



wwPDB EM Validation Summary Report ⓘ

Aug 11, 2026 – 09:14 am BST

PDB ID : 9TI7 / pdb_00009ti7
EMDB ID : EMD-55946
Title : Staphylococcus aureus 70S ribosome with E-site tRNA and RRF oriented towards the LSU (postTC-RRF-LSU-2)
Authors : Gonzalez-Lopez, A.; Selmer, M.
Deposited on : 2025-12-05
Resolution : 2.76 Å (reported)
Based on initial models : 9GHG, .

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:

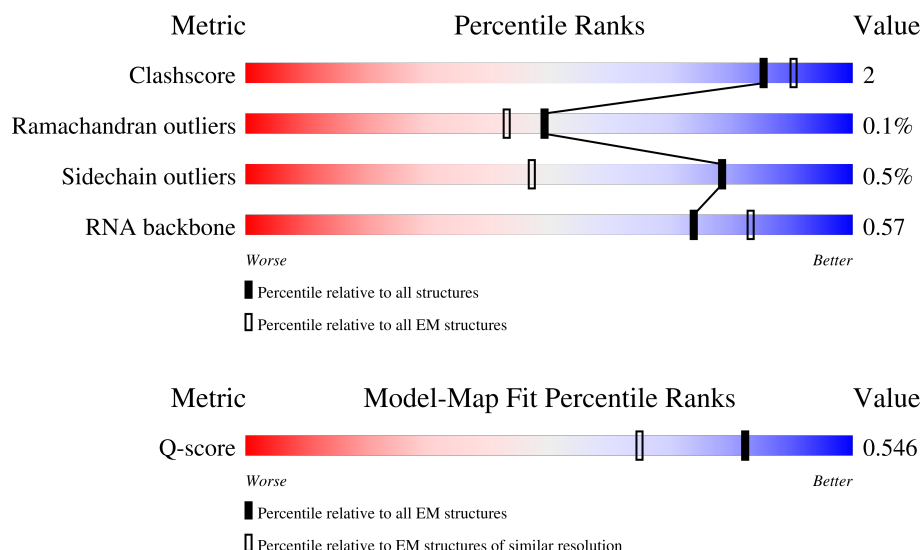
EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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 2.76 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	10642 (2.26 - 3.26)

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	1	62	5% 97% ..
2	2	69	90% 6% .
3	3	59	93% ..

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Mol	Chain	Length	Quality of chain
4	4	84	
5	5	57	
6	6	49	
7	7	45	
8	8	66	
9	9	37	
10	A	2923	
11	B	115	
12	C	186	
13	D	93	
14	G	277	
15	H	220	
16	I	207	
17	J	179	
18	K	178	
19	L	140	
20	M	145	
21	N	122	
22	O	146	
23	P	144	
24	Q	122	
25	R	119	
26	S	116	
27	T	118	
28	U	102	

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Mol	Chain	Length	Quality of chain
29	V	117	
30	W	91	
31	X	105	
32	Y	217	
33	Z	94	
34	a	1555	
35	b	24	
36	c	255	
37	d	217	
38	e	200	
39	f	166	
40	g	98	
41	h	156	
42	i	132	
43	j	132	
44	k	102	
45	l	129	
46	m	137	
47	n	121	
48	o	61	
49	p	89	
50	q	91	
51	r	87	
52	s	80	
53	t	92	

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Mol	Chain	Length	Quality of chain
54	u	83	 95%

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 142554 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	61	Total	C	N	O	S	0	0
			482	298	104	79	1		

- Molecule 2 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	65	Total	C	N	O	S	0	0
			535	329	100	105	1		

- Molecule 3 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	3	57	Total	C	N	O	0	0
			446	277	84	85		

- Molecule 4 is a protein called 50S ribosomal protein L31 type B.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	59	Total	C	N	O	S	0	0
			485	310	76	96	3		

- Molecule 5 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	53	Total	C	N	O	S	0	0
			422	256	86	75	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5	?	-	ARG	deletion	UNP Q2FZF1

- Molecule 6 is a protein called Large ribosomal subunit protein bL33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	48	Total	C	N	O	S	0	0
			402	245	79	73	5		

- Molecule 7 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	44	Total	C	N	O	S	0	0
			373	228	90	54	1		

- Molecule 8 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	8	65	Total	C	N	O	S	0	0
			531	330	115	84	2		

- Molecule 9 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	9	37	Total	C	N	O	S	0	0
			297	186	60	46	5		

- Molecule 10 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	A	2800	Total	C	N	O	P	0	0
			60048	26816	10994	19438	2800		

- Molecule 11 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	B	113	Total	C	N	O	P	0	0
			2408	1076	431	788	113		

- Molecule 12 is a protein called Ribosome-recycling factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	C	183	Total	C	N	O	S	0	0
			1419	866	255	293	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	GLY	-	expression tag	UNP Q2FZ21
C	-1	HIS	-	expression tag	UNP Q2FZ21

- Molecule 13 is a RNA chain called tRNA(Ser3).

Mol	Chain	Residues	Atoms						AltConf	Trace
13	D	93	Total	C	N	O	P	S	0	0
			2000	893	365	648	92	2		

- Molecule 14 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	G	273	Total	C	N	O	S		0	0
			2085	1297	413	370	5			

- Molecule 15 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	H	215	Total	C	N	O	S		0	0
			1628	1018	299	306	5			

- Molecule 16 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	I	205	Total	C	N	O	S		0	0
			1569	983	287	297	2			

- Molecule 17 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	J	177	Total	C	N	O	S		0	0
			1403	891	242	263	7			

- Molecule 18 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	K	177	Total	C	N	O	S		0	0
			1382	858	253	268	3			

- Molecule 19 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	L	136	Total	C	N	O	S	0	0
			1010	635	175	195	5		

- Molecule 20 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	M	145	Total	C	N	O	S	0	0
			1151	717	211	220	3		

- Molecule 21 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	N	122	Total	C	N	O	S	0	0
			920	572	174	170	4		

- Molecule 22 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	O	146	Total	C	N	O	S	0	0
			1099	680	215	203	1		

- Molecule 23 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	P	136	Total	C	N	O	S	0	0
			1089	698	206	181	4		

- Molecule 24 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Q	120	Total	C	N	O	S	0	0
			952	584	182	185	1		

- Molecule 25 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	R	119	Total	C	N	O	S	0	0
			922	574	174	173	1		

- Molecule 26 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	S	114	Total	C	N	O	0	0
			922	580	185	157		

- Molecule 27 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	T	117	Total	C	N	O	S	0	0
			953	599	191	159	4		

- Molecule 28 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	U	102	Total	C	N	O	S	0	0
			799	506	142	150	1		

- Molecule 29 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	V	111	Total	C	N	O	S	0	0
			853	532	163	155	3		

- Molecule 30 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	W	90	Total	C	N	O	S	0	0
			734	461	132	137	4		

- Molecule 31 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	X	102	Total	C	N	O	S	0	0
			787	497	144	144	2		

- Molecule 32 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Y	94	Total	C	N	O	S	0	0
			738	471	131	134	2		

- Molecule 33 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	Z	76	Total	C	N	O	0	0
			585	361	114	110		

- Molecule 34 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	a	1512	Total	C	N	O	P	0	0
			32401	14472	5916	10501	1512		

- Molecule 35 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	b	18	Total	C	N	O	P	0	0
			396	177	82	119	18		

- Molecule 36 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	c	221	Total	C	N	O	S	0	0
			1781	1136	310	328	7		

- Molecule 37 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	d	204	Total	C	N	O	S	0	0
			1609	1012	302	293	2		

- Molecule 38 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	e	199	Total	C	N	O	S	0	0
			1617	1020	302	293	2		

- Molecule 39 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	f	157	Total	C	N	O	S	0	0
			1169	735	214	218	2		

- Molecule 40 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	g	94	Total	C	N	O	S	0	0
			781	494	137	147	3		

- Molecule 41 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	h	146	Total	C	N	O	S	0	0
			1165	727	222	212	4		

- Molecule 42 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	i	131	Total	C	N	O	S	0	0
			1032	652	183	193	4		

- Molecule 43 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	j	128	Total	C	N	O	S	0	0
			1017	629	203	184	1		

- Molecule 44 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	k	98	Total	C	N	O	S	0	0
			783	494	143	145	1		

- Molecule 45 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	l	118	Total	C	N	O	S	0	0
			877	542	166	166	3		

- Molecule 46 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	m	135	Total	C	N	O	S	0	0
			1058	658	214	184	2		

- Molecule 47 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	n	114	Total	C	N	O	S	0	0
			909	559	180	169	1		

- Molecule 48 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	o	60	Total	C	N	O	S	0	0
			502	317	100	80	5		

- Molecule 49 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	p	86	Total	C	N	O	S	0	0
			721	445	148	127	1		

- Molecule 50 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	q	90	Total	C	N	O	S	0	0
			712	448	132	131	1		

- Molecule 51 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	r	81	Total	C	N	O	S	0	0
			671	424	121	125	1		

- Molecule 52 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	s	64	Total	C	N	O	S	0	0
			525	335	97	90	3		

- Molecule 53 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	t	83	Total	C	N	O	S	0	0
			672	432	122	116	2		

- Molecule 54 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	u	81	Total	C	N	O	S	0	0
			611	370	120	119	2		

- Molecule 55 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
55	5	1	Total	Zn	0
			1	1	
55	9	1	Total	Zn	0
			1	1	
55	o	1	Total	Zn	0
			1	1	

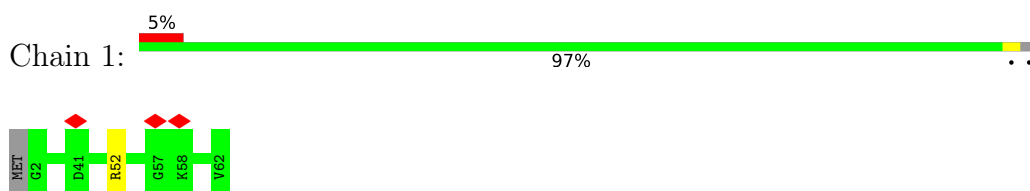
- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	A	94	Total	Mg	0
			94	94	
56	G	1	Total	Mg	0
			1	1	
56	a	18	Total	Mg	0
			18	18	

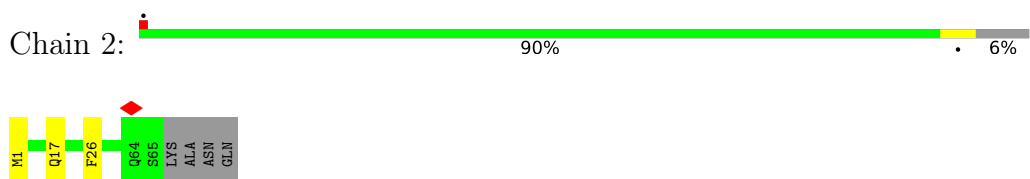
3 Residue-property plots [i](#)

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

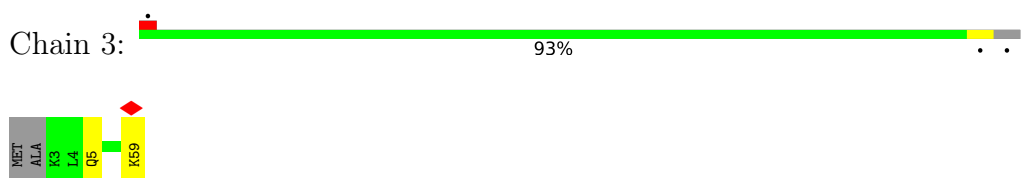
- Molecule 1: 50S ribosomal protein L28



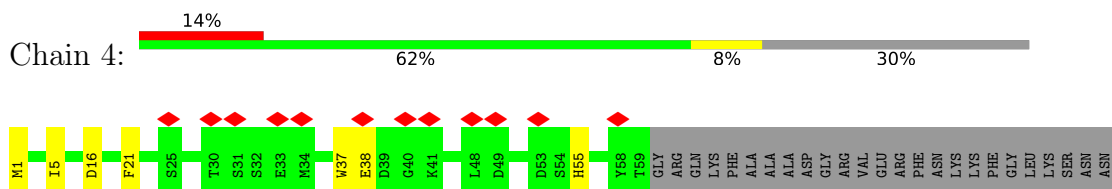
- Molecule 2: 50S ribosomal protein L29



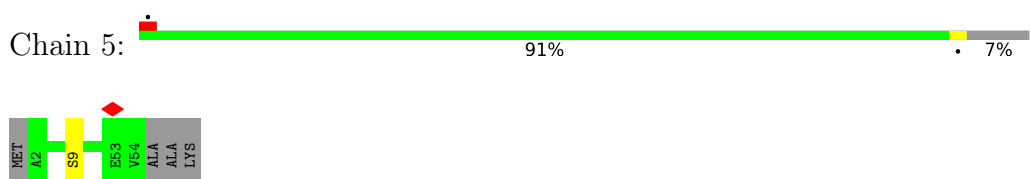
- Molecule 3: 50S ribosomal protein L30



- Molecule 4: 50S ribosomal protein L31 type B



- Molecule 5: Large ribosomal subunit protein bL32

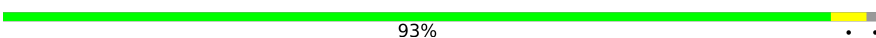


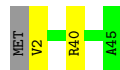
- Molecule 6: Large ribosomal subunit protein bL33A

