



wwPDB EM Validation Summary Report ⓘ

Nov 2, 2022 – 11:02 PM EDT

PDB ID : 5U9F
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:

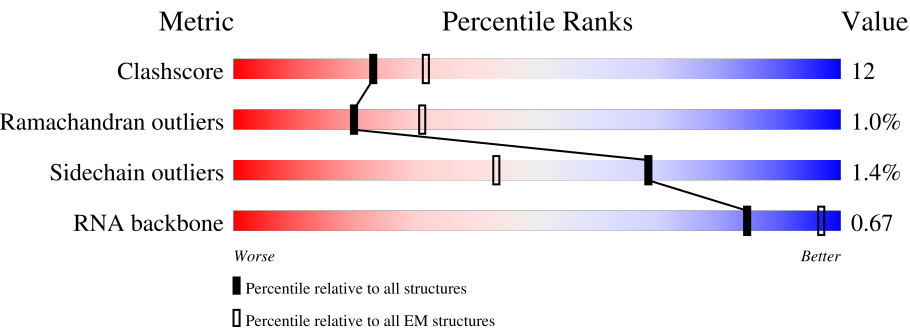
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance i

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

The reported resolution of this entry is 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.









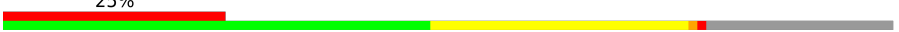





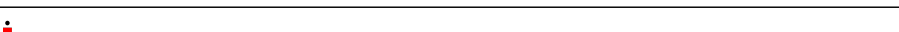

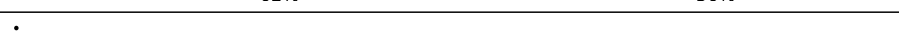

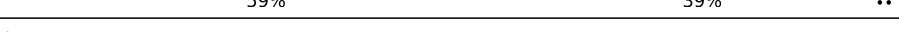








Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	A	1539	
2	01	2903	
3	02	119	
4	Y	72	
5	W	77	
5	X	77	
6	03	234	

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Mol	Chain	Length	Quality of chain
7	04	273	 67% 32% .
8	05	209	 67% 33% .
9	06	201	 65% 34% .
10	07	179	 56% 42% ..
11	08	177	 64% 34% ..
12	09	149	 55% 72% 27% .
13	10	165	 25% 48% 29% .. 21%
14	11	142	 17% 52% 47% .
15	12	142	 70% 30% .
16	13	123	 54% 41% . .
17	14	144	 65% 34% .
18	15	136	 68% 30% .
19	16	127	 58% 35% . 6%
20	17	117	 62% 36% ..
21	18	115	 66% 33% .
22	19	118	 59% 39% ..
23	20	103	 75% 24% .
24	21	110	 68% 32% .
25	22	100	 56% 36% . 7%
26	23	104	 62% 37% .
27	24	94	 69% 30% .
28	25	85	 49% 35% . 12%
29	26	78	 62% 36% ..
30	27	63	 59% 38% .
31	28	59	 66% 32% .




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Mol	Chain	Length	Quality of chain
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	
53	O	89	
54	P	82	
55	Q	84	
56	R	75	

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Mol	Chain	Length	Quality of chain
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 (three-letter code: 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

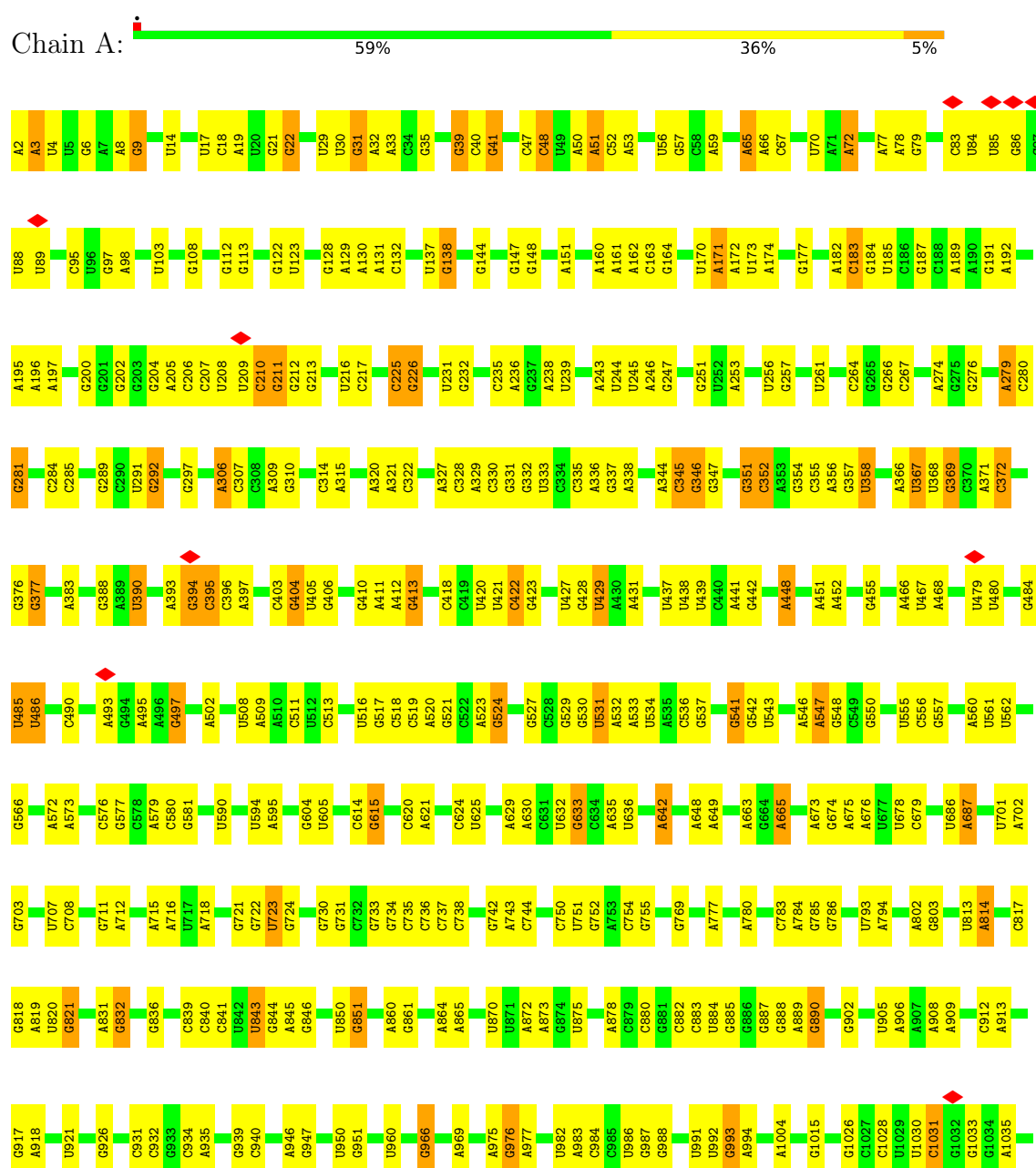
- Molecule 61 is ZINC ION (three-letter code: ZN) (formula: Zn).

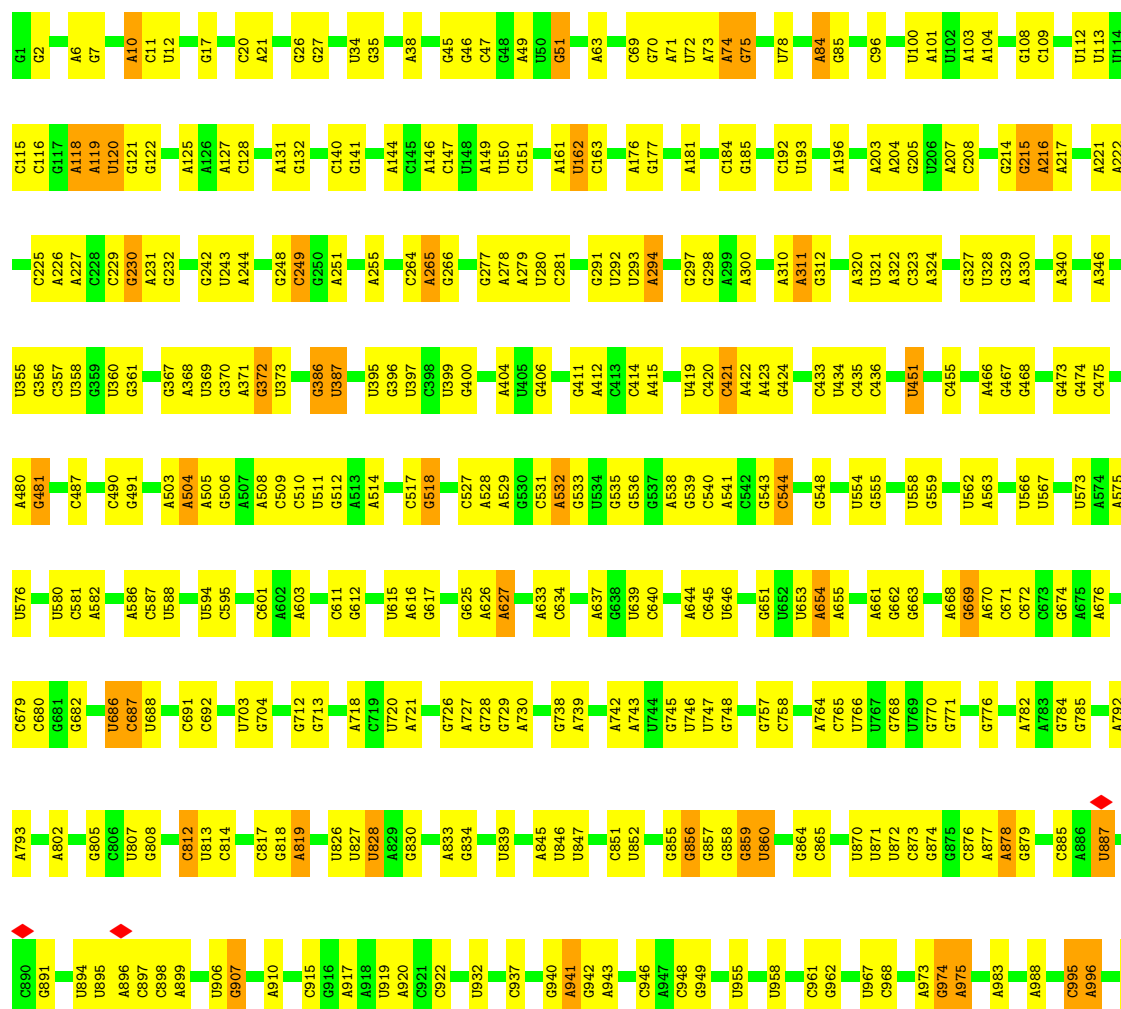
Mol	Chain	Residues	Atoms		AltConf
61	34	1	Total 1	Zn 1	0

3 Residue-property plots

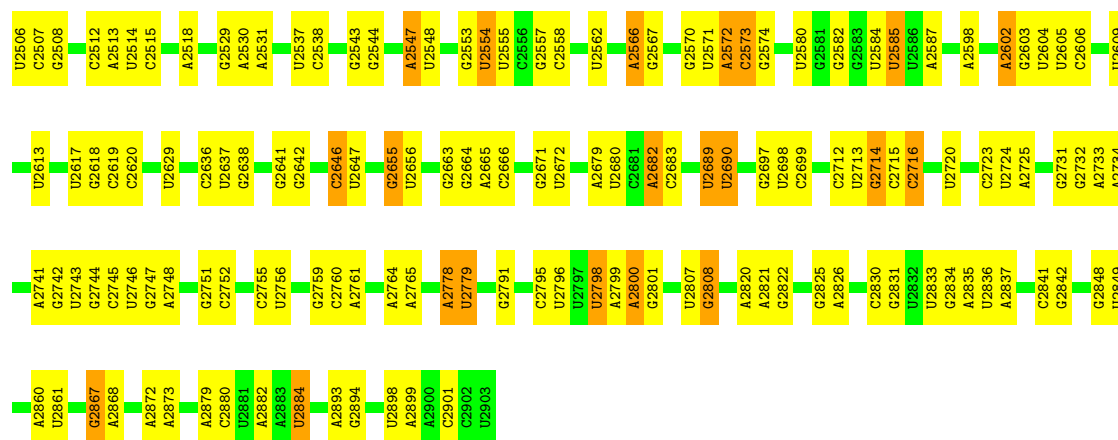
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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



