



Full wwPDB EM Validation Report ⓘ

Oct 13, 2022 – 04:03 am BST

PDB ID : 7PIP
EMDB ID : EMD-13446
Title : 70S ribosome with EF-Tu-tRNA and P-site tRNA in pseudouridimycin-treated Mycoplasma pneumoniae cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-08-23
Resolution : 9.30 Å (reported)
Based on initial models : 4V5L, 7OOC, 7OOD, 4V7C

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

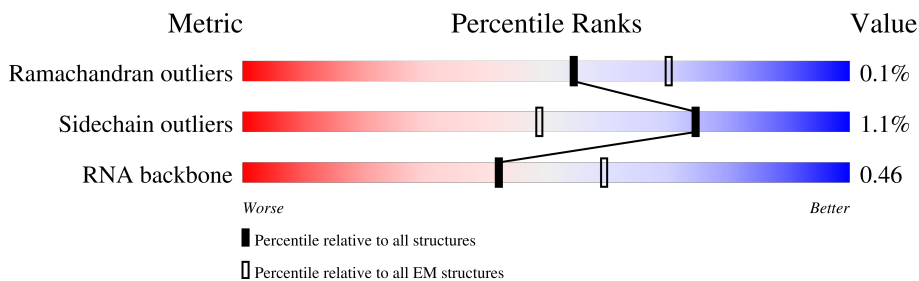
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

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 9.30 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	0	48	
2	1	59	
3	2	37	
4	9	394	
5	A	294	
6	B	273	
7	C	205	
8	D	219	

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Mol	Chain	Length	Quality of chain
9	E	215	21% 77% 22%
10	F	155	21% 99%
11	G	142	16% 95%
12	H	132	23% 96%
13	I	108	25% 91% 6%
14	J	121	20% 94% 6%
15	K	139	14% 94%
16	L	124	18% 91% 5%
17	M	61	30% 98%
18	N	86	12% 97%
19	O	94	85% 15%
20	P	85	16% 98%
21	Q	104	15% 62% 38%
22	R	87	29% 97%
23	S	87	87% 11%
24	T	60	10% 88% 12%
25	a	287	12% 99%
26	b	287	15% 79% 20%
27	c	212	17% 99%
28	d	180	26% 97%
29	e	184	23% 95%
30	f	149	68% 93%
31	g	161	30% 69% 6% 25%
32	h	137	35% 93% 7%
33	i	146	17% 99%

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Mol	Chain	Length	Quality of chain
34	j	122	31% 98%
35	k	151	12% 98%
36	l	139	10% 97%
37	m	124	7% 96%
38	n	116	14% 96%
39	o	119	13% 95%
40	p	127	90% 10%
41	q	100	14% 99%
42	r	159	6% 86% 13%
43	s	237	8% 38% 61%
44	t	111	27% 99%
45	u	104	12% 82% 17%
46	v	65	14% 97%
47	w	111	90% 10%
48	x	97	16% 43% 55%
49	y	57	14% 93% 5%
50	z	53	8% 91% 6%
51	3	2907	69% 30%
52	4	108	60% 35%
53	5	1520	71% 27%
54	6	76	8% 59% 41%
54	7	76	12% 59% 41%

2 Entry composition

There are 54 unique types of molecules in this entry. The entry contains 149091 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
			Total	C	N	O	S		
1	0	47	380	236	81	61	2	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	59	477	300	99	77	1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	2	37	304	189	65	46	4	0	0

- Molecule 4 is a protein called Elongation factor Tu.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	9	393	3021	1892	533	583	13	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	A	240	1921	1226	334	352	9	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	B	215	1698	1073	313	307	5	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	C	203	Total	C	N	O	S	0	0
			1660	1051	314	290	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	D	153	Total	C	N	O	S	0	0
			1173	742	226	202	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	E	167	Total	C	N	O	S	0	0
			1362	857	240	263	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	F	154	Total	C	N	O	S	0	0
			1246	785	239	216	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	G	141	Total	C	N	O	S	0	0
			1110	723	193	192	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	H	128	Total	C	N	O	S	0	0
			1028	655	191	181	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	I	101	Total	C	N	O	S	0	0
			809	523	142	143	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	J	114	Total	C	N	O	S	0	0
			829	514	153	156	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	K	136	Total	C	N	O	S	0	0
			1076	680	213	181	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L	118	Total	C	N	O	S	0	0
			951	594	191	166			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	M	60	Total	C	N	O	S	0	0
			474	302	96	72	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	N	83	Total	C	N	O	S	0	0
			673	428	125	120			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	O	80	Total	C	N	O	S	0	0
			646	414	119	111	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	P	83	Total	C	N	O	S	0	0
			675	425	135	115			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Q	65	Total	C	N	O	S	0	0
			535	342	103	86	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
22	R	84	Total	C	N	O	S	0	0
			682	435	127	118	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
23	S	77	Total	C	N	O	0	0
			629	383	135	111		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	T	53	Total	C	N	O	S	0	0
			471	295	103	72	1		

- Molecule 25 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	a	285	Total	C	N	O	S	0	0
			2225	1385	437	397	6		

- Molecule 26 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	b	229	Total	C	N	O	S	0	0
			1762	1119	318	318	7		

- Molecule 27 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	c	210	Total	C	N	O	S	0	0
			1644	1047	297	297	3		

- Molecule 28 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	d	175	1388	893	245	246	4	0	0

- Molecule 29 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	e	176	1396	899	247	250		0	0

- Molecule 30 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	f	145	1160	746	204	207	3	0	0

- Molecule 31 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	g	121	910	580	158	169	3	0	0

- Molecule 32 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	h	128	959	616	160	177	6	0	0

- Molecule 33 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	i	144	1164	737	213	209	5	0	0

- Molecule 34 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	j	122	944	595	178	167	4	0	0

- Molecule 35 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	k	148	Total	C	N	O	0	0
			1153	731	226	196		

- Molecule 36 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	l	136	Total	C	N	O	S	0	0
			1079	694	196	182	7		

- Molecule 37 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	m	119	Total	C	N	O	S	0	0
			958	609	175	171	3		

- Molecule 38 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	n	112	Total	C	N	O	S	0	0
			889	557	175	155	2		

- Molecule 39 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	o	115	Total	C	N	O	S	0	0
			938	592	180	165	1		

- Molecule 40 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	p	114	Total	C	N	O	S	0	0
			947	603	188	154	2		

- Molecule 41 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	q	99	Total	C	N	O	S	0	0
			811	525	148	134	4		

- Molecule 42 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	r	139	Total	C	N	O	S	0	0
			1068	663	207	191	7		

- Molecule 43 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	s	92	Total	C	N	O	S	0	0
			720	475	122	122	1		

- Molecule 44 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	t	111	Total	C	N	O	S	0	0
			872	550	166	153	3		

- Molecule 45 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	u	86	Total	C	N	O	S	0	0
			657	409	130	117	1		

- Molecule 46 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	v	63	Total	C	N	O	S	0	0
			513	317	108	87	1		

- Molecule 47 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	w	100	Total	C	N	O	0	0
			818	517	153	148		

- Molecule 48 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	x	44	Total	C	N	O	S	0	0
			344	221	55	64	4		

- Molecule 49 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	y	56	Total	C	N	O	S	0	0
			452	274	98	75	5		

- Molecule 50 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	z	50	Total	C	N	O	S	0	0
			408	255	81	68	4		

- Molecule 51 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	3	2878	Total	C	N	O	P	0	0
			61664	27558	11236	19995	2875		

- Molecule 52 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	4	105	Total	C	N	O	P	0	0
			2239	1003	409	724	103		

- Molecule 53 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	5	1493	Total	C	N	O	P	0	0
			31943	14279	5792	10382	1490		

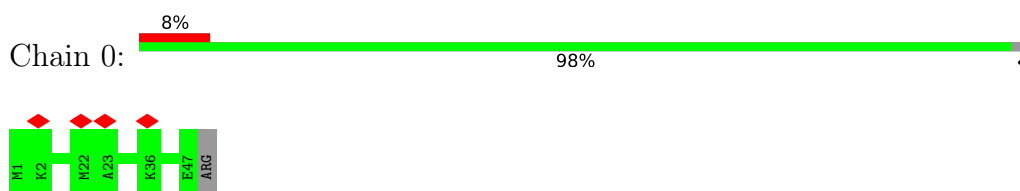
- Molecule 54 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	6	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		
54	7	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		

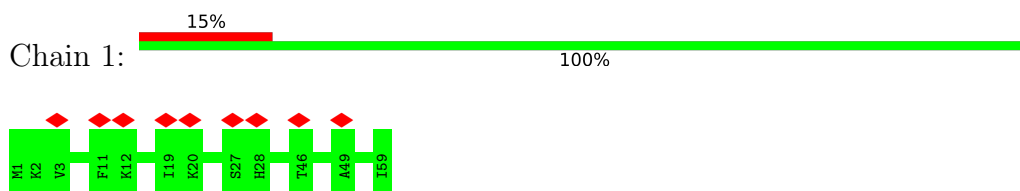
3 Residue-property plots

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

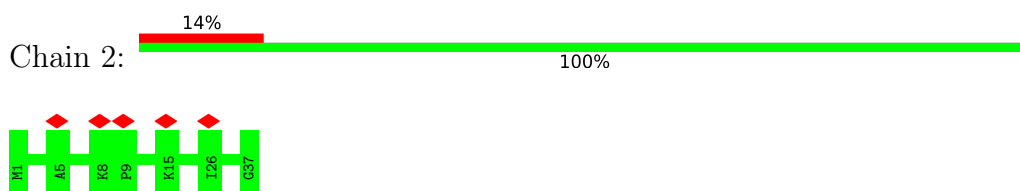
- Molecule 1: 50S ribosomal protein L34



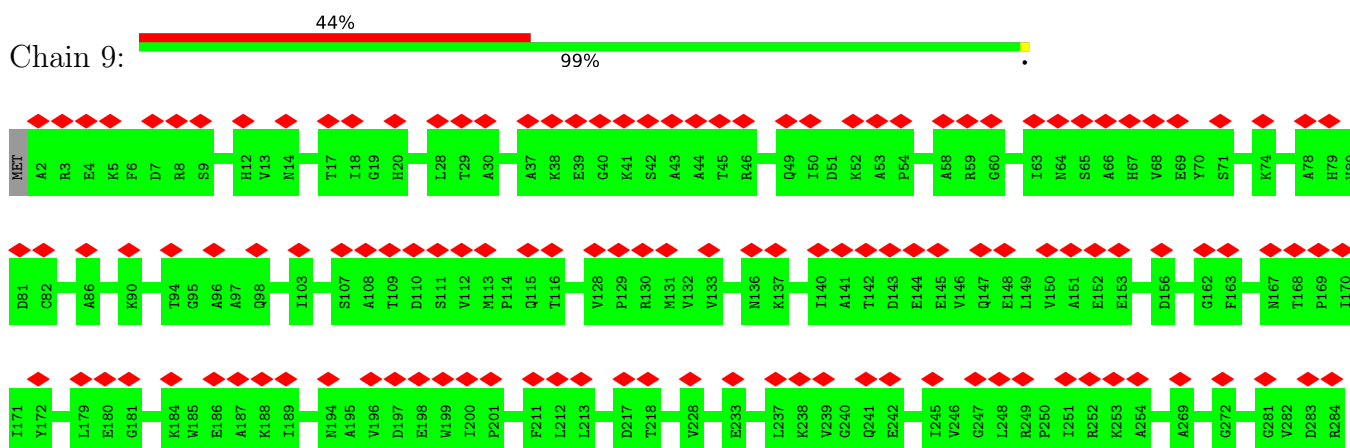
- Molecule 2: 50S ribosomal protein L35

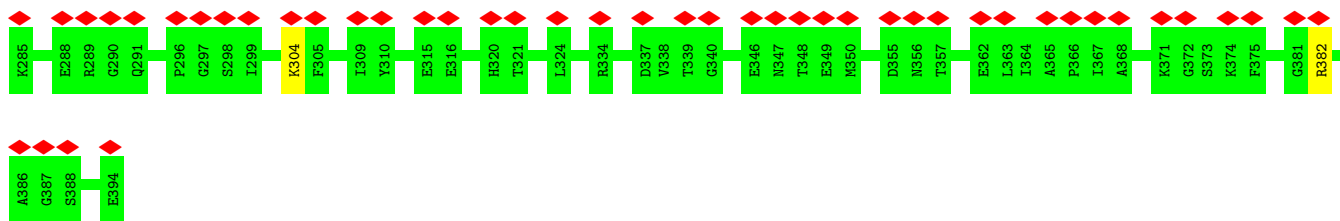


- Molecule 3: 50S ribosomal protein L36

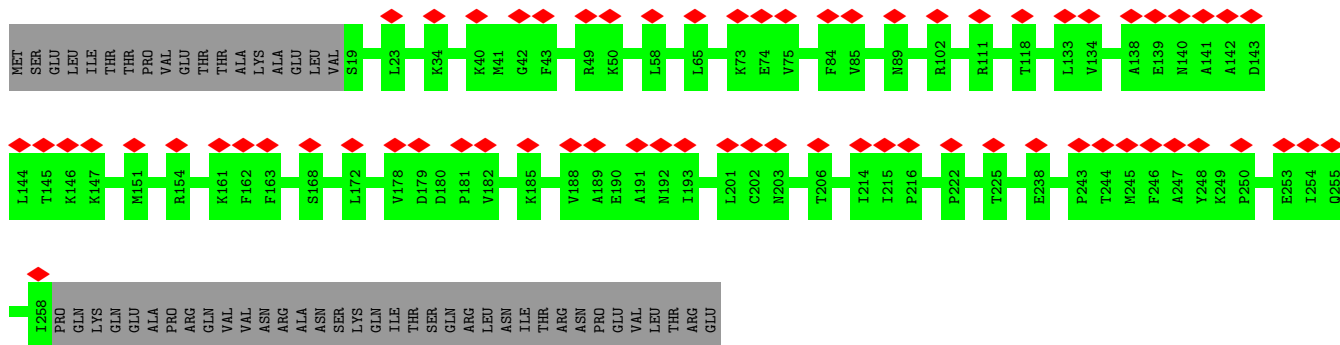
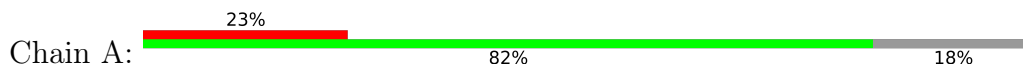


- Molecule 4: Elongation factor Tu

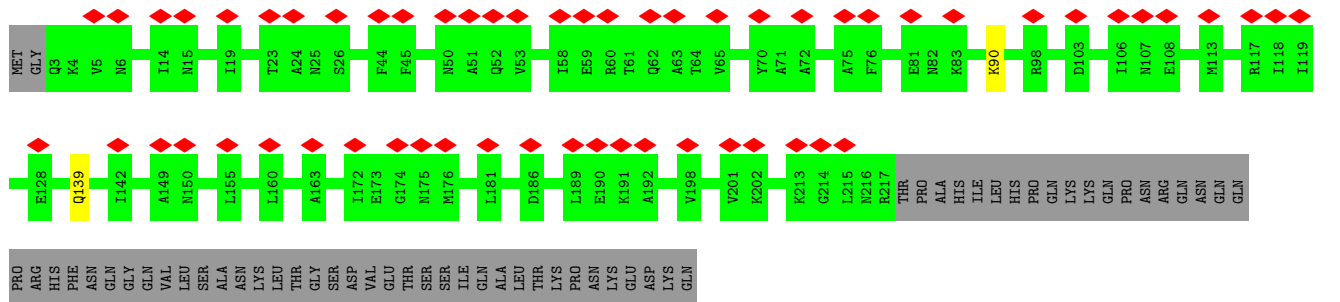
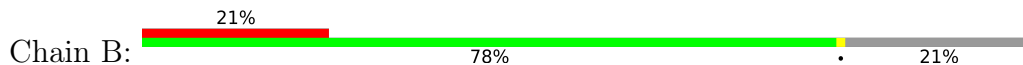




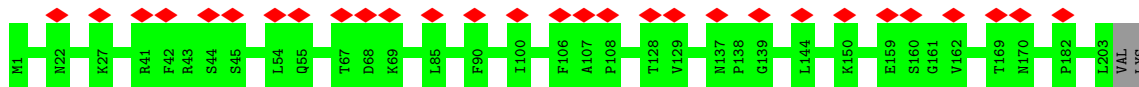
- Molecule 5: 30S ribosomal protein S2



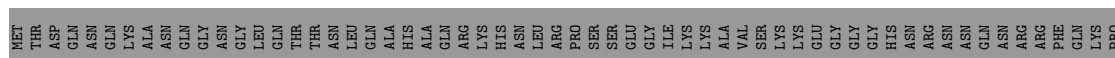
- Molecule 6: 30S ribosomal protein S3

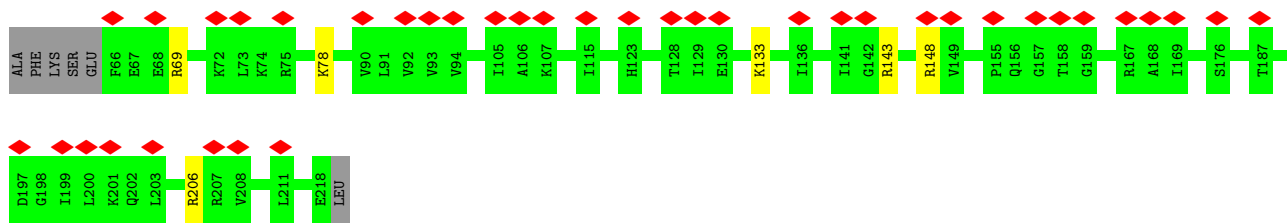


- Molecule 7: 30S ribosomal protein S4

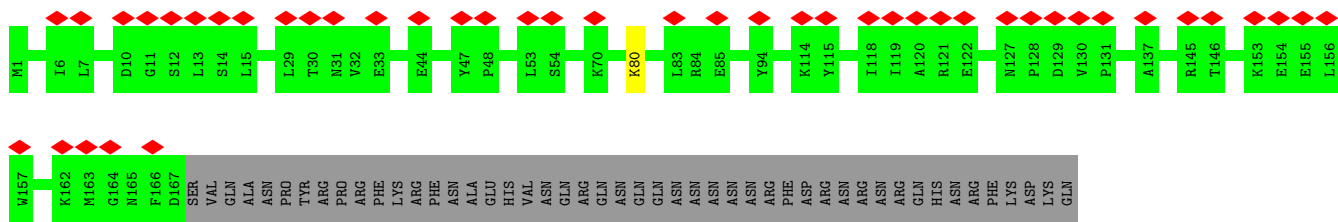
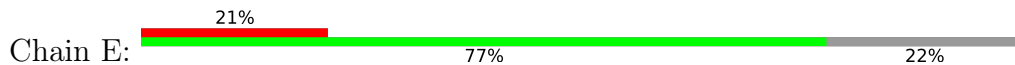