Chain 6:  92% 6%

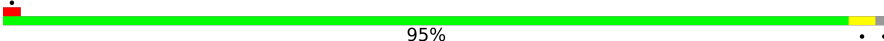


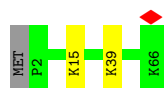
- Molecule 7: 50S ribosomal protein L34

Chain 7:  93%



- Molecule 8: 50S ribosomal protein L35

Chain 8:  95%



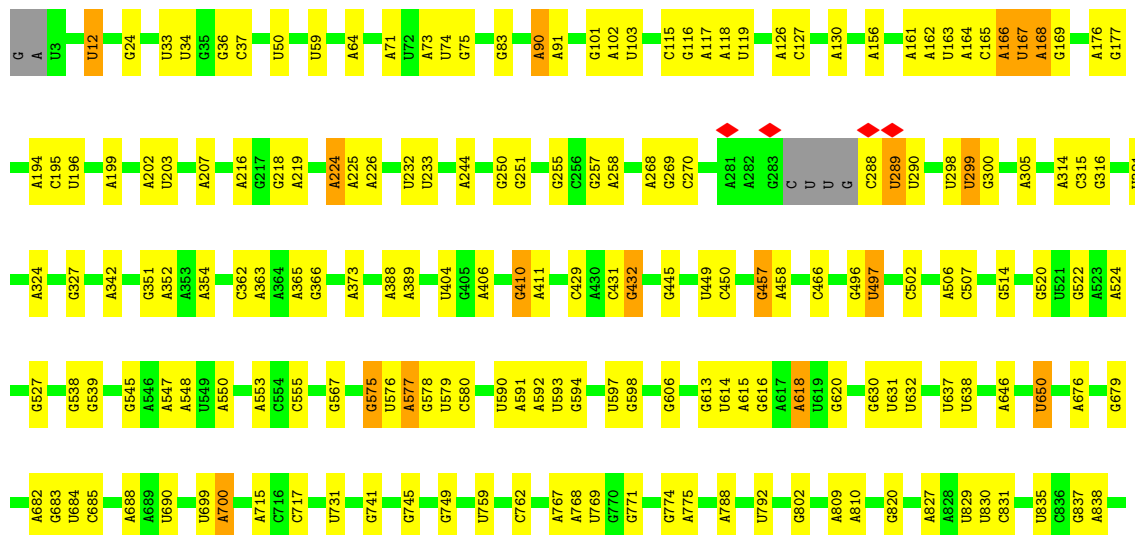
- Molecule 9: 50S ribosomal protein L36

Chain 9:  89% 11%

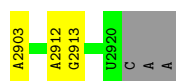


- Molecule 10: 23S rRNA

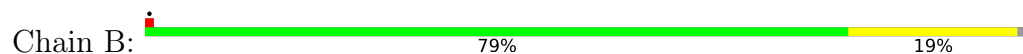
Chain A:  74% 19%



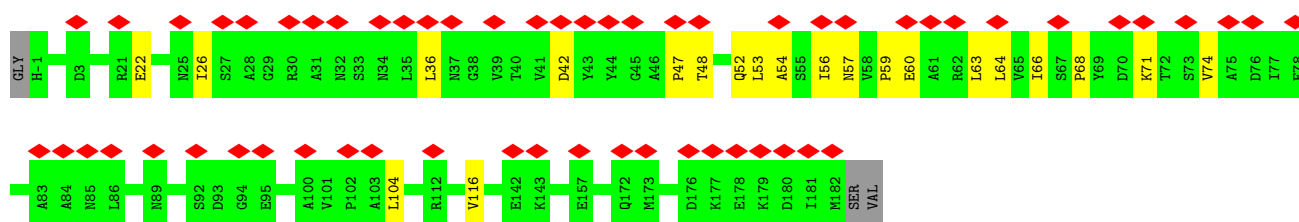
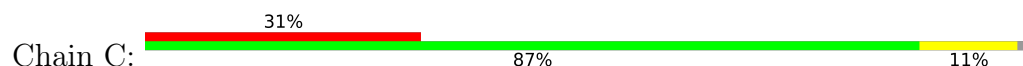
A2717	G2532	U2390	A2252	C2070	G1772	C1606	U1457	U1109	A946	A847
G2718	A2545	C2391	A2261	A2076	A1789	A1616	A1458	U1110	U947	G850
G2736	G2552	C2392	G2266	C2077	G1790	U1625	A1459	A1111	A955	G851
A2740	G2557	A2396	G2265	C2082	G1791	U1630	U1463	A1113	A956	G852
G2741	U2558	U2400	G2266	G2083	A1800	G1631	U1464	A1114	G853	G853
U2753	A2403	U2400	G2278	A2086	A1801	U1802	A1471	G1115	C960	G854
G2759	A2404	A2403	C2285	A2087	U1806	U1806	A1472	C1116	U856	U855
U2760	A2405	A2404	C2285	A2088	U1807	U1807	A1473	A1117	C957	C957
C2761	G2406	A2405	A2285	A2089	U1808	U1808	C1474	U1118	U862	G863
G2762	U2407	A2406	A2285	A2090	C1809	U1809	G1480	C1119	U871	U871
G2769	C2408	A2407	G2298	G2094	A1810	U1810	A1481	U1120	U872	U872
U2770	G2409	C2408	G2298	U2095	A1811	U1811	U1482	U1121	U873	U873
G2771	A2410	A2409	A2305	G2096	A1812	U1812	G1490	C1122	U884	U884
G2774	G2411	A2410	G2306	G2097	A1813	U1813	G1497	U1123	G901	G901
A2775	C2412	A2411	G2310	A2098	A1814	U1814	A1497	A1124	A902	A902
A2776	U2419	A2412	U2311	U2125	C1817	U1817	C1511	U1127	A903	A903
A2777	U2429	A2413	C2312	C	A1818	U1818	U1512	A1128	G904	G904
G2778	C2430	A2414	A2313	G	C1827	U1827	A1513	A1129	G907	G907
G2779	U2611	A2415	A2314	G	U1828	U1828	A1514	A1130	A908	A908
U2780	U2612	A2416	A2315	G	A1829	U1829	A1514	G1131	C910	C910
U2781	C2433	A2417	G2316	U2126	A1856	U1856	G1526	A1132	A911	A911
C2782	G2436	A2418	A2325	C	U1843	U1843	A1533	G1133	C912	C912
U2783	U2450	A2419	G2326	G	G1844	U1844	A1536	U1134	G914	G914
A2784	C2637	A2420	G2330	U2020	U1845	U1845	A1537	A1135	A920	A920
A2791	U2451	A2421	C2331	G2026	A1856	U1856	U1540	A1155	C921	C921
A2792	A2452	A2422	U2332	C2026	A1874	U1874	U1546	G1156	A923	A923
G2793	G2453	A2423	U2333	G2037	A1875	U1875	C1547	A1170	G924	G924
U2805	G2454	A2424	U2334	A2040	A1880	U1880	A1546	A1171	G	G
U2806	G2455	A2425	G2335	A2047	A1881	U1881	C1547	A1172	G	G
G2807	A2456	A2426	G2335	A2057	U1887	U1887	U1552	U1174	C	C
C2816	U2457	A2427	A2338	A2058	C1898	U1898	A1553	A1175	C	C
U2824	A2461	A2428	U2339	A2059	U1899	U1899	A1560	G1176	C	C
U2825	C2468	A2429	C2340	G2052	U1909	U1909	A1569	A1177	U	U
U2826	G2472	A2430	A2347	C2053	C1909	U1909	G1572	C1178	C	C
U2827	A2475	A2431	A2348	C2054	A1916	U1916	A1578	U1179	C	C
U2828	U2476	A2432	A2349	G2054	A1927	U1927	C1579	U1185	U	U
U2851	C2479	A2433	A2354	A2057	G1932	U1932	A	A1186	C	C
U2852	A2480	A2434	A2355	A2058	G1933	U1933	U	C1197	C	C
G2872	U2481	A2435	A2356	A2059	U1937	U1937	U	A1090	U	U
C2873	A2496	A2436	A2357	A2060	U1938	U1938	G	G1091	U	U
U2887	U2518	A2437	U2370	U2061	A1939	U1939	G1585	A1101	A	A
A2888	C2526	A2438	A2372	G2062	A1940	U1940	U	U1215	C942	C942
G2892	U2531	A2439	A2373	C2063	A1941	U1941	U	U1216	C943	C943
A2893	G2529	A2440	A2374	A	A1942	U1942	G1586	U1217	G944	G944
C2894	U2532	A2441	C2377	A	A1943	U1943	U1601	C1107	A945	A945
U2716	U2533	A2442	G2378	A	A1944	U1944	U	C1108		



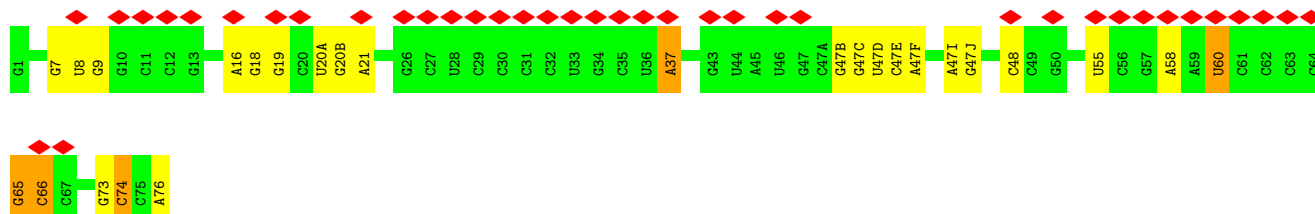
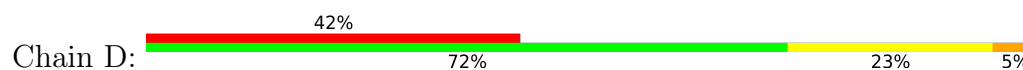
• Molecule 11: 5S rRNA



• Molecule 12: Ribosome-recycling factor



• Molecule 13: tRNA(Ser3)



• Molecule 14: 50S ribosomal protein L2



• Molecule 15: 50S ribosomal protein L3

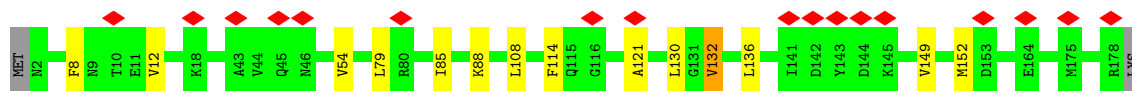


• Molecule 16: 50S ribosomal protein L4

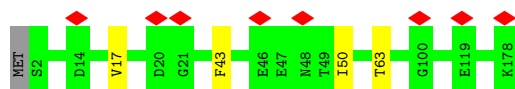




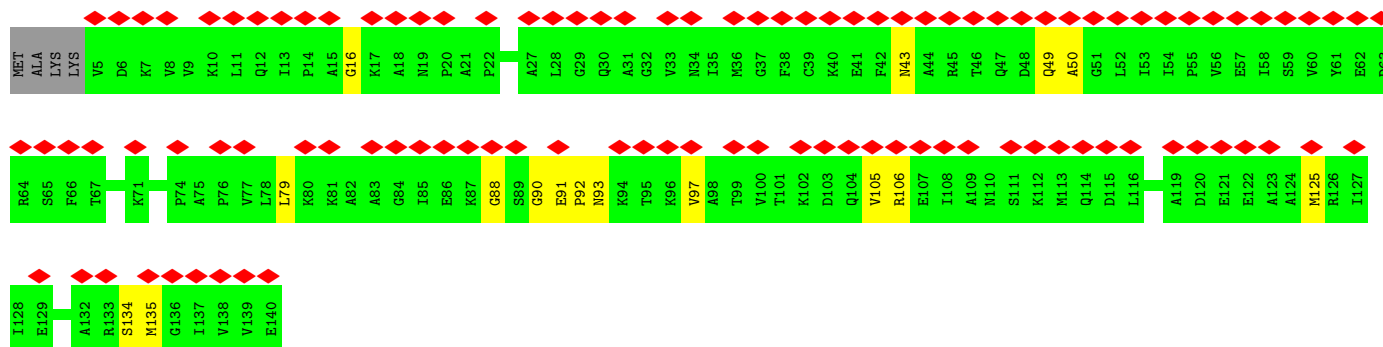
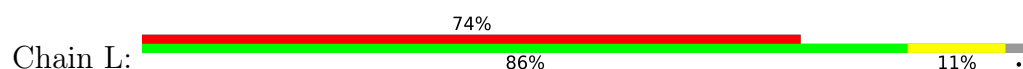
- Molecule 17: 50S ribosomal protein L5



- Molecule 18: Large ribosomal subunit protein uL6



- Molecule 19: Large ribosomal subunit protein uL11



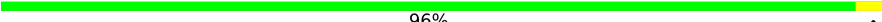
- Molecule 20: 50S ribosomal protein L13

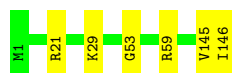


- Molecule 21: 50S ribosomal protein L14



- Molecule 22: 50S ribosomal protein L15

Chain O:  96% .



- Molecule 23: 50S ribosomal protein L16

Chain P:  89% 6% 6%



- Molecule 24: 50S ribosomal protein L17

Chain Q:  90% 8% .

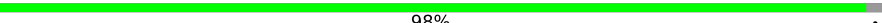


- Molecule 25: 50S ribosomal protein L18

Chain R:  98% .



- Molecule 26: 50S ribosomal protein L19

Chain S:  98% .

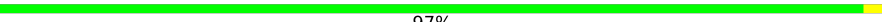


- Molecule 27: 50S ribosomal protein L20

Chain T:  95% . .



- Molecule 28: 50S ribosomal protein L21

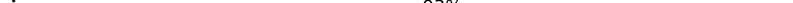
Chain U:  97% .



- Molecule 29: 50S ribosomal protein L22

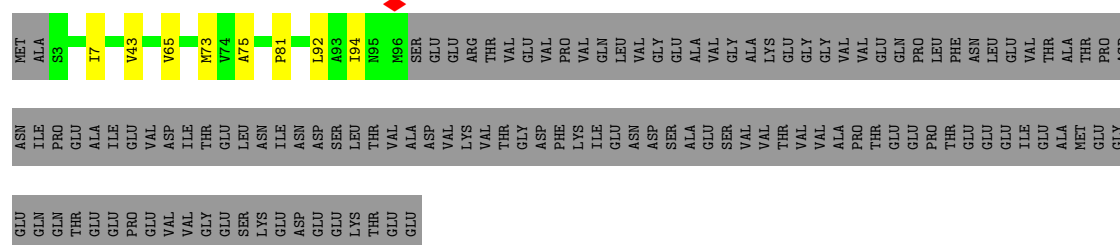
M1	R11	P14	A42	Y62 D63	E78	R88	R92	K111	GLU	GLU	ALA	LYS	GLU	ALA
----	-----	-----	-----	------------	-----	-----	-----	------	-----	-----	-----	-----	-----	-----

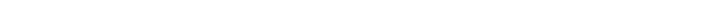
-

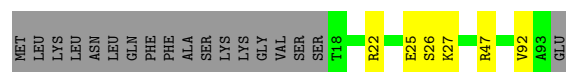
- Chain X:  5% 93% ..

