



wwPDB EM Validation Summary Report ⓘ

Jul 7, 2024 – 02:23 pm BST

PDB ID : 7OW7
EMDB ID : EMD-13094
Title : EIF6-bound large subunit of the human ribosome
Authors : Faille, A.; Warren, A.J.
Deposited on : 2021-06-16
Resolution : 2.40 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.dev92
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

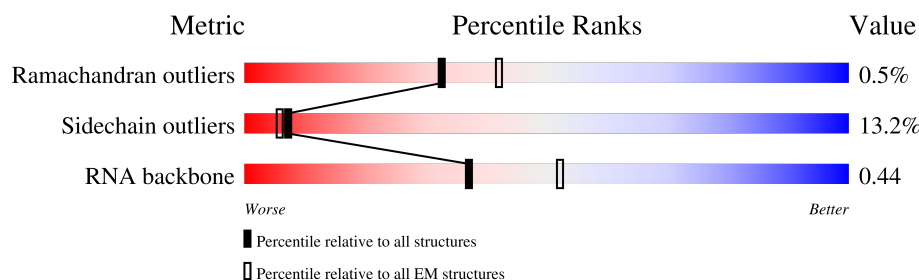
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.40 Å.

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













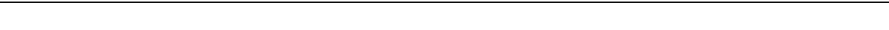

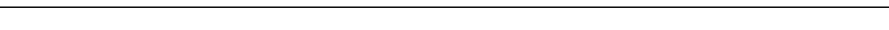
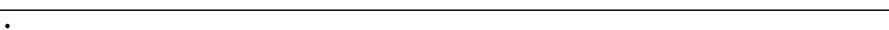











Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	A	5070	
2	B	121	
3	C	157	
4	D	257	
5	E	430	
6	F	427	
7	G	297	
8	H	288	


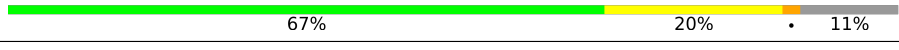
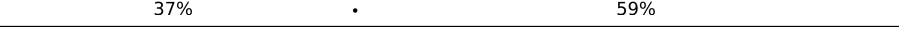




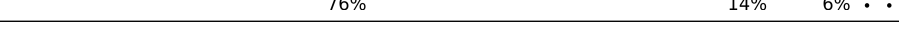


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Mol	Chain	Length	Quality of chain
9	m	248	
10	n	266	
11	o	190	
12	p	214	
13	q	178	
14	r	211	
15	s	220	
16	t	204	
17	I	203	
18	J	184	
19	K	188	
20	L	196	
21	M	176	
22	N	160	
23	R	156	
24	S	145	
25	T	136	
26	U	148	
27	V	159	
28	W	115	
29	X	125	
30	Y	135	
31	Z	110	
32	a	117	
33	b	123	

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Mol	Chain	Length	Quality of chain
34	c	105	
35	d	97	
36	e	70	
37	f	157	
38	i	106	
39	j	92	
40	k	137	
41	P	245	
42	Q	140	
43	u	157	

2 Entry composition

There are 49 unique types of molecules in this entry. The entry contains 137413 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 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3303	Total	C	N	O	P	1	0
			70929	31625	12982	23019	3303		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	148	Total	C	N	O	P	0	0
			3153	1408	564	1034	147		

- Molecule 4 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	246	Total	C	N	O	S	0	0
			1887	1183	387	311	6		

- Molecule 5 is a protein called 60S ribosomal protein L3 isoform a.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	395	Total	C	N	O	S	1	0
			3194	2034	600	545	15		

- Molecule 6 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	359	Total	C	N	O	S	0	0
			2855	1797	571	474	13		

- Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	293	Total	C	N	O	S	0	0
			2376	1505	432	425	14		

- Molecule 8 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	221	Total	C	N	O	S	0	0
			1767	1138	335	290	4		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	40	ARG	GLY	conflict	UNP Q02878
H	41	ASN	LYS	conflict	UNP Q02878

- Molecule 9 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	m	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 10 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	n	223	Total	C	N	O	S	0	0
			1809	1153	349	303	4		

- Molecule 11 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	o	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 12 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	p	158	Total	C	N	O	S	0	0
			1283	819	238	216	10		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
p	49	CYS	GLY	conflict	UNP Q96L21

- Molecule 13 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	q	170	Total	C	N	O	S	0	0
			1358	858	253	241	6		

- Molecule 14 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	r	206	Total	C	N	O	S	0	0
			1664	1041	345	274	4		

- Molecule 15 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	s	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 16 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	t	203	Total	C	N	O	S	2	0
			1720	1086	361	269	4		

- Molecule 17 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	I	199	Total	C	N	O	S	0	0
			1634	1053	319	257	5		

- Molecule 18 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	J	152	Total	C	N	O	S	0	0
			1233	771	240	213	9		

- Molecule 19 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	K	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 20 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L	137	Total	C	N	O	S	0	0
			1137	716	235	178	8		

- Molecule 21 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	M	176	Total	C	N	O	S	0	0
			1461	930	284	236	11		

- Molecule 22 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	N	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 23 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	R	119	Total	C	N	O	S	0	0
			976	624	183	168	1		

- Molecule 24 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	S	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 25 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	T	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 26 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	U	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 27 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	V	104	Total	C	N	O	S	0	0
			837	518	185	130	4		

- Molecule 28 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	W	100	Total	C	N	O	S	0	0
			772	490	136	139	7		

- Molecule 29 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	X	106	Total	C	N	O	S	0	0
			868	551	170	145	2		

- Molecule 30 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Y	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 31 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Z	109	Total	C	N	O	S	1	0
			879	557	174	144	4		

- Molecule 32 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	a	112	Total	C	N	O	S	0	0
			888	555	183	144	6		

- Molecule 33 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	b	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 34 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	c	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 35 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	d	86	Total	C	N	O	S	1	0
			713	442	155	111	5		

- Molecule 36 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	e	29	Total	C	N	O	S	0	0
			249	163	47	38	1		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
e	16	PRO	ARG	conflict	UNP P63173
e	23	ILE	VAL	conflict	UNP P63173

- Molecule 37 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	f	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 38 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	i	97	Total	C	N	O	S	0	0
			794	498	161	129	6		

- Molecule 39 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	j	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 40 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	k	124	Total	C	N	O	S	0	0
			992	615	206	167	4		

- Molecule 41 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	P	225	Total	C	N	O	S	0	0
			1712	1065	295	340	12		

- Molecule 42 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Q	134	Total	C	N	O	S	0	0
			993	625	187	176	5		

- Molecule 43 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	u	62	Total	C	N	O	S	0	0
			519	332	101	83	3		

- Molecule 44 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
44	A	209	Total	Mg	0
			209	209	
44	B	3	Total	Mg	0
			3	3	
44	C	6	Total	Mg	0
			6	6	
44	J	1	Total	Mg	0
			1	1	
44	L	2	Total	Mg	0
			2	2	
44	Q	2	Total	Mg	0
			2	2	

- Molecule 45 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
45	A	1	Total 1	Zn 1	0
45	a	1	Total 1	Zn 1	0
45	d	1	Total 1	Zn 1	0
45	i	1	Total 1	Zn 1	0
45	j	1	Total 1	Zn 1	0

- Molecule 46 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
46	A	139	Total 139	K 139	0
46	B	1	Total 1	K 1	0
46	D	3	Total 3	K 3	0
46	o	1	Total 1	K 1	0
46	p	1	Total 1	K 1	0
46	t	1	Total 1	K 1	0
46	J	1	Total 1	K 1	0
46	N	1	Total 1	K 1	0
46	V	1	Total 1	K 1	0
46	Y	1	Total 1	K 1	0
46	Z	1	Total 1	K 1	0
46	f	1	Total 1	K 1	0
46	i	1	Total 1	K 1	0

- Molecule 47 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		AltConf
47	A	3	Total 3	Na 3	0
47	t	1	Total 1	Na 1	0

- Molecule 48 is BROMIDE ION (three-letter code: BR) (formula: Br).

Mol	Chain	Residues	Atoms		AltConf
48	G	1	Total 1	Br 1	0

- Molecule 49 is water.

Mol	Chain	Residues	Atoms		AltConf
49	A	6577	Total 6577	O 6577	0
49	B	132	Total 132	O 132	0
49	C	280	Total 280	O 280	0
49	D	109	Total 109	O 109	0
49	E	139	Total 139	O 139	0
49	F	182	Total 182	O 182	0
49	G	34	Total 34	O 34	0
49	H	36	Total 36	O 36	0
49	m	101	Total 101	O 101	0
49	n	35	Total 35	O 35	0
49	o	11	Total 11	O 11	0
49	p	12	Total 12	O 12	0
49	q	5	Total 5	O 5	0
49	r	84	Total 84	O 84	0
49	s	14	Total 14	O 14	0

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Mol	Chain	Residues	Atoms		AltConf
49	t	153	Total 153	O 153	0
49	I	87	Total 87	O 87	0
49	J	66	Total 66	O 66	0
49	K	130	Total 130	O 130	0
49	L	37	Total 37	O 37	0
49	M	53	Total 53	O 53	0
49	N	71	Total 71	O 71	0
49	R	29	Total 29	O 29	0
49	S	40	Total 40	O 40	0
49	T	6	Total 6	O 6	0
49	U	80	Total 80	O 80	0
49	V	27	Total 27	O 27	0
49	W	6	Total 6	O 6	0
49	X	24	Total 24	O 24	0
49	Y	96	Total 96	O 96	0
49	Z	58	Total 58	O 58	0
49	a	52	Total 52	O 52	0
49	b	38	Total 38	O 38	0
49	c	15	Total 15	O 15	0
49	d	56	Total 56	O 56	0
49	e	1	Total 1	O 1	0

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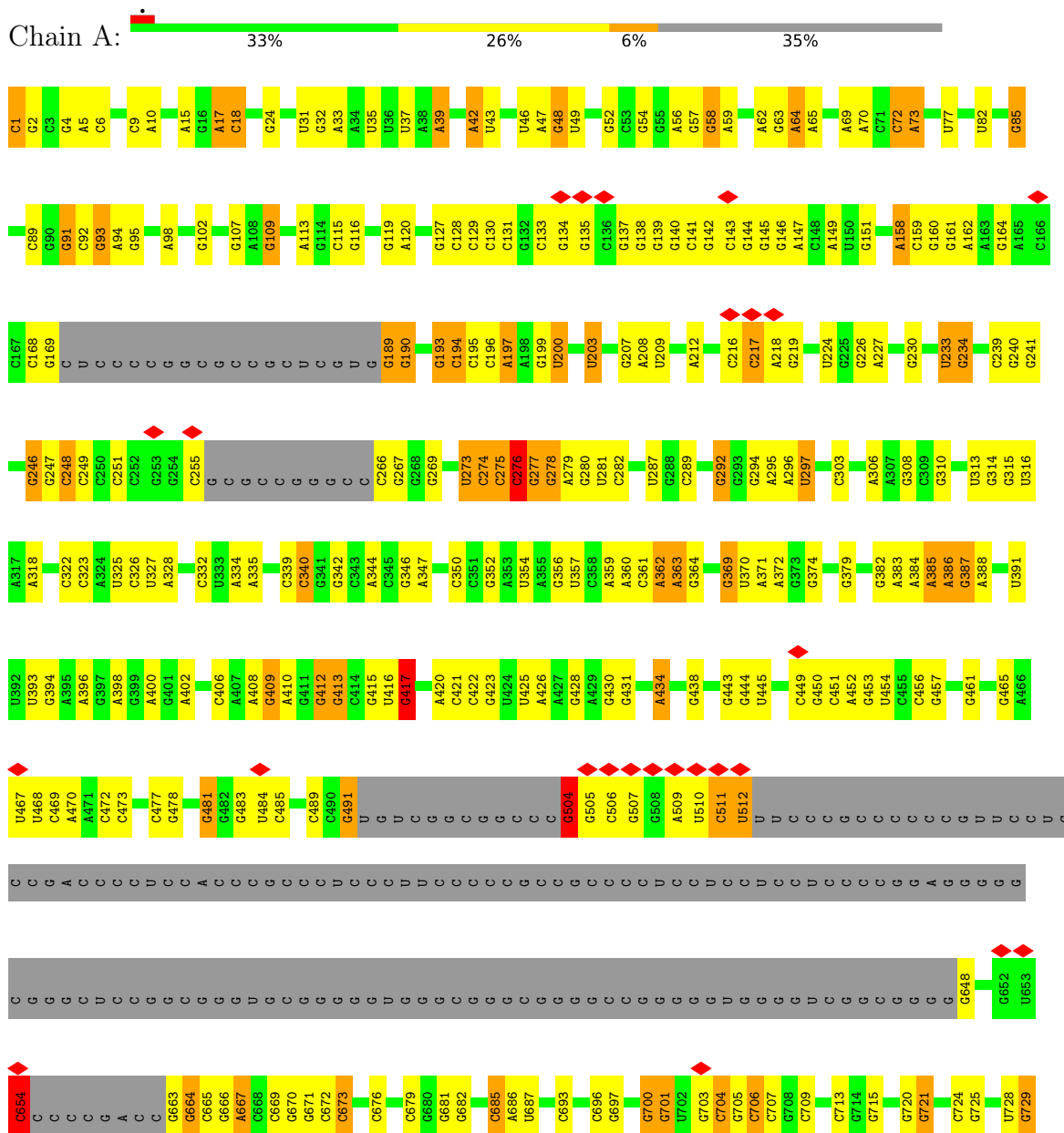
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Mol	Chain	Residues	Atoms		AltConf
49	f	12	Total 12	O 12	0
49	i	35	Total 35	O 35	0
49	j	24	Total 24	O 24	0
49	k	59	Total 59	O 59	0
49	P	1	Total 1	O 1	0
49	Q	31	Total 31	O 31	0
49	u	6	Total 6	O 6	0

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.

