



## wwPDB EM Validation Summary Report ⓘ

Apr 1, 2025 – 11:14 pm BST

PDB ID : 6HA8 / pdb\_00006ha8  
EMDB ID : EMD-0177  
Title : Cryo-EM structure of the ABCF protein VmlR bound to the Bacillus subtilis ribosome  
Authors : Crowe-McAuliffe, C.; Graf, M.; Huter, P.; Abdelshahid, M.; Novacek, J.; Wilson, D.N.  
Deposited on : 2018-08-07  
Resolution : 3.50 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](mailto: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>.

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

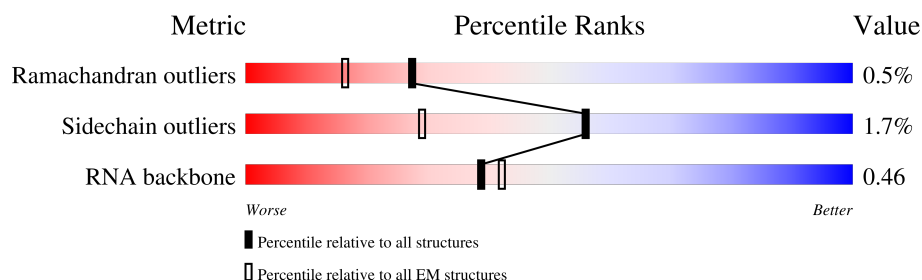
EMDB validation analysis : 0.0.1.dev117  
Mogul : 1.8.4, CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.42

# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:  
*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.50 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	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	2928	
2	B	112	
3	C	277	
4	D	209	
5	E	207	
6	F	179	
7	G	179	
8	J	145	

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Mol	Chain	Length	Quality of chain
9	K	122	
10	L	146	
11	M	144	
12	N	120	
13	O	120	
14	P	115	
15	Q	119	
16	R	102	
17	S	113	
18	T	95	
19	U	103	
20	V	548	
21	W	94	
22	X	62	
23	Y	66	
24	Z	59	
25	0	59	
26	1	49	
27	2	44	
28	3	66	
29	4	37	
30	6	66	
31	7	3	
32	8	232	
33	a	1554	

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Mol	Chain	Length	Quality of chain
34	b	246	
35	c	218	
36	d	200	
37	e	166	
38	f	95	
39	g	156	
40	h	132	
41	i	130	
42	j	102	
43	k	131	
44	l	138	
45	m	121	
46	n	61	
47	o	89	
48	p	90	
49	q	87	
50	r	79	
51	s	92	
52	t	88	
53	x	75	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
54	TEL	A	3001	X	-	-	-

## 2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 146404 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2887	Total	C	N	O	P	0	0
			61997	27661	11460	19992	2884		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	112	Total	C	N	O	P	0	0
			2392	1068	435	778	111		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	272	Total	C	N	O	S	0	0
			2083	1296	408	373	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	206	Total	C	N	O	S	0	0
			1569	985	289	290	5		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	176	Total	C	N	O	S	0	0
			1386	882	241	256	7		

- Molecule 7 is a protein called 50S ribosomal protein L6.

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

- Molecule 8 is a protein called 50S ribosomal protein L13.

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

- Molecule 9 is a protein called 50S ribosomal protein L14.

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

- Molecule 10 is a protein called 50S ribosomal protein L15.

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

- Molecule 11 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	M	135	Total	C	N	O	S	0	0
			1076	690	205	176	5		

- Molecule 12 is a protein called 50S ribosomal protein L17.

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

- Molecule 13 is a protein called 50S ribosomal protein L18.

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

- Molecule 14 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	P	115	Total	C	N	O	S	0	0
			944	600	185	158	1		

- Molecule 15 is a protein called 50S ribosomal protein L20.

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

- Molecule 16 is a protein called 50S ribosomal protein L21.

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

- Molecule 17 is a protein called 50S ribosomal protein L22.

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

- Molecule 18 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	T	90	Total	C	N	O	S	0	0
			725	452	134	136	3		

- Molecule 19 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	U	101	Total	C	N	O	S	0	0
			762	478	142	138	4		

- Molecule 20 is a protein called Nucleotide-binding protein ExpZ.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	V	541	Total	C	N	O	S	0	0
			4177	2637	737	796	7		

There are 66 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	-5	MET	-	initiating methionine	UNP P39115
V	-4	HIS	-	expression tag	UNP P39115
V	-3	HIS	-	expression tag	UNP P39115
V	-2	HIS	-	expression tag	UNP P39115
V	-1	HIS	-	expression tag	UNP P39115
V	0	HIS	-	expression tag	UNP P39115
V	1	HIS	-	expression tag	UNP P39115
V	129	GLN	GLU	engineered mutation	UNP P39115
V	432	GLN	GLU	engineered mutation	UNP P39115
V	486	ALA	-	expression tag	UNP P39115
V	487	ALA	-	expression tag	UNP P39115
V	488	ALA	-	expression tag	UNP P39115
V	489	ALA	-	expression tag	UNP P39115
V	490	ALA	-	expression tag	UNP P39115
V	491	ALA	-	expression tag	UNP P39115
V	492	ALA	-	expression tag	UNP P39115
V	493	ALA	-	expression tag	UNP P39115
V	494	ALA	-	expression tag	UNP P39115
V	495	ALA	-	expression tag	UNP P39115
V	496	ALA	-	expression tag	UNP P39115
V	497	ALA	-	expression tag	UNP P39115
V	498	ALA	-	expression tag	UNP P39115
V	499	ALA	-	expression tag	UNP P39115
V	500	ALA	-	expression tag	UNP P39115
V	501	ALA	-	expression tag	UNP P39115
V	502	ALA	-	expression tag	UNP P39115
V	503	ALA	-	expression tag	UNP P39115
V	504	ALA	-	expression tag	UNP P39115
V	505	ALA	-	expression tag	UNP P39115
V	506	ALA	-	expression tag	UNP P39115
V	507	ALA	-	expression tag	UNP P39115
V	508	ALA	-	expression tag	UNP P39115
V	509	ALA	-	expression tag	UNP P39115
V	510	ALA	-	expression tag	UNP P39115
V	511	ALA	-	expression tag	UNP P39115
V	512	ALA	-	expression tag	UNP P39115
V	513	ALA	-	expression tag	UNP P39115
V	514	ALA	-	expression tag	UNP P39115
V	515	ALA	-	expression tag	UNP P39115
V	516	ALA	-	expression tag	UNP P39115
V	517	ALA	-	expression tag	UNP P39115
V	518	ALA	-	expression tag	UNP P39115
V	519	ALA	-	expression tag	UNP P39115

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Chain	Residue	Modelled	Actual	Comment	Reference
V	520	ALA	-	expression tag	UNP P39115
V	521	ALA	-	expression tag	UNP P39115
V	522	ALA	-	expression tag	UNP P39115
V	523	ALA	-	expression tag	UNP P39115
V	524	ALA	-	expression tag	UNP P39115
V	525	ALA	-	expression tag	UNP P39115
V	526	ALA	-	expression tag	UNP P39115
V	527	ALA	-	expression tag	UNP P39115
V	528	ALA	-	expression tag	UNP P39115
V	529	ALA	-	expression tag	UNP P39115
V	530	ALA	-	expression tag	UNP P39115
V	531	ALA	-	expression tag	UNP P39115
V	532	ALA	-	expression tag	UNP P39115
V	533	ALA	-	expression tag	UNP P39115
V	534	ALA	-	expression tag	UNP P39115
V	535	ALA	-	expression tag	UNP P39115
V	536	ALA	-	expression tag	UNP P39115
V	537	ALA	-	expression tag	UNP P39115
V	538	ALA	-	expression tag	UNP P39115
V	539	ALA	-	expression tag	UNP P39115
V	540	ALA	-	expression tag	UNP P39115
V	541	ALA	-	expression tag	UNP P39115
V	542	ALA	-	expression tag	UNP P39115

- Molecule 21 is a protein called 50S ribosomal protein L27.

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

- Molecule 22 is a protein called 50S ribosomal protein L28.

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

- Molecule 23 is a protein called 50S ribosomal protein L29.

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

- Molecule 24 is a protein called 50S ribosomal protein L30.

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

- Molecule 25 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	0	54	Total	C	N	O	S	0	0
			426	262	86	71	7		

- Molecule 26 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	1	48	Total	C	N	O	S	0	0
			401	244	80	73	4		

- Molecule 27 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	2	44	Total	C	N	O	S	0	0
			367	222	89	54	2		

- Molecule 28 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	3	64	Total	C	N	O	S	0	0
			512	321	107	82	2		

- Molecule 29 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	4	37	Total	C	N	O	S	0	0
			296	186	60	45	5		

- Molecule 30 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	6	63	Total	C	N	O	S	0	0
			499	312	91	91	5		

- Molecule 31 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	7	3	Total	C	N	O	P	0	0
			60	27	7	23	3		

- Molecule 32 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	8	212	Total	C	N	O	S	0	0
			1599	1015	273	306	5		

- Molecule 33 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	a	1533	Total	C	N	O	P	0	0
			32891	14667	6034	10657	1533		

- Molecule 34 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	b	218	Total	C	N	O	S	0	0
			1757	1119	309	323	6		

- Molecule 35 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	c	206	Total	C	N	O	S	0	0
			1619	1011	304	301	3		

- Molecule 36 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	d	195	Total	C	N	O	S	0	0
			1568	991	291	284	2		

- Molecule 37 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	e	164	Total	C	N	O	S	0	0
			1218	767	225	224	2		

- Molecule 38 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	f	92	Total	C	N	O	S	0	0
			755	476	132	146	1		

- Molecule 39 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	g	149	Total	C	N	O	S	0	0
			1181	740	220	215	6		

- Molecule 40 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	h	131	Total	C	N	O	S	0	0
			1036	655	191	187	3		

- Molecule 41 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	i	125	Total	C	N	O	S	0	0
			966	599	191	175	1		

- Molecule 42 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	j	95	Total	C	N	O	S	0	0
			761	479	139	141	2		

- Molecule 43 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	k	114	Total	C	N	O	S	0	0
			838	516	164	156	2		

- Molecule 44 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	l	136	Total	C	N	O	S	0	0
			1052	653	211	186	2		

- Molecule 45 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	m	108	Total	C	N	O		
			868	534	176	158	0	0

- Molecule 46 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	n	60	Total	C	N	O	S		
			497	317	98	77	5	0	0

- Molecule 47 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	o	85	Total	C	N	O	S		
			710	436	144	129	1	0	0

- Molecule 48 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	p	88	Total	C	N	O	S		
			695	441	128	124	2	0	0

- Molecule 49 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	q	84	Total	C	N	O	S		
			691	435	128	126	2	0	0

- Molecule 50 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	r	64	Total	C	N	O	S		
			518	332	96	88	2	0	0

- Molecule 51 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	s	78	Total	C	N	O	S		
			633	409	112	110	2	0	0

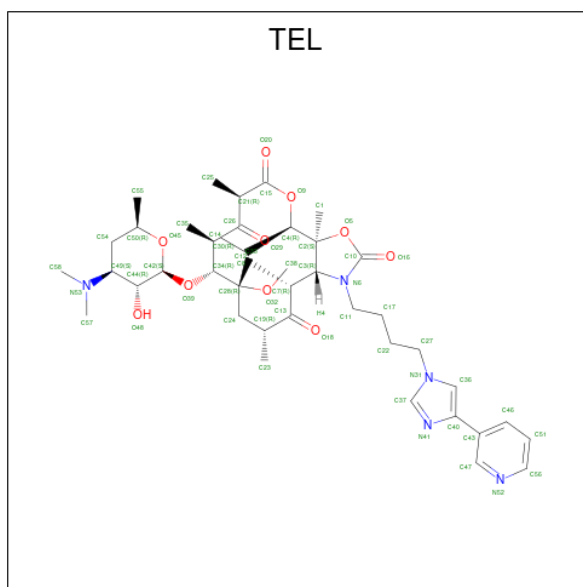
- Molecule 52 is a protein called 30S ribosomal protein S20.

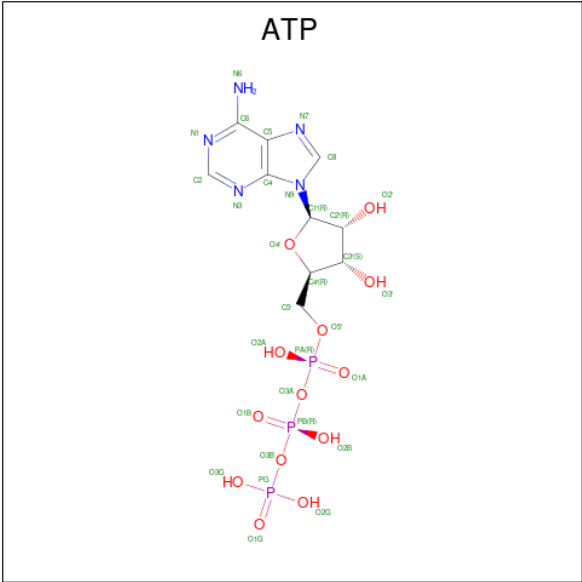
Mol	Chain	Residues	Atoms					AltConf	Trace
52	t	83	Total	C	N	O	S	0	0
			637	390	130	116	1		

- Molecule 53 is a RNA chain called P-tRNA(Leu).

Mol	Chain	Residues	Atoms					AltConf	Trace
53	x	75	Total	C	N	O	P	0	0
			1603	714	284	530	75		

- Molecule 54 is TELITHROMYCIN (CCD ID: TEL) (formula:  $C_{43}H_{65}N_5O_{10}$ ).



