



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 08:50 AM UTC

PDB ID : 6W6L / pdb_00006w6l
EMDB ID : EMD-21435
Title : Cryo-EM structure of the human ribosome-TMCO1 translocon
Authors : Keenan, R.J.; McGilvray, P.T.
Deposited on : 2020-03-17
Resolution : 3.84 Å(reported)
Based on initial models : 6OM0, 5A63, 6FTI

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

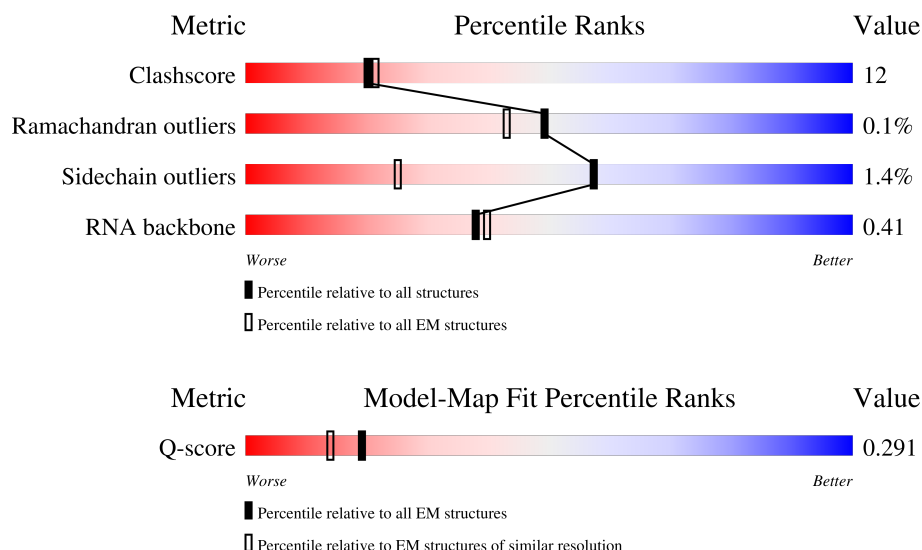
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.84 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.



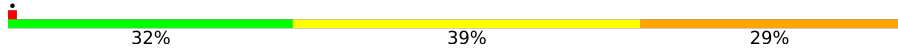
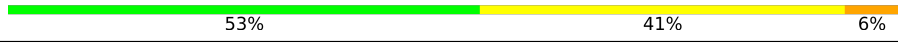
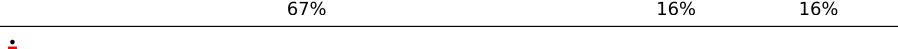
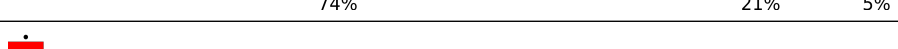
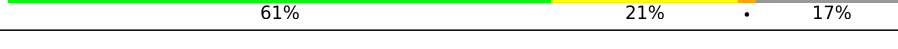
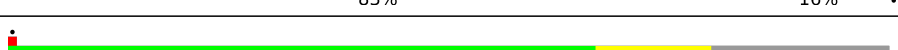
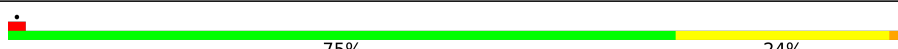
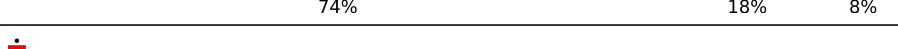
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10198 (3.30 - 4.30)

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	257	
2	B	403	
3	C	427	

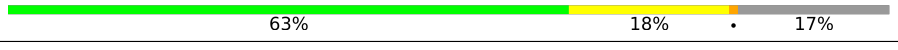
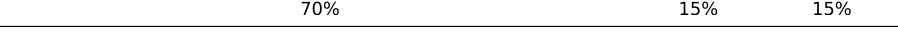
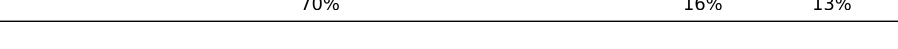
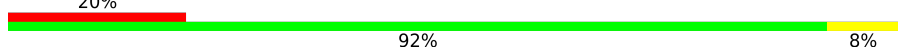
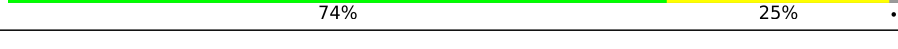
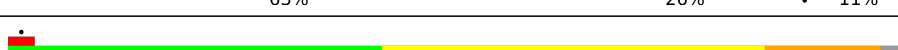
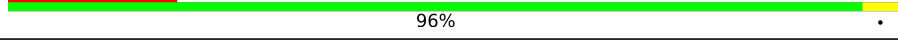
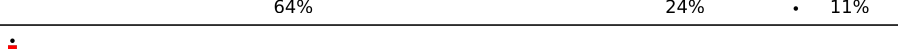
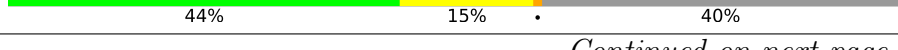
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Mol	Chain	Length	Quality of chain
4	D	157	
5	E	119	
6	F	297	
7	G	288	
8	H	248	
9	I	266	
10	J	192	
11	K	214	
12	L	178	
13	M	211	
14	N	215	
15	O	204	
16	P	203	
17	Q	184	
18	R	188	
19	S	196	
20	T	176	
21	U	160	
22	V	128	
23	W	140	
24	X	157	
25	Y	156	
26	Z	145	
27	a	136	
28	b	148	

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Mol	Chain	Length	Quality of chain
29	c	159	
30	d	115	
31	e	125	
32	f	135	
33	g	110	
34	h	117	
35	i	123	
36	j	105	
37	k	97	
38	l	70	
39	m	51	
40	o	25	
41	p	106	
42	q	92	
43	r	137	
44	t	3579	
45	u	76	
46	v	76	
47	y	27	
48	1	476	
49	2	68	
50	3	96	
51	4	224	
52	5	563	
53	7	483	

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Mol	Chain	Length	Quality of chain
54	6	188	7% 75% 15% • 7%

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 259082 atoms, of which 110309 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 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	246	Total	C	H	N	O	S	0	0
			3870	1183	1983	387	311	6		

- Molecule 2 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	396	Total	C	H	N	O	S	0	0
			6535	2036	3338	601	546	14		

- Molecule 3 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	C	363	Total	C	H	N	O	S	0	0
			5952	1817	3064	577	480	14		

- Molecule 4 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	D	157	Total	C	H	N	O	P	0	0
			5029	1489	1692	587	1104	157		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
5	E	119	Total	C	H	N	O	P	0	0
			3825	1132	1284	454	836	119		

- Molecule 6 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	F	248	Total	C	H	N	O	S	0	0
			4010	1271	1998	358	370	13		

- Molecule 7 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	G	220	Total	C	H	N	O	S	0	0
			3689	1138	1917	335	295	4		

- Molecule 8 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	H	225	Total	C	H	N	O	S	0	0
			3866	1202	1996	358	301	9		

- Molecule 9 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	I	234	Total	C	H	N	O	S	0	0
			3898	1197	2018	362	317	4		

- Molecule 10 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	J	191	Total	C	H	N	O	S	0	0
			3131	960	1605	285	275	6		

- Molecule 11 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	K	152	Total	C	H	N	O	S	0	0
			2508	789	1270	233	208	8		

- Molecule 12 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	L	169	Total	C	H	N	O	S	0	0
			2739	855	1386	252	240	6		

- Molecule 13 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	M	205	Total	C	H	N	O	S	0	0
			3421	1036	1764	344	273	4		

- Molecule 14 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	N	138	Total	C	H	N	O	S	0	0
			2328	725	1197	217	182	7		

- Molecule 15 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	O	203	Total	C	H	N	O	S	0	0
			3450	1072	1749	359	266	4		

- Molecule 16 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	P	195	Total	C	H	N	O	S	0	0
			3352	1034	1746	315	252	5		

- Molecule 17 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	Q	153	Total	C	H	N	O	S	0	0
			2511	776	1269	241	216	9		

- Molecule 18 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	R	187	Total	C	H	N	O	S	0	0
			3141	944	1628	314	250	5		

- Molecule 19 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	S	156	Total	C	H	N	O	S	0	0
			2750	816	1439	278	209	8		

- Molecule 20 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	T	175	Total	C	H	N	O	S	0	0
			2942	921	1493	283	234	11		

- Molecule 21 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	U	157	Total	C	H	N	O	S	0	0
			2636	815	1352	250	214	5		

- Molecule 22 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	V	99	Total	C	H	N	O	S	0	0
			1639	518	831	141	147	2		

- Molecule 23 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	W	129	Total	C	H	N	O	S	0	0
			2000	613	1031	182	169	5		

- Molecule 24 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	X	61	Total	C	H	N	O	S	0	0
			1032	327	521	100	82	2		

- Molecule 25 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	Y	117	Total	C	H	N	O	S	0	0
			1987	612	1029	180	165	1		

- Molecule 26 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	Z	133	Total	C	H	N	O	S	0	0
			2298	694	1192	224	185	3		

- Molecule 27 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	a	134	Total	C	H	N	O	S	0	0
			2282	712	1179	207	181	3		

- Molecule 28 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	b	147	Total	C	H	N	O	S	0	0
			2375	736	1213	237	186	3		

- Molecule 29 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	c	96	Total	C	H	N	O	S	0	0
			1641	489	854	174	121	3		

- Molecule 30 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	d	95	Total	C	H	N	O	S	0	0
			1512	468	774	131	133	6		

- Molecule 31 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	e	106	Total	C	H	N	O	S	0	0
			1803	555	924	170	152	2		

- Molecule 32 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	f	129	Total	C	H	N	O	S	0	0
			2224	673	1160	220	166	5		