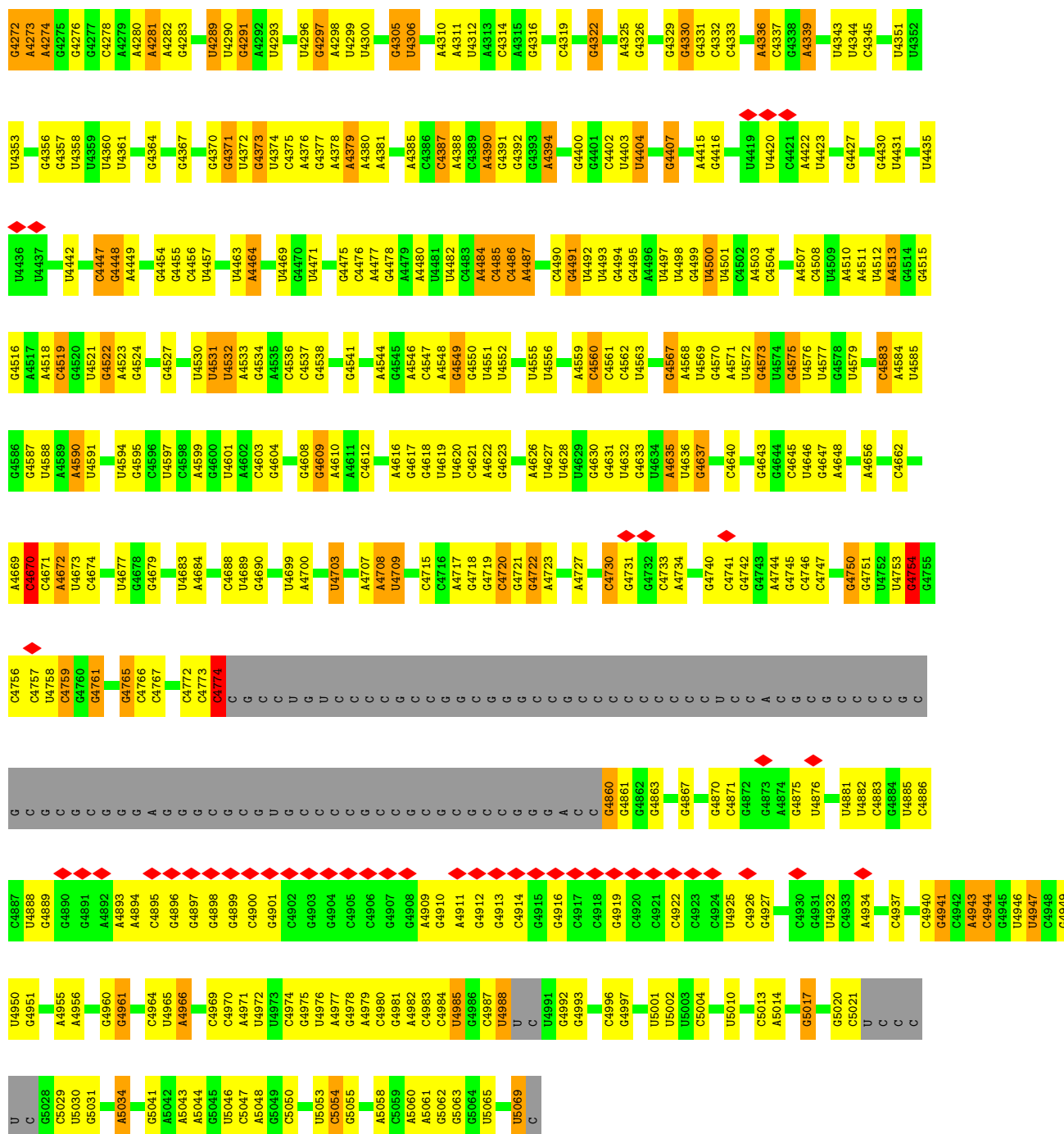
• Molecule 1: 28S rRNA





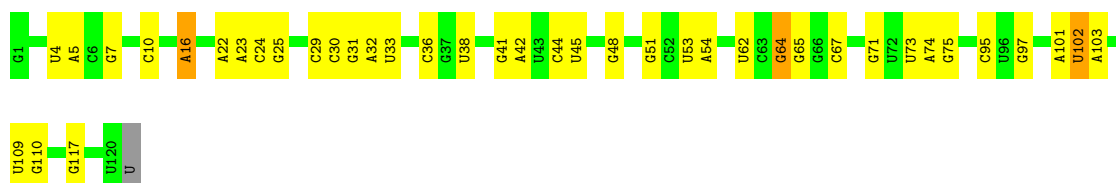
G2831	A2744	G2662	C2558	A2401	C2317	G2049	A	U1822
A2832	A2745	G2663	G2559	G2406	G2318	G2050	U	U1906
A2833	A2746	G2664	C2560	G2407	G2319	C2051	G	A1907
A2834	G2753	U2665	C2561	G2412	G2320	G2052	G	G1826
A2835	G2754	U2666	C2562	U2415	C2323	U2054	A	C1832
A2836	G2755	G2667	G2563	G2416	C2324	G2055	A	G1833
U2837	G2756	G2668	C2564	A2417	G2330	G2056	G	U1834
U2838	G2757	C2669	C2565	U2420	G2331	G2060	U	G1835
U2839	G2760	C2672	C2566	A2421	G2332	G2063	C	A1837
A2840	U2761	G2673	A2567	C2422	G2333	G2064	A	G1842
A2841	G2762	A2674	C2568	A2423	G2339	G2065	A	G1846
A2842	G2763	G2675	C2569	A2424	C2340	C2068	U	G1847
U2843	A2764	A2676	U2570	U2425	G2342	A2069	C	C1848
G2848	G2769	G2679	C2573	U2426	C2347	C2072	C	U1852
A2849	C2770	G2680	G2576	G2427	G2348	C2073	U	G1853
A2850	G2771	C2685	C2579	A2428	A2349	C2074	A	G1854
G2854	C2780	G2686	U2580	G2433	U2350	G2075	G	G1855
G2855	G2781	G2688	A2582	G2434	C2351	C2082	A	A1858
A2856	C2784	G2694	C2583	G2435	U2352	G2083	G	C1931
A2857	G2785	A2695	C2584	C2437	G2355	C2084	U	U1861
A2858	U2786	G2696	C2585	A2438	U2356	G2086	G	G1862
C2861	A2787	A2696	G2586	U2439	G2357	C2087	U	U1863
C2862	U2788	C2702	A2587	U2440	C2357	A2088	G	G1864
C2863	G2789	G2703	C2588	C2441	A2360	G2089	U	G1865
C2866	U2790	C2704	C2589	G2442	U2362	U2090	A	U1866
C2867	C2792	G2705	G2593	U2444	A2367	C	A	A1867
C2868	G2793	G2706	C2594	U2447	A2368	C	C	A1868
U2869	A2794	G2707	C2595	G2448	U2371	G	A	G1869
U2873	G2795	U2708	G2596	A2451	U2372	A	A	U1870
G2876	A2796	C2709	C2597	G2452	C2373	G	C	A1871
G2877	G2797	G2710	A2598	A2453	G2378	C	C	G1872
G2878	U2798	A2599	G2599	G2454	G2379	G	A	A1873
A2882	C2800	A2600	U2530	U2455	G2380	G	U	A1874
G2889	U2803	A2601	G2533	G2456	G2381	G	G	C1875
C2890	C2804	G2602	C2534	C2466	A2382	G	A	U1876
G2897	G2811	C2614	G2535	C2470	U2383	G	C	G1877
G2898	A2812	C2615	A2536	G2471	U2384	G	C	G1878
C2899	G2813	C2616	G2537	A2472	U2385	G	C	A1879
U2900	C2814	G2617	U2538	G2473	G2389	G	C	G1880
G	A2815	C2627	C2539	G2474	U2390	C	C	C1881
G	U2821	U2632	A2543	G2475	G2391	C	C	G1882
G	G2822	U2633	G	A2476	C2392	C	C	G1883
G	G2823	G2643	U	C	G2396	G	A	G1887
G	C2824	G2644	G	G	U2305	G	C	G1890
C	A2825	G2650	G2547	G	G2306	G	C	A1891
C	U2826	C2651	U2554	G	A2395	G	C	A1892
C	G2827	C2652	G2555	G	A2396	G	G	A1896
C	U2828	C2653	G2556	C	G2397	G	U	A1897
C	U2829	G2660	G2557	C	U2398	G	G	C1898
C	G2830	A2743	C2557	A	G2400	G	C	G1899
C							C	C1900

WORLDWIDE
PDB
PROTEIN DATA BANK

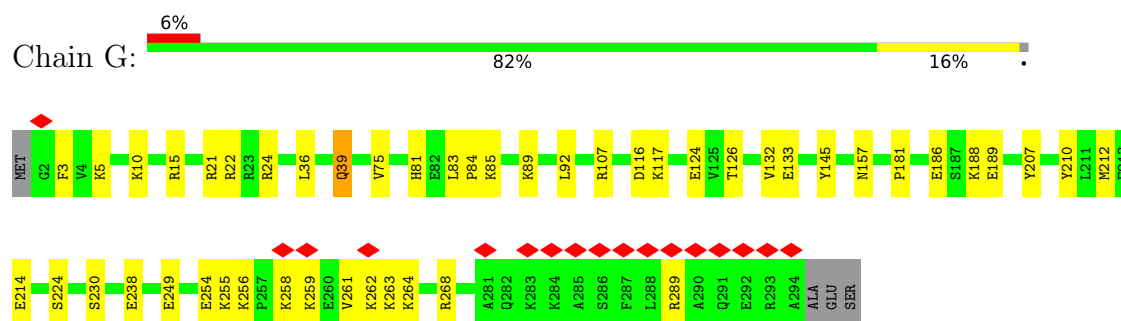


• Molecule 2: 5S rRNA

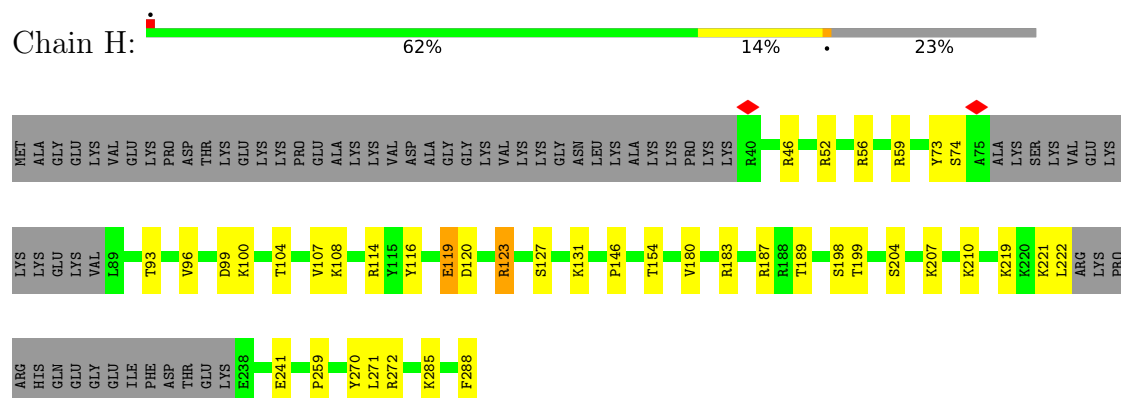
Chain B:



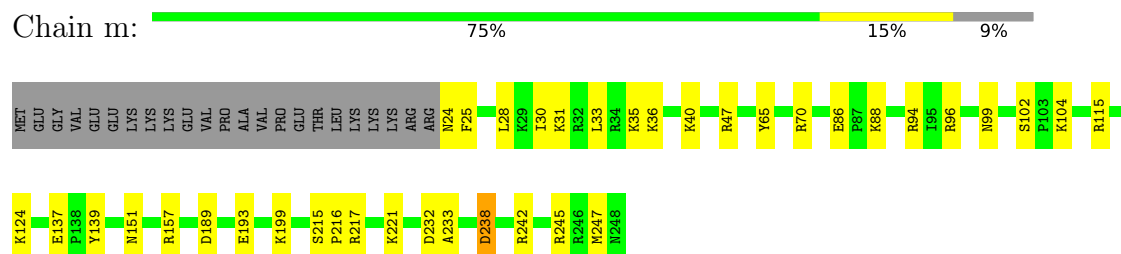
- Molecule 7: 60S ribosomal protein L5



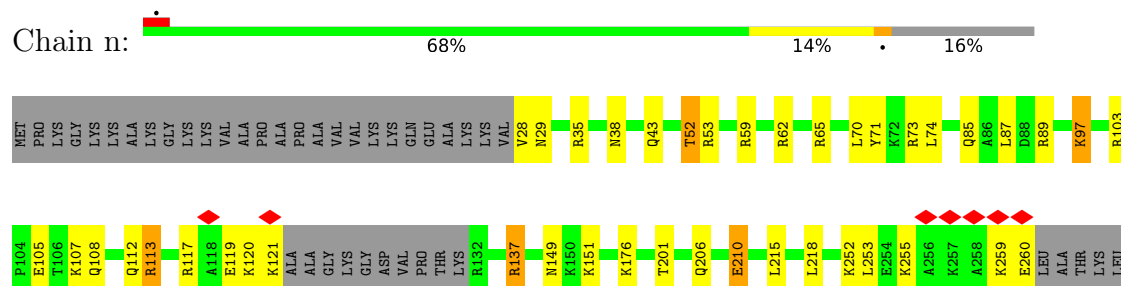
- Molecule 8: 60S ribosomal protein L6



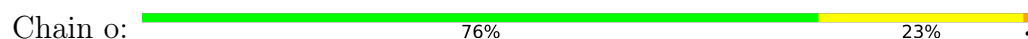
- Molecule 9: 60S ribosomal protein L7

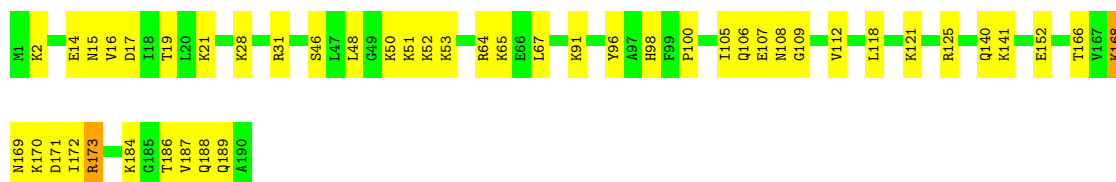


- Molecule 10: 60S ribosomal protein L7a

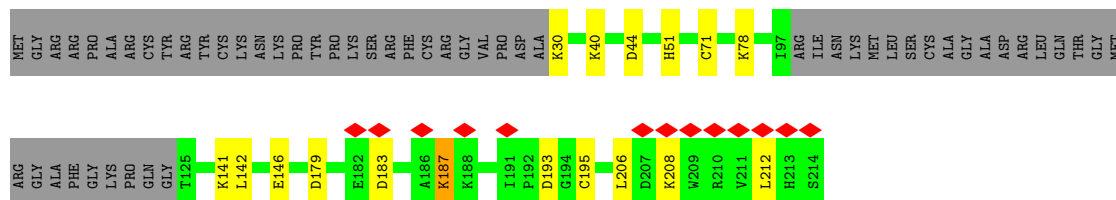


- Molecule 11: 60S ribosomal protein L9

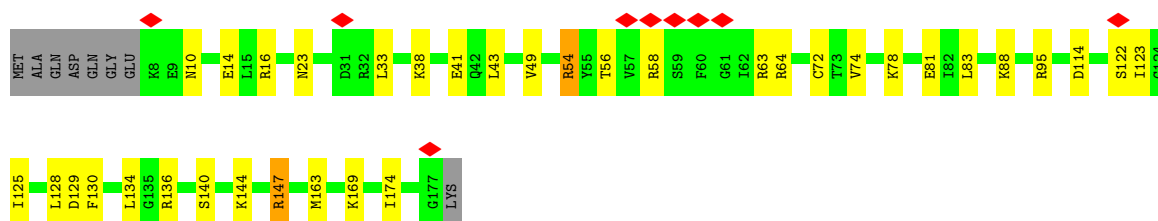
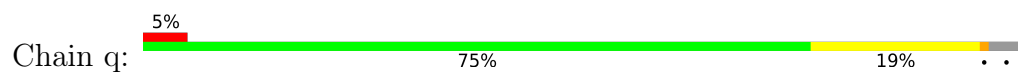




