



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 04:16 PM UTC

PDB ID : 5U9F / pdb_00005u9f
EMDB ID : EMD-8521
Title : 3.2 Å cryo-EM ArfA-RF2 ribosome rescue complex (Structure II)
Authors : Demo, G.; Svidritskiy, E.; Madireddy, R.; Diaz-Avalos, R.; Grant, T.; Grigorieff, N.; Sousa, D.; Korostelev, A.A.
Deposited on : 2016-12-16
Resolution : 3.20 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

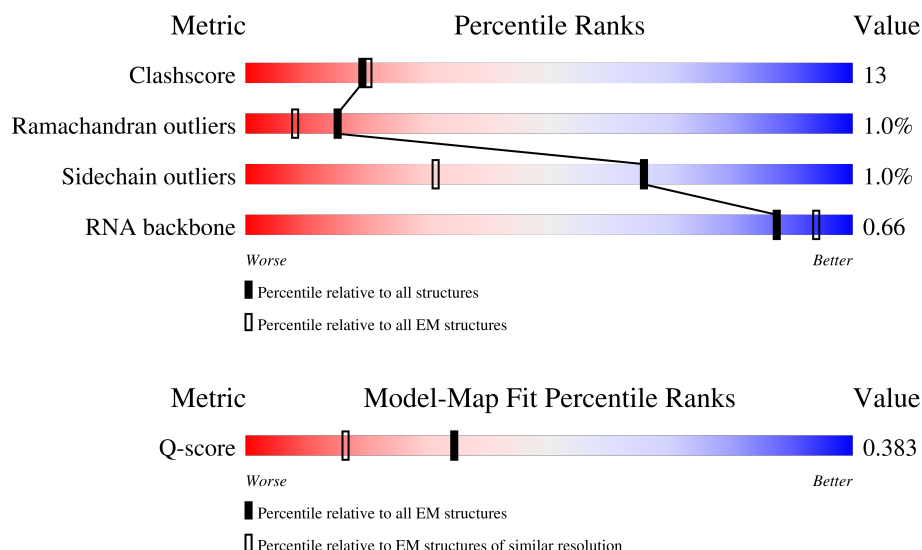
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMD archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.20 Å.

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



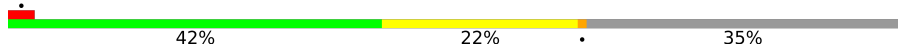
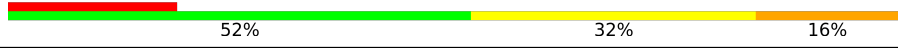
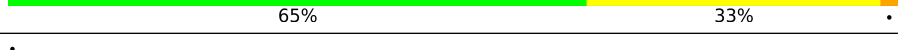
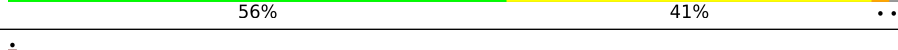
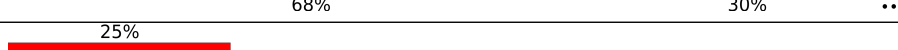
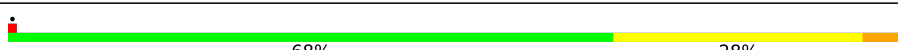
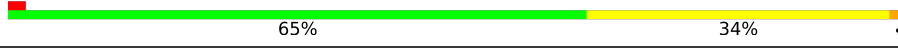
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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

Mol	Chain	Length	Quality of chain
1	A	1539	
2	01	2903	
3	02	119	

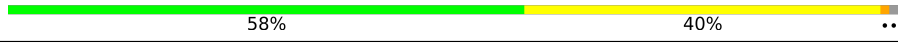
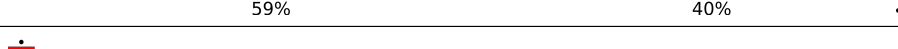
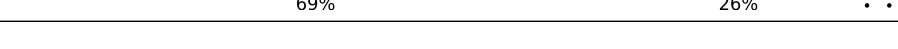
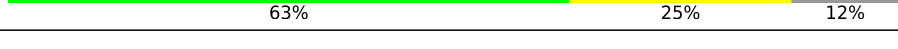
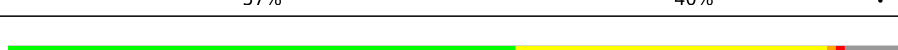
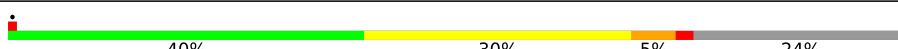
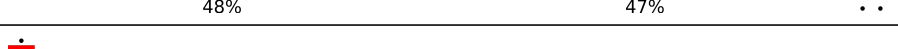
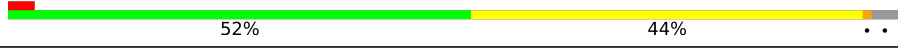
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Mol	Chain	Length	Quality of chain
4	Y	72	
5	W	77	
5	X	77	
6	03	234	
7	04	273	
8	05	209	
9	06	201	
10	07	179	
11	08	177	
12	09	149	
13	10	165	
14	11	142	
15	12	142	
16	13	123	
17	14	144	
18	15	136	
19	16	127	
20	17	117	
21	18	115	
22	19	118	
23	20	103	
24	21	110	
25	22	100	
26	23	104	
27	24	94	

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Mol	Chain	Length	Quality of chain
28	25	85	
29	26	78	
30	27	63	
31	28	59	
32	29	70	
33	30	57	
34	31	55	
35	32	46	
36	33	65	
37	34	38	
38	V	14	
39	Z	365	
40	B	241	
41	C	233	
42	D	206	
43	E	167	
44	F	131	
45	G	156	
46	H	130	
47	I	130	
48	J	103	
49	K	129	
50	L	124	
51	M	118	
52	N	101	

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Mol	Chain	Length	Quality of chain
53	O	89	
54	P	82	
55	Q	84	
56	R	75	
57	S	92	
58	T	87	
59	U	71	

2 Entry composition [i](#)

There are 61 unique types of molecules in this entry. The entry contains 152819 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 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 2 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	01	2903	Total	C	N	O	P	0	0
			62318	27801	11467	20148	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
01	1847	G	A	conflict	GB 2073407

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	02	119	Total	C	N	O	P	0	0
			2546	1135	466	827	118		

- Molecule 4 is a protein called Alternative ribosome-rescue factor A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	Y	47	Total	C	N	O	S	0	0
			377	233	78	65	1		

- Molecule 5 is a RNA chain called fMet-tRNA (P- and E-site).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	X	77	Total	C	N	O	P	0	0
			1622	723	289	534	76		
5	W	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 6 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	03	220	Total	C	N	O	S	0	0
			1353	804	270	277	2		

- Molecule 7 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	04	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 8 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	05	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 9 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	06	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 10 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	07	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 11 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	08	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 12 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	09	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 13 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	10	131	Total	C	N	O	S	0	0
			988	625	175	183	5		

- Molecule 14 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	11	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 15 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	12	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 16 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	13	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 17 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	14	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 18 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	15	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 19 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	16	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 20 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	17	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 21 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	18	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 22 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	19	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 23 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	20	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 24 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	21	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 25 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	22	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 26 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	23	102	Total	C	N	O	0	0
			779	492	146	141		

- Molecule 27 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	24	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 28 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	25	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 29 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	26	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 30 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	27	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 31 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	28	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 32 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	29	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 33 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	30	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 34 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	31	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 35 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	32	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 36 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	33	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 37 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	34	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 38 is a RNA chain called truncated mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	V	14	Total	C	N	O	P	0	0
			306	138	64	91	13		

- Molecule 39 is a protein called Peptide chain release factor RF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Z	361	Total	C	N	O	S	0	0
			2844	1748	503	583	10		

- Molecule 40 is a protein called 30S ribosomal protein S2.

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

- Molecule 41 is a protein called 30S ribosomal protein S3.

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

- Molecule 42 is a protein called 30S ribosomal protein S4.

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

- Molecule 43 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	E	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

- Molecule 44 is a protein called 30S ribosomal protein S6.

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

- Molecule 45 is a protein called 30S ribosomal protein S7.

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

- Molecule 46 is a protein called 30S ribosomal protein S8.

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

- Molecule 47 is a protein called 30S ribosomal protein S9.

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

- Molecule 48 is a protein called 30S ribosomal protein S10.

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

- Molecule 49 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	K	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 50 is a protein called 30S ribosomal protein S12.

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

- Molecule 51 is a protein called 30S ribosomal protein S13.

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

- Molecule 52 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	N	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 53 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	O	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 54 is a protein called 30S ribosomal protein S16.

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

- Molecule 55 is a protein called 30S ribosomal protein S17.

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

- Molecule 56 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	R	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 57 is a protein called 30S ribosomal protein S19.

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

- Molecule 58 is a protein called 30S ribosomal protein S20.

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

- Molecule 59 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	U	65	Total	C	N	O	S	0	0
			544	335	117	91	1		

- Molecule 60 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
60	A	118	Total	Mg	0
			118	118	
60	01	221	Total	Mg	0
			221	221	
60	02	6	Total	Mg	0
			6	6	
60	X	5	Total	Mg	0
			5	5	
60	17	1	Total	Mg	0
			1	1	
60	19	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
60	30	1	Total 1	Mg 1	0
60	31	1	Total 1	Mg 1	0
60	34	1	Total 1	Mg 1	0
60	V	1	Total 1	Mg 1	0
60	W	3	Total 3	Mg 3	0
60	I	1	Total 1	Mg 1	0

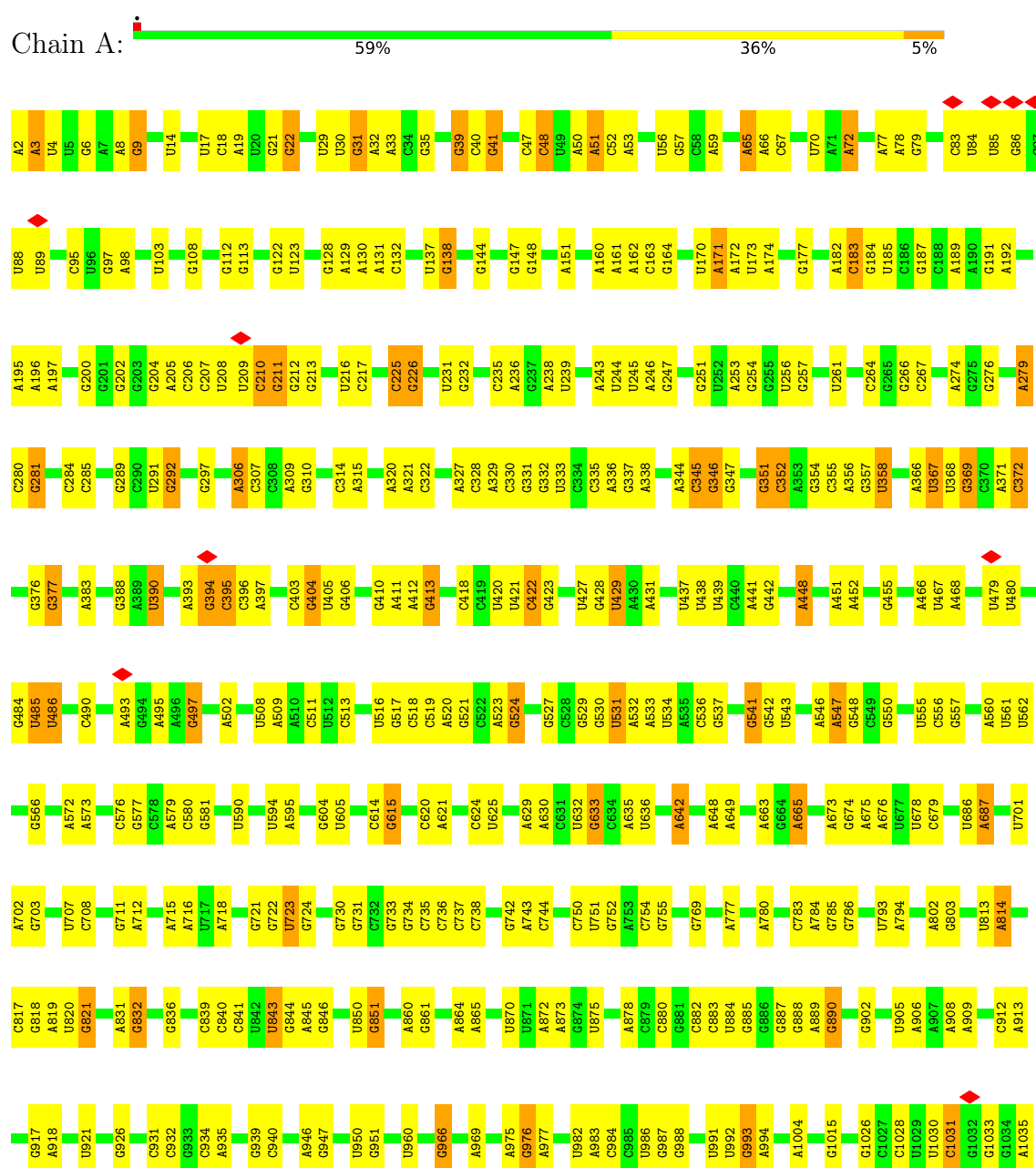
- Molecule 61 is ZINC ION (CCD ID: ZN) (formula: Zn).

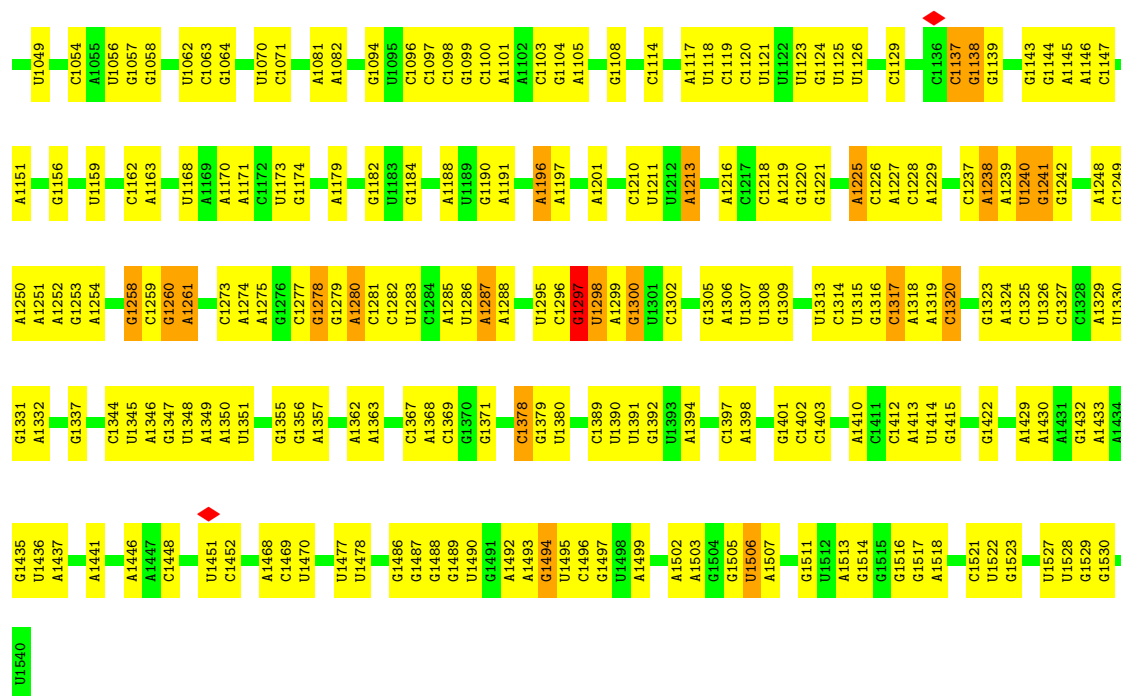
Mol	Chain	Residues	Atoms		AltConf
61	34	1	Total 1	Zn 1	0

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.