- Molecule 33 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	g	109	Total	C	H	N	O	S	0	0
			1788	555	912	174	144	3		

- Molecule 34 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	h	112	Total	C	H	N	O	S	0	0
			1867	555	979	183	144	6		

- Molecule 35 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	i	122	Total	C	H	N	O	S	0	0
			2163	641	1148	205	168	1		

- Molecule 36 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	j	97	Total	C	H	N	O	S	0	0
			1664	497	870	168	124	5		

- Molecule 37 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	k	84	Total	C	H	N	O	S	0	0
			1407	423	718	152	109	5		

- Molecule 38 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	l	69	Total	C	H	N	O	S	0	0
			1206	366	637	103	99	1		

- Molecule 39 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	m	50	Total	C	H	N	O	S	0	0
			927	281	483	98	64	1		

- Molecule 40 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	o	25	Total	C	H	N	O	S	0	0
			529	145	289	64	28	3		

- Molecule 41 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	p	99	Total	C	H	N	O	S	0	0
			1696	510	882	167	131	6		

- Molecule 42 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	q	91	Total	C	H	N	O	S	0	0
			1464	445	756	136	120	7		

- Molecule 43 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	r	122	Total	C	H	N	O	S	0	0
			2021	607	1041	204	165	4		

- Molecule 44 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	t	3510	Total	C	H	N	O	P	0	0
			113261	33507	38018	13757	24469	3510		

- Molecule 45 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	u	75	Total	C	H	N	O	P	0	0
			2402	710	809	278	530	75		

- Molecule 46 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	v	76	Total	C	H	N	O	P	0	0
			2440	721	822	287	534	76		

- Molecule 47 is a protein called Nascent chain mixture.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	y	27	Total	C	H	N	O	0	0
			245	81	110	27	27		

- Molecule 48 is a protein called Protein transport protein Sec61 subunit alpha isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	1	426	Total	C	H	N	O	S	0	0
			6775	2189	3452	535	578	21		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	145	SER	ALA	conflict	UNP P61619
1	343	HIS	TYR	conflict	UNP P61619

- Molecule 49 is a protein called Protein transport protein Sec61 subunit gamma.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	2	62	Total	C	H	N	O	S	0	0
			1021	326	527	86	79	3		

- Molecule 50 is a protein called Protein transport protein Sec61 subunit beta.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	3	29	Total	C	H	N	O	S	0	0
			474	157	245	36	34	2		

- Molecule 51 is a protein called Transmembrane protein 147.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	4	221	Total	C	H	N	O	S	0	0
			3526	1175	1769	272	294	16		

- Molecule 52 is a protein called Nicalin.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	5	516	Total	C	H	N	O	S	0	0
			8173	2595	4083	722	756	17		

- Molecule 53 is a protein called Coiled-coil domain-containing protein 47.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	7	290	Total	C	H	N	O	S	0	0
			4775	1475	2400	435	447	18		

- Molecule 54 is a protein called Calcium load-activated calcium channel.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	6	174	Total	C	H	N	O	S	0	0
			2850	887	1463	239	249	12		

- Molecule 55 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
55	B	1	Total 1	Mg 1	0
55	D	6	Total 6	Mg 6	0
55	E	9	Total 9	Mg 9	0
55	k	1	Total 1	Mg 1	0
55	o	1	Total 1	Mg 1	0
55	t	10	Total 10	Mg 10	0

- Molecule 56 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
56	k	1	Total 1	Zn 1	0
56	p	1	Total 1	Zn 1	0
56	q	1	Total 1	Zn 1	0

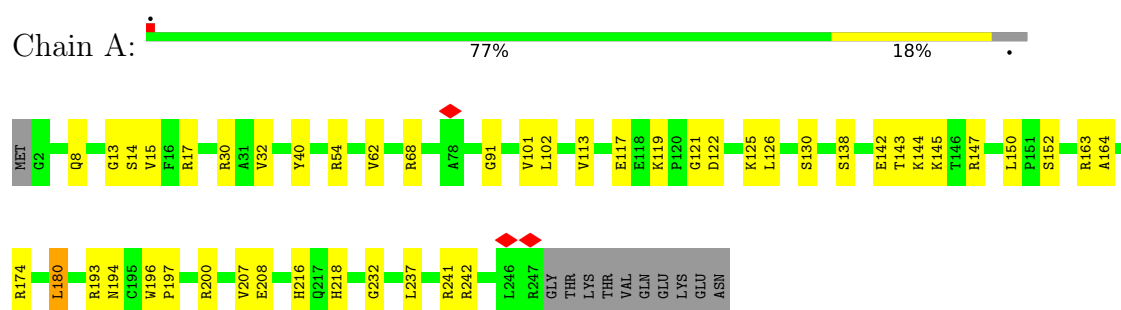
- Molecule 57 is water.