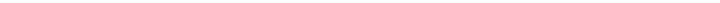


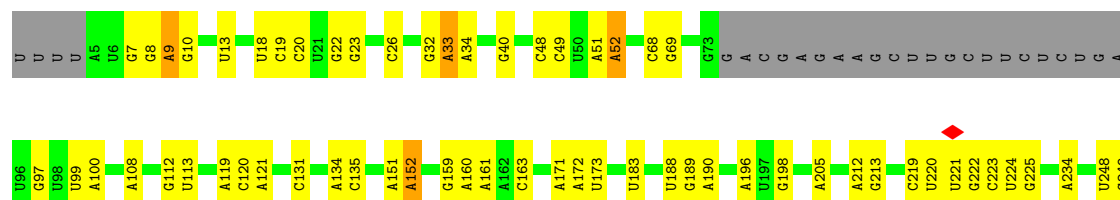
- Chain Y:  40% 1% 57%

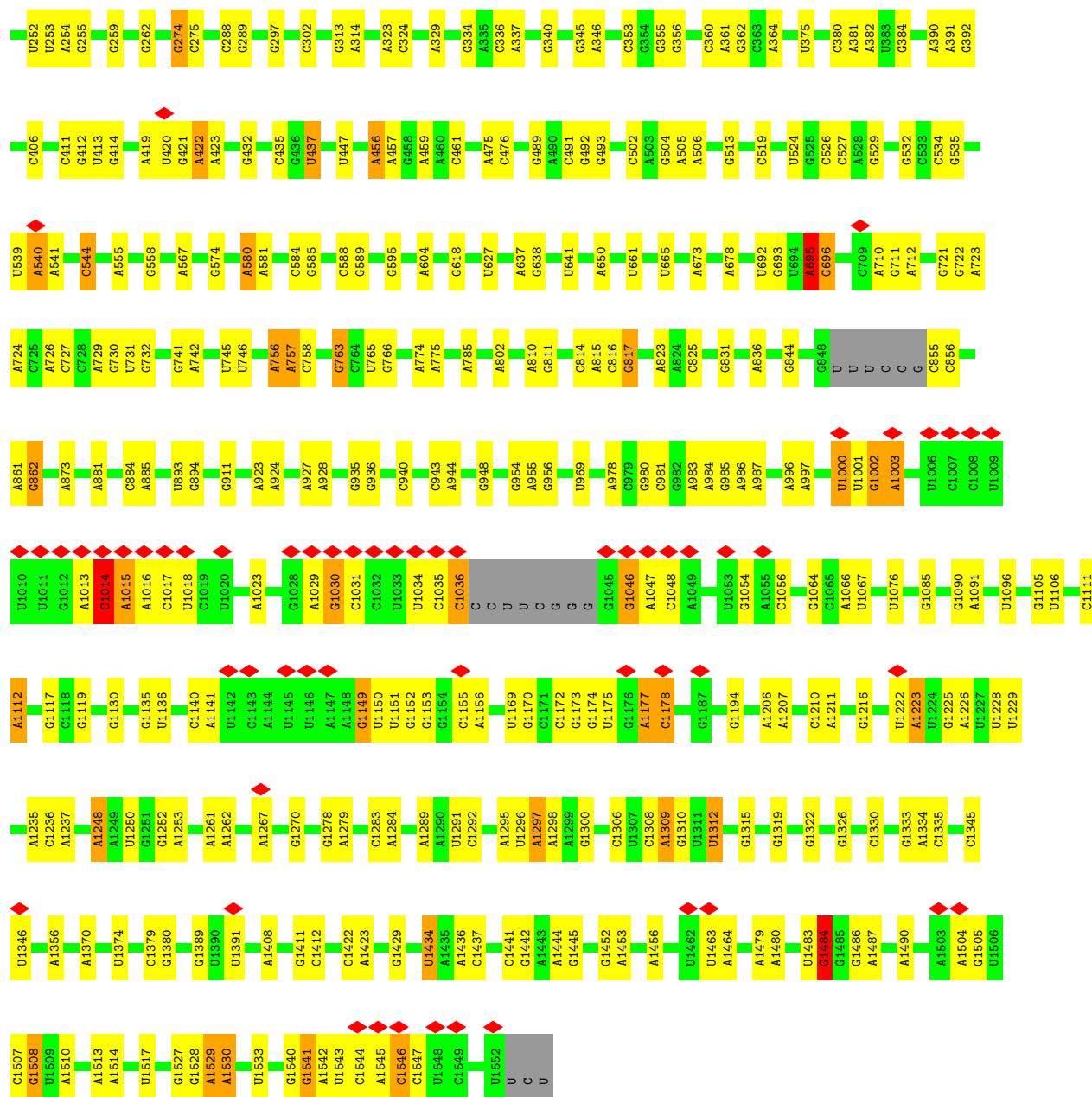


- Chain Z:  74% 6% 19%

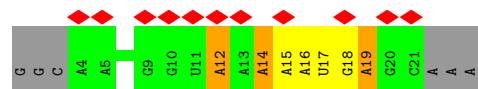


- Chain a:  72% 23%

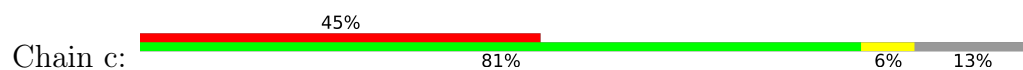


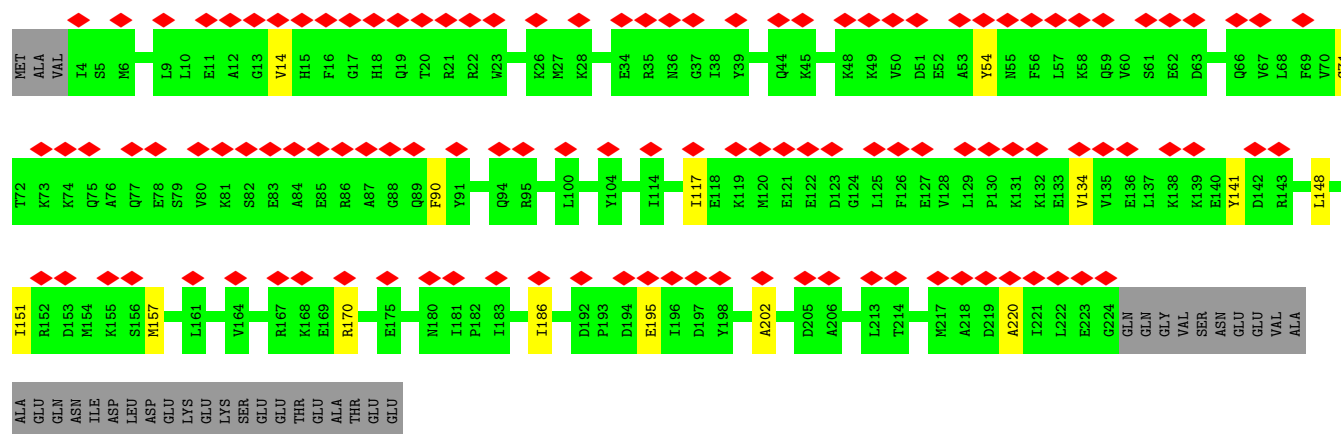


• Molecule 35: mRNA

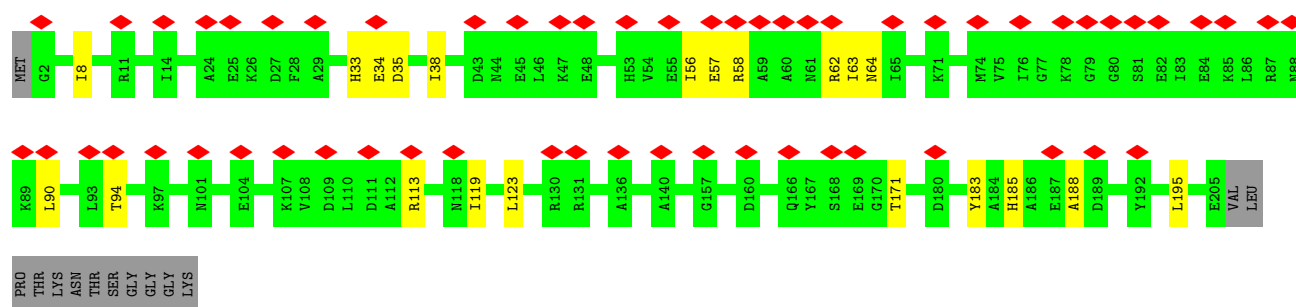
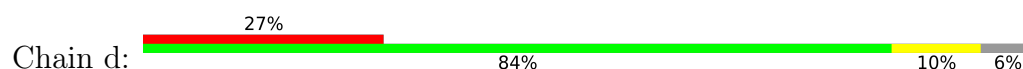


• Molecule 36: 30S ribosomal protein S2

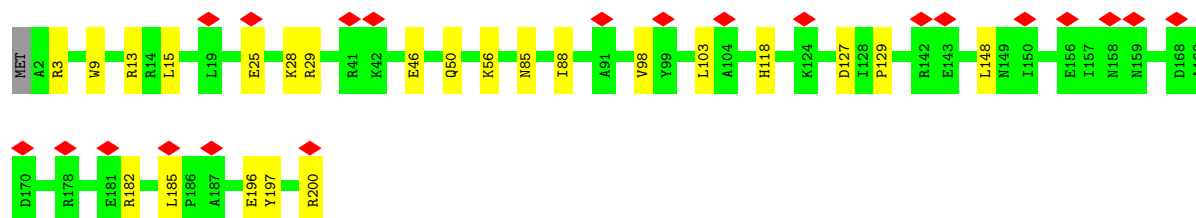
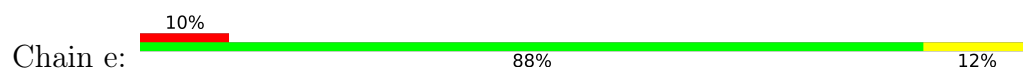




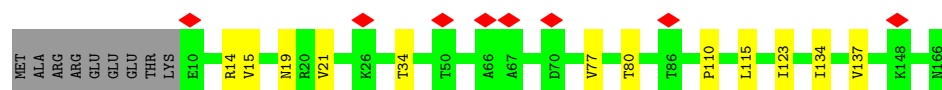
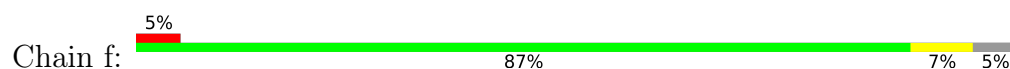
• Molecule 37: 30S ribosomal protein S3



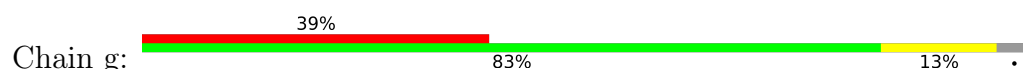
• Molecule 38: 30S ribosomal protein S4

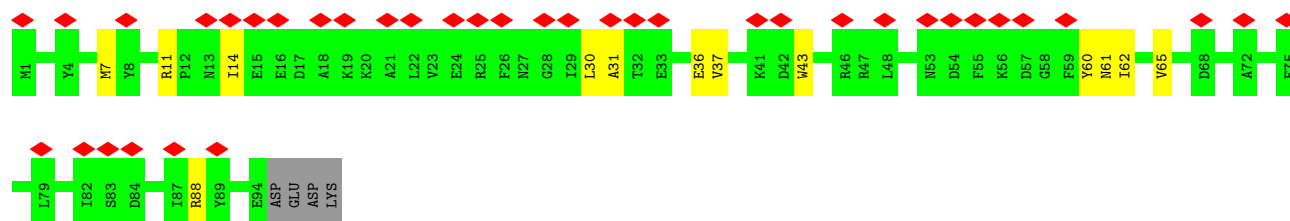


• Molecule 39: 30S ribosomal protein S5



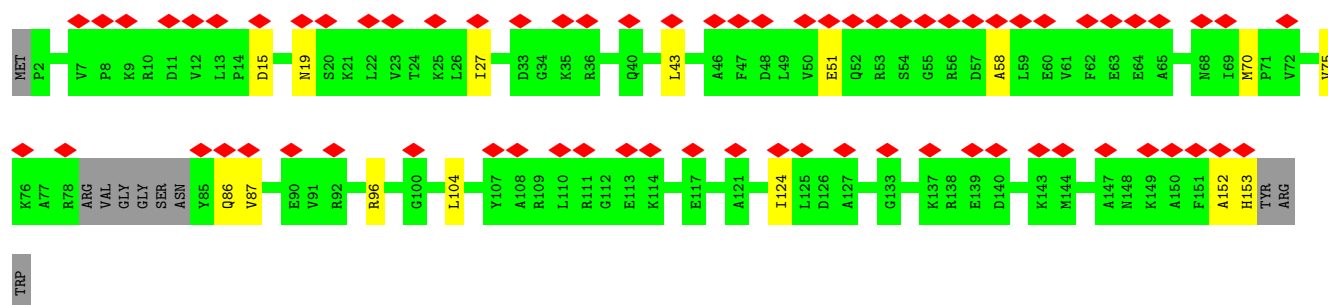
• Molecule 40: 30S ribosomal protein S6





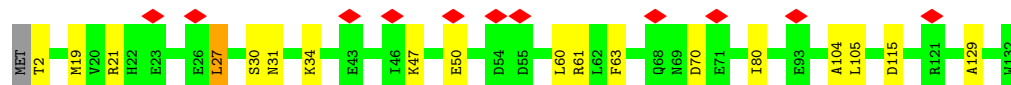
• Molecule 41: 30S ribosomal protein S7

Chain h:



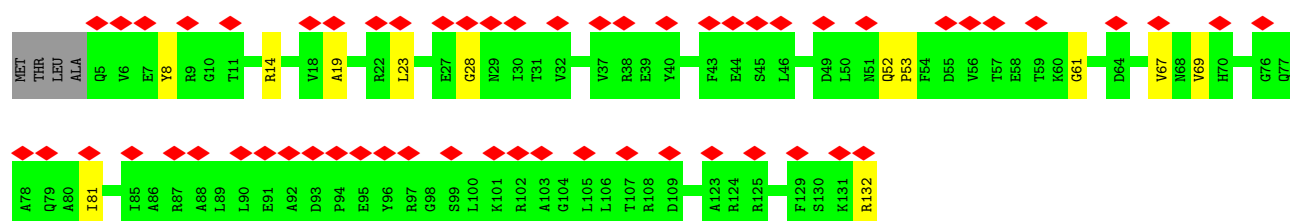
• Molecule 42: 30S ribosomal protein S8

Chain i:



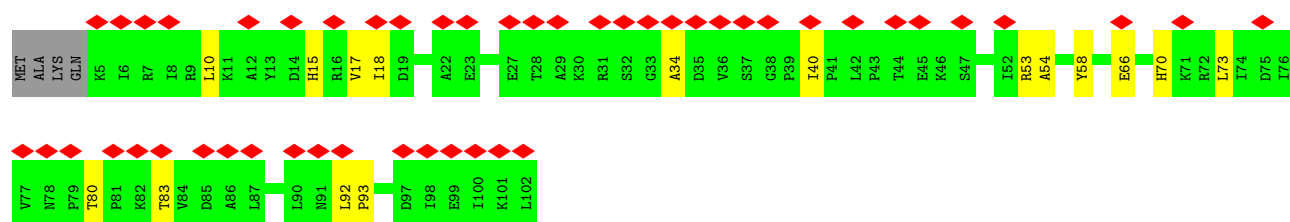
• Molecule 43: 30S ribosomal protein S9

Chain j:

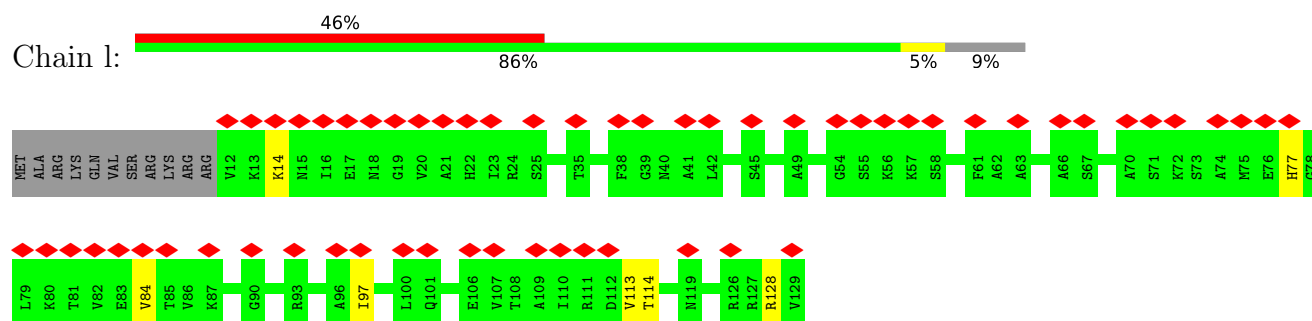


• Molecule 44: Small ribosomal subunit protein uS10

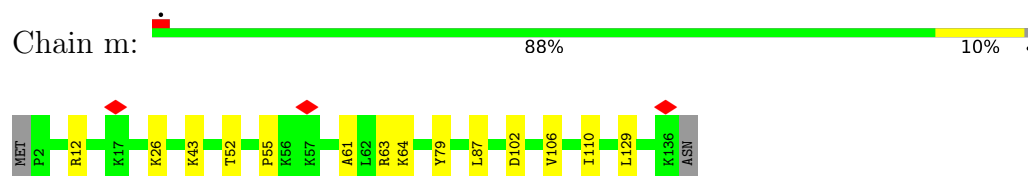
Chain k:



