)	0	100	100
13	G	98/135 (73%)	84 (86%)	14 (14%)	0	100	100
14	H	149/179 (83%)	138 (93%)	11 (7%)	0	100	100
15	I	127/130 (98%)	119 (94%)	8 (6%)	0	100	100
16	J	125/130 (96%)	111 (89%)	14 (11%)	0	100	100
17	K	96/103 (93%)	84 (88%)	12 (12%)	0	100	100
18	L	115/129 (89%)	92 (80%)	23 (20%)	0	100	100
19	M	121/124 (98%)	95 (78%)	26 (22%)	0	100	100
20	N	112/118 (95%)	97 (87%)	13 (12%)	2 (2%)	6	35
21	O	92/101 (91%)	81 (88%)	11 (12%)	0	100	100
22	P	86/89 (97%)	78 (91%)	8 (9%)	0	100	100
23	Q	80/82 (98%)	66 (82%)	14 (18%)	0	100	100
24	R	78/84 (93%)	58 (74%)	19 (24%)	1 (1%)	9	41
25	S	53/75 (71%)	51 (96%)	2 (4%)	0	100	100
26	T	77/92 (84%)	69 (90%)	8 (10%)	0	100	100
27	U	83/87 (95%)	78 (94%)	4 (5%)	1 (1%)	10	42
28	V	49/71 (69%)	37 (76%)	12 (24%)	0	100	100
29	W	94/100 (94%)	80 (85%)	14 (15%)	0	100	100
33	b	269/273 (98%)	230 (86%)	39 (14%)	0	100	100
34	c	207/209 (99%)	187 (90%)	18 (9%)	2 (1%)	12	46
35	d	199/201 (99%)	185 (93%)	14 (7%)	0	100	100
36	e	175/179 (98%)	153 (87%)	22 (13%)	0	100	100
37	f	174/177 (98%)	159 (91%)	13 (8%)	2 (1%)	11	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	g	45/149 (30%)	34 (76%)	11 (24%)	0	100	100
39	h	139/142 (98%)	115 (83%)	24 (17%)	0	100	100
40	i	140/142 (99%)	126 (90%)	14 (10%)	0	100	100
41	j	120/123 (98%)	89 (74%)	30 (25%)	1 (1%)	16	52
42	k	141/144 (98%)	121 (86%)	19 (14%)	1 (1%)	18	55
43	l	134/136 (98%)	118 (88%)	13 (10%)	3 (2%)	5	31
44	m	118/127 (93%)	99 (84%)	17 (14%)	2 (2%)	7	36
45	n	114/117 (97%)	103 (90%)	11 (10%)	0	100	100
46	o	112/115 (97%)	97 (87%)	15 (13%)	0	100	100
47	p	115/118 (98%)	109 (95%)	6 (5%)	0	100	100
48	q	101/103 (98%)	85 (84%)	16 (16%)	0	100	100
49	r	108/110 (98%)	99 (92%)	9 (8%)	0	100	100
50	s	100/104 (96%)	81 (81%)	17 (17%)	2 (2%)	6	33
51	t	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
52	u	73/85 (86%)	62 (85%)	11 (15%)	0	100	100
53	v	75/78 (96%)	64 (85%)	11 (15%)	0	100	100
54	w	61/63 (97%)	54 (88%)	7 (12%)	0	100	100
55	x	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
57	z	48/55 (87%)	42 (88%)	6 (12%)	0	100	100
All	All	6114/6586 (93%)	5314 (87%)	779 (13%)	21 (0%)	37	70