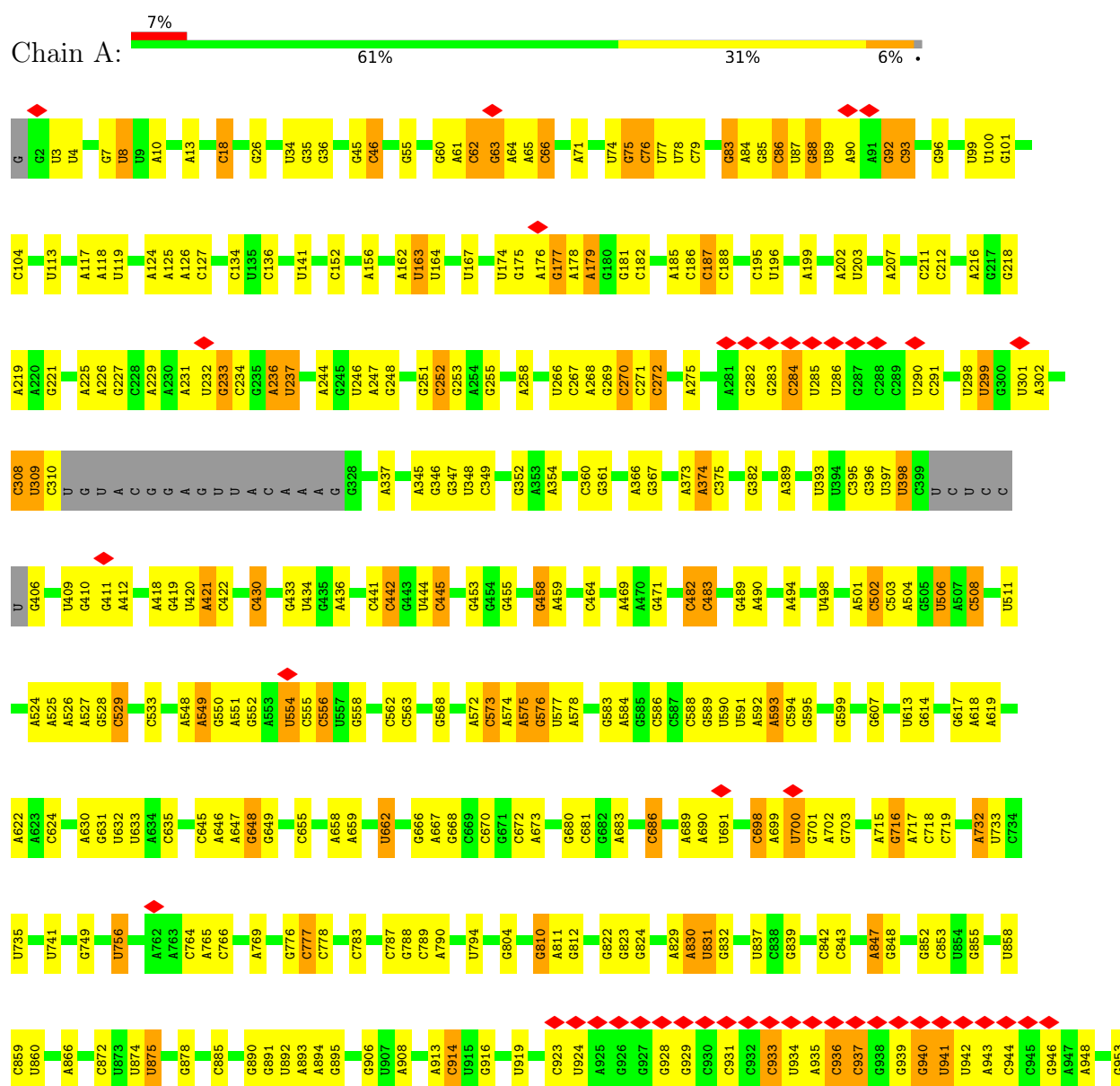


Mol	Chain	Residues	Atoms					AltConf
55	V	1	Total	C	N	O	P	0
			31	10	5	13	3	
55	V	1	Total	C	N	O	P	0
			31	10	5	13	3	

### 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: 23S rRNA

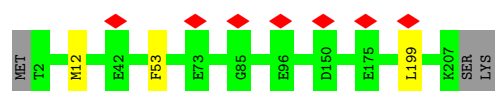




C2102	G2001	G1884	G1782	A1899	U1507	A1404	A1314	U	A1132	A1055	U954
U2105	G2004	A1885	C1783	A1700	C1508	C1415	G1315	U	G133	A1068	A957
C2114	G2009	G1886	A1784	A	A1516	G1416	A1323	C	A1134	A1059	A958
U2121	A2010	G1887	G1785	U	U1522	U1418	A1324		G1135	A1067	C959
G2122	U2020	A1895	A1789	A	G1525	C1422	A1325		U1136	G1068	C962
A2123	G2021	U1899	U1790	C1597	G1526	A1423	A1326		G1137	U1069	G963
A2124	U2022	G1903	G1791	U1602	G1527	C1328	U1327		C1138	G1070	A964
U2125	C2023	G1902	G1793	U1603	U1528	A1424	C1329		G1139	A965	U966
G2126	U2024	G1904	C1794	U1604	U1529	C1425	C1330		U1140	A1072	
U2127	C2025		A1797	C1605	G1530	A1426	C1333		A1141	A1073	A970
U2128	A2026	C1922	C1800	C1606	G1531	U1435	C1334		A1142	U1079	A971
G2129	G2033	G1932	G1801	C1607	A1532	U1436	A1335		U1143	U1086	U972
U2130	A2034	G1935	C1802	A1608	A1533	C1437	C1336		A1144	U1087	A974
A2131	C2035		C1803	C1613	U1535		A1339		G1145	C975	C975
A2132	G2050	A1941	U1716	A1614	A1536		A1340		C1146	U1088	U976
C2133	U2051	A1942	G1717				U1341		U1147	C977	U977
A2134	C2052	A1943	G1718	C1617	C1539	U1448	C1342		C1148	C980	C980
G2135	C2053	U1944	G1719	A1622	A1541	C1449	C1343		A1149	U1091	C981
C2136	U2055	U1945	C1720	C1626	A1542	C1450	U1345		C1150	A1092	
U2137		U1946		U1628	C1543	U1451	A1346		U1151	G1093	A987
U2138	A2059	U1952	G1726	A1628	C1544	A1453	U1350		G1152	A1096	G992
G2139	A2060	C1953	A1727	G1632	U1549	U1457	U1351		U1153	A1097	A999
U2140	A2062		G1731	G1633	C1550	G1460	U1352		U1154	C1098	
A2141	G2063	A1956	U1738	A1631	C1552		C1353		G1155	C1099	A1003
C2142	C2064	A1957	C1739	G1634	U	A1464	G1362		A1157	A1100	A1006
A2143	G2065	G1958	G1747	G1634	C1553	A1465	C1363		U1158	G1102	G1007
G2144		G1959	G1748	C1644	A1555	U1466	U1365		G1160	A1103	C1011
G2145	G2068		G1749	C1645	A1556	G1467	U1366		A1161	U1104	A1019
A2146	U2069	C1963	U1750	A1653	G1557		G1367		G1162	G1105	A1020
U2147	U2070	A1966	G1751	A1654	G1558		U1368		U1106	U1106	
A2148	A2071	A1967	G1752	A1655	C1559	A1472	A1369		U1107	A1026	A1026
G2149	C2072	U1968	C1753	C1656	U1560	A1473	C1370		G1108	C1027	A1027
G2150	C2076	U1969	G1757	C1657	G1561	C1474	C1371		A1173	C1028	C1028
U2151	A2078	C1971	U1758	G1658	A1562	G1475	C1372		A1174	A1029	A1029
A2152	C2079	U1972	U1759		G1563	C1476	U1373		G1177	G1109	G1030
G2153	A2080	A1973	A1760	A1661	C1564		C1374		U1178	C1110	C1031
G2154	G2081	U1847	G1761	A1671	G1565	G1481	A1375		U1111	C1032	
A2155	C2084	A1848	G1762	A1672	G1566		G1376		U1112	A1036	A1036
G2156	G2085	U1849	C1766	A1679	U1567	U1484	U1379		A1113	C1037	C1037
C2157		U1985	A1767	A1680	G1568	G1485			G1114	C1041	C1041
C2158	A2089		G1769	A1691	U1570	G1486	C1384		A1115	A1042	A1042
U2159	G2090	C1991	C1770	U1692	G1571	G1488	G1385		A1116	U1045	U1045
C2160	A2091	C1992	G1771	C1872	C1572	A1490	A1388		G1117	C1118	C1118
C2161	C2093	C1993	A1776	G1693	C1573		C1389		A1119	G1120	G1051
G2162	C2094	C1994	G1777	G1694	U	A1499	U1500		G1121	C1121	C1052
		C1995	A1778	A1695	A	U1501	G1390		A1126	A1126	A1054
	G2098	G1997	G1779	G1696	A	G1502	U1391		G1185	C1122	
A2165		A1998	G1780	A1697	U	A1506	G1397		U1179	U1127	
C2166	G2101	A1999	A1883	G1698					A1186	U1128	
C2167		A2000							U1187	U1129	
G2168									A1188	A1130	
G2169									A1189	A1131	
A2170									A1197	C1125	
G2171									G1198	A1126	
C2172									C1199	A1126	
G2173									G1200	A1126	
C2174									A1201	A1126	
C2175									G1203	A1126	
									A1210	A1126	
									C1216	A1126	

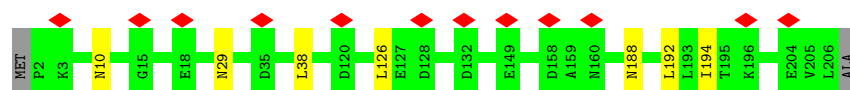


Chain D:  97%



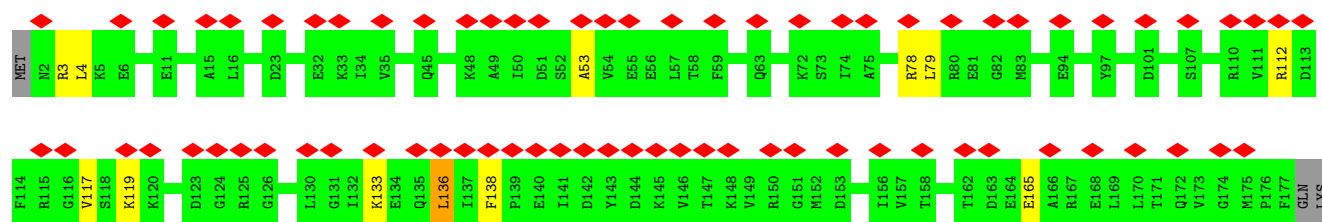
- Molecule 5: 50S ribosomal protein L4

Chain E:  96%



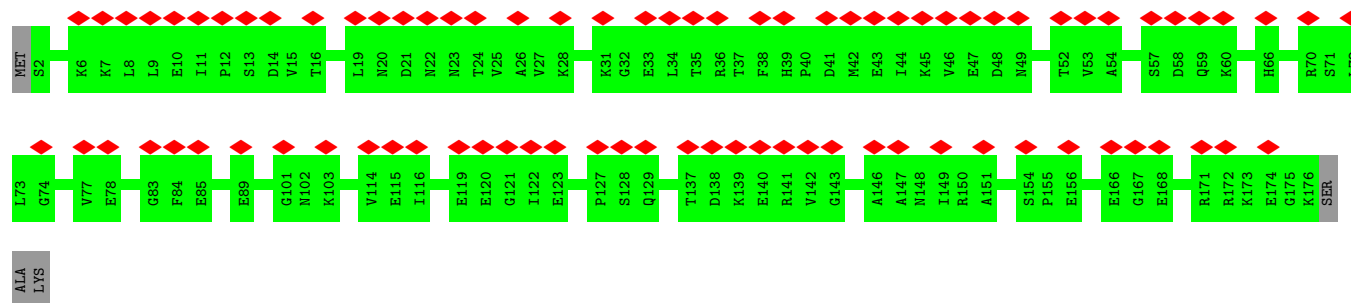
- Molecule 6: 50S ribosomal protein L5

Chain F:  92% 6%



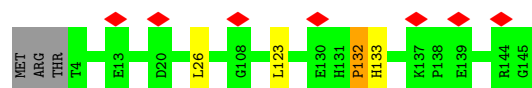
- Molecule 7: 50S ribosomal protein L6

Chain G:  98%



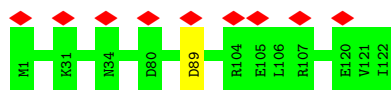
- Molecule 8: 50S ribosomal protein L13

Chain J:  95%

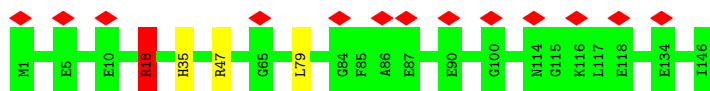


- Molecule 9: 50S ribosomal protein L14

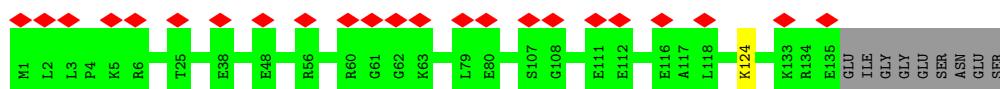
Chain K:  99%



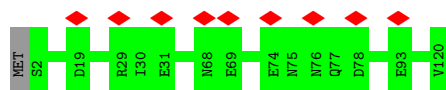
- Molecule 10: 50S ribosomal protein L15



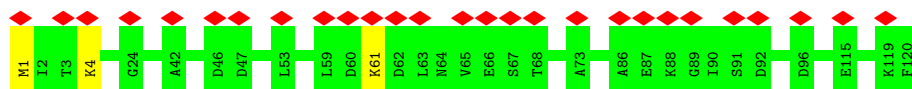
- Molecule 11: 50S ribosomal protein L16



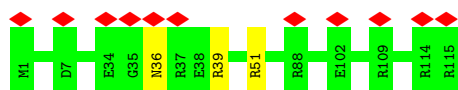
- Molecule 12: 50S ribosomal protein L17



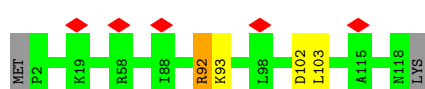
- Molecule 13: 50S ribosomal protein L18



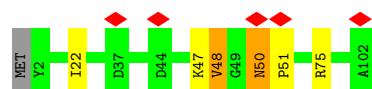
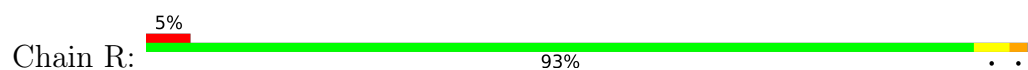
- Molecule 14: 50S ribosomal protein L19



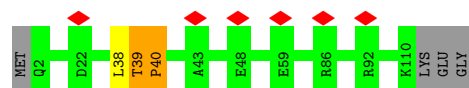
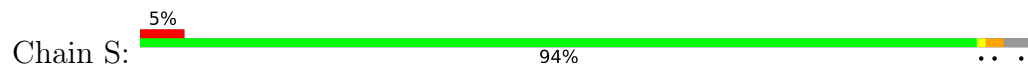
- Molecule 15: 50S ribosomal protein L20



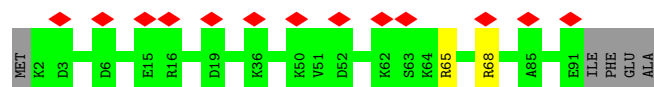
- Molecule 16: 50S ribosomal protein L21



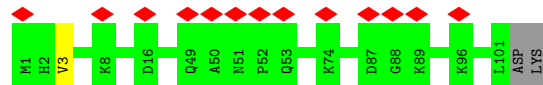
- Molecule 17: 50S ribosomal protein L22



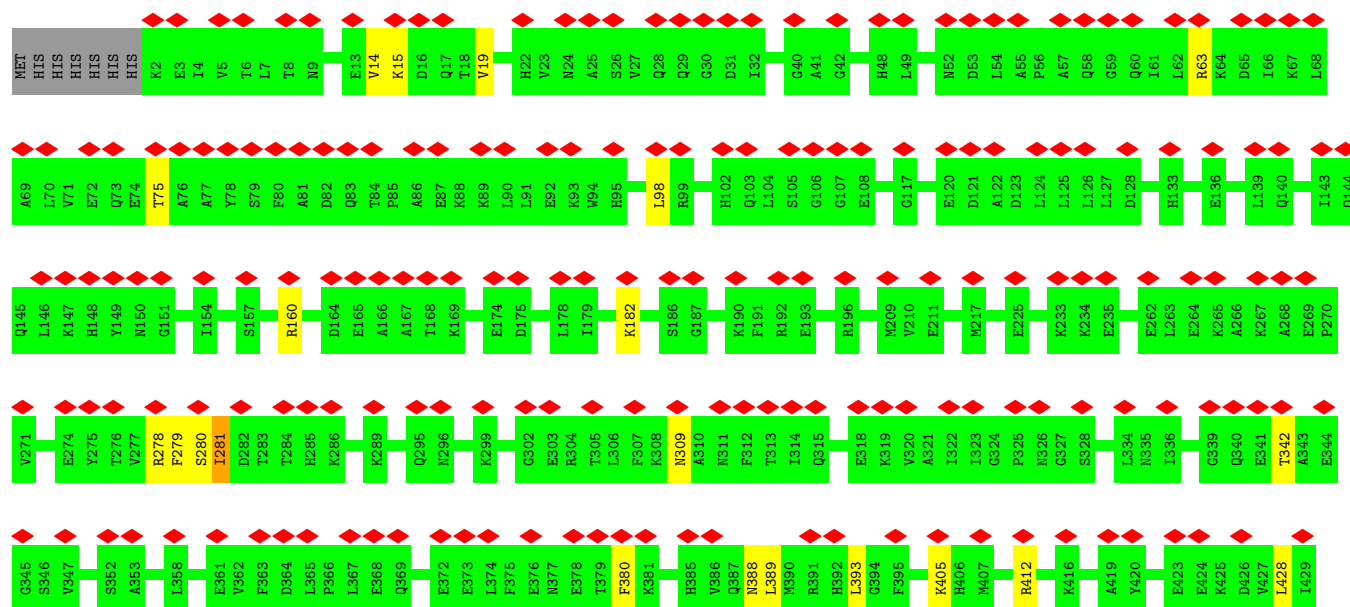
- Molecule 18: 50S ribosomal protein L23