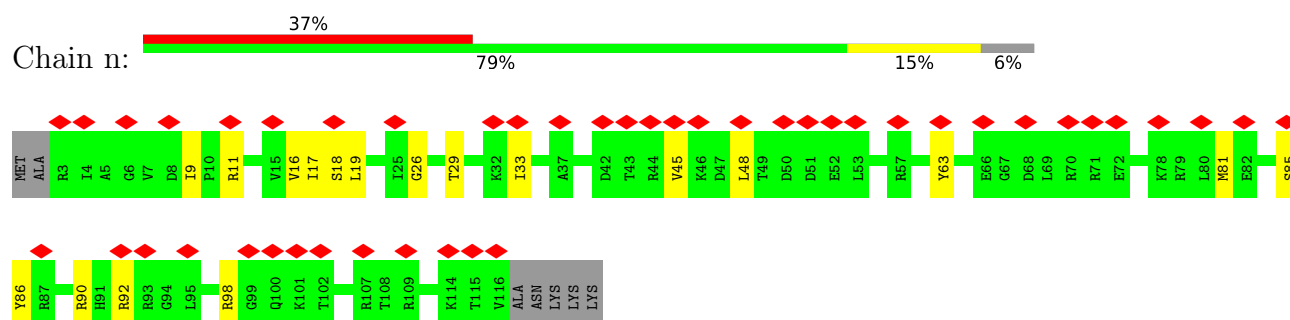
- Molecule 45: 30S ribosomal protein S11



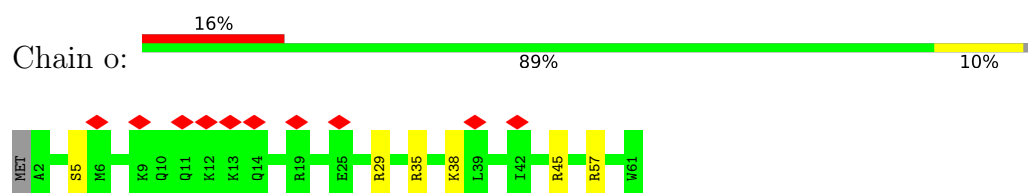
- Molecule 46: 30S ribosomal protein S12



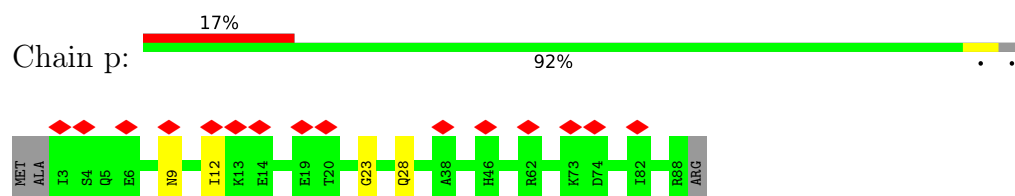
- Molecule 47: 30S ribosomal protein S13



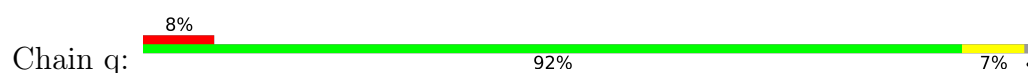
- Molecule 48: 30S ribosomal protein S14 type Z

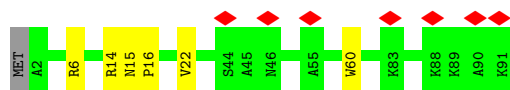


- Molecule 49: 30S ribosomal protein S15

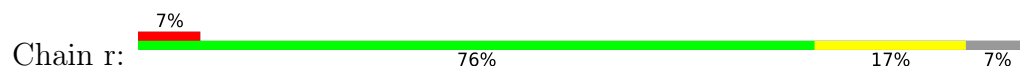


- Molecule 50: 30S ribosomal protein S16

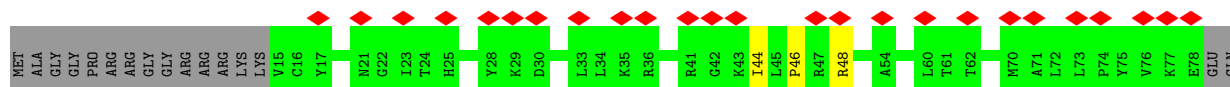
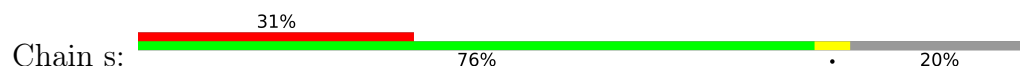




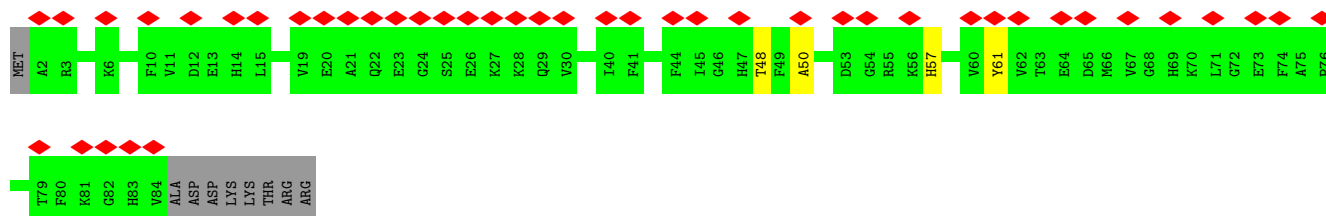
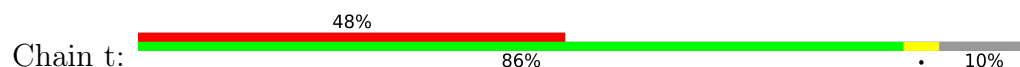
- Molecule 51: 30S ribosomal protein S17



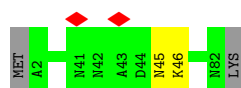
- Molecule 52: 30S ribosomal protein S18



- Molecule 53: 30S ribosomal protein S19



- Molecule 54: 30S ribosomal protein S20



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	24569	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1000	Depositor
Magnification	165000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	31.280	Depositor
Minimum map value	-18.021	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.974	Depositor
Recommended contour level	2.2	Depositor
Map size (Å)	403.19998, 403.19998, 403.19998	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.672, 0.672, 0.672	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 3TD, H2U, 2MA, OMG, G7M, MG, 4OC, MA6, T6A, 2MG, UR3, ZN, 5MC, 5MU, 4SU, PSU, RSP

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	1	0.49	0/488	0.82	0/649
2	2	0.44	0/536	1.04	0/713
3	3	0.49	0/448	0.99	0/601
4	4	0.51	0/499	0.90	0/674
5	5	0.51	0/429	0.86	0/571
6	6	0.47	0/407	0.88	0/545
7	7	0.50	0/377	0.98	0/491
8	8	0.49	0/536	0.89	0/701
9	9	0.52	0/300	0.85	0/393
10	A	0.52	0/67024	0.82	30/104521 (0.0%)
11	B	0.55	0/2692	0.77	0/4193
12	C	0.48	0/1428	1.04	0/1922
13	D	0.59	2/2088 (0.1%)	0.77	0/3255
14	G	0.51	0/2120	0.88	0/2847
15	H	0.50	0/1652	0.88	0/2216
16	I	0.48	0/1592	0.92	0/2148
17	J	0.47	0/1421	0.96	0/1907
18	K	0.49	0/1400	0.92	0/1881
19	L	0.53	0/1024	1.01	0/1384
20	M	0.48	0/1173	0.86	0/1578
21	N	0.49	0/927	0.89	0/1243
22	O	0.50	0/1113	0.90	0/1482
23	P	0.49	0/1113	0.89	0/1493
24	Q	0.45	0/956	0.94	0/1277
25	R	0.48	0/931	0.95	0/1244
26	S	0.50	0/934	0.85	0/1249
27	T	0.47	0/965	0.99	0/1276
28	U	0.47	0/809	0.83	0/1080
29	V	0.50	0/861	0.89	0/1159
30	W	0.47	0/742	0.91	0/989
31	X	0.51	0/796	0.91	0/1063

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Y	0.47	0/746	0.90	0/1000
33	Z	0.48	0/591	0.89	0/785
34	a	0.55	1/36095 (0.0%)	0.78	5/56278 (0.0%)
35	b	0.58	0/446	0.81	0/695
36	c	0.48	0/1808	1.02	0/2426
37	d	0.48	0/1631	0.94	0/2190
38	e	0.49	0/1647	0.96	0/2211
39	f	0.51	0/1183	0.92	0/1595
40	g	0.46	0/792	0.94	0/1062
41	h	0.49	0/1181	1.04	0/1587
42	i	0.49	0/1044	0.95	0/1401
43	j	0.50	0/1033	0.92	0/1386
44	k	0.51	0/795	0.96	0/1071
45	l	0.54	0/892	0.94	0/1203
46	m	0.52	0/1075	0.86	0/1439
47	n	0.49	0/916	1.07	0/1228
48	o	0.50	0/512	0.93	0/678
49	p	0.47	0/730	1.03	0/975
50	q	0.50	0/723	0.95	0/971
51	r	0.47	0/679	0.90	1/907 (0.1%)
52	s	0.49	0/534	1.01	0/716
53	t	0.50	0/690	0.96	0/926
54	u	0.46	0/611	1.07	0/817
All	All	0.52	3/154135 (0.0%)	0.84	36/230292 (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
14	G	0	1
29	V	0	1
37	d	0	1
39	f	0	1
40	g	0	1
43	j	0	2
46	m	0	1
51	r	0	1
All	All	0	9

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	a	535	G7M	O3'-P	5.14	1.61	1.56
13	D	37	T6A	O3'-P	5.03	1.61	1.56
13	D	8	4SU	O3'-P	5.02	1.61	1.56

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	a	1484	G	O3'-P-O5'	-7.74	92.38	104.00
10	A	2673	C	O3'-P-O5'	-7.50	92.75	104.00
10	A	299	U	O3'-P-O5'	-6.70	93.95	104.00
10	A	1962	G	O3'-P-O5'	-6.59	94.12	104.00
10	A	207	A	O3'-P-O5'	-6.33	94.50	104.00

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
14	G	13	ARG	Sidechain
29	V	92	ARG	Sidechain
37	d	62	ARG	Sidechain
39	f	14	ARG	Sidechain
40	g	88	ARG	Sidechain

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	1	482	0	523	2	0
2	2	535	0	566	2	0
3	3	446	0	486	1	0
4	4	485	0	458	4	0
5	5	422	0	426	1	0
6	6	402	0	413	2	0
7	7	373	0	420	2	0
8	8	531	0	599	2	0
9	9	297	0	339	2	0
10	A	60048	0	30201	192	0
11	B	2408	0	1218	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	C	1419	0	1450	11	0
13	D	2000	0	1020	8	0
14	G	2085	0	2192	6	0
15	H	1628	0	1667	5	0
16	I	1569	0	1614	5	0
17	J	1403	0	1457	8	0
18	K	1382	0	1415	2	0
19	L	1010	0	1047	20	0
20	M	1151	0	1145	1	0
21	N	920	0	981	4	0
22	O	1099	0	1142	3	0
23	P	1089	0	1155	5	0
24	Q	952	0	999	7	0
25	R	922	0	968	1	0
26	S	922	0	994	0	0
27	T	953	0	1027	3	0
28	U	799	0	836	2	0
29	V	853	0	914	5	0
30	W	734	0	767	3	0
31	X	787	0	853	2	0
32	Y	738	0	787	6	0
33	Z	585	0	597	4	0
34	a	32401	0	16329	130	0
35	b	396	0	197	4	0
36	c	1781	0	1844	8	0
37	d	1609	0	1668	11	0
38	e	1617	0	1646	15	0
39	f	1169	0	1229	6	0
40	g	781	0	784	4	0
41	h	1165	0	1204	8	0
42	i	1032	0	1082	11	0
43	j	1017	0	1039	5	0
44	k	783	0	825	9	0
45	l	877	0	895	4	0
46	m	1058	0	1130	8	0
47	n	909	0	959	11	0
48	o	502	0	523	6	0
49	p	721	0	751	2	0
50	q	712	0	744	4	0
51	r	671	0	708	8	0
52	s	525	0	554	2	0
53	t	672	0	677	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
54	u	611	0	655	1	0
55	5	1	0	0	0	0
55	9	1	0	0	0	0
55	o	1	0	0	0	0
56	A	94	0	0	0	0
56	G	1	0	0	0	0
56	a	18	0	0	0	0
All	All	142554	0	96119	505	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 2.

The worst 5 of 505 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)
10:A:1120:C:O2'	19:L:91:GLU:HA	1.69	0.90
19:L:79:LEU:HD23	19:L:135:MET:SD	2.20	0.81
10:A:1120:C:O2'	19:L:92:PRO:HD2	1.81	0.81
47:n:11:ARG:HA	47:n:45:VAL:HB	1.63	0.80
44:k:34:ALA:HB2	44:k:83:THR:HG21	1.74	0.70

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1	59/62 (95%)	58 (98%)	1 (2%)	0	100	100
2	2	63/69 (91%)	63 (100%)	0	0	100	100
3	3	55/59 (93%)	54 (98%)	1 (2%)	0	100	100
4	4	57/84 (68%)	56 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	5	51/57 (90%)	49 (96%)	2 (4%)	0	100	100
6	6	46/49 (94%)	46 (100%)	0	0	100	100
7	7	42/45 (93%)	41 (98%)	1 (2%)	0	100	100
8	8	63/66 (96%)	62 (98%)	1 (2%)	0	100	100
9	9	35/37 (95%)	35 (100%)	0	0	100	100
12	C	181/186 (97%)	179 (99%)	2 (1%)	0	100	100
14	G	271/277 (98%)	265 (98%)	6 (2%)	0	100	100
15	H	213/220 (97%)	206 (97%)	7 (3%)	0	100	100
16	I	203/207 (98%)	200 (98%)	3 (2%)	0	100	100
17	J	175/179 (98%)	172 (98%)	3 (2%)	0	100	100
18	K	175/178 (98%)	169 (97%)	6 (3%)	0	100	100
19	L	134/140 (96%)	130 (97%)	4 (3%)	0	100	100
20	M	143/145 (99%)	140 (98%)	3 (2%)	0	100	100
21	N	120/122 (98%)	113 (94%)	7 (6%)	0	100	100
22	O	144/146 (99%)	138 (96%)	5 (4%)	1 (1%)	18	34
23	P	134/144 (93%)	132 (98%)	2 (2%)	0	100	100
24	Q	118/122 (97%)	114 (97%)	4 (3%)	0	100	100
25	R	117/119 (98%)	113 (97%)	4 (3%)	0	100	100
26	S	112/116 (97%)	111 (99%)	1 (1%)	0	100	100
27	T	115/118 (98%)	115 (100%)	0	0	100	100
28	U	100/102 (98%)	98 (98%)	2 (2%)	0	100	100
29	V	109/117 (93%)	108 (99%)	1 (1%)	0	100	100
30	W	88/91 (97%)	87 (99%)	1 (1%)	0	100	100
31	X	100/105 (95%)	95 (95%)	5 (5%)	0	100	100
32	Y	92/217 (42%)	88 (96%)	4 (4%)	0	100	100
33	Z	74/94 (79%)	70 (95%)	4 (5%)	0	100	100
36	c	219/255 (86%)	211 (96%)	7 (3%)	1 (0%)	24	43
37	d	202/217 (93%)	190 (94%)	12 (6%)	0	100	100
38	e	197/200 (98%)	194 (98%)	3 (2%)	0	100	100
39	f	155/166 (93%)	150 (97%)	5 (3%)	0	100	100
40	g	92/98 (94%)	90 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	h	142/156 (91%)	141 (99%)	1 (1%)	0	100	100
42	i	129/132 (98%)	124 (96%)	5 (4%)	0	100	100
43	j	126/132 (96%)	119 (94%)	7 (6%)	0	100	100
44	k	96/102 (94%)	94 (98%)	2 (2%)	0	100	100
45	l	116/129 (90%)	107 (92%)	9 (8%)	0	100	100
46	m	133/137 (97%)	130 (98%)	3 (2%)	0	100	100
47	n	112/121 (93%)	107 (96%)	5 (4%)	0	100	100
48	o	58/61 (95%)	58 (100%)	0	0	100	100
49	p	84/89 (94%)	82 (98%)	2 (2%)	0	100	100
50	q	88/91 (97%)	84 (96%)	4 (4%)	0	100	100
51	r	79/87 (91%)	75 (95%)	3 (4%)	1 (1%)	9	18
52	s	62/80 (78%)	61 (98%)	1 (2%)	0	100	100
53	t	81/92 (88%)	80 (99%)	1 (1%)	0	100	100
54	u	79/83 (95%)	78 (99%)	1 (1%)	0	100	100
All	All	5639/6101 (92%)	5482 (97%)	154 (3%)	3 (0%)	49	71