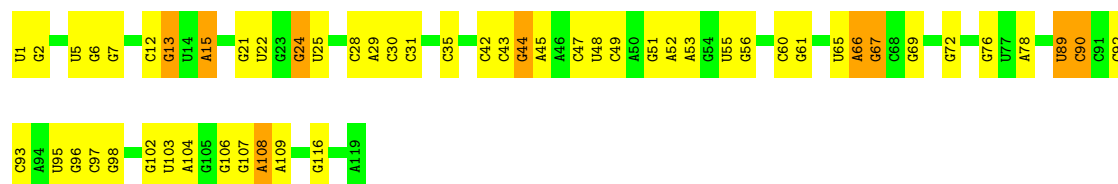


G2391	A2392	G2393	C2394	U2402	C2403	U2404	G2405	A2406	U2423	G2428	G2429	A2430	U2431	A2432	U2441	A2448	U2449	A2450	A2451	G2455	G2456	U2457	G2458	C2462	C2466	C2467	A2468	A2469	C2475	A2476	U2477	A2478	U2479	G2485	G2486	G2487	G2488	U2491	U2492	U2493	G2494	C2498	G2502	A2503	U2504	G2505									
C2313	A2314	G2315	G2316	A2317	G2318	G2319	U2320	U2321	A2322	G2323	U2324	G2325	G2326	A2327	A2328	U2329	U2330	G2331	G2332	A2333	C2334	G2345	G2346	C2347	U2348	G2349	C2350	G2351	A2352	G2353	C2354	G2355	U2356	G2357	C2358	G2359	G2360	G2361	G2364	G2365	A2366	G2367	C2368	A2369	A2376	A2377	A2381	G2382	G2383	U2384	G2385	A2388	G2389	U2390	
C2222	A2119	G2120	G2121	U2122	G2123	G2124	G2128	U2131	U2132	G2133	A2134	G2135	G2136	U2137	G2140	G2141	C2145	G2146	A2147	G2148	G2156	C2164	G2165	U2166	A2167	G2168	A2170	A2171	U2172	A2173	C2177	A2183	A2184	U2189	G2190	A2191	U2192	G2193	U2194	U2195	G2196	U2197	A2198	U2203	G2204	A2205	A2212	G2216	U2213	G2221					
A2031	G1929	G1930	U1931	A1932	G1933	C1934	G1935	A1936	A1937	A1938	U1943	U1944	U1955	U1963	G1964	C1965	A1966	C1967	G1968	A1969	U1970	G2061	A2062	C2065	C2066	G2067	U2068	G2069	A2070	A2071	C2072	C2073	U2074	U2075	U2086	G2087	A2088	C2089	A2090	A2094	A2095	C2104	U2105	U2106	U2111	G2112	U2113	G2114	G2115	G2116	U2118				
G1807	A1808	A1809	A1810	G1811	G1816	G1817	U1818	G1824	U1825	G1826	U1827	A1829	C1838	G1839	G1846	G1847	A1848	U1856	G1857	A1858	G1869	C1870	G1874	G1875	A1885	A1890	A1901	G1906	C1909	G1910	U1911	A1912	A1913	C1914	U1917	A1918	A1919	C1920	U1923	C1924	A1928														
G1697	A1698	G1699	A1700	A1701	U1709	G1710	G1715	U1716	C1726	C1727	G1728	U1729	G1730	G1731	U1736	G1737	G1738	A1739	G1740	A1744	A1745	G1753	A1754	A1755	G1756	A1757	U1758	A1759	C1760	C1764	A1773	G1774	U1775	G1776	A1783	C1790	A1791	A1794	C1795	U1796	G1797	C1800	A1801	A1802	A1803										
C1564	C1565	A1566	A1569	A1570	A1571	A1572	C1575	U1576	G1592	A1593	U1594	G1601	U1602	A1603	C1606	C1607	A1608	A1490	U1497	C1507	A1508	A1509	G1510	A1515	G1516	G1521	A1522	U1523	G1524	A1528	G1529	G1530	A1535	C1536	G1537	A1545	C1546	G1547	A1548	A1549	C1550	A1551	G1555	G1560											
G1444	C1447	G1448	G1449	G1450	C1451	G1452	U1458	U1459	U1460	C1461	U1468	U1475	U1476	C1480	U1481	G1482	A1490	U1497	C1507	A1508	A1509	G1510	A1515	G1516	G1521	A1522	U1523	G1524	A1528	G1529	G1530	A1535	C1536	G1537	A1545	C1546	G1547	A1548	A1549	C1550	A1551	G1555	G1560												
U1012	C1013	U1019	A1020	A1021	G1022	G1026	A1027	A1028	A1029	G1030	G1031	A1032	U1033	G1034	U1035	G1036	G1037	G1038	A1039	A1040	G1041	A1046	G1047	G1055	G1056	A1057	U1058	G1059	U1060	U1061	G1062	C1150	G1063	C1064	U1065	U1066	A1067	G1068	A1069	A1070	G1071	A1072	A1073	G1074	G1075	C1076	A1077	U1078	U1079	A1080	U1081	U1082	U1083	A1084	A1085



• Molecule 3: 5S ribosomal RNA

Chain 02: 55% 38% 8%



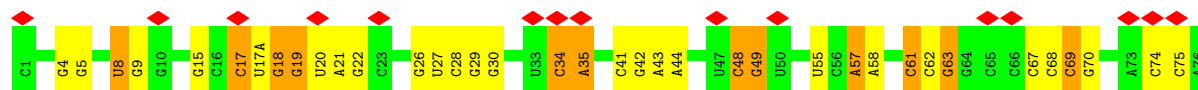
• Molecule 4: Alternative ribosome-rescue factor A

Chain Y: 40% 25% 35%



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

Chain X: 19% 52% 32% 16%



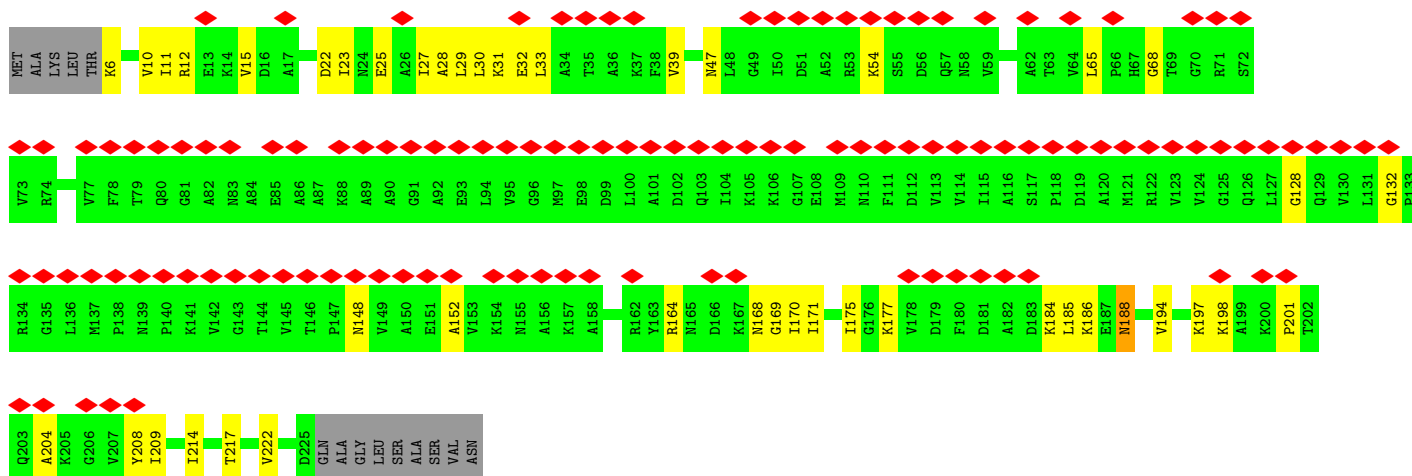
• Molecule 5: fMet-tRNA (P- and E-site)

Chain W: 75% 22% 3%



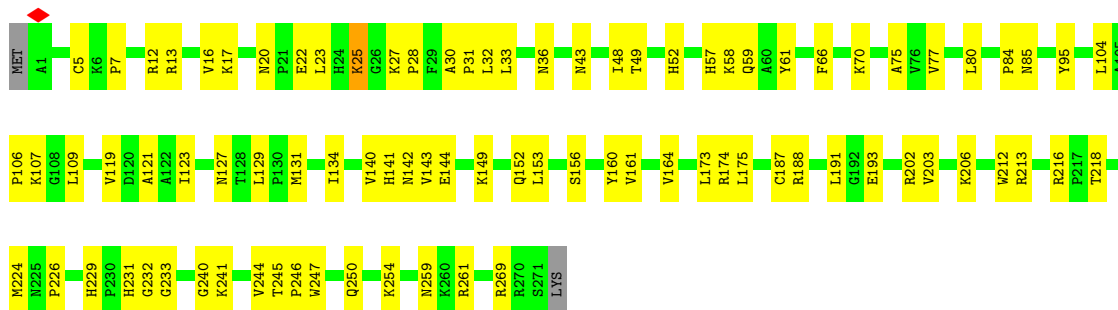
• Molecule 6: 50S ribosomal protein L1

Chain 03: 51% 75% 19% 6%



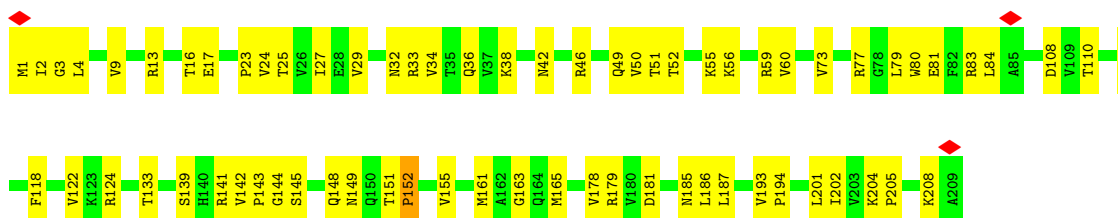
- Molecule 7: 50S ribosomal protein L2

Chain 04: 67% 32% .