- Molecule 8: 30S ribosomal protein S5

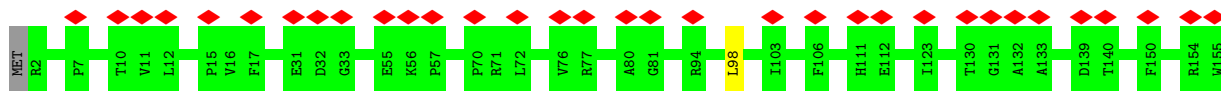




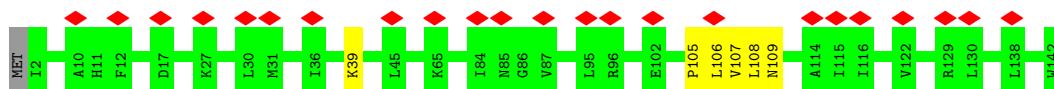
- Molecule 9: 30S ribosomal protein S6



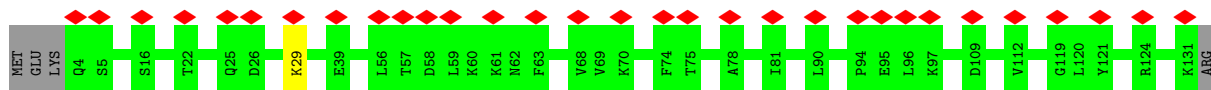
- Molecule 10: 30S ribosomal protein S7



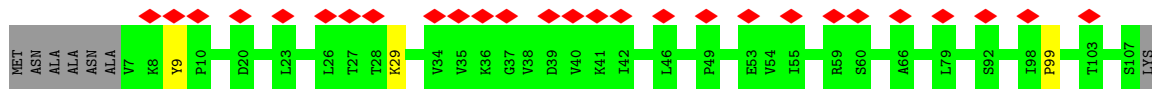
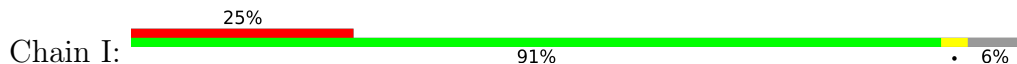
- Molecule 11: 30S ribosomal protein S8



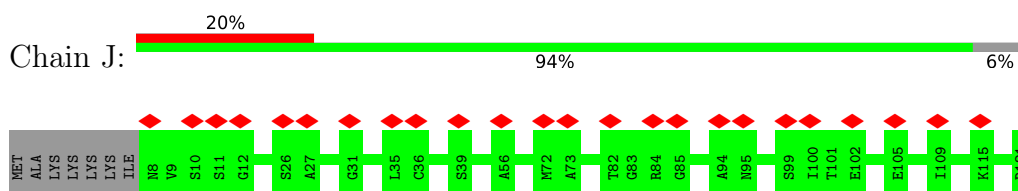
- Molecule 12: 30S ribosomal protein S9



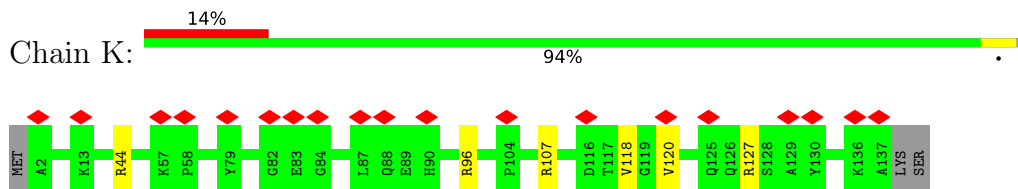
- Molecule 13: 30S ribosomal protein S10



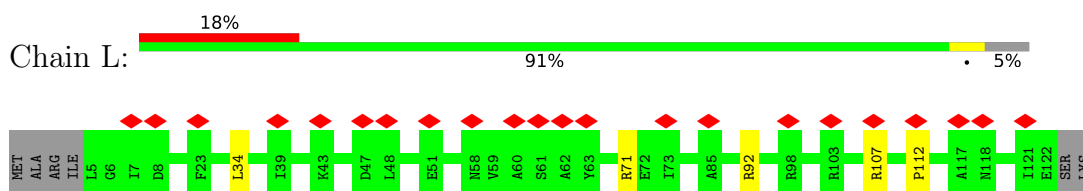
- Molecule 14: 30S ribosomal protein S11



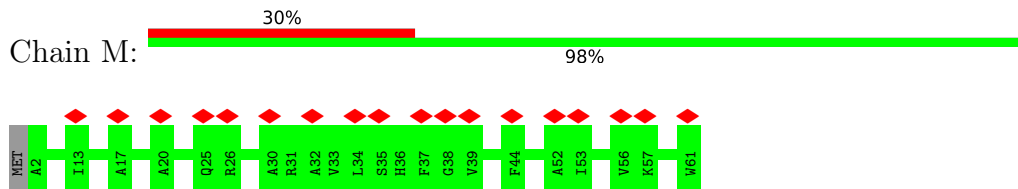
- Molecule 15: 30S ribosomal protein S12



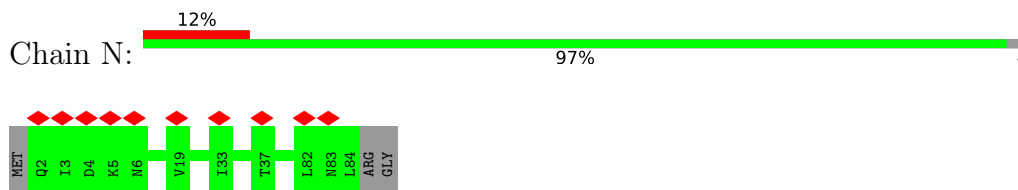
- Molecule 16: 30S ribosomal protein S13



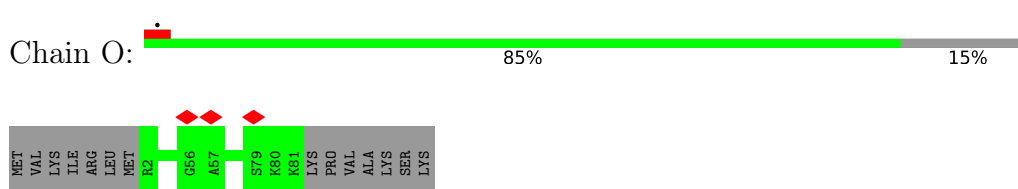
- Molecule 17: 30S ribosomal protein S14 type Z



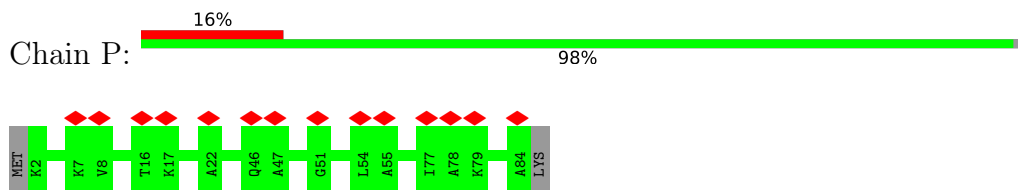
- Molecule 18: 30S ribosomal protein S15



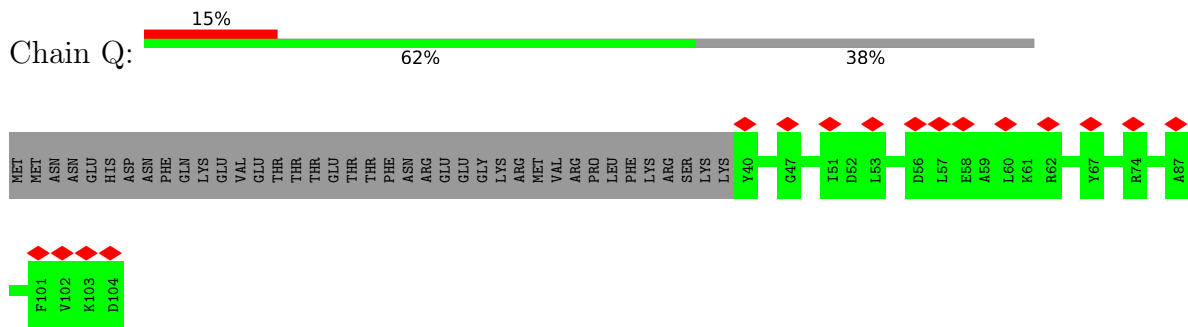
- Molecule 19: 30S ribosomal protein S16



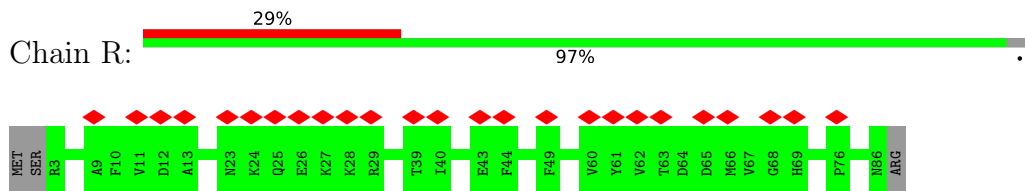
- Molecule 20: 30S ribosomal protein S17



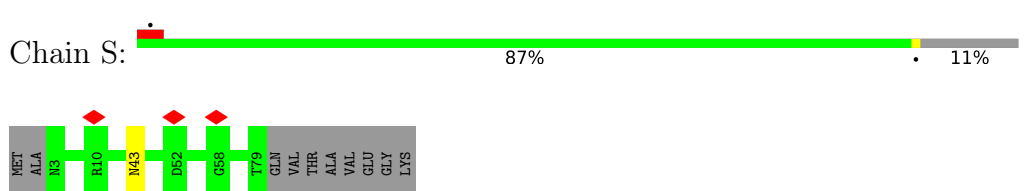
• Molecule 21: 30S ribosomal protein S18



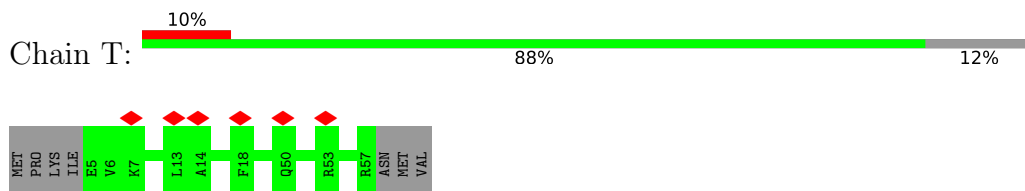
• Molecule 22: 30S ribosomal protein S19



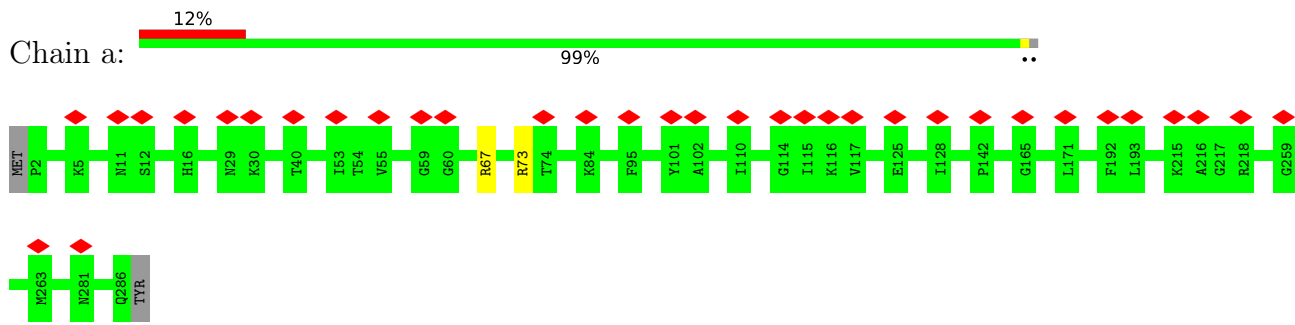
• Molecule 23: 30S ribosomal protein S20



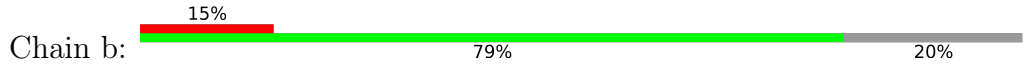
• Molecule 24: 30S ribosomal protein S21

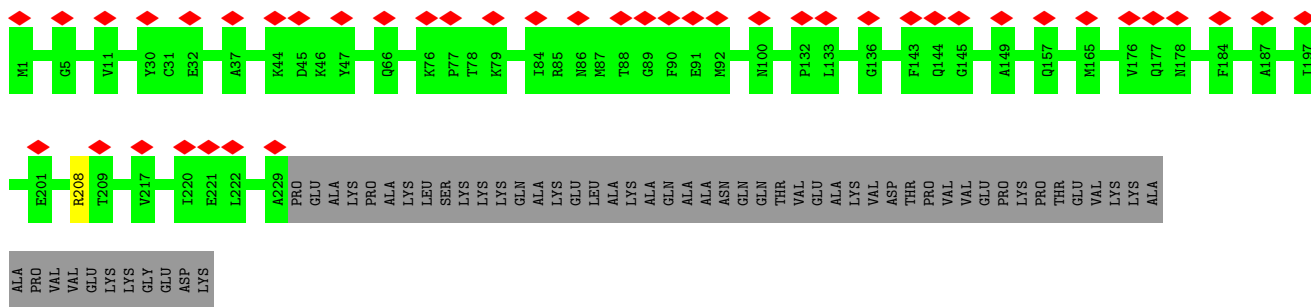


• Molecule 25: 50S ribosomal protein L2

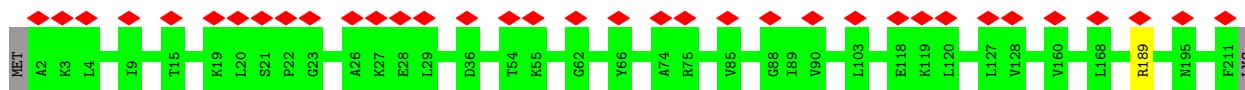


• Molecule 26: 50S ribosomal protein L3

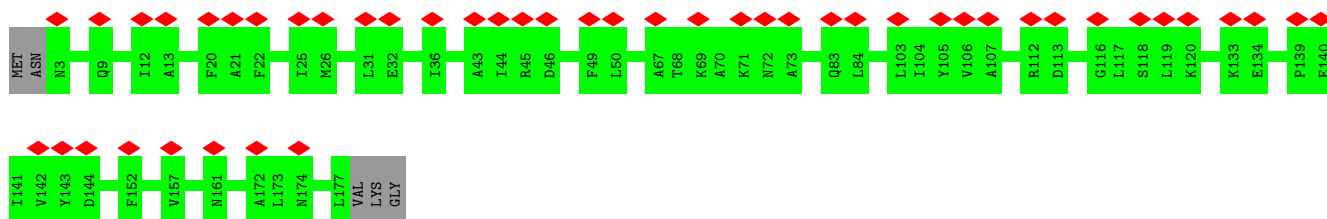




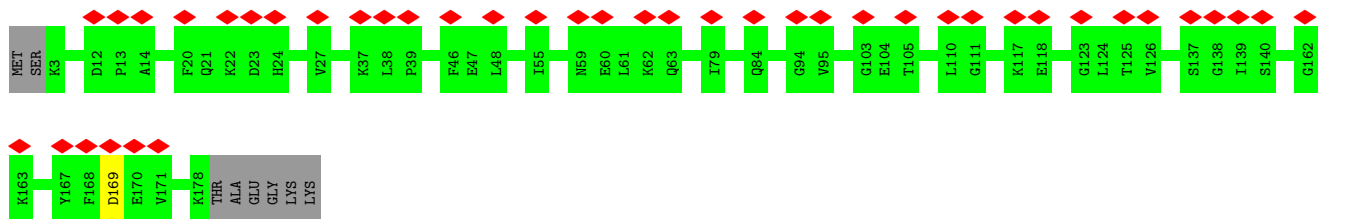
• Molecule 27: 50S ribosomal protein L4



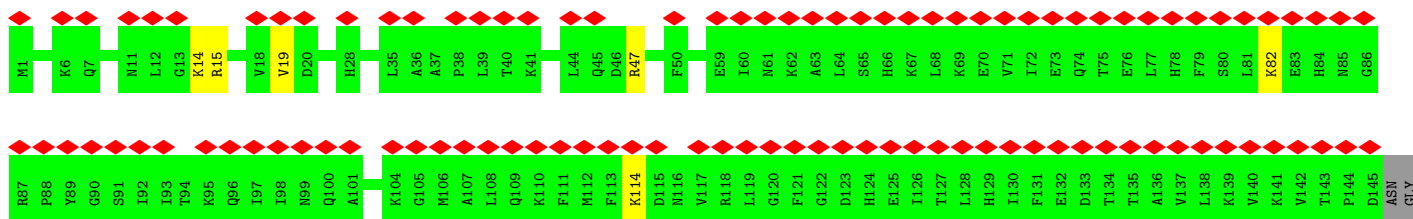
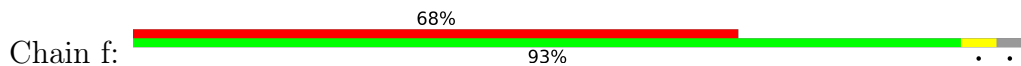
• Molecule 28: 50S ribosomal protein L5