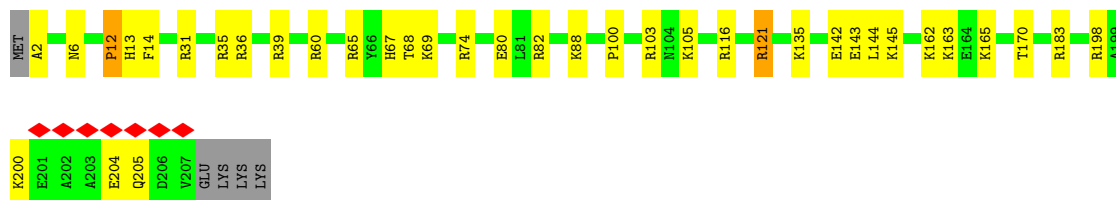
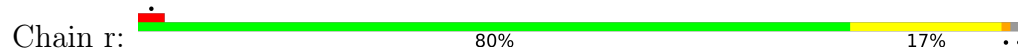
- Molecule 12: 60S ribosomal protein L10-like



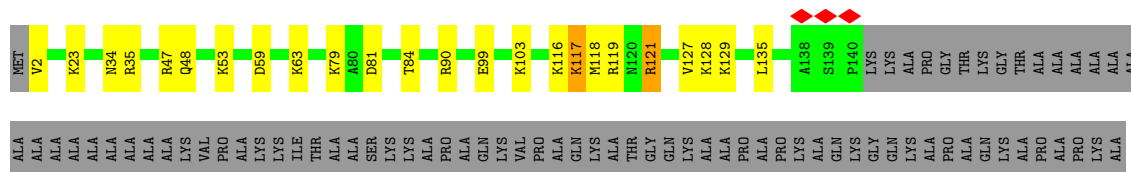
- Molecule 13: 60S ribosomal protein L11



- Molecule 14: 60S ribosomal protein L13




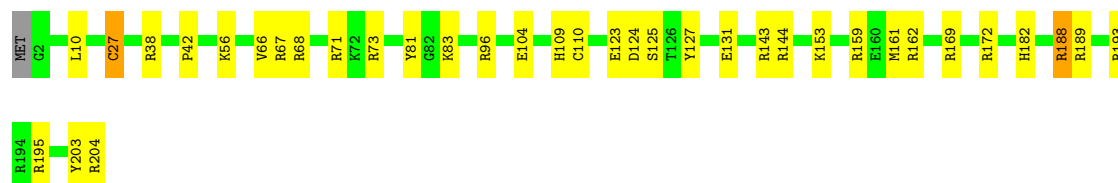
- Molecule 15: 60S ribosomal protein L14




SER
GLY
LYS
LYS
ALA

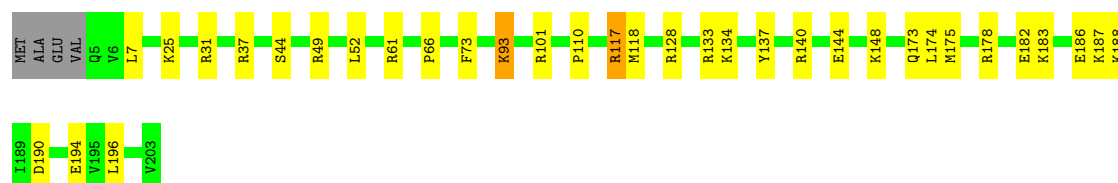
- Molecule 16: 60S ribosomal protein L15

Chain t:  82% 17%



- Molecule 17: 60S ribosomal protein L13a

Chain I:  81% 16%




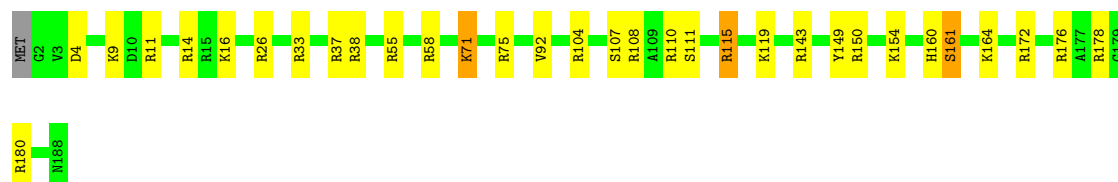
- Molecule 18: 60S ribosomal protein L17

Chain J:  70% 12% 17%



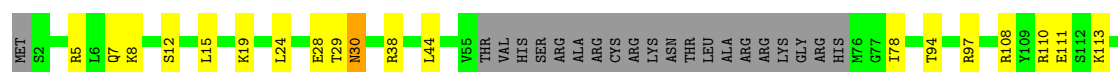
- Molecule 19: 60S ribosomal protein L18

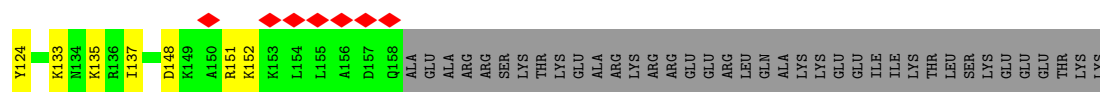
Chain K:  82% 15%



- Molecule 20: 60S ribosomal protein L19

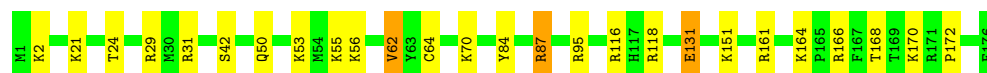
Chain L:  57% 13% 30%





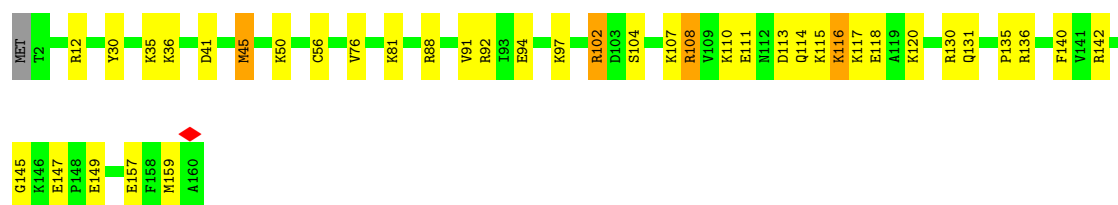
- Molecule 21: 60S ribosomal protein L18a

Chain M: 85% 13% •



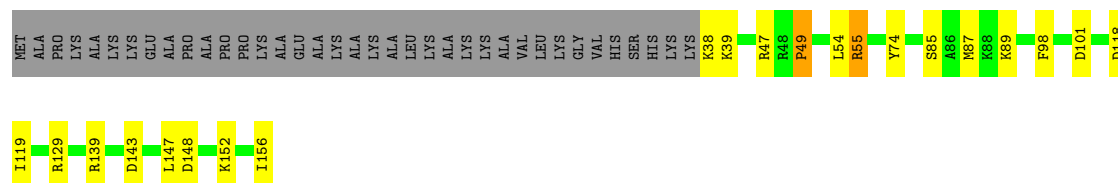
- Molecule 22: 60S ribosomal protein L21

Chain N: 75% 22% ••



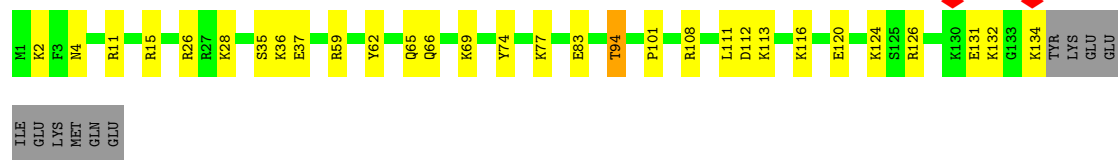
- Molecule 23: 60S ribosomal protein L23a

Chain R: 63% 12% • 24%



- Molecule 24: 60S ribosomal protein L26

Chain S: 72% 20% • 8%




- Molecule 25: 60S ribosomal protein L27

Chain T: 81% 18% •



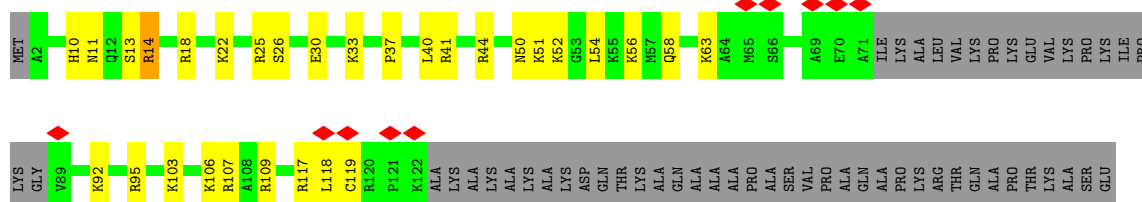
- Molecule 26: 60S ribosomal protein L27a

Chain U:  84% 14% ..



- Molecule 27: 60S ribosomal protein L29

Chain V:  6% 47% 18% • 35%



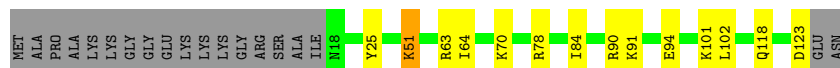
- Molecule 28: 60S ribosomal protein L30

Chain W:  68% 18% • 13%




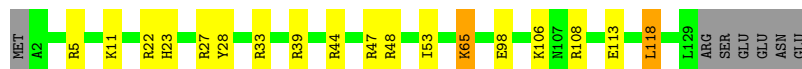
- Molecule 29: 60S ribosomal protein L31

Chain X:  74% 10% • 15%




- Molecule 30: 60S ribosomal protein L32

Chain Y:  81% 12% • 5%




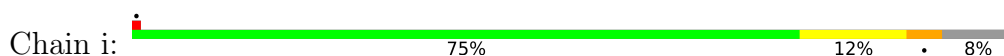
- Molecule 31: 60S ribosomal protein L35a

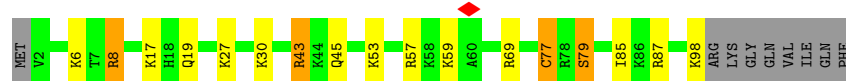
Chain Z:  86% 13% •



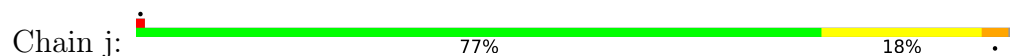
- Molecule 32: 60S ribosomal protein L34

Chain a:  76% 20% •

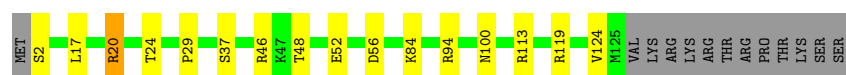
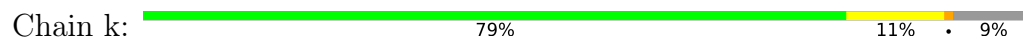




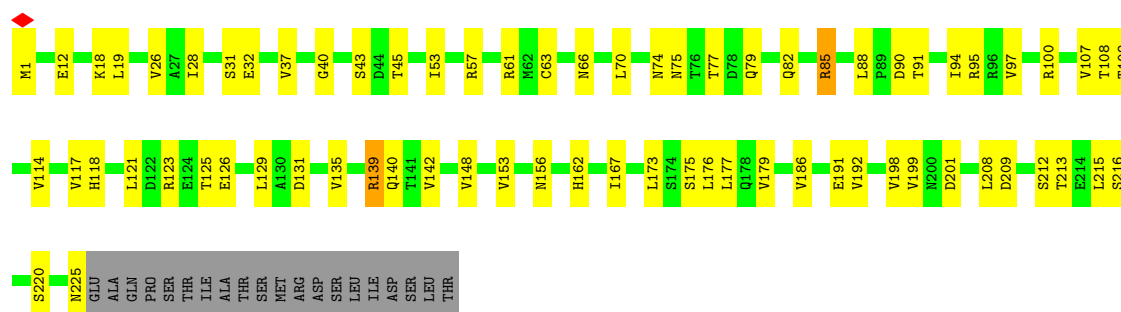
- Molecule 39: 60S ribosomal protein L37a



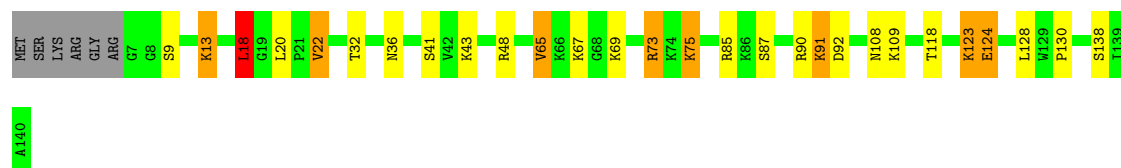
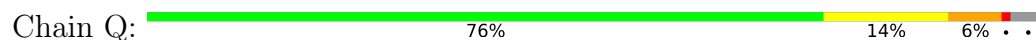
- Molecule 40: 60S ribosomal protein L28