5 of 21 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	1	32	ILE
20	N	67	GLY
37	f	48	ASN
2	1	33	LEU
3	2	21	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	38/38 (100%)	37 (97%)	1 (3%)	40	61
2	1	51/52 (98%)	50 (98%)	1 (2%)	48	66
3	2	34/34 (100%)	34 (100%)	0	100	100
4	3	148/149 (99%)	148 (100%)	0	100	100
5	5	359/359 (100%)	359 (100%)	0	100	100
6	6	47/48 (98%)	46 (98%)	1 (2%)	47	65
9	C	180/199 (90%)	180 (100%)	0	100	100
10	D	170/190 (90%)	166 (98%)	4 (2%)	43	63
11	E	172/173 (99%)	171 (99%)	1 (1%)	78	80
12	F	113/126 (90%)	113 (100%)	0	100	100
13	G	87/116 (75%)	86 (99%)	1 (1%)	65	74
14	H	124/147 (84%)	124 (100%)	0	100	100
15	I	104/105 (99%)	103 (99%)	1 (1%)	68	76
16	J	105/107 (98%)	105 (100%)	0	100	100
17	K	86/90 (96%)	85 (99%)	1 (1%)	63	73
18	L	90/99 (91%)	90 (100%)	0	100	100
19	M	103/104 (99%)	103 (100%)	0	100	100
20	N	92/96 (96%)	90 (98%)	2 (2%)	45	64
21	O	79/84 (94%)	79 (100%)	0	100	100
22	P	75/77 (97%)	75 (100%)	0	100	100
23	Q	65/65 (100%)	65 (100%)	0	100	100
24	R	74/78 (95%)	74 (100%)	0	100	100
25	S	48/65 (74%)	48 (100%)	0	100	100
26	T	70/79 (89%)	70 (100%)	0	100	100
27	U	65/66 (98%)	64 (98%)	1 (2%)	57	70
28	V	44/61 (72%)	43 (98%)	1 (2%)	44	64
29	W	83/84 (99%)	82 (99%)	1 (1%)	63	73
33	b	216/218 (99%)	210 (97%)	6 (3%)	38	59
34	c	164/164 (100%)	160 (98%)	4 (2%)	43	63
35	d	165/165 (100%)	165 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	e	148/150 (99%)	146 (99%)	2 (1%)	59	71
37	f	137/138 (99%)	136 (99%)	1 (1%)	76	79
38	g	38/114 (33%)	38 (100%)	0	100	100
39	h	109/110 (99%)	108 (99%)	1 (1%)	70	76
40	i	116/116 (100%)	113 (97%)	3 (3%)	40	61
41	j	103/104 (99%)	101 (98%)	2 (2%)	50	67
42	k	102/103 (99%)	100 (98%)	2 (2%)	48	66
43	l	109/109 (100%)	108 (99%)	1 (1%)	70	76
44	m	100/103 (97%)	98 (98%)	2 (2%)	48	66
45	n	86/87 (99%)	86 (100%)	0	100	100
46	o	99/100 (99%)	99 (100%)	0	100	100
47	p	89/90 (99%)	88 (99%)	1 (1%)	65	74
48	q	84/84 (100%)	84 (100%)	0	100	100
49	r	93/93 (100%)	92 (99%)	1 (1%)	65	74
50	s	83/85 (98%)	82 (99%)	1 (1%)	63	73
51	t	78/78 (100%)	77 (99%)	1 (1%)	61	72
52	u	56/63 (89%)	55 (98%)	1 (2%)	51	67
53	v	67/68 (98%)	67 (100%)	0	100	100
54	w	55/55 (100%)	55 (100%)	0	100	100
55	x	48/49 (98%)	48 (100%)	0	100	100
57	z	45/49 (92%)	45 (100%)	0	100	100
All	All	5096/5386 (95%)	5051 (99%)	45 (1%)	68	76

5 of 45 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
37	f	98	VAL
42	k	89	VAL
39	h	71	THR
40	i	52	ASP
43	l	89	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 83 such sidechains are listed below:

Mol	Chain	Res	Type
37	f	143	GLN
45	n	43	ASN
39	h	31	GLN
42	k	35	HIS
49	r	7	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	X	58/73 (79%)	30 (51%)	0
31	Z	58/76 (76%)	24 (41%)	1 (1%)
32	a	117/118 (99%)	21 (17%)	0
56	y	63/77 (81%)	19 (30%)	0
7	A	2902/2903 (99%)	740 (25%)	13 (0%)
8	B	1538/1539 (99%)	427 (27%)	3 (0%)
All	All	4736/4786 (98%)	1261 (26%)	17 (0%)

5 of 1261 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	A	10	A
7	A	14	A
7	A	23	G
7	A	34	U
7	A	42	A

5 of 17 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	B	428	G
31	Z	13	C
7	A	1730	C
7	A	1904	G
7	A	1913	A

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

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.

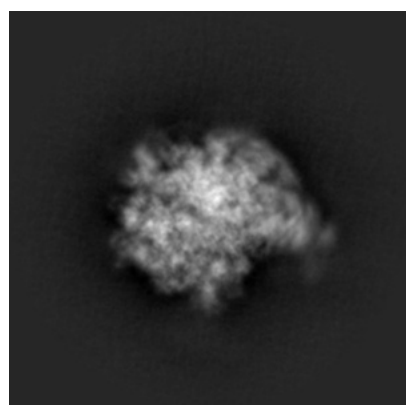
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30611. These allow visual inspection of the internal detail of the map and identification of artifacts.

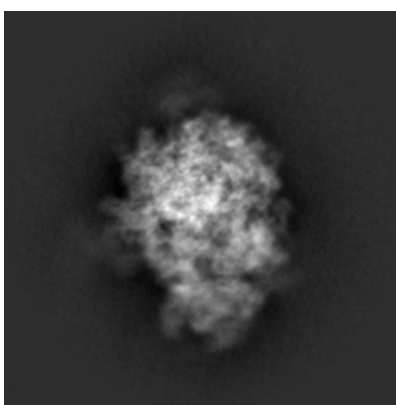
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

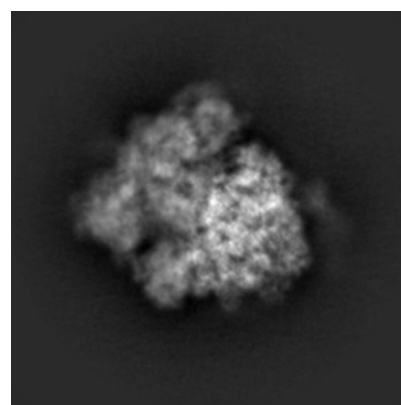
6.1.1 Primary map



X



Y

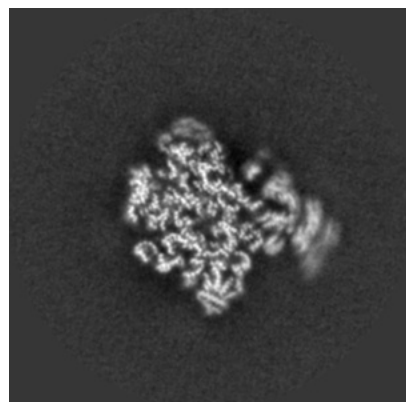


Z

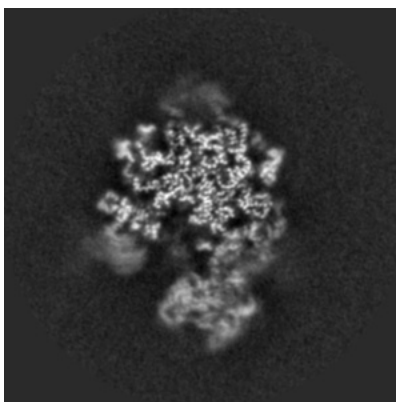
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