Mol	Chain	Residues	Atoms		AltConf
57	u	1	Total 1	O 1	0

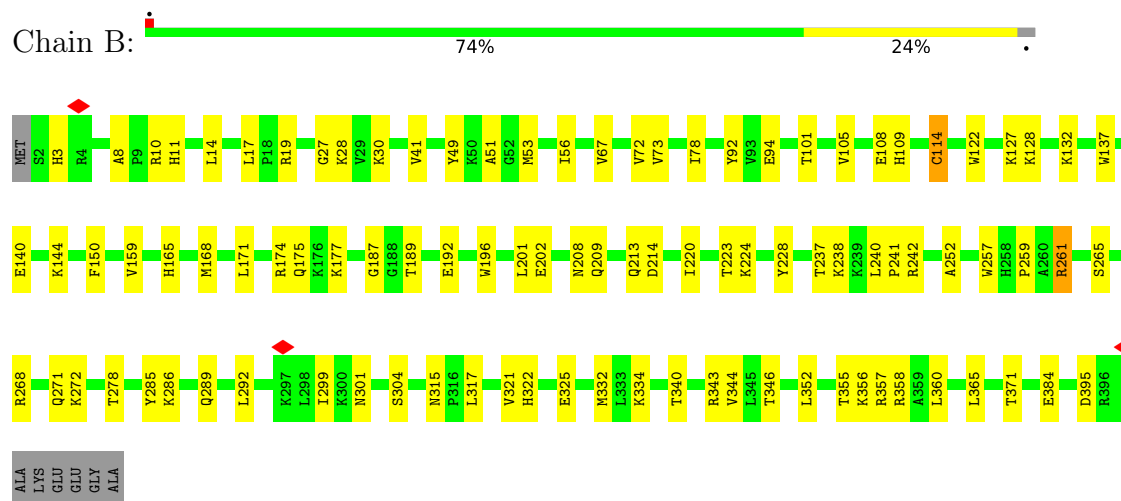
3 Residue-property plots

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

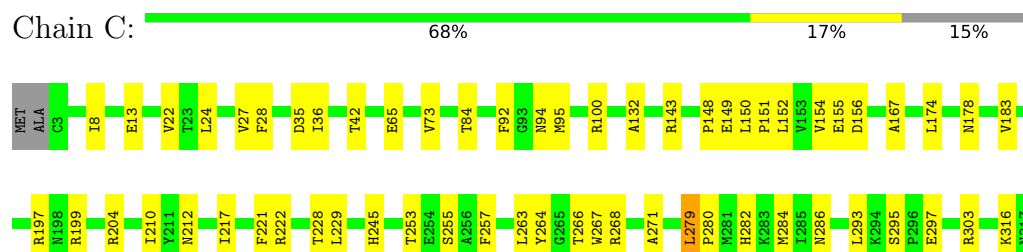
• Molecule 1: 60S ribosomal protein L8

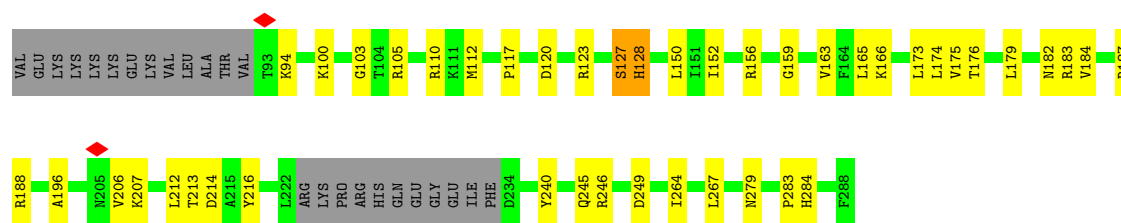


• Molecule 2: 60S ribosomal protein L3



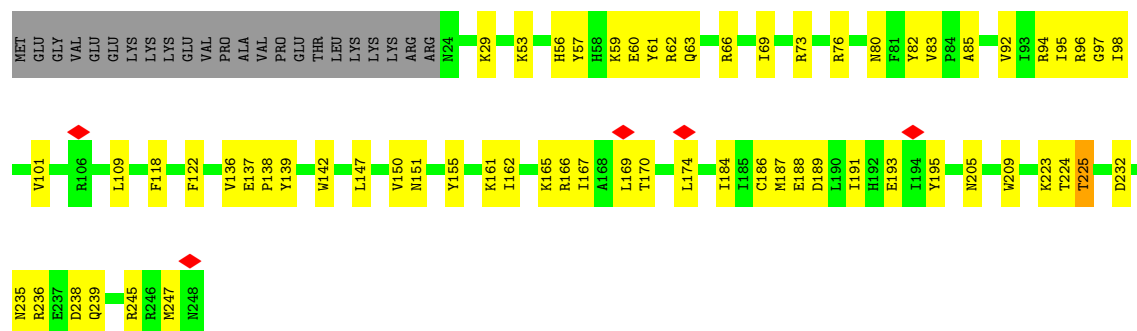
• Molecule 3: 60S ribosomal protein L4





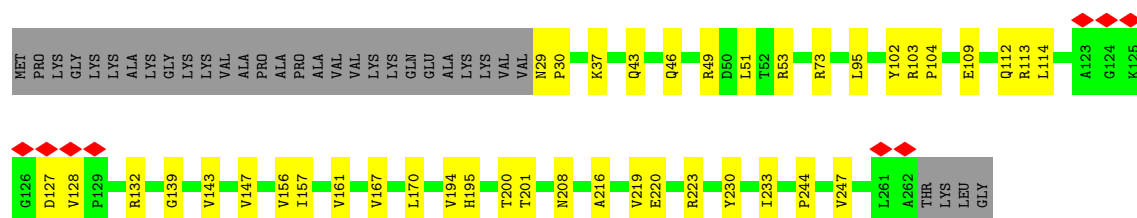
• Molecule 8: 60S ribosomal protein L7

Chain H: 65% 25% 9%



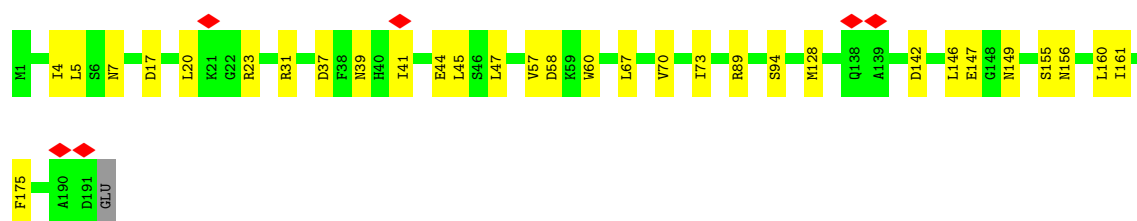
• Molecule 9: 60S ribosomal protein L7a

Chain I: 73% 15% 12%



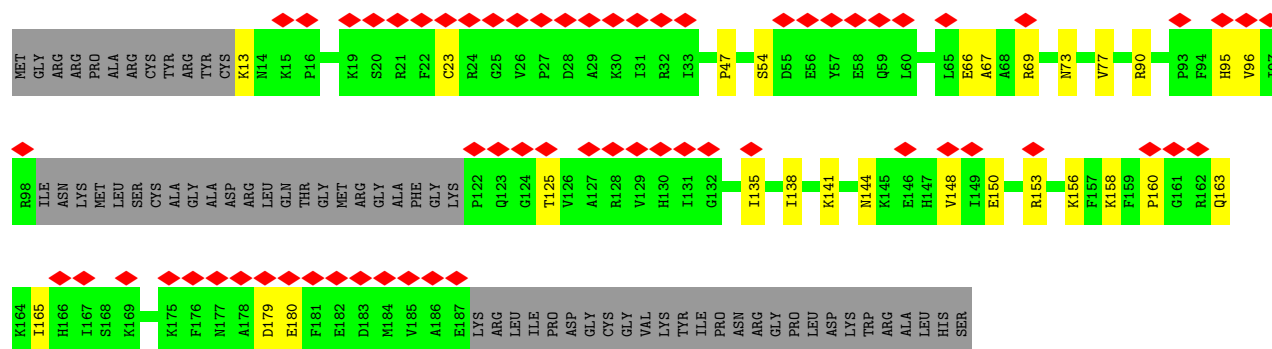
• Molecule 10: 60S ribosomal protein L9

Chain J: 83% 16% .

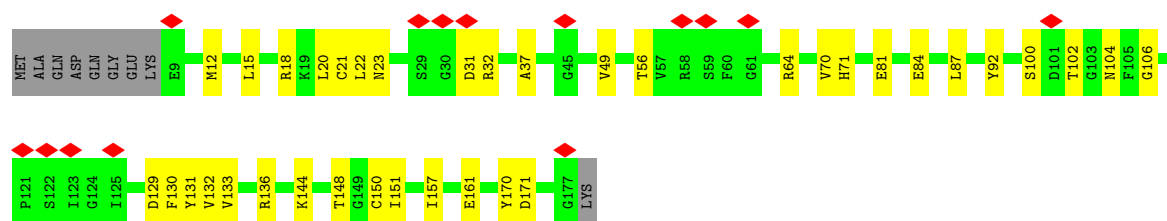


• Molecule 11: 60S ribosomal protein L10

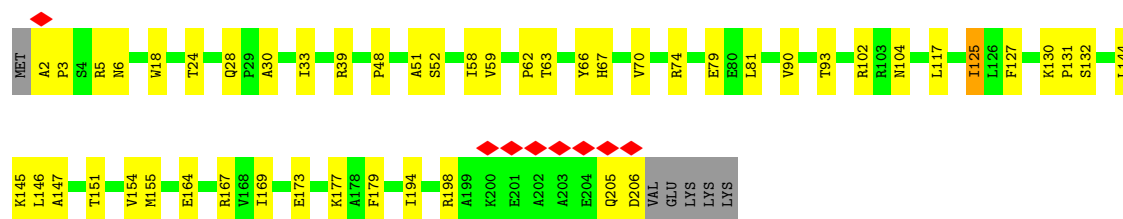
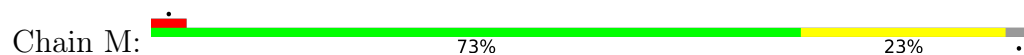
Chain K: 30% 58% 13% 29%



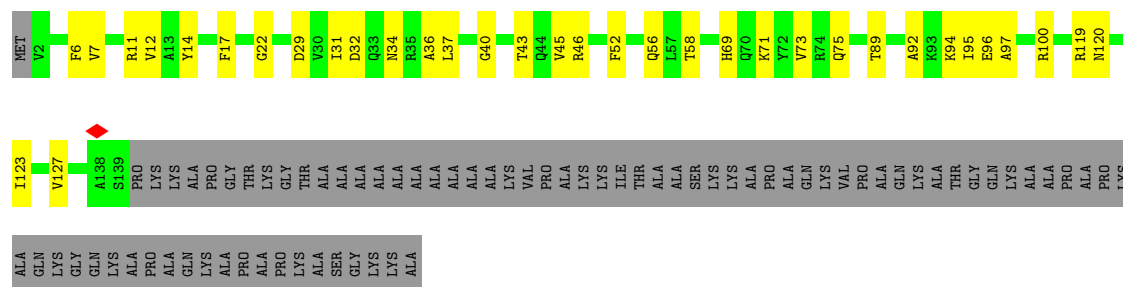
• Molecule 12: 60S ribosomal protein L11



• Molecule 13: 60S ribosomal protein L13

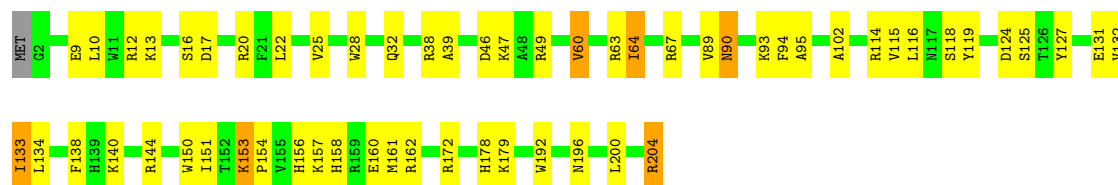


• Molecule 14: 60S ribosomal protein L14



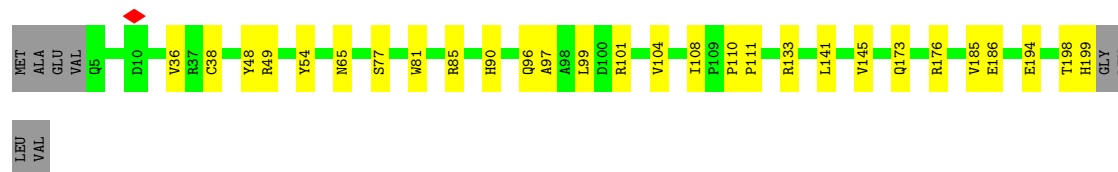
• Molecule 15: 60S ribosomal protein L15





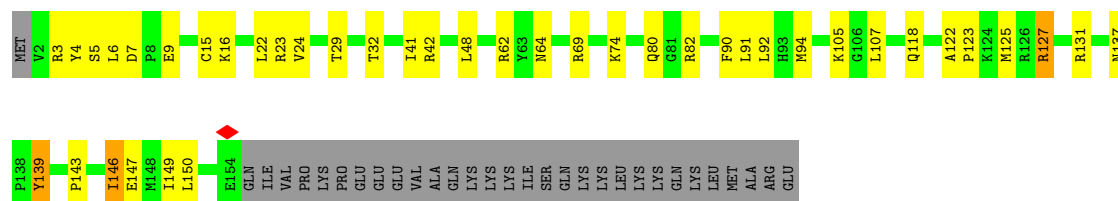
- Molecule 16: 60S ribosomal protein L13a

Chain P: 82% 14% .



- Molecule 17: 60S ribosomal protein L17

Chain Q: 61% 21% 17% .



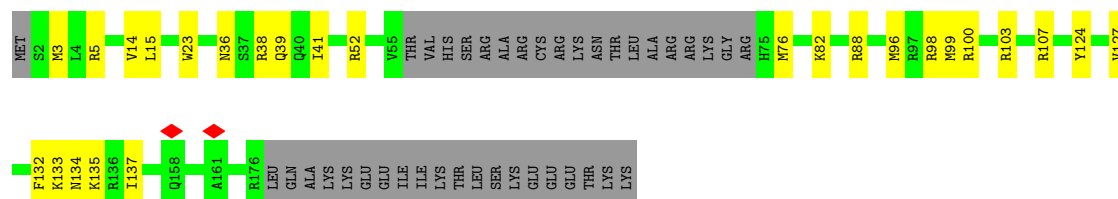
- Molecule 18: 60S ribosomal protein L18

Chain R: 83% 16% .