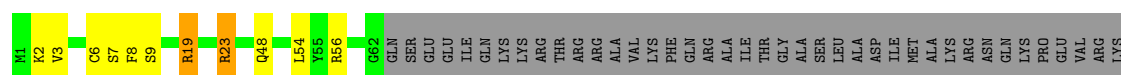
- Molecule 41: Eukaryotic translation initiation factor 6



- Molecule 42: 60S ribosomal protein L23



- Molecule 43: 60S ribosomal protein L24



ALA	GLN	ARG	GLU	GLN	ALA	ILE	ARG	ALA	LYS	GLU	ALA	LYS	LYS	LYS	LYS	GLN	ALA	SER	LYS	LYS	THR	ALA	MET	ALA	ALA	ALA	LYS	ALA	PRO	THR	LYS	ALA	ALA	PRO	LYS	GLN	LYS	ILE	VAL	LYS	PRO	VAL	LYS	VAL	SER	ALA	PRO	ARG	VAL	GLY	GLY	LYS	ARG
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	30000	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.235	Depositor
Minimum map value	-0.004	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	424.96, 424.96, 424.96	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: OMG, NA, BR, OMC, K, 5MC, OMU, ZN, PSU, MG, 6MZ, A2M, UR3, 1MA

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.23	255/76620 (0.3%)	1.48	1340/119500 (1.1%)
2	B	0.95	8/2858 (0.3%)	1.27	28/4455 (0.6%)
3	C	1.26	13/3450 (0.4%)	1.51	58/5372 (1.1%)
4	D	0.82	3/1925 (0.2%)	1.63	28/2581 (1.1%)
5	E	0.72	1/3265 (0.0%)	1.46	35/4369 (0.8%)
6	F	0.80	4/2909 (0.1%)	1.66	68/3908 (1.7%)
7	G	0.52	0/2422	1.25	9/3244 (0.3%)
8	H	0.58	1/1801 (0.1%)	1.30	16/2418 (0.7%)
9	m	0.80	2/1905 (0.1%)	1.48	28/2539 (1.1%)
10	n	0.53	0/1840	1.29	14/2476 (0.6%)
11	o	0.45	0/1537	1.10	4/2066 (0.2%)
12	p	0.39	0/1312	0.94	2/1754 (0.1%)
13	q	0.42	0/1381	0.99	5/1848 (0.3%)
14	r	0.68	0/1695	1.41	21/2270 (0.9%)
15	s	0.54	0/1161	1.27	10/1554 (0.6%)
16	t	0.91	2/1766 (0.1%)	1.68	41/2366 (1.7%)
17	I	0.73	1/1666 (0.1%)	1.53	19/2228 (0.9%)
18	J	0.84	1/1259 (0.1%)	1.49	13/1689 (0.8%)
19	K	0.82	1/1537 (0.1%)	1.69	31/2052 (1.5%)
20	L	0.59	0/1150	1.30	6/1523 (0.4%)
21	M	0.67	0/1501	1.44	14/2013 (0.7%)
22	N	0.69	0/1326	1.52	20/1770 (1.1%)
23	R	0.62	0/993	1.43	10/1334 (0.7%)
24	S	0.79	1/1132 (0.1%)	1.52	10/1504 (0.7%)
25	T	0.49	0/1130	1.16	4/1507 (0.3%)
26	U	0.86	2/1191 (0.2%)	1.60	18/1591 (1.1%)
27	V	0.61	1/850 (0.1%)	1.46	13/1123 (1.2%)
28	W	0.52	0/783	1.19	3/1052 (0.3%)
29	X	0.65	0/883	1.35	5/1190 (0.4%)
30	Y	0.89	1/1071 (0.1%)	1.60	16/1429 (1.1%)
31	Z	0.82	0/901	1.54	10/1206 (0.8%)
32	a	0.79	1/898 (0.1%)	1.53	14/1197 (1.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	b	0.64	1/1023 (0.1%)	1.44	11/1351 (0.8%)
34	c	0.58	0/843	1.48	18/1115 (1.6%)
35	d	0.92	2/732 (0.3%)	1.76	22/968 (2.3%)
36	e	0.41	0/251	1.00	0/330
37	f	0.64	0/454	1.43	6/599 (1.0%)
38	i	0.56	0/807	1.42	10/1065 (0.9%)
39	j	0.84	1/718 (0.1%)	1.73	19/953 (2.0%)
40	k	0.80	1/1007 (0.1%)	1.49	11/1351 (0.8%)
41	P	0.41	0/1736	0.96	1/2362 (0.0%)
42	Q	0.83	0/1007	1.59	15/1350 (1.1%)
43	u	0.73	1/532 (0.2%)	1.30	3/708 (0.4%)
All	All	1.05	304/135228 (0.2%)	1.46	2029/199280 (1.0%)

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
1	A	0	59
3	C	0	2
8	H	0	1
21	M	0	1
33	b	0	1
34	c	0	2
43	u	0	1
All	All	0	67

The worst 5 of 304 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	4273	A	O3'-P	18.99	1.83	1.61
32	a	2	VAL	N-CA	14.24	1.74	1.46
1	A	3823	G	O3'-P	13.95	1.77	1.61
1	A	3663	A	O3'-P	-10.66	1.48	1.61
3	C	150	C	O3'-P	-10.39	1.48	1.61

The worst 5 of 2029 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	109	G	O5'-P-OP1	-31.06	73.42	110.70
1	A	277	G	O5'-P-OP1	-29.77	74.98	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	109	G	O5'-P-OP2	-29.56	75.23	110.70
4	D	193	ARG	NE-CZ-NH2	-27.76	106.42	120.30
1	A	2333	G	O5'-P-OP2	-22.64	83.54	110.70

There are no chirality outliers.

5 of 67 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	275	C	Sidechain
1	A	276	C	Sidechain
1	A	292	G	Sidechain
1	A	91	G	Sidechain
1	A	93	G	Sidechain

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	D	244/257 (95%)	234 (96%)	9 (4%)	1 (0%)	34	48
5	E	394/430 (92%)	373 (95%)	20 (5%)	1 (0%)	41	55
6	F	357/427 (84%)	341 (96%)	16 (4%)	0	100	100
7	G	291/297 (98%)	280 (96%)	10 (3%)	1 (0%)	41	55
8	H	215/288 (75%)	202 (94%)	13 (6%)	0	100	100
9	m	223/248 (90%)	214 (96%)	9 (4%)	0	100	100
10	n	219/266 (82%)	202 (92%)	15 (7%)	2 (1%)	17	25
11	o	188/190 (99%)	169 (90%)	12 (6%)	7 (4%)	3	2

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	p	154/214 (72%)	146 (95%)	8 (5%)	0	100	100
13	q	168/178 (94%)	157 (94%)	10 (6%)	1 (1%)	25	36
14	r	204/211 (97%)	195 (96%)	9 (4%)	0	100	100
15	s	137/220 (62%)	128 (93%)	9 (7%)	0	100	100
16	t	203/204 (100%)	196 (97%)	7 (3%)	0	100	100
17	I	197/203 (97%)	192 (98%)	5 (2%)	0	100	100
18	J	150/184 (82%)	148 (99%)	2 (1%)	0	100	100
19	K	185/188 (98%)	176 (95%)	9 (5%)	0	100	100
20	L	133/196 (68%)	130 (98%)	1 (1%)	2 (2%)	10	14
21	M	174/176 (99%)	170 (98%)	4 (2%)	0	100	100
22	N	157/160 (98%)	146 (93%)	10 (6%)	1 (1%)	25	36
23	R	117/156 (75%)	116 (99%)	1 (1%)	0	100	100
24	S	132/145 (91%)	124 (94%)	7 (5%)	1 (1%)	19	29
25	T	133/136 (98%)	122 (92%)	11 (8%)	0	100	100
26	U	145/148 (98%)	140 (97%)	4 (3%)	1 (1%)	22	32
27	V	100/159 (63%)	91 (91%)	9 (9%)	0	100	100
28	W	98/115 (85%)	91 (93%)	7 (7%)	0	100	100
29	X	104/125 (83%)	100 (96%)	4 (4%)	0	100	100
30	Y	126/135 (93%)	125 (99%)	1 (1%)	0	100	100
31	Z	108/110 (98%)	108 (100%)	0	0	100	100
32	a	110/117 (94%)	105 (96%)	5 (4%)	0	100	100
33	b	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
34	c	100/105 (95%)	93 (93%)	4 (4%)	3 (3%)	4	3
35	d	85/97 (88%)	82 (96%)	3 (4%)	0	100	100
36	e	25/70 (36%)	24 (96%)	1 (4%)	0	100	100
37	f	48/157 (31%)	45 (94%)	3 (6%)	0	100	100
38	i	95/106 (90%)	87 (92%)	6 (6%)	2 (2%)	7	8
39	j	89/92 (97%)	81 (91%)	7 (8%)	1 (1%)	14	20
40	k	122/137 (89%)	121 (99%)	1 (1%)	0	100	100
41	P	223/245 (91%)	173 (78%)	44 (20%)	6 (3%)	5	5
42	Q	132/140 (94%)	122 (92%)	7 (5%)	3 (2%)	6	7

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	u	60/157 (38%)	56 (93%)	3 (5%)	1 (2%)	9	11
All	All	6265/7312 (86%)	5923 (94%)	308 (5%)	34 (0%)	32	41

5 of 34 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	o	98	HIS
11	o	187	VAL
11	o	188	GLN
38	i	79	SER
39	j	39	CYS

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	D	189/199 (95%)	178 (94%)	11 (6%)	20	32
5	E	345/368 (94%)	312 (90%)	33 (10%)	8	12
6	F	297/348 (85%)	270 (91%)	27 (9%)	9	14
7	G	245/250 (98%)	206 (84%)	39 (16%)	2	3
8	H	193/253 (76%)	165 (86%)	28 (14%)	3	3
9	m	194/215 (90%)	179 (92%)	15 (8%)	13	20
10	n	193/223 (86%)	162 (84%)	31 (16%)	2	3
11	o	169/169 (100%)	132 (78%)	37 (22%)	1	1
12	p	138/182 (76%)	122 (88%)	16 (12%)	5	7
13	q	142/149 (95%)	109 (77%)	33 (23%)	1	1
14	r	172/177 (97%)	151 (88%)	21 (12%)	5	6
15	s	118/161 (73%)	101 (86%)	17 (14%)	3	3
16	t	173/172 (101%)	166 (96%)	7 (4%)	31	49
17	I	171/174 (98%)	153 (90%)	18 (10%)	7	9
18	J	133/163 (82%)	122 (92%)	11 (8%)	11	17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	K	164/165 (99%)	152 (93%)	12 (7%)	14	22
20	L	121/175 (69%)	102 (84%)	19 (16%)	2	3
21	M	157/157 (100%)	138 (88%)	19 (12%)	5	6
22	N	139/140 (99%)	115 (83%)	24 (17%)	2	2
23	R	107/133 (80%)	94 (88%)	13 (12%)	5	6
24	S	124/135 (92%)	105 (85%)	19 (15%)	2	3
25	T	117/118 (99%)	96 (82%)	21 (18%)	2	2
26	U	120/121 (99%)	113 (94%)	7 (6%)	20	32
27	V	83/126 (66%)	62 (75%)	21 (25%)	0	0
28	W	84/97 (87%)	64 (76%)	20 (24%)	0	0
29	X	93/110 (84%)	83 (89%)	10 (11%)	6	9
30	Y	114/121 (94%)	107 (94%)	7 (6%)	18	30
31	Z	89/89 (100%)	85 (96%)	4 (4%)	27	44
32	a	96/100 (96%)	85 (88%)	11 (12%)	5	7
33	b	109/110 (99%)	95 (87%)	14 (13%)	4	5
34	c	86/89 (97%)	69 (80%)	17 (20%)	1	1
35	d	74/80 (92%)	69 (93%)	5 (7%)	16	25
36	e	29/65 (45%)	26 (90%)	3 (10%)	7	10
37	f	47/130 (36%)	41 (87%)	6 (13%)	4	5
38	i	86/94 (92%)	77 (90%)	9 (10%)	7	9
39	j	74/75 (99%)	64 (86%)	10 (14%)	4	4
40	k	107/121 (88%)	101 (94%)	6 (6%)	21	34
41	P	195/213 (92%)	129 (66%)	66 (34%)	0	0
42	Q	102/107 (95%)	79 (78%)	23 (22%)	1	1
43	u	54/126 (43%)	46 (85%)	8 (15%)	3	3
All	All	5443/6200 (88%)	4725 (87%)	718 (13%)	7	4

5 of 718 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
25	T	100	VAL
34	c	66	ASP
26	U	130	SER

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Mol	Chain	Res	Type
25	T	93	LYS
29	X	63	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 144 such sidechains are listed below:

Mol	Chain	Res	Type
30	Y	107	ASN
43	u	48	GLN
32	a	100	GLN
39	j	56	HIS
12	p	92	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	3280/5070 (64%)	711 (21%)	151 (4%)
2	B	119/121 (98%)	16 (13%)	6 (5%)
3	C	145/157 (92%)	21 (14%)	4 (2%)
All	All	3544/5348 (66%)	748 (21%)	161 (4%)

5 of 748 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	2	G
1	A	4	G
1	A	15	A
1	A	17	A
1	A	18	C

5 of 161 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	4228	OMG
1	A	4910	G
1	A	4265	U
1	A	4449	A
1	A	5061	A