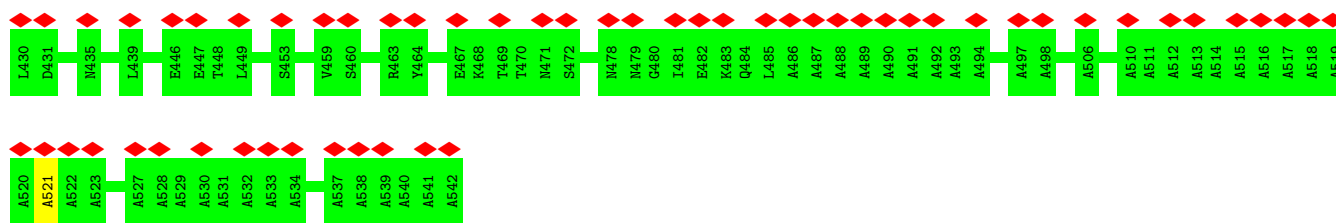


- Molecule 19: 50S ribosomal protein L24

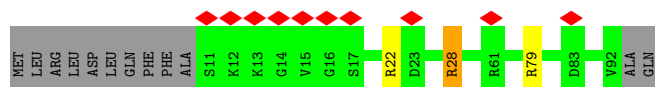
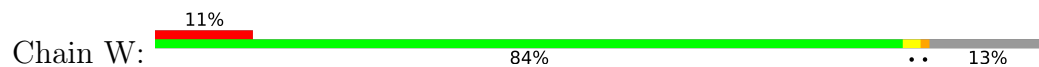


- Molecule 20: Nucleotide-binding protein ExpZ

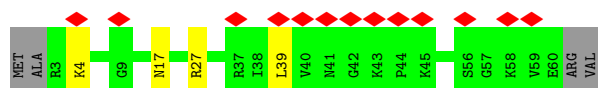
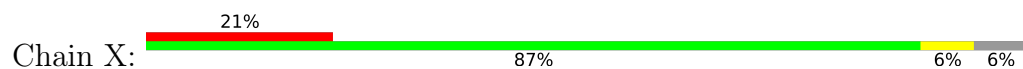




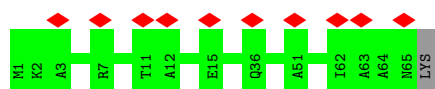
- Molecule 21: 50S ribosomal protein L27



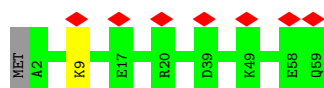
- Molecule 22: 50S ribosomal protein L28



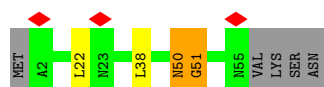
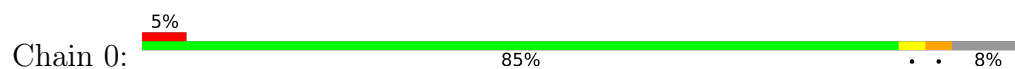
- Molecule 23: 50S ribosomal protein L29



- Molecule 24: 50S ribosomal protein L30

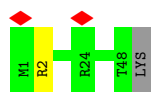


- Molecule 25: 50S ribosomal protein L32

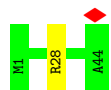


- Molecule 26: 50S ribosomal protein L33 1

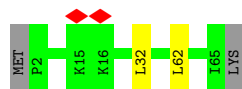




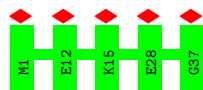
- Molecule 27: 50S ribosomal protein L34



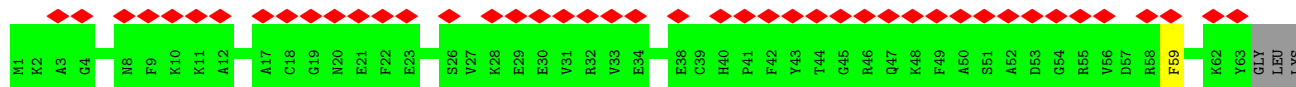
- Molecule 28: 50S ribosomal protein L35



- Molecule 29: 50S ribosomal protein L36



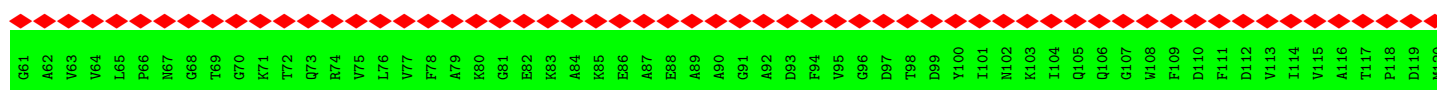
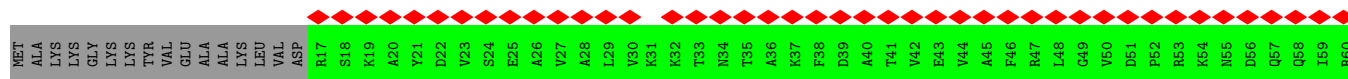
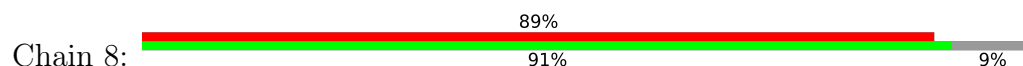
- Molecule 30: 50S ribosomal protein L31

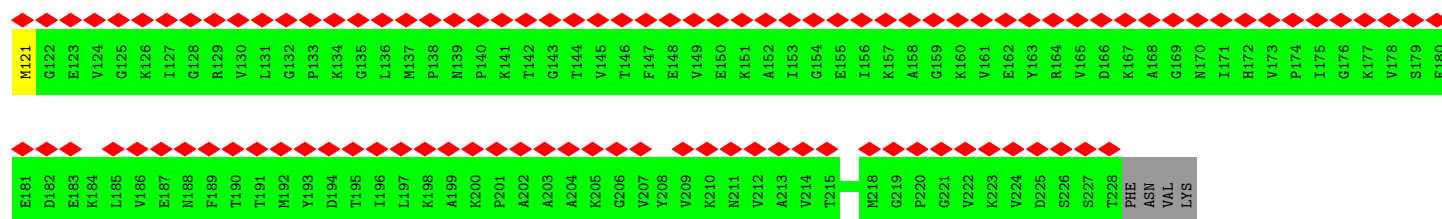


- Molecule 31: mRNA

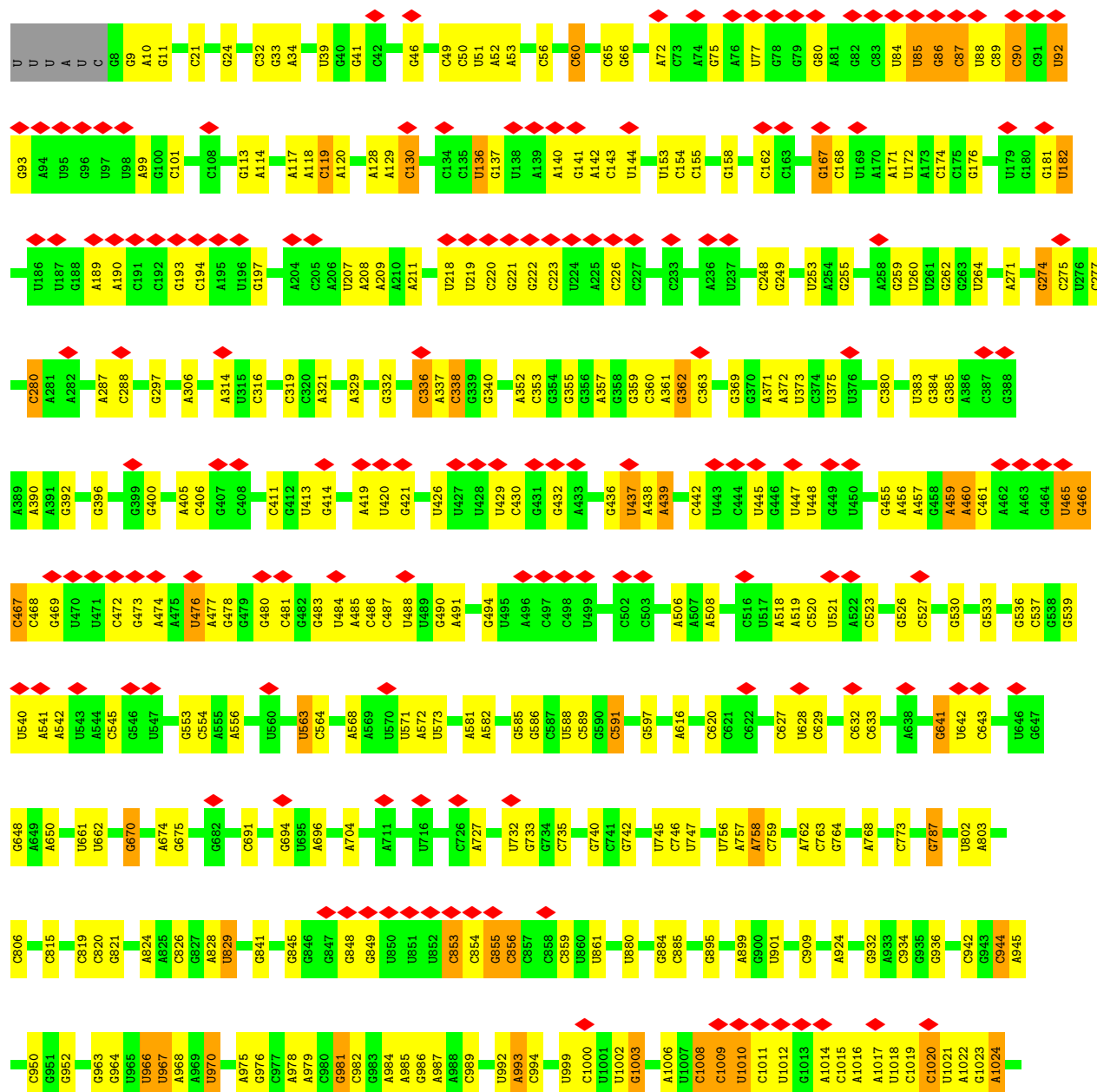


- Molecule 32: 50S ribosomal protein L1

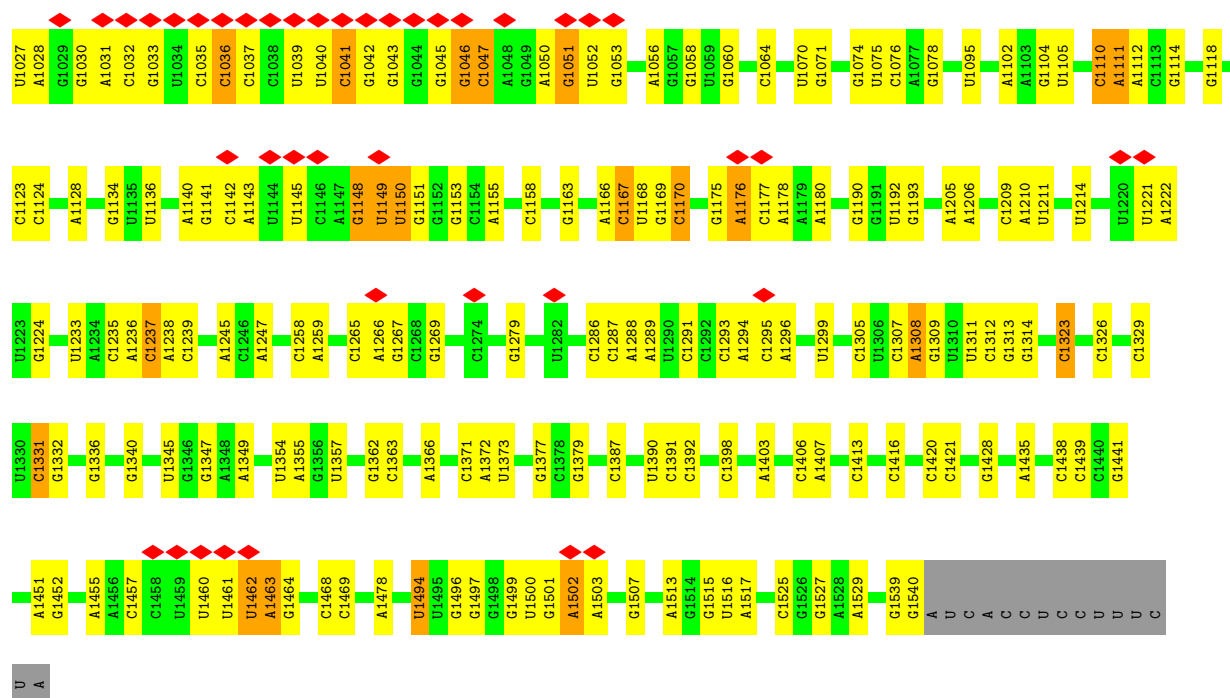




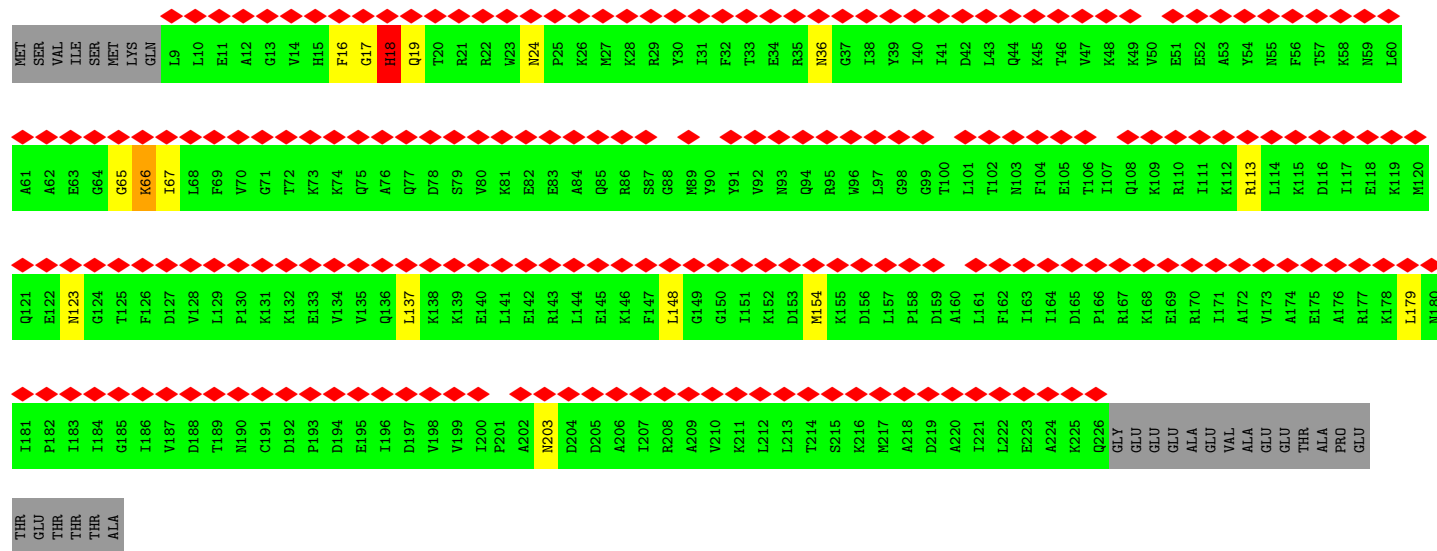
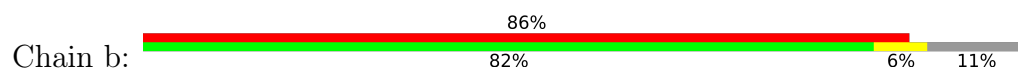
• Molecule 33: 16S rRNA