- Molecule 19: 60S ribosomal protein L19

Chain S: 66% 13% 20%

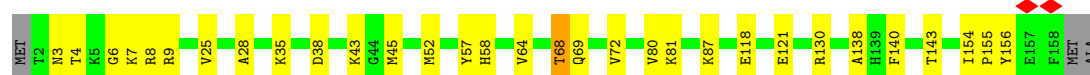
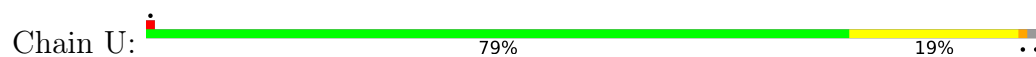


- Molecule 20: 60S ribosomal protein L18a

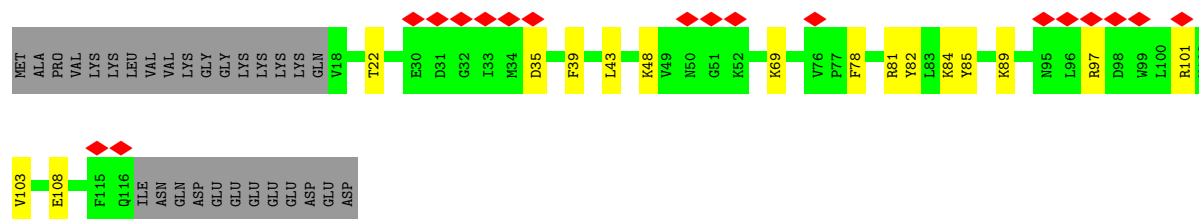
Chain T: 75% 24% ..



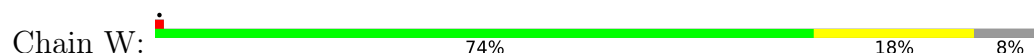
- Molecule 21: 60S ribosomal protein L21



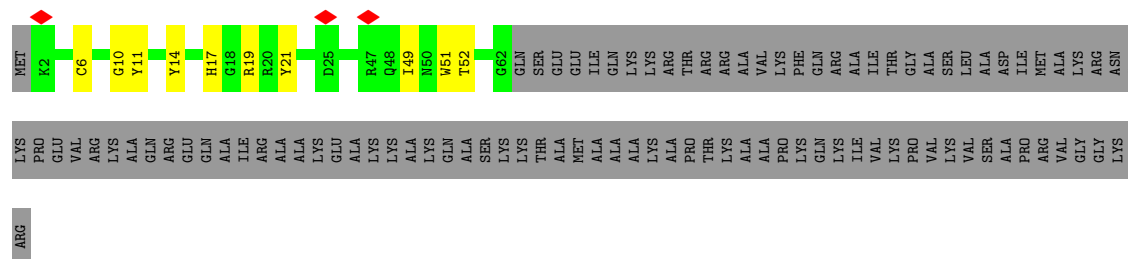
- Molecule 22: 60S ribosomal protein L22



- Molecule 23: 60S ribosomal protein L23

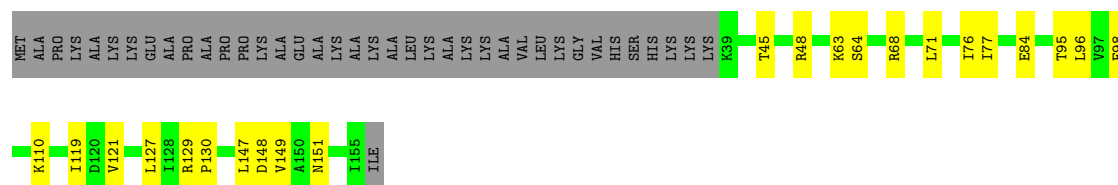


- Molecule 24: 60S ribosomal protein L24

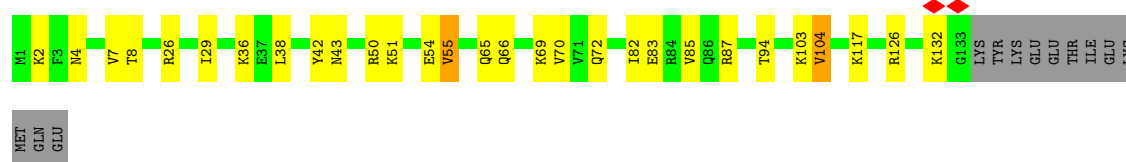


- Molecule 25: 60S ribosomal protein L23a

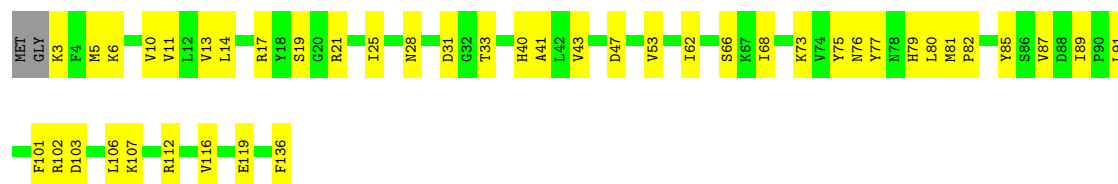




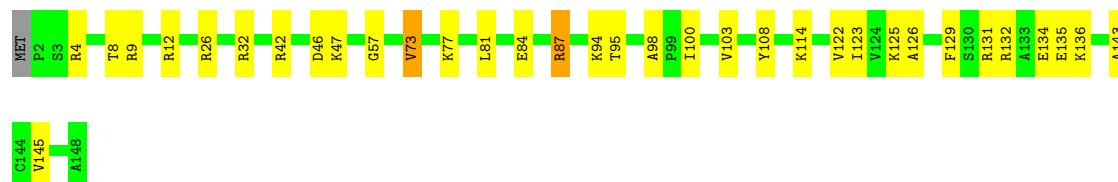
- Molecule 26: 60S ribosomal protein L26



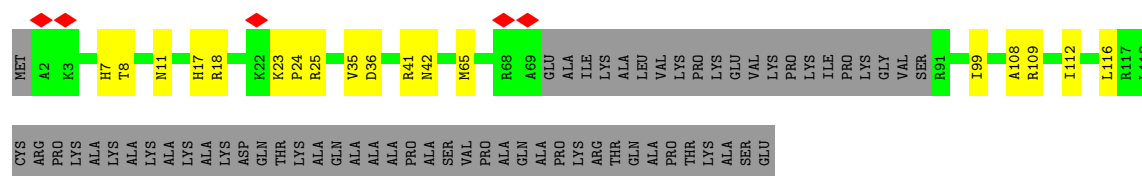
- Molecule 27: 60S ribosomal protein L27



- Molecule 28: 60S ribosomal protein L27a



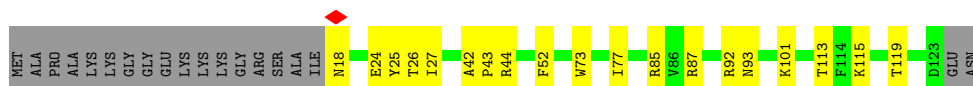
- Molecule 29: 60S ribosomal protein L29



- Molecule 30: 60S ribosomal protein L30



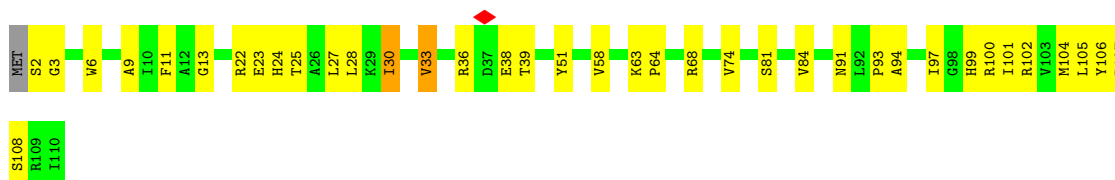
- Molecule 31: 60S ribosomal protein L31



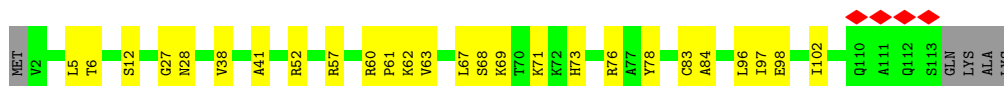
- Molecule 32: 60S ribosomal protein L32



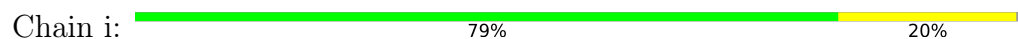
- Molecule 33: 60S ribosomal protein L35a



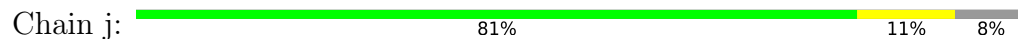
- Molecule 34: 60S ribosomal protein L34



- Molecule 35: 60S ribosomal protein L35

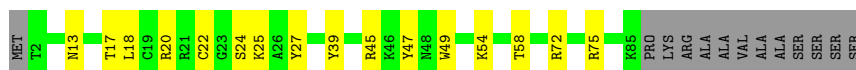


- Molecule 36: 60S ribosomal protein L36

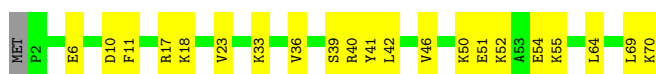




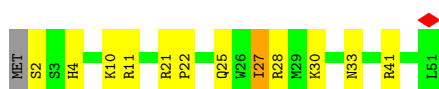
- Molecule 37: 60S ribosomal protein L37



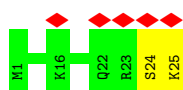
- Molecule 38: 60S ribosomal protein L38



- Molecule 39: 60S ribosomal protein L39



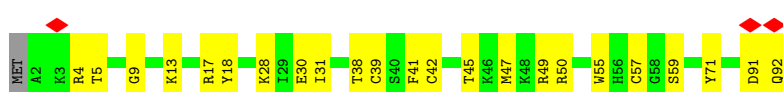
- Molecule 40: 60S ribosomal protein L41