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

117 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$
1	PSU	A	4521	46,1,44	18,21,22	2.44	8 (44%)	22,30,33	4.68	13 (59%)
1	OMC	A	2422	1,44	19,22,23	2.58	6 (31%)	26,31,34	9.61	12 (46%)
1	PSU	A	1860	1	18,21,22	1.88	3 (16%)	22,30,33	3.07	4 (18%)
1	PSU	A	4420	1	18,21,22	1.62	2 (11%)	22,30,33	2.13	6 (27%)
1	OMG	A	4618	46,1	18,26,27	1.94	4 (22%)	19,38,41	3.03	8 (42%)
1	PSU	A	4353	46,1	18,21,22	2.53	7 (38%)	22,30,33	4.81	14 (63%)
1	OMU	A	2415	1	19,22,23	1.63	5 (26%)	26,31,34	5.14	12 (46%)
1	OMC	A	3869	1	19,22,23	2.00	6 (31%)	26,31,34	2.63	8 (30%)
1	A2M	A	4590	1	18,25,26	2.13	5 (27%)	18,36,39	2.79	10 (55%)
1	PSU	A	5010	1	18,21,22	1.49	2 (11%)	22,30,33	2.12	5 (22%)
1	OMC	A	2351	1,44	19,22,23	2.43	9 (47%)	26,31,34	2.55	13 (50%)
1	PSU	A	1677	46,1	18,21,22	3.32	11 (61%)	22,30,33	3.93	10 (45%)
1	OMG	A	4623	1	18,26,27	2.66	6 (33%)	19,38,41	2.76	7 (36%)
1	PSU	A	4471	1	18,21,22	1.42	5 (27%)	22,30,33	3.37	9 (40%)
1	PSU	A	1683	46,1	18,21,22	2.86	10 (55%)	22,30,33	4.18	13 (59%)
1	PSU	A	1781	1	18,21,22	2.03	3 (16%)	22,30,33	2.83	6 (27%)
1	PSU	A	4442	1	18,21,22	1.85	3 (16%)	22,30,33	4.30	9 (40%)
1	A2M	A	2815	1	18,25,26	1.50	3 (16%)	18,36,39	1.80	3 (16%)
1	OMU	A	4498	46,1	19,22,23	1.35	3 (15%)	26,31,34	2.60	9 (34%)
1	OMG	A	3627	1	18,26,27	1.78	5 (27%)	19,38,41	2.78	5 (26%)
1	1MA	A	1322	1,44	16,25,26	2.29	6 (37%)	18,37,40	2.59	7 (38%)
1	OMC	A	3841	1	19,22,23	2.07	6 (31%)	26,31,34	1.96	7 (26%)
3	PSU	C	55	3	18,21,22	1.41	3 (16%)	22,30,33	3.59	10 (45%)
1	PSU	A	3637	46,1	18,21,22	2.21	7 (38%)	22,30,33	4.12	12 (54%)
1	PSU	A	4457	1	18,21,22	2.02	6 (33%)	22,30,33	3.47	9 (40%)
1	OMG	A	1316	46,1	18,26,27	1.85	6 (33%)	19,38,41	2.87	8 (42%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMC	A	2861	1	19,22,23	1.53	4 (21%)	26,31,34	1.07	3 (11%)
1	OMU	A	3925	1	19,22,23	1.74	5 (26%)	26,31,34	3.99	13 (50%)
1	OMG	A	4392	1	18,26,27	1.70	5 (27%)	19,38,41	3.30	6 (31%)
1	5MC	A	4447	46,1	18,22,23	1.88	2 (11%)	26,32,35	3.20	14 (53%)
1	A2M	A	2401	1	18,25,26	1.35	2 (11%)	18,36,39	2.51	10 (55%)
1	PSU	A	4673	46,1	18,21,22	2.18	5 (27%)	22,30,33	4.58	13 (59%)
1	OMG	A	1625	46,1	18,26,27	1.67	5 (27%)	19,38,41	3.29	12 (63%)
1	PSU	A	4972	46,1	18,21,22	2.31	6 (33%)	22,30,33	4.72	14 (63%)
1	A2M	A	4571	1	18,25,26	1.38	1 (5%)	18,36,39	2.87	9 (50%)
1	6MZ	A	4220	1	18,25,26	1.51	4 (22%)	16,36,39	4.45	6 (37%)
1	A2M	A	1524	1	18,25,26	2.03	6 (33%)	18,36,39	3.08	6 (33%)
1	PSU	A	2632	1	18,21,22	1.72	3 (16%)	22,30,33	2.03	7 (31%)
1	OMU	A	4227	1	19,22,23	1.76	5 (26%)	26,31,34	5.63	16 (61%)
1	OMU	A	4306	1	19,22,23	2.46	6 (31%)	26,31,34	3.34	13 (50%)
1	PSU	A	1862	1	18,21,22	1.70	3 (16%)	22,30,33	3.15	11 (50%)
1	OMG	A	2424	1	18,26,27	1.96	7 (38%)	19,38,41	4.36	12 (63%)
1	PSU	A	4423	1	18,21,22	1.61	2 (11%)	22,30,33	2.00	5 (22%)
1	OMC	A	3701	46,1	19,22,23	1.49	3 (15%)	26,31,34	2.25	9 (34%)
1	PSU	A	3853	1,44	18,21,22	2.65	10 (55%)	22,30,33	5.12	11 (50%)
1	PSU	A	4312	1	18,21,22	1.79	6 (33%)	22,30,33	3.63	12 (54%)
1	PSU	A	3695	46,1	18,21,22	1.88	5 (27%)	22,30,33	2.50	7 (31%)
1	PSU	A	1792	46,1	18,21,22	1.36	1 (5%)	22,30,33	2.27	7 (31%)
1	OMG	A	3744	1	18,26,27	1.57	5 (27%)	19,38,41	2.45	11 (57%)
1	PSU	A	3729	1	18,21,22	1.85	5 (27%)	22,30,33	2.96	9 (40%)
1	OMC	A	4536	1	19,22,23	2.11	9 (47%)	26,31,34	2.51	12 (46%)
1	PSU	A	4299	1	18,21,22	2.27	6 (33%)	22,30,33	4.39	10 (45%)
1	PSU	A	4293	1	18,21,22	1.53	4 (22%)	22,30,33	3.96	12 (54%)
3	PSU	C	69	3	18,21,22	2.05	4 (22%)	22,30,33	2.92	9 (40%)
1	PSU	A	3639	1	18,21,22	2.56	6 (33%)	22,30,33	4.59	12 (54%)
1	A2M	A	3785	1	18,25,26	1.31	2 (11%)	18,36,39	2.52	7 (38%)
1	A2M	A	1534	1,44	18,25,26	2.25	6 (33%)	18,36,39	2.19	6 (33%)
1	A2M	A	3830	1	18,25,26	1.72	4 (22%)	18,36,39	1.98	3 (16%)
1	PSU	A	1744	46,1	18,21,22	1.78	2 (11%)	22,30,33	2.71	8 (36%)
1	PSU	A	4403	46,1	18,21,22	2.32	6 (33%)	22,30,33	3.73	10 (45%)
1	OMU	A	4620	1	19,22,23	2.06	6 (31%)	26,31,34	4.12	14 (53%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMC	A	2365	1,44	19,22,23	1.46	4 (21%)	26,31,34	2.49	10 (38%)
1	5MC	A	3782	1,44	18,22,23	1.67	4 (22%)	26,32,35	1.79	4 (15%)
1	PSU	A	4689	1	18,21,22	1.86	5 (27%)	22,30,33	3.06	11 (50%)
1	PSU	A	4431	46,1	18,21,22	1.26	2 (11%)	22,30,33	2.49	6 (27%)
1	PSU	A	4532	46,1	18,21,22	2.86	9 (50%)	22,30,33	4.16	17 (77%)
1	A2M	A	400	1	18,25,26	1.53	3 (16%)	18,36,39	2.24	5 (27%)
1	OMG	A	2364	1	18,26,27	2.34	7 (38%)	19,38,41	3.48	13 (68%)
1	PSU	A	4361	46,1	18,21,22	1.69	5 (27%)	22,30,33	3.92	9 (40%)
1	OMG	A	4494	1	18,26,27	2.10	7 (38%)	19,38,41	3.01	8 (42%)
1	PSU	A	2508	1	18,21,22	1.97	7 (38%)	22,30,33	3.11	10 (45%)
1	PSU	A	3920	1,44	18,21,22	2.52	9 (50%)	22,30,33	4.23	13 (59%)
1	PSU	A	1536	1	18,21,22	2.70	8 (44%)	22,30,33	4.92	13 (59%)
1	A2M	A	398	1	18,25,26	2.08	4 (22%)	18,36,39	2.40	5 (27%)
1	OMG	A	1522	1	18,26,27	2.44	6 (33%)	19,38,41	2.60	9 (47%)
1	OMU	A	2837	1	19,22,23	2.33	6 (31%)	26,31,34	3.98	11 (42%)
1	PSU	A	4296	1	18,21,22	1.80	5 (27%)	22,30,33	3.04	13 (59%)
1	PSU	A	4579	1	18,21,22	1.70	4 (22%)	22,30,33	3.51	11 (50%)
3	OMG	C	75	3	18,26,27	1.27	1 (5%)	19,38,41	1.55	5 (26%)
1	A2M	A	1871	46,1,44	18,25,26	1.67	4 (22%)	18,36,39	2.38	7 (38%)
1	A2M	A	2363	1,44	18,25,26	1.73	4 (22%)	18,36,39	3.32	8 (44%)
1	OMC	A	3887	1	19,22,23	1.18	1 (5%)	26,31,34	3.82	13 (50%)
1	OMC	A	2824	1	19,22,23	1.51	5 (26%)	26,31,34	2.81	13 (50%)
1	PSU	A	2839	1	18,21,22	1.77	4 (22%)	22,30,33	3.73	15 (68%)
1	A2M	A	1326	1	18,25,26	1.74	3 (16%)	18,36,39	2.64	6 (33%)
1	PSU	A	4552	1	18,21,22	1.83	7 (38%)	22,30,33	4.53	14 (63%)
1	OMG	A	4499	1	18,26,27	1.50	4 (22%)	19,38,41	1.68	4 (21%)
1	PSU	A	3884	46,1	18,21,22	2.87	10 (55%)	22,30,33	4.09	14 (63%)
1	OMG	A	2876	1	18,26,27	2.01	1 (5%)	19,38,41	2.31	3 (15%)
1	PSU	A	1782	1	18,21,22	2.55	4 (22%)	22,30,33	3.13	9 (40%)
1	A2M	A	3867	1	18,25,26	1.81	4 (22%)	18,36,39	1.57	4 (22%)
1	PSU	A	4576	1	18,21,22	1.61	5 (27%)	22,30,33	3.23	12 (54%)
1	OMG	A	4228	1	18,26,27	3.20	9 (50%)	19,38,41	5.35	14 (73%)
1	PSU	A	3851	1	18,21,22	1.64	4 (22%)	22,30,33	4.68	16 (72%)
1	PSU	A	1582	1	18,21,22	1.92	3 (16%)	22,30,33	4.03	15 (68%)
1	PSU	A	3844	1	18,21,22	2.32	5 (27%)	22,30,33	4.20	13 (59%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	A2M	A	3825	1	18,25,26	1.36	3 (16%)	18,36,39	2.63	7 (38%)
1	PSU	A	4493	46,1	18,21,22	1.30	2 (11%)	22,30,33	7.39	13 (59%)
1	OMU	A	3818	46,1	19,22,23	1.93	6 (31%)	26,31,34	3.62	11 (42%)
1	A2M	A	3718	1	18,25,26	1.57	3 (16%)	18,36,39	1.94	6 (33%)
1	OMC	A	2804	1	19,22,23	1.54	3 (15%)	26,31,34	1.91	9 (34%)
1	OMC	A	4456	1	19,22,23	1.74	5 (26%)	26,31,34	2.64	14 (53%)
1	UR3	A	4530	1	19,22,23	2.00	5 (26%)	26,32,35	2.91	14 (53%)
1	OMG	A	3899	1	18,26,27	2.57	7 (38%)	19,38,41	1.54	3 (15%)
1	PSU	A	3715	1	18,21,22	1.94	4 (22%)	22,30,33	1.86	7 (31%)
1	PSU	A	4500	46,1	18,21,22	1.75	5 (27%)	22,30,33	4.02	9 (40%)
1	OMG	A	4196	1,44	18,26,27	1.40	1 (5%)	19,38,41	1.90	4 (21%)
1	A2M	A	3724	1	18,25,26	1.49	3 (16%)	18,36,39	1.60	4 (22%)
1	OMG	A	3792	1	18,26,27	1.73	4 (22%)	19,38,41	2.08	6 (31%)
1	OMC	A	3808	46,1	19,22,23	1.24	1 (5%)	26,31,34	1.91	7 (26%)
1	PSU	A	4628	1	18,21,22	2.41	6 (33%)	22,30,33	4.28	14 (63%)
1	A2M	A	4523	1,44	18,25,26	1.76	6 (33%)	18,36,39	2.68	7 (38%)
1	PSU	A	5001	46,1	18,21,22	1.69	5 (27%)	22,30,33	3.58	12 (54%)
1	OMG	A	4637	46,1	18,26,27	1.61	3 (16%)	19,38,41	2.55	6 (31%)
1	OMG	A	4370	1,44	18,26,27	1.45	4 (22%)	19,38,41	3.67	7 (36%)
1	A2M	A	2787	46,1,44	18,25,26	1.59	4 (22%)	18,36,39	3.24	10 (55%)
1	OMC	A	1340	1	19,22,23	1.45	5 (26%)	26,31,34	2.73	12 (46%)