• Molecule 29: 50S ribosomal protein L6

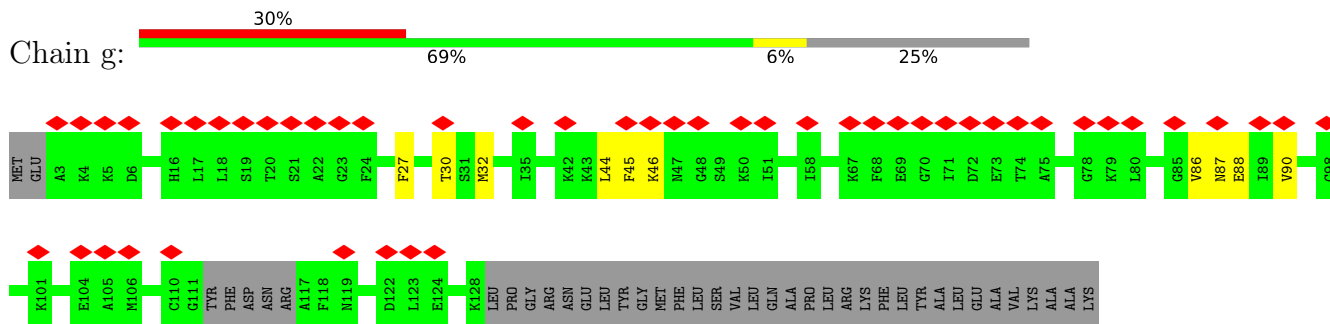


• Molecule 30: 50S ribosomal protein L9

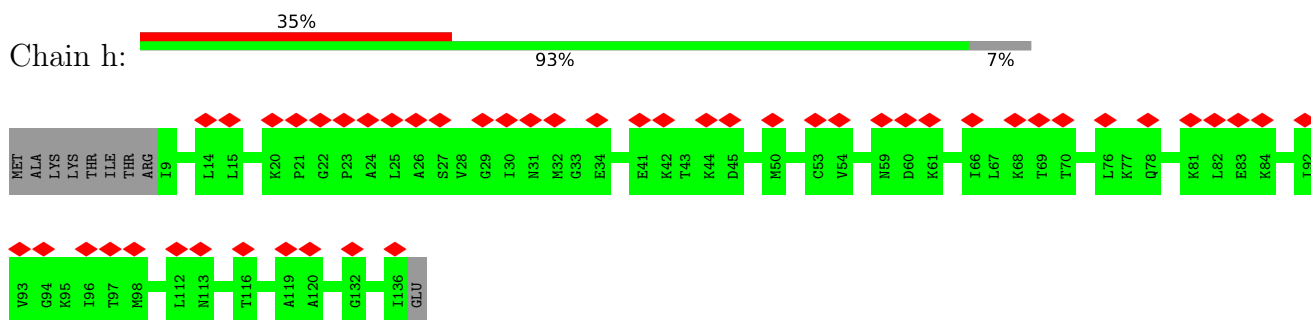


VAL
LYS

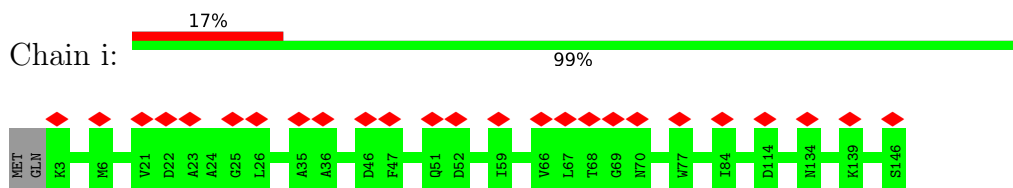
- Molecule 31: 50S ribosomal protein L10



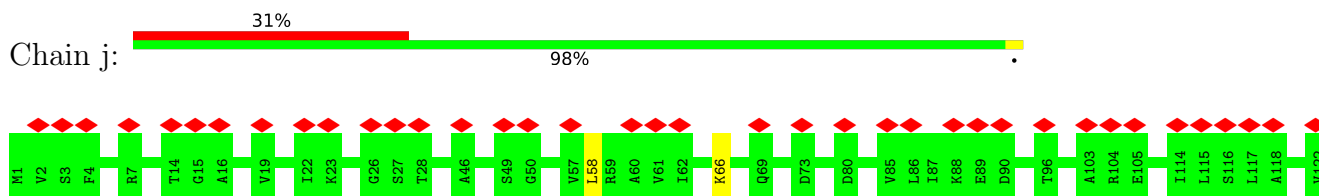
- Molecule 32: 50S ribosomal protein L11



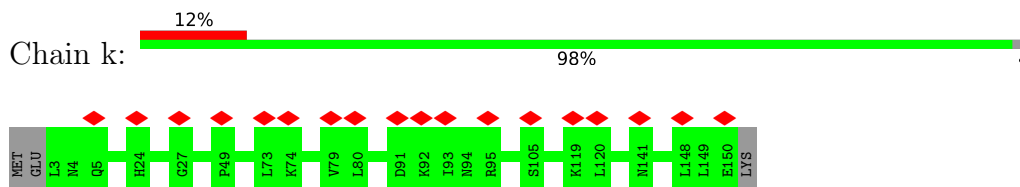
- Molecule 33: 50S ribosomal protein L13



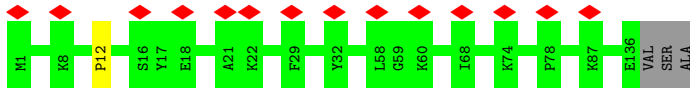
- Molecule 34: 50S ribosomal protein L14



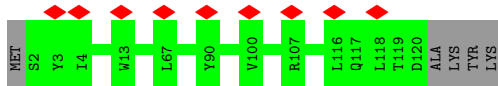
- Molecule 35: 50S ribosomal protein L15



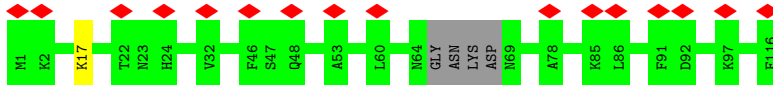
- Molecule 36: 50S ribosomal protein L16



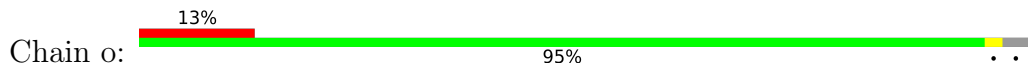
- Molecule 37: 50S ribosomal protein L17



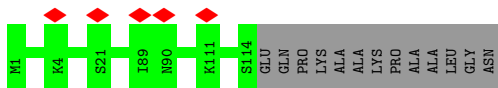
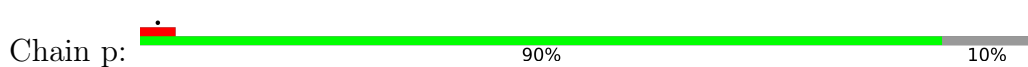
- Molecule 38: 50S ribosomal protein L18



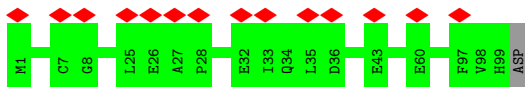
- Molecule 39: 50S ribosomal protein L19



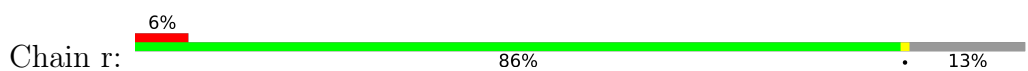
- Molecule 40: 50S ribosomal protein L20

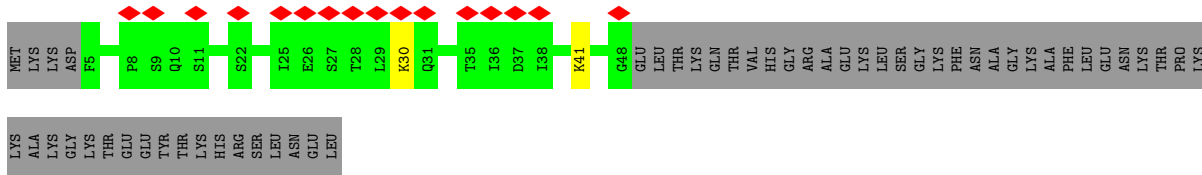


- Molecule 41: 50S ribosomal protein L21

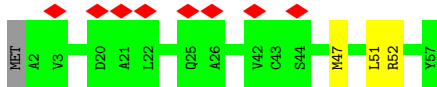
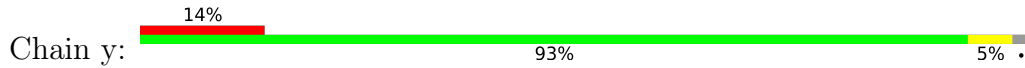


- Molecule 42: 50S ribosomal protein L22

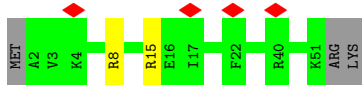
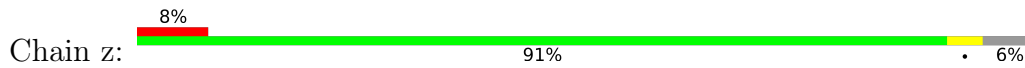




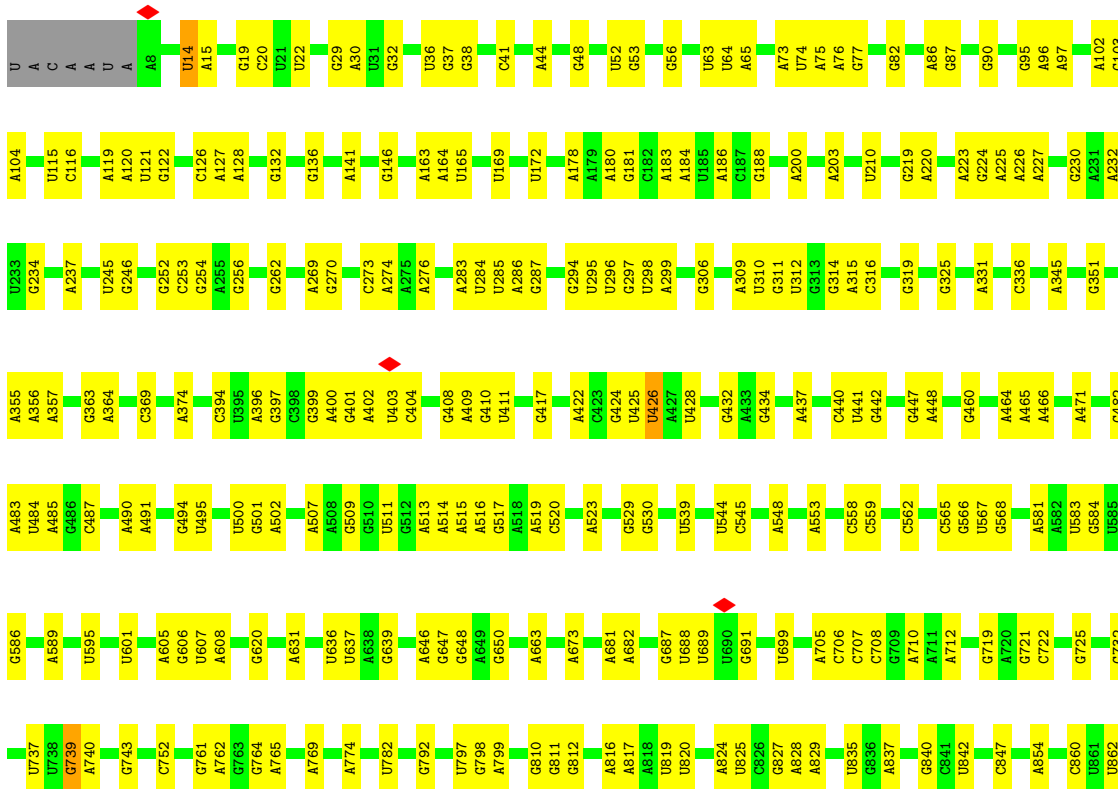
• Molecule 49: 50S ribosomal protein L32



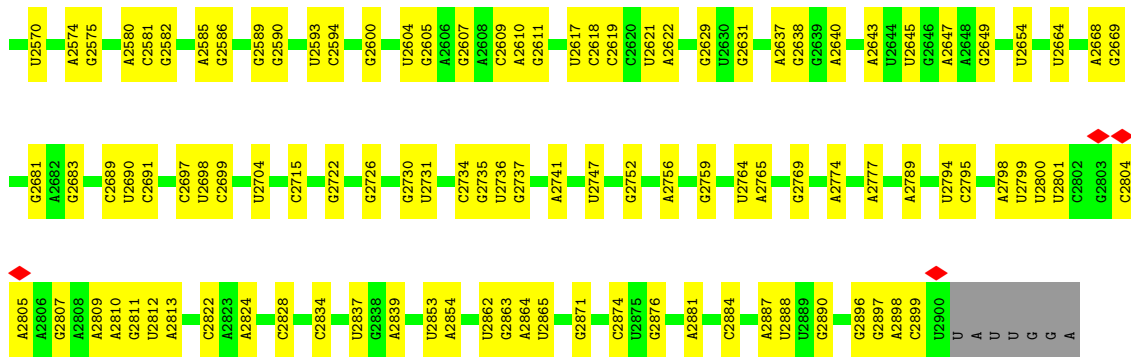
• Molecule 50: 50S ribosomal protein L33 1



• Molecule 51: 23S ribosomal RNA



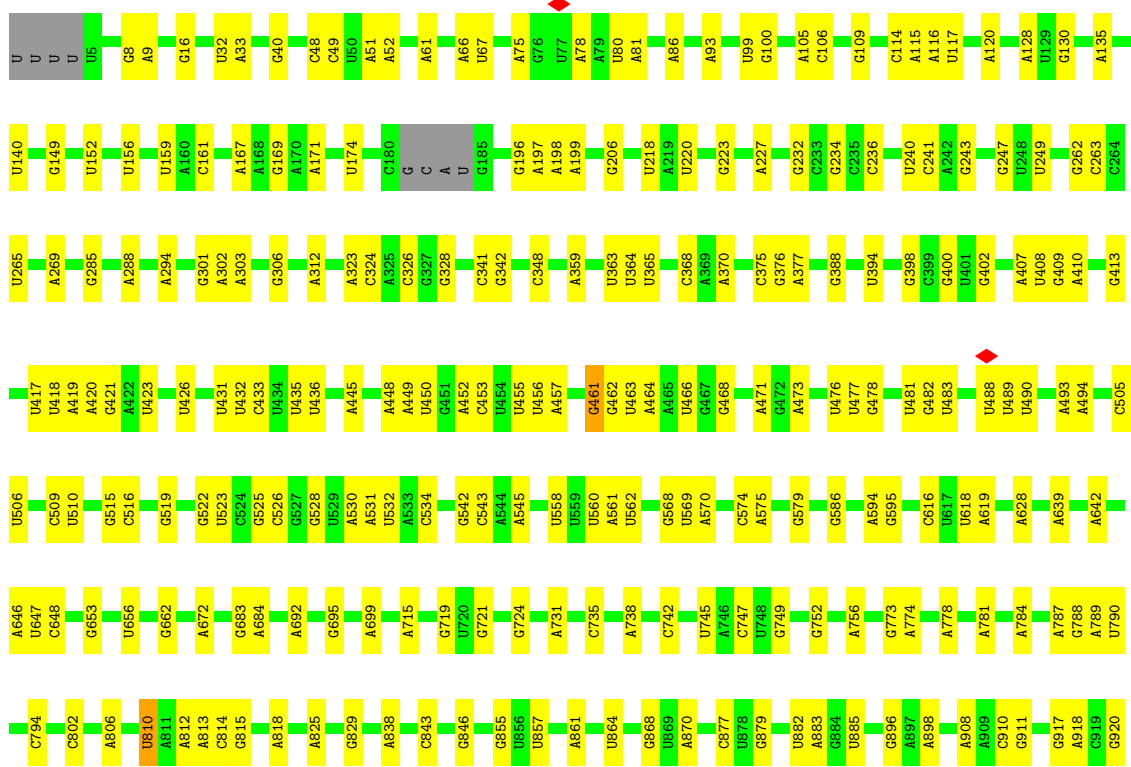
U863	U864	U865	U866	C880	U881	C882	A883	A884	A885	U886	A887	G895	U902	A903	C904	U905	G906	G914	G917	C921	C922	A	C	C	U	A	G928	G929	C930	G931	U932	A933	C934	U935	G936	A937	A940	U944	A947	C949	U952	G953	A964	U968	A969	U970				
A977	G982	U983	C984	G989	A1002	G1005	U1006	C1007	A1008	U1009	G1010	A1016	A1019	A1026	U1027	C1028	A1029	U1035	C1041	C1044	A1045	A1046	A1047	U1048	U1049	A1052	A1055	A1061	A1062	U1068	G1075	A1080	A1081	A1082	A1089															
G1090	G1091	U1095	U1096	C1099	A1102	G1103	A1104	A1105	U1106	C1107	A1108	C1111	G1115	A1123	G1124	U1125	G1126	A1130	A1131	C1132	U1141	G1145	A1146	G1147	U1151	U1154	U1165	G1166	U1167	A1168	A1169	C1170	G1171	U1176	A1177	A1178	C1187	G1188	G1189	A1190	A1191	U1192	U1193	A1202						
G1903	A1204	A1208	U1209	A1210	U1211	C1212	G1215	A1216	A1217	U1218	A1219	A1225	U1234	U1235	A1250	G1251	G1252	A1256	G1257	G1265	G1266	A1267	U1268	A1274	A1277	G1278	U1279	G1280	A1281	G1282	A1283	A1284	U1285	G1286	A1292	U1297	A1298	A1299	C1300	G1301	C1302	U1303	U1304	G1305	A1314	A1315				
U1316	C1317	A1322	C1325	A1328	U1329	U1330	G1331	G1338	U1341	G1353	G1356	U1357	U1360	U1368	U1369	A1370	G1371	U1374	G1375	G1376	A1377	C1378	U1380	A1387	G1388	A1393	A1406	U1407	G1408	A1412	A1420	A1421	U1422	A1423	U1424	U1425	A1431	U1434	C1444	U1445										
U1448	C1456	A1457	G1463	U1466	U1467	A1480	U1481	U1482	G1483	U1486	U1487	A1497	A1502	U1506	G1507	U1508	A1509	A1510	A1513	U1514	A1515	C1518	A1519	C1523	G1528	A1534	A1537	A1541	U1546	G1550	U1559	G1681	G1682	G1683	A1684	G1685	U1686	G1687	A1688	A1692										
A1570	G1571	A1577	G1582	U1583	U1584	A1585	U1586	A1588	U1589	U1593	G1594	A1600	A1603	G1607	U1612	G1615	G1616	U1617	U1618	A1619	A1630	A1631	G1632	A1641	G1642	A1643	C1645	C1651	A1652	C1653	A1661	A1669	G1681	G1682	G1683	A1684	G1685	U1686	G1687	A1688	A1692									
U1693	A1694	C1697	A1698	A1699	G1700	G1701	A1702	G1708	C1717	C1718	U1727	A1728	G1729	G1733	A1734	U1735	G1736	G1737	G1747	U1748	A1751	U1764	G1765	A1766	U1767	G1768	A1769	C1771	G1772	A1780	U1784	A1788	C1789	A1792	G1806	C1807	C1808	A1809	C1813	A1816	A1817	U1823								
A1828	A1836	C1839	G1842	C1845	C1850	A1855	G1866	U1871	U1872	A1873	A1883	C1886	U1890	A1891	A1892	C1893	C1902	A1903	G1906	A1907	G1913	C1916	A1920	C1921	U1922	A1923	A1934	U1938	A1943	A1944	A1945	U1950	A1951	G1952	U1953	G1954	G1955													
A1961	U1962	C1965	C1970	G1971	C1972	U1977	U1978	G1979	G1982	U1998	C1999	U2000	C2003	U2009	A2010	C2011	A2020	G2027	A2124	G2028	U2029	A2030	A2037	A2038	G2039	A2040	A2041	A2042	C2043	C2044	C2045	G2050	A2055	A2056	C2062	G2063	G2064	A2067	G2068	A2069	C2070	C2071	G2076	A2077	A2078					
U2083	A2084	G2087	A2095	U2099	G2100	G2106	A2107	C2108	A2109	U2110	U2111	A2112	U2113	C2114	A2115	U2116	U2117	U2118	A2119	A2123	A2124	U2125	A2126	A2127	G2128	U2129	G2130	G2131	G2132	A2133	G2134	C2135	U2138	C2139	G2140	C2152	U2153	A2154	G2155	U2159	G2284	G2285	A2286	U2291	A2165	U2166	A2170	A2171	A2172	G2173
U2180	A2181	C2182	C2187	U2188	U2193	G2194	U2195	G2198	C2199	U2200	G2201	U2202	U2203	C2204	U2205	A2206	G2211	U2218	U2219	A2220	U2221	C2222	U2226	U2227	U2228	A2231	A2232	A2233	G2246	G2247	G2258	G2267	A2274	A2275	A2276	U2280	G2284	G2285	A2286	U2291	A2294	A2295	A2296							
G2297	C2305	U2312	U2313	U2314	G2315	A2316	U2317	U2327	G2333	U2334	A2335	U2340	G2341	U2342	U2343	U2344	U2351	U2352	C2355	U2358	U2359	A2362	U2365	A2366	C2367	U2380	U2387	G2391	U2392	C2393	A2396	G2397	U2414	A2415	A2422	U2431	C2432	U2433	A2434	U2435	G2436	G2437	A2438	U2439						
A2442	A2443	G2444	U2449	G2455	A2456	U2457	A2458	A2459	C2460	U2468	C2475	A2484	U2485	A2486	U2487	G2492	A2495	G2498	U2499	G2502	G2503	C2504	C2505	C2506	C2507	G2510	G2513	U2514	A2521	C2525	A2526	C2528	A2538	A2539	G2543	G2544	A2545	G2551	U2555	C2556	G2557									