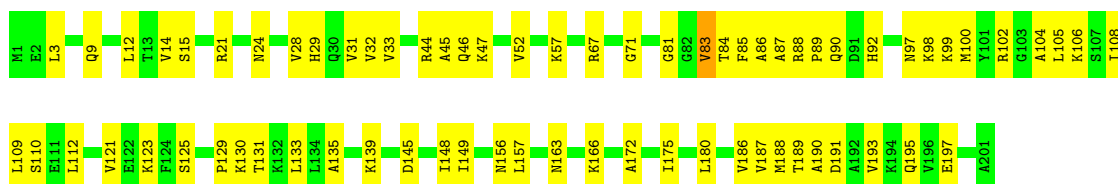
- Molecule 8: 50S ribosomal protein L3

Chain 05: 67% 33%

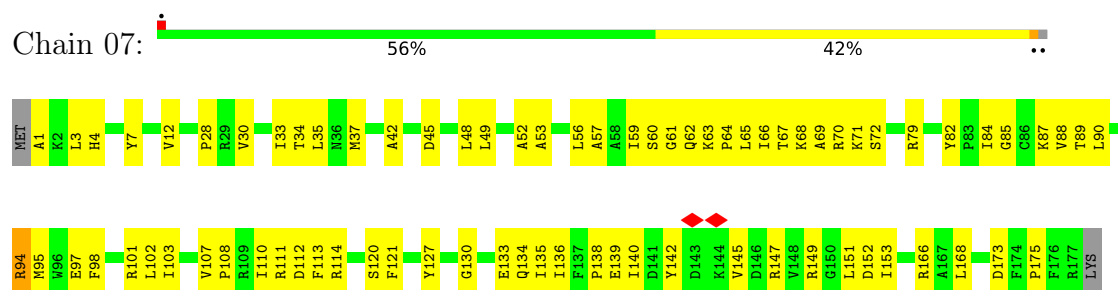


- Molecule 9: 50S ribosomal protein L4

Chain 06: 65% 34%



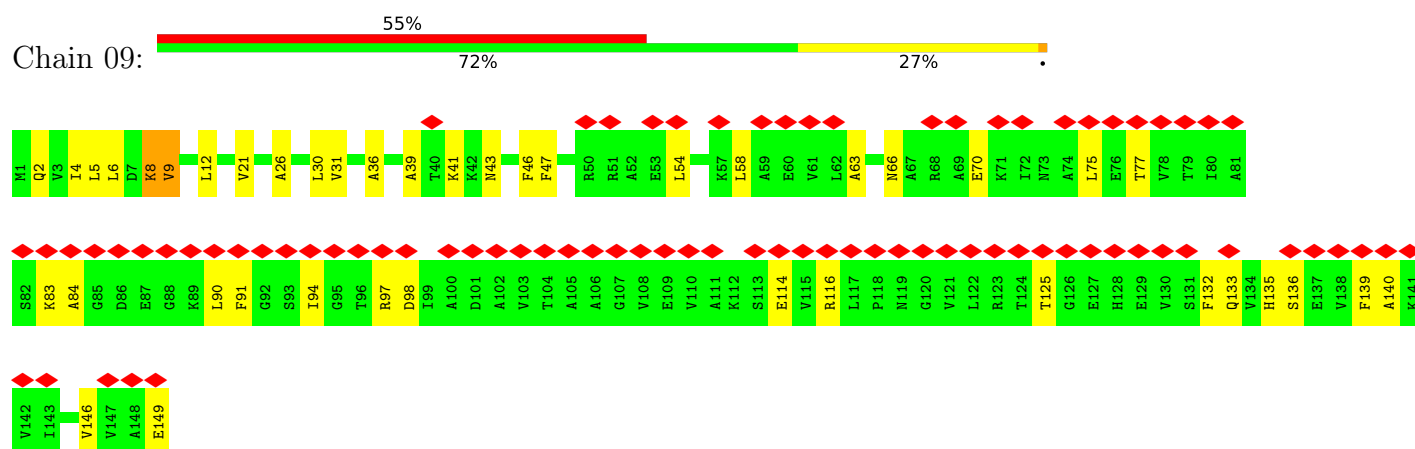
- Molecule 10: 50S ribosomal protein L5



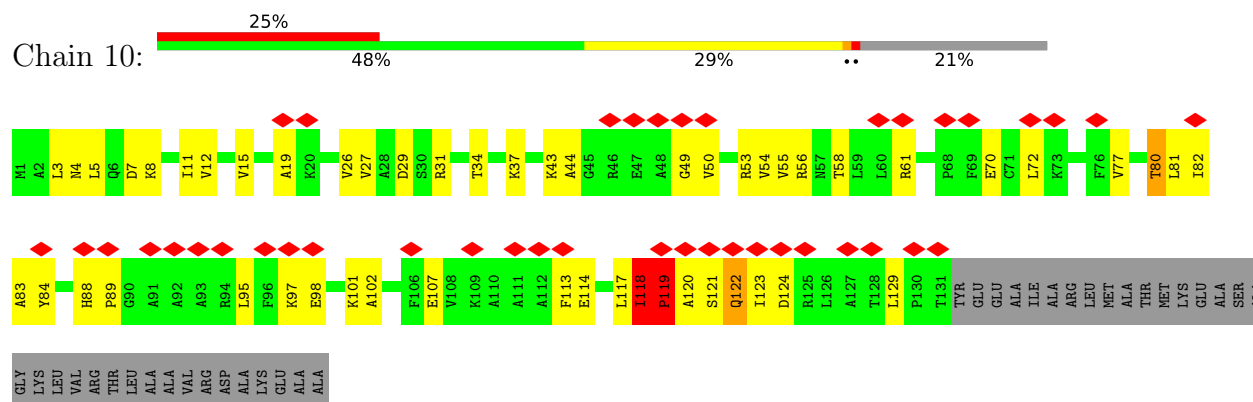
- Molecule 11: 50S ribosomal protein L6



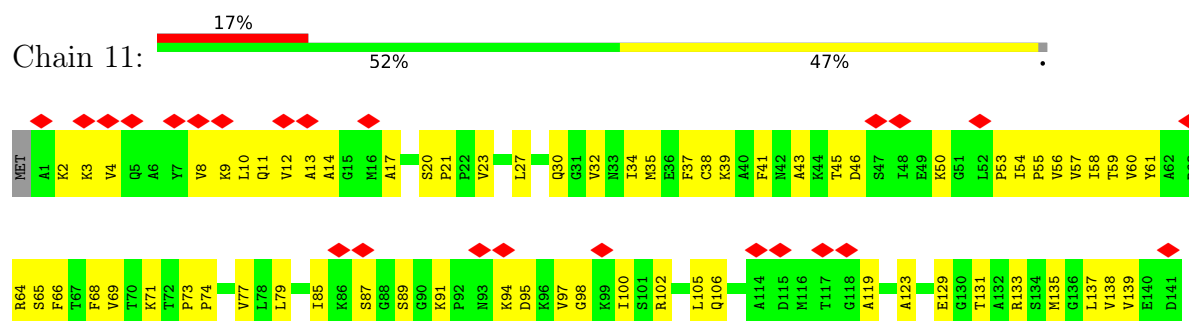
- Molecule 12: 50S ribosomal protein L9



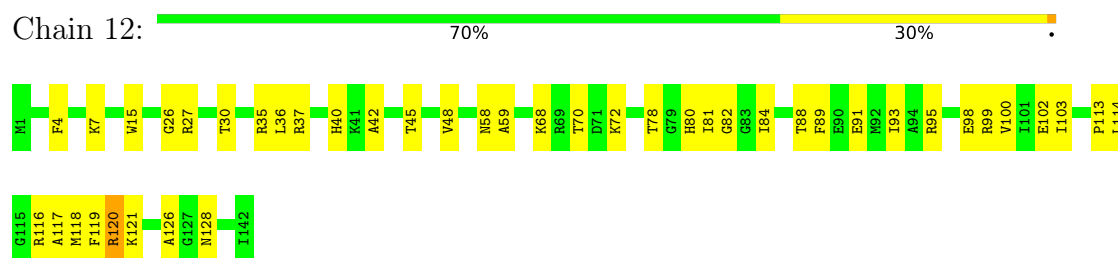
- Molecule 13: 50S ribosomal protein L10



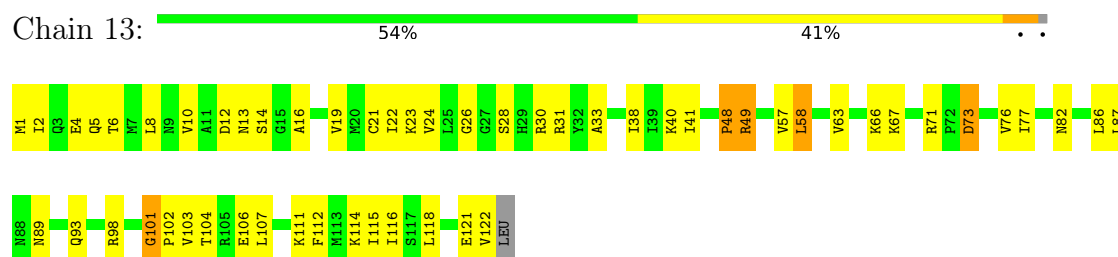
- Molecule 14: 50S ribosomal protein L11



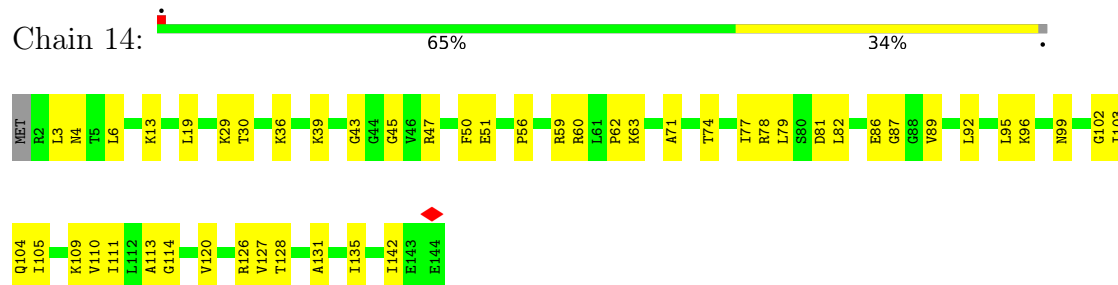
- Molecule 15: 50S ribosomal protein L13



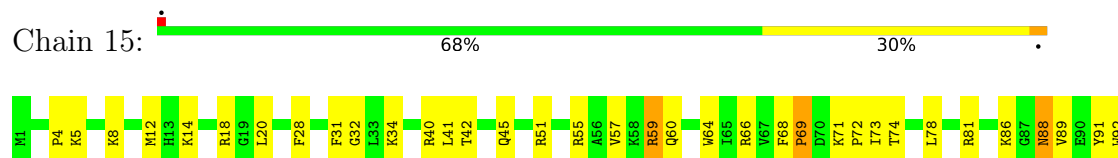
- Molecule 16: 50S ribosomal protein L14



- Molecule 17: 50S ribosomal protein L15

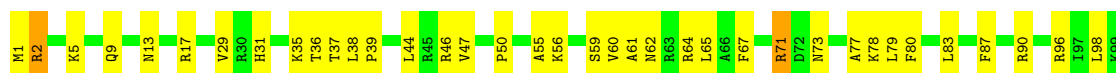


- Molecule 18: 50S ribosomal protein L16





- Molecule 19: 50S ribosomal protein L17



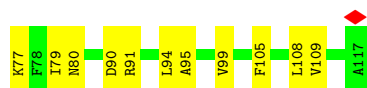
- Molecule 20: 50S ribosomal protein L18



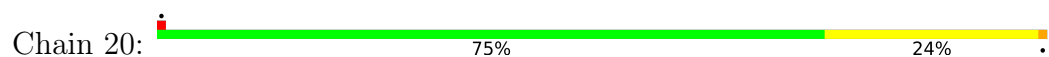
- Molecule 21: 50S ribosomal protein L19