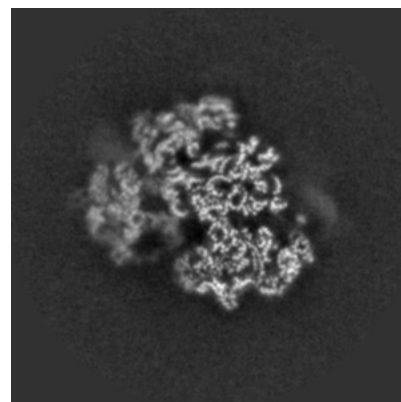
6.2.1 Primary map



X Index: 160



Y Index: 160

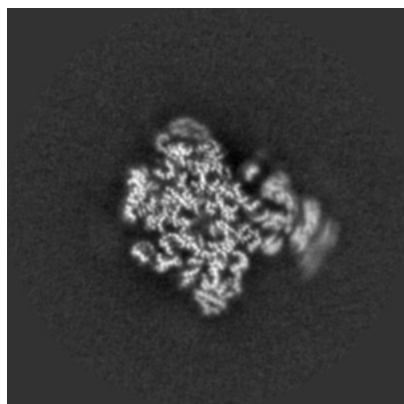


Z Index: 160

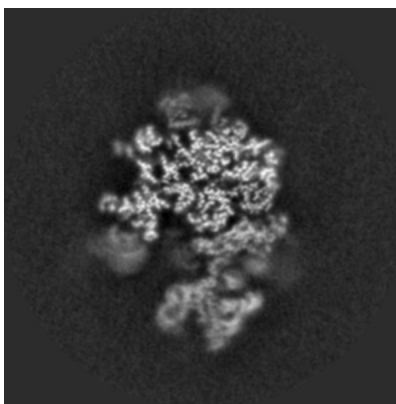
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

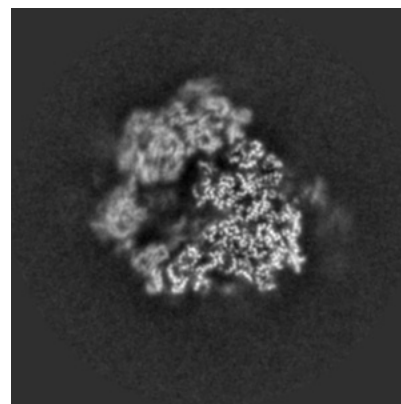
6.3.1 Primary map



X Index: 161



Y Index: 165

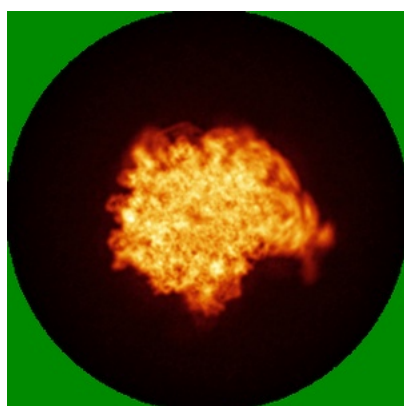


Z Index: 147

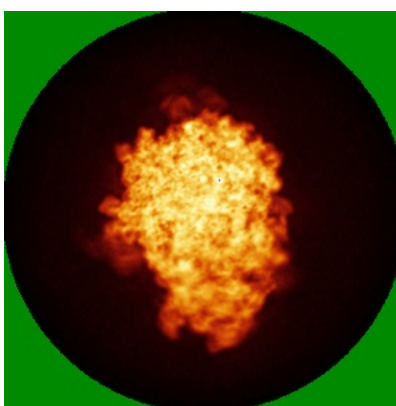
The images above show the largest variance slices of the map in three orthogonal directions.

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

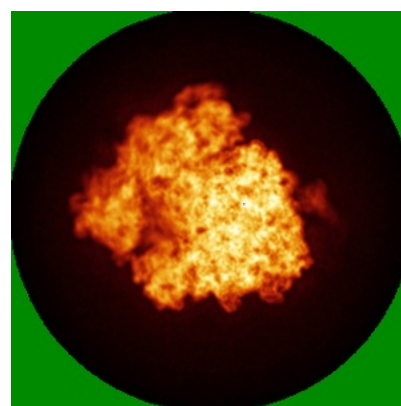
6.4.1 Primary map



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 0.005. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