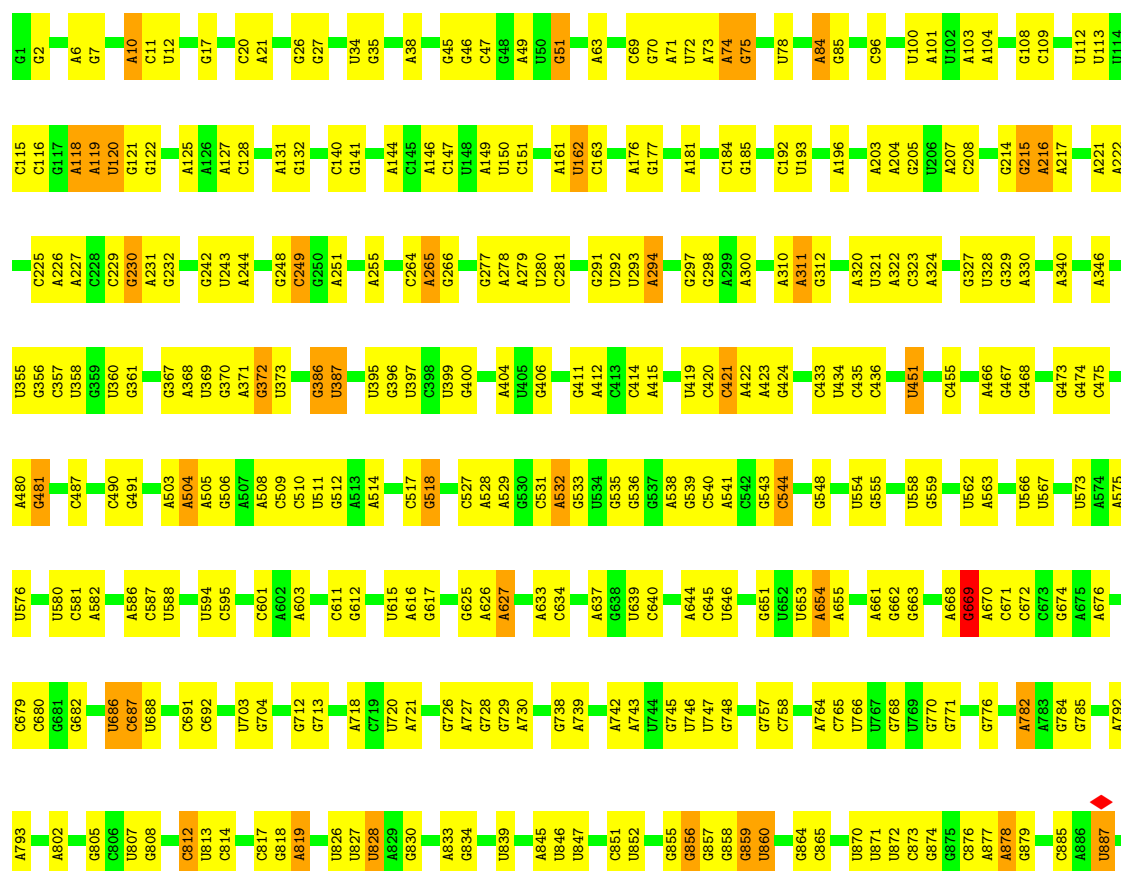
• Molecule 1: 16S ribosomal RNA



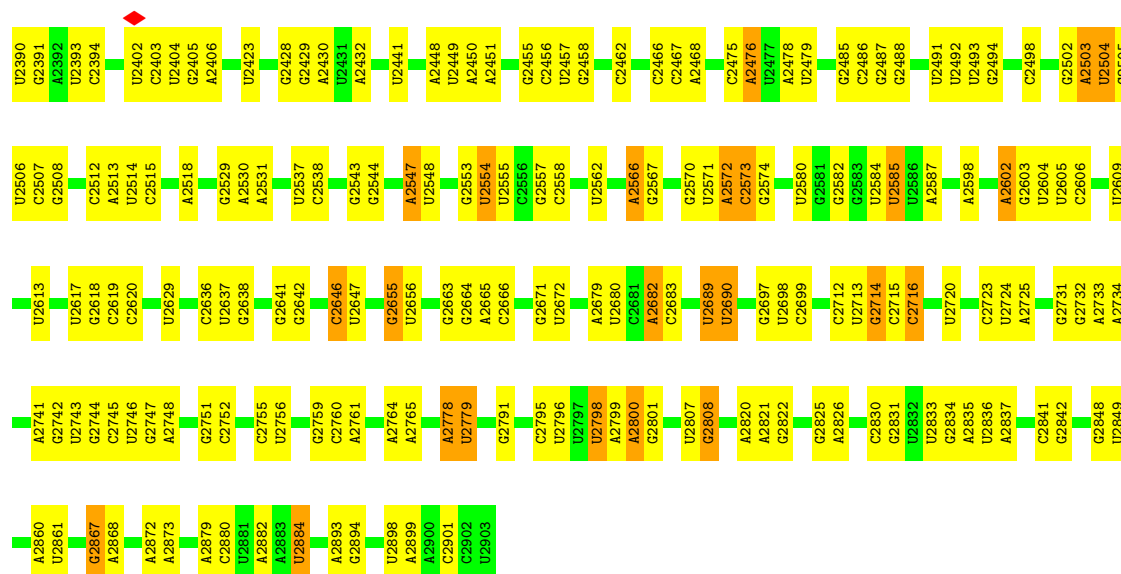


• Molecule 2: 23S ribosomal RNA

Chain 01: 62% 33% 5%

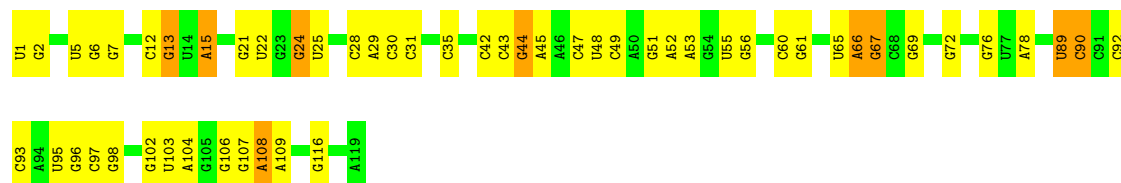


U2312	G2221	U2118	A2031	G1929	G1807	C1564	G1444	U1352	U1203	A1086	U1012	C890
C2313	C2222	A2119	G2032	G1930	A1808	C1565	C1447	A1353	A1204	G1087	U1012	C891
A2314	A2225	G2120	A2033	U1931	A1809	A1566	G1448	A1353	C1013	A1088	C1013	U894
G2315		G2121	U2034	A1932	G1699		G1449	C1357	G1210	A1089	U1019	U895
A2316		U2122	G2035	G1934	A1700	A1569	G1450	C1358	C1212	C1092	A1020	A896
G2317		G2123	C2036	G1935	A1701	A1571	C1451	G1359	A1213	G1093	A1021	C897
C2318		G2124		G1936	U1709	A1572	G1452	A1359	U1094	U1094	G1022	C898
G2319		G2128	U2039	A1937	G1710			G1361	G1225	A1096	G1026	A899
U2320		G2128	G2040	A1938		U1575	U1458	A1365	A1230	U1027	G1027	U906
U2321		U2131	C2043		G1715	U1576	G1459	A1366	U1231	C1104	A1028	G907
G2322		U2132	G2048	U1943	U1716	C1592	U1460	A1367	G1031	U1105	C1030	A910
U2323		G2133	G2049	U1944	G1826	A1593	C1461	G1368	C1243	C1103	A1032	C915
G2324		A2134	C2050	U1945	U1827	U1594			G1250	U1108	U1033	G916
G2325		A2135	A2051		G1828		U1468	A1373	C1261	A1111	G1034	G917
C2326		U2137	G2052	U1963	G1728	G1601	U1476	A1378	G1251	A1112	U1035	A918
A2327		U2137	A2053	A1964	C1729	U1602	U1476	U1379	G1252	U1113	G1036	U919
G2328		G2140	G2054	C1965	G1730	A1803		A1383	A1253	U1130	G1038	A920
C2329		G2141	C2055	A1966	G1731		C1480	C1386	G1256	G1131	A1039	C921
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G2331		C2145	A2059	A1968	G1737	C1607	G1482	U1394	G1259	A1133	G1041	U932
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U2333		A2147	U1970	G1971	U1739	C1611	U1497	C1398	G1055	G1138	G1056	G940
G2334		G2148	A2062	G1972	G1740	A1616		C1404	G1057	G1139	G1058	A941
A2345		G2156	C2065	G1973	A1744	A1637	C1507	U1405	A1061	C1140	G1062	G942
C2346		C2164	C2066	A1978	A1745	C1638	C1508	U1406	U1060	U1141	G1063	A943
U2347		C2165	G2067	G1979	G1753	C1639	A1509	U1409	G1149	A1142	G1064	C946
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U2356		U2172	G2073	G1992	A1759	C1645	U1522	G1421	U1067	C1170	U1067	C961
G2357		A2173	U2074	U1993	C1760	U1649	U1523	G1422	G1068	G1171	G1068	G962
A2358		C2177	U2075	C1996	G1764	G1652	G1530	G1424	A1069	U1070	A1070	U967
C2359		U2189	U2086	C1997	A1783	C1653	A1536	G1425	C1071	G1071	G1071	C968
G2360		G2190	G2087	G2004	A1790	U1657	G1537	G1426	G1072	U1175	G1072	A973
C2361		U2192	A2088	A2005	G1791	C1658	A1545	A1427	C1073	U1180	C1073	G974
G2362		A2184	C2089	C2006	A1791	G1776	G1546	G1429	A1073	U1181	A1073	A975
C2363		U2193	A2090	U2011	A1913		C1547	G1432	G1074	U1182	G1074	A983
A2364		G2195	C2104	G2012	C1914	A1664	G1548	A1433	C1075	U1183	C1075	A988
G2365		U2196	U2105	A2015	A1915	A1665	C1549	A1434	C1076	U1186	A1080	C995
C2366		C2197	U2106	A2019	A1916	A1666	A1551	G1436	C1077	U1187	U1081	A996
G2367		A2198	U2107	A2020	U1917	G1667		C1437	C1078	G1187	U1082	
C2368		U2199	U2108	A2021	G1796	G1668		U1438	C1079	G1188	U1083	
A2369		G2200	U2109	C2022	U1918	A1669		A1439	A1080	G1189	A1084	C1005
G2370		U2203	U2110	G2023	A1919	A1670			A1085			
C2371		G2204	G2112	C2024	C1920	G1674						
A2372		U2205	U2113	G2025	U1923	A1801						
G2373		A2206	G2114	U2026	C1924	A1802						
C2374		U2207	G2115	G2027	A1803	G1685						
A2375		A2208	A2117	A2030	A1928	G1687						



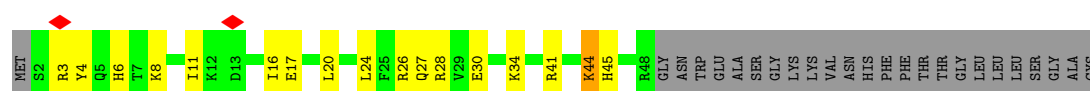
- Molecule 3: 5S ribosomal RNA

Chain 02:



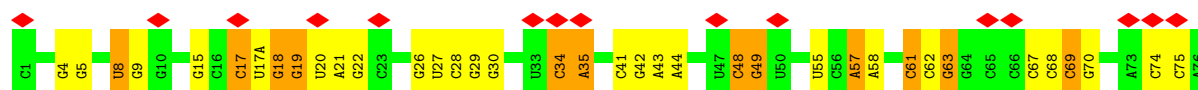
- Molecule 4: Alternative ribosome-rescue factor A

Chain Y:



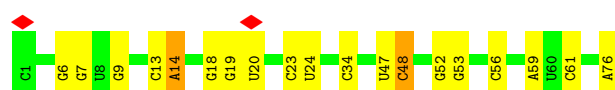
- Molecule 5: fMet-tRNA (P- and E-site)

Chain X:



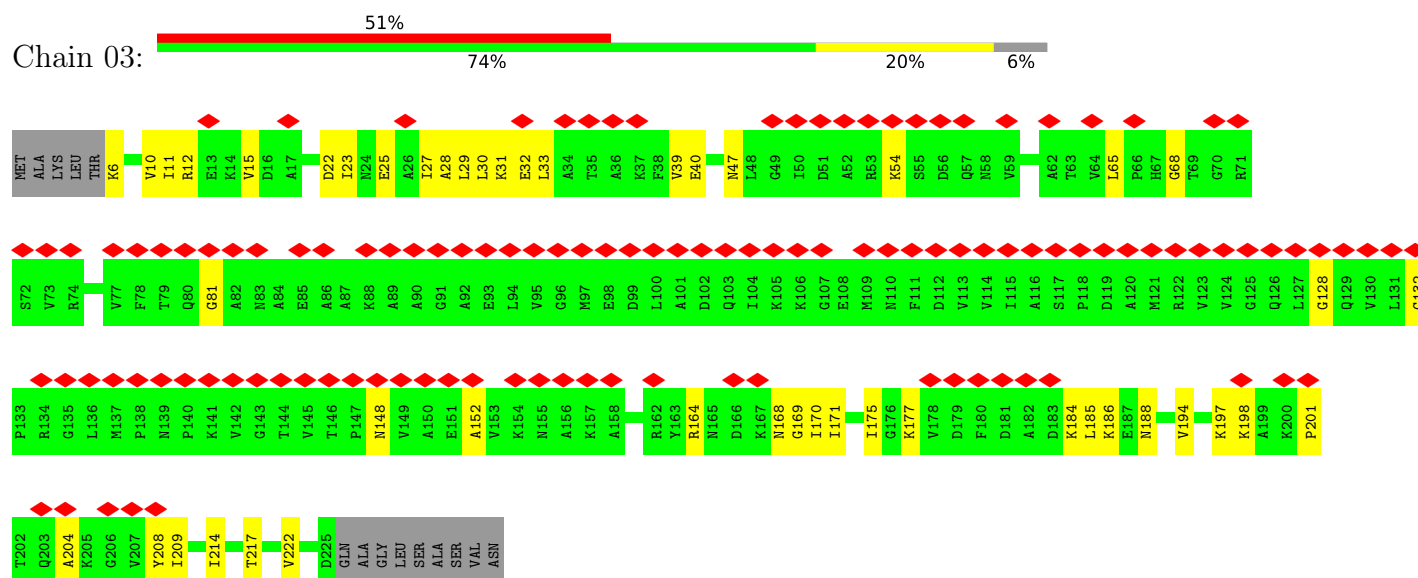
- Molecule 5: fMet-tRNA (P- and E-site)