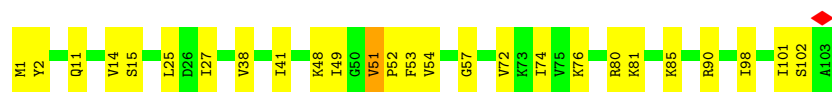


- Molecule 22: 50S ribosomal protein L20

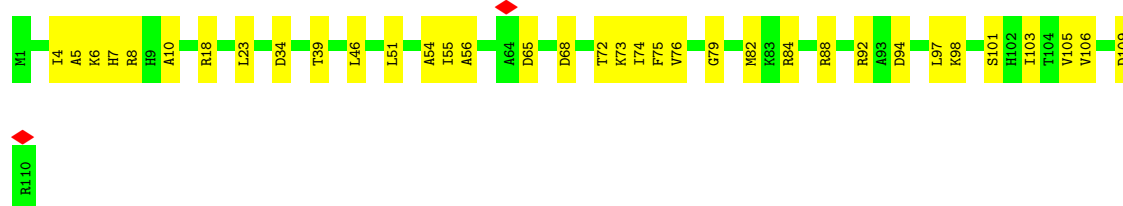


- Molecule 23: 50S ribosomal protein L21

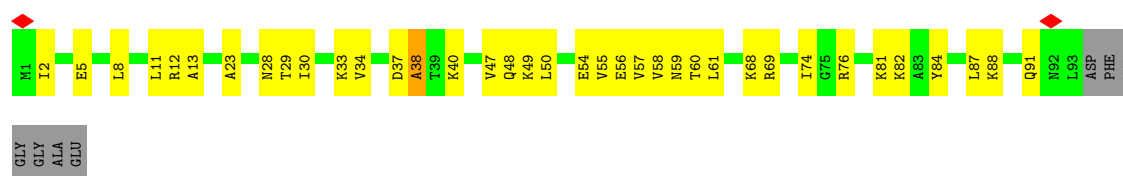




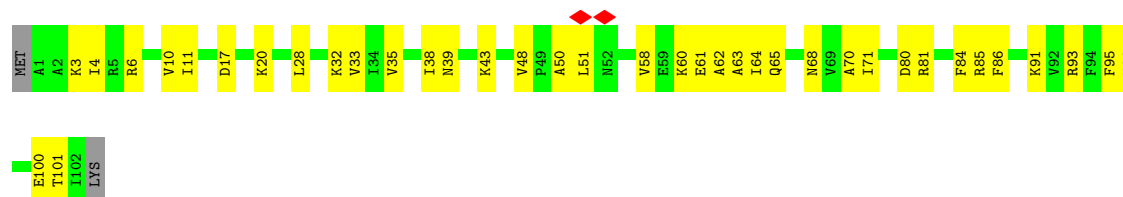
- Molecule 24: 50S ribosomal protein L22



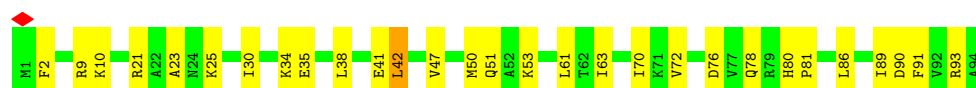
- Molecule 25: 50S ribosomal protein L23



- Molecule 26: 50S ribosomal protein L24



- Molecule 27: 50S ribosomal protein L25



- Molecule 28: 50S ribosomal protein L27



- Molecule 29: 50S ribosomal protein L28

Chain 26:  62% 36% ..



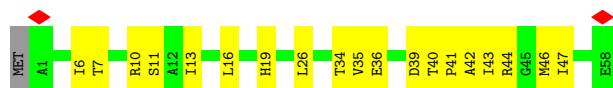
- Molecule 30: 50S ribosomal protein L29

Chain 27:  59% 38% .



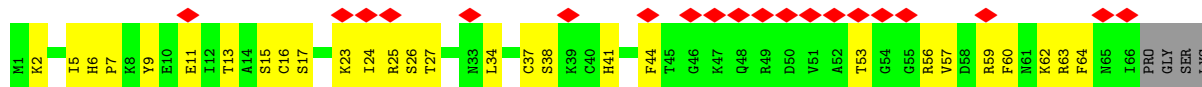
- Molecule 31: 50S ribosomal protein L30

Chain 28:  66% 32% .



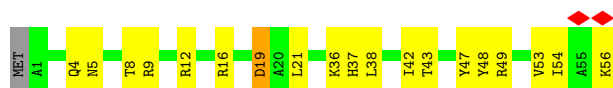
- Molecule 32: 50S ribosomal protein L31

Chain 29:  29% 54% 40% 6%



- Molecule 33: 50S ribosomal protein L32

Chain 30:  65% 32% ..



- Molecule 34: 50S ribosomal protein L33

Chain 31:  71% 20% 9%



- Molecule 35: 50S ribosomal protein L34

Chain 32:  57% 43%



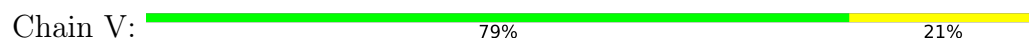
- Molecule 36: 50S ribosomal protein L35



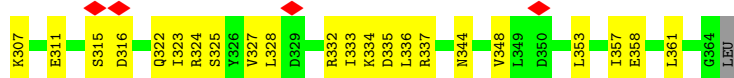
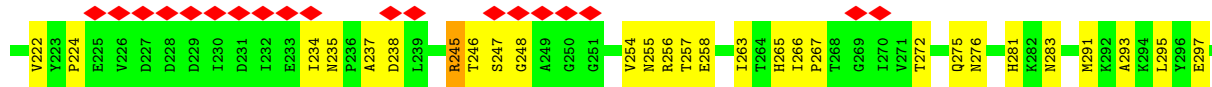
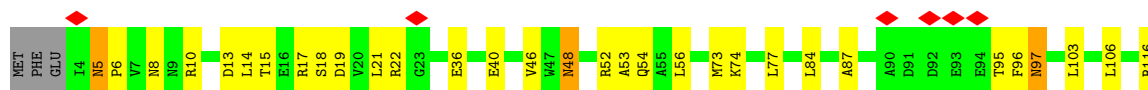
- Molecule 37: 50S ribosomal protein L36



- Molecule 38: truncated mRNA

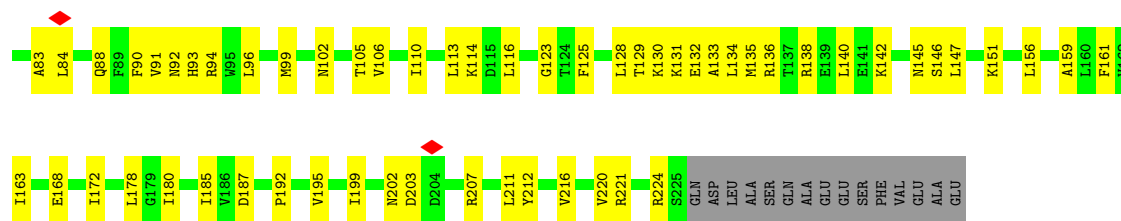


- Molecule 39: Peptide chain release factor RF2



- Molecule 40: 30S ribosomal protein S2





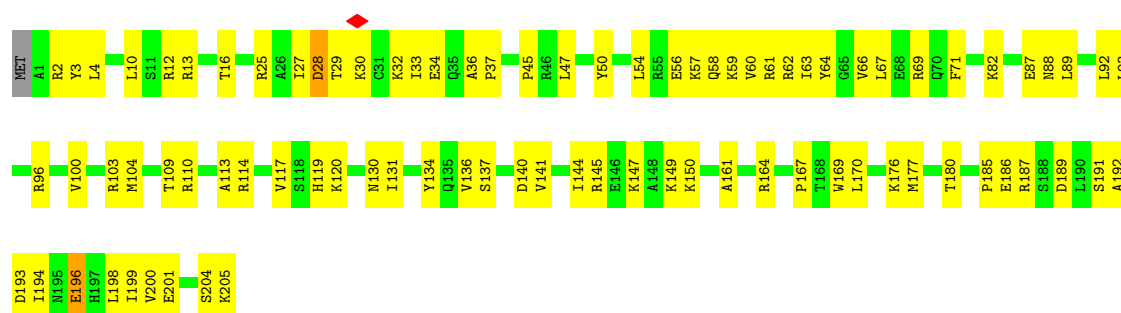
• Molecule 41: 30S ribosomal protein S3

Chain C: 64% 25% 12%



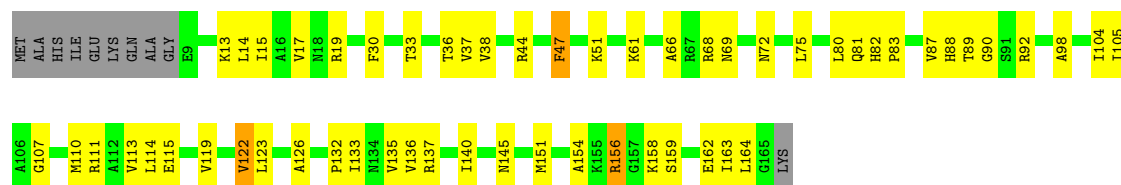
• Molecule 42: 30S ribosomal protein S4

Chain D: 58% 41% .



• Molecule 43: 30S ribosomal protein S5

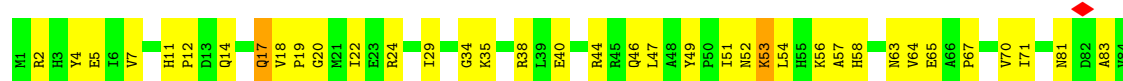
Chain E: 60% 32% . 6%



• Molecule 44: 30S ribosomal protein S6

Chain F: 40% 33% . 24%





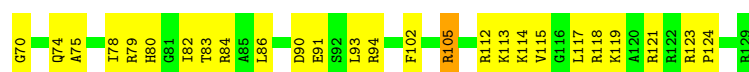
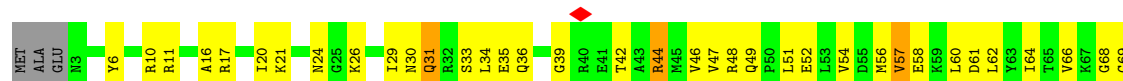
- Molecule 45: 30S ribosomal protein S7



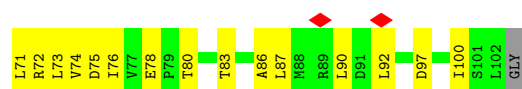
- Molecule 46: 30S ribosomal protein S8



- Molecule 47: 30S ribosomal protein S9

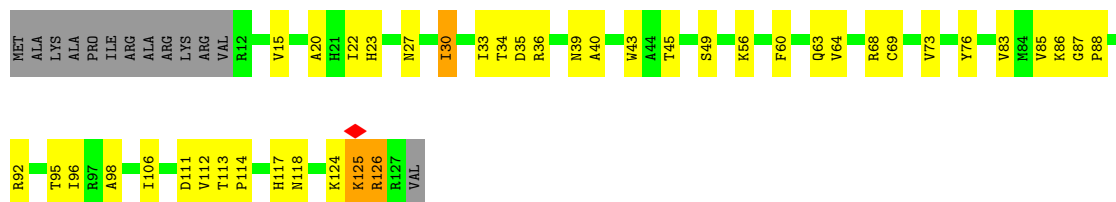


- Molecule 48: 30S ribosomal protein S10



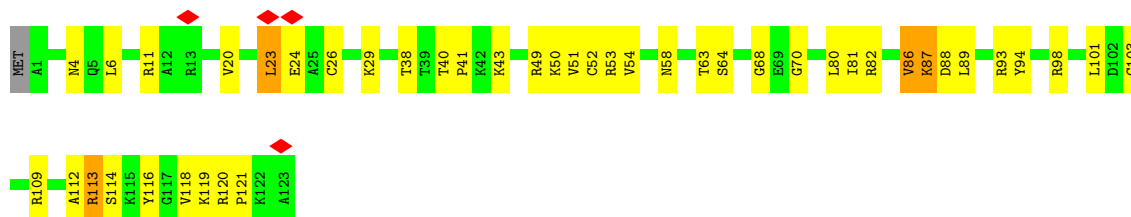
- Molecule 49: 30S ribosomal protein S11

Chain K:  57% 30% 10%



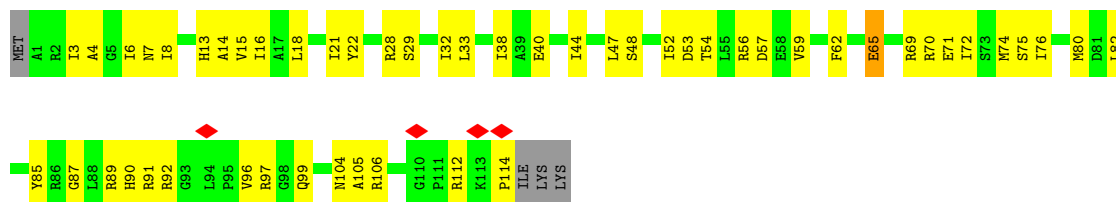
- Molecule 50: 30S ribosomal protein S12