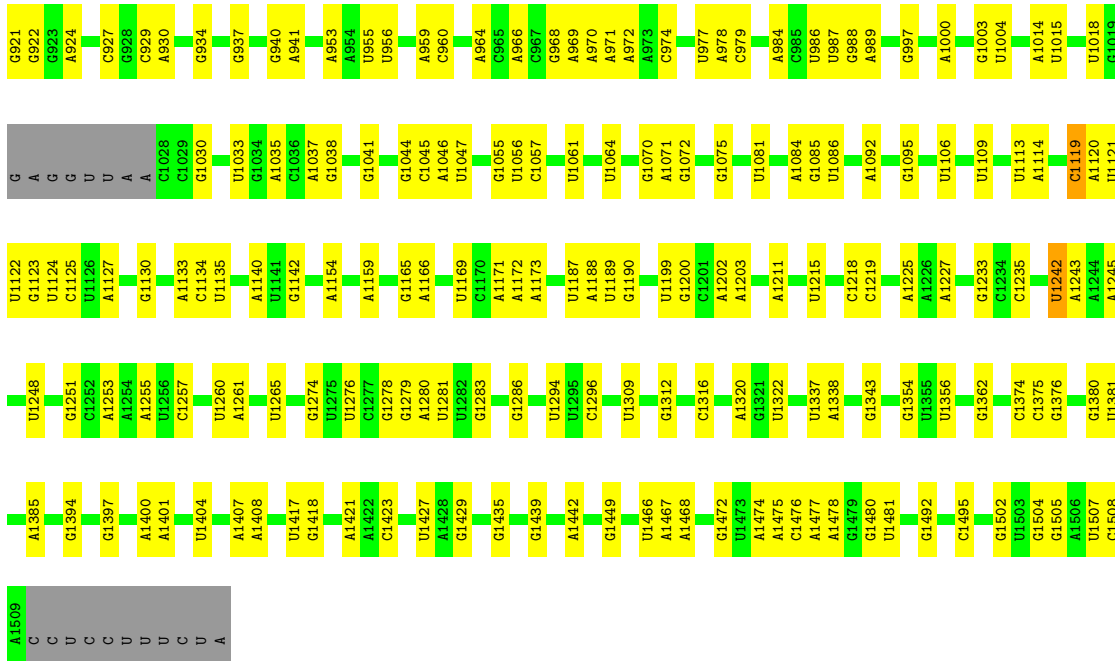


• Molecule 52: 5S ribosomal RNA

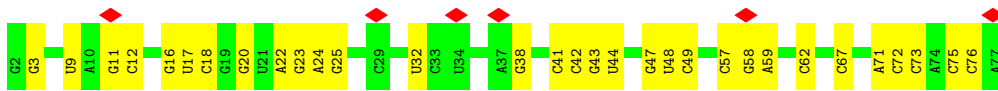


• Molecule 53: 16S ribosomal RNA





• Molecule 54: tRNA-Phe



• Molecule 54: tRNA-Phe



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	1128	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 ($e^-/\text{\AA}^2$)	3.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3750	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.595	Depositor
Minimum map value	-0.633	Depositor
Average map value	0.020	Depositor
Map value standard deviation	0.113	Depositor
Recommended contour level	0.39	Depositor
Map size (Å)	435.328, 435.328, 435.328	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.7005, 1.7005, 1.7005	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.24	0/383	0.51	0/504
2	1	0.23	0/484	0.46	0/637
3	2	0.22	0/306	0.48	0/401
4	9	0.25	0/3071	0.49	0/4147
5	A	0.25	0/1954	0.48	0/2642
6	B	0.25	0/1721	0.50	0/2323
7	C	0.26	0/1691	0.47	0/2267
8	D	0.25	0/1188	0.52	0/1593
9	E	0.26	0/1384	0.51	0/1867
10	F	0.26	0/1266	0.51	1/1700 (0.1%)
11	G	0.28	0/1126	0.58	0/1517
12	H	0.25	0/1044	0.46	0/1395
13	I	0.31	0/820	0.65	2/1103 (0.2%)
14	J	0.26	0/844	0.49	0/1136
15	K	0.28	0/1094	0.56	0/1468
16	L	0.27	0/962	0.54	1/1289 (0.1%)
17	M	0.24	0/483	0.47	0/643
18	N	0.26	0/679	0.47	0/907
19	O	0.26	0/659	0.53	0/885
20	P	0.24	0/684	0.46	0/913
21	Q	0.25	0/545	0.52	0/730
22	R	0.25	0/698	0.54	0/936
23	S	0.23	0/631	0.37	0/838
24	T	0.29	0/475	0.60	0/621
25	a	0.23	0/2267	0.46	0/3044
26	b	0.29	0/1795	0.55	0/2412
27	c	0.25	0/1671	0.50	0/2246
28	d	0.28	0/1409	0.52	0/1894
29	e	0.28	0/1420	0.55	0/1912
30	f	0.26	0/1183	0.56	0/1587
31	g	0.36	0/916	0.57	0/1222
32	h	0.27	0/968	0.50	0/1298
33	i	0.25	0/1186	0.50	0/1592
34	j	0.24	0/953	0.54	1/1275 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	k	0.25	0/1170	0.49	0/1559
36	l	0.27	0/1104	0.52	0/1481
37	m	0.24	0/973	0.52	0/1309
38	n	0.26	0/897	0.49	0/1198
39	o	0.24	0/948	0.49	0/1262
40	p	0.24	0/961	0.44	0/1278
41	q	0.26	0/828	0.56	0/1111
42	r	0.24	0/1077	0.48	0/1441
43	s	0.26	0/732	0.51	0/988
44	t	0.25	0/879	0.52	0/1165
45	u	0.25	0/665	0.52	0/884
46	v	0.30	0/519	0.56	0/695
47	w	0.24	0/826	0.49	0/1104
48	x	0.38	0/353	0.51	0/474
49	y	0.31	0/457	0.52	0/601
50	z	0.25	0/412	0.53	0/547
51	3	0.21	0/69073	0.81	31/107710 (0.0%)
52	4	0.24	0/2505	0.87	4/3902 (0.1%)
53	5	0.20	0/35768	0.79	15/55764 (0.0%)
54	6	0.23	0/1808	0.88	0/2817
54	7	0.23	0/1808	0.88	0/2817
All	All	0.22	0/161723	0.74	55/241051 (0.0%)

There are no bond length outliers.

All (55) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	I	99	PRO	CA-N-CD	-8.78	99.21	111.50
53	5	843	C	N3-C2-O2	-8.42	116.01	121.90
51	3	559	C	N3-C2-O2	-7.66	116.54	121.90
52	4	79	U	C2-N1-C1'	7.49	126.69	117.70
51	3	1916	C	N3-C2-O2	-7.18	116.87	121.90
52	4	79	U	N1-C2-O2	7.01	127.71	122.80
51	3	1718	C	N3-C2-O2	-6.83	117.12	121.90
51	3	1697	C	N3-C2-O2	-6.75	117.17	121.90
51	3	1341	U	C2-N1-C1'	6.66	125.69	117.70
51	3	708	C	N3-C2-O2	-6.64	117.25	121.90
52	4	79	U	N3-C2-O2	-6.61	117.57	122.20
34	j	58	LEU	CA-CB-CG	6.57	130.41	115.30
53	5	810	U	N1-C2-O2	6.50	127.35	122.80
51	3	1341	U	N1-C2-O2	6.47	127.33	122.80
53	5	648	C	N1-C2-O2	6.44	122.76	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	5	648	C	N3-C2-O2	-6.27	117.51	121.90
53	5	810	U	N3-C2-O2	-6.20	117.86	122.20
53	5	463	U	C2-N1-C1'	6.10	125.02	117.70
53	5	1219	C	N3-C2-O2	-6.09	117.64	121.90
51	3	2070	C	C2-N1-C1'	5.99	125.38	118.80
51	3	426	U	C2-N1-C1'	5.95	124.83	117.70
51	3	1341	U	N3-C2-O2	-5.93	118.05	122.20
53	5	810	U	C2-N1-C1'	5.87	124.74	117.70
51	3	1902	C	N3-C2-O2	-5.85	117.81	121.90
51	3	1507	G	O4'-C1'-N9	5.84	112.87	108.20
53	5	974	C	N1-C2-O2	5.83	122.40	118.90
51	3	1717	C	N1-C2-O2	5.79	122.38	118.90
53	5	1242	U	O4'-C1'-N1	5.76	112.80	108.20
53	5	461	G	O4'-C1'-N9	5.65	112.72	108.20
51	3	708	C	C6-N1-C2	-5.57	118.07	120.30
51	3	707	C	N1-C2-O2	5.54	122.22	118.90
53	5	1119	C	N1-C2-O2	5.52	122.21	118.90
51	3	904	C	C2-N1-C1'	5.49	124.83	118.80
51	3	2070	C	N1-C2-O2	5.37	122.12	118.90
51	3	739	G	O4'-C1'-N9	5.25	112.40	108.20
16	L	34	LEU	CA-CB-CG	5.25	127.37	115.30
53	5	974	C	C2-N1-C1'	5.24	124.56	118.80
53	5	463	U	N1-C2-O2	5.21	126.44	122.80
51	3	1507	G	C8-N9-C1'	5.19	133.75	127.00
51	3	1316	U	N1-C2-O2	5.19	126.43	122.80
51	3	1507	G	C4-N9-C1'	-5.18	119.77	126.50
51	3	1893	C	N1-C2-O2	5.17	122.00	118.90
13	I	99	PRO	N-CD-CG	-5.13	95.50	103.20
51	3	440	C	C2-N1-C1'	5.10	124.41	118.80
51	3	2199	C	N3-C2-O2	-5.09	118.34	121.90
10	F	98	LEU	CA-CB-CG	5.08	126.97	115.30
51	3	2691	C	N1-C2-O2	5.07	121.94	118.90
51	3	2874	C	N3-C2-O2	-5.06	118.36	121.90
51	3	1316	U	C2-N1-C1'	5.05	123.76	117.70
51	3	19	G	C5-C6-O6	5.05	131.63	128.60
51	3	14	U	C2-N1-C1'	5.04	123.75	117.70
52	4	54	U	P-O3'-C3'	5.02	125.72	119.70
53	5	843	C	N1-C2-O2	5.01	121.91	118.90
51	3	394	C	N3-C2-O2	-5.01	118.39	121.90
51	3	881	A	P-O3'-C3'	5.01	125.71	119.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	45/48 (94%)	43 (96%)	2 (4%)	0	100	100
2	1	57/59 (97%)	53 (93%)	4 (7%)	0	100	100
3	2	35/37 (95%)	31 (89%)	4 (11%)	0	100	100
4	9	391/394 (99%)	360 (92%)	31 (8%)	0	100	100
5	A	238/294 (81%)	212 (89%)	26 (11%)	0	100	100
6	B	213/273 (78%)	200 (94%)	13 (6%)	0	100	100
7	C	201/205 (98%)	191 (95%)	10 (5%)	0	100	100
8	D	151/219 (69%)	143 (95%)	8 (5%)	0	100	100
9	E	165/215 (77%)	143 (87%)	22 (13%)	0	100	100
10	F	152/155 (98%)	137 (90%)	15 (10%)	0	100	100
11	G	139/142 (98%)	123 (88%)	15 (11%)	1 (1%)	22	63
12	H	126/132 (96%)	121 (96%)	5 (4%)	0	100	100
13	I	99/108 (92%)	84 (85%)	15 (15%)	0	100	100
14	J	112/121 (93%)	106 (95%)	6 (5%)	0	100	100
15	K	134/139 (96%)	117 (87%)	17 (13%)	0	100	100
16	L	116/124 (94%)	104 (90%)	11 (10%)	1 (1%)	17	57
17	M	58/61 (95%)	55 (95%)	3 (5%)	0	100	100
18	N	81/86 (94%)	80 (99%)	1 (1%)	0	100	100
19	O	78/94 (83%)	70 (90%)	8 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	P	81/85 (95%)	79 (98%)	2 (2%)	0	100	100
21	Q	63/104 (61%)	54 (86%)	9 (14%)	0	100	100
22	R	82/87 (94%)	72 (88%)	10 (12%)	0	100	100
23	S	75/87 (86%)	75 (100%)	0	0	100	100
24	T	51/60 (85%)	49 (96%)	2 (4%)	0	100	100
25	a	283/287 (99%)	261 (92%)	22 (8%)	0	100	100
26	b	227/287 (79%)	209 (92%)	18 (8%)	0	100	100
27	c	208/212 (98%)	196 (94%)	12 (6%)	0	100	100
28	d	173/180 (96%)	160 (92%)	13 (8%)	0	100	100
29	e	174/184 (95%)	165 (95%)	8 (5%)	1 (1%)	25	66
30	f	143/149 (96%)	128 (90%)	14 (10%)	1 (1%)	22	63
31	g	117/161 (73%)	107 (92%)	7 (6%)	3 (3%)	5	31
32	h	126/137 (92%)	115 (91%)	11 (9%)	0	100	100
33	i	142/146 (97%)	128 (90%)	14 (10%)	0	100	100
34	j	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
35	k	146/151 (97%)	137 (94%)	9 (6%)	0	100	100
36	l	134/139 (96%)	125 (93%)	8 (6%)	1 (1%)	22	63
37	m	117/124 (94%)	114 (97%)	3 (3%)	0	100	100
38	n	108/116 (93%)	98 (91%)	10 (9%)	0	100	100
39	o	113/119 (95%)	102 (90%)	11 (10%)	0	100	100
40	p	112/127 (88%)	109 (97%)	3 (3%)	0	100	100
41	q	97/100 (97%)	85 (88%)	12 (12%)	0	100	100
42	r	137/159 (86%)	124 (90%)	13 (10%)	0	100	100
43	s	90/237 (38%)	86 (96%)	4 (4%)	0	100	100
44	t	109/111 (98%)	101 (93%)	8 (7%)	0	100	100
45	u	84/104 (81%)	81 (96%)	3 (4%)	0	100	100
46	v	61/65 (94%)	61 (100%)	0	0	100	100
47	w	96/111 (86%)	91 (95%)	5 (5%)	0	100	100
48	x	42/97 (43%)	35 (83%)	7 (17%)	0	100	100
49	y	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
50	z	48/53 (91%)	47 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	6204/7064 (88%)	5732 (92%)	464 (8%)	8 (0%)	54	86

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
31	g	88	GLU
29	e	169	ASP
31	g	32	MET
31	g	30	THR
11	G	105	PRO
16	L	112	PRO
36	l	12	PRO
30	f	19	VAL

5.3.2 Protein sidechains [i](#)

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	40/41 (98%)	40 (100%)	0	100	100
2	1	51/51 (100%)	51 (100%)	0	100	100
3	2	35/35 (100%)	35 (100%)	0	100	100
4	9	324/325 (100%)	322 (99%)	2 (1%)	86	92
5	A	212/262 (81%)	212 (100%)	0	100	100
6	B	180/232 (78%)	178 (99%)	2 (1%)	73	84
7	C	181/183 (99%)	181 (100%)	0	100	100
8	D	123/178 (69%)	117 (95%)	6 (5%)	25	50
9	E	150/196 (76%)	149 (99%)	1 (1%)	84	90
10	F	131/132 (99%)	131 (100%)	0	100	100
11	G	123/124 (99%)	118 (96%)	5 (4%)	30	55
12	H	111/115 (96%)	110 (99%)	1 (1%)	78	87
13	I	95/99 (96%)	93 (98%)	2 (2%)	53	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	J	91/97 (94%)	91 (100%)	0	100	100
15	K	117/120 (98%)	111 (95%)	6 (5%)	24	48
16	L	100/105 (95%)	97 (97%)	3 (3%)	41	63
17	M	47/48 (98%)	47 (100%)	0	100	100
18	N	76/78 (97%)	76 (100%)	0	100	100
19	O	69/82 (84%)	69 (100%)	0	100	100
20	P	73/75 (97%)	73 (100%)	0	100	100
21	Q	56/94 (60%)	56 (100%)	0	100	100
22	R	74/77 (96%)	74 (100%)	0	100	100
23	S	70/77 (91%)	69 (99%)	1 (1%)	67	80
24	T	49/56 (88%)	49 (100%)	0	100	100
25	a	241/243 (99%)	239 (99%)	2 (1%)	81	89
26	b	186/233 (80%)	185 (100%)	1 (0%)	88	93
27	c	182/184 (99%)	181 (100%)	1 (0%)	88	93
28	d	150/154 (97%)	150 (100%)	0	100	100
29	e	153/159 (96%)	153 (100%)	0	100	100
30	f	123/134 (92%)	118 (96%)	5 (4%)	30	55
31	g	96/129 (74%)	89 (93%)	7 (7%)	14	39
32	h	102/110 (93%)	102 (100%)	0	100	100
33	i	126/128 (98%)	126 (100%)	0	100	100
34	j	103/103 (100%)	102 (99%)	1 (1%)	76	86
35	k	123/126 (98%)	123 (100%)	0	100	100
36	l	113/115 (98%)	113 (100%)	0	100	100
37	m	105/109 (96%)	105 (100%)	0	100	100
38	n	96/99 (97%)	95 (99%)	1 (1%)	76	86
39	o	101/105 (96%)	99 (98%)	2 (2%)	55	74
40	p	100/108 (93%)	100 (100%)	0	100	100
41	q	90/91 (99%)	90 (100%)	0	100	100
42	r	116/132 (88%)	114 (98%)	2 (2%)	60	78
43	s	82/208 (39%)	81 (99%)	1 (1%)	71	83
44	t	96/96 (100%)	95 (99%)	1 (1%)	76	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	u	69/85 (81%)	68 (99%)	1 (1%)	67	80
46	v	58/60 (97%)	58 (100%)	0	100	100
47	w	87/98 (89%)	87 (100%)	0	100	100
48	x	41/86 (48%)	39 (95%)	2 (5%)	25	50
49	y	48/49 (98%)	45 (94%)	3 (6%)	18	43
50	z	47/50 (94%)	45 (96%)	2 (4%)	29	53
All	All	5412/6076 (89%)	5351 (99%)	61 (1%)	74	84