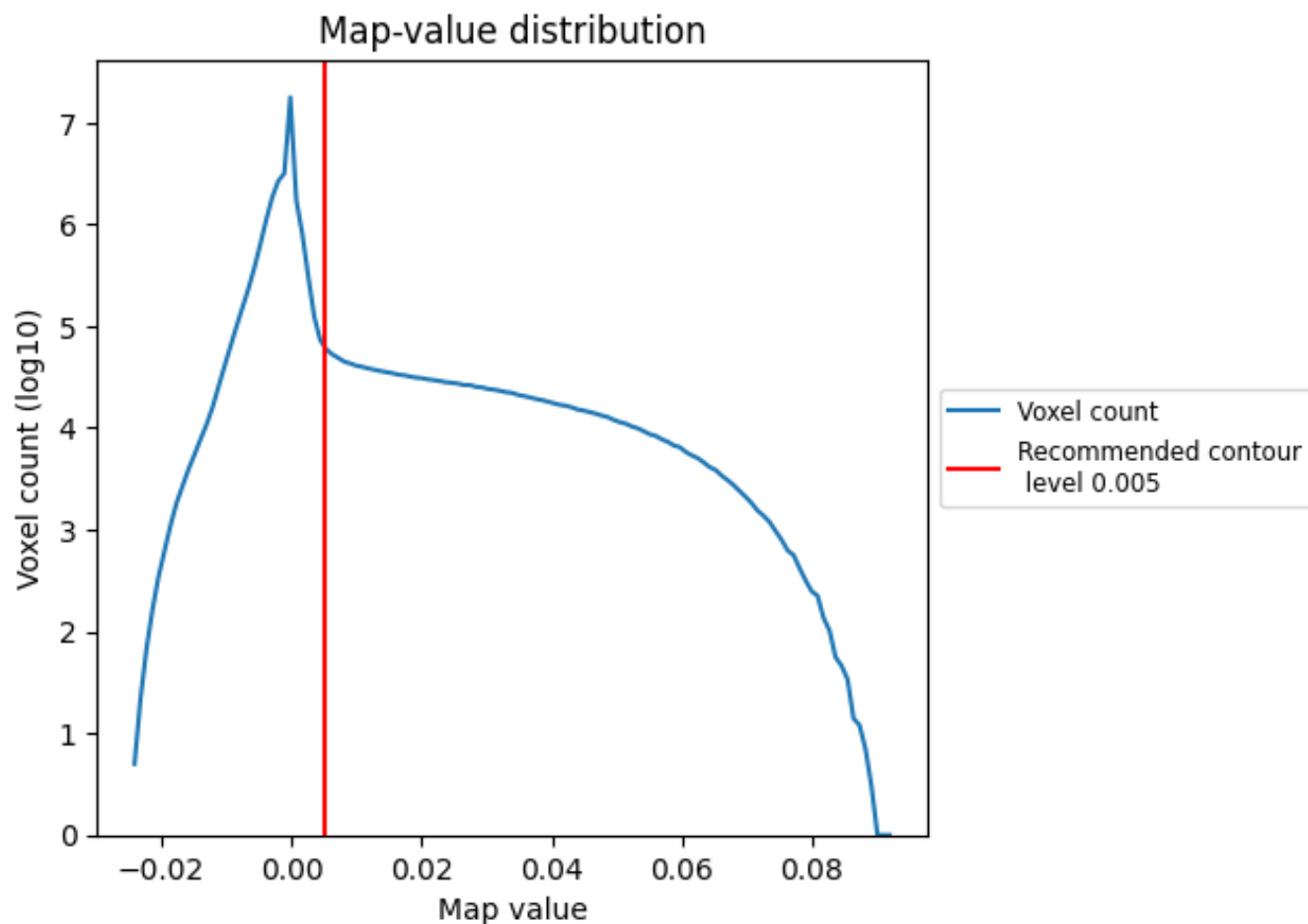
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

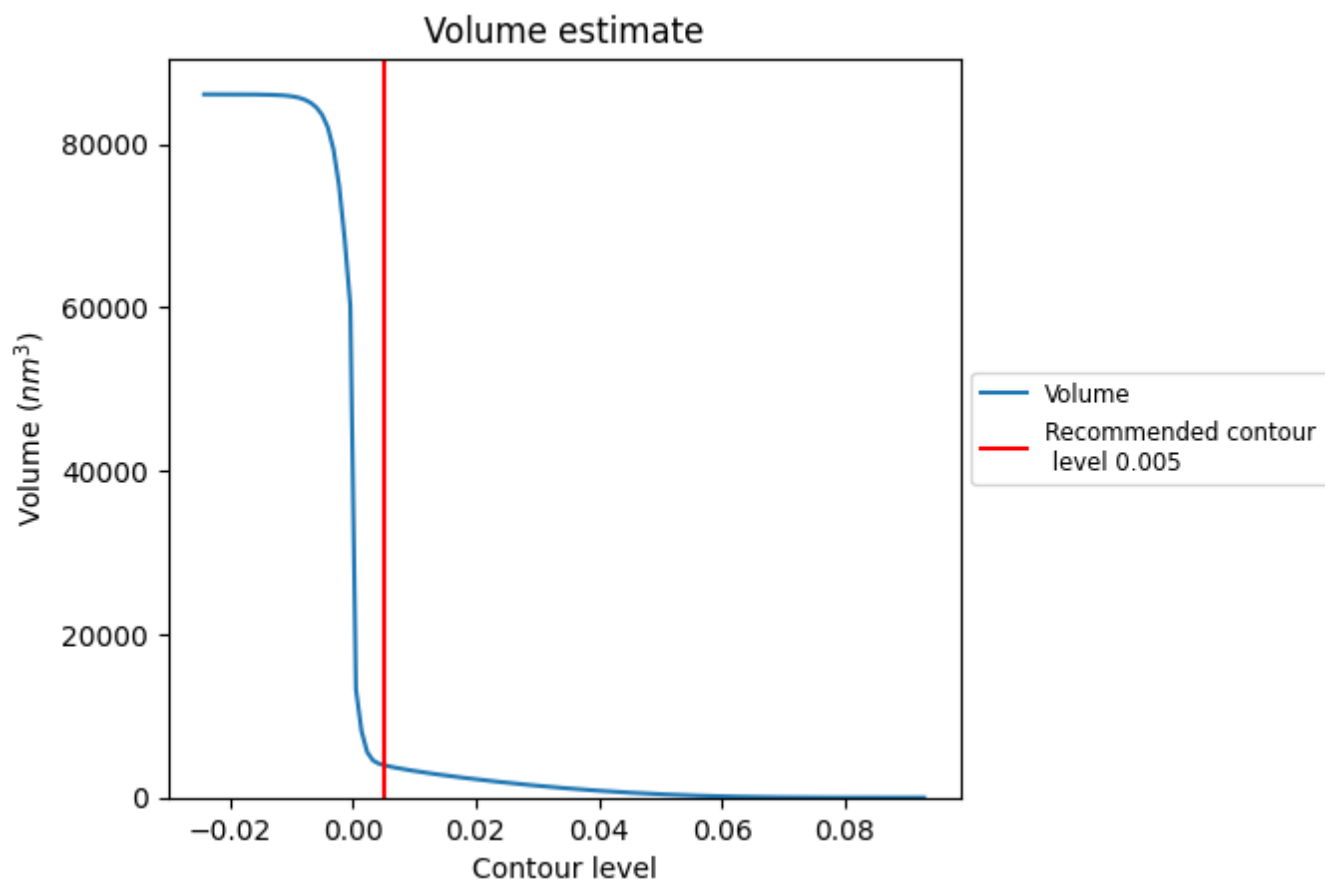
This section contains the results of statistical analysis of the map.