Chain L:  64% 32% 2%



- Molecule 51: 30S ribosomal protein S13

Chain M:  53% 43% 2%



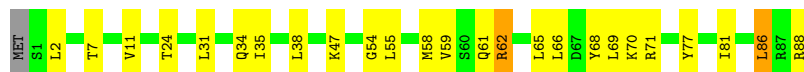
- Molecule 52: 30S ribosomal protein S14

Chain N:  47% 46% 6%

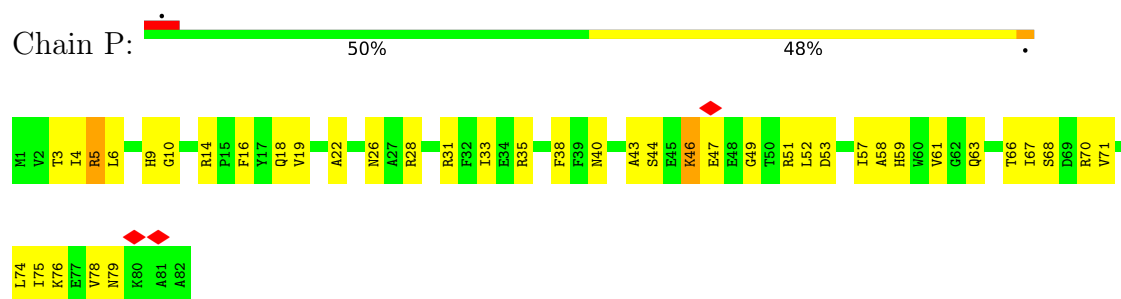


- Molecule 53: 30S ribosomal protein S15

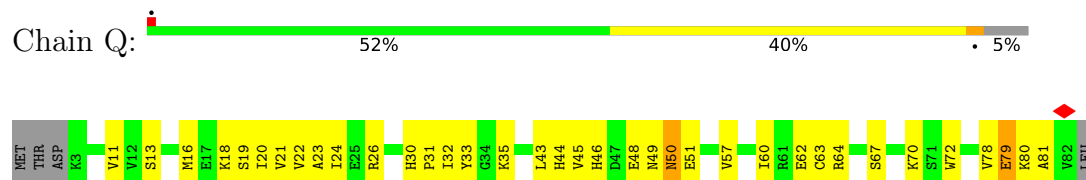
Chain O:  71% 26% 2%



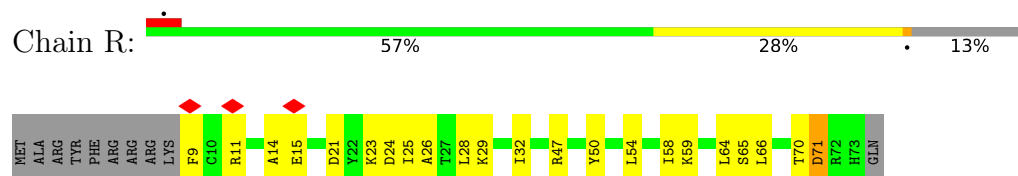
- Molecule 54: 30S ribosomal protein S16



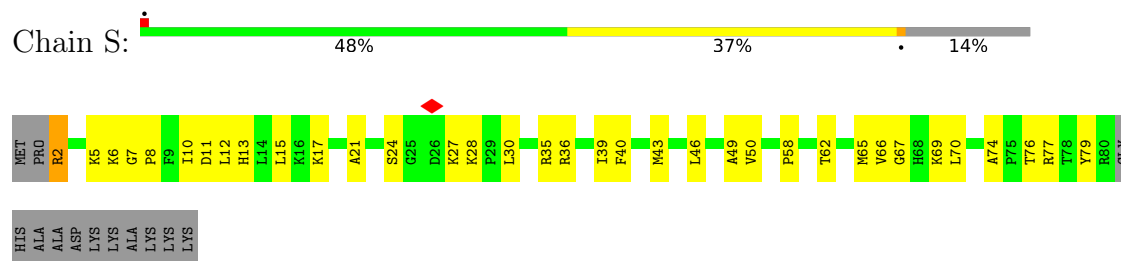
- Molecule 55: 30S ribosomal protein S17



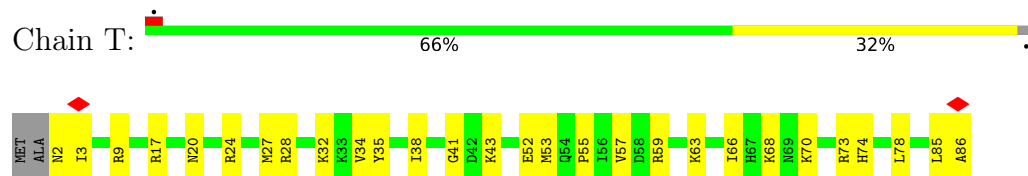
- Molecule 56: 30S ribosomal protein S18



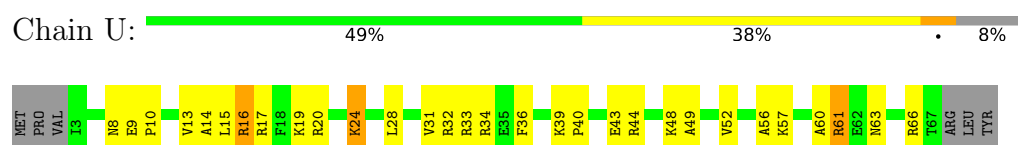
- Molecule 57: 30S ribosomal protein S19



- Molecule 58: 30S ribosomal protein S20



- 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 (Å)	388.80002, 388.80002, 388.80002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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	0.25	0/36963	0.65	0/57662
2	01	0.25	0/69797	0.65	1/108890 (0.0%)
3	02	0.26	0/2847	0.65	0/4440
4	Y	0.30	0/383	0.51	0/504
5	W	0.24	0/1832	0.64	0/2855
5	X	0.29	0/1811	0.66	0/2822
6	03	0.29	0/1361	0.57	0/1796
7	04	0.30	0/2121	0.61	0/2852
8	05	0.33	0/1586	0.60	0/2134
9	06	0.31	0/1571	0.59	0/2113
10	07	0.32	0/1434	0.56	0/1926
11	08	0.30	0/1343	0.60	0/1816
12	09	0.32	0/1122	0.64	0/1515
13	10	0.40	0/1001	0.93	3/1350 (0.2%)
14	11	0.32	0/1046	0.60	0/1410
15	12	0.31	0/1152	0.56	0/1551
16	13	0.32	0/947	0.63	1/1268 (0.1%)
17	14	0.31	0/1054	0.58	0/1403
18	15	0.33	0/1093	0.59	0/1460
19	16	0.32	0/973	0.57	0/1301
20	17	0.29	0/902	0.54	0/1209
21	18	0.31	0/929	0.56	0/1242
22	19	0.30	0/960	0.47	0/1278
23	20	0.33	0/829	0.64	1/1107 (0.1%)
24	21	0.29	0/864	0.59	0/1156
25	22	0.31	0/744	0.59	0/994
26	23	0.33	0/787	0.59	0/1051
27	24	0.31	0/766	0.53	0/1025
28	25	0.34	0/582	0.59	0/769
29	26	0.31	0/635	0.54	0/848
30	27	0.28	0/510	0.49	0/677
31	28	0.29	0/453	0.55	0/605

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
32	29	0.34	0/531	0.56	0/709
33	30	0.30	0/450	0.57	0/599
34	31	0.33	0/416	0.54	0/554
35	32	0.32	0/380	0.57	0/498
36	33	0.30	0/513	0.58	0/676
37	34	0.23	0/303	0.40	0/397
38	V	0.20	0/345	0.60	0/538
39	Z	0.28	0/2884	0.49	0/3884
40	B	0.32	0/1735	0.58	1/2338 (0.0%)
41	C	0.30	0/1651	0.54	0/2225
42	D	0.29	0/1665	0.58	0/2227
43	E	0.33	0/1169	0.66	0/1573
44	F	0.33	0/835	0.71	2/1128 (0.2%)
45	G	0.29	0/1195	0.53	0/1602
46	H	0.29	0/989	0.56	0/1326
47	I	0.31	0/1034	0.63	0/1375
48	J	0.29	0/796	0.60	0/1077
49	K	0.32	0/885	0.59	1/1195 (0.1%)
50	L	0.32	0/969	0.68	0/1300
51	M	0.28	0/892	0.59	0/1193
52	N	0.37	0/817	0.73	3/1088 (0.3%)
53	O	0.28	0/722	0.50	0/964
54	P	0.34	0/659	0.60	0/884
55	Q	0.33	0/657	0.59	0/881
56	R	0.29	0/544	0.51	0/731
57	S	0.32	0/652	0.58	0/877
58	T	0.30	0/671	0.48	0/888
59	U	0.36	0/550	0.71	0/728
All	All	0.27	0/165307	0.63	13/246484 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
52	N	0	1

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	10	118	ILE	C-N-CD	-18.15	80.67	120.60
13	10	118	ILE	C-N-CA	7.52	153.59	122.00
52	N	55	SER	N-CA-C	6.88	129.58	111.00
49	K	125	LYS	N-CA-C	6.75	129.21	111.00
40	B	16	GLY	N-CA-C	6.51	129.38	113.10

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	477	0
2	01	62318	0	31345	788	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	78	0
8	05	1565	0	1616	68	0
9	06	1552	0	1619	56	0
10	07	1410	0	1447	72	0
11	08	1323	0	1374	56	0
12	09	1111	0	1148	31	0
13	10	988	0	1025	47	0
14	11	1032	0	1088	56	0
15	12	1129	0	1162	44	0
16	13	938	0	1012	51	0
17	14	1045	0	1117	46	0
18	15	1074	0	1157	38	0
19	16	960	0	1000	47	0
20	17	892	0	923	39	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	23	0
25	22	738	0	807	26	0
26	23	779	0	834	32	0
27	24	753	0	780	27	0
28	25	575	0	592	30	0
29	26	625	0	655	25	0
30	27	509	0	543	25	0
31	28	449	0	491	14	0
32	29	522	0	524	26	0
33	30	444	0	461	24	0
34	31	409	0	440	8	0
35	32	377	0	418	19	0
36	33	504	0	574	19	0
37	34	302	0	340	23	0
38	V	306	0	154	1	0
39	Z	2844	0	2739	113	0
40	B	1704	0	1732	77	0
41	C	1624	0	1699	50	0
42	D	1643	0	1710	82	0
43	E	1156	0	1199	55	0
44	F	817	0	808	36	0
45	G	1181	0	1240	45	0
46	H	979	0	1034	32	0
47	I	1022	0	1070	65	0
48	J	786	0	828	54	0
49	K	869	0	878	44	0
50	L	955	0	1019	42	0
51	M	883	0	944	52	0
52	N	805	0	847	63	0
53	O	714	0	737	19	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	45	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	3184	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 12.