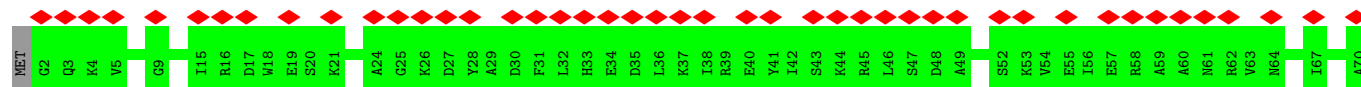
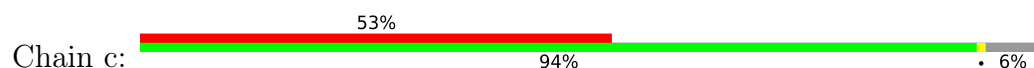


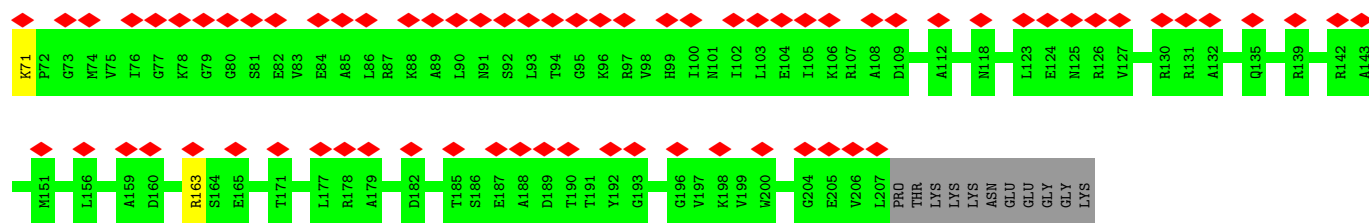


• Molecule 34: 30S ribosomal protein S2

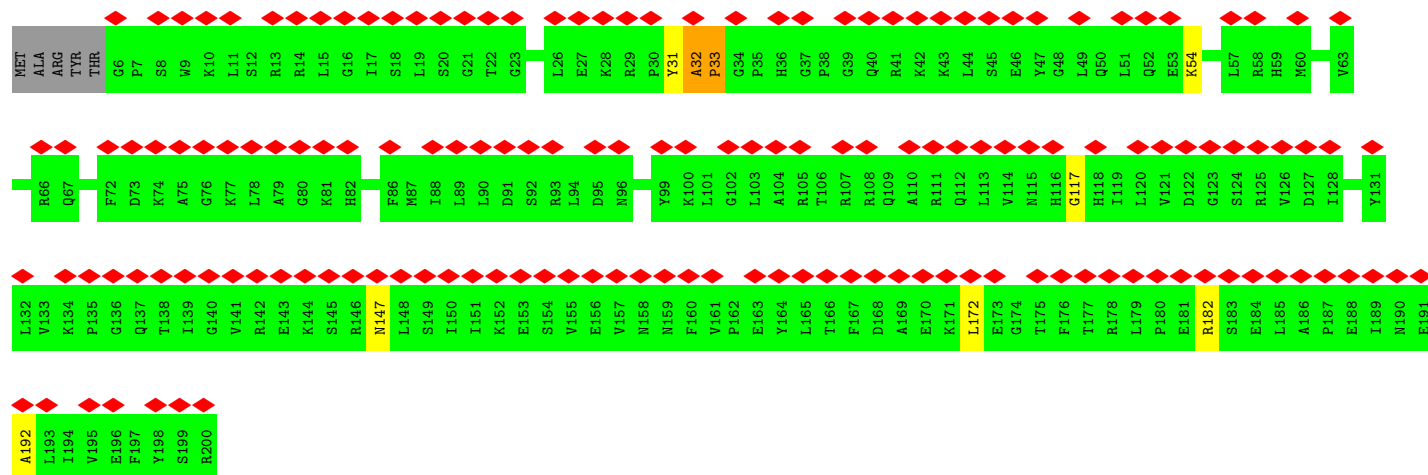
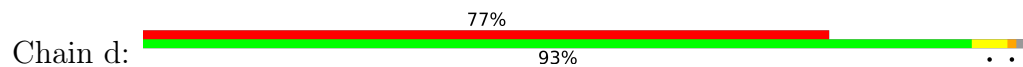


• Molecule 35: 30S ribosomal protein S3

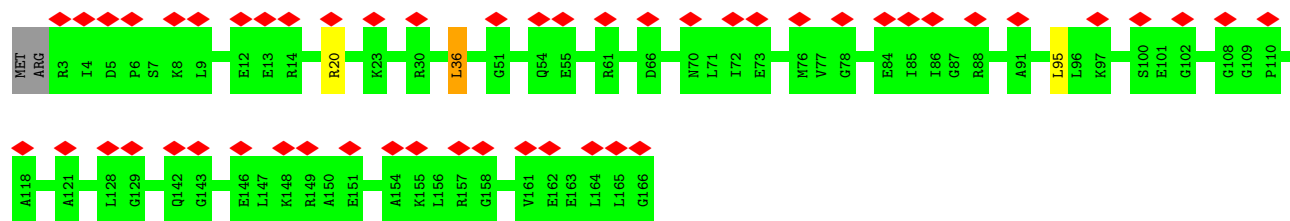




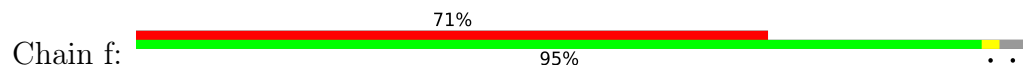
- Molecule 36: 30S ribosomal protein S4



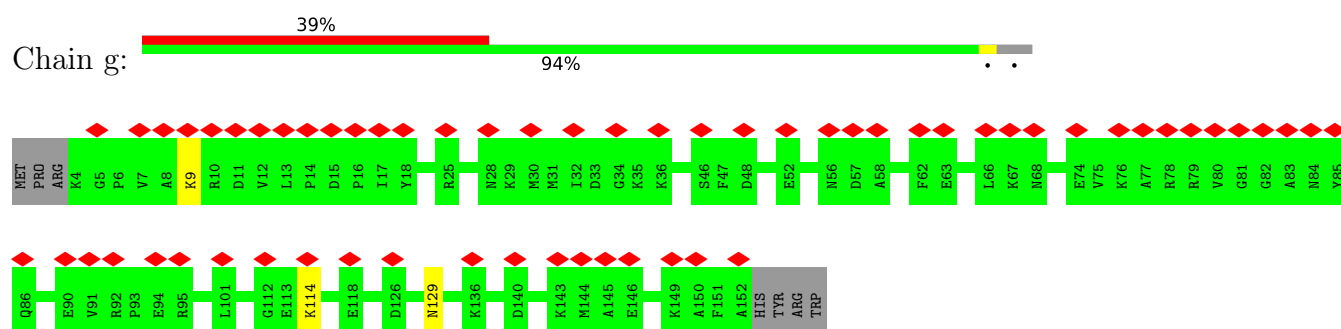
- Molecule 37: 30S ribosomal protein S5



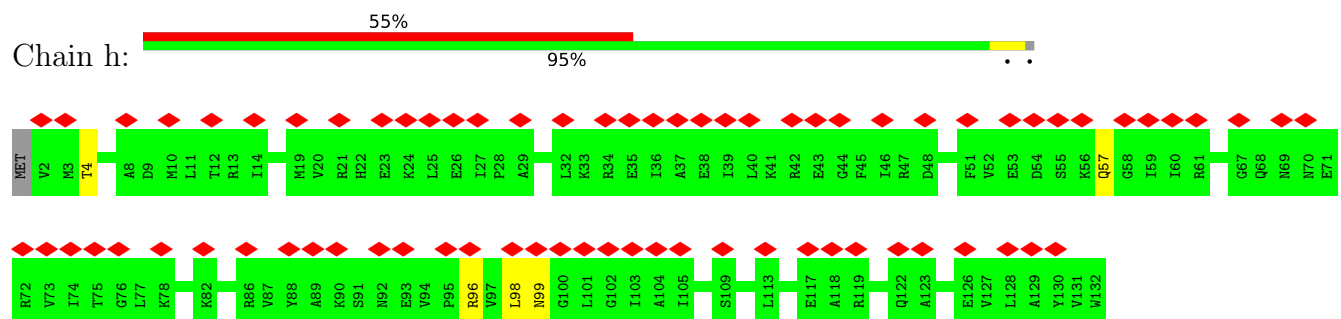
- Molecule 38: 30S ribosomal protein S6



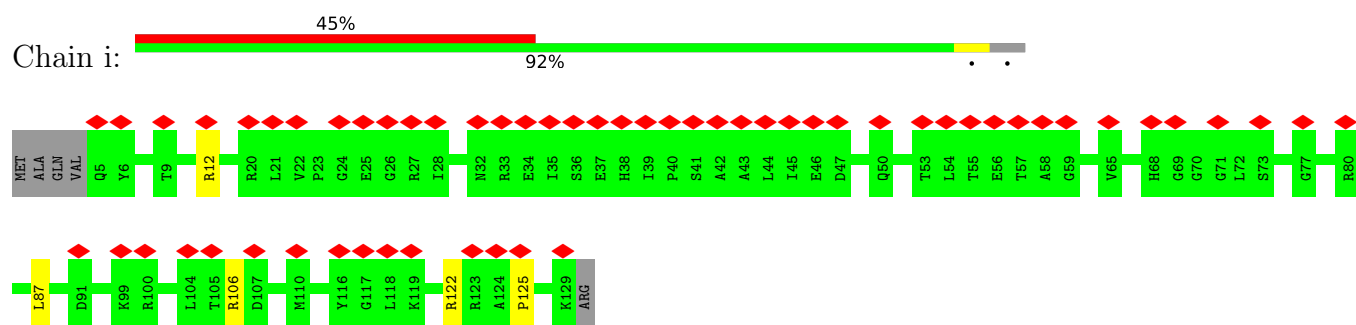
- Molecule 39: 30S ribosomal protein S7



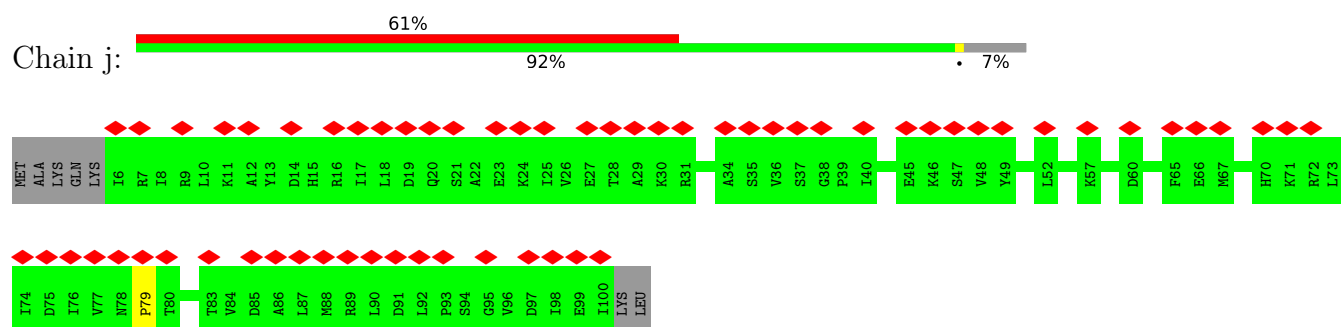
- Molecule 40: 30S ribosomal protein S8



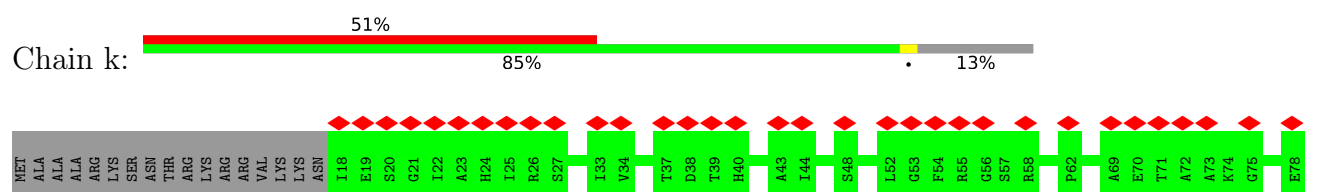
- Molecule 41: 30S ribosomal protein S9

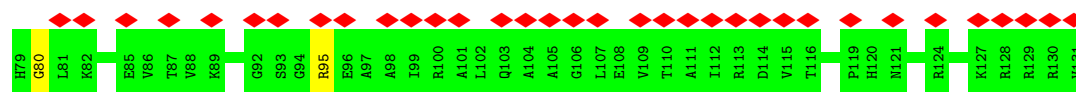


- Molecule 42: 30S ribosomal protein S10

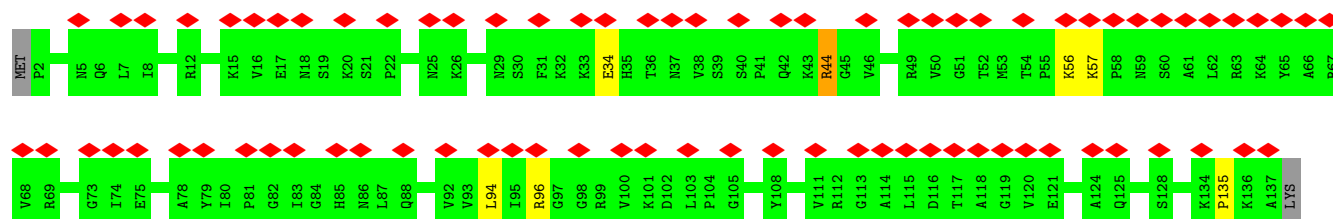
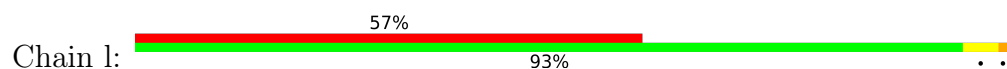


- Molecule 43: 30S ribosomal protein S11

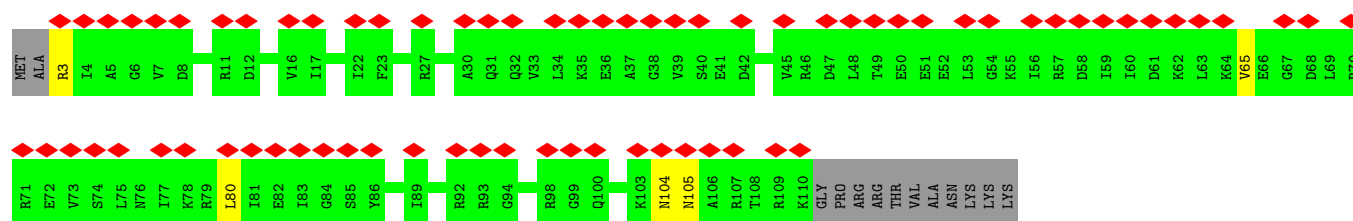
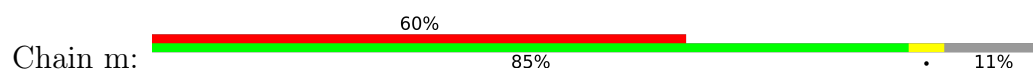




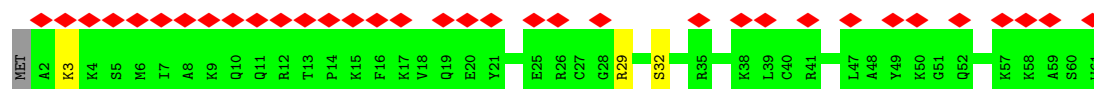
- Molecule 44: 30S ribosomal protein S12