Chain W:



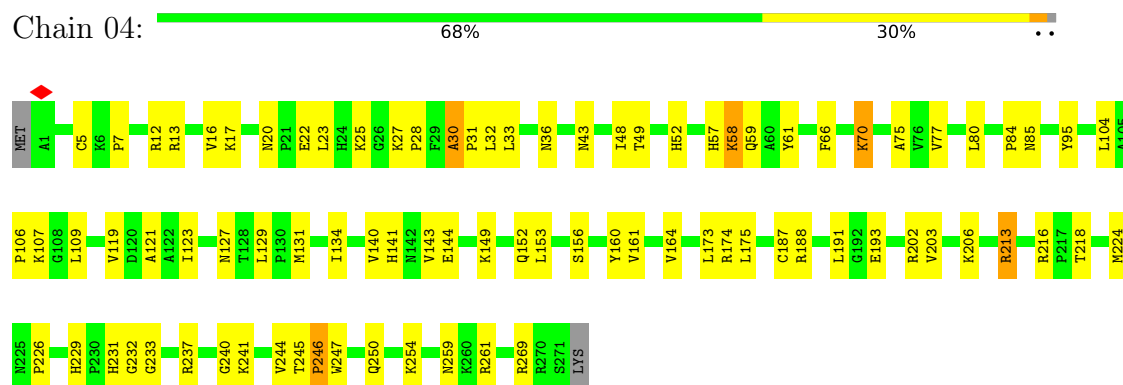
- Molecule 6: 50S ribosomal protein L1

Chain 03:



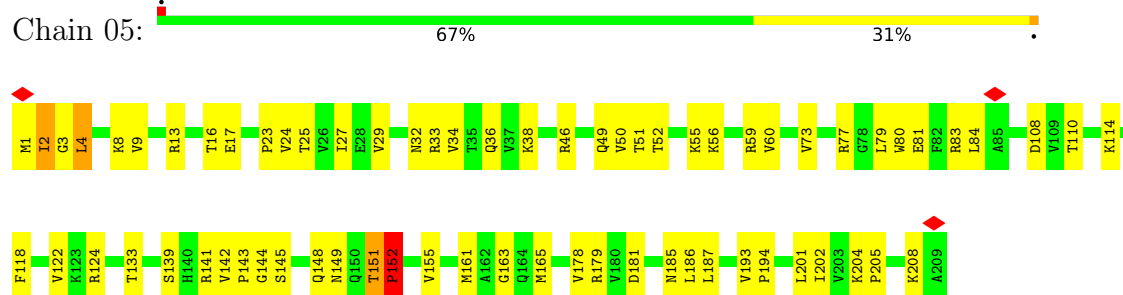
- Molecule 7: 50S ribosomal protein L2

Chain 04:



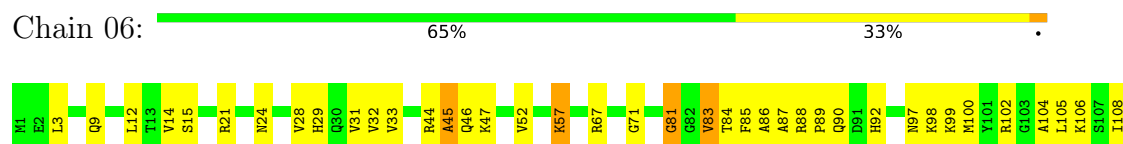
- Molecule 8: 50S ribosomal protein L3

Chain 05:



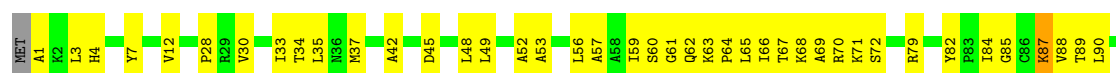
- Molecule 9: 50S ribosomal protein L4

Chain 06:

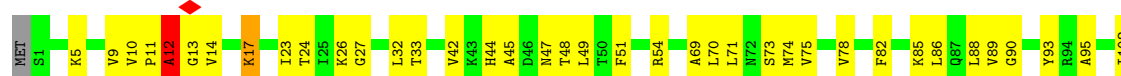




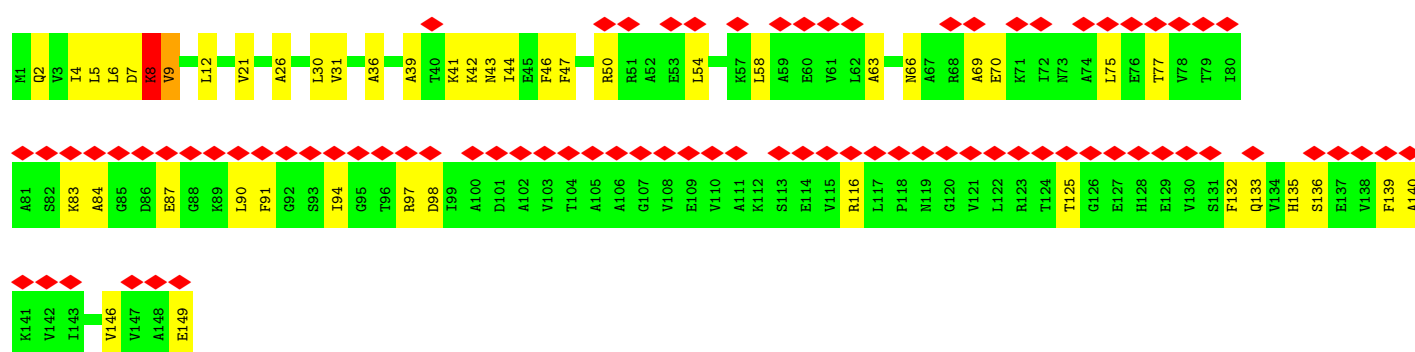
• Molecule 10: 50S ribosomal protein L5



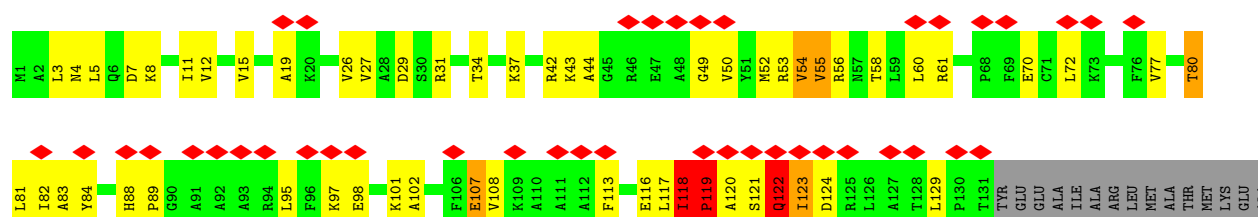
• Molecule 11: 50S ribosomal protein L6



• Molecule 12: 50S ribosomal protein L9

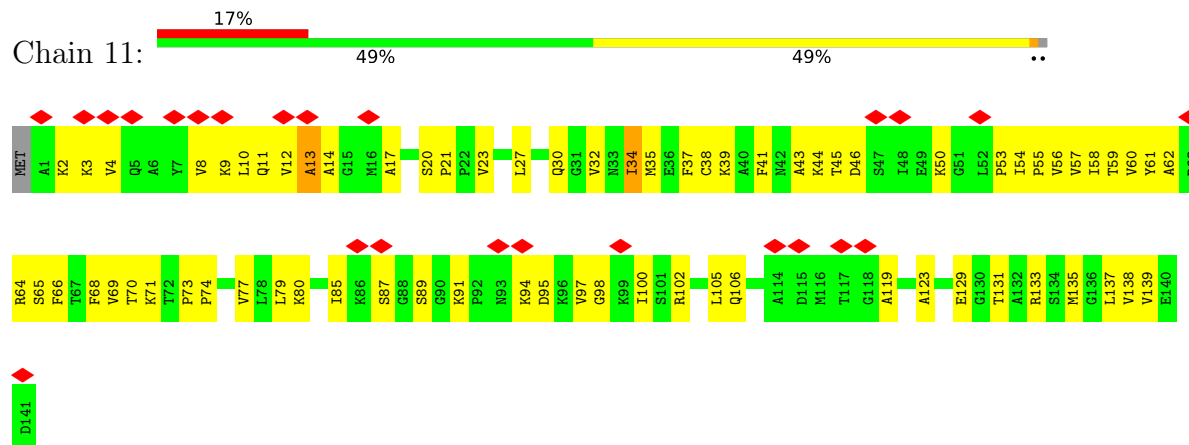


• Molecule 13: 50S ribosomal protein L10

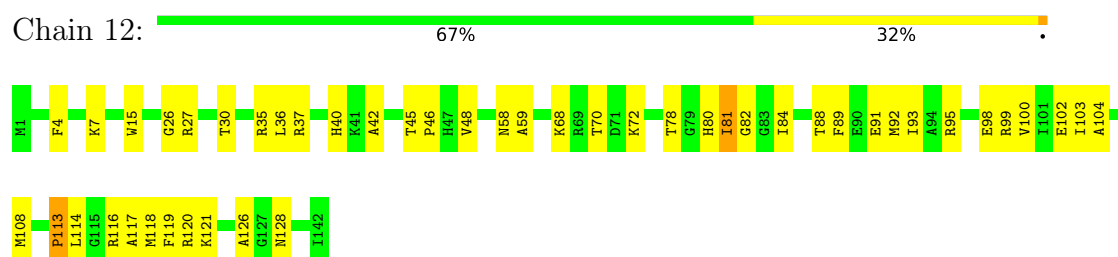


SER
ALA
GLY
LYS
LEU
VAL
ARG
THR
LEU
ALA
ALA
VAL
ARG
ASP
ALA
LYS
GLU
ALA
ALA

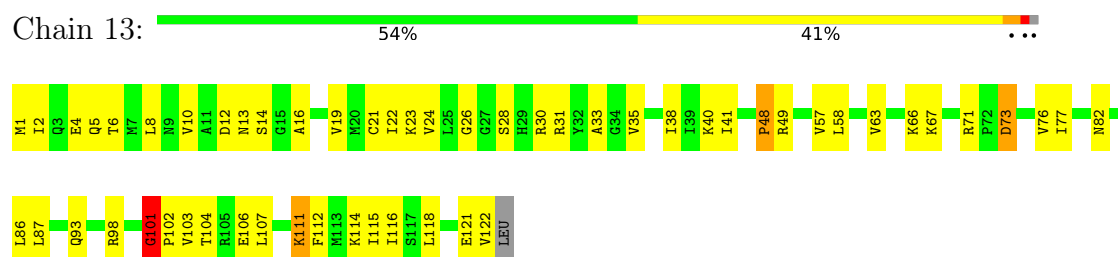
• Molecule 14: 50S ribosomal protein L11



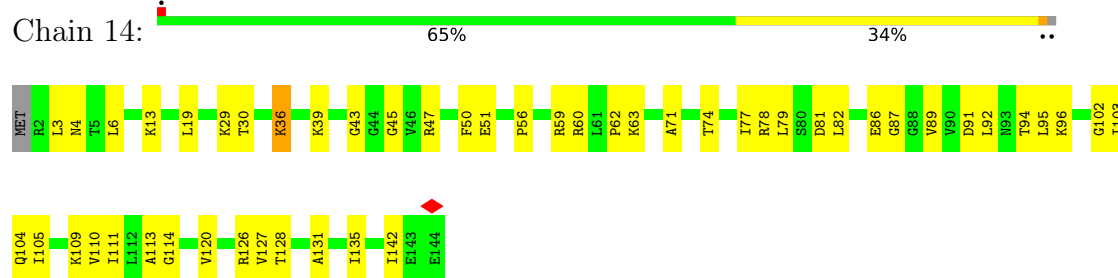
• Molecule 15: 50S ribosomal protein L13



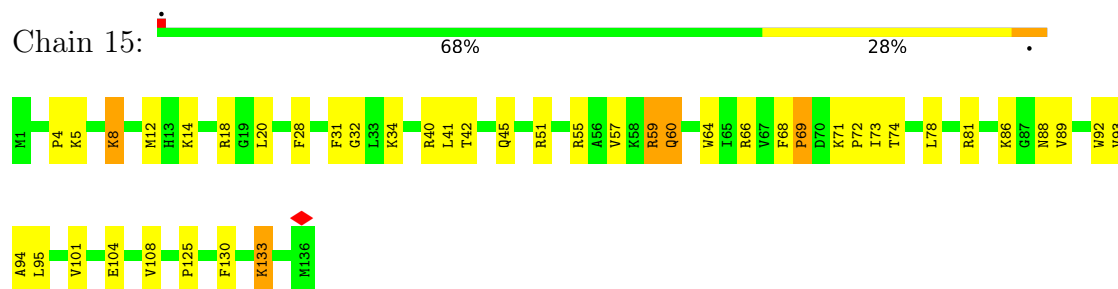
• Molecule 16: 50S ribosomal protein L14



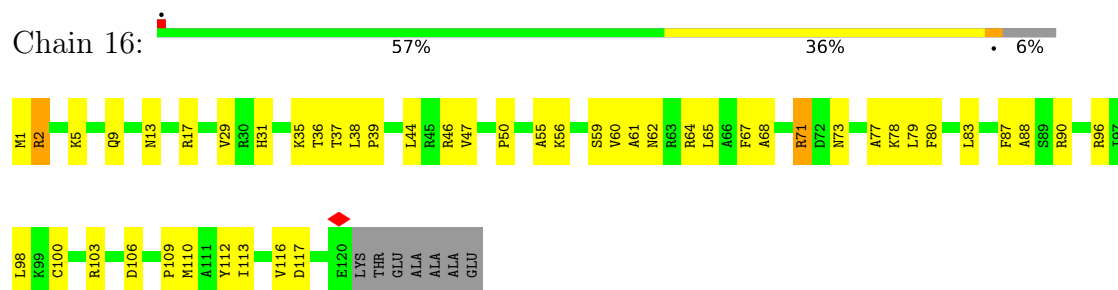
• Molecule 17: 50S ribosomal protein L15