The worst 5 of 3184 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
1:A:291:U:H2'	1:A:292:G:H5''	1.31	1.12
13:10:117:LEU:C	13:10:119:PRO:HD2	1.71	1.10
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%)	22	61
8	05	207/209 (99%)	189 (91%)	17 (8%)	1 (0%)	29	67
9	06	199/201 (99%)	180 (90%)	17 (8%)	2 (1%)	15	54
10	07	175/179 (98%)	155 (89%)	20 (11%)	0	100	100
11	08	174/177 (98%)	154 (88%)	17 (10%)	3 (2%)	9	42
12	09	147/149 (99%)	131 (89%)	13 (9%)	3 (2%)	7	38
13	10	129/165 (78%)	95 (74%)	28 (22%)	6 (5%)	2	17
14	11	139/142 (98%)	120 (86%)	18 (13%)	1 (1%)	22	61
15	12	140/142 (99%)	133 (95%)	7 (5%)	0	100	100
16	13	120/123 (98%)	100 (83%)	18 (15%)	2 (2%)	9	42
17	14	141/144 (98%)	128 (91%)	13 (9%)	0	100	100
18	15	134/136 (98%)	125 (93%)	7 (5%)	2 (2%)	10	44
19	16	118/127 (93%)	106 (90%)	11 (9%)	1 (1%)	19	58
20	17	114/117 (97%)	102 (90%)	11 (10%)	1 (1%)	17	56
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%)	15	54
24	21	108/110 (98%)	97 (90%)	11 (10%)	0	100	100
25	22	91/100 (91%)	77 (85%)	13 (14%)	1 (1%)	14	51
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%)	5	30
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%)	6	34
36	33	62/65 (95%)	53 (86%)	7 (11%)	2 (3%)	4	26
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%)	41	74
40	B	216/241 (90%)	188 (87%)	26 (12%)	2 (1%)	17	56
41	C	204/233 (88%)	189 (93%)	15 (7%)	0	100	100
42	D	203/206 (98%)	177 (87%)	25 (12%)	1 (0%)	29	67
43	E	155/167 (93%)	125 (81%)	29 (19%)	1 (1%)	25	64
44	F	98/131 (75%)	77 (79%)	16 (16%)	5 (5%)	2	15
45	G	149/156 (96%)	134 (90%)	14 (9%)	1 (1%)	22	61
46	H	127/130 (98%)	115 (91%)	12 (9%)	0	100	100
47	I	125/130 (96%)	101 (81%)	22 (18%)	2 (2%)	9	43
48	J	96/103 (93%)	85 (88%)	9 (9%)	2 (2%)	7	37
49	K	114/129 (88%)	102 (90%)	11 (10%)	1 (1%)	17	56
50	L	121/124 (98%)	92 (76%)	23 (19%)	6 (5%)	2	16
51	M	112/118 (95%)	94 (84%)	16 (14%)	2 (2%)	8	41
52	N	98/101 (97%)	79 (81%)	13 (13%)	6 (6%)	1	12
53	O	86/89 (97%)	79 (92%)	7 (8%)	0	100	100
54	P	80/82 (98%)	65 (81%)	13 (16%)	2 (2%)	5	32
55	Q	78/84 (93%)	63 (81%)	14 (18%)	1 (1%)	12	47
56	R	63/75 (84%)	60 (95%)	3 (5%)	0	100	100
57	S	77/92 (84%)	69 (90%)	7 (9%)	1 (1%)	12	47
58	T	83/87 (95%)	81 (98%)	2 (2%)	0	100	100
59	U	63/71 (89%)	44 (70%)	17 (27%)	2 (3%)	4	26
All	All	6468/6864 (94%)	5705 (88%)	696 (11%)	67 (1%)	20	54

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%)	38 (100%)	0	100	100
6	03	106/181 (59%)	104 (98%)	2 (2%)	57	81
7	04	216/218 (99%)	213 (99%)	3 (1%)	67	86
8	05	164/164 (100%)	162 (99%)	2 (1%)	71	88
9	06	165/165 (100%)	164 (99%)	1 (1%)	86	94
10	07	148/150 (99%)	147 (99%)	1 (1%)	84	94
11	08	137/138 (99%)	136 (99%)	1 (1%)	84	94
12	09	114/114 (100%)	113 (99%)	1 (1%)	78	91
13	10	100/123 (81%)	98 (98%)	2 (2%)	55	80
14	11	109/110 (99%)	109 (100%)	0	100	100
15	12	116/116 (100%)	115 (99%)	1 (1%)	78	91
16	13	103/104 (99%)	99 (96%)	4 (4%)	32	67
17	14	102/103 (99%)	101 (99%)	1 (1%)	76	90
18	15	109/109 (100%)	107 (98%)	2 (2%)	59	82
19	16	100/104 (96%)	99 (99%)	1 (1%)	76	90
20	17	86/87 (99%)	84 (98%)	2 (2%)	50	78
21	18	99/100 (99%)	98 (99%)	1 (1%)	76	90
22	19	89/90 (99%)	88 (99%)	1 (1%)	73	88
23	20	84/84 (100%)	84 (100%)	0	100	100
24	21	93/93 (100%)	92 (99%)	1 (1%)	73	88
25	22	80/84 (95%)	80 (100%)	0	100	100
26	23	83/85 (98%)	83 (100%)	0	100	100
27	24	78/78 (100%)	77 (99%)	1 (1%)	69	87
28	25	57/63 (90%)	56 (98%)	1 (2%)	59	82
29	26	67/68 (98%)	66 (98%)	1 (2%)	65	85
30	27	55/55 (100%)	53 (96%)	2 (4%)	35	69

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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%)	59 (100%)	0	100	100
33	30	47/48 (98%)	46 (98%)	1 (2%)	53	79
34	31	45/49 (92%)	44 (98%)	1 (2%)	52	79
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%)	33 (97%)	1 (3%)	42	74
39	Z	303/311 (97%)	298 (98%)	5 (2%)	60	83
40	B	180/199 (90%)	176 (98%)	4 (2%)	52	79
41	C	170/190 (90%)	170 (100%)	0	100	100
42	D	172/173 (99%)	169 (98%)	3 (2%)	60	83
43	E	119/126 (94%)	116 (98%)	3 (2%)	47	77
44	F	87/112 (78%)	85 (98%)	2 (2%)	50	78
45	G	124/129 (96%)	122 (98%)	2 (2%)	62	84
46	H	104/105 (99%)	103 (99%)	1 (1%)	76	90
47	I	105/107 (98%)	102 (97%)	3 (3%)	42	74
48	J	86/90 (96%)	85 (99%)	1 (1%)	71	88
49	K	89/99 (90%)	86 (97%)	3 (3%)	37	70
50	L	103/104 (99%)	102 (99%)	1 (1%)	76	90
51	M	92/96 (96%)	92 (100%)	0	100	100
52	N	83/84 (99%)	83 (100%)	0	100	100
53	O	76/77 (99%)	74 (97%)	2 (3%)	46	76
54	P	65/65 (100%)	63 (97%)	2 (3%)	40	72
55	Q	74/78 (95%)	73 (99%)	1 (1%)	67	86
56	R	56/65 (86%)	55 (98%)	1 (2%)	59	82
57	S	70/79 (89%)	69 (99%)	1 (1%)	67	86
58	T	65/66 (98%)	64 (98%)	1 (2%)	65	85
59	U	55/61 (90%)	53 (96%)	2 (4%)	35	69
All	All	5298/5593 (95%)	5225 (99%)	73 (1%)	68	86

5 of 73 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
47	I	105	ARG
59	U	16	ARG
49	K	30	ILE
54	P	5	ARG
21	18	2	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 134 such sidechains are listed below:

Mol	Chain	Res	Type
49	K	39	ASN
50	L	72	ASN
54	P	40	ASN
23	20	11	GLN
22	19	36	GLN

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%)	19 (25%)	1 (1%)
All	All	4723/4729 (99%)	541 (11%)	9 (0%)

5 of 541 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 monosaccharides 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.

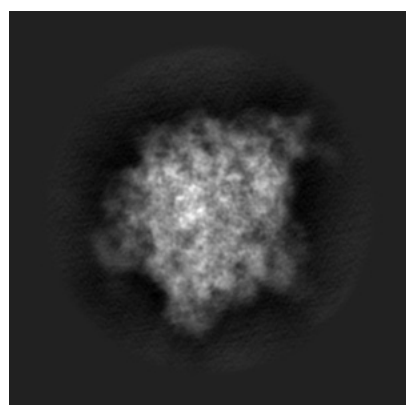
6 Map visualisation [i](#)

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.

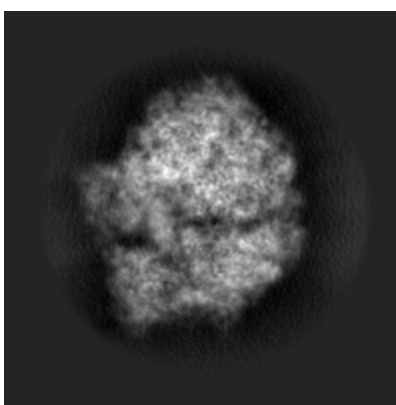
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

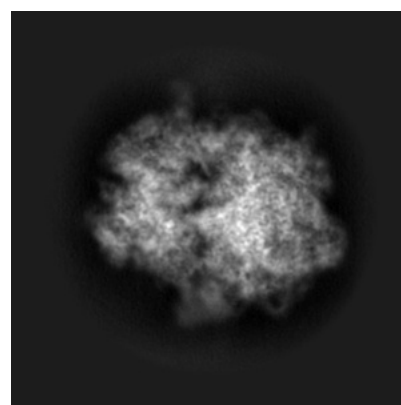
6.1.1 Primary map



X



Y

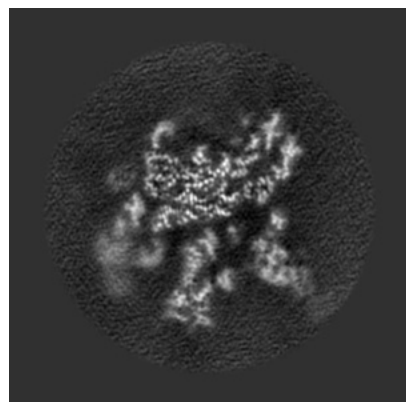


Z

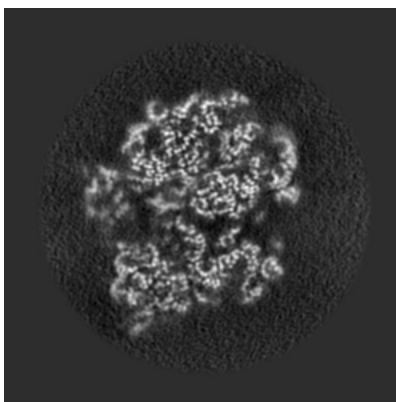
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

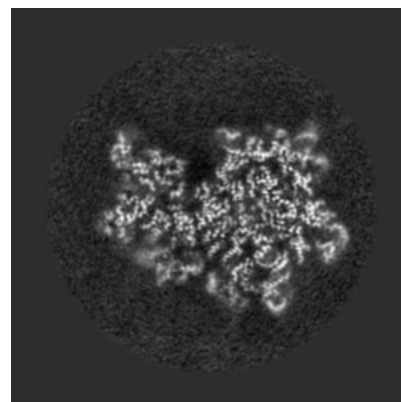
6.2.1 Primary map



X Index: 160



Y Index: 160

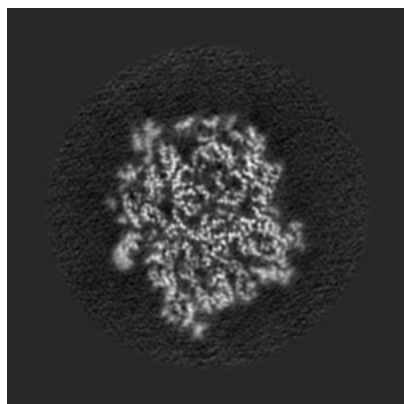


Z Index: 160

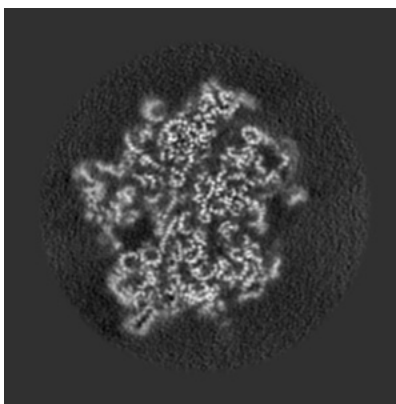
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

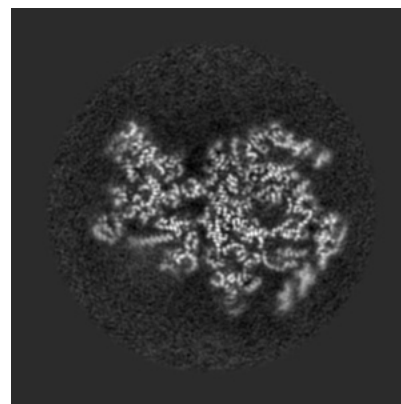
6.3.1 Primary map



X Index: 188



Y Index: 154

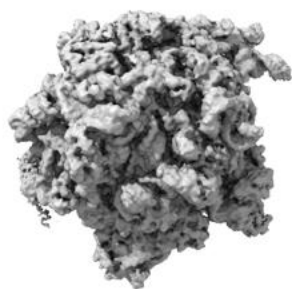


Z Index: 170

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

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.