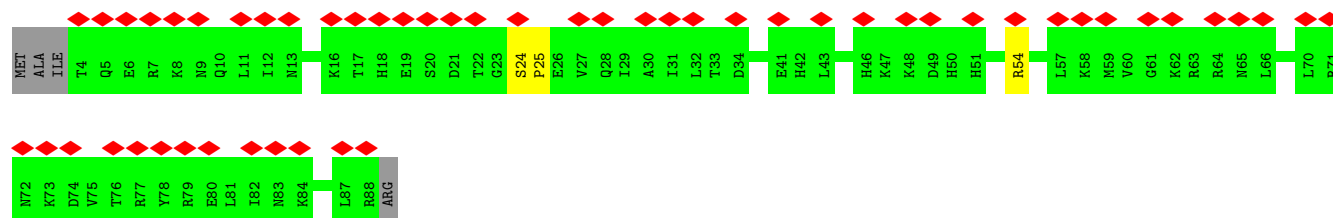
- Molecule 45: 30S ribosomal protein S13



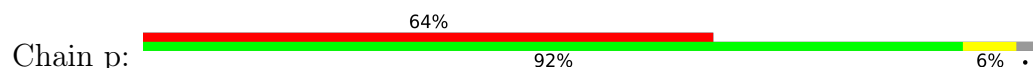
- Molecule 46: 30S ribosomal protein S14

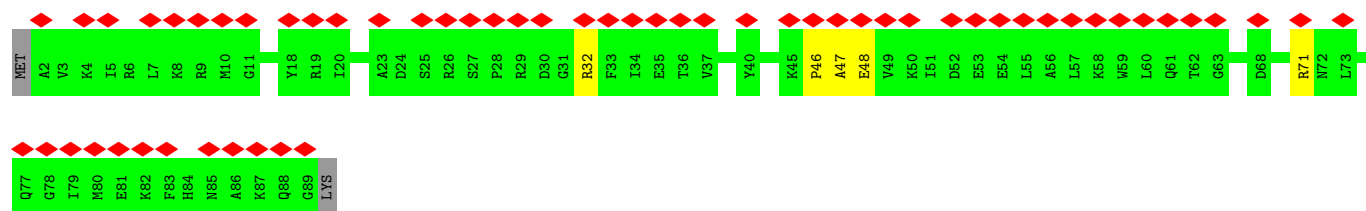


- Molecule 47: 30S ribosomal protein S15

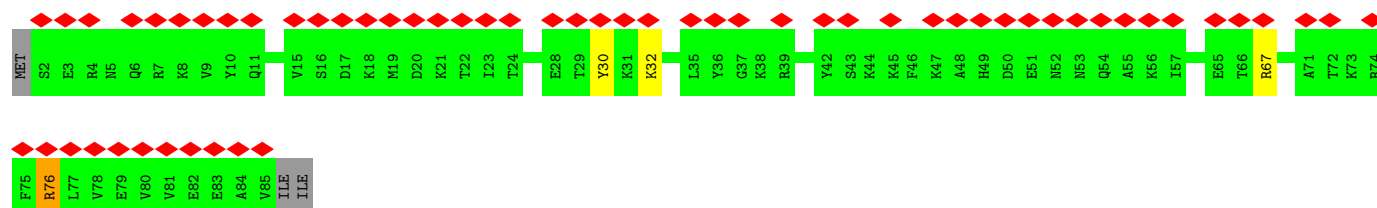
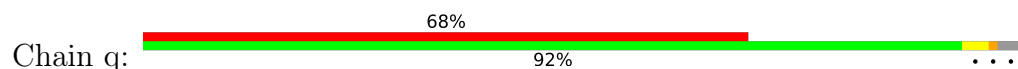


- Molecule 48: 30S ribosomal protein S16

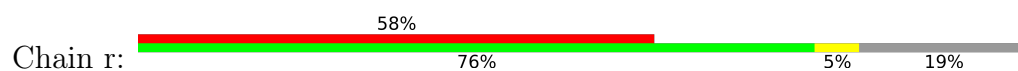




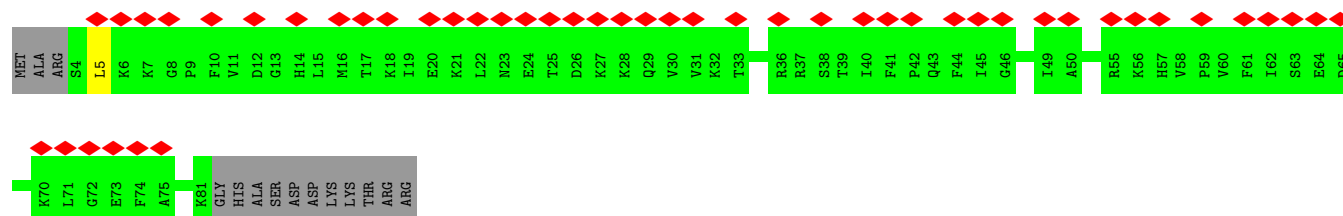
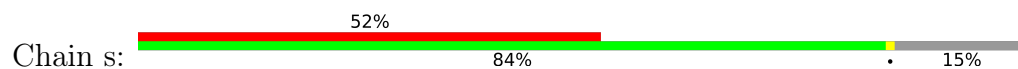
• Molecule 49: 30S ribosomal protein S17



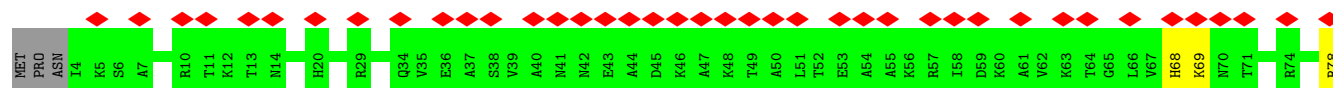
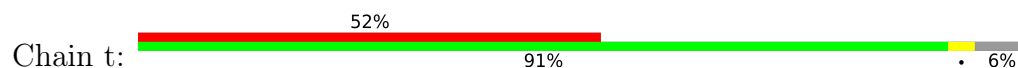
• Molecule 50: 30S ribosomal protein S18

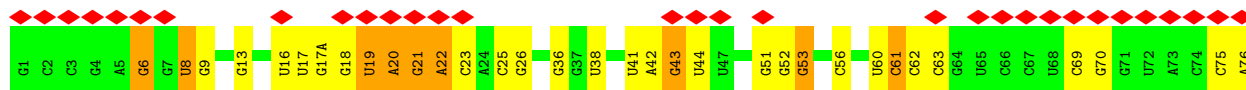


• Molecule 51: 30S ribosomal protein S19



• Molecule 52: 30S ribosomal protein S20





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	28972	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 ( $e^-/\text{\AA}^2$ )	1.425	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	0.634	Depositor
Minimum map value	-0.379	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.027	Depositor
Recommended contour level	0.11	Depositor
Map size ( $\text{\AA}$ )	381.96, 381.96, 381.96	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.061, 1.061, 1.061	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ATP, TEL

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	1.05	17/69438 (0.0%)	1.31	711/108311 (0.7%)
2	B	0.79	0/2675	1.34	36/4170 (0.9%)
3	C	0.59	0/2120	0.76	0/2845
4	D	0.61	0/1591	0.75	1/2132 (0.0%)
5	E	0.54	0/1580	0.74	2/2132 (0.1%)
6	F	0.44	0/1405	0.83	4/1887 (0.2%)
7	G	0.40	0/1360	0.70	0/1832
8	J	0.57	0/1146	0.78	0/1542
9	K	0.60	0/927	0.79	1/1245 (0.1%)
10	L	0.53	0/1093	0.77	2/1457 (0.1%)
11	M	0.55	0/1099	0.76	0/1468
12	N	0.54	0/960	0.74	0/1284
13	O	0.45	0/921	0.77	0/1236
14	P	0.55	0/957	0.77	0/1279
15	Q	0.62	0/952	0.81	2/1266 (0.2%)
16	R	0.62	0/797	0.87	4/1070 (0.4%)
17	S	0.54	0/851	0.78	2/1146 (0.2%)
18	T	0.52	0/731	0.71	0/974
19	U	0.51	1/772 (0.1%)	0.75	0/1032
20	V	0.41	0/4247	0.72	3/5736 (0.1%)
21	W	0.62	0/638	0.94	2/847 (0.2%)
22	X	0.46	0/448	0.77	1/596 (0.2%)
23	Y	0.44	0/531	0.70	0/707
24	Z	0.47	0/457	0.79	0/613
25	0	0.61	0/433	0.81	0/574
26	1	0.57	0/406	0.76	1/540 (0.2%)
27	2	0.58	0/370	0.78	0/483
28	3	0.55	0/519	0.70	0/680
29	4	0.47	0/299	0.66	0/393
30	6	0.42	0/509	0.72	0/678
31	7	0.61	0/65	1.36	2/98 (2.0%)
32	8	0.32	0/1624	0.66	0/2192



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	a	0.63	1/36826 (0.0%)	1.23	291/57450 (0.5%)
34	b	0.35	0/1782	0.71	3/2392 (0.1%)
35	c	0.38	0/1641	0.67	0/2208
36	d	0.36	0/1598	0.72	0/2147
37	e	0.39	0/1230	0.75	1/1655 (0.1%)
38	f	0.32	0/766	0.61	0/1031
39	g	0.38	0/1196	0.75	0/1604
40	h	0.36	0/1048	0.75	0/1407
41	i	0.38	0/979	0.76	2/1315 (0.2%)
42	j	0.38	0/773	0.70	0/1044
43	k	0.35	0/852	0.70	1/1153 (0.1%)
44	l	0.37	0/1069	0.79	3/1435 (0.2%)
45	m	0.36	0/873	0.76	1/1166 (0.1%)
46	n	0.41	0/507	0.82	1/672 (0.1%)
47	o	0.33	0/718	0.62	0/960
48	p	0.39	0/708	0.73	0/950
49	q	0.40	0/699	0.79	1/933 (0.1%)
50	r	0.33	0/526	0.67	0/705
51	s	0.35	0/649	0.69	0/872
52	t	0.36	0/639	0.65	0/852
53	x	0.65	0/1790	1.52	28/2787 (1.0%)
All	All	0.81	19/158790 (0.0%)	1.17	1106/237183 (0.5%)

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
3	C	0	1
4	D	0	1
6	F	0	3
8	J	0	1
10	L	0	2
13	O	0	1
15	Q	0	1
16	R	0	2
17	S	0	1
20	V	0	11
25	0	0	2
30	6	0	1
34	b	0	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
36	d	0	5
37	e	0	1
38	f	0	1
39	g	0	2
40	h	0	1
44	l	0	2
45	m	0	3
47	o	0	1
49	q	0	1
50	r	0	2
All	All	0	51

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	631	G	N9-C4	-7.63	1.31	1.38
1	A	830	A	N9-C4	-6.90	1.33	1.37
1	A	1067	A	N9-C4	-6.87	1.33	1.37
1	A	574	A	N9-C4	-6.32	1.34	1.37
1	A	631	G	C2-N3	-5.92	1.28	1.32

The worst 5 of 1106 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	a	1502	A	C8-N9-C4	-14.51	100.00	105.80
53	x	6	G	O5'-P-OP2	-14.04	93.07	105.70
1	A	756	U	N3-C2-O2	-12.07	113.75	122.20
1	A	2054	C	C5-C6-N1	12.06	127.03	121.00
1	A	2243	C	N1-C2-O2	11.98	126.09	118.90

There are no chirality outliers.

5 of 51 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	153	GLN	Peptide
4	D	53	PHE	Peptide
6	F	117	VAL	Peptide
6	F	138	PHE	Peptide
6	F	53	ALA	Peptide

## 5.2 Too-close contacts

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

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	270/277 (98%)	253 (94%)	17 (6%)	0	100	100
4	D	204/209 (98%)	195 (96%)	9 (4%)	0	100	100
5	E	203/207 (98%)	187 (92%)	16 (8%)	0	100	100
6	F	174/179 (97%)	159 (91%)	15 (9%)	0	100	100
7	G	173/179 (97%)	153 (88%)	20 (12%)	0	100	100
8	J	140/145 (97%)	129 (92%)	9 (6%)	2 (1%)	9	40
9	K	120/122 (98%)	110 (92%)	10 (8%)	0	100	100
10	L	144/146 (99%)	137 (95%)	7 (5%)	0	100	100
11	M	133/144 (92%)	125 (94%)	8 (6%)	0	100	100
12	N	117/120 (98%)	108 (92%)	9 (8%)	0	100	100
13	O	118/120 (98%)	107 (91%)	11 (9%)	0	100	100
14	P	113/115 (98%)	105 (93%)	8 (7%)	0	100	100
15	Q	115/119 (97%)	107 (93%)	6 (5%)	2 (2%)	7	36
16	R	99/102 (97%)	83 (84%)	15 (15%)	1 (1%)	13	46
17	S	107/113 (95%)	92 (86%)	13 (12%)	2 (2%)	6	34
18	T	88/95 (93%)	84 (96%)	4 (4%)	0	100	100
19	U	99/103 (96%)	86 (87%)	13 (13%)	0	100	100
20	V	539/548 (98%)	464 (86%)	73 (14%)	2 (0%)	30	64
21	W	80/94 (85%)	71 (89%)	9 (11%)	0	100	100
22	X	56/62 (90%)	46 (82%)	10 (18%)	0	100	100
23	Y	63/66 (96%)	60 (95%)	3 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
24	Z	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
25	0	52/59 (88%)	49 (94%)	2 (4%)	1 (2%)	6	34
26	1	46/49 (94%)	43 (94%)	3 (6%)	0	100	100
27	2	42/44 (96%)	41 (98%)	1 (2%)	0	100	100
28	3	62/66 (94%)	60 (97%)	2 (3%)	0	100	100
29	4	35/37 (95%)	32 (91%)	3 (9%)	0	100	100
30	6	61/66 (92%)	53 (87%)	8 (13%)	0	100	100
32	8	210/232 (90%)	192 (91%)	18 (9%)	0	100	100
34	b	216/246 (88%)	188 (87%)	24 (11%)	4 (2%)	6	34
35	c	204/218 (94%)	185 (91%)	19 (9%)	0	100	100
36	d	193/200 (96%)	173 (90%)	18 (9%)	2 (1%)	13	46
37	e	162/166 (98%)	150 (93%)	12 (7%)	0	100	100
38	f	90/95 (95%)	83 (92%)	7 (8%)	0	100	100
39	g	147/156 (94%)	136 (92%)	11 (8%)	0	100	100
40	h	129/132 (98%)	107 (83%)	20 (16%)	2 (2%)	8	38
41	i	123/130 (95%)	104 (85%)	18 (15%)	1 (1%)	16	51
42	j	93/102 (91%)	83 (89%)	9 (10%)	1 (1%)	12	45
43	k	112/131 (86%)	100 (89%)	12 (11%)	0	100	100
44	l	134/138 (97%)	117 (87%)	16 (12%)	1 (1%)	19	53
45	m	106/121 (88%)	94 (89%)	11 (10%)	1 (1%)	14	49
46	n	58/61 (95%)	46 (79%)	11 (19%)	1 (2%)	7	36
47	o	83/89 (93%)	79 (95%)	3 (4%)	1 (1%)	11	43
48	p	86/90 (96%)	76 (88%)	7 (8%)	3 (4%)	3	24
49	q	82/87 (94%)	77 (94%)	5 (6%)	0	100	100
50	r	62/79 (78%)	57 (92%)	5 (8%)	0	100	100
51	s	76/92 (83%)	66 (87%)	10 (13%)	0	100	100
52	t	81/88 (92%)	76 (94%)	3 (4%)	2 (2%)	4	29
All	All	5956/6298 (95%)	5382 (90%)	545 (9%)	29 (0%)	27	59