- Molecule 41: 60S ribosomal protein L36a

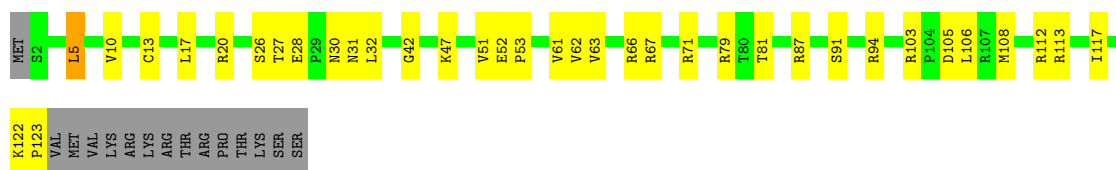


- Molecule 42: 60S ribosomal protein L37a



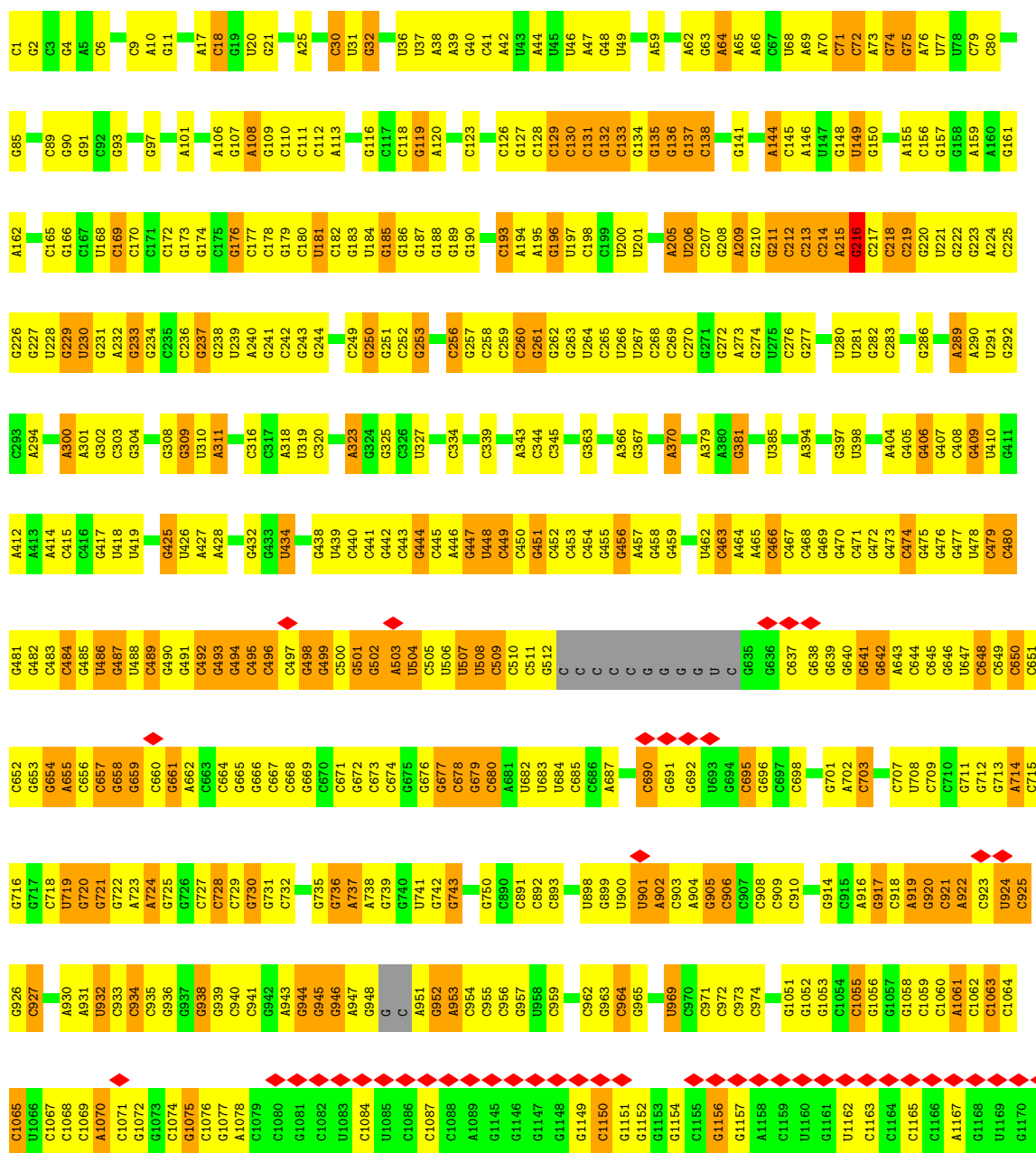
- Molecule 43: 60S ribosomal protein L28