All (61) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	9	304	LYS
4	9	382	ARG
6	B	90	LYS
6	B	139	GLN
8	D	69	ARG
8	D	78	LYS
8	D	133	LYS
8	D	143	ARG
8	D	148	ARG
8	D	206	ARG
9	E	80	LYS
11	G	39	LYS
11	G	106	LEU
11	G	107	VAL
11	G	108	LEU
11	G	109	ASN
12	H	29	LYS
13	I	9	TYR
13	I	29	LYS
15	K	44	ARG
15	K	96	ARG
15	K	107	ARG
15	K	118	VAL
15	K	120	VAL
15	K	127	ARG
16	L	71	ARG
16	L	92	ARG
16	L	107	ARG
23	S	43	ASN

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Mol	Chain	Res	Type
25	a	67	ARG
25	a	73	ARG
26	b	208	ARG
27	c	189	ARG
30	f	14	LYS
30	f	15	ARG
30	f	47	ARG
30	f	82	LYS
30	f	114	LYS
31	g	27	PHE
31	g	44	LEU
31	g	45	PHE
31	g	46	LYS
31	g	86	VAL
31	g	87	ASN
31	g	90	VAL
34	j	66	LYS
38	n	17	LYS
39	o	56	ARG
39	o	95	LYS
42	r	9	ARG
42	r	128	ARG
43	s	5	ASN
44	t	96	LYS
45	u	18	LYS
48	x	30	LYS
48	x	41	LYS
49	y	47	MET
49	y	51	LEU
49	y	52	ARG
50	z	8	ARG
50	z	15	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
3	2	30	GLN
4	9	12	HIS
4	9	194	ASN
4	9	302	HIS
5	A	51	HIS
7	C	52	GLN

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Mol	Chain	Res	Type
7	C	81	GLN
11	G	58	GLN
15	K	25	HIS
15	K	125	GLN
18	N	2	GLN
18	N	35	GLN
20	P	5	GLN
20	P	42	HIS
22	R	53	ASN
23	S	63	ASN
26	b	171	HIS
27	c	50	HIS
27	c	81	ASN
29	e	77	ASN
30	f	124	HIS
33	i	126	HIS
34	j	56	GLN
35	k	39	GLN
35	k	83	ASN
36	l	13	HIS
36	l	108	ASN
42	r	7	GLN
42	r	38	ASN
44	t	17	ASN
47	w	64	ASN
50	z	28	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
51	3	2875/2907 (98%)	849 (29%)	29 (1%)
52	4	103/108 (95%)	38 (36%)	3 (2%)
53	5	1490/1520 (98%)	411 (27%)	7 (0%)
54	6	75/76 (98%)	30 (40%)	2 (2%)
54	7	75/76 (98%)	30 (40%)	2 (2%)
All	All	4618/4687 (98%)	1358 (29%)	43 (0%)

All (1358) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
51	3	14	U

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Mol	Chain	Res	Type
51	3	15	A
51	3	20	C
51	3	22	U
51	3	29	G
51	3	30	A
51	3	32	G
51	3	36	U
51	3	37	G
51	3	38	G
51	3	41	C
51	3	44	A
51	3	48	G
51	3	52	U
51	3	53	G
51	3	56	G
51	3	63	U
51	3	64	U
51	3	65	A
51	3	73	A
51	3	74	U
51	3	75	A
51	3	76	A
51	3	77	G
51	3	82	G
51	3	86	A
51	3	87	G
51	3	90	G
51	3	95	G
51	3	96	A
51	3	97	A
51	3	102	A
51	3	103	G
51	3	104	A
51	3	115	U
51	3	116	C
51	3	119	A
51	3	120	A
51	3	121	U
51	3	122	G
51	3	126	C
51	3	127	A
51	3	128	A

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Mol	Chain	Res	Type
51	3	132	G
51	3	136	G
51	3	141	A
51	3	146	G
51	3	163	A
51	3	164	A
51	3	165	U
51	3	169	U
51	3	172	U
51	3	178	A
51	3	180	A
51	3	181	G
51	3	183	A
51	3	184	A
51	3	186	A
51	3	188	G
51	3	200	A
51	3	203	A
51	3	210	U
51	3	219	G
51	3	220	A
51	3	223	A
51	3	224	G
51	3	225	A
51	3	226	A
51	3	227	A
51	3	230	G
51	3	232	A
51	3	234	G
51	3	237	A
51	3	245	U
51	3	246	G
51	3	252	G
51	3	253	C
51	3	254	G
51	3	256	G
51	3	262	G
51	3	269	A
51	3	270	G
51	3	273	C
51	3	274	A
51	3	276	A

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Mol	Chain	Res	Type
51	3	283	A
51	3	284	U
51	3	285	U
51	3	286	A
51	3	287	G
51	3	294	G
51	3	295	U
51	3	296	U
51	3	297	G
51	3	298	U
51	3	299	A
51	3	306	G
51	3	310	U
51	3	312	U
51	3	314	G
51	3	315	A
51	3	316	C
51	3	319	G
51	3	325	G
51	3	331	A
51	3	336	C
51	3	345	A
51	3	351	G
51	3	355	A
51	3	356	A
51	3	357	A
51	3	363	G
51	3	364	A
51	3	369	C
51	3	374	A
51	3	396	A
51	3	397	G
51	3	399	G
51	3	400	A
51	3	401	G
51	3	402	A
51	3	403	U
51	3	404	C
51	3	408	G
51	3	409	A
51	3	410	G
51	3	411	U

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Mol	Chain	Res	Type
51	3	417	G
51	3	422	A
51	3	424	G
51	3	425	U
51	3	426	U
51	3	428	U
51	3	432	G
51	3	434	G
51	3	437	A
51	3	441	U
51	3	442	G
51	3	447	G
51	3	448	A
51	3	460	G
51	3	464	A
51	3	465	A
51	3	466	A
51	3	471	A
51	3	482	G
51	3	483	A
51	3	484	U
51	3	485	A
51	3	487	C
51	3	490	A
51	3	491	A
51	3	494	G
51	3	495	U
51	3	500	U
51	3	501	G
51	3	502	A
51	3	507	A
51	3	509	G
51	3	511	U
51	3	514	A
51	3	515	A
51	3	516	A
51	3	517	G
51	3	519	A
51	3	520	C
51	3	523	A
51	3	529	G
51	3	530	G

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Mol	Chain	Res	Type
51	3	539	U
51	3	544	U
51	3	545	C
51	3	548	A
51	3	553	A
51	3	558	C
51	3	562	C
51	3	565	C
51	3	566	G
51	3	567	U
51	3	568	G
51	3	581	A
51	3	583	U
51	3	584	G
51	3	586	G
51	3	589	A
51	3	595	U
51	3	601	U
51	3	605	A
51	3	606	G
51	3	607	U
51	3	608	A
51	3	620	G
51	3	631	A
51	3	636	U
51	3	637	U
51	3	639	G
51	3	646	A
51	3	647	G
51	3	648	G
51	3	650	G
51	3	663	A
51	3	673	A
51	3	681	A
51	3	682	A
51	3	687	G
51	3	689	U
51	3	691	G
51	3	699	U
51	3	705	A
51	3	706	C
51	3	710	A

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Mol	Chain	Res	Type
51	3	712	A
51	3	719	G
51	3	721	G
51	3	722	C
51	3	725	G
51	3	732	G
51	3	737	U
51	3	739	G
51	3	740	A
51	3	743	G
51	3	752	C
51	3	761	G
51	3	762	A
51	3	764	G
51	3	765	A
51	3	769	A
51	3	774	A
51	3	782	U
51	3	792	G
51	3	797	U
51	3	798	G
51	3	799	A
51	3	810	G
51	3	811	G
51	3	812	G
51	3	816	A
51	3	817	A
51	3	819	U
51	3	820	U
51	3	824	A
51	3	825	U
51	3	827	G
51	3	828	A
51	3	829	A
51	3	835	U
51	3	837	A
51	3	840	G
51	3	842	U
51	3	847	C
51	3	854	A
51	3	860	C
51	3	862	U

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Mol	Chain	Res	Type
51	3	863	U
51	3	864	A
51	3	865	A
51	3	866	G
51	3	880	C
51	3	881	A
51	3	882	C
51	3	883	A
51	3	885	A
51	3	887	A
51	3	895	G
51	3	902	U
51	3	904	C
51	3	906	G
51	3	914	G
51	3	917	G
51	3	922	C
51	3	930	C
51	3	931	G
51	3	932	U
51	3	933	A
51	3	936	G
51	3	937	A
51	3	940	A
51	3	944	U
51	3	947	A
51	3	949	C
51	3	953	G
51	3	964	A
51	3	968	U
51	3	970	U
51	3	977	A
51	3	982	G
51	3	984	C
51	3	989	G
51	3	994	U
51	3	997	G
51	3	998	C
51	3	1001	C
51	3	1002	A
51	3	1005	G
51	3	1007	C

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Mol	Chain	Res	Type
51	3	1008	A
51	3	1009	A
51	3	1010	G
51	3	1016	A
51	3	1019	A
51	3	1026	A
51	3	1027	U
51	3	1029	A
51	3	1035	U
51	3	1041	C
51	3	1044	C
51	3	1046	A
51	3	1048	A
51	3	1049	U
51	3	1052	A
51	3	1055	A
51	3	1061	A
51	3	1062	A
51	3	1068	U
51	3	1075	G
51	3	1080	A
51	3	1081	A
51	3	1082	A
51	3	1089	A
51	3	1091	G
51	3	1095	U
51	3	1096	U
51	3	1099	C
51	3	1102	A
51	3	1103	G
51	3	1104	A
51	3	1105	A
51	3	1106	G
51	3	1107	C
51	3	1108	A
51	3	1111	C
51	3	1115	G
51	3	1123	A
51	3	1124	G
51	3	1125	U
51	3	1126	G
51	3	1130	A

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Mol	Chain	Res	Type
51	3	1132	C
51	3	1141	U
51	3	1145	G
51	3	1146	A
51	3	1147	G
51	3	1151	U
51	3	1154	U
51	3	1165	U
51	3	1166	G
51	3	1167	U
51	3	1168	A
51	3	1169	A
51	3	1170	C
51	3	1171	G
51	3	1176	U
51	3	1177	A
51	3	1178	A
51	3	1187	C
51	3	1189	G
51	3	1191	A
51	3	1193	U
51	3	1202	A
51	3	1204	A
51	3	1208	A
51	3	1209	U
51	3	1210	A
51	3	1212	C
51	3	1215	G
51	3	1216	U
51	3	1217	G
51	3	1219	U
51	3	1225	A
51	3	1234	U
51	3	1235	U
51	3	1250	A
51	3	1251	G
51	3	1253	G
51	3	1256	A
51	3	1257	G
51	3	1265	G
51	3	1266	G
51	3	1267	A

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Mol	Chain	Res	Type
51	3	1268	U
51	3	1274	A
51	3	1277	A
51	3	1279	U
51	3	1281	A
51	3	1283	A
51	3	1284	A
51	3	1285	U
51	3	1286	G
51	3	1292	A
51	3	1297	U
51	3	1298	A
51	3	1300	C
51	3	1301	G
51	3	1302	C
51	3	1304	U
51	3	1305	G
51	3	1314	A
51	3	1316	U
51	3	1317	C
51	3	1322	A
51	3	1325	C
51	3	1328	A
51	3	1329	U
51	3	1330	U
51	3	1331	G
51	3	1338	G
51	3	1353	G
51	3	1356	G
51	3	1357	U
51	3	1360	U
51	3	1368	U
51	3	1369	U
51	3	1371	G
51	3	1374	U
51	3	1376	G
51	3	1378	C
51	3	1380	U
51	3	1387	A
51	3	1388	G
51	3	1393	A
51	3	1406	A

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Mol	Chain	Res	Type
51	3	1407	U
51	3	1408	G
51	3	1412	A
51	3	1420	A
51	3	1422	U
51	3	1423	A
51	3	1424	U
51	3	1425	U
51	3	1431	A
51	3	1434	U
51	3	1444	C
51	3	1445	U
51	3	1448	U
51	3	1456	C
51	3	1457	A
51	3	1463	G
51	3	1466	U
51	3	1467	U
51	3	1480	A
51	3	1481	U
51	3	1482	U
51	3	1483	G
51	3	1486	U
51	3	1487	U
51	3	1497	A
51	3	1502	A
51	3	1506	U
51	3	1507	G
51	3	1508	G
51	3	1510	A
51	3	1513	A
51	3	1515	A
51	3	1518	C
51	3	1519	A
51	3	1523	C
51	3	1528	G
51	3	1534	A
51	3	1537	A
51	3	1541	A
51	3	1546	U
51	3	1550	G
51	3	1559	A

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Mol	Chain	Res	Type
51	3	1571	G
51	3	1577	A
51	3	1582	G
51	3	1584	U
51	3	1585	A
51	3	1586	U
51	3	1587	U
51	3	1588	A
51	3	1589	A
51	3	1593	U
51	3	1594	G
51	3	1600	A
51	3	1603	A
51	3	1607	G
51	3	1612	U
51	3	1615	G
51	3	1616	G
51	3	1617	U
51	3	1618	U
51	3	1619	A
51	3	1630	A
51	3	1632	C
51	3	1641	A
51	3	1642	G
51	3	1643	A
51	3	1644	A
51	3	1645	C
51	3	1651	C
51	3	1653	C
51	3	1661	A
51	3	1669	A
51	3	1681	G
51	3	1682	C
51	3	1683	G
51	3	1685	G
51	3	1687	G
51	3	1688	A
51	3	1692	A
51	3	1694	A
51	3	1698	A
51	3	1699	A
51	3	1701	G

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Mol	Chain	Res	Type
51	3	1702	A
51	3	1708	G
51	3	1727	U
51	3	1728	A
51	3	1729	G
51	3	1733	G
51	3	1734	A
51	3	1735	A
51	3	1737	G
51	3	1747	G
51	3	1748	U
51	3	1751	A
51	3	1764	U
51	3	1765	G
51	3	1766	A
51	3	1768	G
51	3	1769	A
51	3	1770	A
51	3	1771	C
51	3	1772	G
51	3	1780	A
51	3	1784	U
51	3	1788	A
51	3	1789	C
51	3	1792	A
51	3	1806	G
51	3	1807	C
51	3	1809	A
51	3	1813	C
51	3	1816	A
51	3	1817	A
51	3	1823	U
51	3	1828	A
51	3	1836	A
51	3	1839	C
51	3	1842	G
51	3	1845	C
51	3	1850	C
51	3	1855	A
51	3	1866	G
51	3	1871	U
51	3	1873	A

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Mol	Chain	Res	Type
51	3	1883	A
51	3	1886	C
51	3	1890	U
51	3	1891	A
51	3	1892	A
51	3	1903	A
51	3	1906	G
51	3	1907	A
51	3	1913	G
51	3	1920	A
51	3	1921	C
51	3	1923	A
51	3	1934	A
51	3	1938	U
51	3	1943	A
51	3	1944	A
51	3	1945	A
51	3	1950	U
51	3	1951	A
51	3	1952	G
51	3	1953	U
51	3	1955	G
51	3	1961	A
51	3	1962	U
51	3	1965	C
51	3	1970	C
51	3	1971	G
51	3	1972	C
51	3	1977	A
51	3	1978	U
51	3	1979	G
51	3	1982	G
51	3	1998	U
51	3	1999	G
51	3	2000	U
51	3	2003	C
51	3	2009	U
51	3	2011	G
51	3	2020	A
51	3	2027	G
51	3	2028	G
51	3	2030	A

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Mol	Chain	Res	Type
51	3	2037	A
51	3	2038	A
51	3	2039	G
51	3	2040	A
51	3	2041	C
51	3	2043	C
51	3	2045	C
51	3	2050	G
51	3	2055	A
51	3	2056	A
51	3	2062	C
51	3	2063	G
51	3	2064	G
51	3	2067	A
51	3	2068	G
51	3	2069	A
51	3	2070	C
51	3	2071	C
51	3	2076	G
51	3	2078	A
51	3	2083	U
51	3	2084	A
51	3	2087	G
51	3	2095	A
51	3	2099	U
51	3	2100	G
51	3	2106	G
51	3	2107	A
51	3	2109	A
51	3	2111	U
51	3	2112	A
51	3	2114	C
51	3	2115	A
51	3	2117	G
51	3	2123	A
51	3	2124	A
51	3	2125	U
51	3	2127	G
51	3	2130	A
51	3	2131	G
51	3	2133	A
51	3	2135	C

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Mol	Chain	Res	Type
51	3	2139	C
51	3	2140	G
51	3	2152	C
51	3	2153	U
51	3	2154	A
51	3	2155	G
51	3	2165	A
51	3	2166	U
51	3	2171	A
51	3	2173	G
51	3	2180	U
51	3	2182	C
51	3	2193	U
51	3	2194	G
51	3	2195	U
51	3	2198	G
51	3	2200	U
51	3	2201	G
51	3	2202	U
51	3	2203	U
51	3	2204	C
51	3	2206	A
51	3	2211	G
51	3	2218	U
51	3	2220	A
51	3	2221	U
51	3	2222	C
51	3	2226	U
51	3	2227	U
51	3	2228	U
51	3	2231	A
51	3	2233	A
51	3	2246	G
51	3	2247	G
51	3	2258	G
51	3	2267	G
51	3	2274	A
51	3	2275	A
51	3	2276	A
51	3	2280	U
51	3	2284	G
51	3	2286	A

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Mol	Chain	Res	Type
51	3	2291	U
51	3	2294	A
51	3	2295	A
51	3	2296	A
51	3	2297	G
51	3	2305	C
51	3	2312	G
51	3	2313	U
51	3	2315	G
51	3	2316	G
51	3	2317	A
51	3	2327	U
51	3	2333	G
51	3	2335	A
51	3	2340	U
51	3	2341	G
51	3	2342	U
51	3	2343	A
51	3	2351	U
51	3	2352	U
51	3	2355	C
51	3	2358	U
51	3	2362	A
51	3	2365	U
51	3	2367	C
51	3	2380	U
51	3	2387	U
51	3	2391	G
51	3	2393	C
51	3	2396	A
51	3	2397	G
51	3	2414	U
51	3	2415	A
51	3	2422	G
51	3	2431	U
51	3	2433	A
51	3	2435	C
51	3	2436	G
51	3	2437	G
51	3	2438	A
51	3	2439	U
51	3	2442	A