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
22	O	29	LYS
36	c	71	GLY
51	r	68	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	
1	1	51/52 (98%)	51 (100%)	0	100	100
2	2	59/62 (95%)	59 (100%)	0	100	100
3	3	52/53 (98%)	52 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	4	56/75 (75%)	55 (98%)	1 (2%)	51	71
5	5	48/50 (96%)	48 (100%)	0	100	100
6	6	46/47 (98%)	46 (100%)	0	100	100
7	7	39/40 (98%)	39 (100%)	0	100	100
8	8	56/57 (98%)	56 (100%)	0	100	100
9	9	35/35 (100%)	35 (100%)	0	100	100
12	C	160/162 (99%)	158 (99%)	2 (1%)	61	76
14	G	220/224 (98%)	220 (100%)	0	100	100
15	H	173/177 (98%)	172 (99%)	1 (1%)	78	88
16	I	168/169 (99%)	167 (99%)	1 (1%)	78	88
17	J	156/158 (99%)	154 (99%)	2 (1%)	61	76
18	K	154/155 (99%)	153 (99%)	1 (1%)	78	88
19	L	108/111 (97%)	107 (99%)	1 (1%)	70	82
20	M	123/123 (100%)	123 (100%)	0	100	100
21	N	100/100 (100%)	100 (100%)	0	100	100
22	O	112/112 (100%)	111 (99%)	1 (1%)	70	82
23	P	113/119 (95%)	113 (100%)	0	100	100
24	Q	101/102 (99%)	101 (100%)	0	100	100
25	R	95/95 (100%)	94 (99%)	1 (1%)	65	79
26	S	100/102 (98%)	100 (100%)	0	100	100
27	T	97/98 (99%)	97 (100%)	0	100	100
28	U	86/86 (100%)	86 (100%)	0	100	100
29	V	90/94 (96%)	89 (99%)	1 (1%)	65	79
30	W	81/82 (99%)	81 (100%)	0	100	100
31	X	87/90 (97%)	87 (100%)	0	100	100
32	Y	83/190 (44%)	83 (100%)	0	100	100
33	Z	59/75 (79%)	58 (98%)	1 (2%)	53	71
36	c	192/221 (87%)	191 (100%)	1 (0%)	81	89
37	d	165/175 (94%)	164 (99%)	1 (1%)	78	88
38	e	174/175 (99%)	173 (99%)	1 (1%)	78	88
39	f	123/131 (94%)	122 (99%)	1 (1%)	73	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	g	82/86 (95%)	78 (95%)	4 (5%)	22	43
41	h	124/132 (94%)	124 (100%)	0	100	100
42	i	112/113 (99%)	111 (99%)	1 (1%)	70	82
43	j	106/109 (97%)	106 (100%)	0	100	100
44	k	88/91 (97%)	87 (99%)	1 (1%)	65	79
45	l	94/104 (90%)	94 (100%)	0	100	100
46	m	117/119 (98%)	117 (100%)	0	100	100
47	n	99/104 (95%)	98 (99%)	1 (1%)	68	81
48	o	52/53 (98%)	52 (100%)	0	100	100
49	p	79/81 (98%)	79 (100%)	0	100	100
50	q	76/77 (99%)	76 (100%)	0	100	100
51	r	76/82 (93%)	76 (100%)	0	100	100
52	s	57/68 (84%)	57 (100%)	0	100	100
53	t	72/80 (90%)	72 (100%)	0	100	100
54	u	67/69 (97%)	67 (100%)	0	100	100
All	All	4863/5165 (94%)	4839 (100%)	24 (0%)	78	89

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
37	d	90	LEU
40	g	36	GLU
39	f	15	VAL
40	g	43	TRP
17	J	132	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 47 such sidechains are listed below:

Mol	Chain	Res	Type
32	Y	38	ASN
40	g	77	GLN
36	c	93	ASN
38	e	149	ASN
41	h	153	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	2796/2923 (95%)	384 (13%)	79 (2%)
11	B	112/115 (97%)	15 (13%)	5 (4%)
13	D	92/93 (98%)	13 (14%)	2 (2%)
34	a	1508/1555 (96%)	233 (15%)	0
35	b	17/24 (70%)	5 (29%)	0
All	All	4525/4710 (96%)	650 (14%)	86 (1%)

5 of 650 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
10	A	12	U
10	A	33	U
10	A	34	U
10	A	64	A
10	A	71	A

5 of 86 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
10	A	1945	A
10	A	2777	A
10	A	2094	G
10	A	2409	G
10	A	2816	C

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

22 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
10	2MA	A	2530	10,56	22,25,26	0.24	0	33,37,40	0.71	1 (3%)
34	5MC	a	976	34	18,22,23	0.33	0	26,32,35	0.51	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
10	G7M	A	2601	10,56	23,26,27	0.70	1 (4%)	35,39,42	0.54	0
10	H2U	A	2476	10	18,21,22	0.62	0	21,30,33	0.74	1 (4%)
34	MA6	a	1530	34	23,26,27	0.28	0	34,38,41	0.65	1 (2%)
10	2MG	A	2472	10	23,26,27	0.37	0	32,38,41	0.35	0
13	5MU	D	54	13	19,22,23	0.27	0	28,32,35	0.27	0
34	4OC	a	1412	34	20,23,24	0.38	0	26,32,35	0.49	0
13	H2U	D	20(A)	13	18,21,22	0.64	0	21,30,33	0.90	1 (4%)
34	2MG	a	975	34	23,26,27	0.39	0	32,38,41	0.36	0
13	4SU	D	8	13	18,21,22	0.40	0	26,30,33	1.13	3 (11%)
13	PSU	D	55	13	18,21,22	0.92	1 (5%)	22,30,33	0.56	0
34	UR3	a	1509	34	19,22,23	0.31	0	26,32,35	0.67	0
10	3TD	A	1942	10	18,22,23	0.97	1 (5%)	22,32,35	0.92	0
34	MA6	a	1529	34	23,26,27	0.25	0	34,38,41	0.67	1 (2%)
13	T6A	D	37	13,35	31,34,35	0.48	0	44,49,52	0.65	1 (2%)
10	5MU	A	1966	10	19,22,23	0.32	0	28,32,35	0.37	0
34	G7M	a	535	34	23,26,27	0.71	1 (4%)	35,39,42	0.57	0
13	RSP	D	32	13	17,21,22	0.39	0	22,30,33	0.61	0
10	OMG	A	2580	10	23,26,27	0.33	0	33,38,41	0.38	0
10	5MU	A	792	10	19,22,23	0.25	0	28,32,35	0.39	0
10	OMG	A	2278	10	23,26,27	0.33	0	33,38,41	0.52	1 (3%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
10	2MA	A	2530	10,56	-	2/7/25/26	0/3/3/3
34	5MC	a	976	34	-	0/7/25/26	0/2/2/2
10	G7M	A	2601	10,56	-	0/7/25/26	0/3/3/3
10	H2U	A	2476	10	-	0/7/38/39	0/2/2/2
34	MA6	a	1530	34	-	3/11/29/30	0/3/3/3
10	2MG	A	2472	10	-	0/9/27/28	0/3/3/3
13	5MU	D	54	13	-	0/7/25/26	0/2/2/2
34	4OC	a	1412	34	-	0/9/29/30	0/2/2/2
13	H2U	D	20(A)	13	-	5/7/38/39	0/2/2/2
34	2MG	a	975	34	-	0/9/27/28	0/3/3/3
13	4SU	D	8	13	-	0/7/25/26	0/2/2/2
13	PSU	D	55	13	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	UR3	a	1509	34	-	2/7/25/26	0/2/2/2
10	3TD	A	1942	10	-	0/7/25/26	0/2/2/2
34	MA6	a	1529	34	-	0/11/29/30	0/3/3/3
13	T6A	D	37	13,35	-	0/23/41/42	0/3/3/3
10	5MU	A	1966	10	-	0/7/25/26	0/2/2/2
34	G7M	a	535	34	-	2/7/25/26	0/3/3/3
13	RSP	D	32	13	-	0/7/25/26	0/2/2/2
10	OMG	A	2580	10	-	0/9/27/28	0/3/3/3
10	5MU	A	792	10	-	0/7/25/26	0/2/2/2
10	OMG	A	2278	10	-	1/9/27/28	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	A	1942	3TD	C6-C5	3.66	1.39	1.35
13	D	55	PSU	C6-C5	3.60	1.39	1.35
34	a	535	G7M	C8-N7	2.48	1.37	1.33
10	A	2601	G7M	C8-N7	2.38	1.37	1.33

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	D	8	4SU	C4-N3-C2	-4.04	123.41	127.34
34	a	1529	MA6	C2-N1-C6	2.88	118.56	111.75
34	a	1530	MA6	C2-N1-C6	2.86	118.51	111.75
13	D	8	4SU	C5-C4-N3	2.57	117.08	114.69
10	A	2278	OMG	O2'-C2'-C1'	2.39	113.73	109.08

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
34	a	1530	MA6	O4'-C4'-C5'-O5'
34	a	1530	MA6	C3'-C4'-C5'-O5'
10	A	2278	OMG	C1'-C2'-O2'-CM2
34	a	535	G7M	C3'-C4'-C5'-O5'
13	D	20(A)	H2U	C3'-C4'-C5'-O5'

There are no ring outliers.

7 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	A	2530	2MA	1	0
10	A	2476	H2U	1	0
10	A	2472	2MG	1	0
34	a	1412	4OC	1	0
10	A	1942	3TD	1	0
34	a	1529	MA6	1	0
13	D	37	T6A	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 116 ligands modelled in this entry, 116 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.

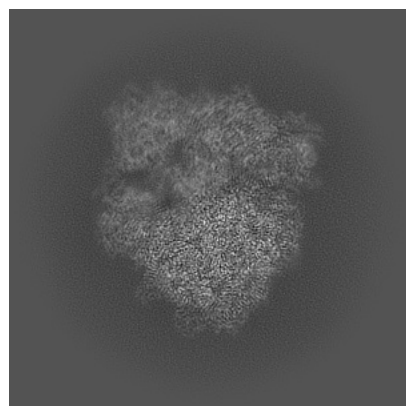
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-55946. These allow visual inspection of the internal detail of the map and identification of artifacts.

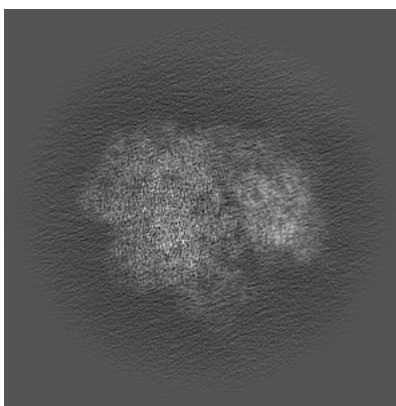
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

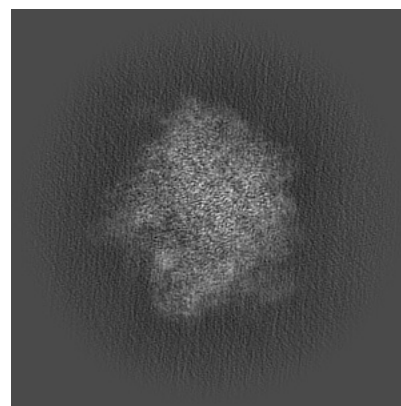
6.1.1 Primary map



X

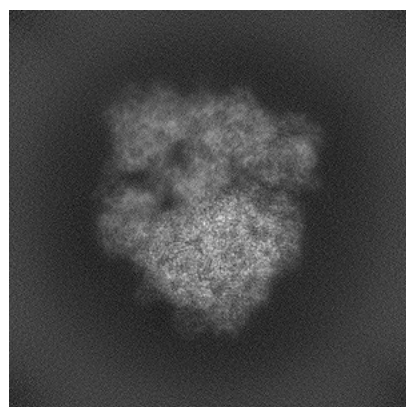


Y

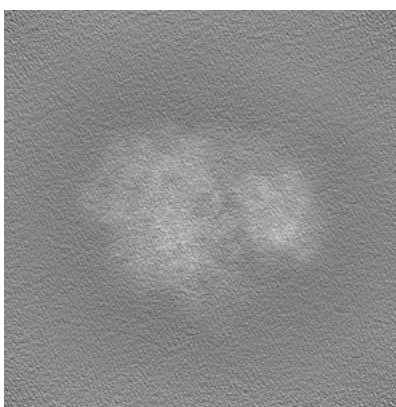


Z

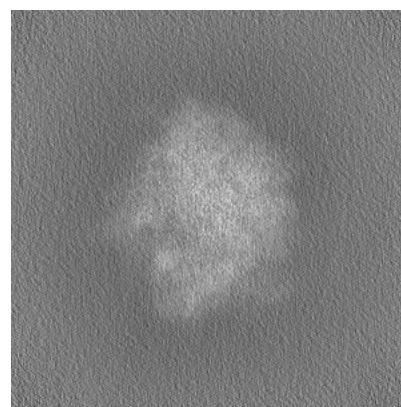
6.1.2 Raw map



X



Y

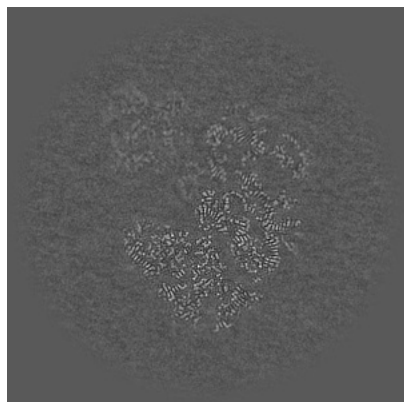


Z

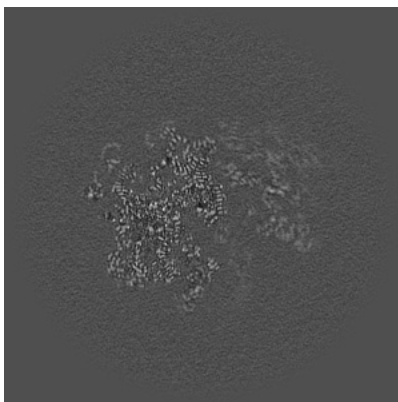
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