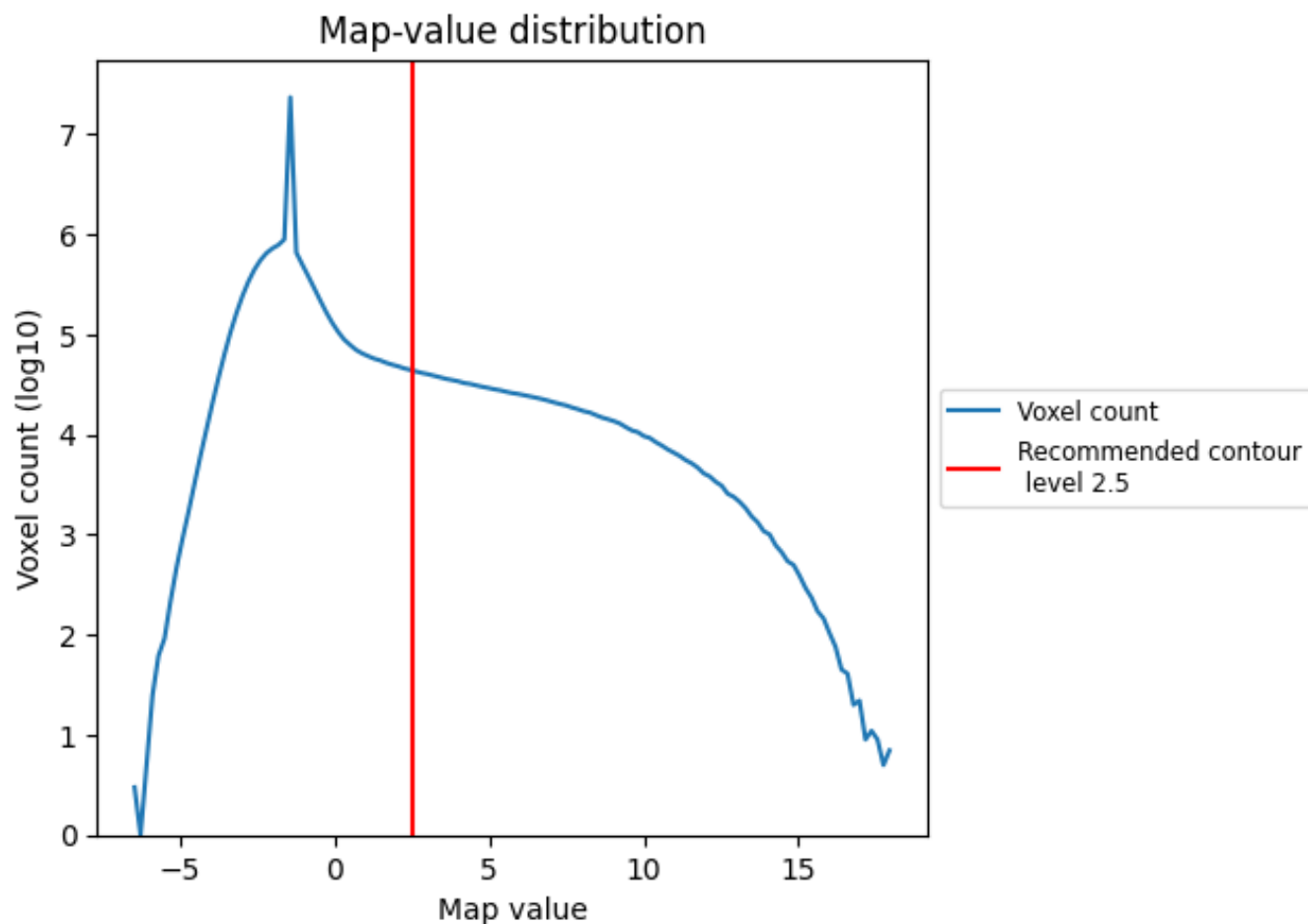
6.5 Mask visualisation

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

7 Map analysis [i](#)

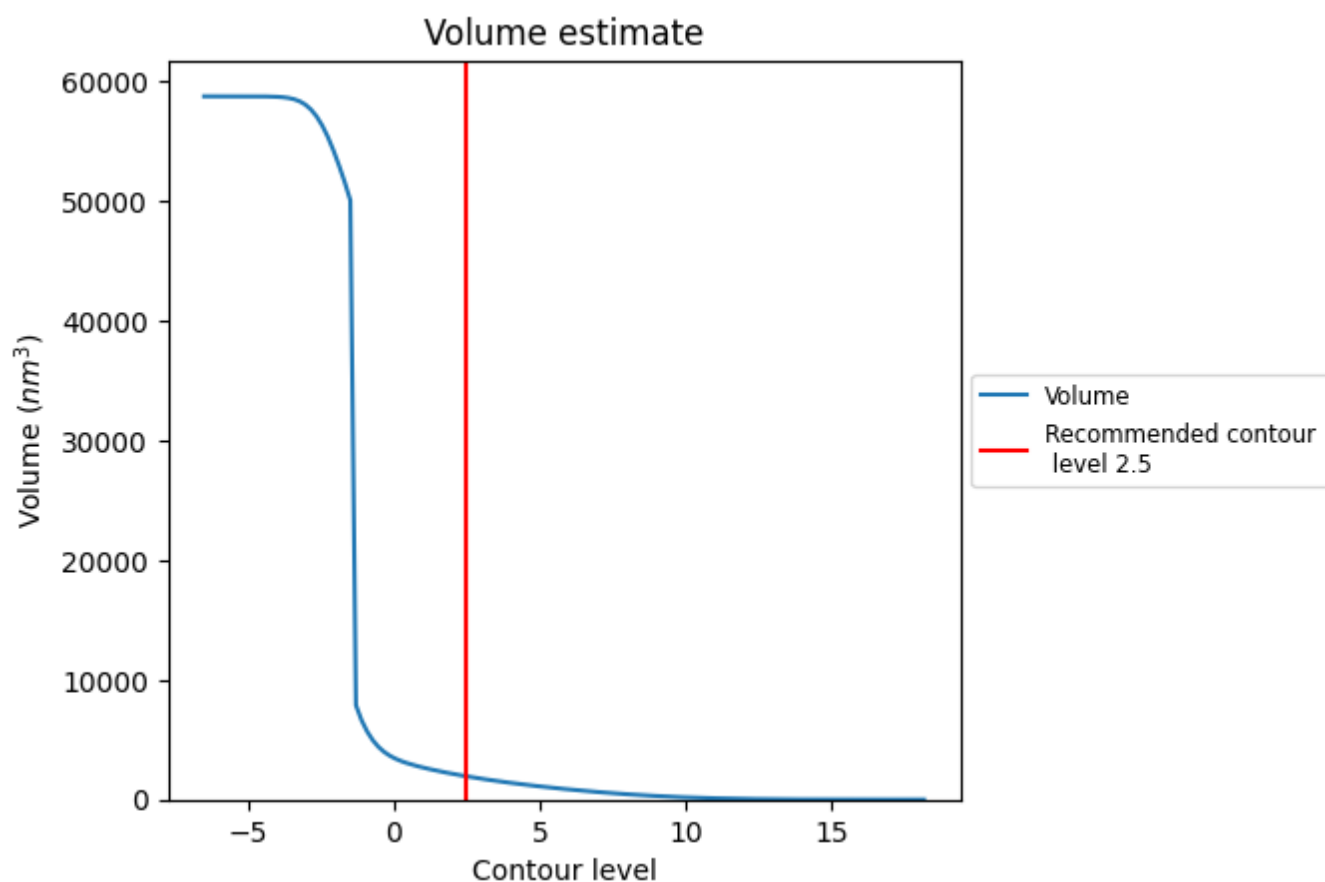
This section contains the results of statistical analysis of the map.

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.

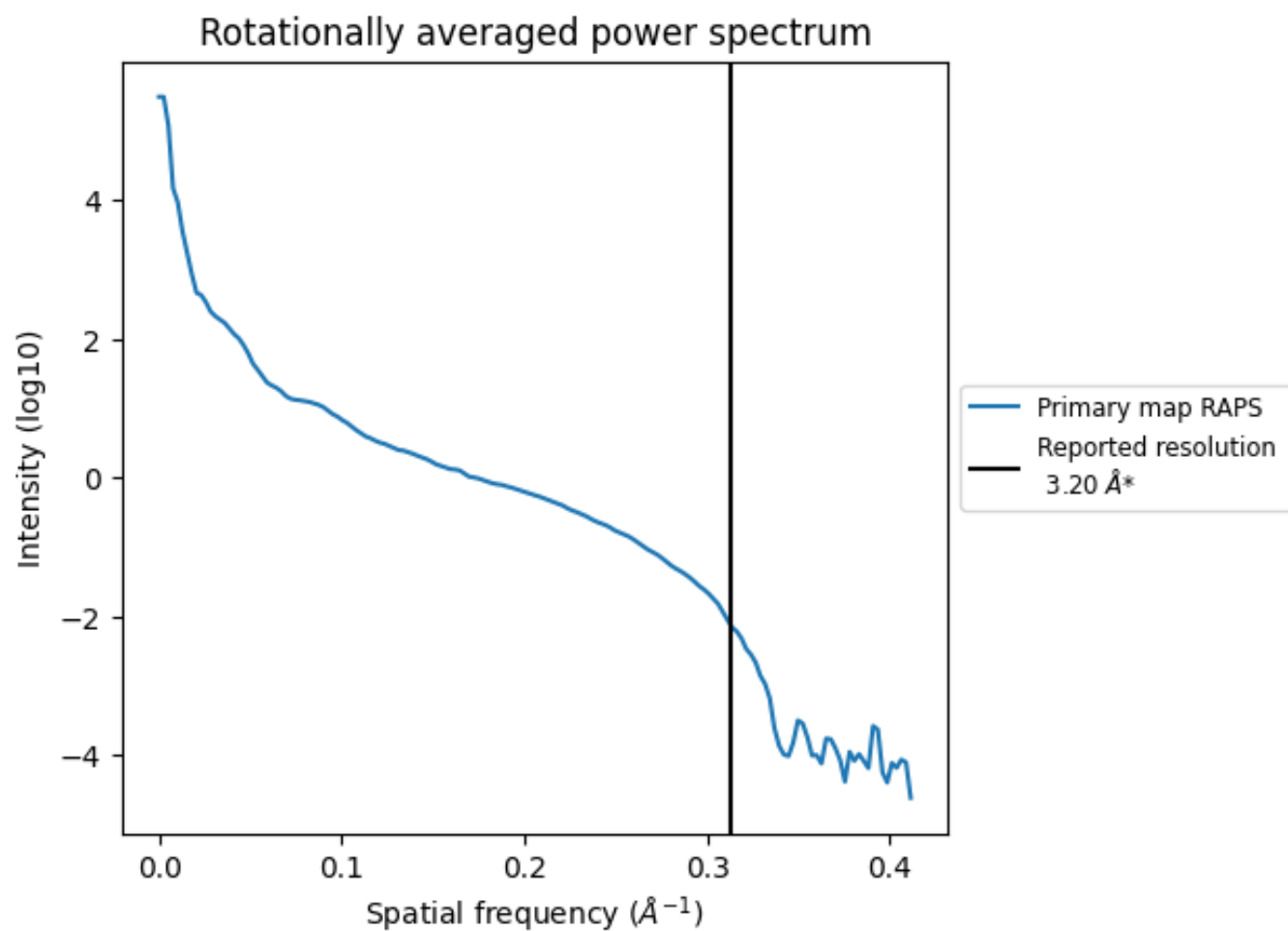
7.2 Volume estimate [i](#)