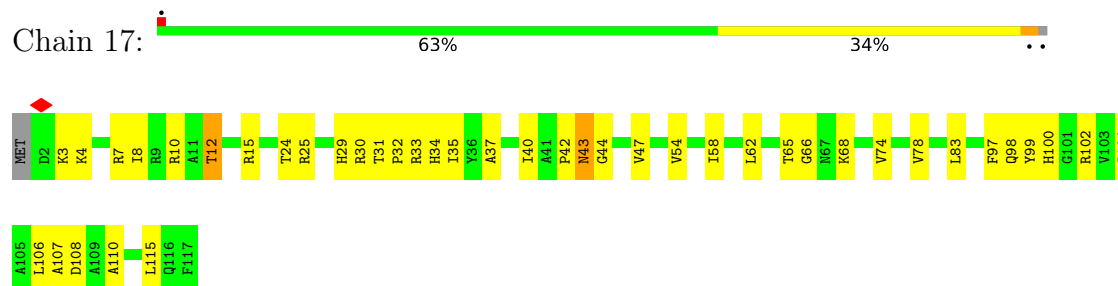
• Molecule 18: 50S ribosomal protein L16



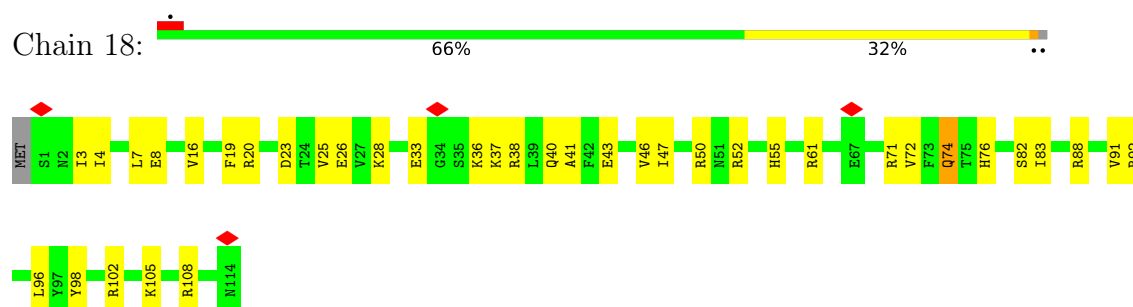
- Molecule 19: 50S ribosomal protein L17



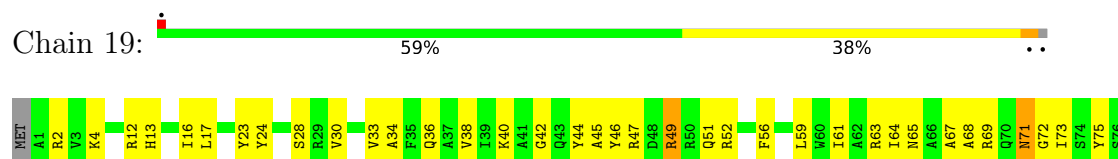
- Molecule 20: 50S ribosomal protein L18



- Molecule 21: 50S ribosomal protein L19

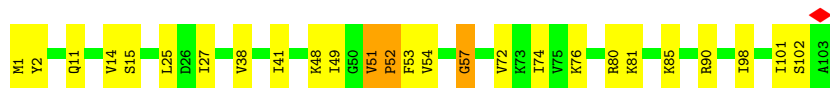
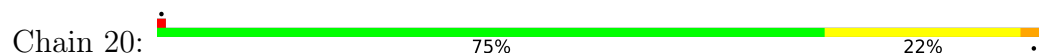


- Molecule 22: 50S ribosomal protein L20

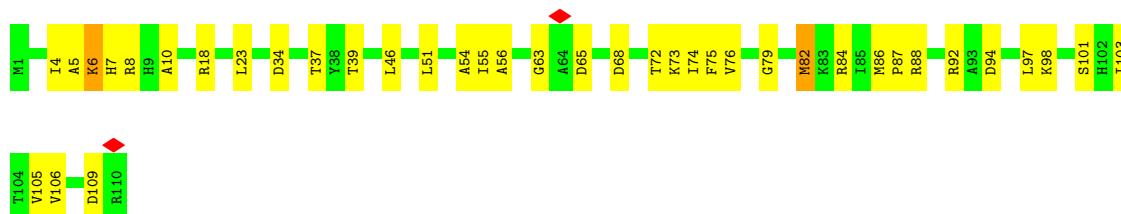




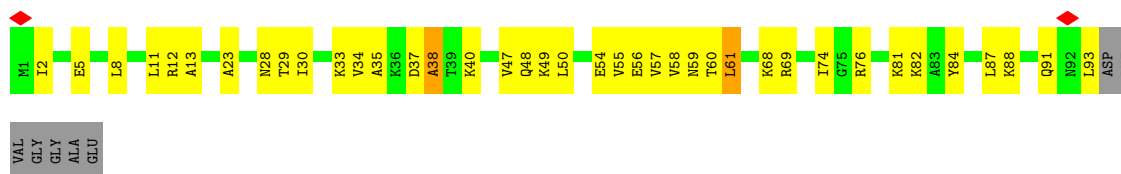
- Molecule 23: 50S ribosomal protein L21



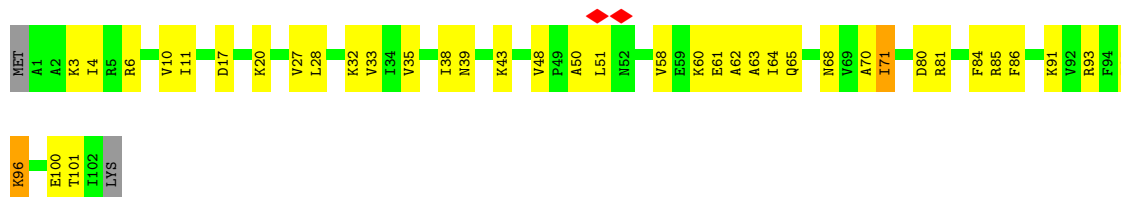
- Molecule 24: 50S ribosomal protein L22



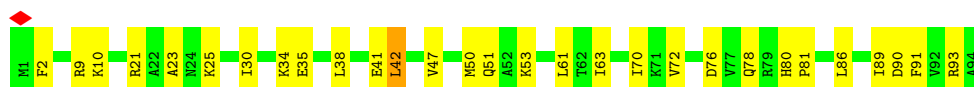
- Molecule 25: 50S ribosomal protein L23



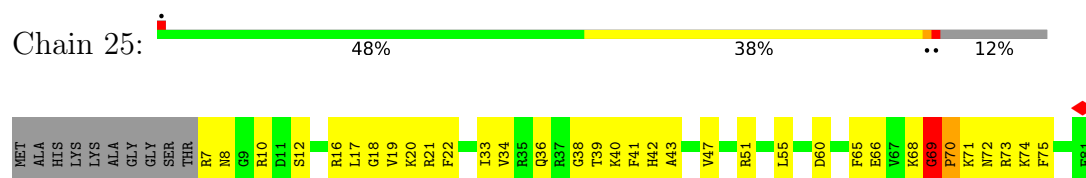
- Molecule 26: 50S ribosomal protein L24



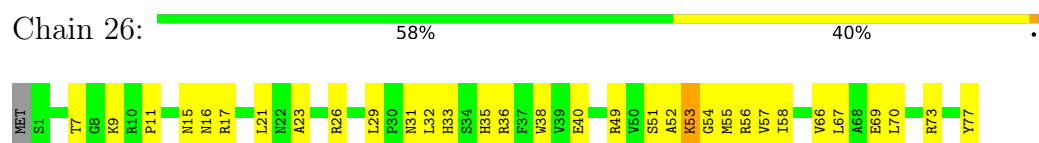
- Molecule 27: 50S ribosomal protein L25



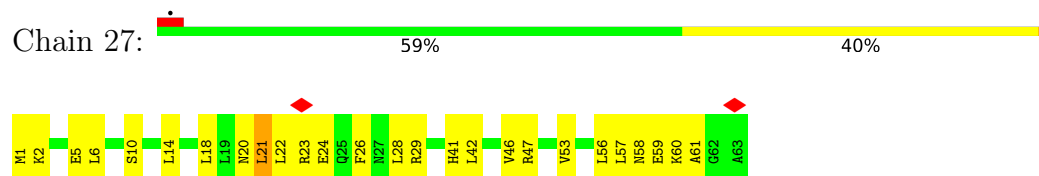
- Molecule 28: 50S ribosomal protein L27



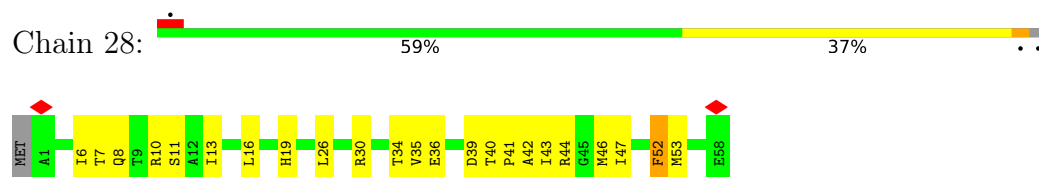
- Molecule 29: 50S ribosomal protein L28



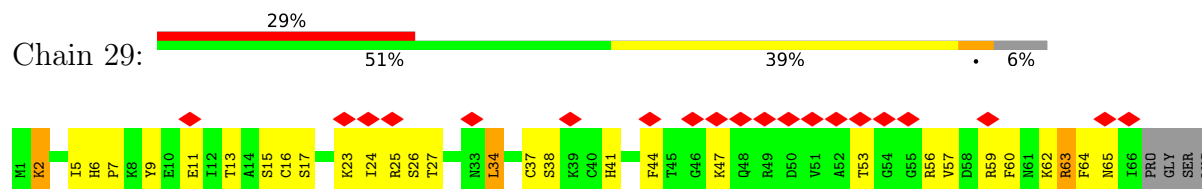
- Molecule 30: 50S ribosomal protein L29



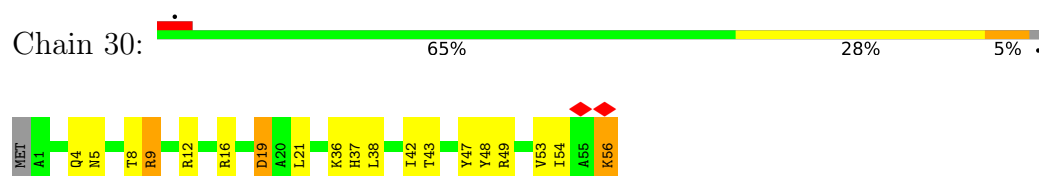
- Molecule 31: 50S ribosomal protein L30



- Molecule 32: 50S ribosomal protein L31



- Molecule 33: 50S ribosomal protein L32

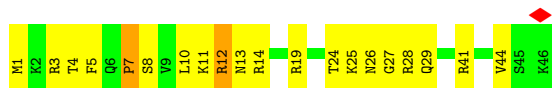


- Molecule 34: 50S ribosomal protein L33

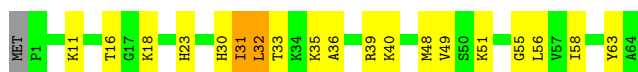




- Molecule 35: 50S ribosomal protein L34



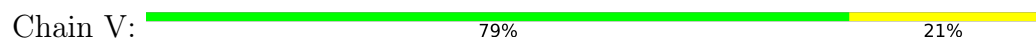
- Molecule 36: 50S ribosomal protein L35



- Molecule 37: 50S ribosomal protein L36



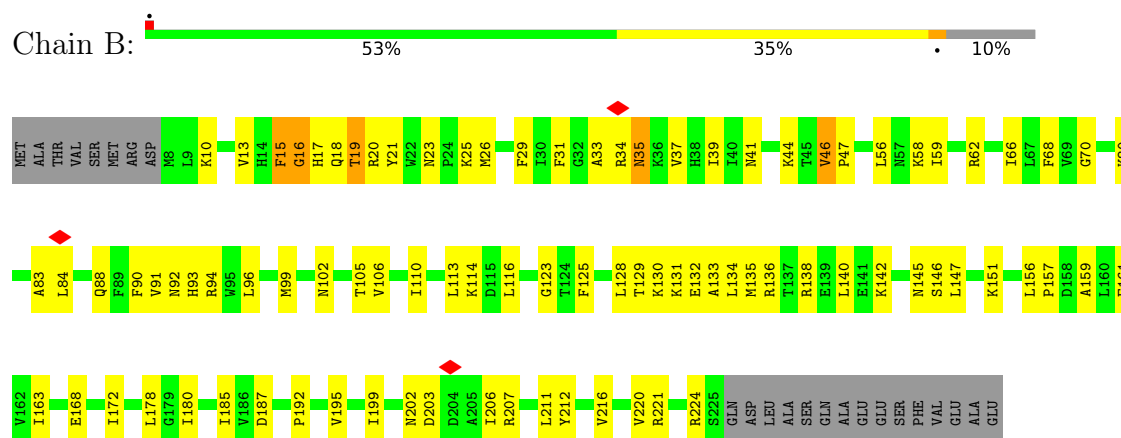
- Molecule 38: truncated mRNA



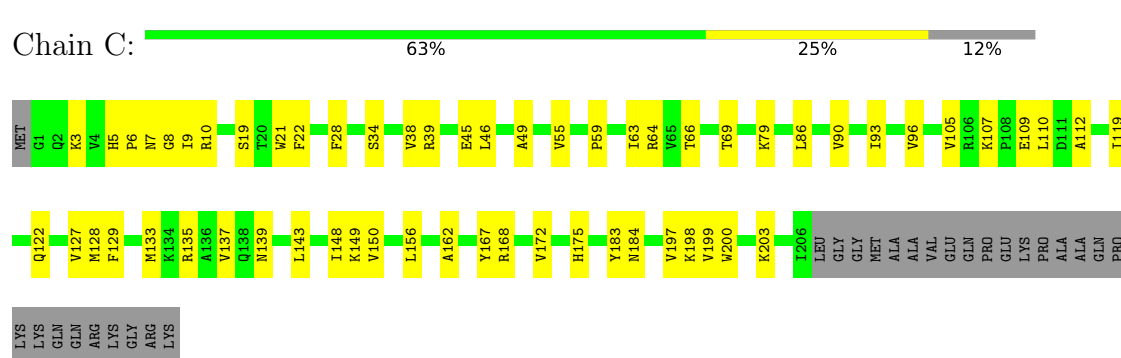
- Molecule 39: Peptide chain release factor RF2