5 of 29 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	J	133	HIS

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Mol	Chain	Res	Type
15	Q	93	LYS
17	S	40	PRO
20	V	280	SER
34	b	18	HIS

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	220/225 (98%)	218 (99%)	2 (1%)	75	86
4	D	167/170 (98%)	166 (99%)	1 (1%)	84	91
5	E	169/170 (99%)	164 (97%)	5 (3%)	36	63
6	F	151/154 (98%)	144 (95%)	7 (5%)	23	52
7	G	148/151 (98%)	148 (100%)	0	100	100
8	J	120/123 (98%)	118 (98%)	2 (2%)	56	75
9	K	101/101 (100%)	101 (100%)	0	100	100
10	L	110/110 (100%)	108 (98%)	2 (2%)	54	74
11	M	109/116 (94%)	108 (99%)	1 (1%)	75	86
12	N	99/100 (99%)	99 (100%)	0	100	100
13	O	93/93 (100%)	91 (98%)	2 (2%)	47	70
14	P	100/100 (100%)	97 (97%)	3 (3%)	36	63
15	Q	96/98 (98%)	96 (100%)	0	100	100
16	R	83/84 (99%)	81 (98%)	2 (2%)	44	68
17	S	90/93 (97%)	90 (100%)	0	100	100
18	T	81/85 (95%)	79 (98%)	2 (2%)	42	67
19	U	85/87 (98%)	85 (100%)	0	100	100
20	V	424/431 (98%)	417 (98%)	7 (2%)	56	75
21	W	64/74 (86%)	61 (95%)	3 (5%)	22	51
22	X	47/50 (94%)	44 (94%)	3 (6%)	14	41

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	Y	56/57 (98%)	56 (100%)	0	100	100
24	Z	52/53 (98%)	51 (98%)	1 (2%)	52	73
25	0	48/53 (91%)	45 (94%)	3 (6%)	15	42
26	1	46/47 (98%)	46 (100%)	0	100	100
27	2	39/39 (100%)	38 (97%)	1 (3%)	41	66
28	3	54/56 (96%)	52 (96%)	2 (4%)	29	58
29	4	35/35 (100%)	35 (100%)	0	100	100
30	6	53/55 (96%)	53 (100%)	0	100	100
32	8	169/185 (91%)	168 (99%)	1 (1%)	84	91
34	b	189/212 (89%)	182 (96%)	7 (4%)	29	58
35	c	168/178 (94%)	166 (99%)	2 (1%)	67	82
36	d	169/173 (98%)	165 (98%)	4 (2%)	44	68
37	e	128/130 (98%)	126 (98%)	2 (2%)	58	76
38	f	81/84 (96%)	80 (99%)	1 (1%)	67	82
39	g	125/132 (95%)	124 (99%)	1 (1%)	79	88
40	h	111/112 (99%)	109 (98%)	2 (2%)	54	74
41	i	98/102 (96%)	96 (98%)	2 (2%)	50	72
42	j	86/92 (94%)	86 (100%)	0	100	100
43	k	86/100 (86%)	85 (99%)	1 (1%)	67	82
44	l	114/116 (98%)	111 (97%)	3 (3%)	41	66
45	m	94/104 (90%)	94 (100%)	0	100	100
46	n	53/54 (98%)	52 (98%)	1 (2%)	52	73
47	o	80/83 (96%)	79 (99%)	1 (1%)	65	81
48	p	74/76 (97%)	72 (97%)	2 (3%)	40	65
49	q	77/80 (96%)	74 (96%)	3 (4%)	27	56
50	r	56/64 (88%)	54 (96%)	2 (4%)	30	59
51	s	70/81 (86%)	69 (99%)	1 (1%)	62	79
52	t	66/70 (94%)	65 (98%)	1 (2%)	60	77
All	All	5034/5238 (96%)	4948 (98%)	86 (2%)	56	75

5 of 86 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	c	71	LYS
43	k	95	ARG
36	d	54	LYS
38	f	77	ARG
46	n	29	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 78 such sidechains are listed below:

Mol	Chain	Res	Type
38	f	61	GLN
47	o	42	HIS
39	g	142	HIS
44	l	90	HIS
49	q	49	HIS

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2876/2928 (98%)	857 (29%)	90 (3%)
2	B	111/112 (99%)	40 (36%)	3 (2%)
31	7	2/3 (66%)	0	0
33	a	1532/1554 (98%)	411 (26%)	0
53	x	73/75 (97%)	29 (39%)	0
All	All	4594/4672 (98%)	1337 (29%)	93 (2%)

5 of 1337 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
1	A	8	U
1	A	10	A
1	A	13	A
1	A	18	C

5 of 93 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1530	G
1	A	1883	A
1	A	1543	U
1	A	1751	U

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Mol	Chain	Res	Type
1	A	2127	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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

3 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
55	ATP	V	900	20	26,33,33	0.91	1 (3%)	31,52,52	1.66	6 (19%)
55	ATP	V	901	-	26,33,33	0.98	1 (3%)	31,52,52	1.83	4 (12%)
54	TEL	A	3001	-	59,62,62	1.29	4 (6%)	77,92,92	1.97	13 (16%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
55	ATP	V	900	20	-	3/18/38/38	0/3/3/3
55	ATP	V	901	-	-	4/18/38/38	0/3/3/3
54	TEL	A	3001	-	1/1/19/19	14/73/108/108	0/4/5/5

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



Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	A	3001	TEL	O5-C10	5.85	1.45	1.35
54	A	3001	TEL	O9-C15	4.91	1.45	1.34
54	A	3001	TEL	C36-N31	-2.79	1.34	1.38
54	A	3001	TEL	O5-C2	-2.74	1.43	1.47
55	V	901	ATP	C5-C4	2.38	1.47	1.40

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	A	3001	TEL	O9-C15-C21	9.27	120.30	110.88
54	A	3001	TEL	C11-N6-C10	6.88	130.94	122.25
55	V	901	ATP	PB-O3B-PG	-6.13	111.78	132.83
54	A	3001	TEL	C17-C11-N6	-5.42	104.94	113.31
55	V	901	ATP	PA-O3A-PB	-5.15	115.17	132.83

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
54	A	3001	TEL	C21

5 of 21 torsion outliers are listed below:

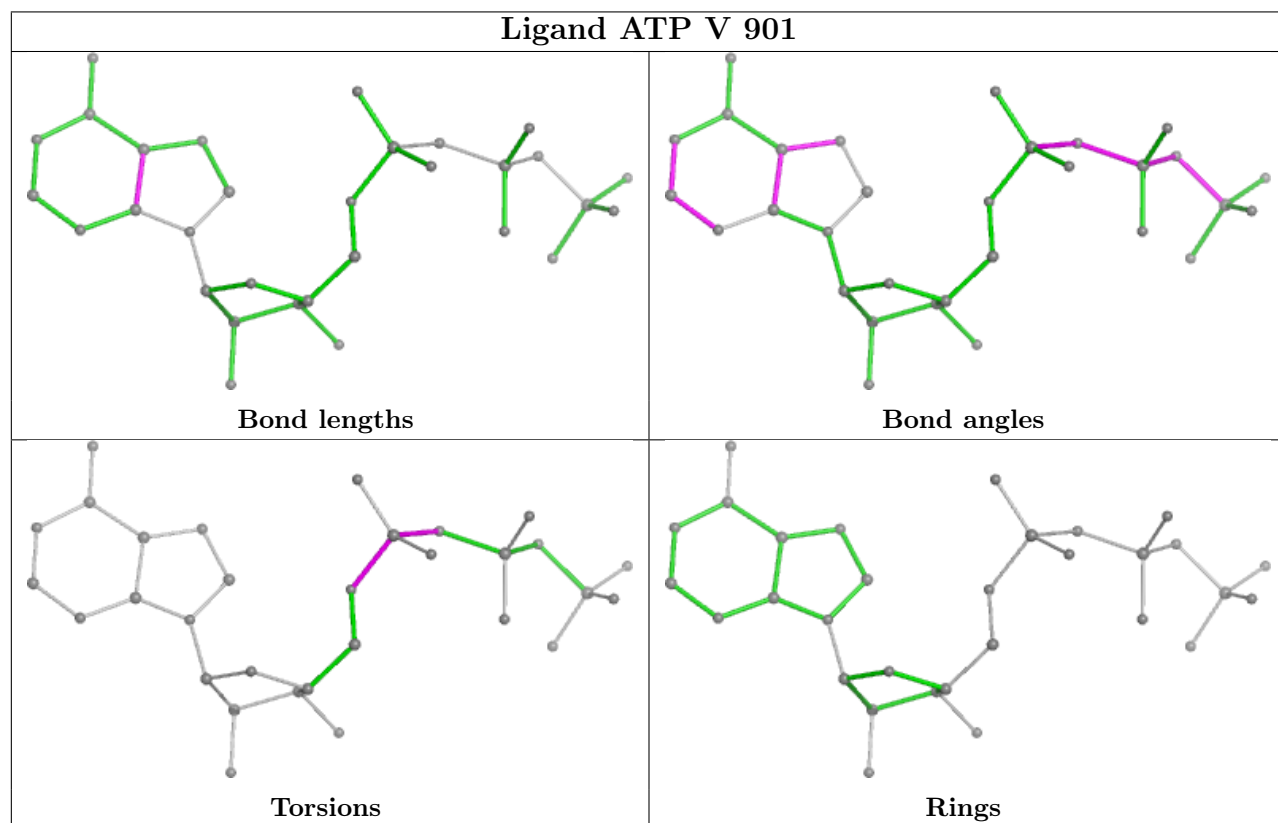
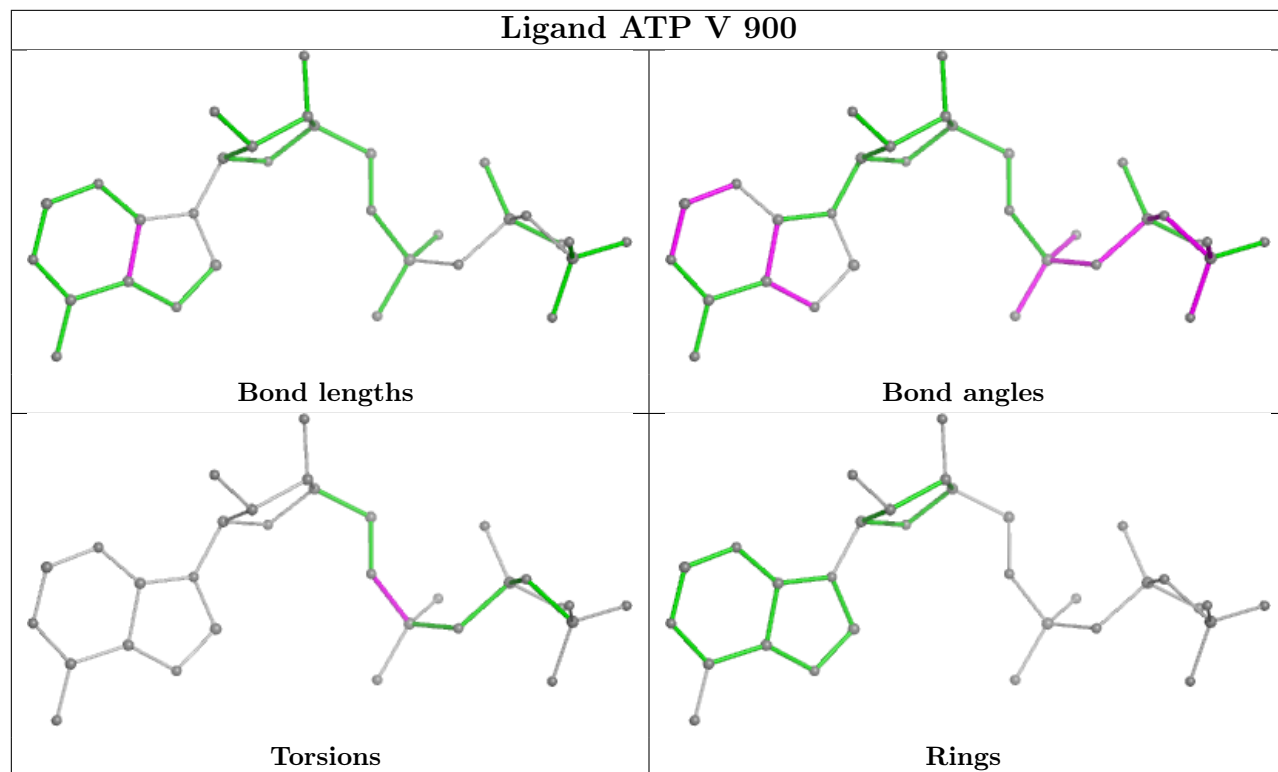
Mol	Chain	Res	Type	Atoms
54	A	3001	TEL	C15-C21-C26-O29
54	A	3001	TEL	C15-C21-C26-C30
55	V	900	ATP	C5'-O5'-PA-O1A
55	V	901	ATP	C5'-O5'-PA-O1A
54	A	3001	TEL	C21-C15-O9-C4

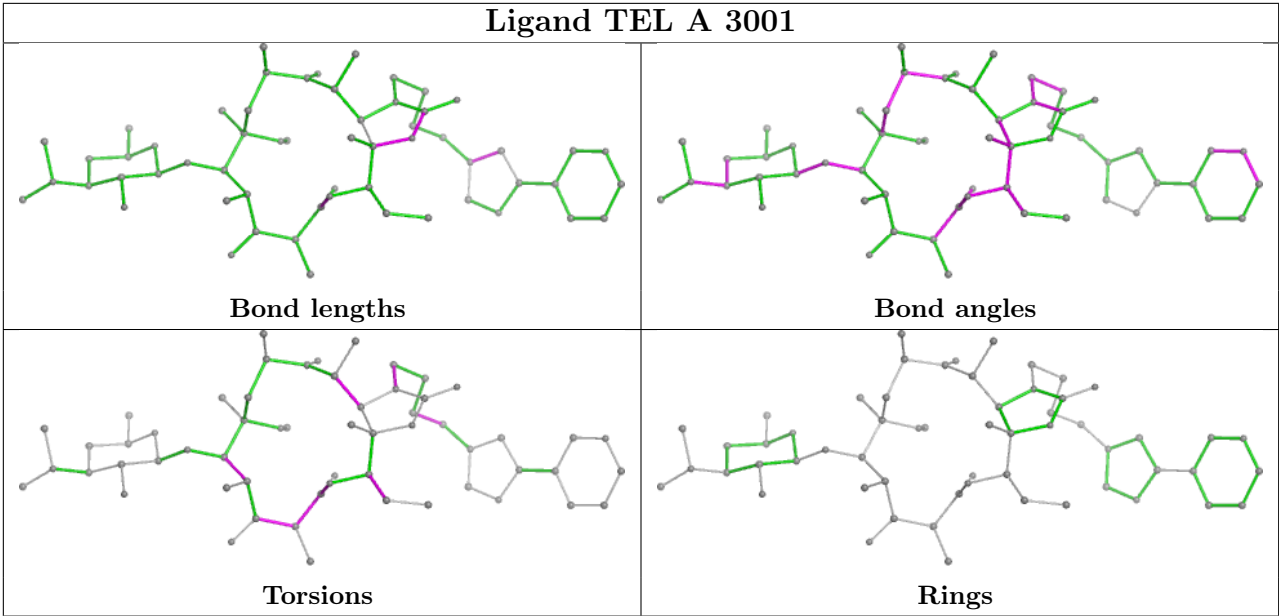
There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient

equivalents in the CSD to analyse the geometry.