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
1	PSU	A	4521	46,1,44	-	0/7/25/26	0/2/2/2
1	OMC	A	2422	1,44	-	1/9/27/28	0/2/2/2
1	PSU	A	1860	1	-	0/7/25/26	0/2/2/2
1	PSU	A	4420	1	-	0/7/25/26	0/2/2/2
1	OMG	A	4618	46,1	-	0/5/27/28	0/3/3/3
1	PSU	A	4353	46,1	-	0/7/25/26	0/2/2/2
1	OMU	A	2415	1	-	1/9/27/28	0/2/2/2
1	OMC	A	3869	1	-	1/9/27/28	0/2/2/2
1	A2M	A	4590	1	-	1/5/27/28	0/3/3/3
1	PSU	A	5010	1	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMC	A	2351	1,44	-	2/9/27/28	0/2/2/2
1	PSU	A	1677	46,1	-	1/7/25/26	0/2/2/2
1	OMG	A	4623	1	-	0/5/27/28	0/3/3/3
1	PSU	A	4471	1	-	0/7/25/26	0/2/2/2
1	PSU	A	1683	46,1	-	0/7/25/26	0/2/2/2
1	PSU	A	1781	1	-	0/7/25/26	0/2/2/2
1	PSU	A	4442	1	-	0/7/25/26	0/2/2/2
1	A2M	A	2815	1	-	3/5/27/28	0/3/3/3
1	OMU	A	4498	46,1	-	0/9/27/28	0/2/2/2
1	OMG	A	3627	1	-	0/5/27/28	0/3/3/3
1	1MA	A	1322	1,44	-	0/3/25/26	0/3/3/3
1	OMC	A	3841	1	-	0/9/27/28	0/2/2/2
3	PSU	C	55	3	-	0/7/25/26	0/2/2/2
1	PSU	A	3637	46,1	-	0/7/25/26	0/2/2/2
1	PSU	A	4457	1	-	0/7/25/26	0/2/2/2
1	OMG	A	1316	46,1	-	0/5/27/28	0/3/3/3
1	OMC	A	2861	1	-	0/9/27/28	0/2/2/2
1	OMU	A	3925	1	-	0/9/27/28	0/2/2/2
1	OMG	A	4392	1	-	0/5/27/28	0/3/3/3
1	5MC	A	4447	46,1	-	4/7/25/26	0/2/2/2
1	A2M	A	2401	1	-	0/5/27/28	0/3/3/3
1	PSU	A	4673	46,1	-	0/7/25/26	0/2/2/2
1	OMG	A	1625	46,1	-	1/5/27/28	0/3/3/3
1	PSU	A	4972	46,1	-	2/7/25/26	0/2/2/2
1	A2M	A	4571	1	-	0/5/27/28	0/3/3/3
1	6MZ	A	4220	1	-	0/5/27/28	0/3/3/3
1	A2M	A	1524	1	-	1/5/27/28	0/3/3/3
1	PSU	A	2632	1	-	0/7/25/26	0/2/2/2
1	OMU	A	4227	1	-	2/9/27/28	0/2/2/2
1	OMU	A	4306	1	-	0/9/27/28	0/2/2/2
1	PSU	A	1862	1	-	0/7/25/26	0/2/2/2
1	OMG	A	2424	1	-	2/5/27/28	0/3/3/3
1	PSU	A	4423	1	-	0/7/25/26	0/2/2/2
1	OMC	A	3701	46,1	-	5/9/27/28	0/2/2/2
1	PSU	A	3853	1,44	-	0/7/25/26	0/2/2/2
1	PSU	A	4312	1	-	0/7/25/26	0/2/2/2
1	PSU	A	3695	46,1	-	0/7/25/26	0/2/2/2
1	PSU	A	1792	46,1	-	2/7/25/26	0/2/2/2
1	OMG	A	3744	1	-	0/5/27/28	0/3/3/3
1	PSU	A	3729	1	-	1/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMC	A	4536	1	-	0/9/27/28	0/2/2/2
1	PSU	A	4299	1	-	0/7/25/26	0/2/2/2
1	PSU	A	4293	1	-	0/7/25/26	0/2/2/2
3	PSU	C	69	3	-	0/7/25/26	0/2/2/2
1	PSU	A	3639	1	-	0/7/25/26	0/2/2/2
1	A2M	A	3785	1	-	2/5/27/28	0/3/3/3
1	A2M	A	1534	1,44	-	2/5/27/28	0/3/3/3
1	A2M	A	3830	1	-	3/5/27/28	0/3/3/3
1	PSU	A	1744	46,1	-	0/7/25/26	0/2/2/2
1	PSU	A	4403	46,1	-	0/7/25/26	0/2/2/2
1	OMU	A	4620	1	-	0/9/27/28	0/2/2/2
1	OMC	A	2365	1,44	-	2/9/27/28	0/2/2/2
1	5MC	A	3782	1,44	-	0/7/25/26	0/2/2/2
1	PSU	A	4689	1	-	1/7/25/26	0/2/2/2
1	PSU	A	4431	46,1	-	0/7/25/26	0/2/2/2
1	PSU	A	4532	46,1	-	0/7/25/26	0/2/2/2
1	A2M	A	400	1	-	1/5/27/28	0/3/3/3
1	OMG	A	2364	1	-	2/5/27/28	0/3/3/3
1	PSU	A	4361	46,1	-	0/7/25/26	0/2/2/2
1	OMG	A	4494	1	-	0/5/27/28	0/3/3/3
1	PSU	A	2508	1	-	0/7/25/26	0/2/2/2
1	PSU	A	3920	1,44	-	0/7/25/26	0/2/2/2
1	PSU	A	1536	1	-	0/7/25/26	0/2/2/2
1	A2M	A	398	1	-	1/5/27/28	0/3/3/3
1	OMG	A	1522	1	-	0/5/27/28	0/3/3/3
1	OMU	A	2837	1	-	0/9/27/28	0/2/2/2
1	PSU	A	4296	1	-	1/7/25/26	0/2/2/2
1	PSU	A	4579	1	-	0/7/25/26	0/2/2/2
3	OMG	C	75	3	-	1/5/27/28	0/3/3/3
1	A2M	A	1871	46,1,44	-	0/5/27/28	0/3/3/3
1	A2M	A	2363	1,44	-	0/5/27/28	0/3/3/3
1	OMC	A	3887	1	-	0/9/27/28	0/2/2/2
1	OMC	A	2824	1	-	0/9/27/28	0/2/2/2
1	PSU	A	2839	1	-	2/7/25/26	0/2/2/2
1	A2M	A	1326	1	-	0/5/27/28	0/3/3/3
1	PSU	A	4552	1	-	0/7/25/26	0/2/2/2
1	OMG	A	4499	1	-	0/5/27/28	0/3/3/3
1	PSU	A	3884	46,1	-	0/7/25/26	0/2/2/2
1	OMG	A	2876	1	-	0/5/27/28	0/3/3/3
1	PSU	A	1782	1	-	0/7/25/26	0/2/2/2
1	A2M	A	3867	1	-	0/5/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	A	4576	1	-	0/7/25/26	0/2/2/2
1	OMG	A	4228	1	-	1/5/27/28	0/3/3/3
1	PSU	A	3851	1	-	1/7/25/26	0/2/2/2
1	PSU	A	1582	1	-	1/7/25/26	0/2/2/2
1	PSU	A	3844	1	-	1/7/25/26	0/2/2/2
1	A2M	A	3825	1	-	1/5/27/28	0/3/3/3
1	PSU	A	4493	46,1	-	0/7/25/26	0/2/2/2
1	OMU	A	3818	46,1	-	1/9/27/28	0/2/2/2
1	A2M	A	3718	1	-	1/5/27/28	0/3/3/3
1	OMC	A	2804	1	-	0/9/27/28	0/2/2/2
1	OMC	A	4456	1	-	0/9/27/28	0/2/2/2
1	UR3	A	4530	1	-	1/7/25/26	0/2/2/2
1	OMG	A	3899	1	-	0/5/27/28	0/3/3/3
1	PSU	A	3715	1	-	0/7/25/26	0/2/2/2
1	PSU	A	4500	46,1	-	3/7/25/26	0/2/2/2
1	OMG	A	4196	1,44	-	1/5/27/28	0/3/3/3
1	A2M	A	3724	1	-	0/5/27/28	0/3/3/3
1	OMG	A	3792	1	-	0/5/27/28	0/3/3/3
1	OMC	A	3808	46,1	-	1/9/27/28	0/2/2/2
1	PSU	A	4628	1	-	0/7/25/26	0/2/2/2
1	A2M	A	4523	1,44	-	0/5/27/28	0/3/3/3
1	PSU	A	5001	46,1	-	1/7/25/26	0/2/2/2
1	OMG	A	4637	46,1	-	0/5/27/28	0/3/3/3
1	OMG	A	4370	1,44	-	2/5/27/28	0/3/3/3
1	A2M	A	2787	46,1,44	-	0/5/27/28	0/3/3/3
1	OMC	A	1340	1	-	0/9/27/28	0/2/2/2

The worst 5 of 559 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	4228	OMG	O4'-C1'	-9.74	1.27	1.41
1	A	4623	OMG	C6-N1	-8.25	1.25	1.37
1	A	1782	PSU	C6-C5	8.00	1.44	1.35
1	A	1677	PSU	C2'-C1'	-7.78	1.43	1.53
1	A	2422	OMC	C5-C4	7.46	1.60	1.42

The worst 5 of 1103 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2422	OMC	N4-C4-N3	-27.53	69.65	117.97
1	A	2422	OMC	C4-N3-C2	-23.05	83.03	120.25
1	A	4493	PSU	C4-N3-C2	-19.76	97.87	126.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2422	OMC	C5-C4-N4	18.62	149.88	120.57
1	A	4493	PSU	N1-C2-N3	16.91	134.29	115.13

There are no chirality outliers.

5 of 64 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	400	A2M	C1'-C2'-O2'-CM'
1	A	1582	PSU	C3'-C4'-C5'-O5'
1	A	1625	OMG	C3'-C2'-O2'-CM2
1	A	2415	OMU	C1'-C2'-O2'-CM2
1	A	2424	OMG	O4'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 386 ligands modelled in this entry, 386 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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	4273:A	O3'	4274:A	P	1.83
1	A	3823:G	O3'	3824:A	P	1.77

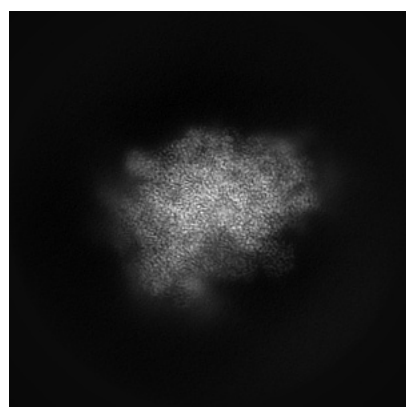
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13094. These allow visual inspection of the internal detail of the map and identification of artifacts.

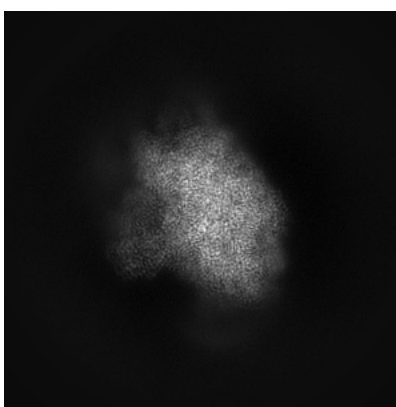
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

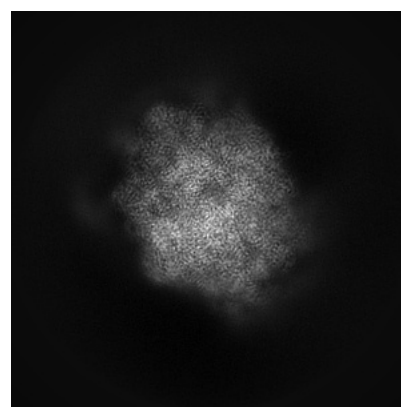
6.1.1 Primary map



X



Y

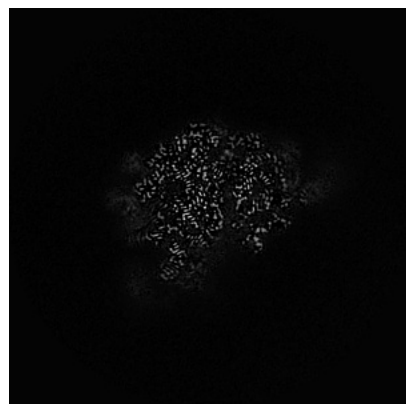


Z

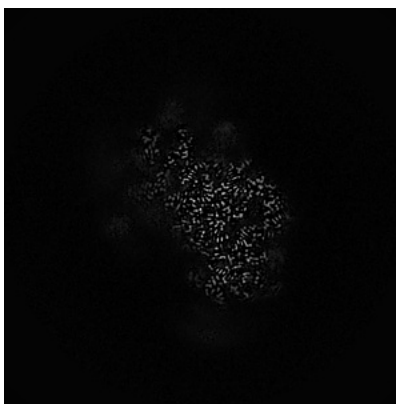
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

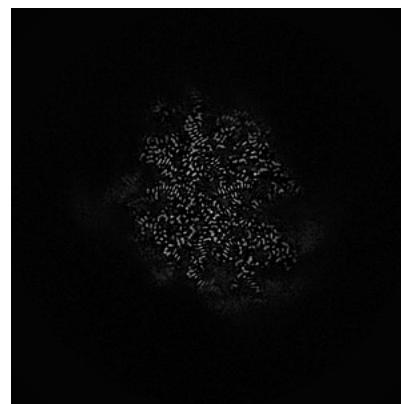
6.2.1 Primary map



X Index: 256



Y Index: 256

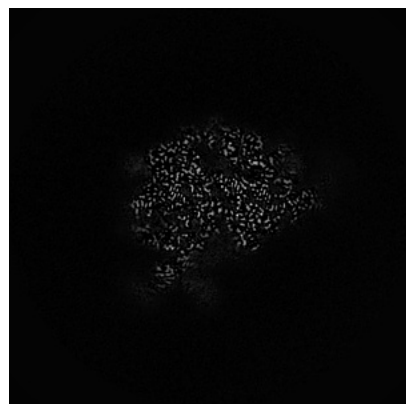


Z Index: 256

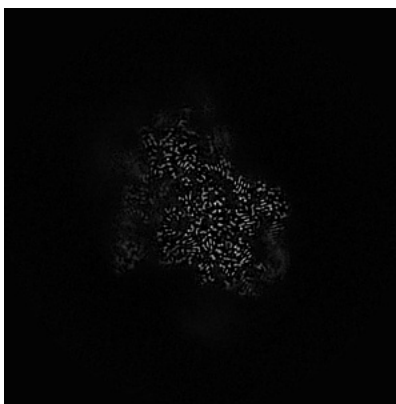
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

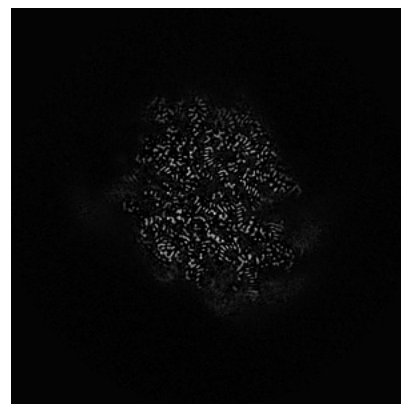
6.3.1 Primary map



X Index: 239



Y Index: 238

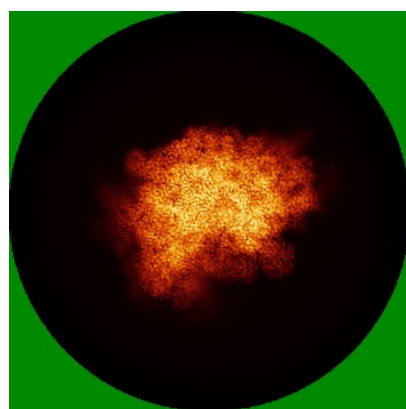


Z Index: 261

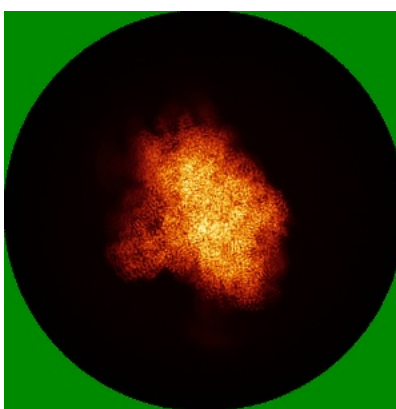
The images above show the largest variance slices of the map in three orthogonal directions.