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Mol	Chain	Res	Type
51	3	2444	G
51	3	2449	U
51	3	2455	G
51	3	2457	U
51	3	2458	A
51	3	2460	C
51	3	2468	U
51	3	2475	C
51	3	2484	A
51	3	2486	A
51	3	2487	U
51	3	2492	G
51	3	2495	A
51	3	2498	G
51	3	2499	U
51	3	2502	G
51	3	2504	C
51	3	2505	A
51	3	2506	C
51	3	2507	C
51	3	2510	G
51	3	2513	G
51	3	2514	U
51	3	2521	A
51	3	2525	C
51	3	2526	A
51	3	2528	C
51	3	2538	A
51	3	2539	A
51	3	2543	G
51	3	2544	G
51	3	2551	G
51	3	2555	U
51	3	2557	G
51	3	2570	U
51	3	2574	A
51	3	2575	G
51	3	2580	A
51	3	2581	C
51	3	2582	G
51	3	2585	A
51	3	2586	G

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Mol	Chain	Res	Type
51	3	2589	G
51	3	2590	G
51	3	2593	U
51	3	2594	C
51	3	2600	G
51	3	2604	U
51	3	2605	G
51	3	2607	G
51	3	2609	C
51	3	2610	A
51	3	2611	G
51	3	2617	U
51	3	2618	C
51	3	2619	C
51	3	2621	U
51	3	2622	A
51	3	2629	G
51	3	2631	G
51	3	2637	A
51	3	2638	G
51	3	2640	A
51	3	2643	A
51	3	2645	U
51	3	2647	A
51	3	2649	G
51	3	2654	U
51	3	2664	U
51	3	2669	G
51	3	2681	G
51	3	2683	G
51	3	2689	C
51	3	2690	U
51	3	2697	C
51	3	2698	U
51	3	2699	C
51	3	2704	U
51	3	2715	C
51	3	2722	G
51	3	2726	G
51	3	2730	G
51	3	2731	U
51	3	2734	C

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Mol	Chain	Res	Type
51	3	2735	G
51	3	2736	U
51	3	2737	G
51	3	2741	A
51	3	2747	U
51	3	2752	G
51	3	2756	A
51	3	2759	G
51	3	2764	U
51	3	2765	A
51	3	2769	G
51	3	2774	A
51	3	2777	A
51	3	2789	A
51	3	2794	U
51	3	2795	C
51	3	2798	A
51	3	2799	U
51	3	2800	U
51	3	2801	U
51	3	2804	C
51	3	2805	A
51	3	2807	G
51	3	2809	A
51	3	2810	A
51	3	2811	G
51	3	2812	U
51	3	2813	A
51	3	2822	C
51	3	2824	A
51	3	2828	C
51	3	2834	C
51	3	2837	U
51	3	2839	A
51	3	2853	U
51	3	2854	A
51	3	2863	G
51	3	2864	A
51	3	2865	U
51	3	2871	G
51	3	2876	G
51	3	2881	A

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Mol	Chain	Res	Type
51	3	2884	C
51	3	2887	A
51	3	2888	U
51	3	2890	G
51	3	2896	G
51	3	2897	G
51	3	2898	A
51	3	2899	C
52	4	8	C
52	4	10	C
52	4	11	A
52	4	20	U
52	4	22	G
52	4	23	A
52	4	25	A
52	4	26	C
52	4	28	C
52	4	31	G
52	4	32	G
52	4	33	U
52	4	35	C
52	4	38	U
52	4	40	U
52	4	41	C
52	4	42	G
52	4	44	A
52	4	48	A
52	4	49	G
52	4	52	G
52	4	55	A
52	4	60	C
52	4	65	G
52	4	66	A
52	4	74	G
52	4	76	A
52	4	77	G
52	4	78	C
52	4	79	U
52	4	80	G
52	4	86	G
52	4	88	G
52	4	89	A

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Mol	Chain	Res	Type
52	4	97	A
52	4	99	A
52	4	102	A
52	4	108	C
53	5	8	G
53	5	9	A
53	5	16	G
53	5	32	U
53	5	33	A
53	5	40	G
53	5	48	C
53	5	49	C
53	5	51	A
53	5	52	A
53	5	61	A
53	5	66	A
53	5	67	U
53	5	75	A
53	5	78	A
53	5	80	U
53	5	81	A
53	5	86	A
53	5	93	A
53	5	99	U
53	5	100	G
53	5	105	A
53	5	106	C
53	5	109	G
53	5	114	C
53	5	115	A
53	5	116	A
53	5	117	U
53	5	120	A
53	5	128	A
53	5	130	G
53	5	135	A
53	5	140	U
53	5	149	G
53	5	152	U
53	5	156	U
53	5	159	U
53	5	161	C

Continued on next page...

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Mol	Chain	Res	Type
53	5	167	A
53	5	169	G
53	5	171	A
53	5	174	U
53	5	197	A
53	5	198	A
53	5	199	A
53	5	206	G
53	5	218	U
53	5	220	U
53	5	223	G
53	5	227	A
53	5	232	G
53	5	234	G
53	5	236	C
53	5	240	U
53	5	241	C
53	5	243	G
53	5	247	G
53	5	249	U
53	5	262	G
53	5	263	C
53	5	265	U
53	5	269	A
53	5	285	G
53	5	288	A
53	5	294	A
53	5	301	G
53	5	302	A
53	5	303	A
53	5	306	G
53	5	312	A
53	5	323	A
53	5	324	C
53	5	326	C
53	5	328	G
53	5	341	C
53	5	342	G
53	5	348	C
53	5	359	A
53	5	363	U
53	5	364	U

Continued on next page...

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Mol	Chain	Res	Type
53	5	365	U
53	5	368	C
53	5	370	A
53	5	375	C
53	5	376	G
53	5	377	A
53	5	388	G
53	5	394	U
53	5	398	G
53	5	400	G
53	5	402	G
53	5	407	A
53	5	408	U
53	5	409	G
53	5	410	A
53	5	413	G
53	5	417	U
53	5	418	U
53	5	419	A
53	5	420	A
53	5	421	G
53	5	423	U
53	5	426	U
53	5	431	U
53	5	432	U
53	5	433	C
53	5	435	U
53	5	436	U
53	5	445	A
53	5	449	A
53	5	450	U
53	5	452	A
53	5	453	C
53	5	455	U
53	5	456	U
53	5	457	A
53	5	461	G
53	5	462	G
53	5	464	A
53	5	466	U
53	5	468	G
53	5	471	A

Continued on next page...

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Mol	Chain	Res	Type
53	5	473	A
53	5	476	U
53	5	477	U
53	5	478	G
53	5	481	U
53	5	482	G
53	5	483	U
53	5	488	U
53	5	489	U
53	5	490	U
53	5	493	A
53	5	494	A
53	5	505	C
53	5	506	U
53	5	509	C
53	5	510	U
53	5	515	G
53	5	516	C
53	5	519	G
53	5	522	G
53	5	523	U
53	5	525	G
53	5	526	C
53	5	528	G
53	5	530	A
53	5	531	A
53	5	532	U
53	5	534	C
53	5	542	G
53	5	543	C
53	5	545	A
53	5	558	U
53	5	560	U
53	5	561	A
53	5	562	U
53	5	568	G
53	5	569	U
53	5	570	A
53	5	574	C
53	5	575	A
53	5	579	G
53	5	586	G

Continued on next page...

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Mol	Chain	Res	Type
53	5	594	A
53	5	595	G
53	5	616	C
53	5	618	U
53	5	619	A
53	5	628	A
53	5	639	A
53	5	642	A
53	5	646	A
53	5	647	U
53	5	653	G
53	5	656	U
53	5	662	G
53	5	672	A
53	5	683	G
53	5	684	A
53	5	692	A
53	5	695	G
53	5	699	A
53	5	715	A
53	5	719	G
53	5	721	G
53	5	724	G
53	5	731	A
53	5	735	C
53	5	738	A
53	5	742	C
53	5	745	U
53	5	747	C
53	5	749	G
53	5	752	G
53	5	756	A
53	5	773	G
53	5	774	A
53	5	778	A
53	5	781	A
53	5	784	A
53	5	787	A
53	5	788	G
53	5	789	A
53	5	790	U
53	5	794	C

Continued on next page...

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Mol	Chain	Res	Type
53	5	802	C
53	5	806	A
53	5	810	U
53	5	812	A
53	5	813	A
53	5	814	C
53	5	815	G
53	5	818	A
53	5	825	A
53	5	829	G
53	5	838	A
53	5	846	G
53	5	855	G
53	5	857	U
53	5	861	A
53	5	864	U
53	5	868	G
53	5	870	A
53	5	877	C
53	5	879	G
53	5	882	U
53	5	883	A
53	5	885	U
53	5	896	G
53	5	898	A
53	5	908	A
53	5	910	C
53	5	911	G
53	5	917	G
53	5	918	A
53	5	921	G
53	5	922	G
53	5	924	A
53	5	927	C
53	5	929	C
53	5	930	A
53	5	934	G
53	5	937	G
53	5	940	G
53	5	941	A
53	5	953	A
53	5	955	U

Continued on next page...

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Mol	Chain	Res	Type
53	5	956	U
53	5	959	A
53	5	960	C
53	5	964	A
53	5	966	A
53	5	968	G
53	5	969	A
53	5	970	A
53	5	971	A
53	5	972	A
53	5	977	U
53	5	978	A
53	5	979	C
53	5	984	A
53	5	986	U
53	5	987	U
53	5	988	G
53	5	989	A
53	5	997	G
53	5	1000	A
53	5	1003	G
53	5	1004	U
53	5	1014	A
53	5	1015	U
53	5	1018	U
53	5	1030	G
53	5	1033	U
53	5	1035	A
53	5	1037	A
53	5	1038	G
53	5	1041	G
53	5	1044	G
53	5	1045	C
53	5	1046	A
53	5	1047	U
53	5	1055	G
53	5	1056	U
53	5	1057	C
53	5	1061	U
53	5	1064	U
53	5	1070	G
53	5	1071	A

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Mol	Chain	Res	Type
53	5	1072	G
53	5	1075	G
53	5	1081	U
53	5	1084	A
53	5	1085	G
53	5	1086	U
53	5	1092	A
53	5	1095	G
53	5	1106	U
53	5	1109	U
53	5	1113	U
53	5	1114	A
53	5	1119	C
53	5	1120	A
53	5	1121	U
53	5	1122	U
53	5	1123	G
53	5	1124	U
53	5	1125	C
53	5	1127	A
53	5	1130	G
53	5	1134	C
53	5	1135	U
53	5	1140	A
53	5	1142	G
53	5	1154	A
53	5	1159	A
53	5	1165	G
53	5	1166	A
53	5	1169	U
53	5	1171	A
53	5	1172	A
53	5	1173	A
53	5	1187	U
53	5	1188	A
53	5	1189	U
53	5	1190	G
53	5	1199	U
53	5	1200	G
53	5	1202	A
53	5	1203	A
53	5	1211	A

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Mol	Chain	Res	Type
53	5	1215	U
53	5	1218	C
53	5	1225	A
53	5	1227	A
53	5	1233	G
53	5	1235	C
53	5	1242	U
53	5	1243	A
53	5	1245	A
53	5	1248	U
53	5	1251	G
53	5	1253	A
53	5	1255	A
53	5	1257	C
53	5	1260	U
53	5	1261	A
53	5	1265	U
53	5	1274	G
53	5	1276	U
53	5	1278	G
53	5	1279	G
53	5	1280	A
53	5	1281	U
53	5	1283	G
53	5	1286	G
53	5	1294	U
53	5	1296	C
53	5	1309	U
53	5	1312	G
53	5	1316	C
53	5	1320	A
53	5	1322	U
53	5	1337	U
53	5	1338	A
53	5	1343	G
53	5	1354	G
53	5	1356	U
53	5	1362	G
53	5	1374	C
53	5	1375	C
53	5	1376	G
53	5	1380	G

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Mol	Chain	Res	Type
53	5	1381	U
53	5	1385	A
53	5	1394	G
53	5	1397	G
53	5	1400	A
53	5	1401	A
53	5	1404	U
53	5	1407	A
53	5	1408	A
53	5	1417	U
53	5	1418	G
53	5	1421	A
53	5	1423	C
53	5	1427	U
53	5	1429	G
53	5	1435	G
53	5	1439	G
53	5	1442	A
53	5	1449	G
53	5	1466	U
53	5	1467	A
53	5	1468	A
53	5	1472	G
53	5	1474	A
53	5	1475	A
53	5	1476	C
53	5	1477	A
53	5	1478	A
53	5	1480	G
53	5	1481	U
53	5	1492	G
53	5	1495	C
53	5	1502	G
53	5	1504	G
53	5	1505	G
53	5	1507	U
53	5	1508	C
54	6	3	G
54	6	9	U
54	6	11	G
54	6	12	C
54	6	17	U

Continued on next page...

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Mol	Chain	Res	Type
54	6	18	C
54	6	20	G
54	6	22	A
54	6	23	G
54	6	24	A
54	6	25	G
54	6	32	U
54	6	38	G
54	6	41	C
54	6	42	C
54	6	43	G
54	6	44	U
54	6	47	G
54	6	48	U
54	6	49	C
54	6	57	C
54	6	58	G
54	6	59	A
54	6	62	C
54	6	67	C
54	6	71	A
54	6	72	C
54	6	73	C
54	6	75	C
54	6	76	C
54	7	3	G
54	7	9	U
54	7	11	G
54	7	12	C
54	7	17	U
54	7	18	C
54	7	20	G
54	7	22	A
54	7	23	G
54	7	24	A
54	7	25	G
54	7	32	U
54	7	38	G
54	7	41	C
54	7	42	C
54	7	43	G
54	7	44	U

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Mol	Chain	Res	Type
54	7	47	G
54	7	48	U
54	7	49	C
54	7	57	C
54	7	58	G
54	7	59	A
54	7	62	C
54	7	67	C
54	7	71	A
54	7	72	C
54	7	73	C
54	7	75	C
54	7	76	C

All (43) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
51	3	309	A
51	3	311	G
51	3	315	A
51	3	410	G
51	3	425	U
51	3	500	U
51	3	513	A
51	3	688	U
51	3	881	A
51	3	935	U
51	3	936	G
51	3	952	U
51	3	1048	A
51	3	1124	G
51	3	1209	U
51	3	1216	U
51	3	1297	U
51	3	1507	G
51	3	1583	G
51	3	1587	U
51	3	1588	A
51	3	2124	A
51	3	2219	U
51	3	2504	C
51	3	2604	U

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Mol	Chain	Res	Type
51	3	2668	A
51	3	2764	U
51	3	2862	U
51	3	2897	G
52	4	10	C
52	4	54	U
52	4	59	A
53	5	8	G
53	5	196	G
53	5	448	A
53	5	618	U
53	5	787	A
53	5	920	G
53	5	1133	A
54	6	16	G
54	6	48	U
54	7	16	G
54	7	48	U

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

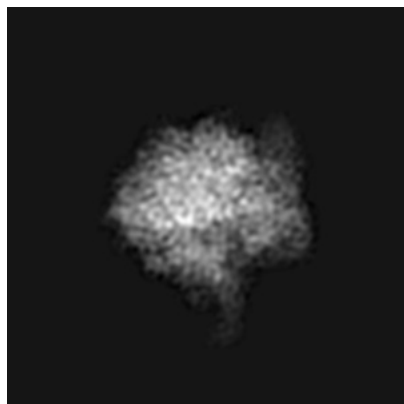
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13446. These allow visual inspection of the internal detail of the map and identification of artifacts.

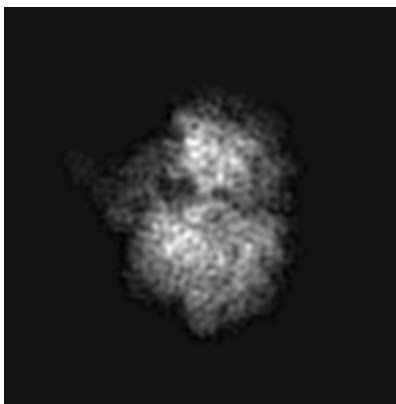
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

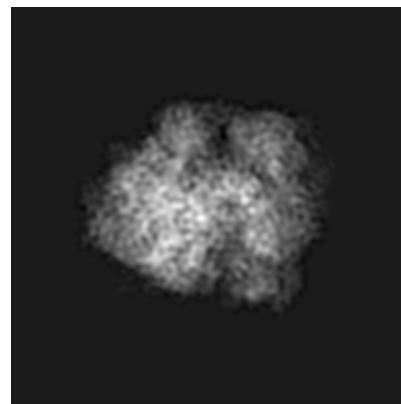
6.1.1 Primary map



X

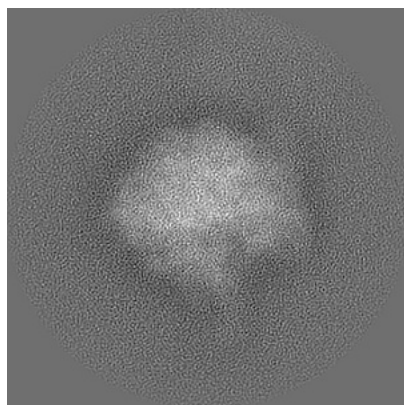


Y

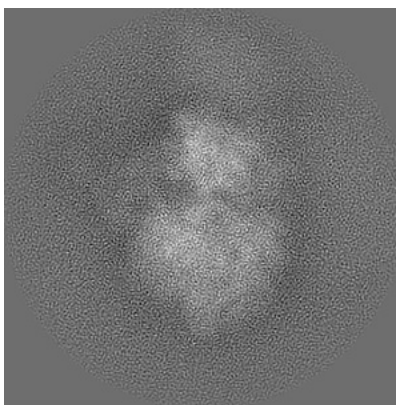


Z

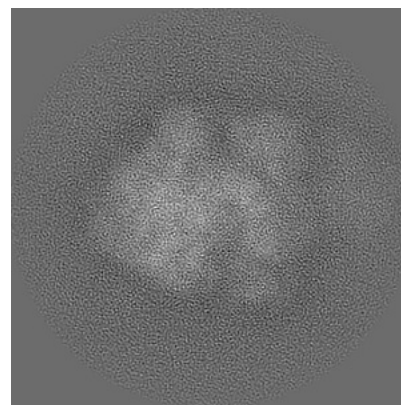
6.1.2 Raw map



X



Y

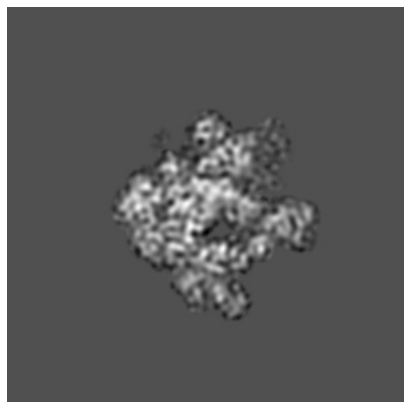


Z

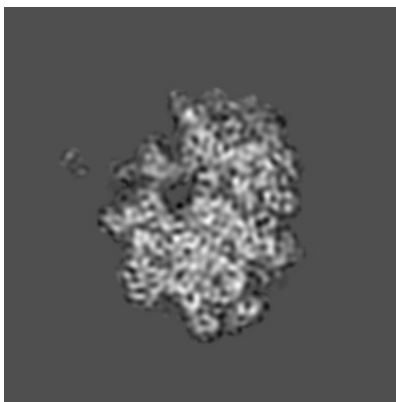
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