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.

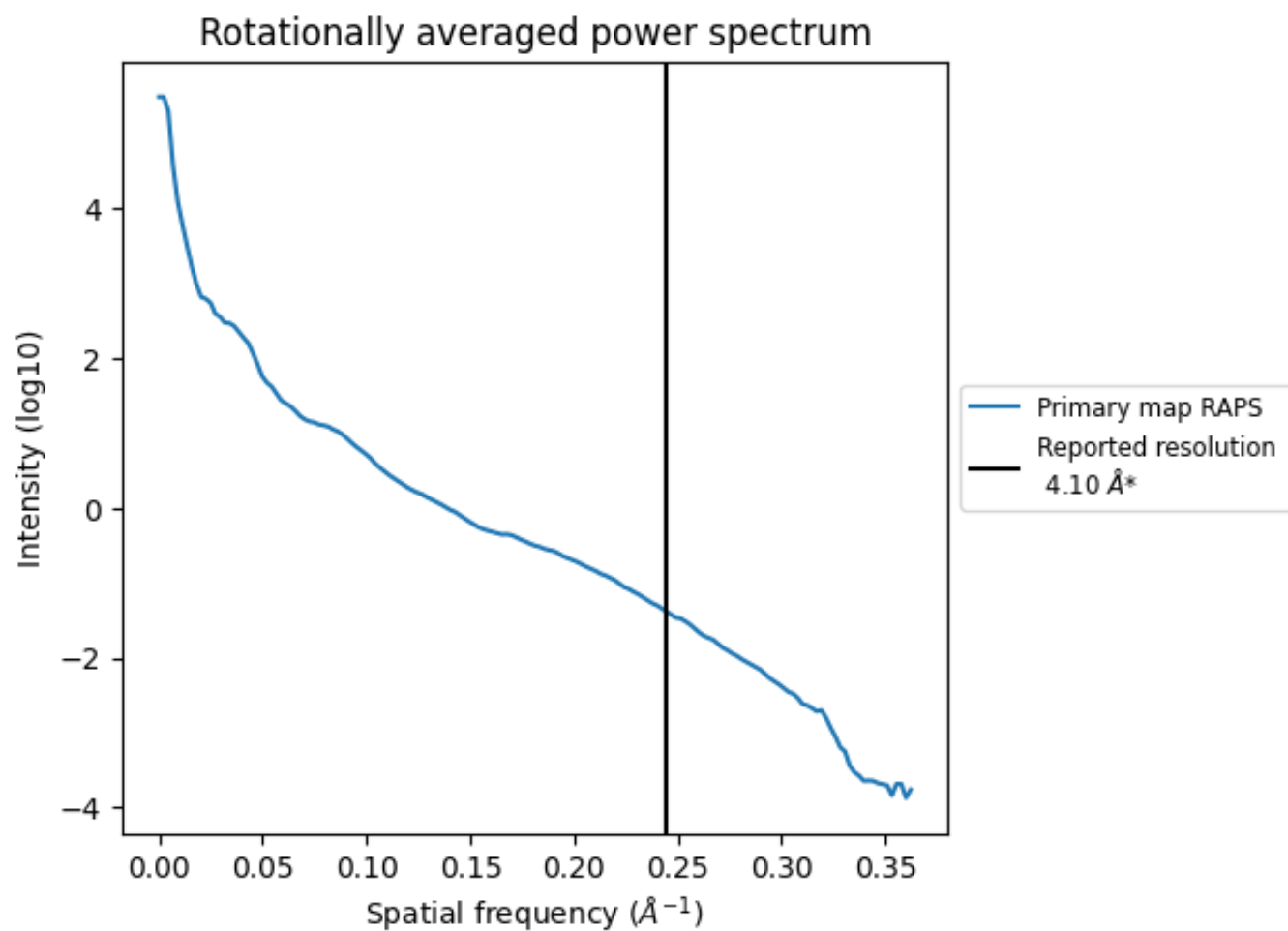
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3991 nm³; this corresponds to an approximate mass of 3605 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 ⓘ