Chain r:  63% 26% 11%



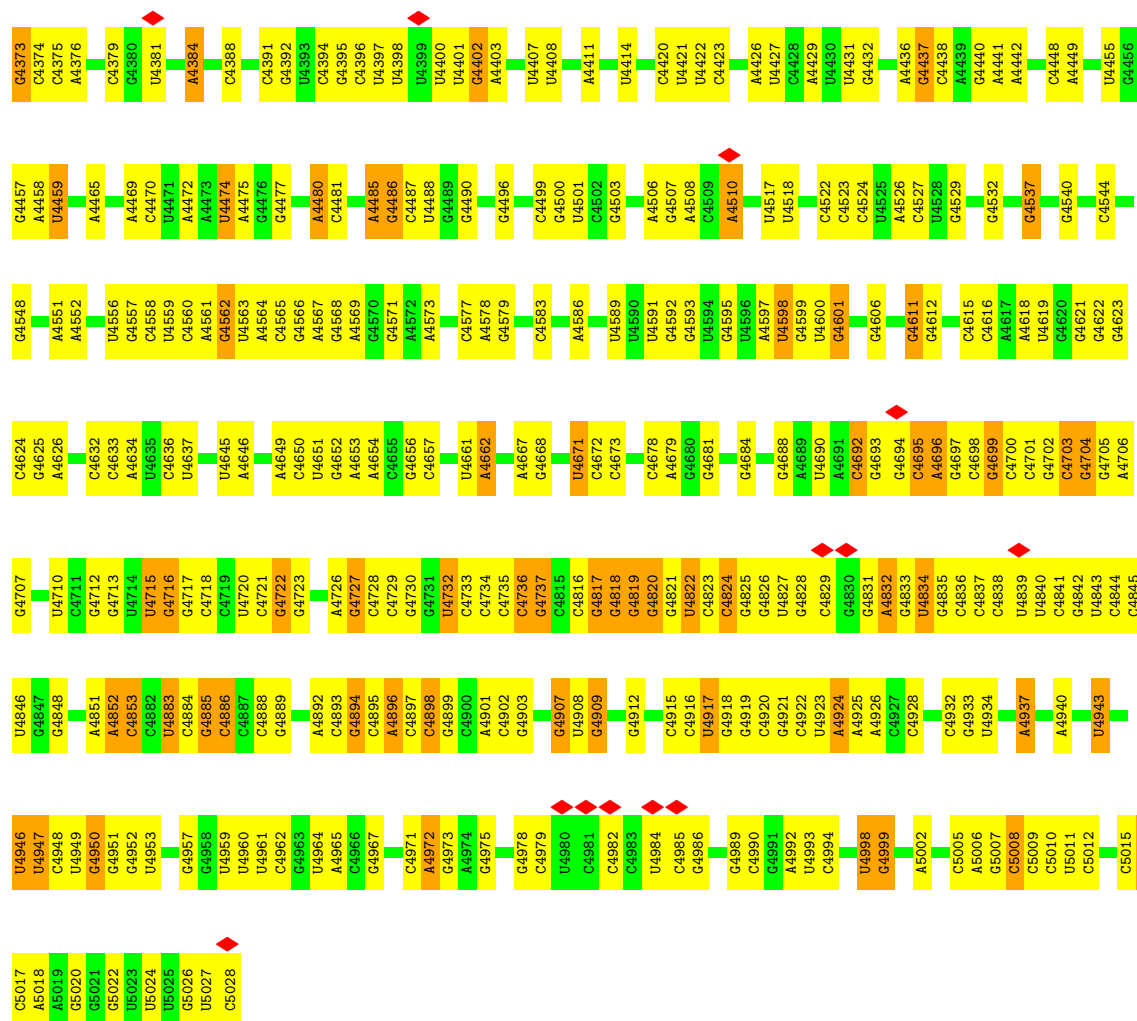
• Molecule 44: 28S ribosomal RNA

Chain t:  42% 43% 13%

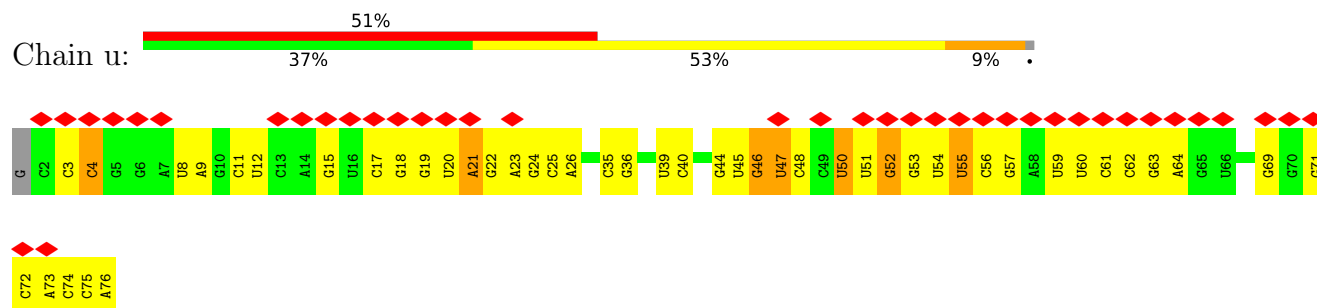


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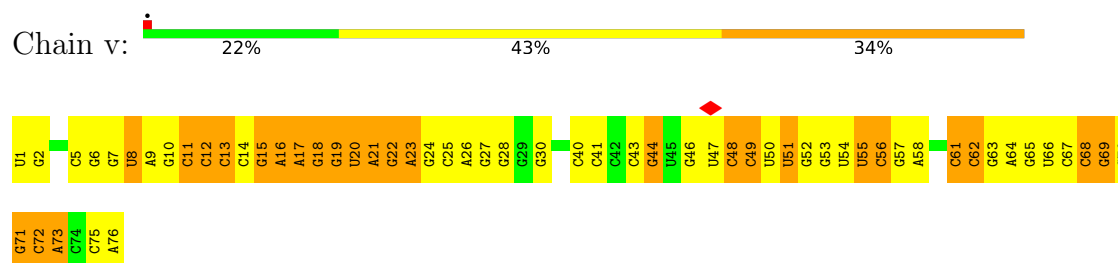
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A2860	A2861	C2862	C2869	U2870	C2871	A2874	C2875	C2876	C2877	C2878	U2879	C2880	C2881	C3569	C3570	C3571	C3572	C3573	C3574	C3575	C3576	U3577	U3578	A3581	C3582	U3587	C3588	C3589	C3590	C3591	C3592	C3593	C3594	C3595	C3596	C3597	C3598	C3599	C3600	C3601	C3605	C3606	U3611	C3612	C3613	C3614	U3615	U3616	C3617	C3618	C3619	C3620	C3621	
G2760	C2766	U2767	U2768	U2769	C2773	C2776	C2777	C2778	C2779	U2780	C2781	C2782	C2785	C2788	U2789	C2790	C2791	C2792	C2793	U2798	C2805	C2806	C2807	C2812	C2813	C2814	C2817	C2823	C2824	C2827	C2828	C2834	C2835	C2838	C2839	C2840	C2841	C2846	C2847	C2851	C2855	C2856	C2857	C2858	C2859	C2860	C2861	C2862	C2863	C2864	C2865			
U2686	U2687	C2688	C2689	C2690	C2691	C2692	C2693	C2694	C2700	C2701	A2704	C2705	U2707	C2708	C2711	C2714	C2717	C2718	U2719	C2720	C2721	C2722	C2723	A2724	C2725	U2726	C2727	C2728	C2729	C2730	C2731	C2732	C2733	C2734	C2735	C2736	C2737	C2738	C2739	C2741	U2742	C2743	C2744	C2745	C2746	C2747	U2748	C2749	C2750	C2751	C2752			
U2607	C2608	U2609	U2610	U2611	U2612	C2613	U2614	U2615	U2616	C2617	U2618	U2619	C2620	C2621	C2622	A2626	C2632	C2633	C2637	C2638	U2645	C2646	C2647	C2648	C2652	C2653	C2654	C2655	C2656	C2657	C2658	C2659	C2660	C2664	C2665	U2666	C2667	C2668	C2669	U2670	U2671	C2672	C2673	C2674	C2675	C2676	C2677	C2678	U2680	C2681	C2682	C2683	C2685	
A2463	U2464	G2465	G2466	C2467	C2468	U2469	C2470	C2471	A2472	U2473	U2474	C2475	C2476	C2477	U2478	C2479	C2480	C2481	C2482	C2483	C2484	C2485	C2486	U2487	C2488	A2492	C2495	C2496	C2499	C2500	C2501	C2502	U2503	U2504	C2505	A2506	C2507	C2512	C2513	C2514	A2515	C2516	U2517	C2518	C2523	U2524	C2525	C2526	C2527	C2528	C2531	A2532	U2533	
G2534	C2535	C2536	C2537	C2538	C2542	C2543	A2544	C2545	C2546	C2547	C2548	U2549	C2550	C2551	C2552	C2553	U2554	C2557	C2558	U2559	A2560	A2561	C2565	C2566	C2567	C2568	C2569	C2570	C2573	C2574	C2578	C2579	C2580	C2581	C2582	C2585	C2586	C2587	C2590	C2591	C2595	C2596	C2597	A2600	C2601	C2602	C2603	U2604	C2605	C2606				



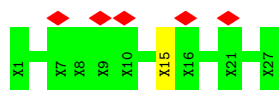
• Molecule 45: tRNA



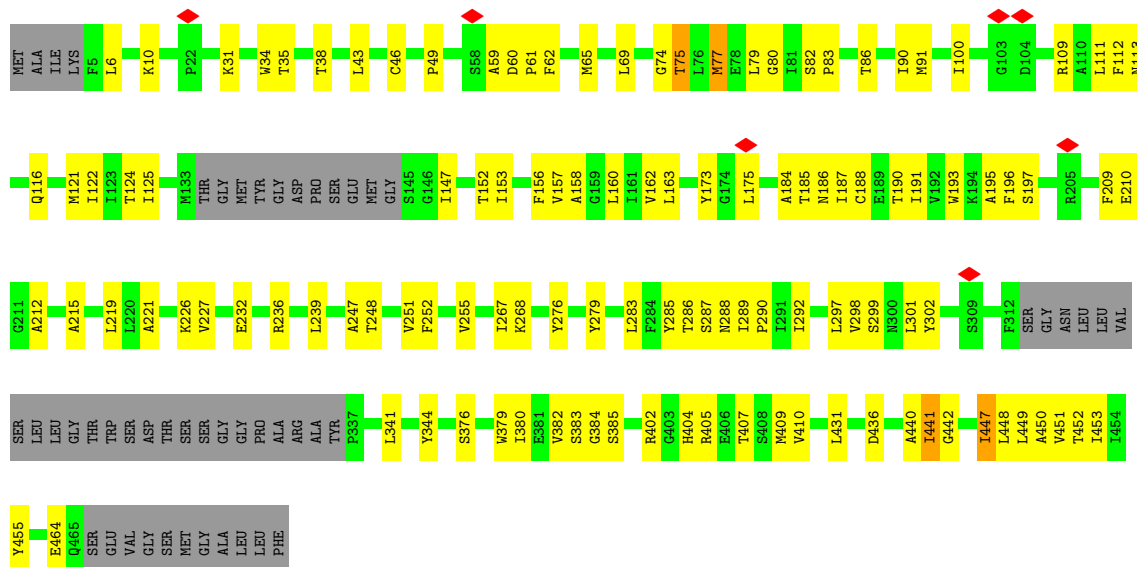
• Molecule 46: tRNA



- Molecule 47: Nascent chain mixture



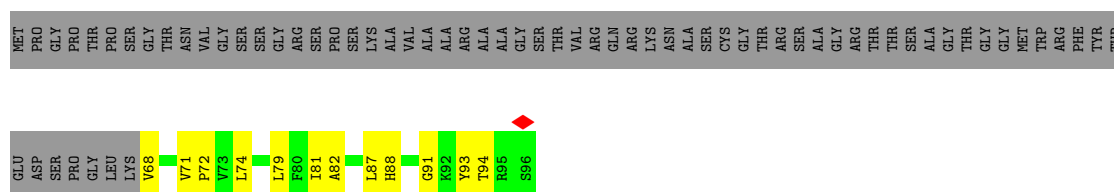
- Molecule 48: Protein transport protein Sec61 subunit alpha isoform 1