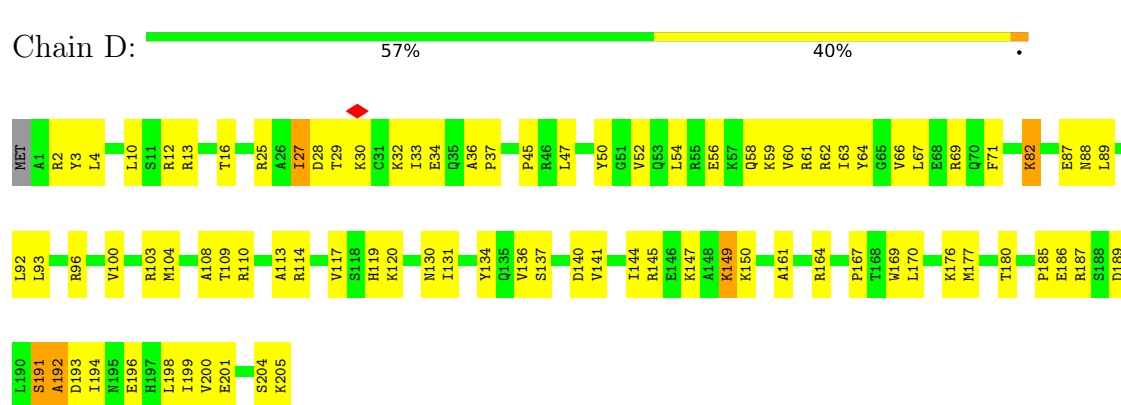
- Molecule 40: 30S ribosomal protein S2



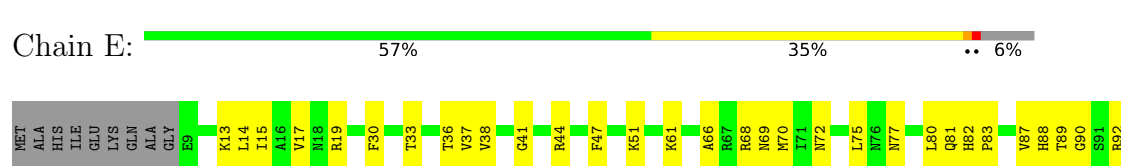
- Molecule 41: 30S ribosomal protein S3



- Molecule 42: 30S ribosomal protein S4

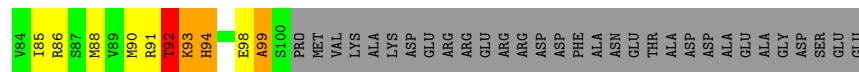


- Molecule 43: 30S ribosomal protein S5

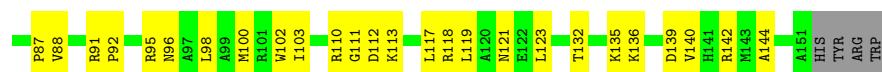




- Molecule 44: 30S ribosomal protein S6



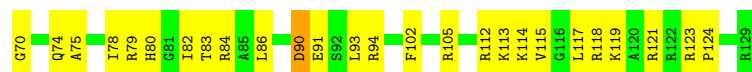
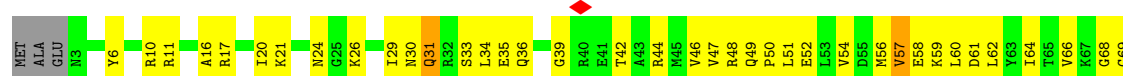
- Molecule 45: 30S ribosomal protein S7



- Molecule 46: 30S ribosomal protein S8

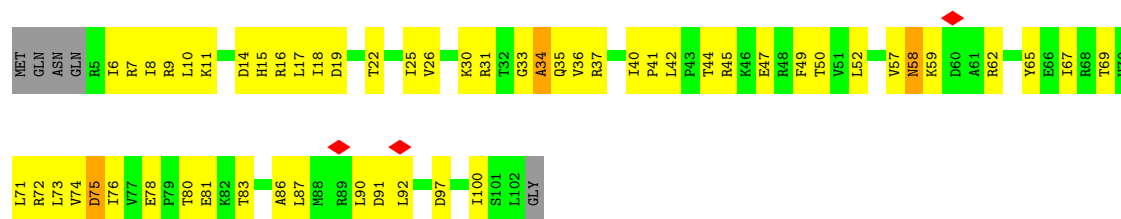


- Molecule 47: 30S ribosomal protein S9

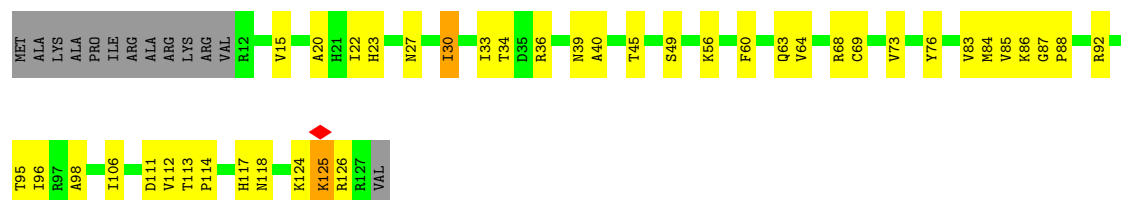


- Molecule 48: 30S ribosomal protein S10

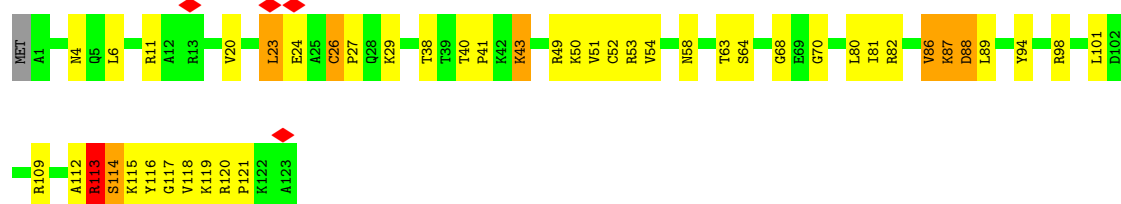




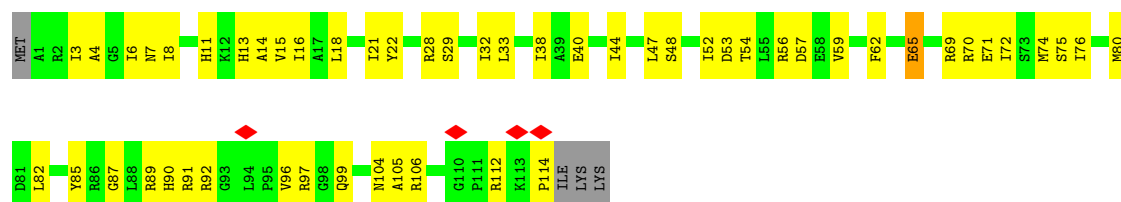
- Molecule 49: 30S ribosomal protein S11



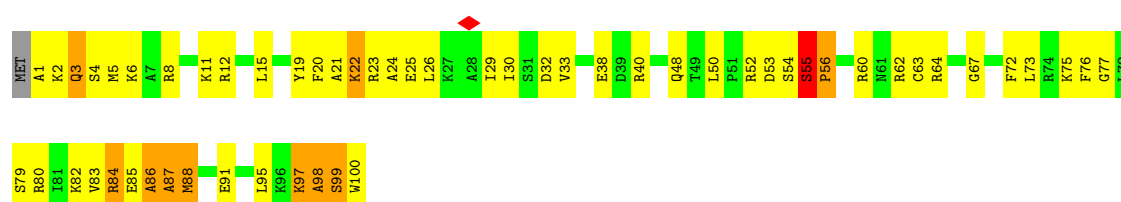
- Molecule 50: 30S ribosomal protein S12



- Molecule 51: 30S ribosomal protein S13



- Molecule 52: 30S ribosomal protein S14



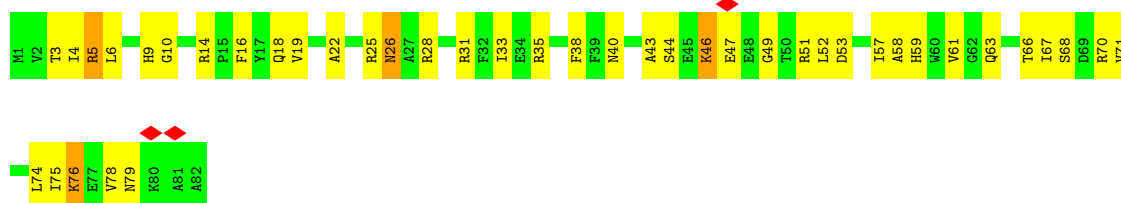
- Molecule 53: 30S ribosomal protein S15

Chain O: 



- Molecule 54: 30S ribosomal protein S16

Chain P: 



- Molecule 55: 30S ribosomal protein S17

Chain Q: 

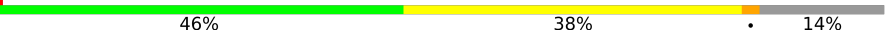


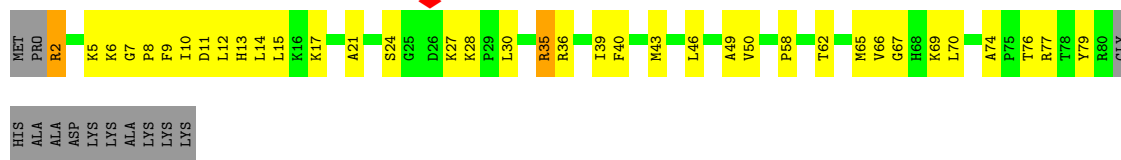
- Molecule 56: 30S ribosomal protein S18

Chain R: 



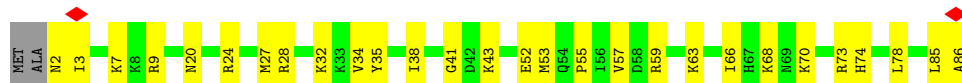
- Molecule 57: 30S ribosomal protein S19

Chain S: 

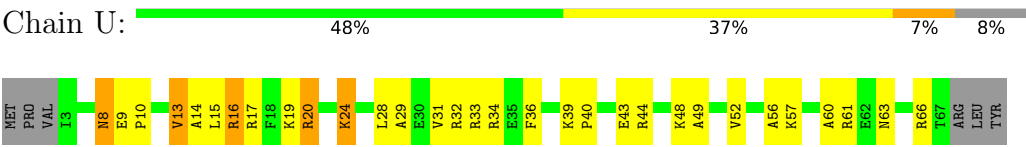


- Molecule 58: 30S ribosomal protein S20

Chain T: 



● Molecule 59: 30S ribosomal protein S21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	96070	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 ($e^-/\text{\AA}^2$)	1.2	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	29000	Depositor
Image detector	DIRECT ELECTRON DE-20 (5k x 3k)	Depositor
Maximum map value	18.146	Depositor
Minimum map value	-6.484	Depositor
Average map value	-1.164	Depositor
Map value standard deviation	1.530	Depositor
Recommended contour level	2.5	Depositor
Map size ($\text{\AA}$)	388.80002, 388.80002, 388.80002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.215, 1.215, 1.215	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.39	0/36963	0.48	1/57662 (0.0%)
2	01	0.39	0/69797	0.48	3/108890 (0.0%)
3	02	0.40	0/2847	0.49	0/4440
4	Y	0.35	0/383	0.68	0/504
5	W	0.39	0/1832	0.45	0/2855
5	X	0.40	0/1811	0.54	0/2822
6	03	0.43	0/1361	0.96	3/1796 (0.2%)
7	04	0.41	0/2121	0.88	4/2852 (0.1%)
8	05	0.42	0/1586	0.85	4/2134 (0.2%)
9	06	0.39	0/1571	0.86	2/2113 (0.1%)
10	07	0.40	0/1434	0.86	1/1926 (0.1%)
11	08	0.38	0/1343	0.82	2/1816 (0.1%)
12	09	0.42	0/1122	0.99	8/1515 (0.5%)
13	10	0.53	0/1001	1.62	13/1350 (1.0%)
14	11	0.45	0/1046	0.93	3/1410 (0.2%)
15	12	0.41	0/1152	0.83	2/1551 (0.1%)
16	13	0.40	0/947	0.90	5/1268 (0.4%)
17	14	0.38	0/1054	0.87	1/1403 (0.1%)
18	15	0.40	0/1093	0.85	1/1460 (0.1%)
19	16	0.41	0/973	0.94	2/1301 (0.2%)
20	17	0.38	0/902	0.85	0/1209
21	18	0.38	0/929	0.82	2/1242 (0.2%)
22	19	0.37	0/960	0.79	1/1278 (0.1%)
23	20	0.37	0/829	0.83	3/1107 (0.3%)
24	21	0.40	0/864	0.90	3/1156 (0.3%)
25	22	0.40	0/744	0.89	1/994 (0.1%)
26	23	0.39	0/787	0.84	0/1051
27	24	0.35	0/766	0.78	0/1025
28	25	0.38	0/582	0.90	3/769 (0.4%)
29	26	0.37	0/635	0.79	1/848 (0.1%)
30	27	0.37	0/510	0.79	0/677
31	28	0.37	0/453	0.81	1/605 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	29	0.44	0/531	0.92	4/709 (0.6%)
33	30	0.38	0/450	0.80	1/599 (0.2%)
34	31	0.39	0/416	0.71	0/554
35	32	0.44	0/380	0.94	2/498 (0.4%)
36	33	0.37	0/513	0.91	1/676 (0.1%)
37	34	0.27	0/303	0.74	0/397
38	V	0.38	0/345	0.50	0/538
39	Z	0.36	0/2884	0.73	2/3884 (0.1%)
40	B	0.40	0/1735	0.92	4/2338 (0.2%)
41	C	0.40	0/1651	0.78	0/2225
42	D	0.39	0/1665	0.92	6/2227 (0.3%)
43	E	0.43	0/1169	1.03	7/1573 (0.4%)
44	F	0.45	0/835	1.07	7/1128 (0.6%)
45	G	0.38	0/1195	0.88	1/1602 (0.1%)
46	H	0.37	0/989	0.82	1/1326 (0.1%)
47	I	0.41	0/1034	0.99	2/1375 (0.1%)
48	J	0.43	0/796	0.94	2/1077 (0.2%)
49	K	0.41	0/885	0.88	1/1195 (0.1%)
50	L	0.44	0/969	1.00	8/1300 (0.6%)
51	M	0.39	0/892	0.93	1/1193 (0.1%)
52	N	0.54	0/817	1.16	9/1088 (0.8%)
53	O	0.37	0/722	0.84	1/964 (0.1%)
54	P	0.41	0/659	0.87	1/884 (0.1%)
55	Q	0.40	0/657	0.88	3/881 (0.3%)
56	R	0.36	0/544	0.85	2/731 (0.3%)
57	S	0.41	0/652	0.89	2/877 (0.2%)
58	T	0.40	0/671	0.93	1/888 (0.1%)
59	U	0.49	0/550	1.15	4/728 (0.5%)
All	All	0.39	0/165307	0.63	143/246484 (0.1%)

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
52	N	0	1

There are no bond length outliers.