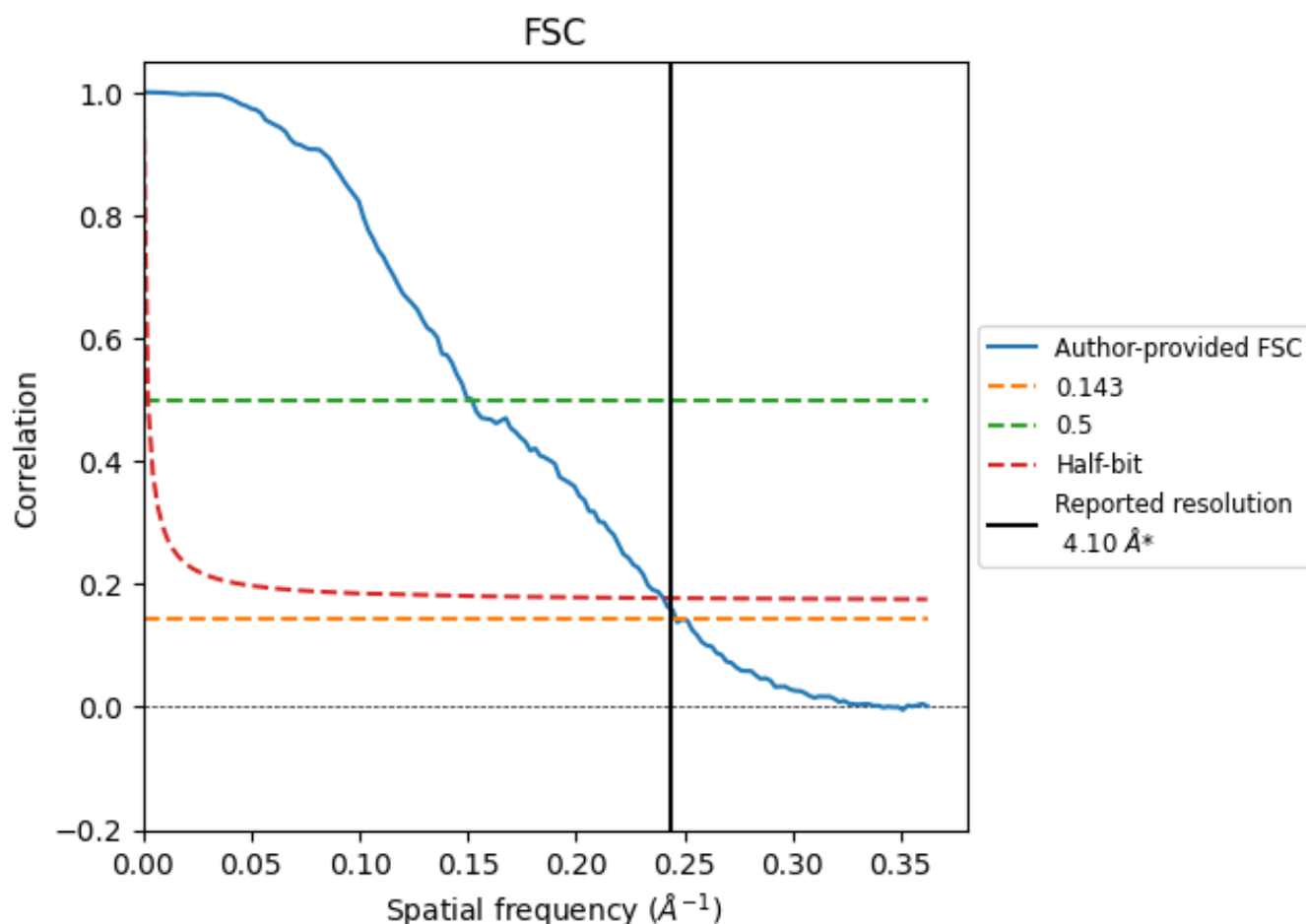


*Reported resolution corresponds to spatial frequency of 0.244 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.244 Å⁻¹