5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	5
53	x	1

The worst 5 of 6 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	x	44:U	O3'	47:U	P	14.81
1	A	182:C	O3'	183:A	P	6.43
1	A	1449:C	O3'	1450:C	P	4.34
1	A	1451:U	O3'	1452:C	P	3.29
1	A	1452:C	O3'	1453:A	P	3.25

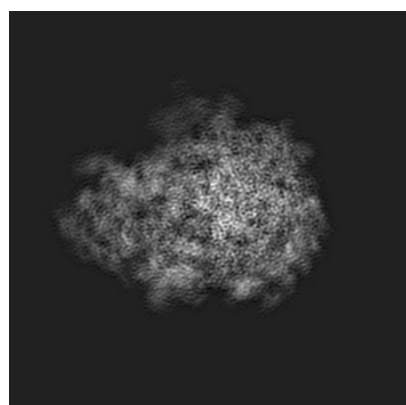
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0177. These allow visual inspection of the internal detail of the map and identification of artifacts.

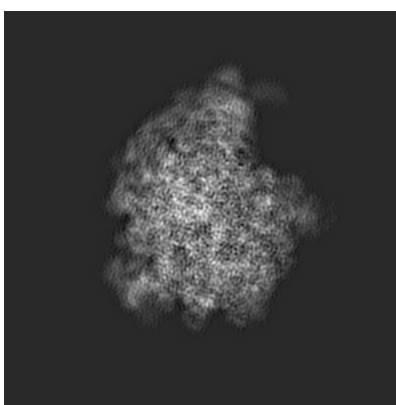
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

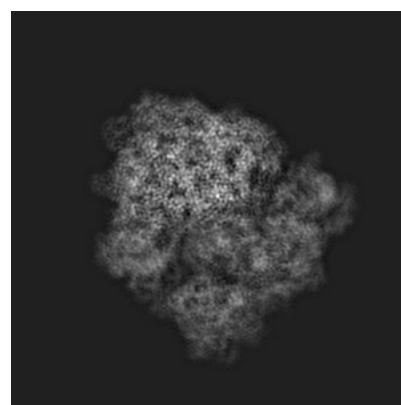
#### 6.1.1 Primary map



X



Y

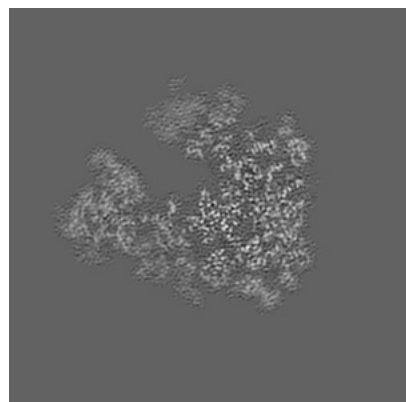


Z

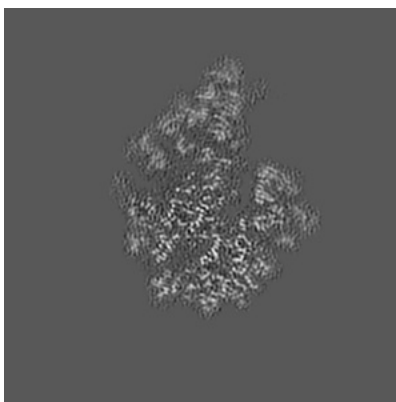
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

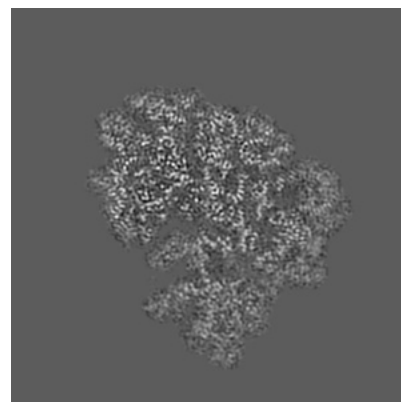
#### 6.2.1 Primary map



X Index: 180



Y Index: 180

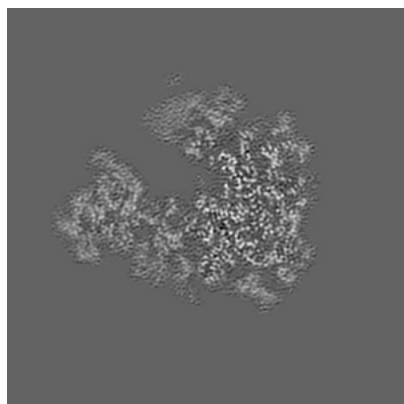


Z Index: 180

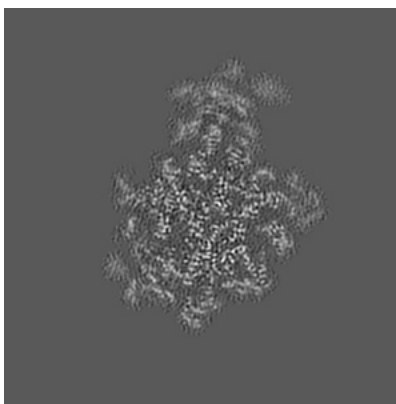
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

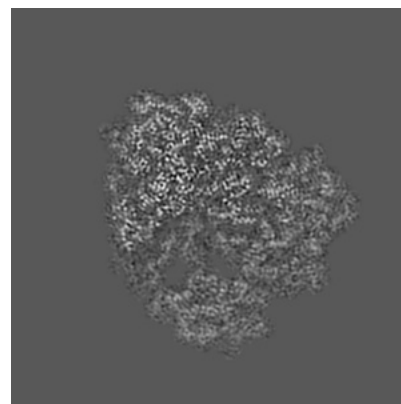
### 6.3.1 Primary map



X Index: 177



Y Index: 199

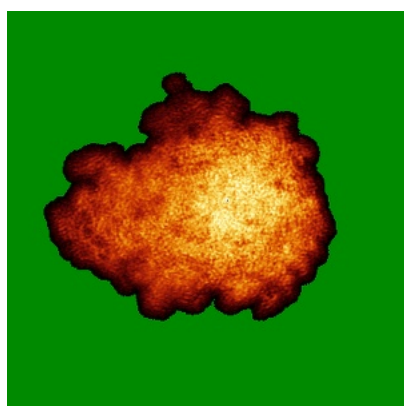


Z Index: 189

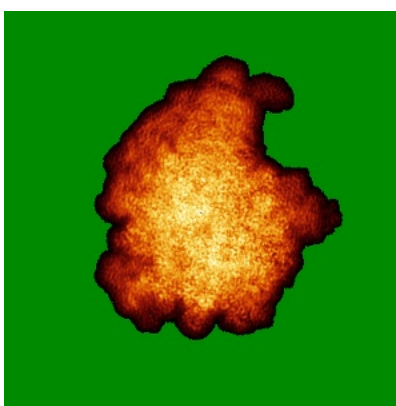
The images above show the largest variance slices of the map in three orthogonal directions.

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

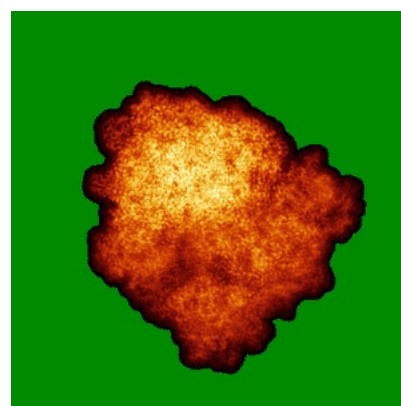
### 6.4.1 Primary map



X



Y

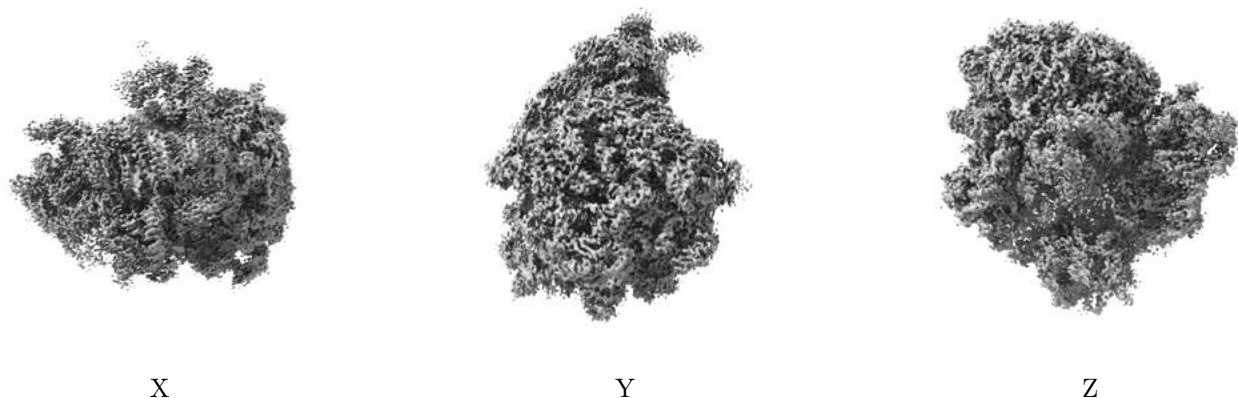


Z

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

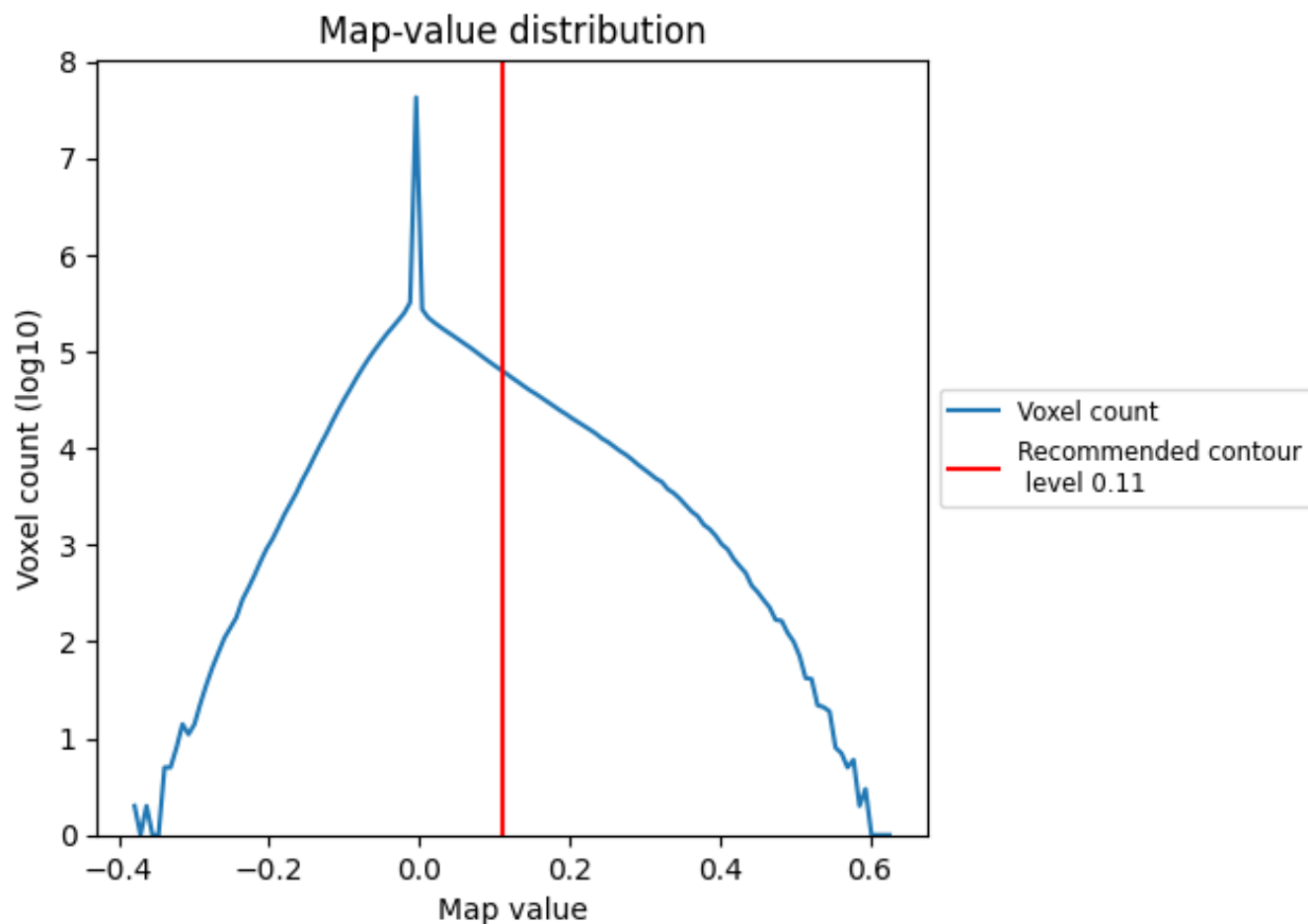
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

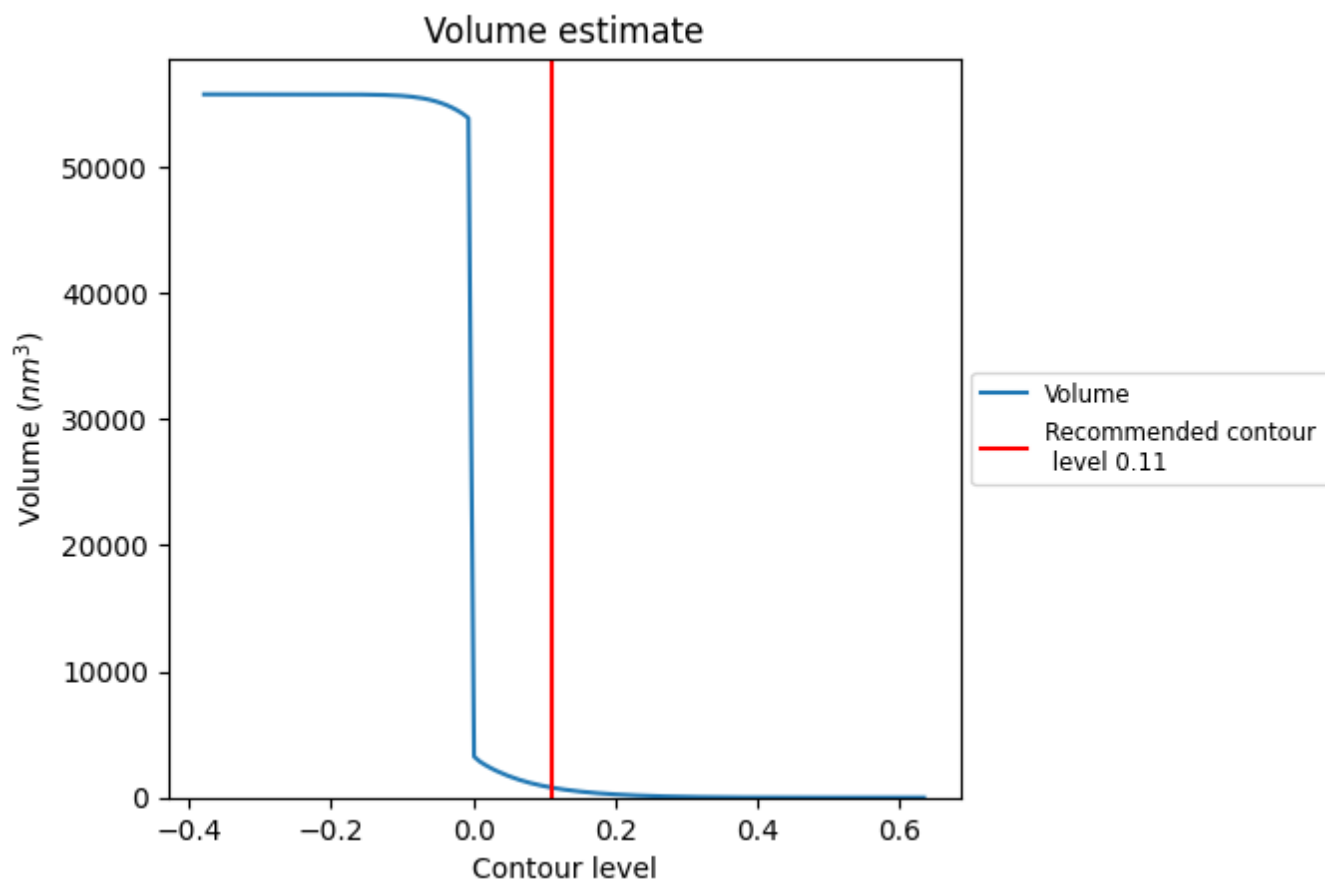
This section contains the results of statistical analysis of the map.