- Molecule 49: Protein transport protein Sec61 subunit gamma

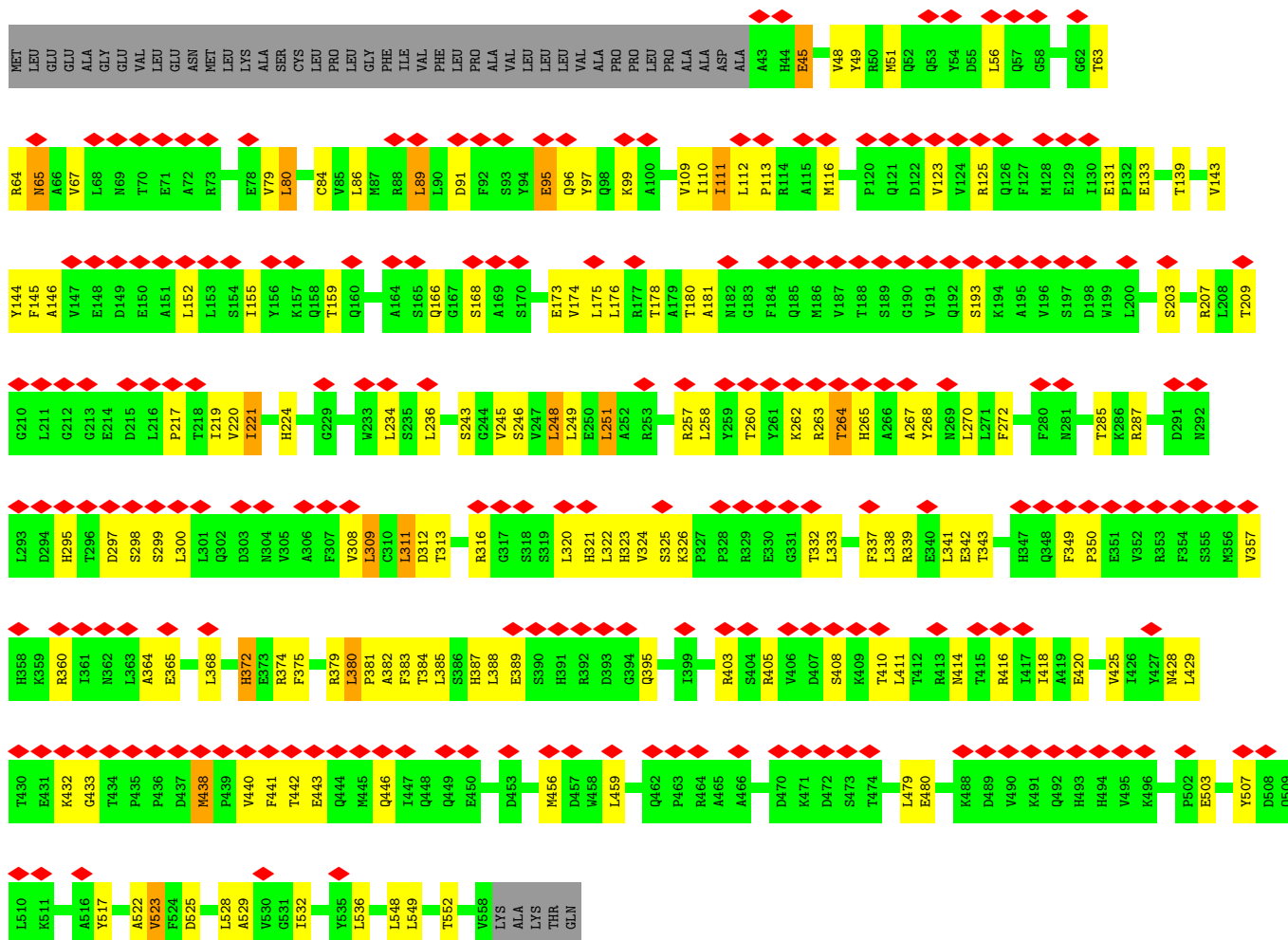


- Molecule 50: Protein transport protein Sec61 subunit beta

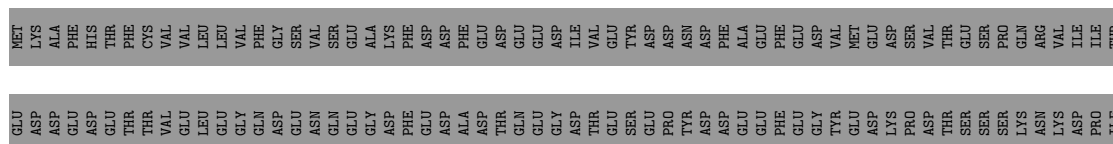
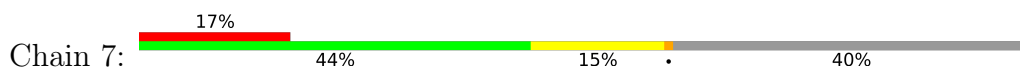


- Molecule 51: Transmembrane protein 147





- Molecule 53: Coiled-coil domain-containing protein 47





M1	L122	L21	L22	L23	L24	L25	L26	L27	L28	L29	L30	L31	L32	L33	L34	L35	L36	L37	L38	L39	L40	L41	L42	L43	L44	L45	L46	L47	L48	L49	L50	L51	L52	L53	L54	L55	L56	L57	L58	L59	L60	L61	L62	L63	L64	L65	L66	L67	L68	L69	L70	L71	L72	L73	L74	L75	L76	L77	L78	L79	L80	L81	L82	L83	L84	L85	L86	L87	L88	L89	L90	L91	L92	L93	L94	L95	L96	L97	L98	L99	L100	L101	L102	L103	L104	L105	L106	L107	L108	L109	L110	L111	L112	L113	L114	L115	L116	L117	L118	L119	L120	L121	L122	L123	L124	L125	L126	L127	L128	L129	L130	L131	L132	L133	L134	L135	L136	L137	L138	L139	L140	L141	L142	L143	L144	L145	L146	L147	L148	L149	L150	L151	L152	L153	L154	L155	L156	L157	L158	L159	L160	L161	L162	L163	L164	L165	L166	L167	L168	L169	L170	L171	L172	L173	L174	L175	L176	L177	L178	L179	L180	L181	L182	L183	L184	L185	L186	L187	L188	L189	L190	L191	L192	L193	L194	L195	L196	L197	L198	L199	L200	L201	L202	L203	L204	L205	L206	L207	L208	L209	L210	L211	L212	L213	L214	L215	L216	L217	L218	L219	L220	L221	L222	L223	L224	L225	L226	L227	L228	L229	L230	L231	L232	L233	L234	L235	L236	L237	L238	L239	L240	L241	L242	L243	L244	L245	L246	L247	L248	L249	L250	L251	L252	L253	L254	L255	L256	L257	L258	L259	L260	L261	L262	L263	L264	L265	L266	L267	L268	L269	L270	L271	L272	L273	L274	L275	L276	L277	L278	L279	L280	L281	L282	L283	L284	L285	L286	L287	L288	L289	L290	L291	L292	L293	L294	L295	L296	L297	L298	L299	L300	L301	L302	L303	L304	L305	L306	L307	L308	L309	L310	L311	L312	L313	L314	L315	L316	L317	L318	L319	L320	L321	L322	L323	L324	L325	L326	L327	L328	L329	L330	L331	L332	L333	L334	L335	L336	L337	L338	L339	L340	L341	L342	L343	L344	L345	L346	L347	L348	L349	L350	L351	L352	L353	L354	L355	L356	L357	L358	L359	L360	L361	L362	L363	L364	L365	L366	L367	L368	L369	L370	L371	L372	L373	L374	L375	L376	L377	L378	L379	L380	L381	L382	L383	L384	L385	L386	L387	L388	L389	L390	L391	L392	L393	L394	L395	L396	L397	L398	L399	L400	L401	L402	L403	L404	L405	L406	L407	L408	L409	L410	L411	L412	L413	L414	L415	L416	L417	L418	L419	L420	L421	L422	L423	L424	L425	L426	L427	L428	L429	L430	L431	L432	L433	L434	L435	L436	L437	L438	L439	L440	L441	L442	L443	L444	L445	L446	L447	L448	L449	L450	L451	L452	L453	L454	L455	L456	L457	L458	L459	L460	L461	L462	L463	L464	L465	L466	L467	L468	L469	L470	L471	L472	L473	L474	L475	L476	L477	L478	L479	L480	L481	L482	L483	L484	L485	L486	L487	L488	L489	L490	L491	L492	L493	L494	L495	L496	L497	L498	L499	L500	L501	L502	L503	L504	L505	L506	L507	L508	L509	L510	L511	L512	L513	L514	L515	L516	L517	L518	L519	L520	L521	L522	L523	L524	L525	L526	L527	L528	L529	L530	L531	L532	L533	L534	L535	L536	L537	L538	L539
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	82684	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.047	Depositor
Minimum map value	-0.019	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0073	Depositor
Map size (Å)	680.0, 680.0, 680.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.36, 1.36, 1.36	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.36	0/1925	0.46	0/2581
2	B	0.30	0/3265	0.44	0/4370
3	C	0.51	0/2942	0.53	0/3951
4	D	0.72	0/3726	0.74	0/5804
5	E	0.25	0/2839	0.38	0/4425
6	F	0.20	0/2052	0.38	0/2755
7	G	0.25	0/1806	0.42	0/2421
8	H	0.31	0/1905	0.48	0/2539
9	I	0.28	0/1913	0.41	0/2576
10	J	0.21	0/1545	0.39	0/2077
11	K	0.14	0/1265	0.33	0/1688
12	L	0.18	0/1376	0.38	0/1841
13	M	0.35	0/1688	0.49	0/2260
14	N	0.24	0/1153	0.37	0/1542
15	O	0.43	0/1746	0.53	0/2338
16	P	0.32	0/1638	0.46	0/2191
17	Q	0.66	0/1268	0.62	0/1701
18	R	0.36	0/1537	0.48	0/2052
19	S	0.44	0/1325	0.54	0/1750
20	T	0.24	0/1488	0.47	0/1997
21	U	0.23	0/1312	0.35	0/1753
22	V	0.16	0/822	0.32	0/1103
23	W	0.25	0/983	0.36	0/1319
24	X	0.26	0/524	0.34	0/698
25	Y	0.72	0/975	0.61	0/1312
26	Z	0.71	0/1123	0.58	0/1493
27	a	0.28	0/1126	0.42	0/1502
28	b	0.37	0/1191	0.47	0/1591
29	c	0.25	0/799	0.45	0/1053
30	d	0.29	0/748	0.44	0/1004
31	e	0.41	0/894	0.49	0/1204
32	f	0.58	0/1082	0.58	0/1443