The worst 5 of 143 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	10	118	ILE	CA-C-N	27.00	153.59	119.84
13	10	118	ILE	C-N-CA	27.00	153.59	119.84
49	K	125	LYS	N-CA-C	11.94	129.21	110.70
13	10	118	ILE	C-N-CD	-10.81	80.67	125.00
13	10	54	VAL	N-CA-C	10.16	122.20	110.62

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
52	N	86	ALA	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	33012	0	16618	474	0
2	01	62318	0	31345	789	0
3	02	2546	0	1292	50	0
4	Y	377	0	383	29	0
5	W	1640	0	837	11	0
5	X	1622	0	827	28	0
6	03	1353	0	1159	38	0
7	04	2082	0	2157	82	0
8	05	1565	0	1616	68	0
9	06	1552	0	1619	56	0
10	07	1410	0	1447	74	0
11	08	1323	0	1374	59	0
12	09	1111	0	1148	32	0
13	10	988	0	1025	51	0
14	11	1032	0	1088	59	0
15	12	1129	0	1162	48	0
16	13	938	0	1012	50	0
17	14	1045	0	1117	46	0
18	15	1074	0	1157	37	0
19	16	960	0	1000	48	0
20	17	892	0	923	40	0
21	18	917	0	965	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	19	947	0	1022	45	0
23	20	816	0	839	25	0
24	21	857	0	922	26	0
25	22	738	0	807	27	0
26	23	779	0	834	31	0
27	24	753	0	780	28	0
28	25	575	0	592	30	0
29	26	625	0	655	27	0
30	27	509	0	543	25	0
31	28	449	0	491	16	0
32	29	522	0	524	27	0
33	30	444	0	461	24	0
34	31	409	0	440	10	0
35	32	377	0	418	19	0
36	33	504	0	574	21	0
37	34	302	0	340	23	0
38	V	306	0	154	1	0
39	Z	2844	0	2739	120	0
40	B	1704	0	1732	79	0
41	C	1624	0	1699	52	0
42	D	1643	0	1710	85	0
43	E	1156	0	1199	59	0
44	F	817	0	808	37	0
45	G	1181	0	1240	48	0
46	H	979	0	1034	32	0
47	I	1022	0	1070	67	0
48	J	786	0	828	56	0
49	K	869	0	878	44	0
50	L	955	0	1019	41	0
51	M	883	0	944	53	0
52	N	805	0	847	64	0
53	O	714	0	737	22	0
54	P	649	0	666	39	0
55	Q	648	0	691	35	0
56	R	535	0	552	19	0
57	S	637	0	665	47	0
58	T	665	0	714	23	0
59	U	544	0	579	43	0
60	01	221	0	0	0	0
60	02	6	0	0	0	0
60	17	1	0	0	0	0
60	19	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	30	1	0	0	0	0
60	31	1	0	0	0	0
60	34	1	0	0	0	0
60	A	118	0	0	0	0
60	I	1	0	0	0	0
60	V	1	0	0	0	0
60	W	3	0	0	0	0
60	X	5	0	0	0	0
61	34	1	0	0	0	0
All	All	152819	0	104018	3245	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 13.

The worst 5 of 3245 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:45:G:H5''	2:01:46:G:H5'	1.26	1.14
13:10:117:LEU:C	13:10:119:PRO:HD2	1.71	1.14
1:A:291:U:H2'	1:A:292:G:H5''	1.31	1.12
1:A:376:G:H2'	1:A:377:G:H5''	1.35	1.07
51:M:3:ILE:HG12	51:M:7:ASN:HB2	1.25	1.07

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	Y	45/72 (62%)	40 (89%)	5 (11%)	0	100	100
6	03	218/234 (93%)	195 (89%)	23 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	04	269/273 (98%)	242 (90%)	25 (9%)	2 (1%)	18	52
8	05	207/209 (99%)	189 (91%)	17 (8%)	1 (0%)	24	59
9	06	199/201 (99%)	180 (90%)	17 (8%)	2 (1%)	12	45
10	07	175/179 (98%)	155 (89%)	20 (11%)	0	100	100
11	08	174/177 (98%)	154 (88%)	17 (10%)	3 (2%)	7	35
12	09	147/149 (99%)	131 (89%)	13 (9%)	3 (2%)	6	31
13	10	129/165 (78%)	95 (74%)	28 (22%)	6 (5%)	2	14
14	11	139/142 (98%)	120 (86%)	18 (13%)	1 (1%)	18	52
15	12	140/142 (99%)	133 (95%)	7 (5%)	0	100	100
16	13	120/123 (98%)	100 (83%)	18 (15%)	2 (2%)	7	35
17	14	141/144 (98%)	128 (91%)	13 (9%)	0	100	100
18	15	134/136 (98%)	125 (93%)	7 (5%)	2 (2%)	8	37
19	16	118/127 (93%)	106 (90%)	11 (9%)	1 (1%)	16	50
20	17	114/117 (97%)	102 (90%)	11 (10%)	1 (1%)	14	47
21	18	112/115 (97%)	98 (88%)	14 (12%)	0	100	100
22	19	115/118 (98%)	113 (98%)	2 (2%)	0	100	100
23	20	101/103 (98%)	84 (83%)	16 (16%)	1 (1%)	12	45
24	21	108/110 (98%)	97 (90%)	11 (10%)	0	100	100
25	22	91/100 (91%)	77 (85%)	13 (14%)	1 (1%)	11	43
26	23	100/104 (96%)	90 (90%)	10 (10%)	0	100	100
27	24	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
28	25	73/85 (86%)	60 (82%)	11 (15%)	2 (3%)	4	25
29	26	75/78 (96%)	69 (92%)	6 (8%)	0	100	100
30	27	61/63 (97%)	60 (98%)	1 (2%)	0	100	100
31	28	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
32	29	64/70 (91%)	55 (86%)	9 (14%)	0	100	100
33	30	54/57 (95%)	49 (91%)	5 (9%)	0	100	100
34	31	48/55 (87%)	45 (94%)	3 (6%)	0	100	100
35	32	44/46 (96%)	38 (86%)	5 (11%)	1 (2%)	5	29
36	33	62/65 (95%)	53 (86%)	7 (11%)	2 (3%)	3	21
37	34	36/38 (95%)	31 (86%)	5 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	Z	359/365 (98%)	332 (92%)	26 (7%)	1 (0%)	36	68
40	B	216/241 (90%)	188 (87%)	26 (12%)	2 (1%)	14	47
41	C	204/233 (88%)	189 (93%)	15 (7%)	0	100	100
42	D	203/206 (98%)	177 (87%)	25 (12%)	1 (0%)	24	59
43	E	155/167 (93%)	125 (81%)	29 (19%)	1 (1%)	21	56
44	F	98/131 (75%)	77 (79%)	16 (16%)	5 (5%)	1	13
45	G	149/156 (96%)	134 (90%)	14 (9%)	1 (1%)	18	52
46	H	127/130 (98%)	115 (91%)	12 (9%)	0	100	100
47	I	125/130 (96%)	101 (81%)	22 (18%)	2 (2%)	7	36
48	J	96/103 (93%)	85 (88%)	9 (9%)	2 (2%)	5	31
49	K	114/129 (88%)	102 (90%)	11 (10%)	1 (1%)	14	47
50	L	121/124 (98%)	92 (76%)	23 (19%)	6 (5%)	1	13
51	M	112/118 (95%)	94 (84%)	16 (14%)	2 (2%)	6	34
52	N	98/101 (97%)	79 (81%)	13 (13%)	6 (6%)	1	9
53	O	86/89 (97%)	79 (92%)	7 (8%)	0	100	100
54	P	80/82 (98%)	65 (81%)	13 (16%)	2 (2%)	4	27
55	Q	78/84 (93%)	63 (81%)	14 (18%)	1 (1%)	9	40
56	R	63/75 (84%)	60 (95%)	3 (5%)	0	100	100
57	S	77/92 (84%)	69 (90%)	7 (9%)	1 (1%)	9	40
58	T	83/87 (95%)	81 (98%)	2 (2%)	0	100	100
59	U	63/71 (89%)	44 (70%)	17 (27%)	2 (3%)	3	21
All	All	6468/6864 (94%)	5705 (88%)	696 (11%)	67 (1%)	15	45

5 of 67 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	06	83	VAL
11	08	12	ALA
12	09	9	VAL
13	10	55	VAL
13	10	119	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	Y	38/59 (64%)	37 (97%)	1 (3%)	40	69
6	03	106/181 (59%)	106 (100%)	0	100	100
7	04	216/218 (99%)	214 (99%)	2 (1%)	70	81
8	05	164/164 (100%)	162 (99%)	2 (1%)	63	79
9	06	165/165 (100%)	164 (99%)	1 (1%)	78	84
10	07	148/150 (99%)	146 (99%)	2 (1%)	59	77
11	08	137/138 (99%)	135 (98%)	2 (2%)	57	76
12	09	114/114 (100%)	114 (100%)	0	100	100
13	10	100/123 (81%)	99 (99%)	1 (1%)	68	80
14	11	109/110 (99%)	108 (99%)	1 (1%)	70	81
15	12	116/116 (100%)	115 (99%)	1 (1%)	70	81
16	13	103/104 (99%)	102 (99%)	1 (1%)	68	80
17	14	102/103 (99%)	102 (100%)	0	100	100
18	15	109/109 (100%)	107 (98%)	2 (2%)	51	74
19	16	100/104 (96%)	99 (99%)	1 (1%)	68	80
20	17	86/87 (99%)	84 (98%)	2 (2%)	44	70
21	18	99/100 (99%)	99 (100%)	0	100	100
22	19	89/90 (99%)	88 (99%)	1 (1%)	65	79
23	20	84/84 (100%)	84 (100%)	0	100	100
24	21	93/93 (100%)	92 (99%)	1 (1%)	65	79
25	22	80/84 (95%)	79 (99%)	1 (1%)	61	78
26	23	83/85 (98%)	80 (96%)	3 (4%)	31	63
27	24	78/78 (100%)	77 (99%)	1 (1%)	61	78
28	25	57/63 (90%)	57 (100%)	0	100	100
29	26	67/68 (98%)	66 (98%)	1 (2%)	57	76
30	27	55/55 (100%)	54 (98%)	1 (2%)	51	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	28	48/49 (98%)	48 (100%)	0	100	100
32	29	59/62 (95%)	58 (98%)	1 (2%)	53	75
33	30	47/48 (98%)	45 (96%)	2 (4%)	26	59
34	31	45/49 (92%)	45 (100%)	0	100	100
35	32	38/38 (100%)	38 (100%)	0	100	100
36	33	51/52 (98%)	51 (100%)	0	100	100
37	34	34/34 (100%)	32 (94%)	2 (6%)	18	50
39	Z	303/311 (97%)	300 (99%)	3 (1%)	68	80
40	B	180/199 (90%)	178 (99%)	2 (1%)	65	79
41	C	170/190 (90%)	170 (100%)	0	100	100
42	D	172/173 (99%)	171 (99%)	1 (1%)	78	84
43	E	119/126 (94%)	118 (99%)	1 (1%)	73	82
44	F	87/112 (78%)	85 (98%)	2 (2%)	44	70
45	G	124/129 (96%)	124 (100%)	0	100	100
46	H	104/105 (99%)	104 (100%)	0	100	100
47	I	105/107 (98%)	104 (99%)	1 (1%)	68	80
48	J	86/90 (96%)	86 (100%)	0	100	100
49	K	89/99 (90%)	88 (99%)	1 (1%)	65	79
50	L	103/104 (99%)	102 (99%)	1 (1%)	68	80
51	M	92/96 (96%)	92 (100%)	0	100	100
52	N	83/84 (99%)	82 (99%)	1 (1%)	63	79
53	O	76/77 (99%)	75 (99%)	1 (1%)	61	78
54	P	65/65 (100%)	61 (94%)	4 (6%)	16	49
55	Q	74/78 (95%)	73 (99%)	1 (1%)	59	77
56	R	56/65 (86%)	56 (100%)	0	100	100
57	S	70/79 (89%)	69 (99%)	1 (1%)	59	77
58	T	65/66 (98%)	65 (100%)	0	100	100
59	U	55/61 (90%)	54 (98%)	1 (2%)	51	74
All	All	5298/5593 (95%)	5244 (99%)	54 (1%)	65	80

5 of 54 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	29	2	LYS
39	Z	307	LYS
54	P	46	LYS
33	30	19	ASP
37	34	23	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 161 such sidechains are listed below:

Mol	Chain	Res	Type
41	C	138	GLN
50	L	28	GLN
42	D	84	ASN
44	F	68	GLN
52	N	61	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1538/1539 (99%)	182 (11%)	1 (0%)
2	01	2902/2903 (99%)	320 (11%)	6 (0%)
3	02	118/119 (99%)	11 (9%)	1 (0%)
38	V	13/14 (92%)	1 (7%)	0
5	W	76/77 (98%)	8 (10%)	0
5	X	76/77 (98%)	20 (26%)	1 (1%)
All	All	4723/4729 (99%)	542 (11%)	9 (0%)

5 of 542 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	3	A
1	A	6	G
1	A	9	G
1	A	22	G
1	A	31	G

5 of 9 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	02	66	A
5	X	17(A)	U
2	01	1020	A

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Mol	Chain	Res	Type
2	01	1130	U
2	01	2296	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](#)

Of 361 ligands modelled in this entry, 361 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

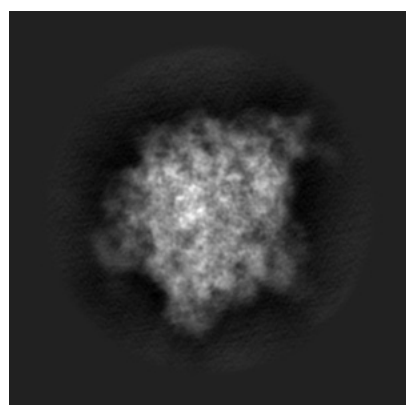
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8521. These allow visual inspection of the internal detail of the map and identification of artifacts.