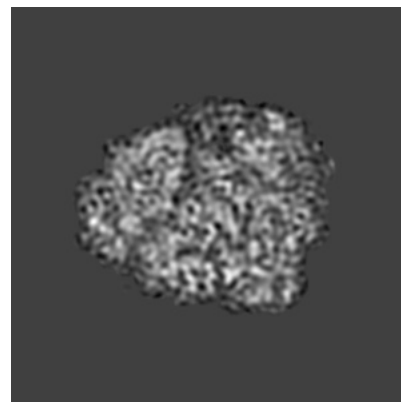
6.2.1 Primary map



X Index: 128

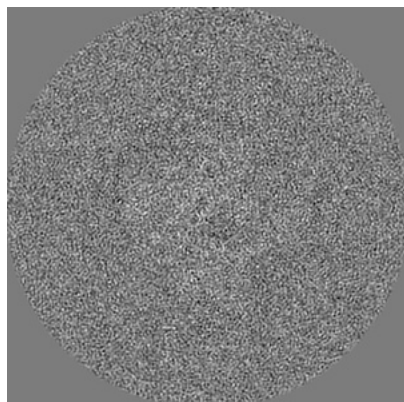


Y Index: 128

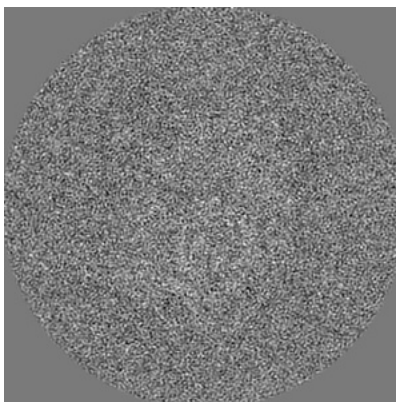


Z Index: 128

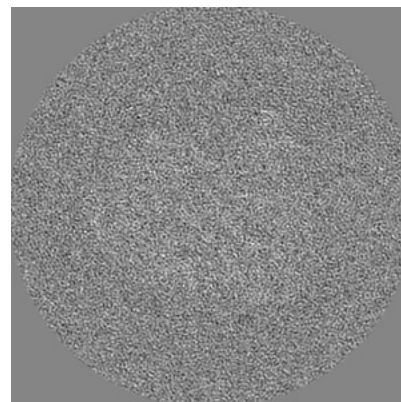
6.2.2 Raw map



X Index: 128



Y Index: 128

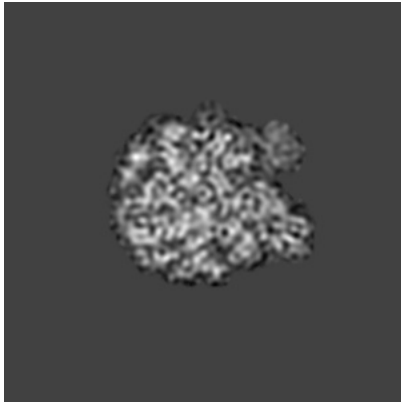


Z Index: 128

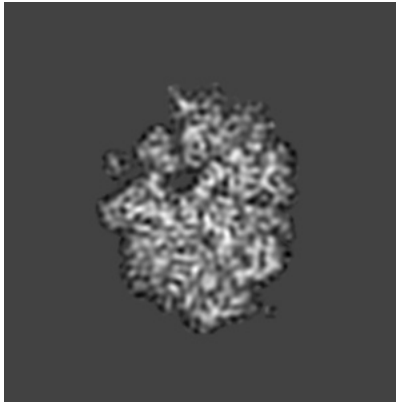
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

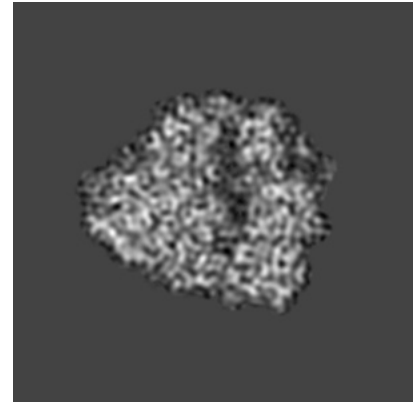
6.3.1 Primary map



X Index: 103

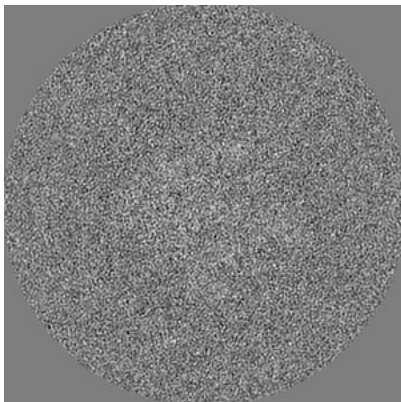


Y Index: 121

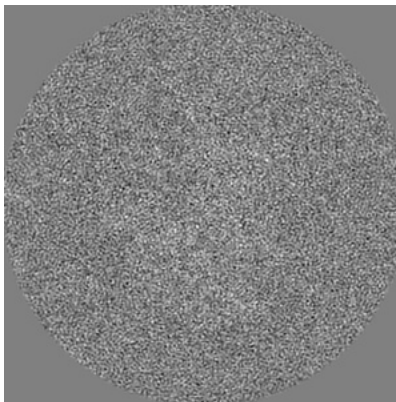


Z Index: 121

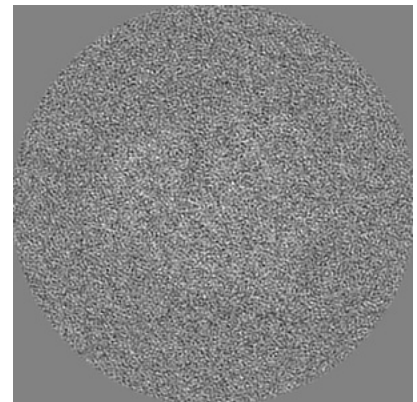
6.3.2 Raw map



X Index: 125



Y Index: 127

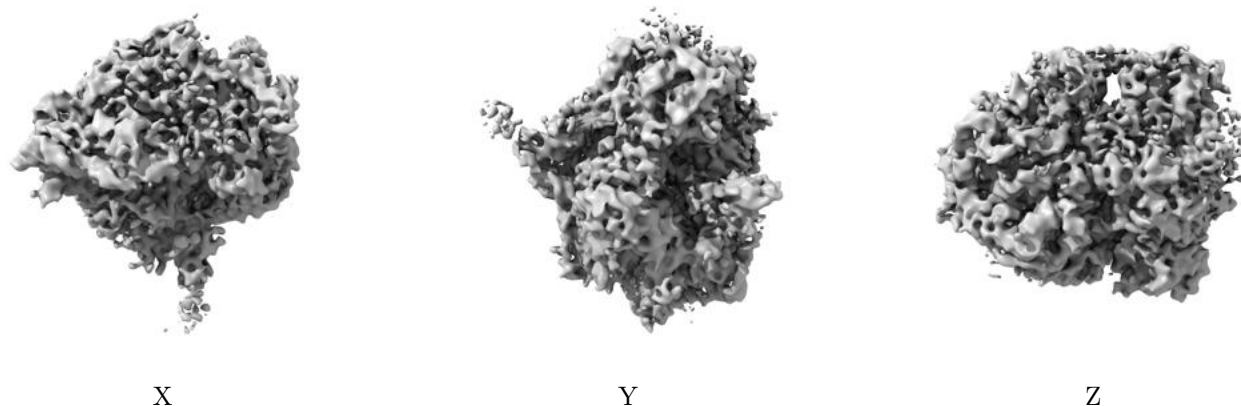


Z Index: 129

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

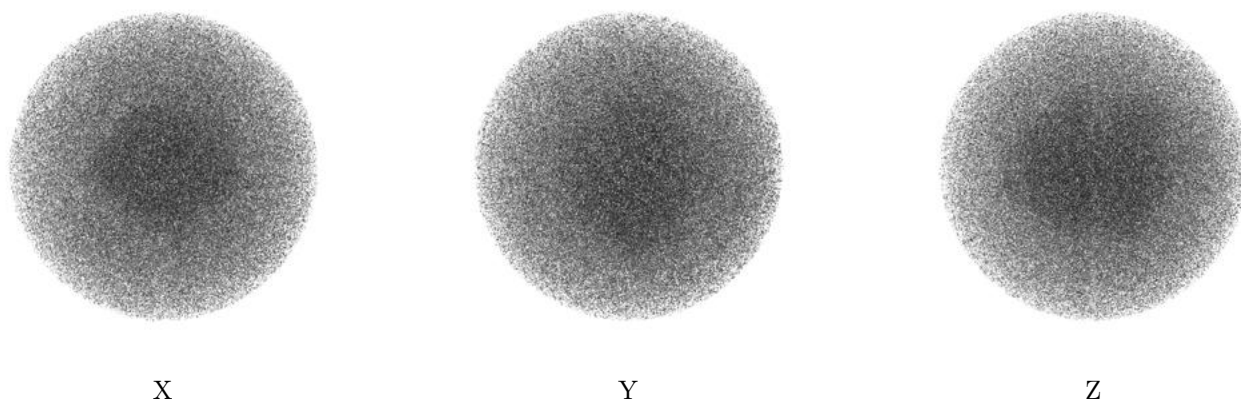
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.39. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map



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

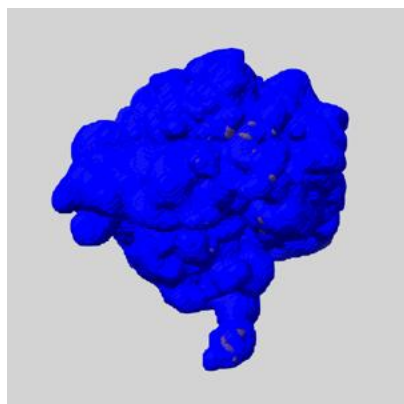
6.5 Mask visualisation [i](#)

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

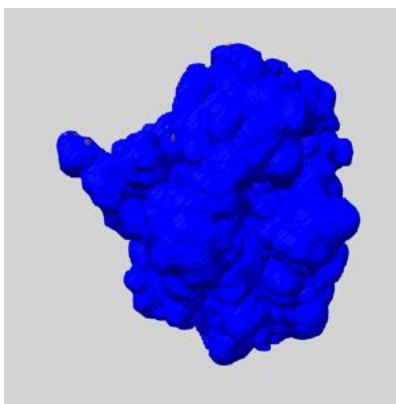
A mask typically either:

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

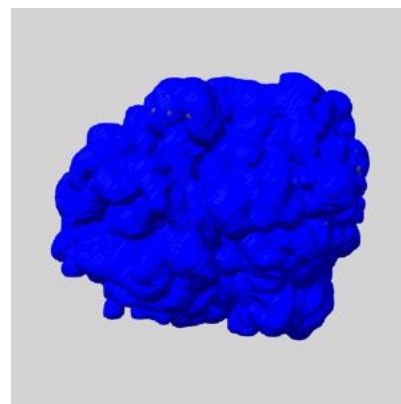
6.5.1 emd_13446_msk_1.map [i](#)



X



Y

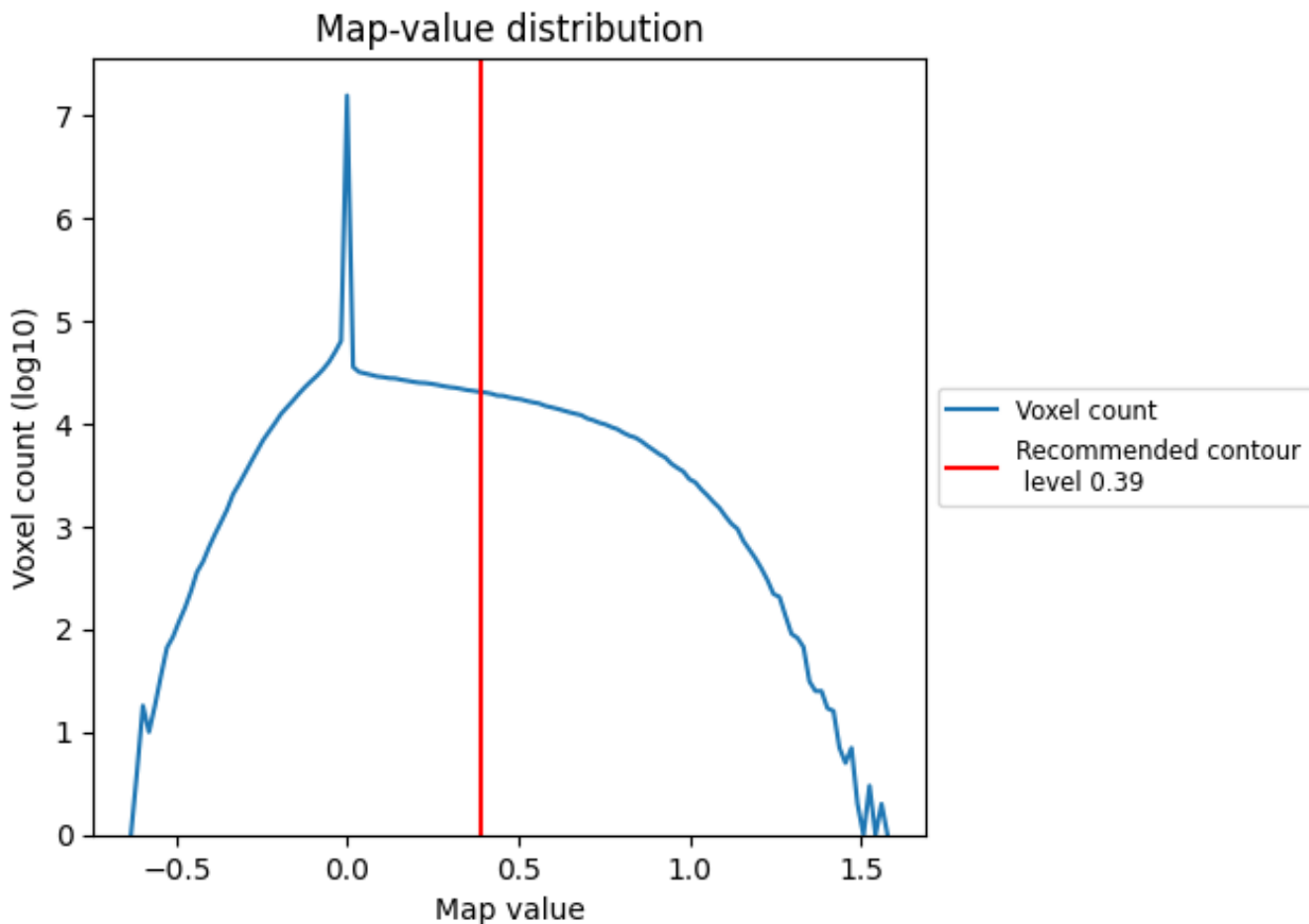


Z

7 Map analysis [i](#)

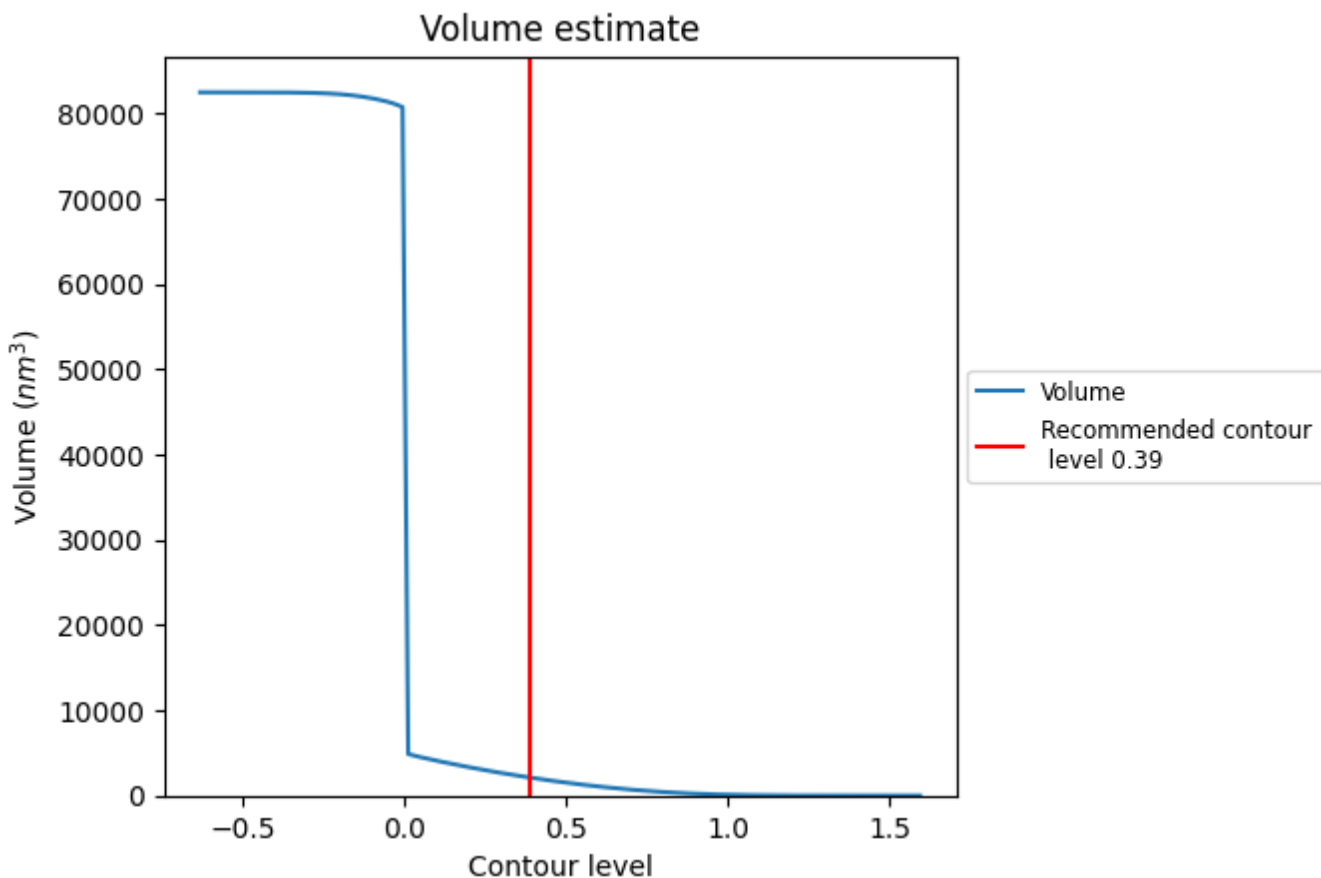
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