### 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](#)

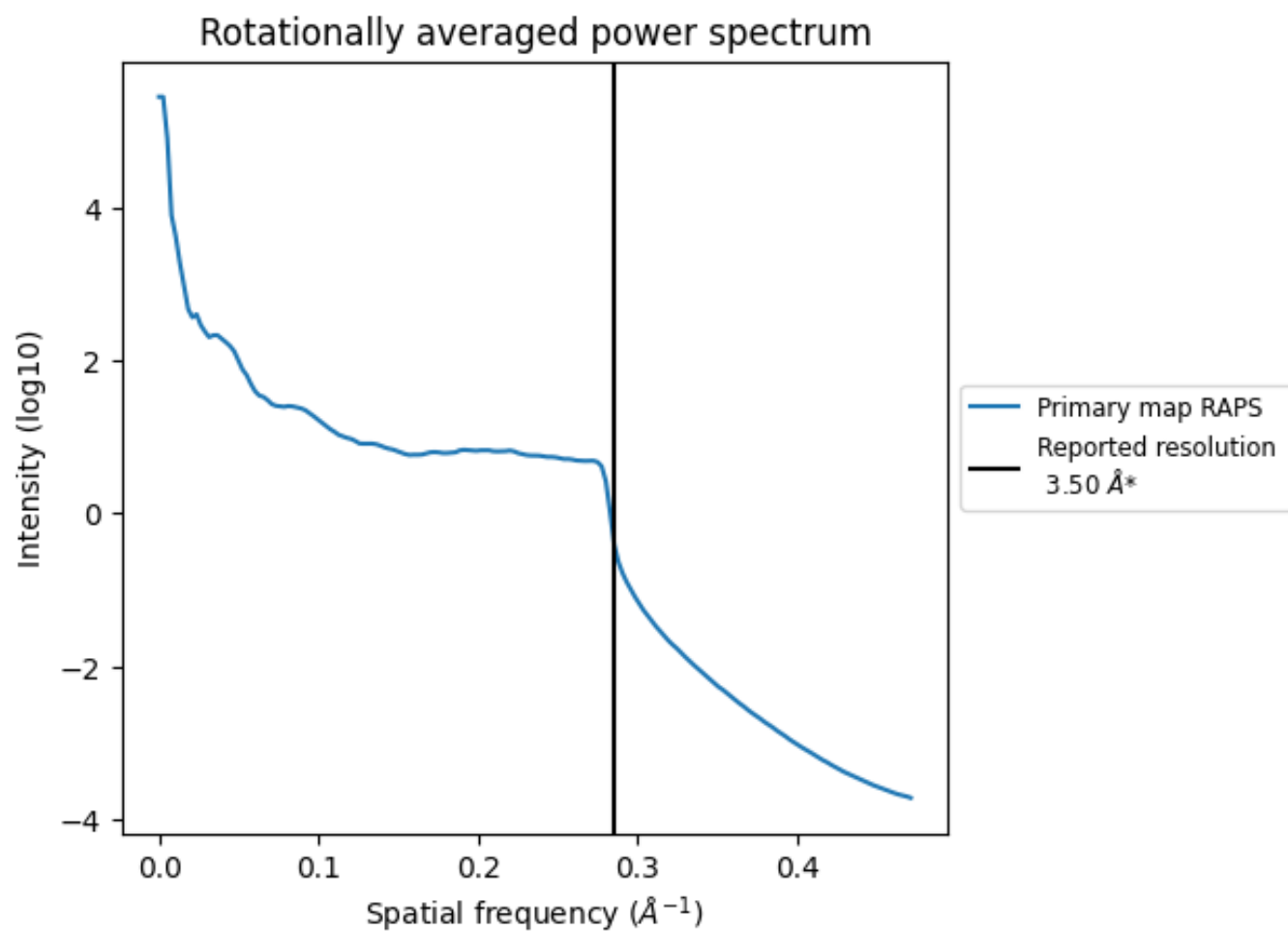


The volume at the recommended contour level is 793 nm<sup>3</sup>; this corresponds to an approximate mass of 716 kDa.

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 0.286 Å<sup>-1</sup>

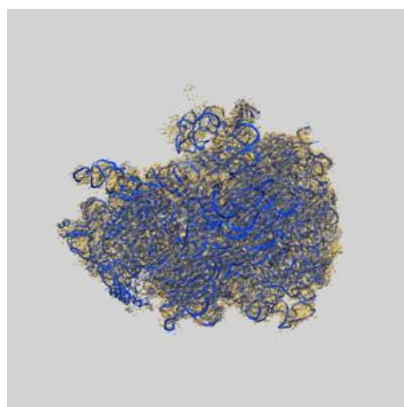
## 8 Fourier-Shell correlation

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

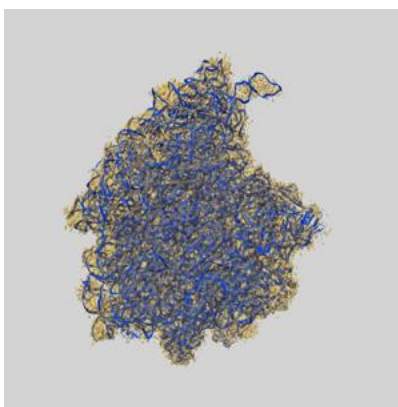
## 9 Map-model fit ⓘ

This section contains information regarding the fit between EMDB map EMD-0177 and PDB model 6HA8. Per-residue inclusion information can be found in section 3 on page 16.

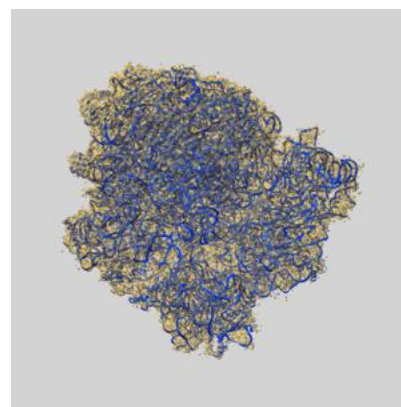
### 9.1 Map-model overlay ⓘ



X



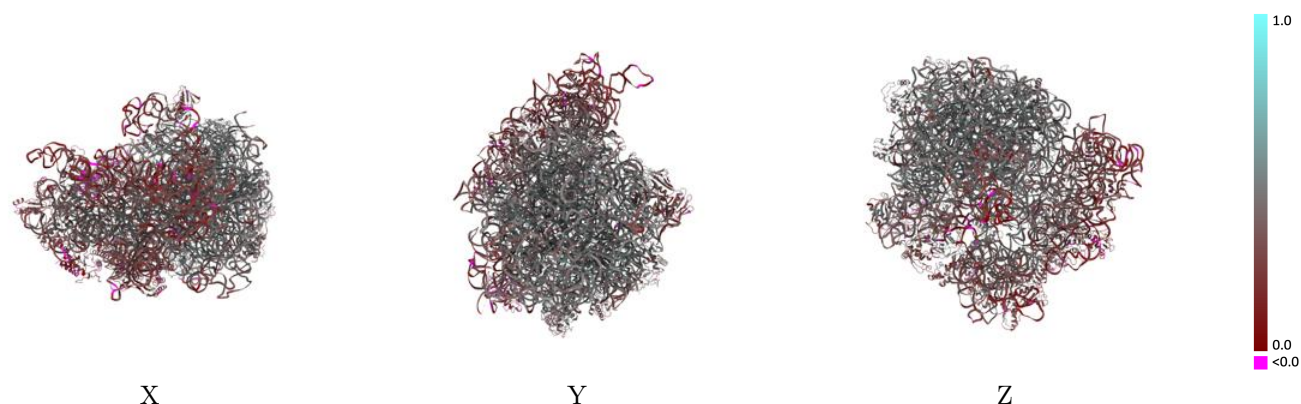
Y



Z

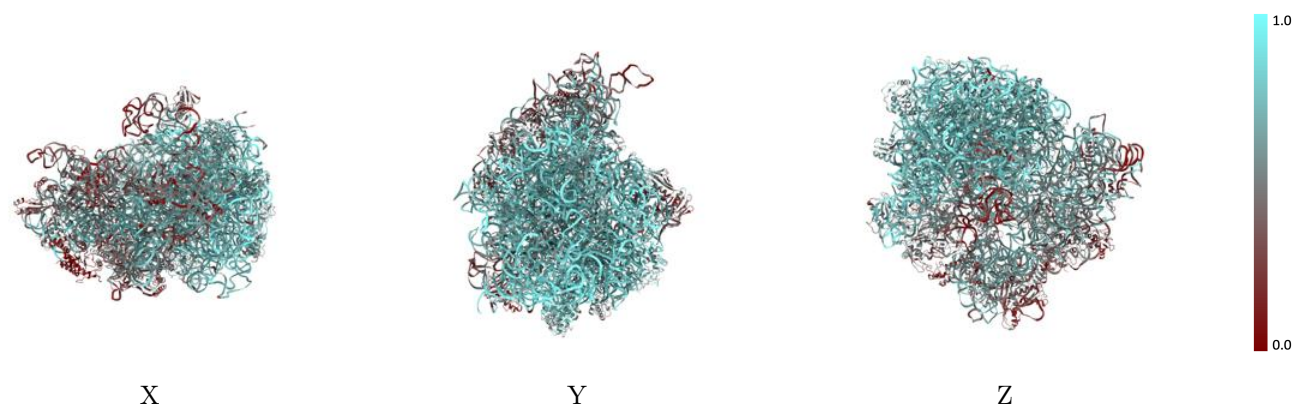
The images above show the 3D surface view of the map at the recommended contour level 0.11 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



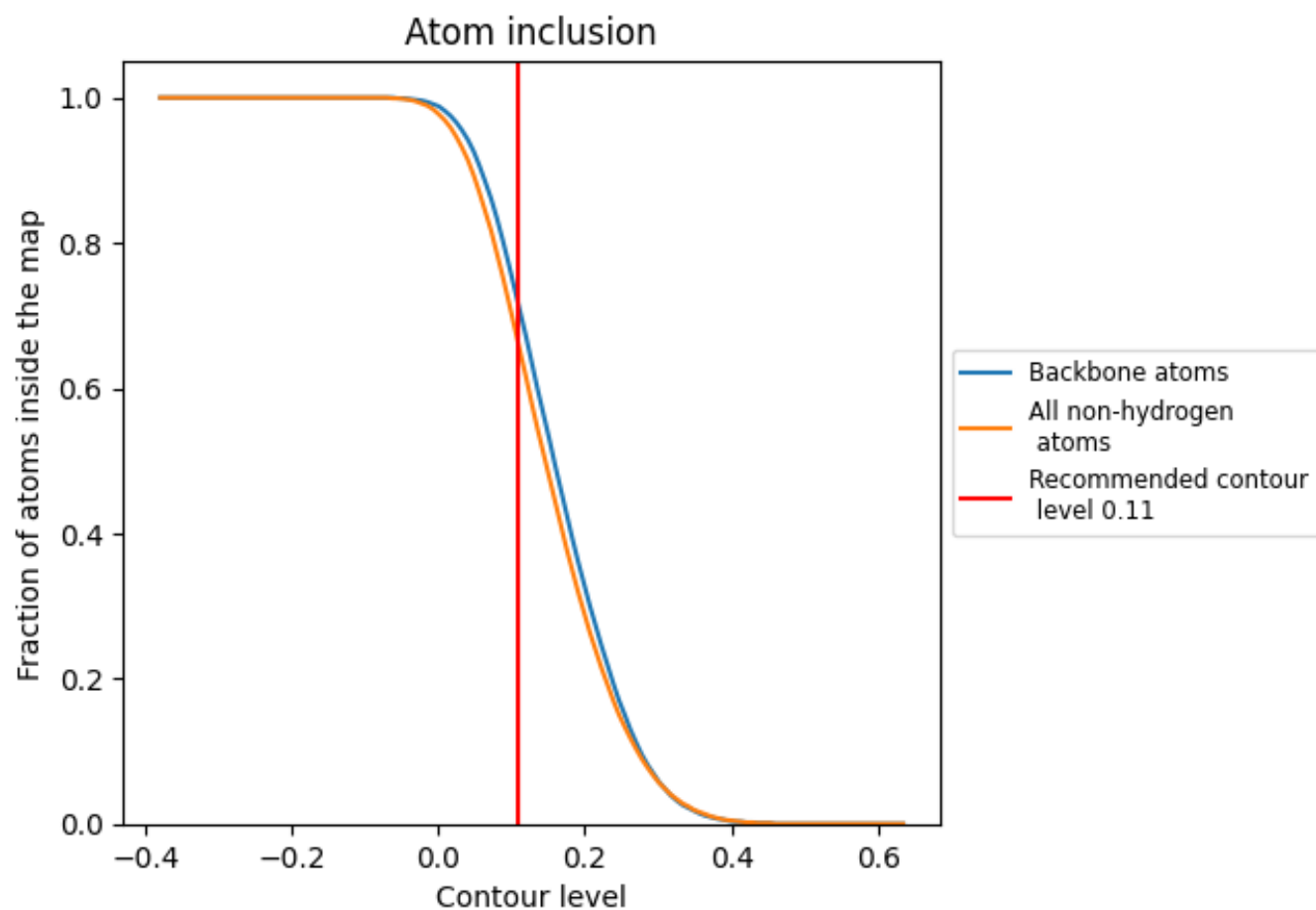
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.11).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 66% 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 (0.11) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6580	 0.3890
0	 0.7190	 0.4870
1	 0.6740	 0.4410
2	 0.7360	 0.5030
3	 0.7260	 0.5080
4	 0.6140	 0.4620
6	 0.2940	 0.2640
7	 0.6670	 0.4050
8	 0.0760	 0.1430
A	 0.7960	 0.4370
B	 0.7850	 0.4020
C	 0.6760	 0.4800
D	 0.6960	 0.4810
E	 0.6820	 0.4500
F	 0.4590	 0.3260
G	 0.4150	 0.3170
J	 0.7100	 0.4720
K	 0.6450	 0.4620
L	 0.6630	 0.4490
M	 0.6350	 0.4500
N	 0.6840	 0.4640
O	 0.5470	 0.3630
P	 0.6320	 0.4500
Q	 0.7070	 0.4500
R	 0.6890	 0.4530
S	 0.7030	 0.4810
T	 0.6140	 0.4430
U	 0.6150	 0.4040
V	 0.4240	 0.3890
W	 0.6490	 0.4500
X	 0.5230	 0.4500
Y	 0.5880	 0.3610
Z	 0.6360	 0.4400
a	 0.6450	 0.3360
b	 0.1210	 0.1970



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Chain	Atom inclusion	Q-score
c	 0.3990	 0.3340
d	 0.2450	 0.2270
e	 0.4970	 0.3750
f	 0.2840	 0.2490
g	 0.4500	 0.3240
h	 0.3960	 0.2870
i	 0.4340	 0.3220
j	 0.3410	 0.3210
k	 0.3790	 0.2970
l	 0.3720	 0.3080
m	 0.3810	 0.2880
n	 0.3810	 0.3480
o	 0.3850	 0.2490
p	 0.3260	 0.2690
q	 0.2850	 0.2390
r	 0.3410	 0.2730
s	 0.3460	 0.2600
t	 0.3710	 0.2630
x	 0.4340	 0.3210