8.2 Resolution estimates [i](#)

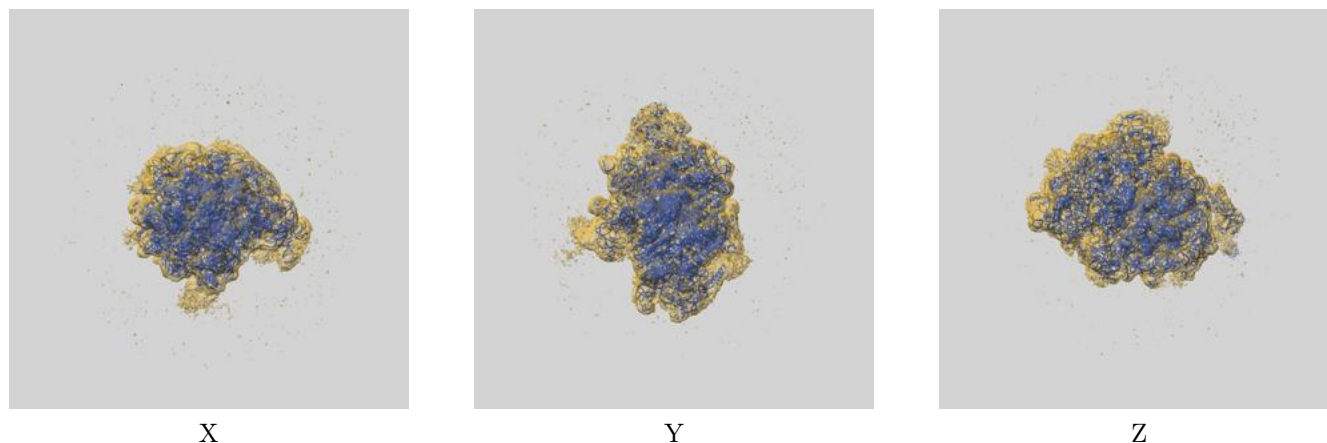
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.10	-	-
Author-provided FSC curve	4.06	6.59	4.16
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

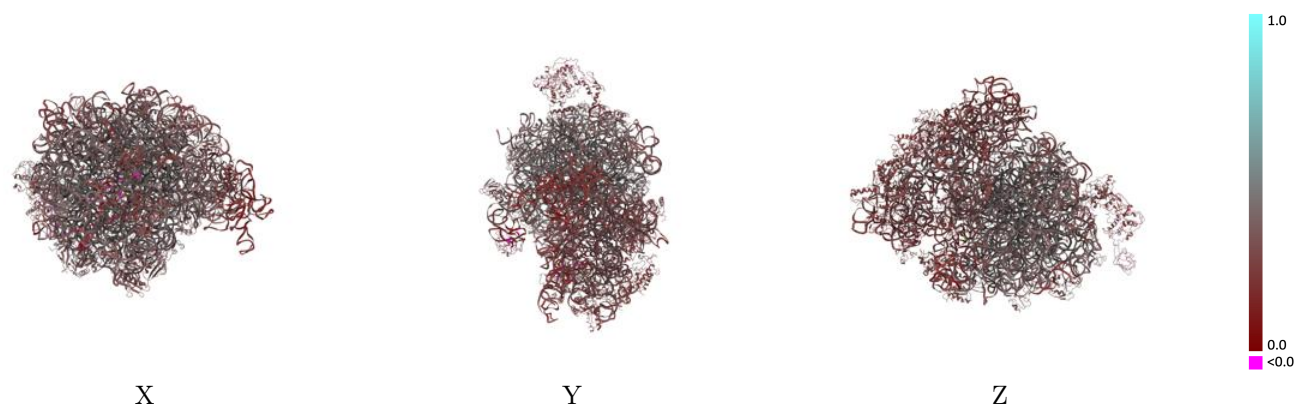
This section contains information regarding the fit between EMDB map EMD-30611 and PDB model 7D80. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

9.1 Map-model overlay [i](#)



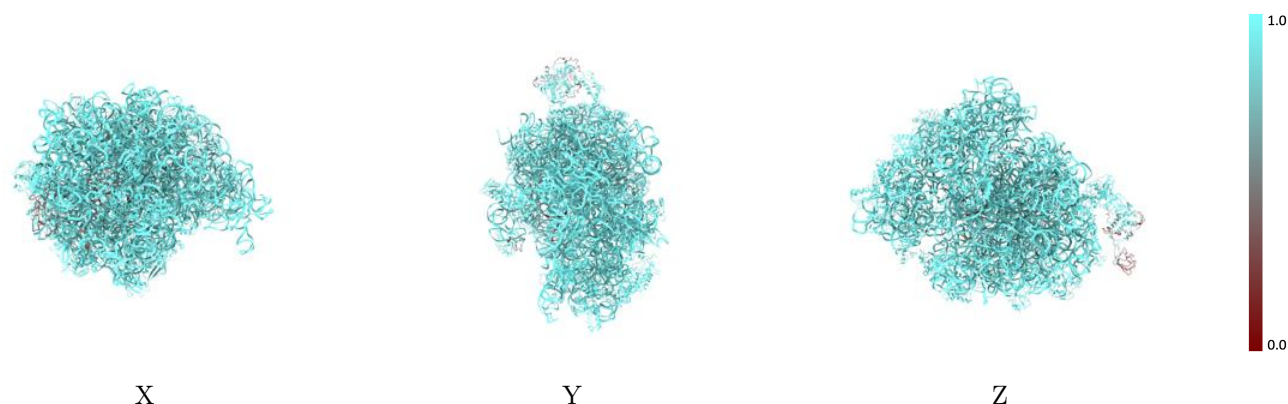
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