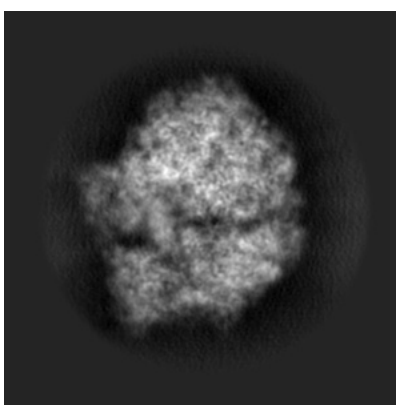
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

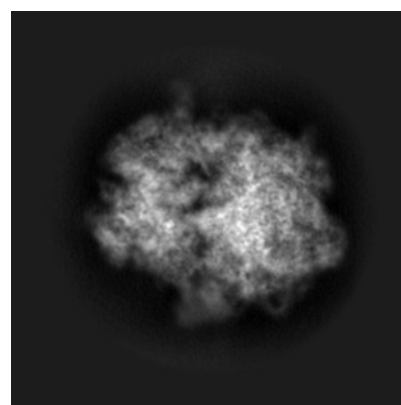
6.1.1 Primary map



X



Y

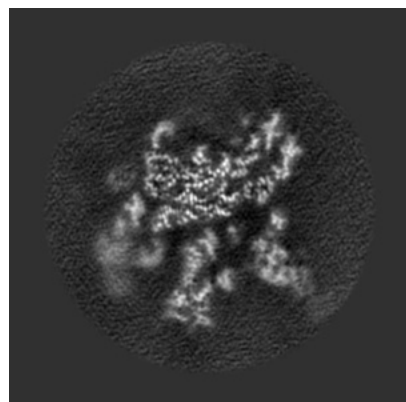


Z

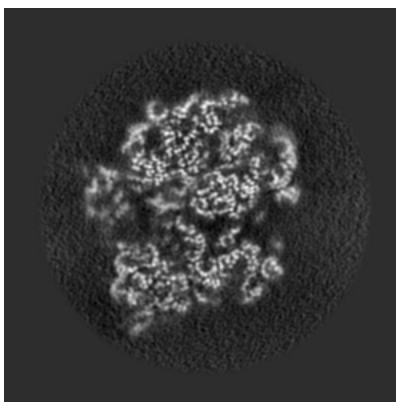
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

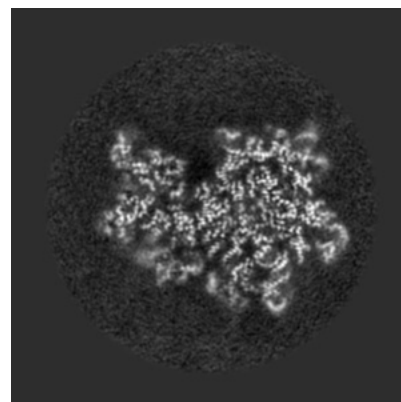
6.2.1 Primary map



X Index: 160



Y Index: 160

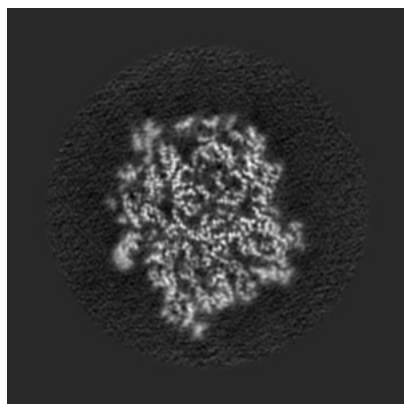


Z Index: 160

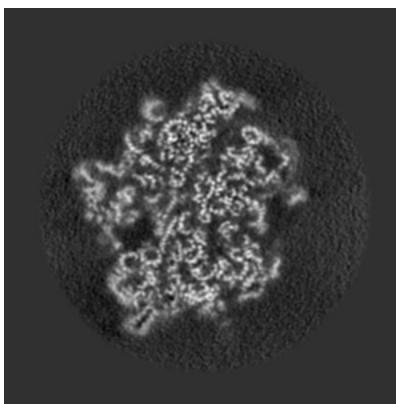
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

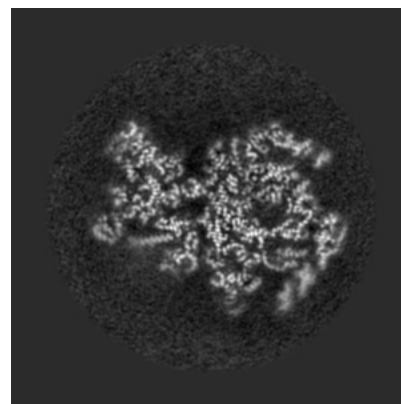
6.3.1 Primary map



X Index: 188



Y Index: 154

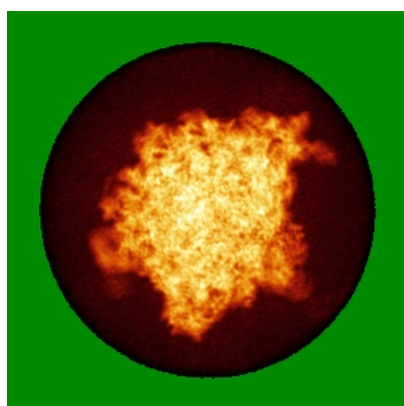


Z Index: 170

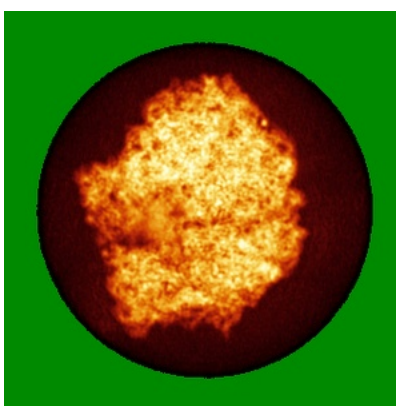
The images above show the largest variance slices of the map in three orthogonal directions.

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

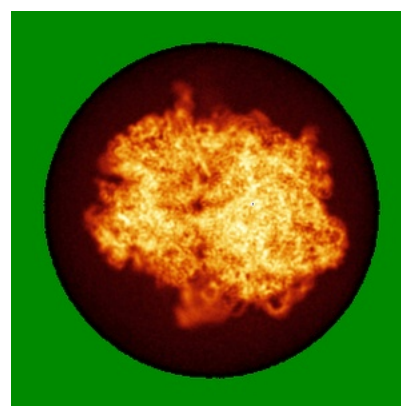
6.4.1 Primary map



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

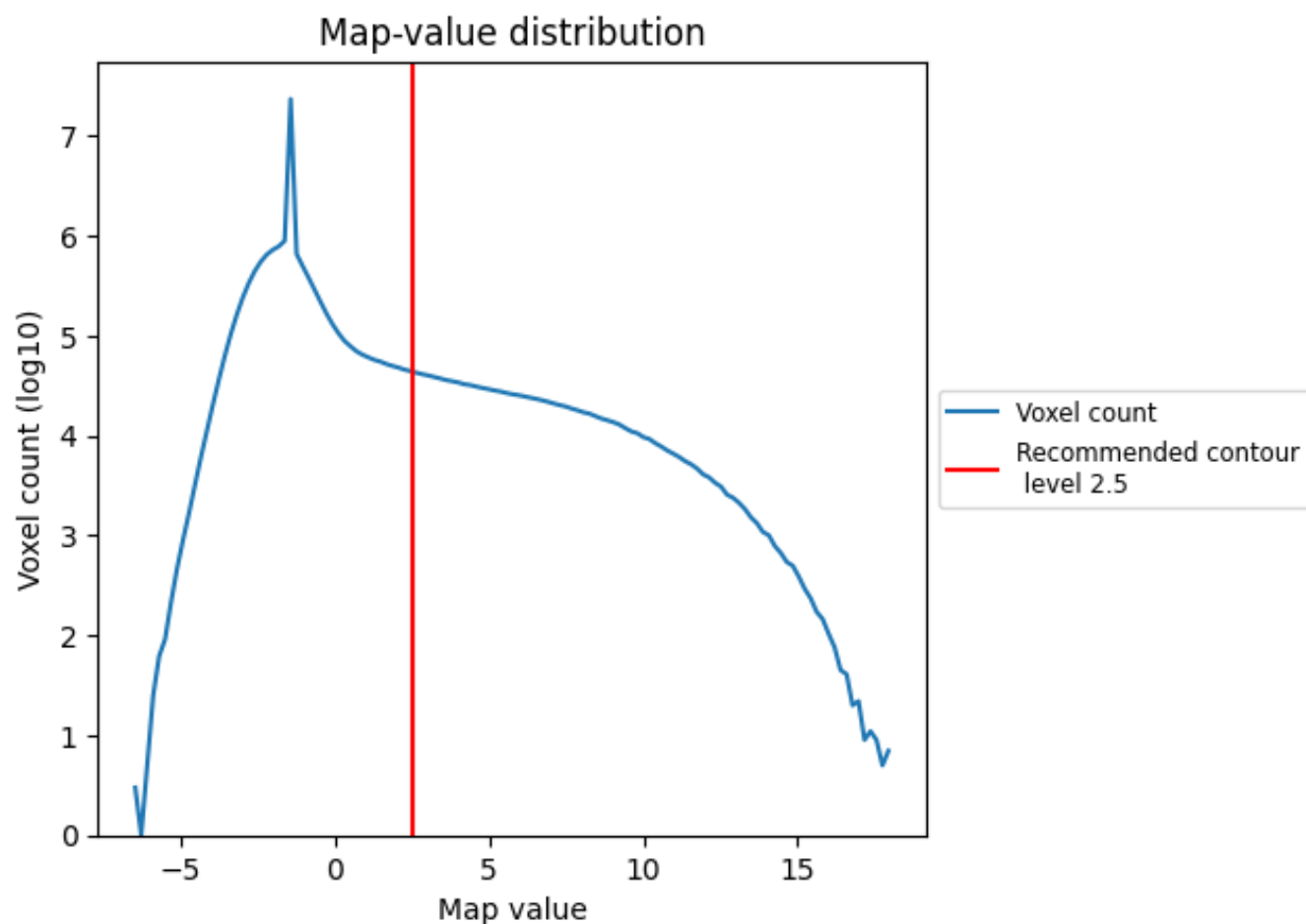
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

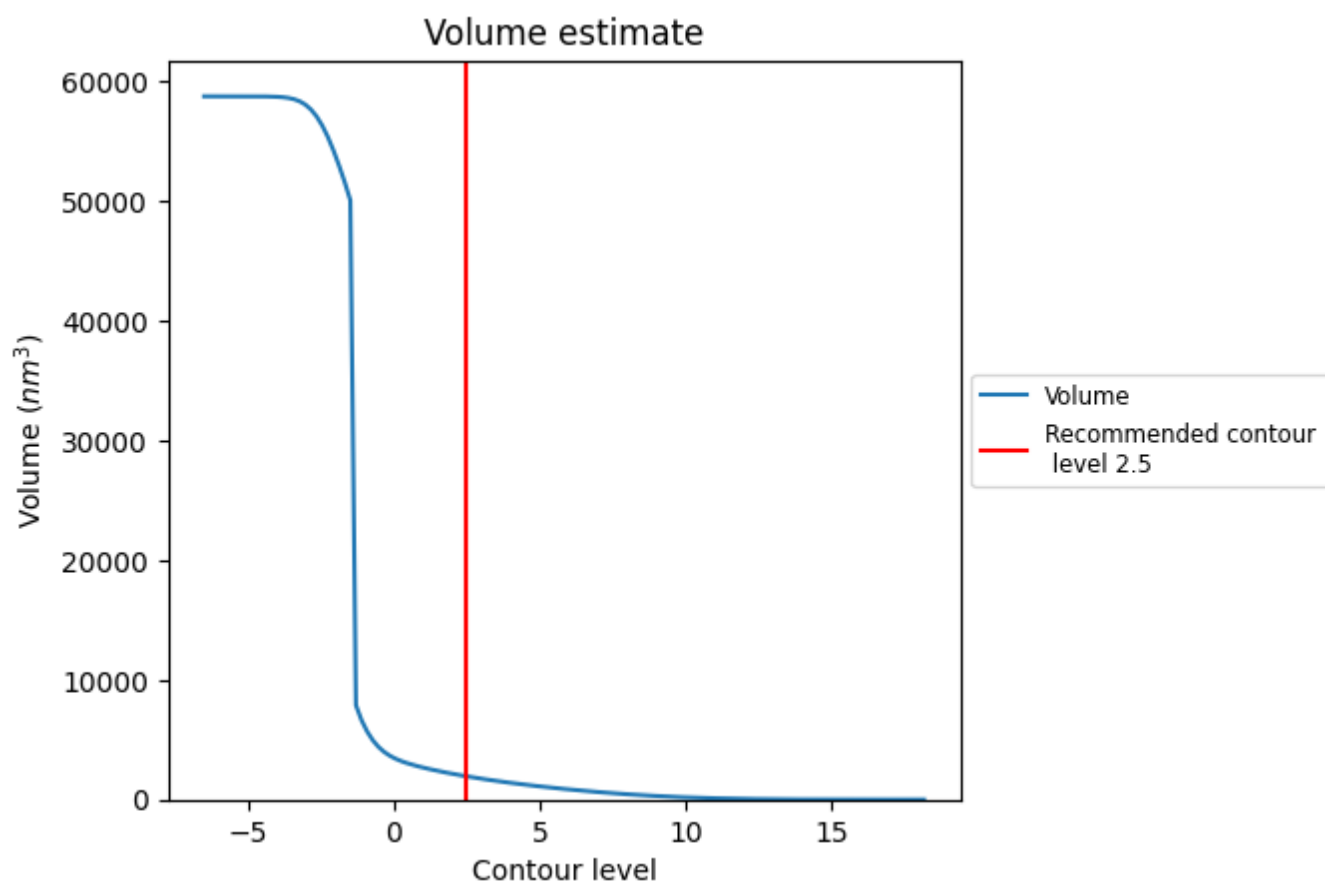
This section contains the results of statistical analysis of the map.

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.