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

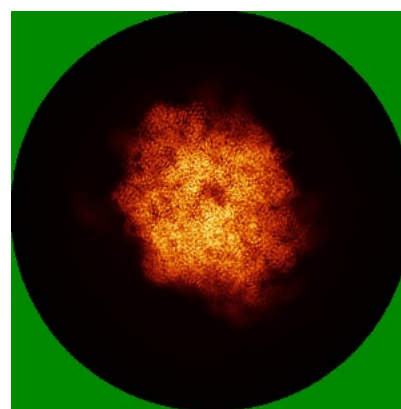
6.4.1 Primary map



X



Y

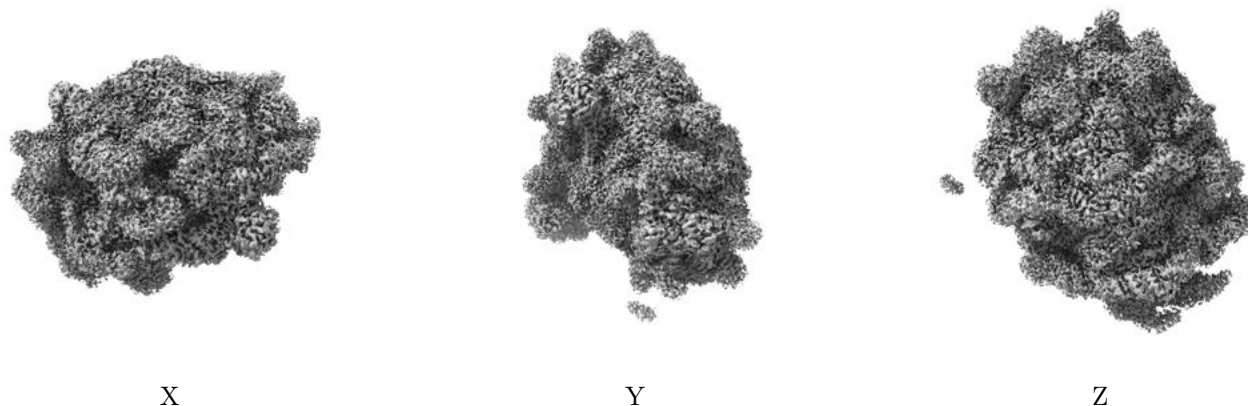


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

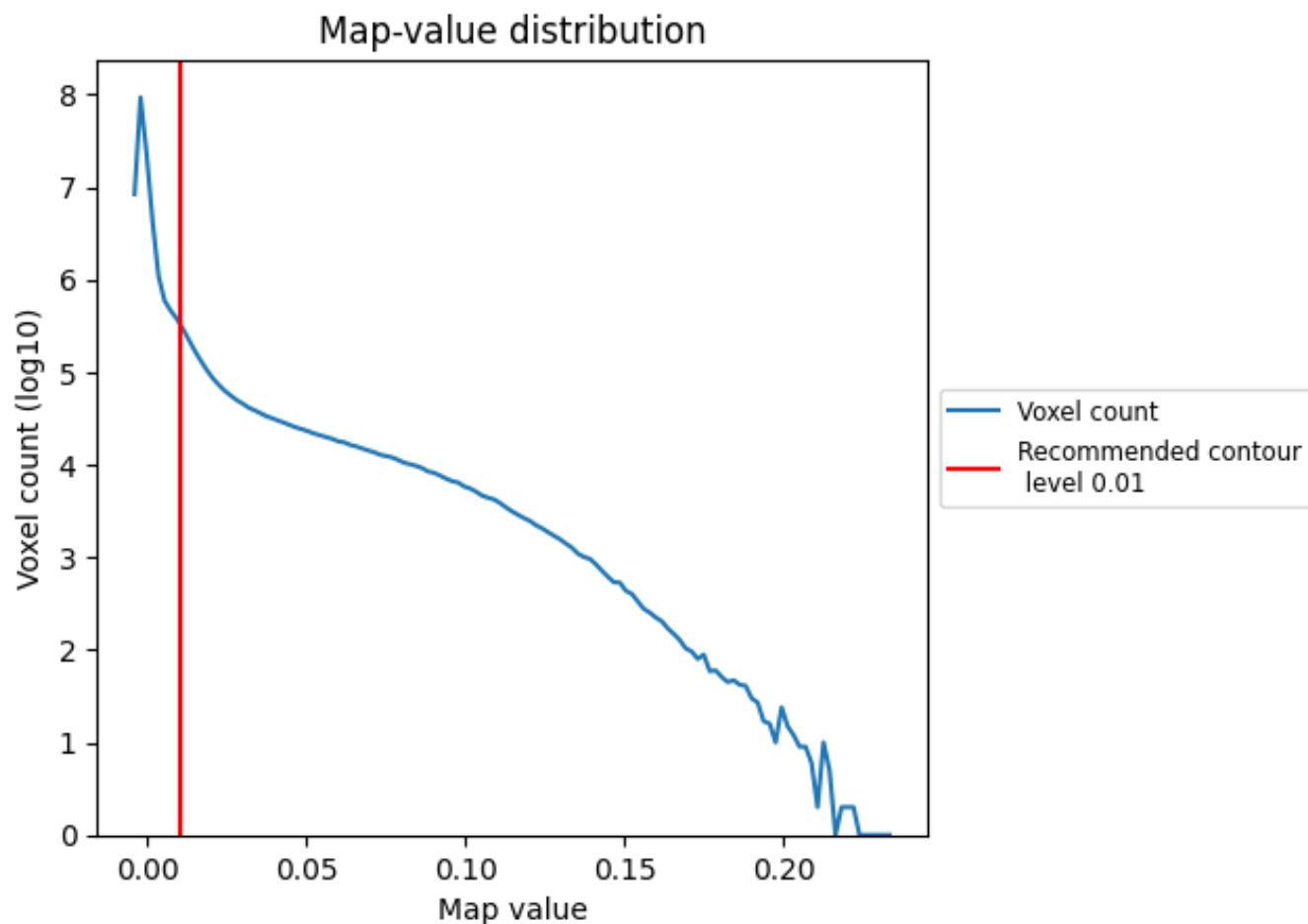
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

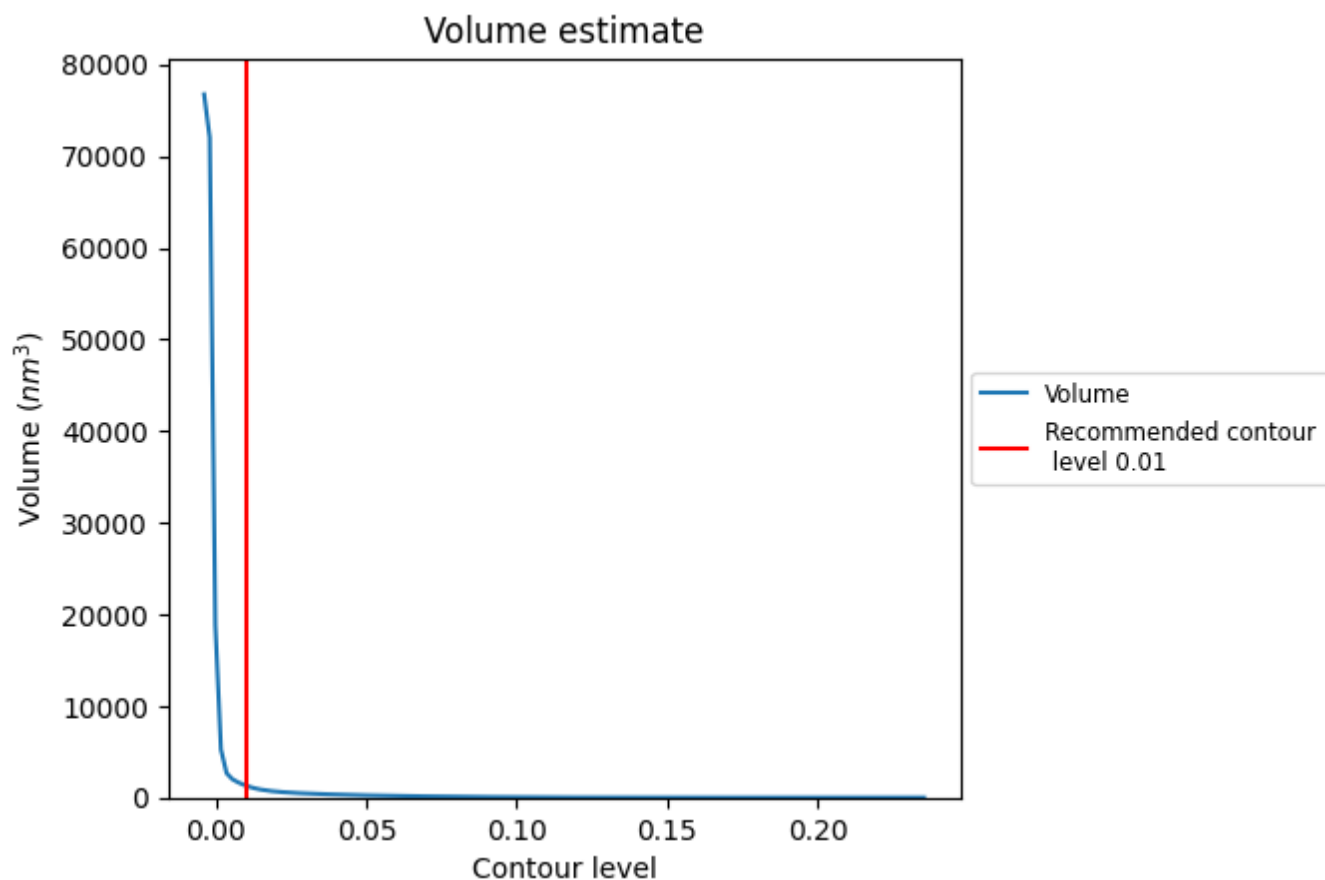
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

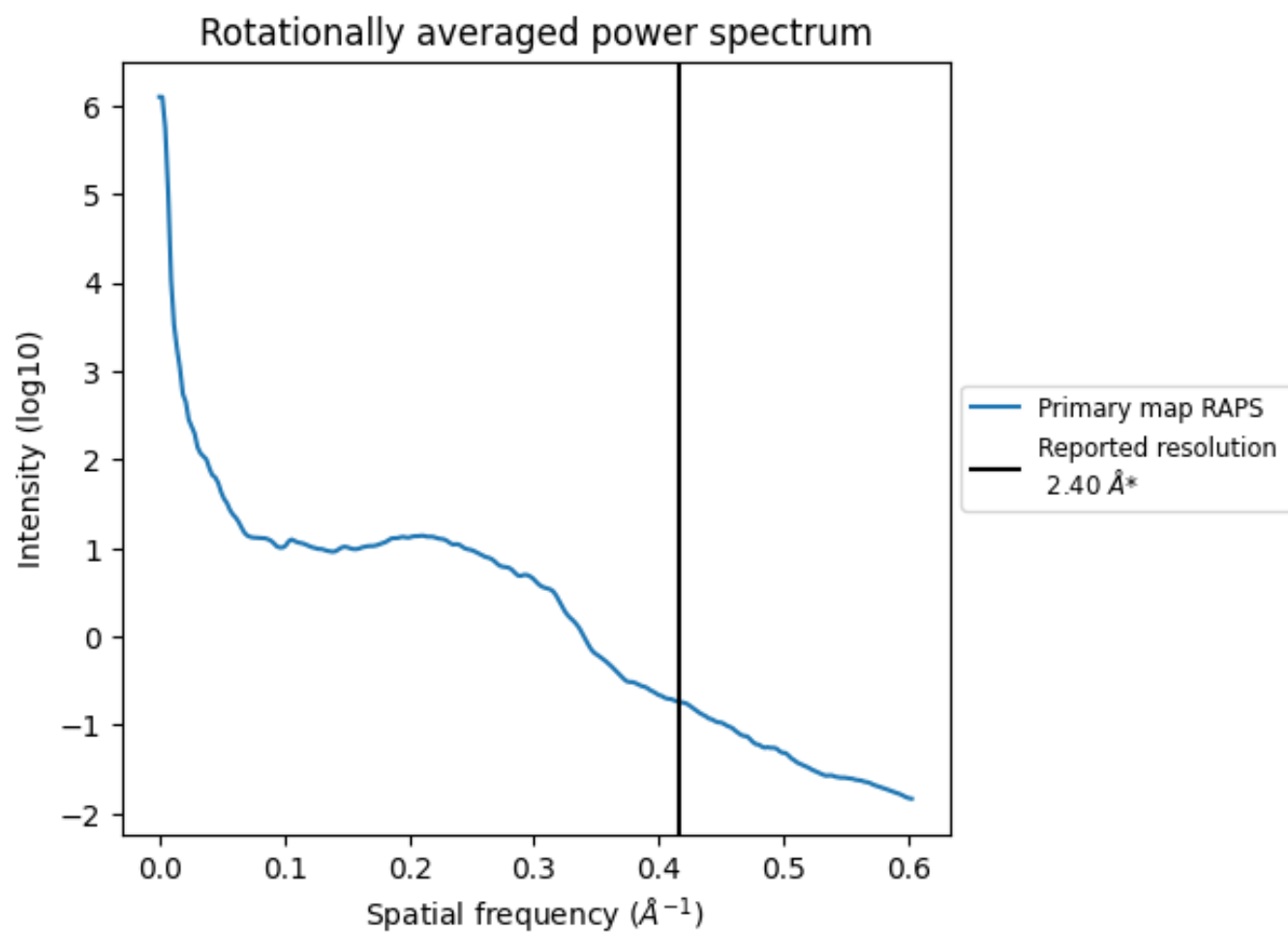
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1295 nm³; this corresponds to an approximate mass of 1170 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 ⓘ