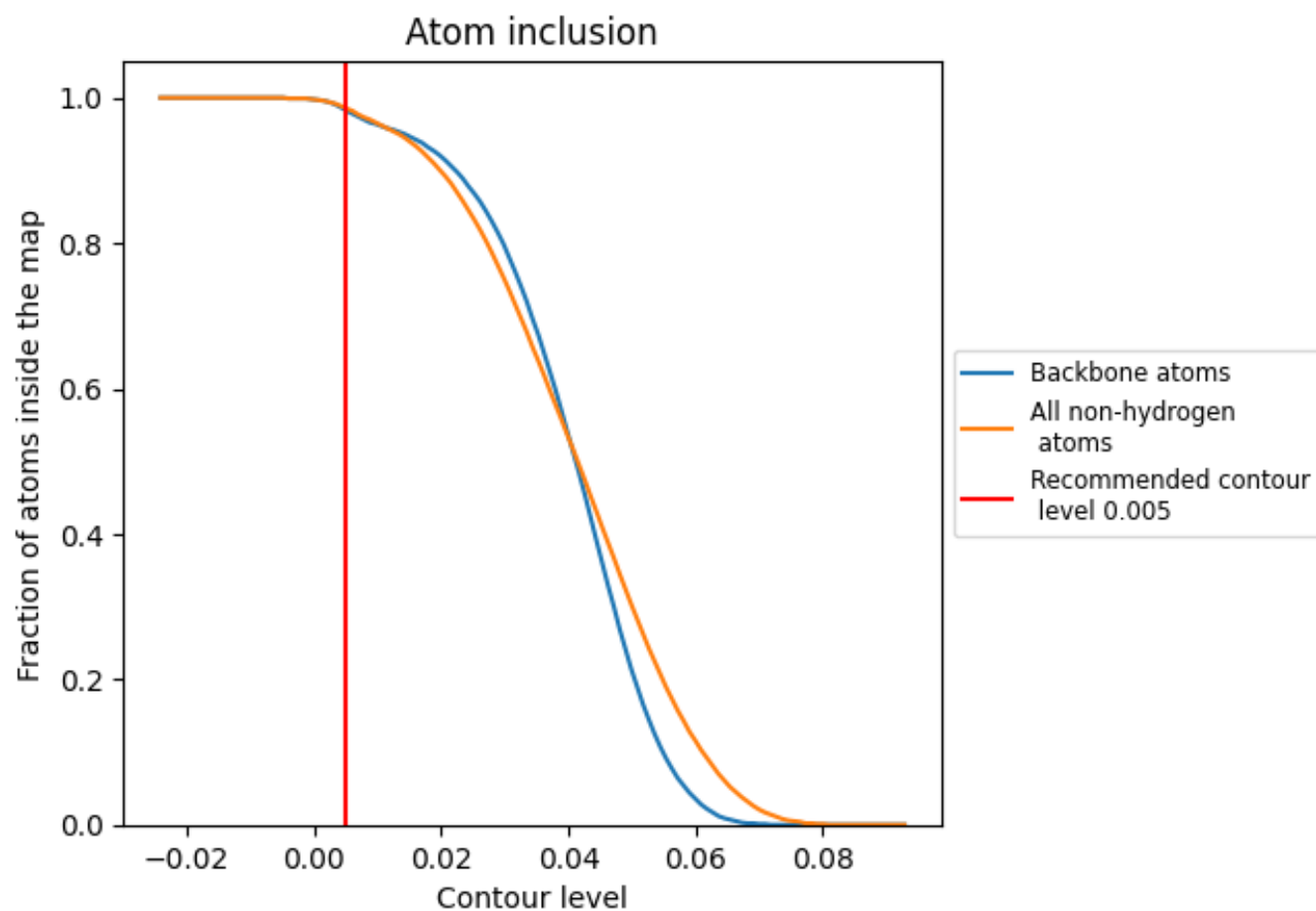
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.005).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 99% 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 (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9860	 0.3390
0	 0.9750	 0.3790
1	 0.9940	 0.3960
2	 1.0000	 0.3610
3	 0.9890	 0.2710
5	 0.6750	 0.2400
6	 1.0000	 0.3920
A	 0.9990	 0.3870
B	 1.0000	 0.3000
C	 1.0000	 0.2690
D	 0.9980	 0.2850
E	 1.0000	 0.2120
F	 0.9980	 0.3040
G	 0.9940	 0.2860
H	 0.9990	 0.2410
I	 0.9990	 0.2790
J	 1.0000	 0.2260
K	 0.9970	 0.2560
L	 0.9970	 0.2910
M	 0.9940	 0.2620
N	 0.9980	 0.2210
O	 1.0000	 0.2350
P	 0.9960	 0.2560
Q	 0.9980	 0.2510
R	 1.0000	 0.2680
S	 1.0000	 0.3140
T	 0.9980	 0.2050
U	 0.9970	 0.2250
V	 0.9930	 0.2600
W	 0.9950	 0.3610
X	 0.9980	 0.2180
Z	 0.5280	 0.2640
a	 1.0000	 0.3520
b	 0.9910	 0.4030
c	 0.9940	 0.4000



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Chain	Atom inclusion	Q-score
d	 0.9970	 0.3740
e	 0.9990	 0.2550
f	 1.0000	 0.3330
g	 1.0000	 0.3360
h	 0.8800	 0.1720
i	 0.9960	 0.3910
j	 0.9910	 0.4010
k	 0.9950	 0.3920
l	 0.9970	 0.3940
m	 0.9980	 0.3800
n	 1.0000	 0.3220
o	 0.9930	 0.3830
p	 0.9990	 0.3670
q	 0.9960	 0.4020
r	 0.9920	 0.3850
s	 0.9960	 0.3580
t	 1.0000	 0.3620
u	 0.9980	 0.4010
v	 0.9970	 0.3730
w	 1.0000	 0.2840
x	 0.9950	 0.3850
y	 0.9700	 0.2890
z	 0.9880	 0.3580