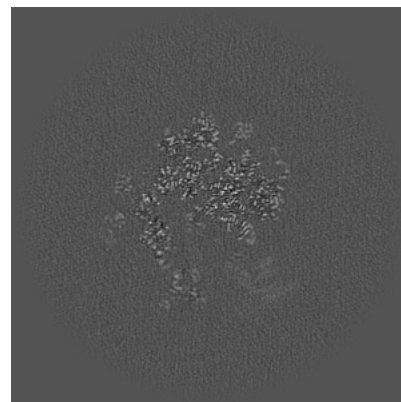
6.2.1 Primary map



X Index: 300

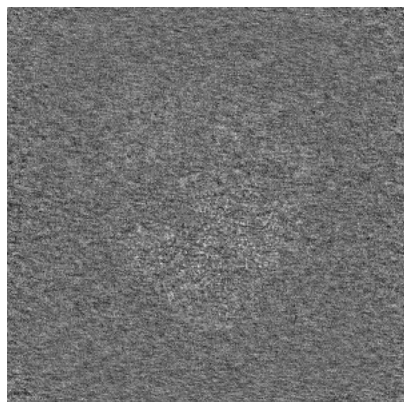


Y Index: 300

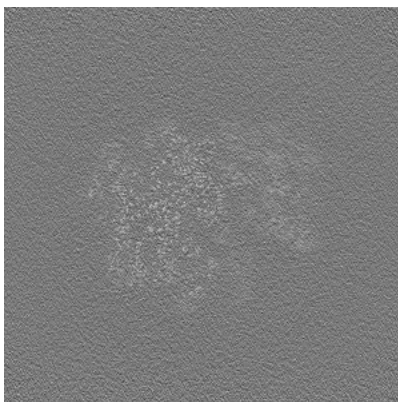


Z Index: 300

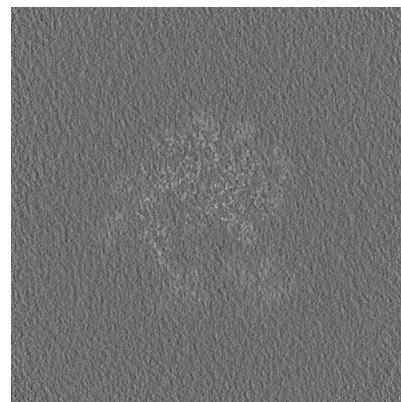
6.2.2 Raw map



X Index: 300



Y Index: 300

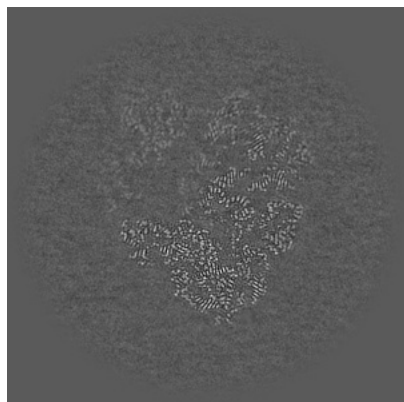


Z Index: 300

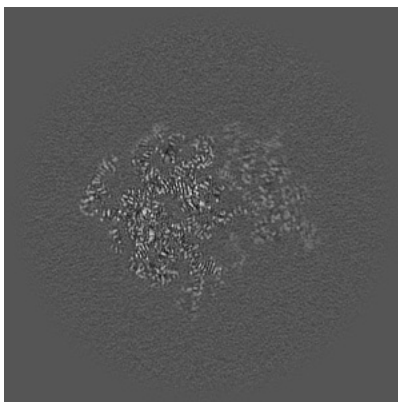
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

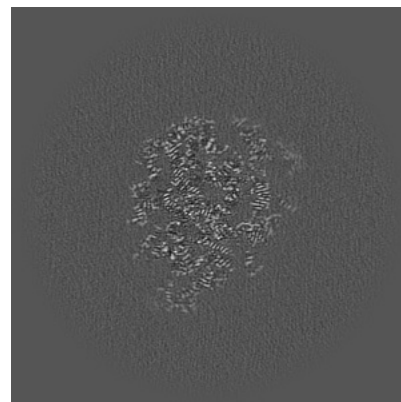
6.3.1 Primary map



X Index: 287

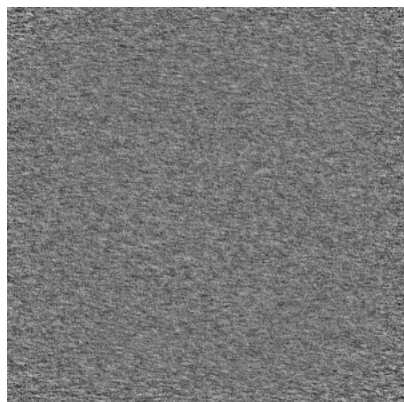


Y Index: 314

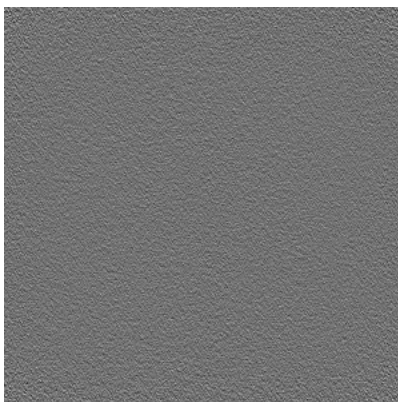


Z Index: 244

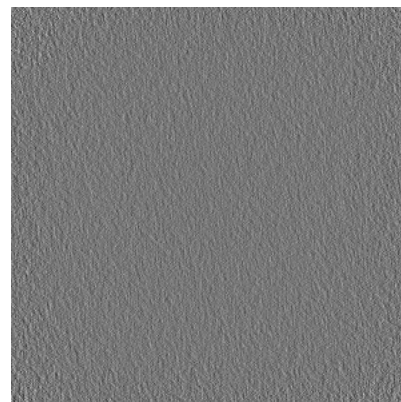
6.3.2 Raw map



X Index: 0



Y Index: 0

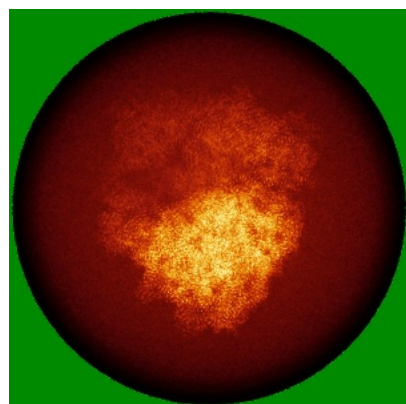


Z Index: 0

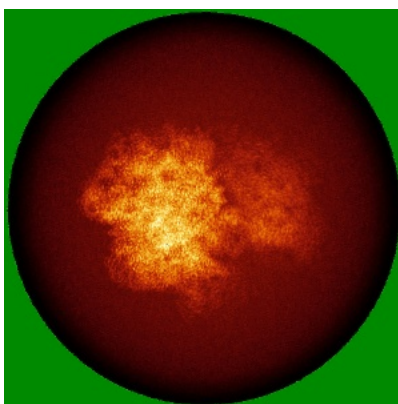
The images above show the largest variance slices of the map in three orthogonal directions.

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

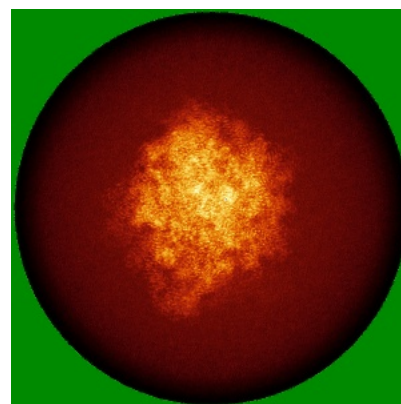
6.4.1 Primary map



X

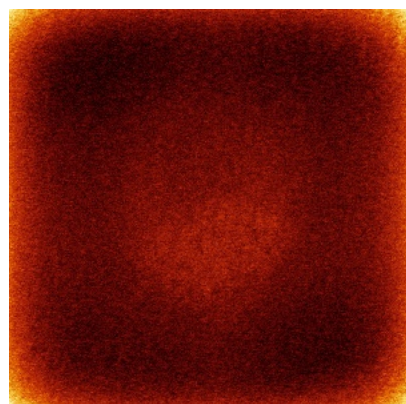


Y

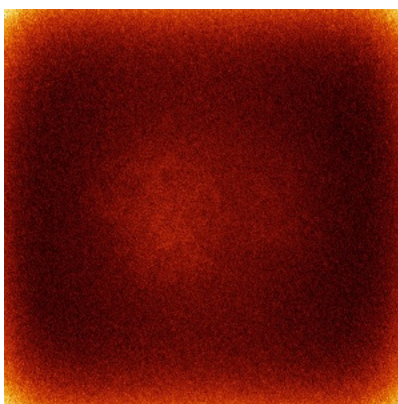


Z

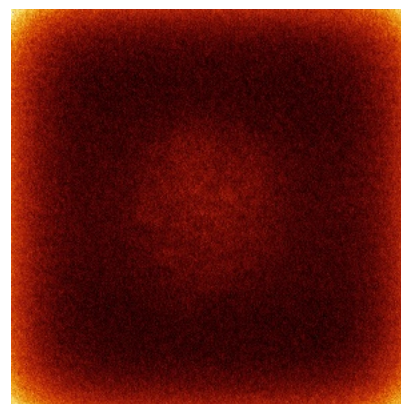
6.4.2 Raw map



X



Y

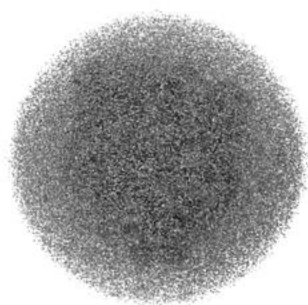


Z

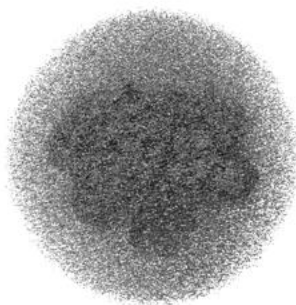
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

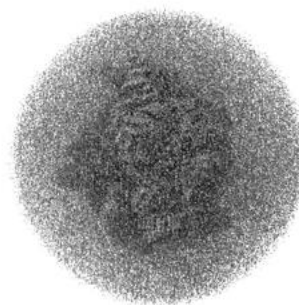
6.5.1 Primary map



X



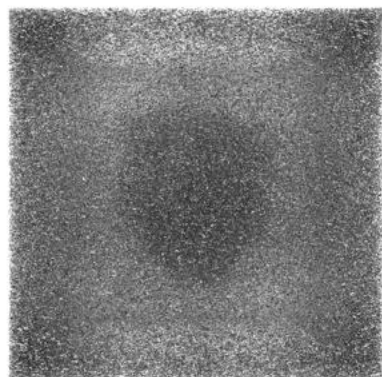
Y



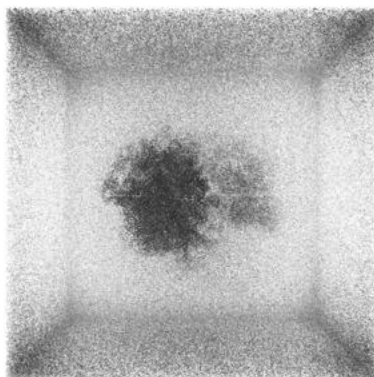
Z

The images above show the 3D surface view of the map at the recommended contour level 2.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

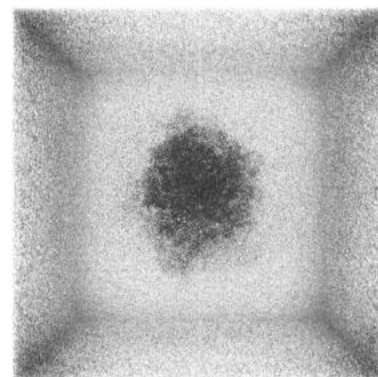
6.5.2 Raw map



X



Y



Z

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

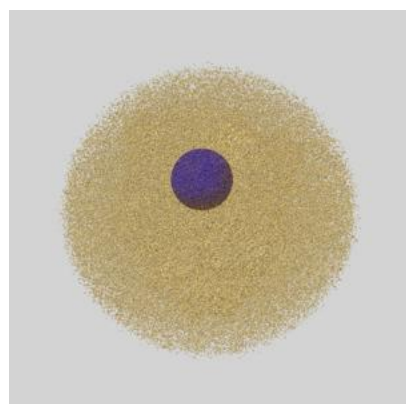
6.6 Mask visualisation [i](#)

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

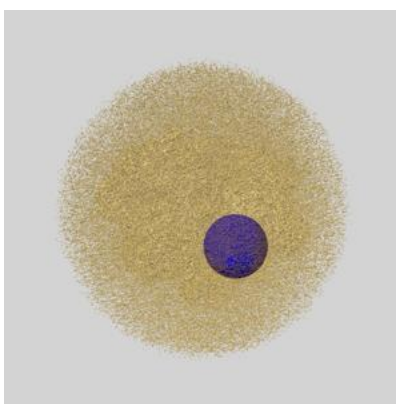
A mask typically either:

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

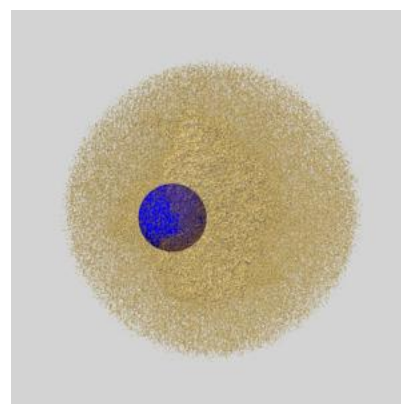
6.6.1 emd_55946_msk_1.map [i](#)



X

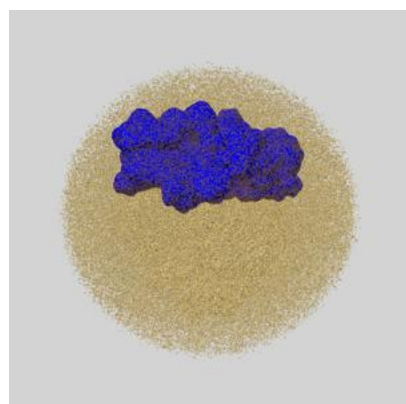


Y

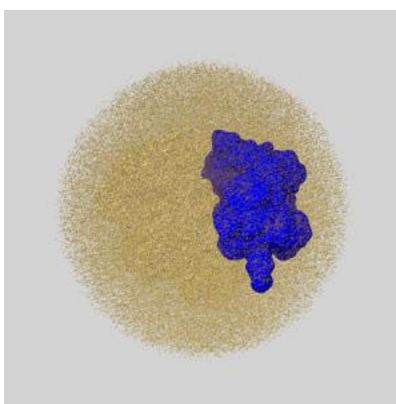


Z

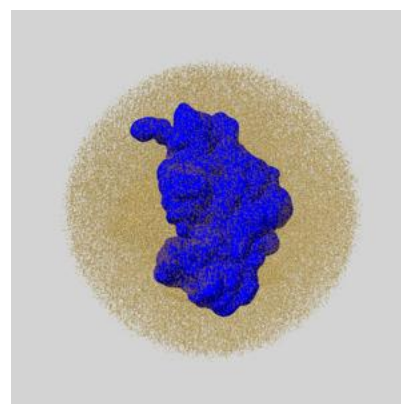
6.6.2 emd_55946_msk_2.map [i](#)