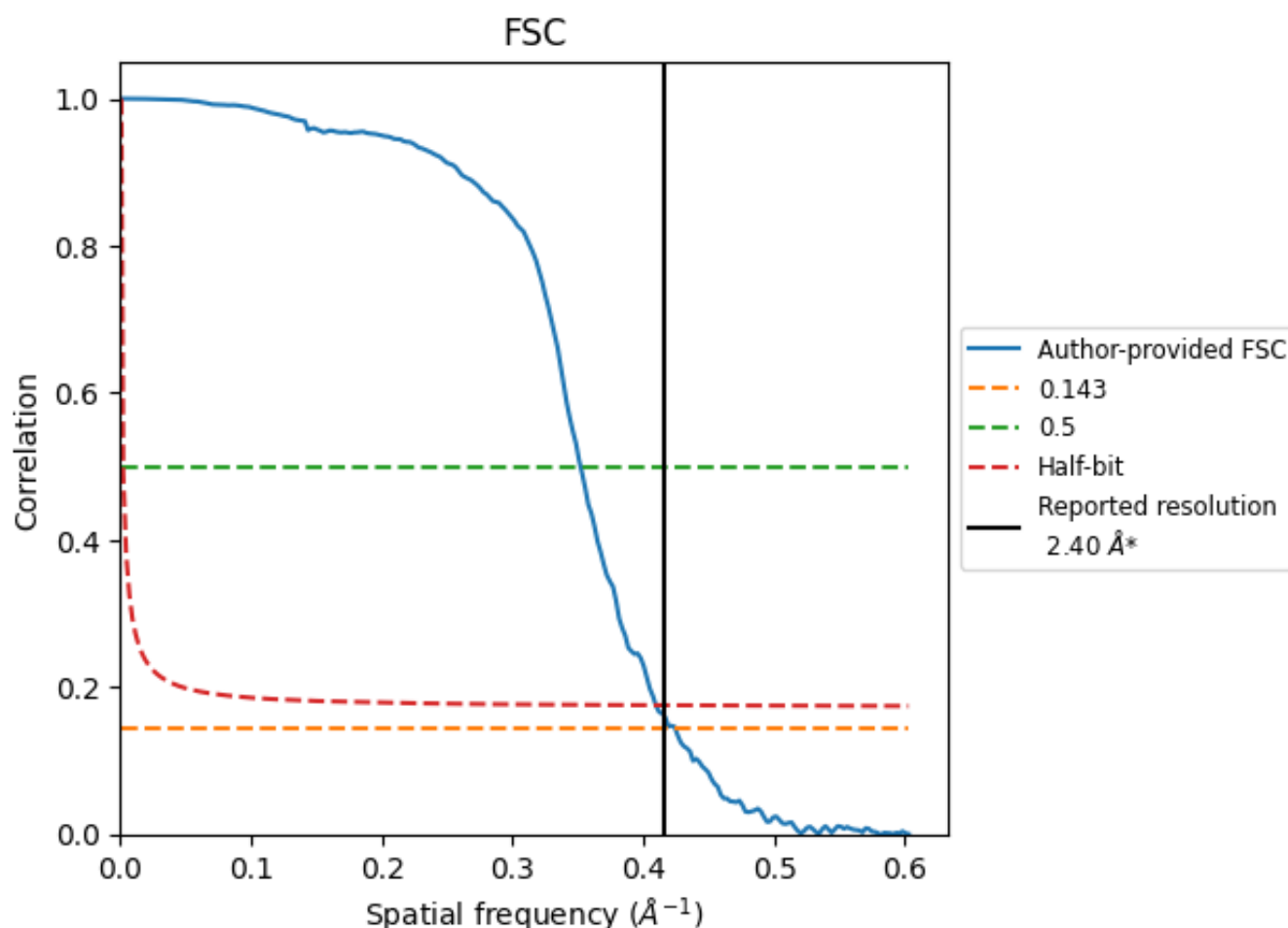


*Reported resolution corresponds to spatial frequency of 0.417 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.417 Å⁻¹

8.2 Resolution estimates [i](#)

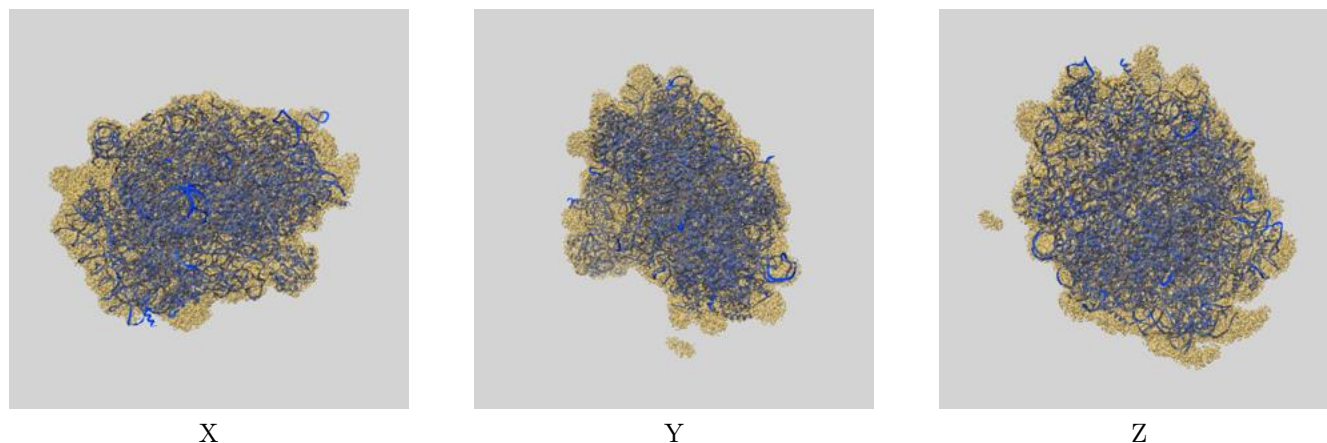
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.40	-	-
Author-provided FSC curve	2.36	2.84	2.44
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

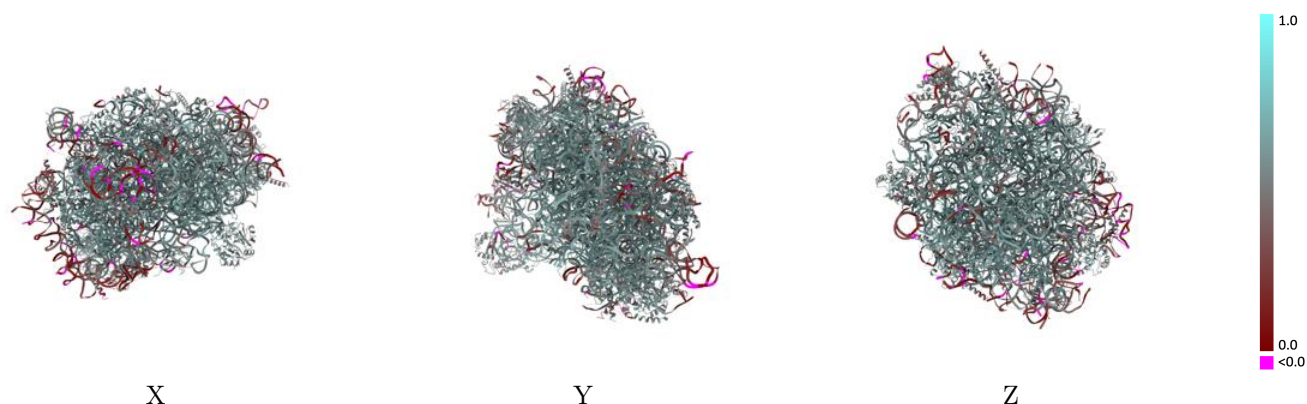
This section contains information regarding the fit between EMDB map EMD-13094 and PDB model 7OW7. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

9.1 Map-model overlay [i](#)



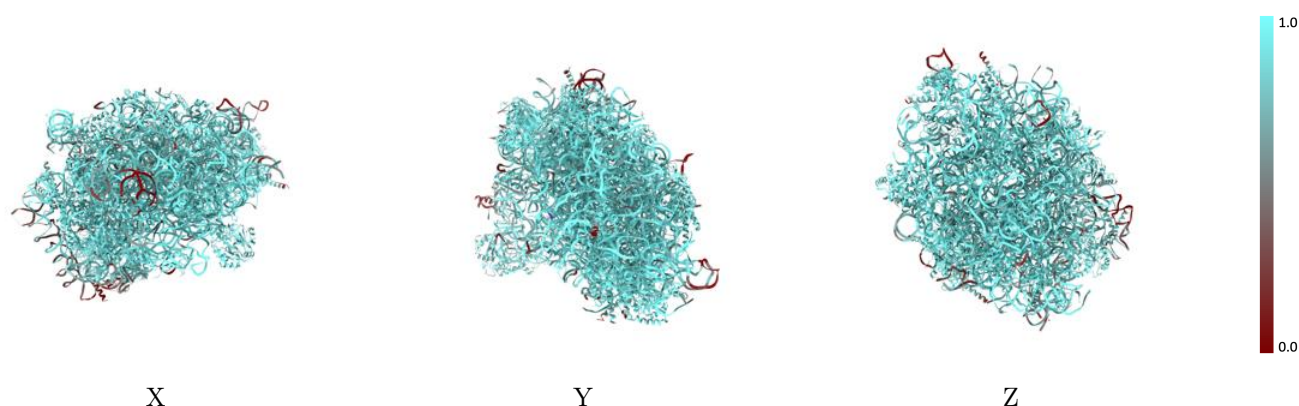
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



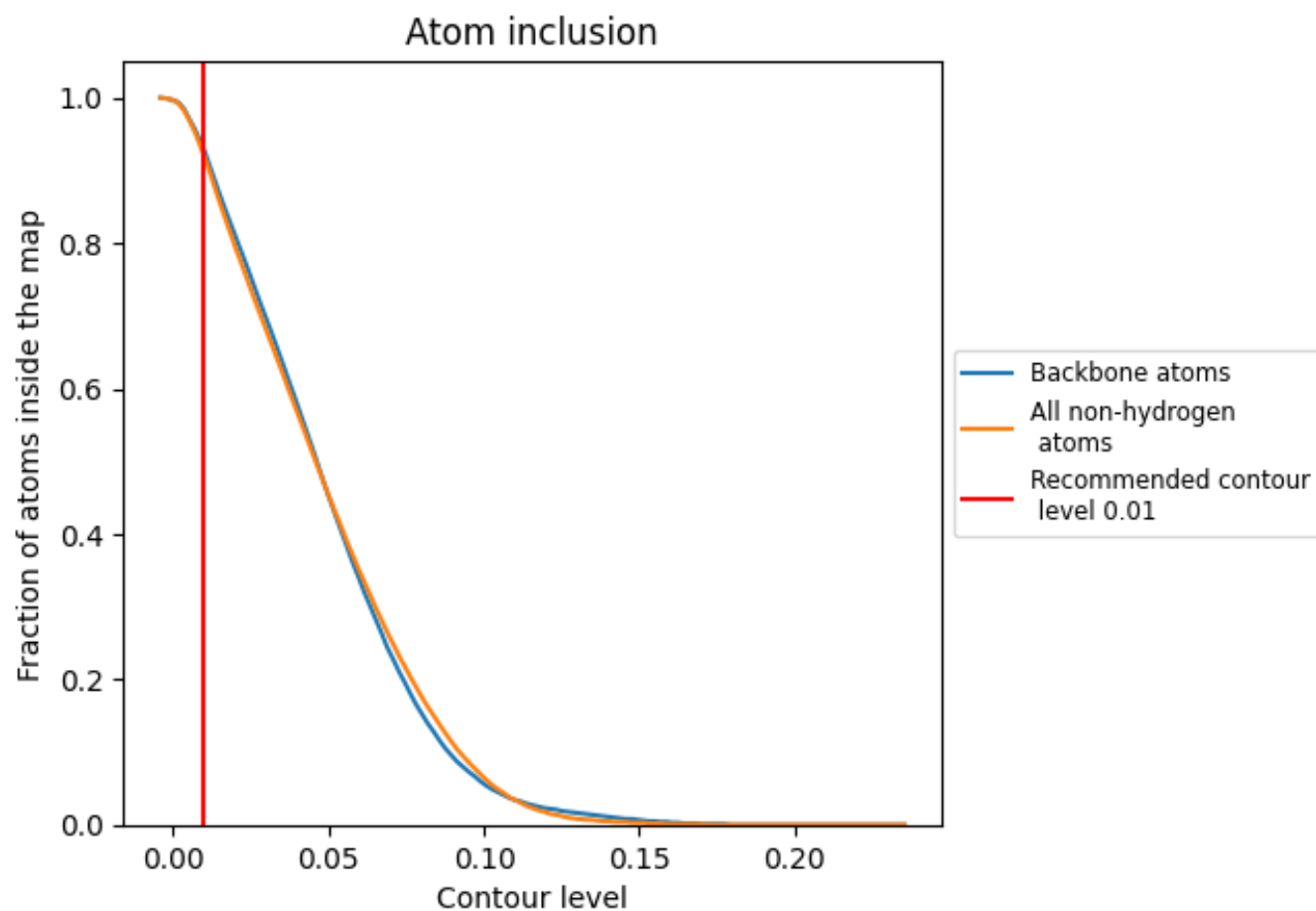
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.01).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ



















The table lists the average atom inclusion at the recommended contour level (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9200	 0.5390
A	 0.9100	 0.5170
B	 0.9820	 0.5800
C	 0.9720	 0.5680
D	 0.9800	 0.6120
E	 0.9510	 0.5750
F	 0.9700	 0.6060
G	 0.8790	 0.5420
H	 0.9240	 0.5500
I	 0.9510	 0.5810
J	 0.9710	 0.5870
K	 0.9790	 0.6260
L	 0.8900	 0.5270
M	 0.9660	 0.5890
N	 0.9530	 0.5920
P	 0.8820	 0.5290
Q	 0.9610	 0.5910
R	 0.9480	 0.5570
S	 0.9240	 0.5500
T	 0.8980	 0.5210
U	 0.9720	 0.6220
V	 0.8640	 0.5150
W	 0.9100	 0.5350
X	 0.9350	 0.5560
Y	 0.9750	 0.6060
Z	 0.9820	 0.6150
a	 0.9150	 0.5470
b	 0.9180	 0.5540
c	 0.8900	 0.5400
d	 0.9750	 0.6080
e	 0.7390	 0.4490
f	 0.9460	 0.5630
i	 0.9300	 0.5710
j	 0.9330	 0.5590
k	 0.9710	 0.6020



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Chain	Atom inclusion	Q-score
m	 0.9660	 0.6060
n	 0.9040	 0.5520
o	 0.9030	 0.5300
p	 0.7930	 0.4490
q	 0.8100	 0.4810
r	 0.9200	 0.5760
s	 0.9150	 0.5410
t	 0.9880	 0.6240
u	 0.9220	 0.5420