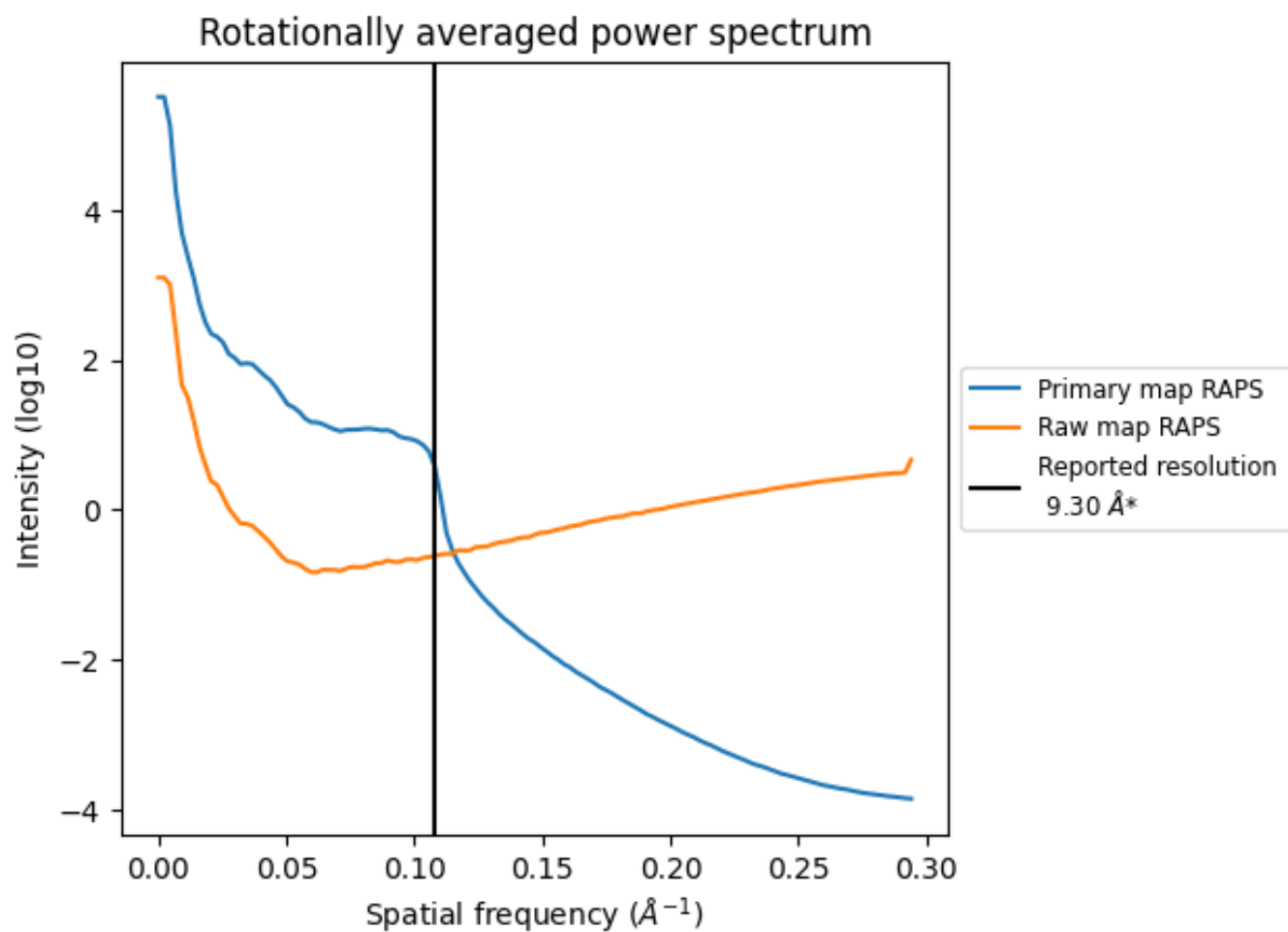
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2100 nm³; this corresponds to an approximate mass of 1897 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 [i](#)

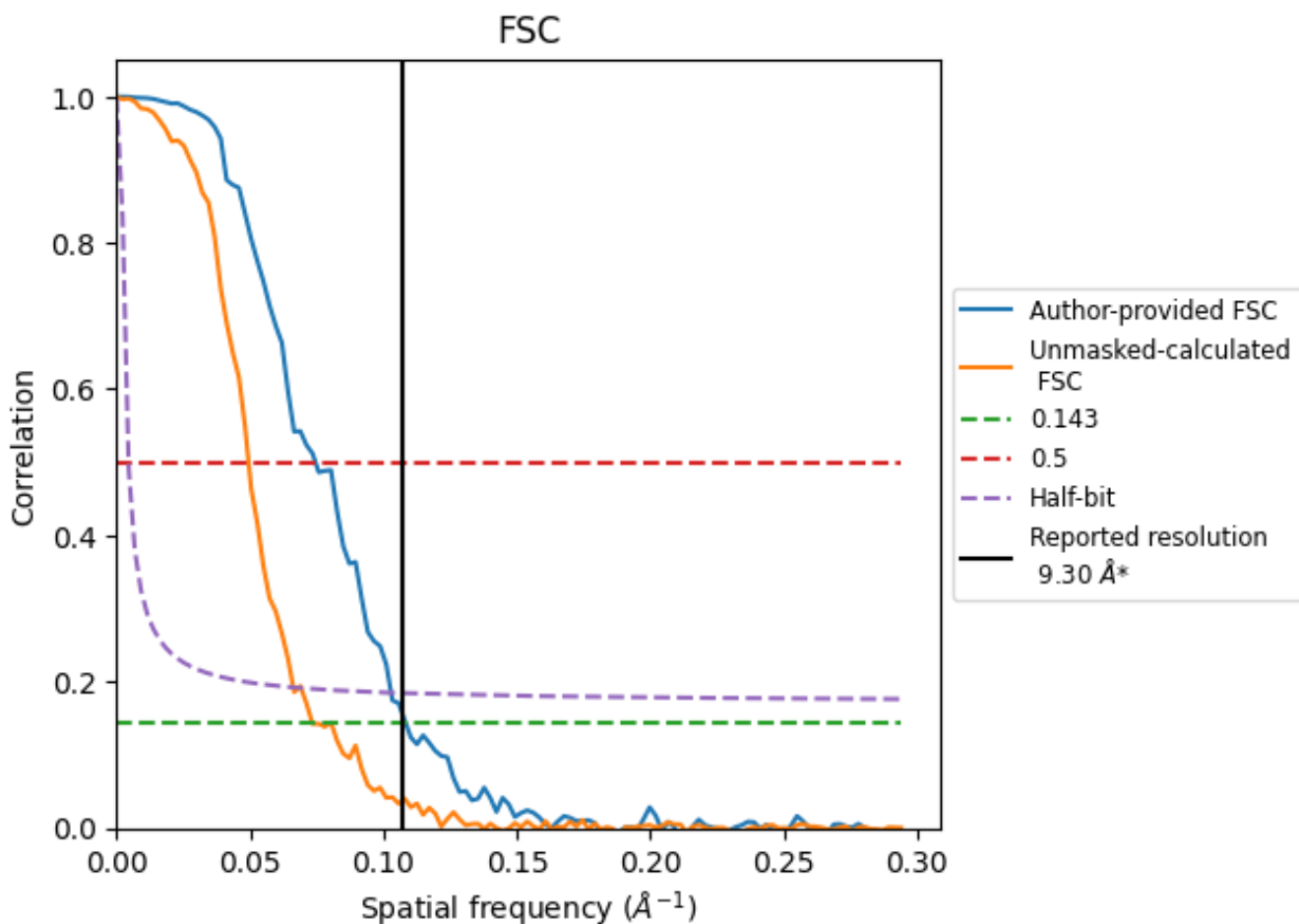


*Reported resolution corresponds to spatial frequency of 0.108 Å⁻¹

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 0.108\AA^{-1}

8.2 Resolution estimates [i](#)

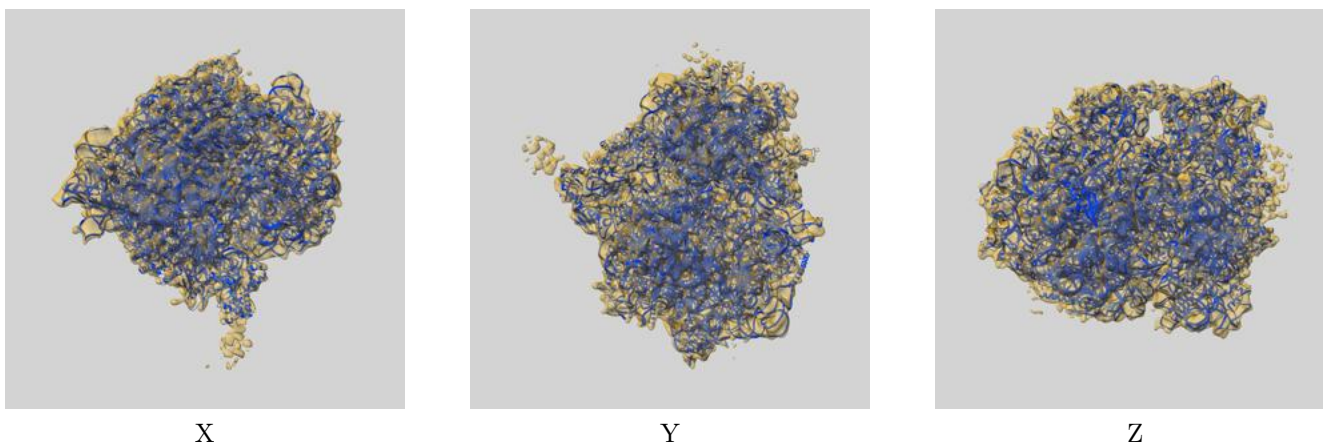
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	9.30	-	-
Author-provided FSC curve	9.23	13.40	9.72
Unmasked-calculated*	13.62	20.16	15.08

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 13.62 differs from the reported value 9.3 by more than 10 %

9 Map-model fit [i](#)

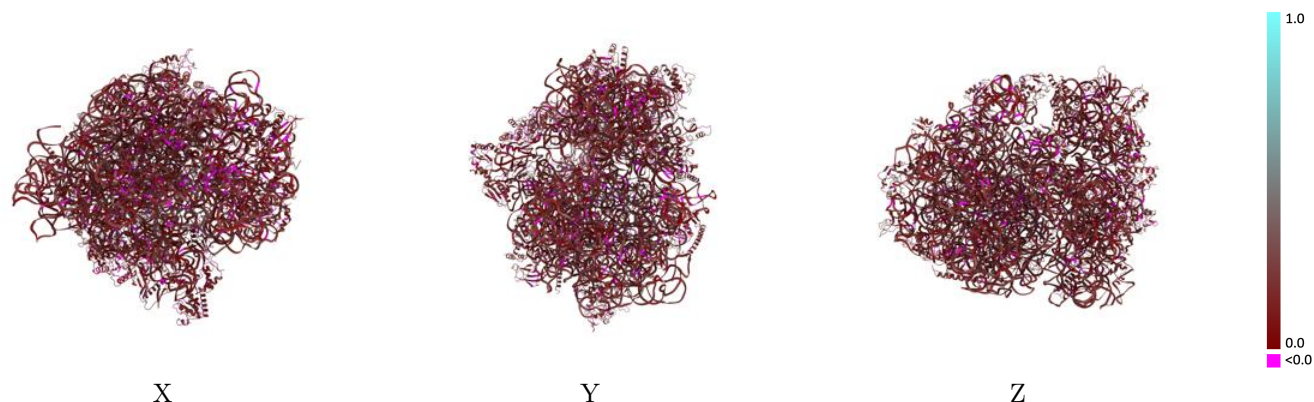
This section contains information regarding the fit between EMDB map EMD-13446 and PDB model 7PIP. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



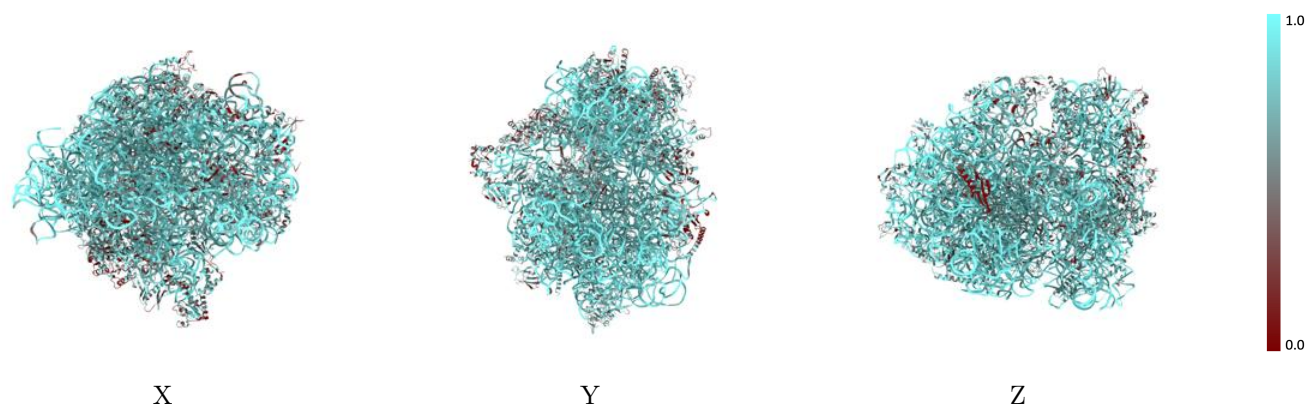
The images above show the 3D surface view of the map at the recommended contour level 0.39 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



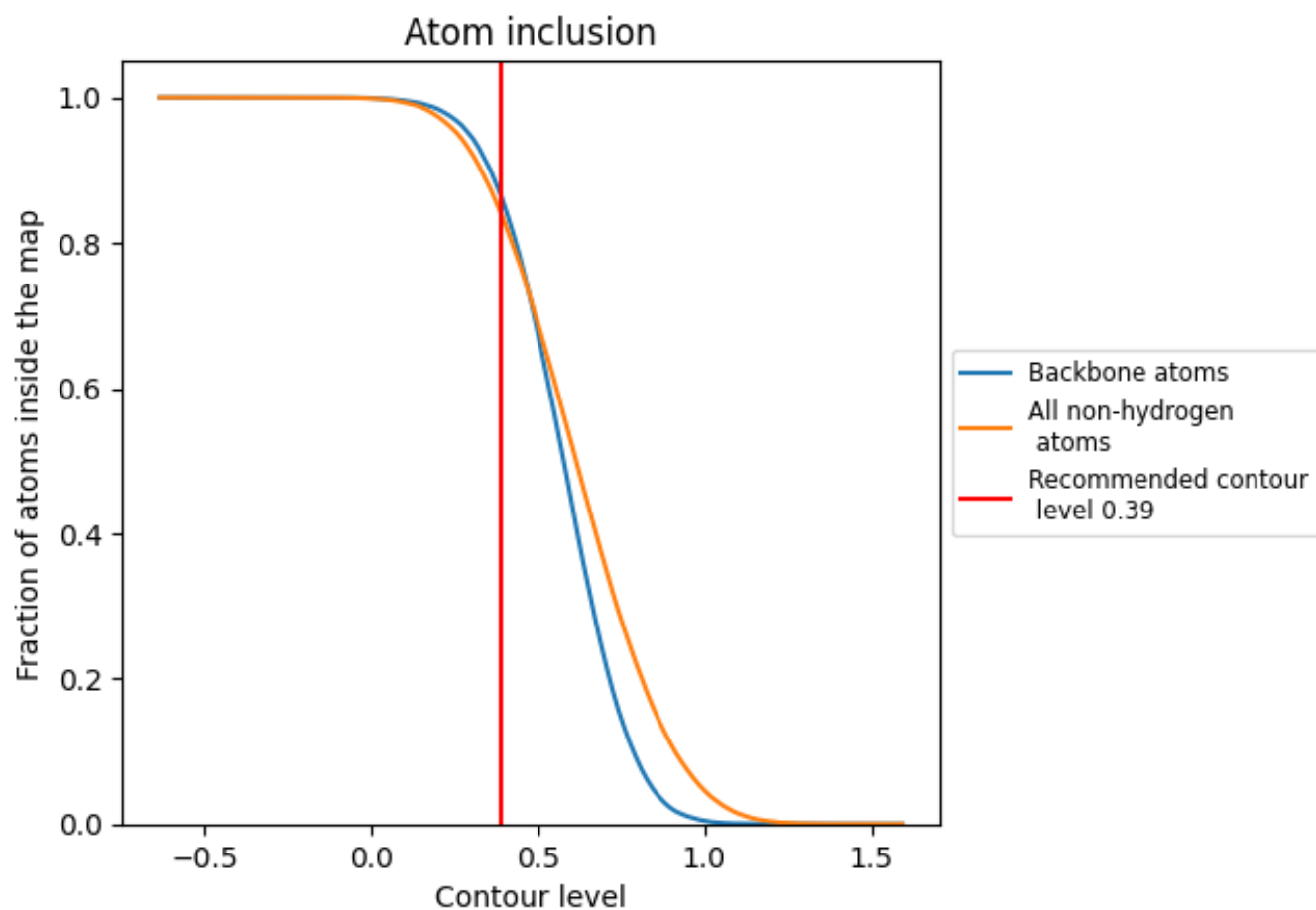
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.39).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 84% 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 (0.39) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8418	 0.1590
0	 0.7945	 0.1400
1	 0.7618	 0.1410
2	 0.7466	 0.1130
3	 0.9413	 0.1680
4	 0.9415	 0.1790
5	 0.9439	 0.1710
6	 0.7849	 0.1530
7	 0.7497	 0.1100
9	 0.4821	 0.1290
A	 0.5774	 0.1580
B	 0.5900	 0.1450
C	 0.6758	 0.1420
D	 0.6323	 0.1390
E	 0.6040	 0.1620
F	 0.6306	 0.1450
G	 0.6581	 0.1360
H	 0.6264	 0.1110
I	 0.6075	 0.1400
J	 0.6401	 0.1270
K	 0.7011	 0.1410
L	 0.6569	 0.1480
M	 0.6242	 0.1050
N	 0.7024	 0.1720
O	 0.8188	 0.1670
P	 0.7306	 0.1640
Q	 0.6202	 0.1360
R	 0.6179	 0.0970
S	 0.7787	 0.1640
T	 0.7188	 0.1880
a	 0.7315	 0.1280
b	 0.6843	 0.1320
c	 0.6904	 0.1490
d	 0.6193	 0.1470
e	 0.6301	 0.1530



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Chain	Atom inclusion	Q-score
f	 0.2463	 0.1380
g	 0.5150	 0.1540
h	 0.5225	 0.1410
i	 0.7029	 0.1310
j	 0.5902	 0.1290
k	 0.7414	 0.1430
l	 0.7280	 0.1410
m	 0.7415	 0.1370
n	 0.6770	 0.1450
o	 0.6817	 0.1550
p	 0.7716	 0.1390
q	 0.6846	 0.1400
r	 0.7960	 0.1710
s	 0.6700	 0.1370
t	 0.6272	 0.1510
u	 0.7641	 0.1170
v	 0.7515	 0.1520
w	 0.7553	 0.1870
x	 0.5394	 0.1620
y	 0.7465	 0.1270
z	 0.7935	 0.1300