X



Y

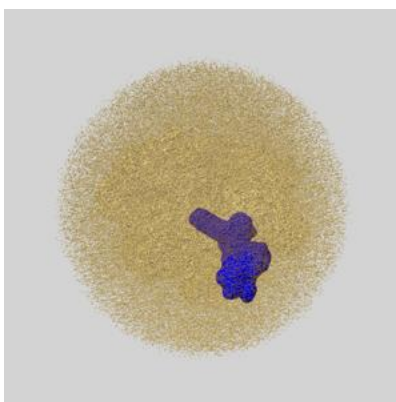


Z

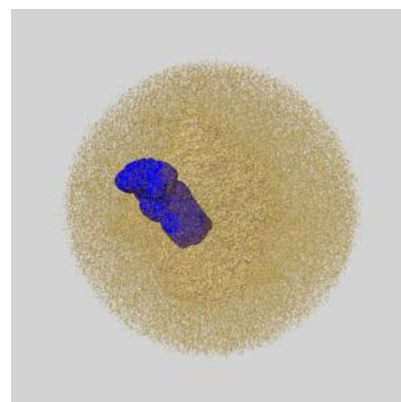
6.6.3 emd_55946_msk_3.map [i](#)



X

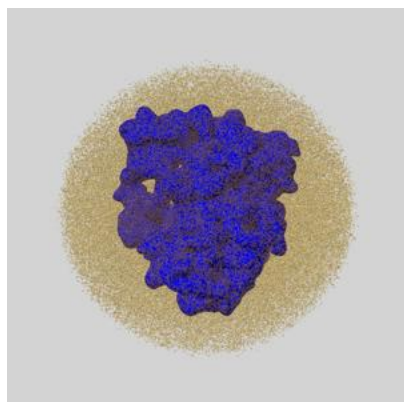


Y

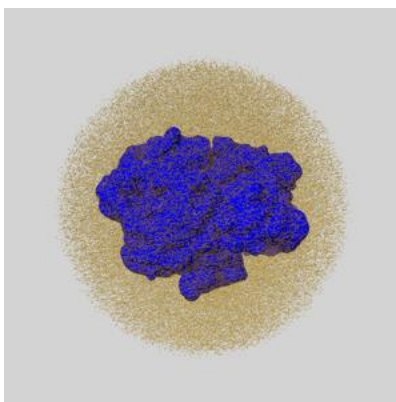


Z

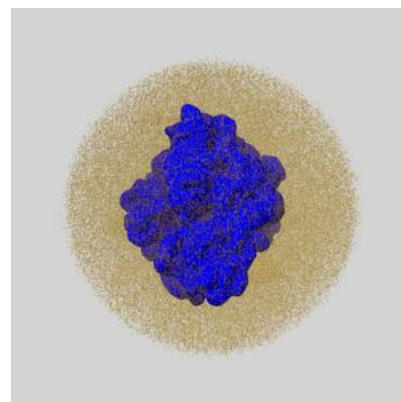
6.6.4 emd_55946_msk_4.map [i](#)



X

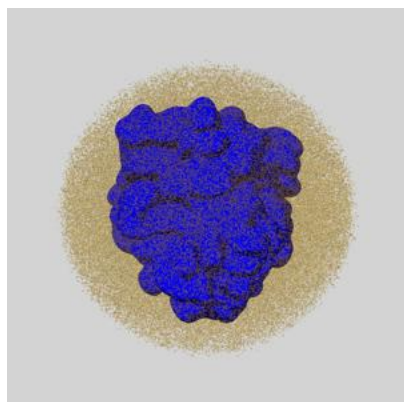


Y

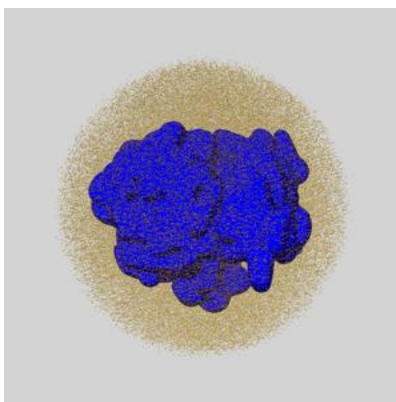


Z

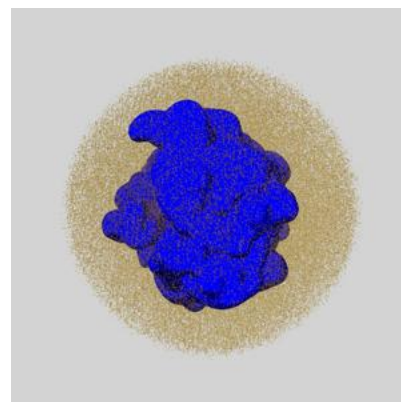
6.6.5 emd_55946_msk_5.map [i](#)



X



Y

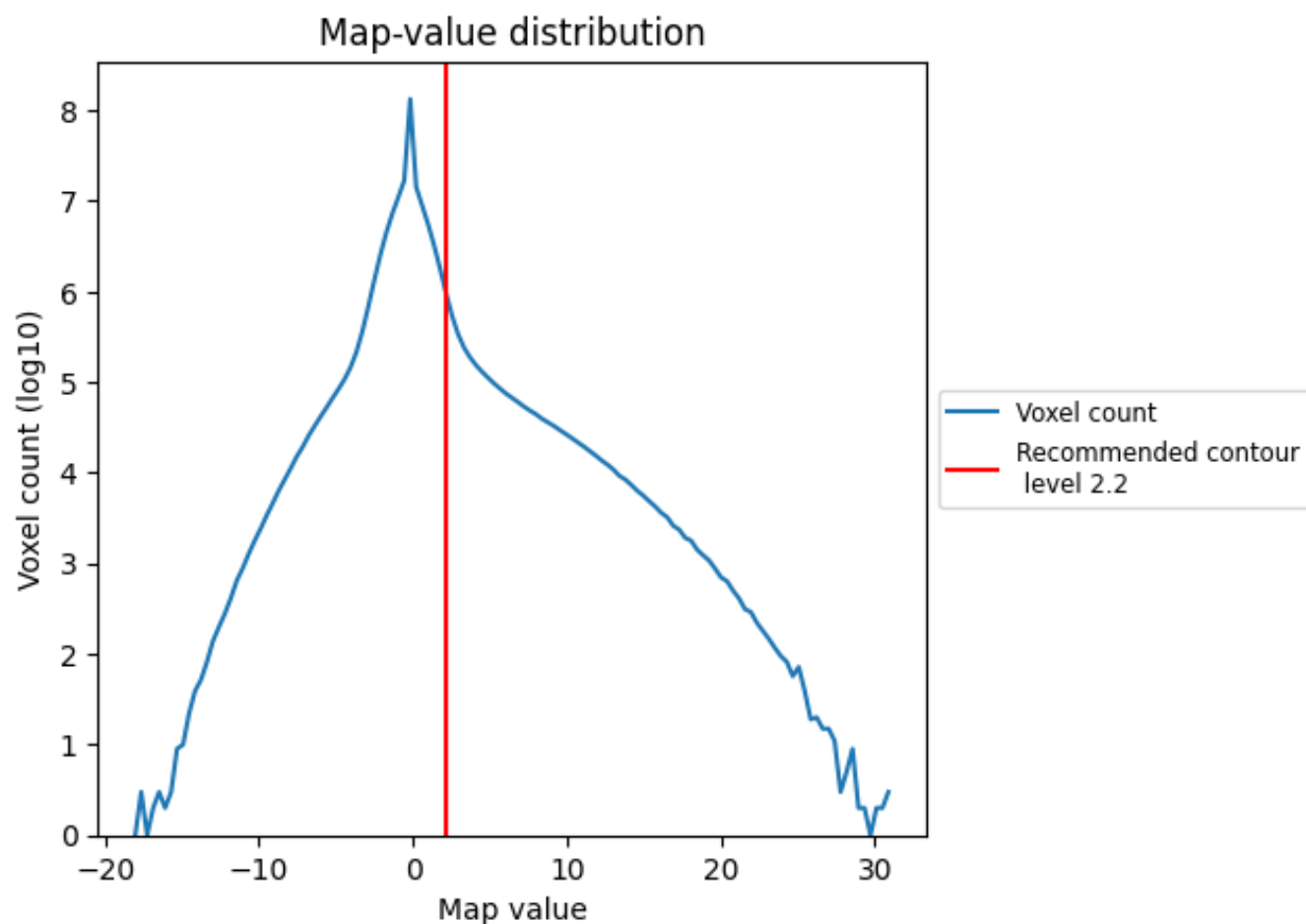


Z

7 Map analysis [i](#)

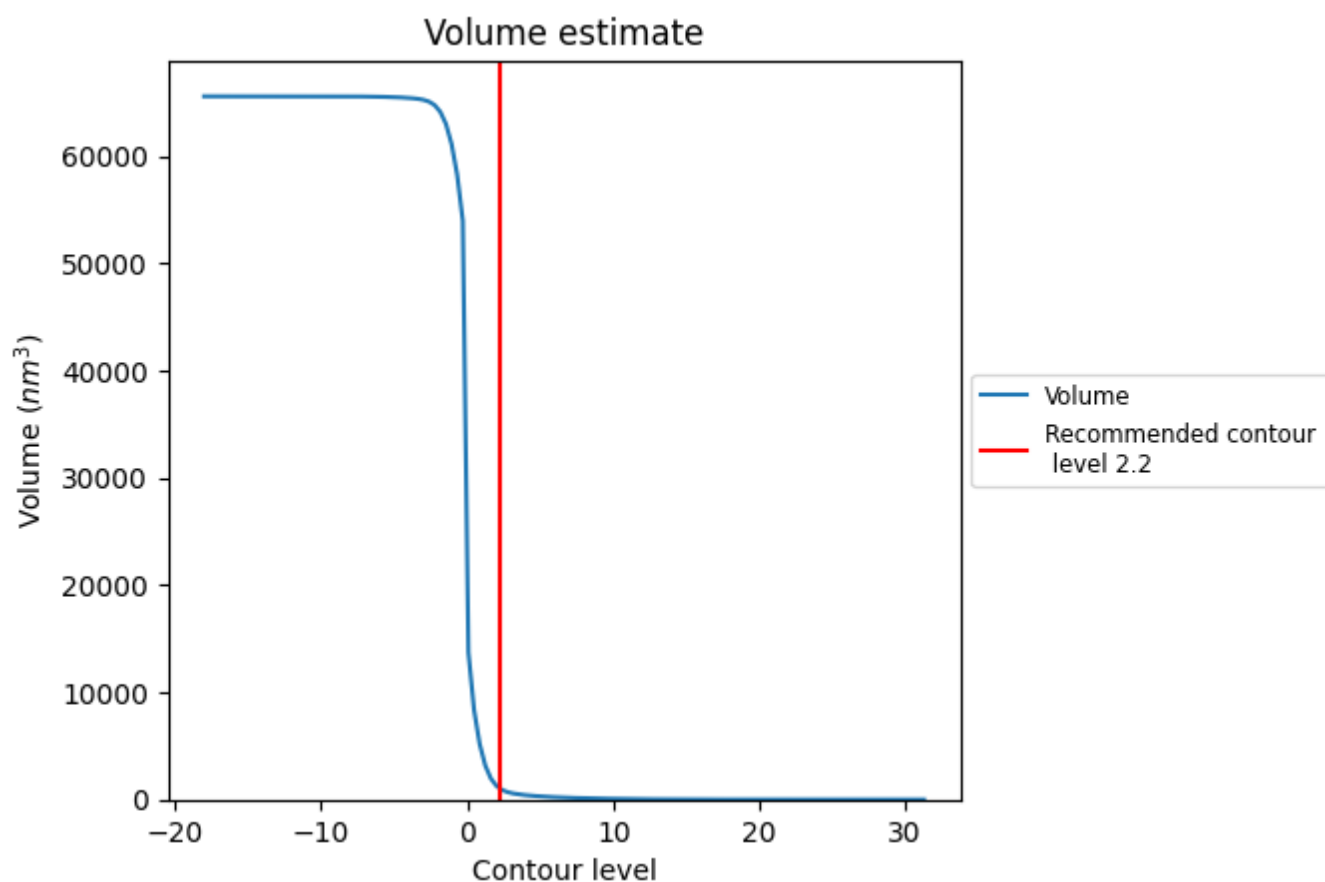
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

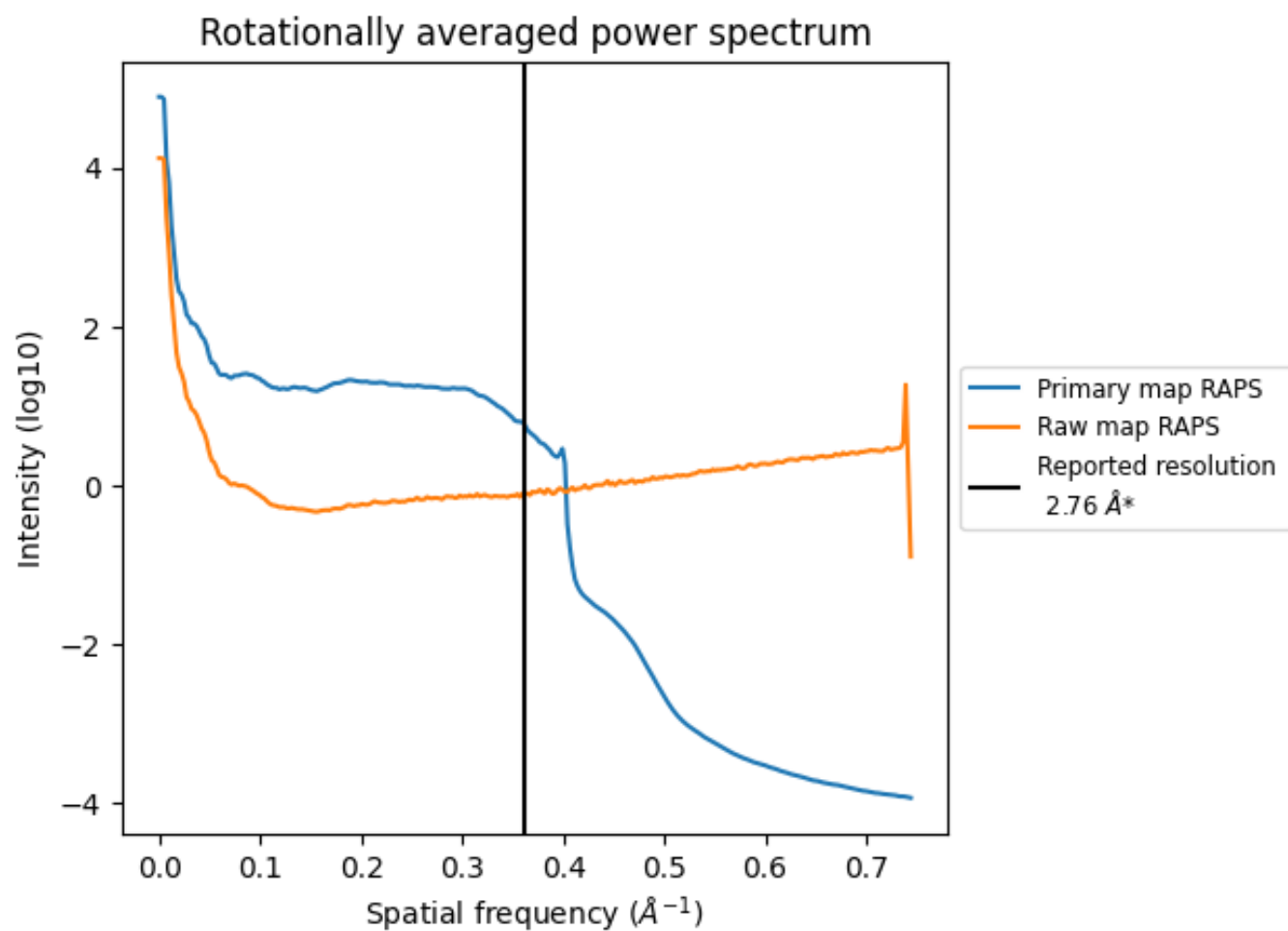
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1080 nm³; this corresponds to an approximate mass of 975 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 ⓘ