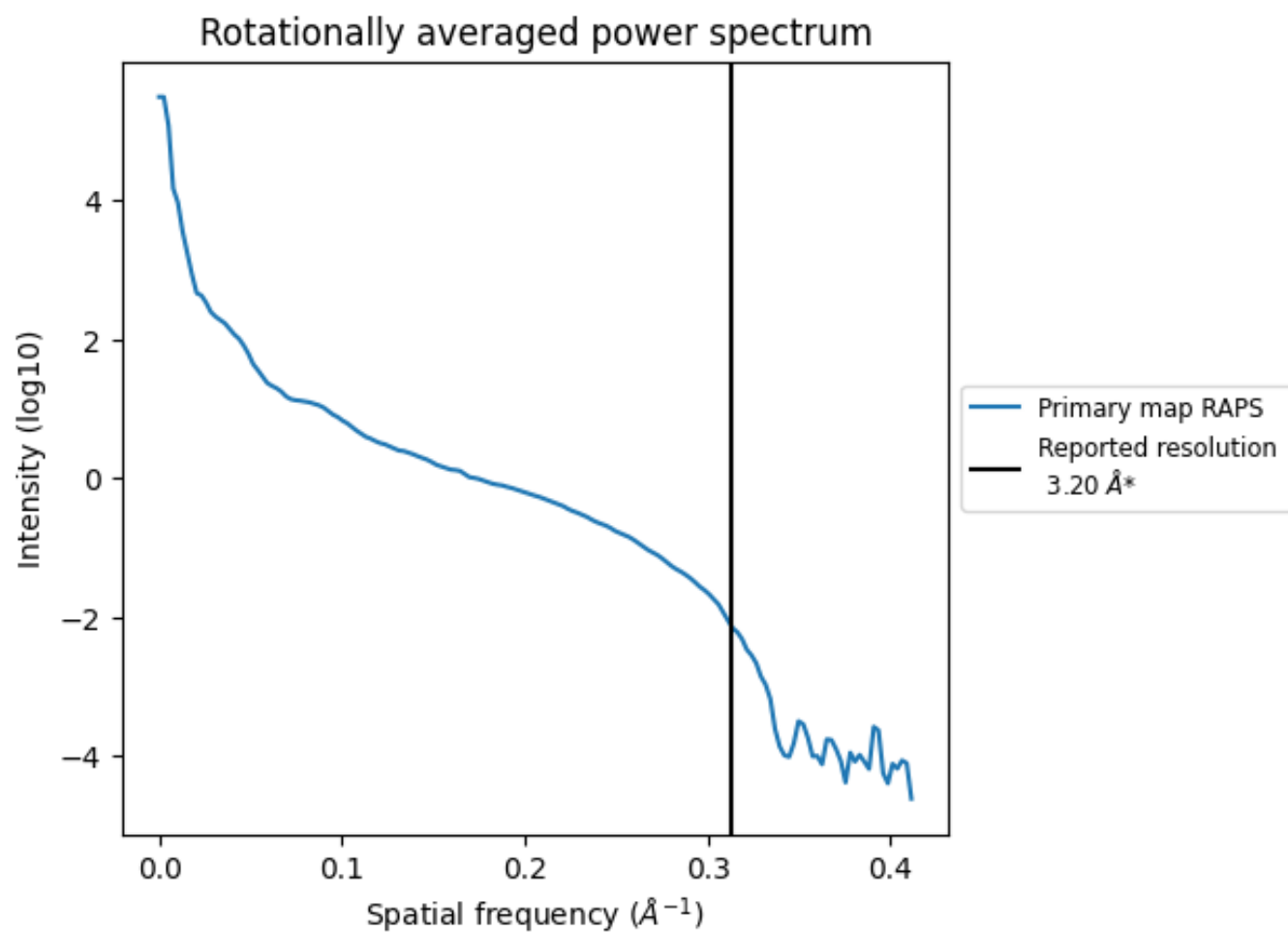
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1941 nm³; this corresponds to an approximate mass of 1753 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 0.312 Å⁻¹

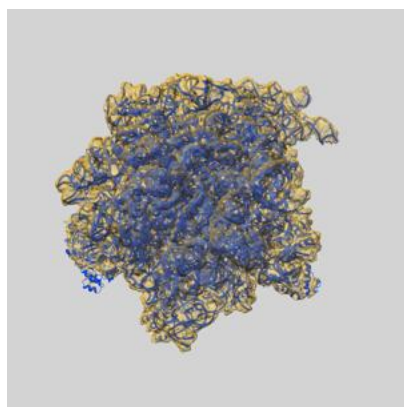
8 Fourier-Shell correlation

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

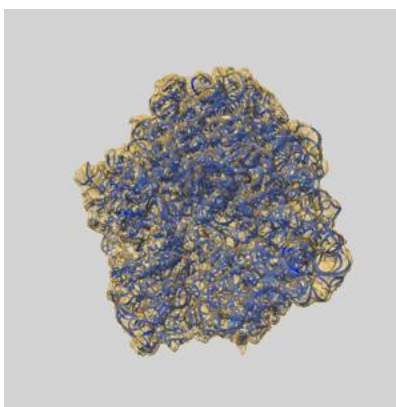
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8521 and PDB model 5U9F. Per-residue inclusion information can be found in section [3](#) on page [16](#).

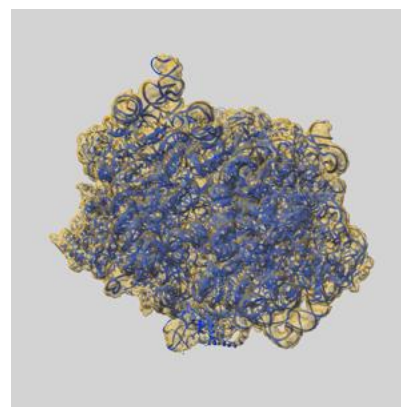
9.1 Map-model overlay [i](#)



X



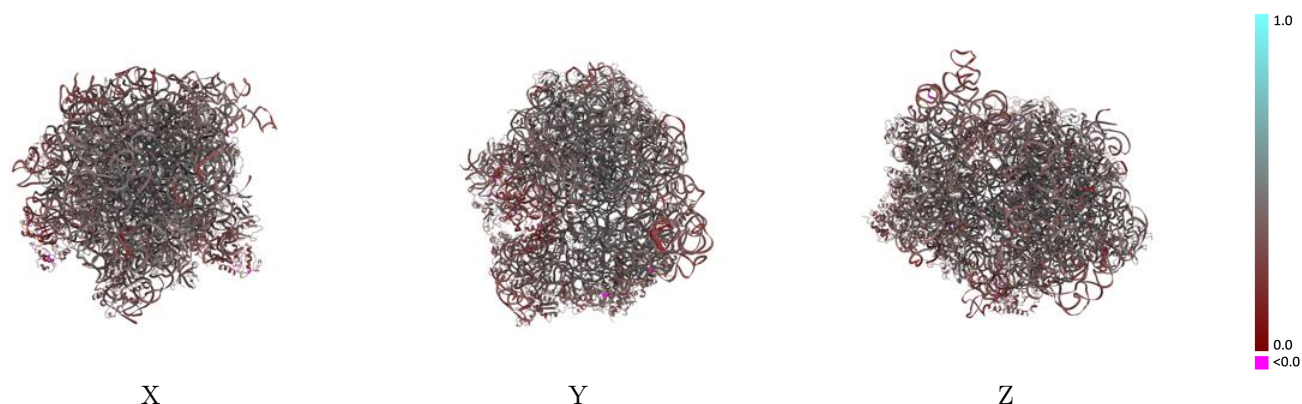
Y



Z

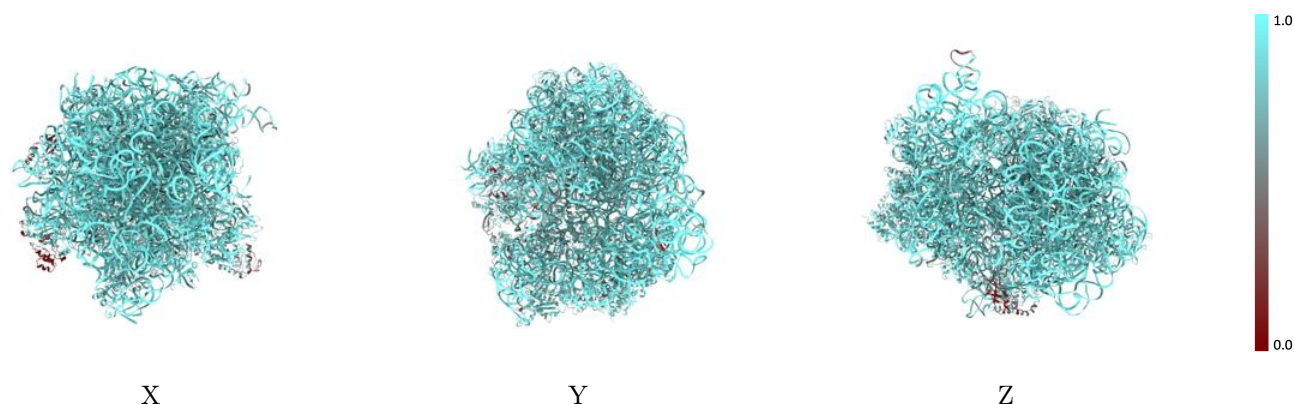
The images above show the 3D surface view of the map at the recommended contour level 2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



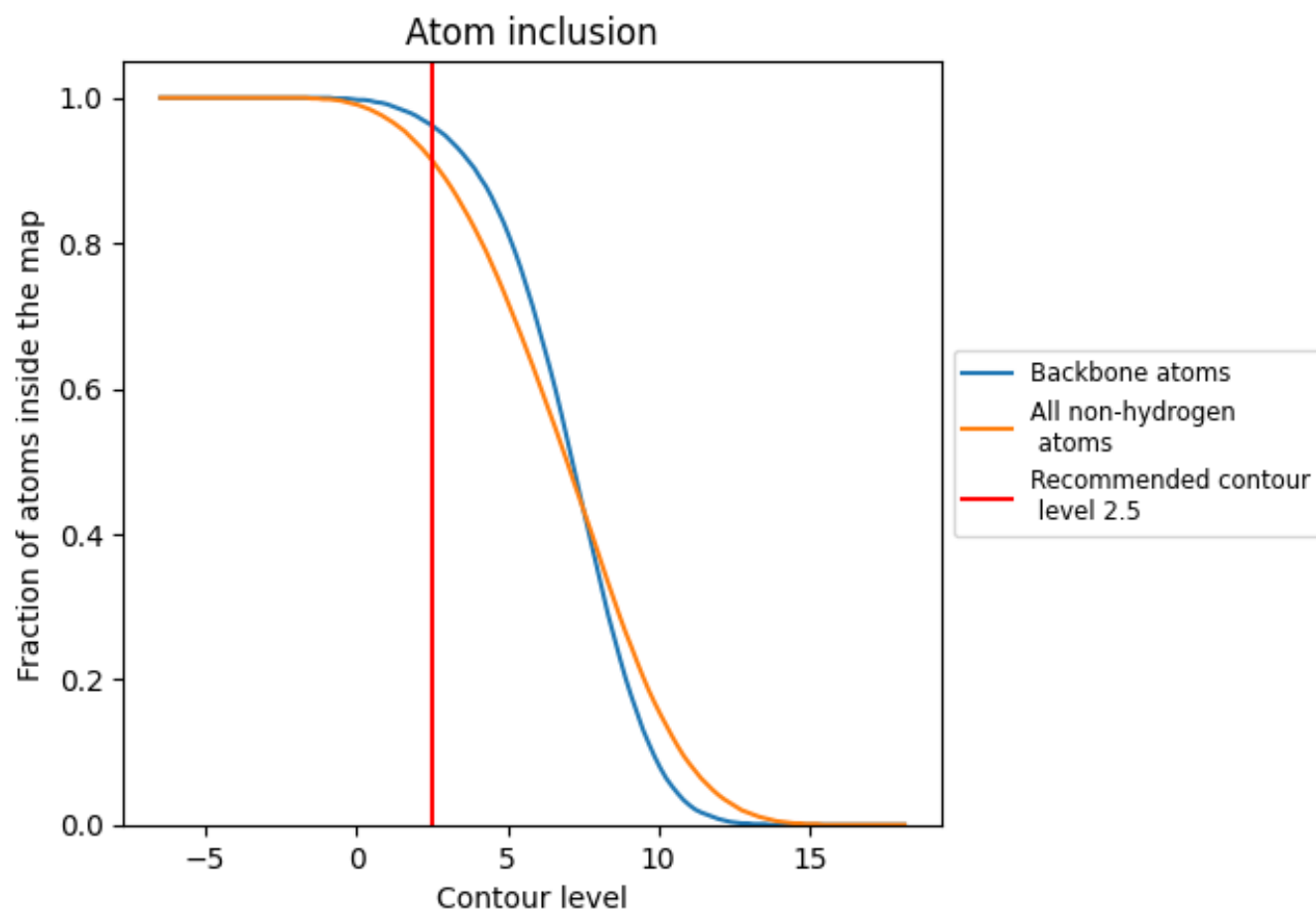
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 91% 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 (2.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9140	 0.3830
01	 0.9760	 0.4040
02	 0.9790	 0.3530
03	 0.4600	 0.1980
04	 0.8360	 0.4350
05	 0.8650	 0.4250
06	 0.8650	 0.4000
07	 0.8590	 0.3230
08	 0.8480	 0.3650
09	 0.3690	 0.3050
10	 0.5420	 0.2120
11	 0.6920	 0.2380
12	 0.8750	 0.4120
13	 0.8030	 0.4230
14	 0.8820	 0.4140
15	 0.8110	 0.4120
16	 0.8930	 0.3900
17	 0.8900	 0.3420
18	 0.8240	 0.4010
19	 0.8770	 0.4080
20	 0.8760	 0.4140
21	 0.8340	 0.4090
22	 0.8010	 0.3790
23	 0.8400	 0.3800
24	 0.8820	 0.3800
25	 0.8940	 0.4230
26	 0.8370	 0.4040
27	 0.8150	 0.3030
28	 0.8440	 0.4040
29	 0.5380	 0.2840
30	 0.8530	 0.4020
31	 0.7980	 0.4010
32	 0.8620	 0.4280
33	 0.8860	 0.4290
34	 0.7790	 0.3680



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Chain	Atom inclusion	Q-score
A	 0.9730	 0.3860
B	 0.8110	 0.3300
C	 0.8190	 0.3740
D	 0.8430	 0.3600
E	 0.8700	 0.4010
F	 0.8130	 0.3530
G	 0.8090	 0.3290
H	 0.8650	 0.3960
I	 0.8570	 0.3340
J	 0.8270	 0.3250
K	 0.8580	 0.3870
L	 0.8280	 0.4250
M	 0.8070	 0.3170
N	 0.8550	 0.3310
O	 0.8730	 0.3590
P	 0.8840	 0.4020
Q	 0.8450	 0.3770
R	 0.8310	 0.3680
S	 0.8570	 0.3540
T	 0.8390	 0.3360
U	 0.7450	 0.2650
V	 0.8730	 0.3070
W	 0.9350	 0.3850
X	 0.6450	 0.2180
Y	 0.7570	 0.3830
Z	 0.6680	 0.3170