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

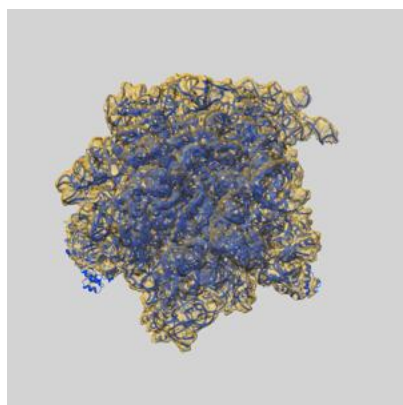
8 Fourier-Shell correlation ⓘ

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

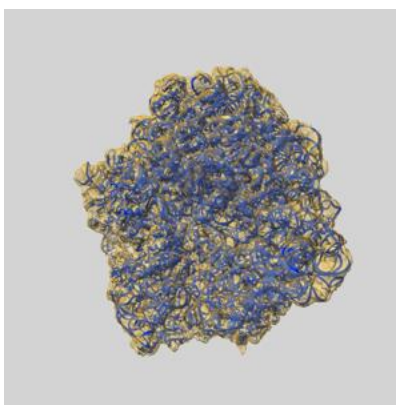
9 Map-model fit [i](#)

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](#).

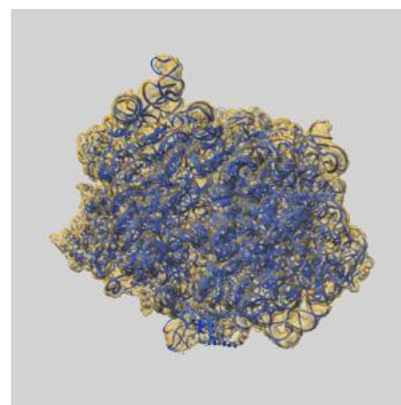
9.1 Map-model overlay [i](#)



X



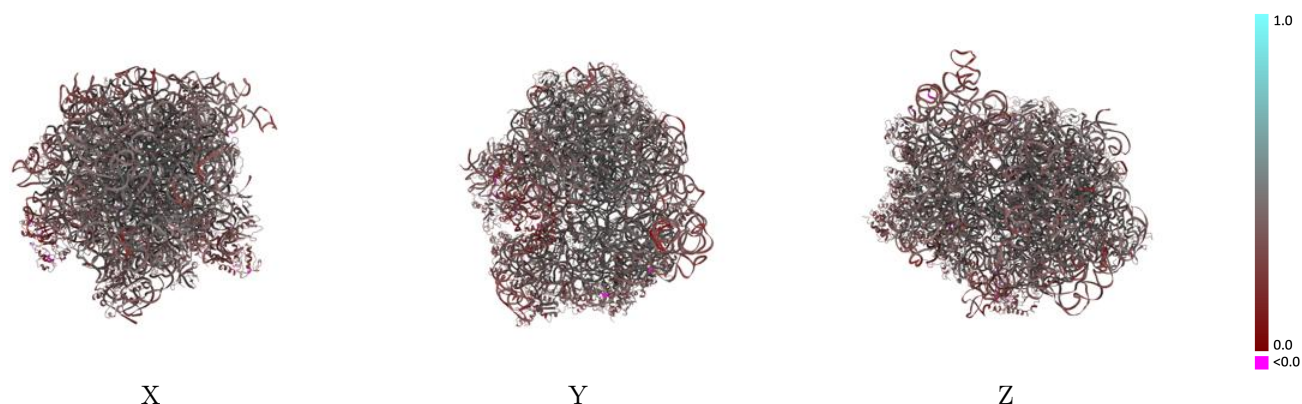
Y



Z

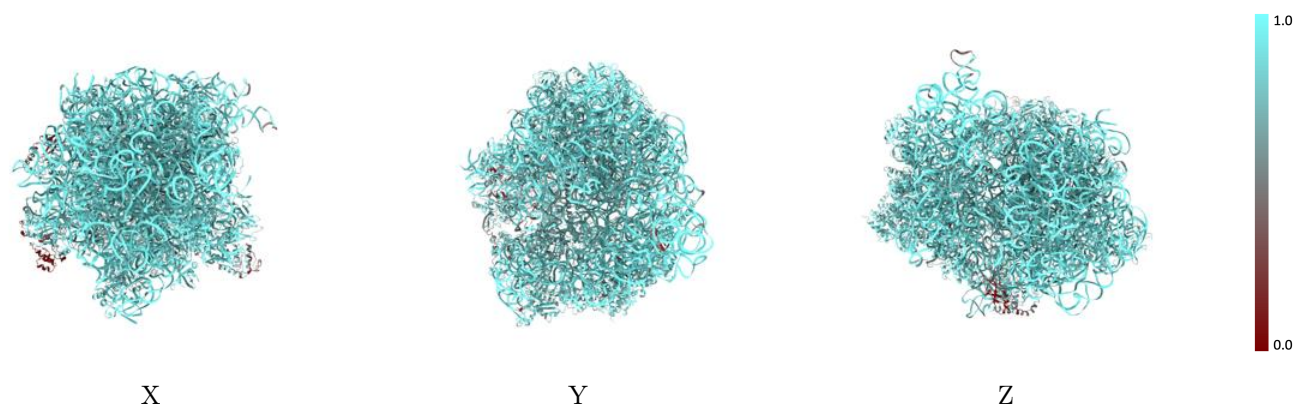
The images above show the 3D surface view of the map at the recommended contour level 2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



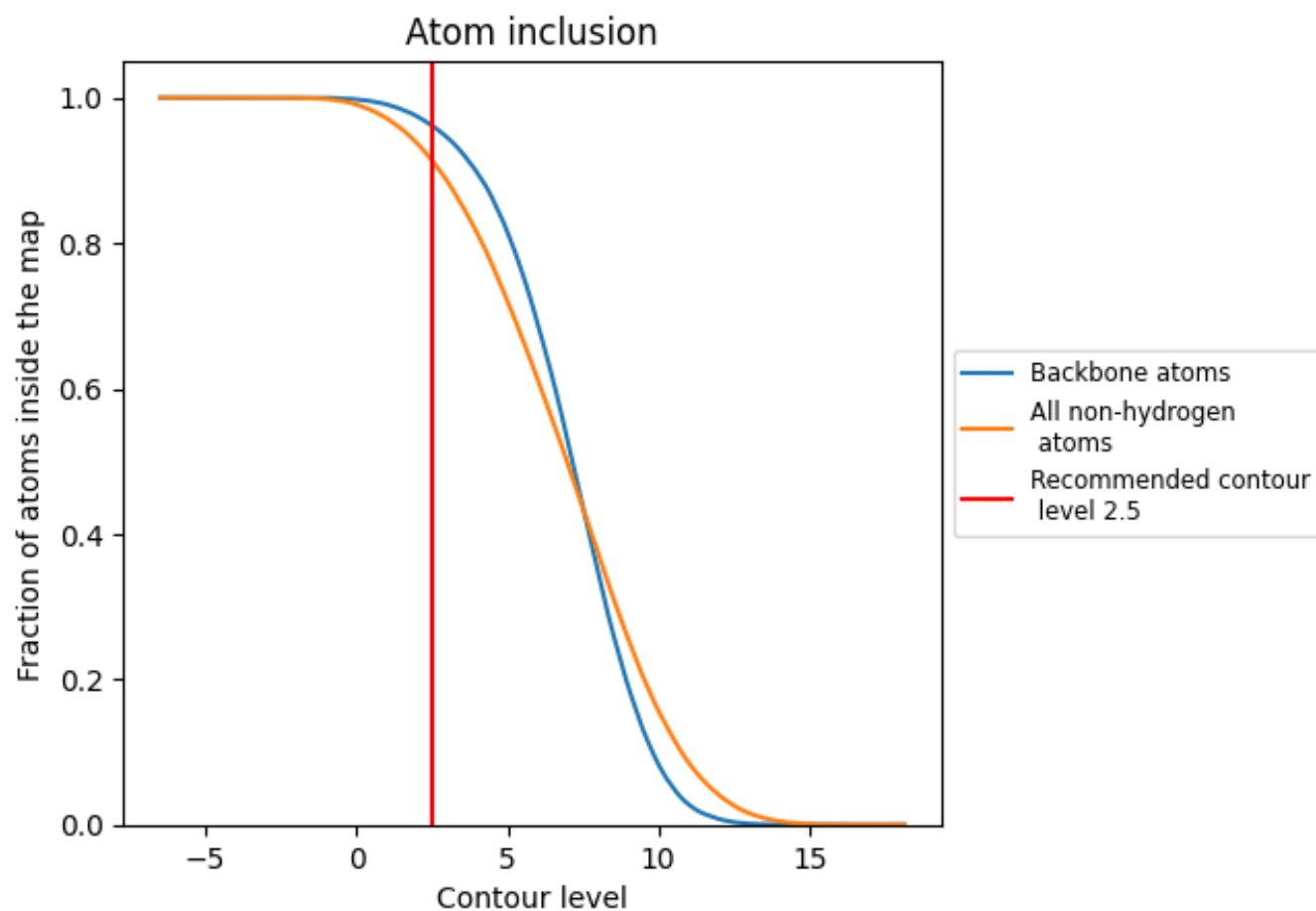
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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	 0.9788	 0.3530
03	 0.4596	 0.1980
04	 0.8363	 0.4350
05	 0.8648	 0.4250
06	 0.8651	 0.4000
07	 0.8587	 0.3230
08	 0.8481	 0.3650
09	 0.3686	 0.3050
10	 0.5424	 0.2120
11	 0.6918	 0.2380
12	 0.8745	 0.4120
13	 0.8028	 0.4230
14	 0.8819	 0.4140
15	 0.8109	 0.4120
16	 0.8926	 0.3890
17	 0.8900	 0.3420
18	 0.8243	 0.4010
19	 0.8768	 0.4080
20	 0.8758	 0.4140
21	 0.8337	 0.4090
22	 0.8006	 0.3790
23	 0.8396	 0.3800
24	 0.8821	 0.3800
25	 0.8945	 0.4230
26	 0.8369	 0.4040
27	 0.8149	 0.3030
28	 0.8444	 0.4040
29	 0.5382	 0.2840
30	 0.8531	 0.4020
31	 0.7985	 0.4010
32	 0.8620	 0.4280
33	 0.8859	 0.4290
34	 0.7789	 0.3680



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Chain	Atom inclusion	Q-score
A	 0.9734	 0.3860
B	 0.8107	 0.3300
C	 0.8188	 0.3740
D	 0.8428	 0.3600
E	 0.8704	 0.4010
F	 0.8128	 0.3530
G	 0.8086	 0.3290
H	 0.8646	 0.3960
I	 0.8571	 0.3340
J	 0.8265	 0.3250
K	 0.8580	 0.3870
L	 0.8284	 0.4250
M	 0.8073	 0.3170
N	 0.8553	 0.3310
O	 0.8725	 0.3590
P	 0.8836	 0.4020
Q	 0.8449	 0.3770
R	 0.8307	 0.3680
S	 0.8567	 0.3540
T	 0.8385	 0.3360
U	 0.7447	 0.2650
V	 0.8730	 0.3070
W	 0.9349	 0.3850
X	 0.6454	 0.2180
Y	 0.7575	 0.3830
Z	 0.6677	 0.3170