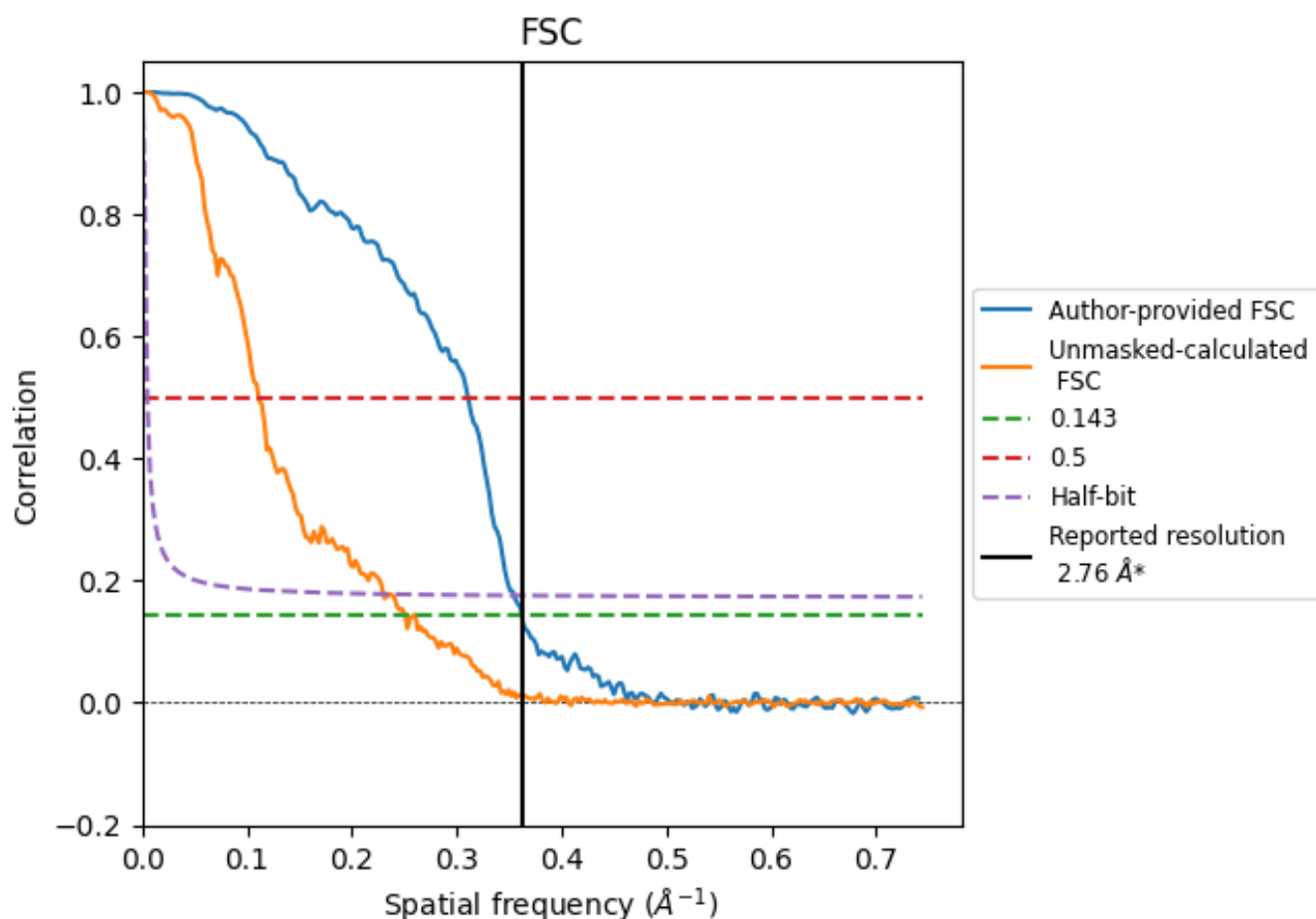


*Reported resolution corresponds to spatial frequency of 0.362 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.362 Å⁻¹

8.2 Resolution estimates [i](#)

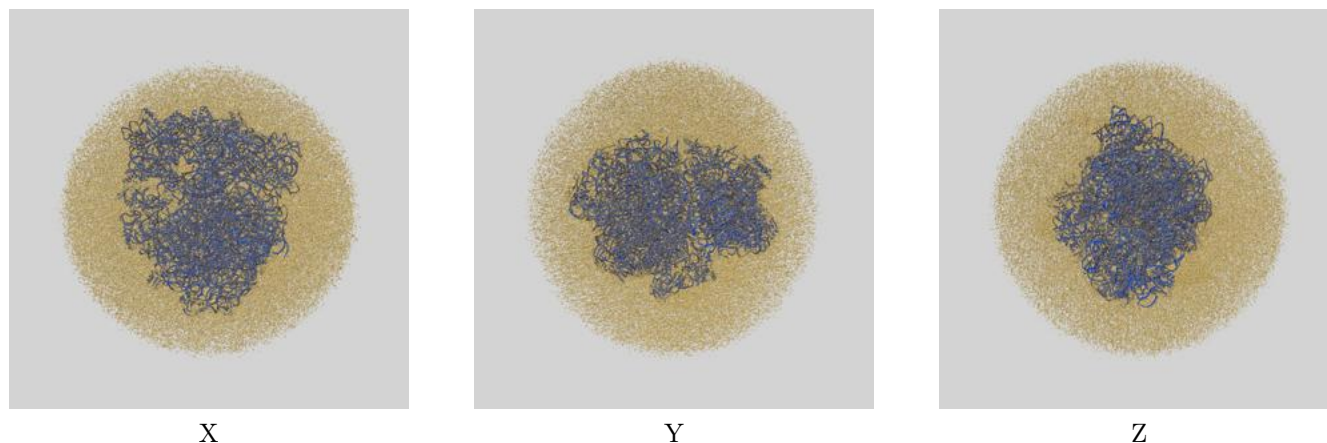
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.76	-	-
Author-provided FSC curve	2.76	3.22	2.82
Unmasked-calculated*	3.99	9.00	4.35

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.99 differs from the reported value 2.76 by more than 10 %

9 Map-model fit [i](#)

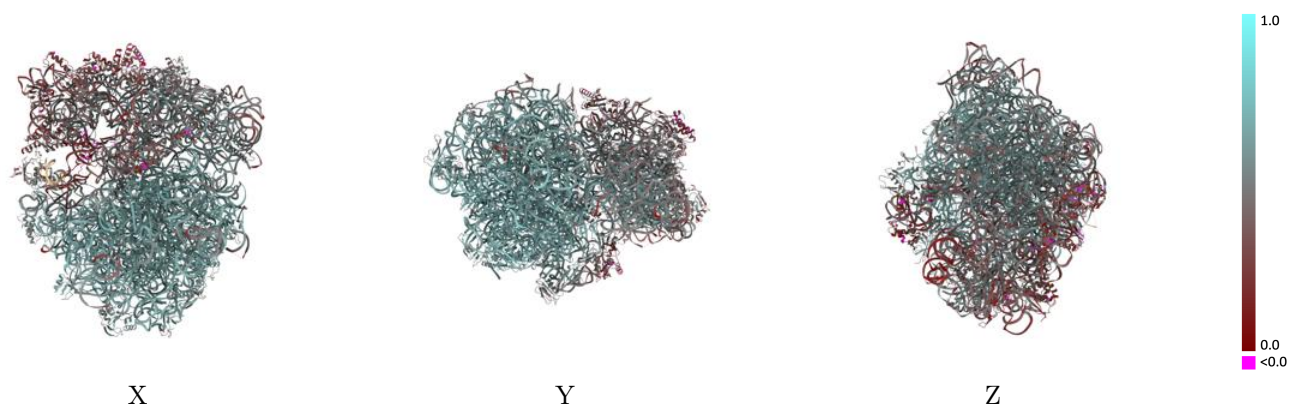
This section contains information regarding the fit between EMDB map EMD-55946 and PDB model 9TI7. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)



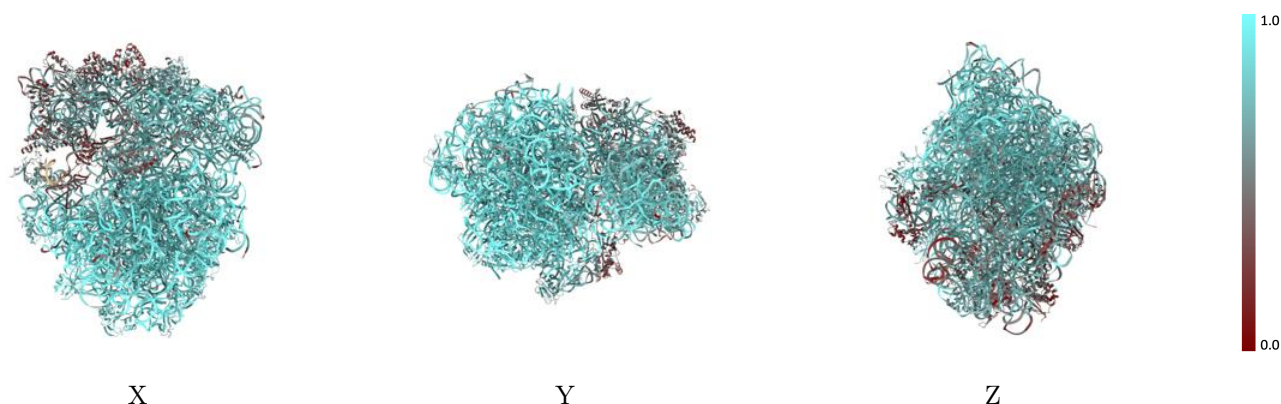
The images above show the 3D surface view of the map at the recommended contour level 2.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



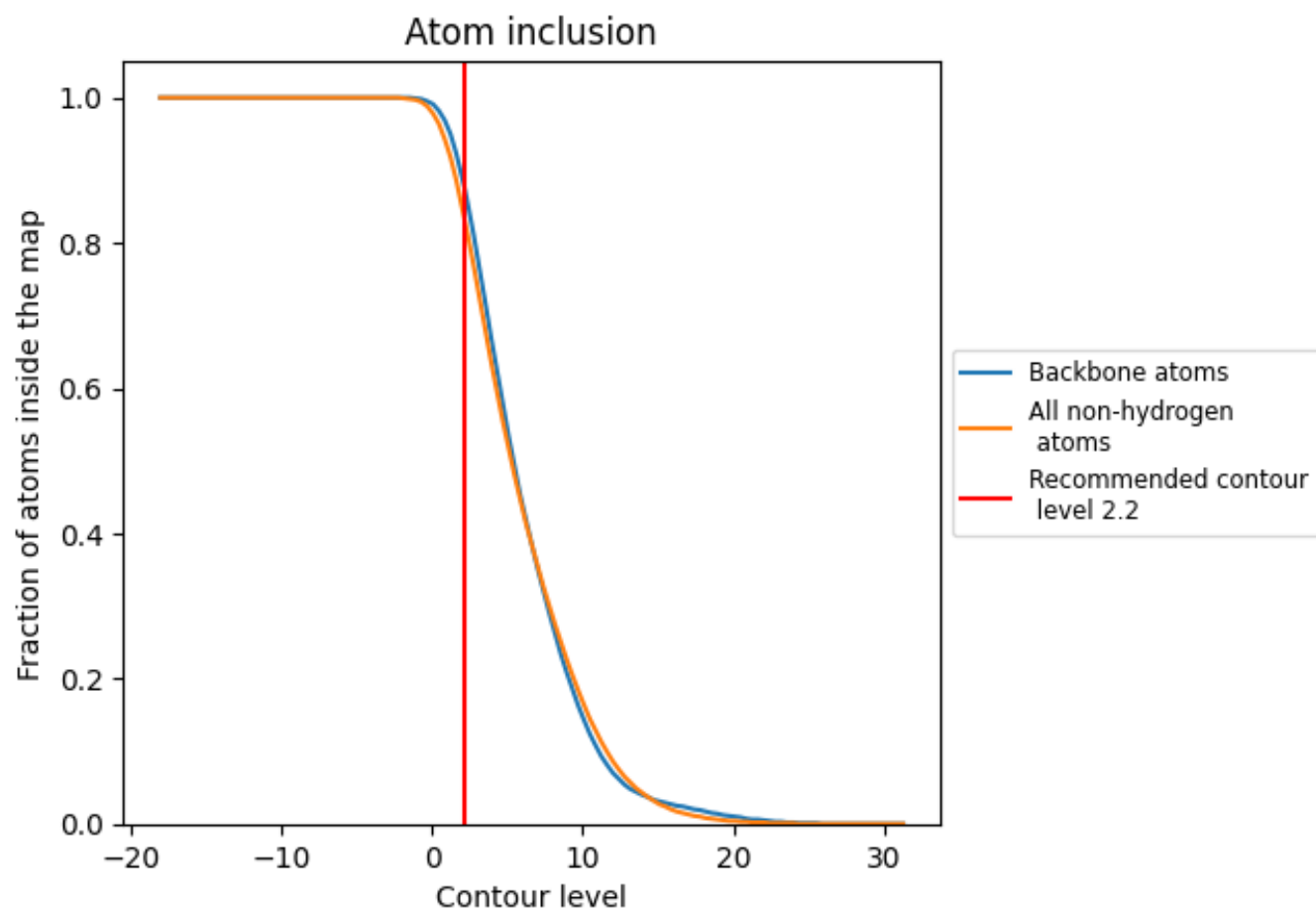
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 83% 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 (2.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8300	 0.5460
1	 0.8810	 0.6130
2	 0.8270	 0.5590
3	 0.9130	 0.6270
4	 0.5590	 0.3990
5	 0.9220	 0.6410
6	 0.8500	 0.5840
7	 0.9690	 0.6650
8	 0.9490	 0.6610
9	 0.9420	 0.6350
A	 0.9520	 0.6300
B	 0.9310	 0.5860
C	 0.5280	 0.3860
D	 0.3830	 0.2440
G	 0.9380	 0.6530
H	 0.9430	 0.6540
I	 0.9030	 0.6180
J	 0.6530	 0.4590
K	 0.7140	 0.5020
L	 0.2710	 0.1990
M	 0.9220	 0.6380
N	 0.9230	 0.6330
O	 0.9090	 0.6290
P	 0.9250	 0.6280
Q	 0.9290	 0.6320
R	 0.8060	 0.5450
S	 0.9120	 0.6180
T	 0.9360	 0.6570
U	 0.9220	 0.6310
V	 0.9340	 0.6380
W	 0.8780	 0.6040
X	 0.7820	 0.5430
Y	 0.7810	 0.5270
Z	 0.9290	 0.6370
a	 0.7860	 0.4770



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Chain	Atom inclusion	Q-score
b	 0.3690	 0.3170
c	 0.3910	 0.2750
d	 0.5140	 0.3720
e	 0.6460	 0.4310
f	 0.6690	 0.4670
g	 0.4430	 0.3060
h	 0.4380	 0.3000
i	 0.6680	 0.4550
j	 0.4270	 0.3120
k	 0.4490	 0.3280
l	 0.4230	 0.2890
m	 0.7540	 0.5300
n	 0.4590	 0.3380
o	 0.5830	 0.4230
p	 0.6210	 0.4090
q	 0.7090	 0.4900
r	 0.6700	 0.4700
s	 0.4540	 0.2990
t	 0.3990	 0.3290
u	 0.7730	 0.5300