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	g	0.33	0/895	0.44	0/1198
34	h	0.41	0/898	0.47	0/1197
35	i	0.66	0/1023	0.63	0/1351
36	j	0.27	0/805	0.42	0/1065
37	k	0.69	0/703	0.61	0/929
38	l	0.37	0/575	0.43	0/761
39	m	0.64	0/454	0.57	0/599
40	o	0.20	0/241	0.42	0/305
41	p	0.28	0/827	0.38	0/1090
42	q	0.34	0/718	0.45	0/953
43	r	0.47	0/995	0.57	0/1334
44	t	0.44	0/84165	0.48	0/131283
45	u	0.18	0/1777	0.49	0/2767
46	v	0.26	0/1806	0.80	0/2813
48	1	0.36	0/3394	0.47	0/4598
49	2	0.37	0/504	0.53	0/673
50	3	0.22	0/236	0.42	0/321
51	4	0.28	0/1808	0.50	0/2459
52	5	0.14	0/4174	0.34	0/5661
53	7	0.22	0/2406	0.46	1/3214 (0.0%)
54	6	0.23	0/1406	0.39	0/1882
All	All	0.41	0/159791	0.48	1/234787 (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
44	t	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	7	356	LYS	N-CA-C	-6.67	96.60	110.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
44	t	216	G	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1887	1983	1983	37	0
2	B	3197	3338	3338	76	0
3	C	2888	3064	3064	63	0
4	D	3337	1692	1692	135	0
5	E	2541	1284	1284	43	0
6	F	2012	1998	1998	40	0
7	G	1772	1917	1917	45	0
8	H	1870	1996	1996	50	0
9	I	1880	2018	2018	28	0
10	J	1526	1605	1605	21	0
11	K	1238	1270	1270	16	0
12	L	1353	1386	1386	24	0
13	M	1657	1764	1764	44	0
14	N	1131	1197	1197	30	0
15	O	1701	1749	1749	45	0
16	P	1606	1746	1745	17	0
17	Q	1242	1269	1269	38	0
18	R	1513	1628	1628	23	0
19	S	1311	1439	1439	24	0
20	T	1449	1493	1493	35	0
21	U	1284	1352	1352	29	0
22	V	808	831	831	18	0
23	W	969	1031	1031	17	0
24	X	511	521	521	8	0
25	Y	958	1029	1029	20	0
26	Z	1106	1192	1192	21	0
27	a	1103	1179	1179	30	0
28	b	1162	1213	1213	34	0
29	c	787	854	854	15	0
30	d	738	774	774	14	0
31	e	879	924	924	11	0
32	f	1064	1160	1160	20	0
33	g	876	912	912	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	h	888	979	979	25	0
35	i	1015	1148	1148	22	0
36	j	794	870	870	11	0
37	k	689	718	717	11	0
38	l	569	637	637	16	0
39	m	444	483	483	11	0
40	o	240	289	289	1	0
41	p	814	882	882	23	0
42	q	708	756	756	19	0
43	r	980	1041	1041	27	0
44	t	75243	38018	38017	1671	0
45	u	1593	809	809	21	0
46	v	1618	822	822	52	0
47	y	135	110	30	1	0
48	1	3323	3452	3452	96	0
49	2	494	527	527	19	0
50	3	229	245	245	9	0
51	4	1757	1769	1769	64	0
52	5	4090	4083	4082	146	0
53	7	2375	2400	2400	53	0
54	6	1387	1463	1463	24	0
55	B	1	0	0	0	0
55	D	6	0	0	0	0
55	E	9	0	0	0	0
55	k	1	0	0	0	0
55	o	1	0	0	0	0
55	t	10	0	0	0	0
56	k	1	0	0	0	0
56	p	1	0	0	0	0
56	q	1	0	0	0	0
57	u	1	0	0	2	0
All	All	148773	110309	110225	3066	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

The worst 5 of 3066 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)
44:t:205:A:N6	44:t:229:G:O6	1.85	1.07
44:t:2553:G:N7	44:t:2739:G:N2	2.06	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:t:135:G:O2'	44:t:136:G:O4'	1.76	1.02
21:U:3:ASN:OD1	21:U:9:ARG:NH2	1.92	1.02
44:t:1064:C:O2	44:t:1201:G:N2	1.92	1.01

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	A	244/257 (95%)	224 (92%)	20 (8%)	0	100	100
2	B	394/403 (98%)	363 (92%)	31 (8%)	0	100	100
3	C	361/427 (84%)	337 (93%)	24 (7%)	0	100	100
6	F	246/297 (83%)	235 (96%)	11 (4%)	0	100	100
7	G	214/288 (74%)	186 (87%)	26 (12%)	2 (1%)	14	47
8	H	223/248 (90%)	207 (93%)	16 (7%)	0	100	100
9	I	232/266 (87%)	221 (95%)	11 (5%)	0	100	100
10	J	189/192 (98%)	173 (92%)	16 (8%)	0	100	100
11	K	148/214 (69%)	141 (95%)	7 (5%)	0	100	100
12	L	167/178 (94%)	155 (93%)	12 (7%)	0	100	100
13	M	203/211 (96%)	180 (89%)	23 (11%)	0	100	100
14	N	136/215 (63%)	127 (93%)	9 (7%)	0	100	100
15	O	201/204 (98%)	181 (90%)	19 (10%)	1 (0%)	24	59
16	P	193/203 (95%)	187 (97%)	6 (3%)	0	100	100
17	Q	151/184 (82%)	147 (97%)	4 (3%)	0	100	100
18	R	185/188 (98%)	175 (95%)	10 (5%)	0	100	100
19	S	152/196 (78%)	146 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	T	173/176 (98%)	165 (95%)	8 (5%)	0	100	100
21	U	155/160 (97%)	146 (94%)	9 (6%)	0	100	100
22	V	97/128 (76%)	95 (98%)	2 (2%)	0	100	100
23	W	127/140 (91%)	123 (97%)	4 (3%)	0	100	100
24	X	59/157 (38%)	57 (97%)	2 (3%)	0	100	100
25	Y	115/156 (74%)	107 (93%)	8 (7%)	0	100	100
26	Z	131/145 (90%)	126 (96%)	5 (4%)	0	100	100
27	a	132/136 (97%)	121 (92%)	11 (8%)	0	100	100
28	b	145/148 (98%)	128 (88%)	17 (12%)	0	100	100
29	c	92/159 (58%)	85 (92%)	7 (8%)	0	100	100
30	d	93/115 (81%)	91 (98%)	2 (2%)	0	100	100
31	e	104/125 (83%)	97 (93%)	7 (7%)	0	100	100
32	f	127/135 (94%)	115 (91%)	12 (9%)	0	100	100
33	g	107/110 (97%)	100 (94%)	7 (6%)	0	100	100
34	h	110/117 (94%)	105 (96%)	5 (4%)	0	100	100
35	i	120/123 (98%)	115 (96%)	5 (4%)	0	100	100
36	j	95/105 (90%)	94 (99%)	1 (1%)	0	100	100
37	k	82/97 (84%)	79 (96%)	3 (4%)	0	100	100
38	l	67/70 (96%)	65 (97%)	2 (3%)	0	100	100
39	m	48/51 (94%)	48 (100%)	0	0	100	100
40	o	23/25 (92%)	23 (100%)	0	0	100	100
41	p	97/106 (92%)	94 (97%)	3 (3%)	0	100	100
42	q	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
43	r	120/137 (88%)	106 (88%)	14 (12%)	0	100	100
48	1	420/476 (88%)	403 (96%)	16 (4%)	1 (0%)	43	74
49	2	60/68 (88%)	59 (98%)	1 (2%)	0	100	100
50	3	27/96 (28%)	25 (93%)	2 (7%)	0	100	100
51	4	219/224 (98%)	206 (94%)	13 (6%)	0	100	100
52	5	514/563 (91%)	472 (92%)	39 (8%)	3 (1%)	21	55
53	7	286/483 (59%)	273 (96%)	13 (4%)	0	100	100
54	6	172/188 (92%)	165 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	7845/9182 (85%)	7357 (94%)	481 (6%)	7 (0%)	49 80

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	G	127	SER
48	1	75	THR
7	G	128	HIS
52	5	432	LYS
15	O	90	ASN

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	A	189/199 (95%)	188 (100%)	1 (0%)	81 81
2	B	345/349 (99%)	343 (99%)	2 (1%)	78 80
3	C	302/348 (87%)	300 (99%)	2 (1%)	76 78
6	F	208/250 (83%)	207 (100%)	1 (0%)	81 81
7	G	195/252 (77%)	193 (99%)	2 (1%)	68 74
8	H	194/215 (90%)	192 (99%)	2 (1%)	68 74
9	I	199/223 (89%)	199 (100%)	0	100 100
10	J	170/171 (99%)	170 (100%)	0	100 100
11	K	132/181 (73%)	132 (100%)	0	100 100
12	L	142/149 (95%)	142 (100%)	0	100 100
13	M	171/177 (97%)	170 (99%)	1 (1%)	78 80
14	N	117/161 (73%)	116 (99%)	1 (1%)	70 75
15	O	171/172 (99%)	166 (97%)	5 (3%)	37 58
16	P	168/174 (97%)	167 (99%)	1 (1%)	78 80
17	Q	134/163 (82%)	131 (98%)	3 (2%)	45 64
18	R	164/165 (99%)	162 (99%)	2 (1%)	63 72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	S	139/175 (79%)	139 (100%)	0	100	100
20	T	156/157 (99%)	154 (99%)	2 (1%)	61	71
21	U	138/140 (99%)	137 (99%)	1 (1%)	76	78
22	V	89/115 (77%)	89 (100%)	0	100	100
23	W	100/107 (94%)	100 (100%)	0	100	100
24	X	53/126 (42%)	53 (100%)	0	100	100
25	Y	105/133 (79%)	105 (100%)	0	100	100
26	Z	123/135 (91%)	119 (97%)	4 (3%)	33	56
27	a	117/118 (99%)	117 (100%)	0	100	100
28	b	120/121 (99%)	117 (98%)	3 (2%)	42	62
29	c	79/126 (63%)	78 (99%)	1 (1%)	61	71
30	d	80/97 (82%)	77 (96%)	3 (4%)	29	53
31	e	97/110 (88%)	97 (100%)	0	100	100
32	f	115/121 (95%)	114 (99%)	1 (1%)	70	75
33	g	88/89 (99%)	85 (97%)	3 (3%)	32	56
34	h	96/100 (96%)	96 (100%)	0	100	100
35	i	109/110 (99%)	107 (98%)	2 (2%)	51	67
36	j	83/89 (93%)	83 (100%)	0	100	100
37	k	71/80 (89%)	71 (100%)	0	100	100
38	l	64/65 (98%)	64 (100%)	0	100	100
39	m	47/48 (98%)	45 (96%)	2 (4%)	26	50
40	o	24/24 (100%)	24 (100%)	0	100	100
41	p	88/94 (94%)	88 (100%)	0	100	100
42	q	74/75 (99%)	74 (100%)	0	100	100
43	r	106/121 (88%)	104 (98%)	2 (2%)	50	66
48	1	362/399 (91%)	357 (99%)	5 (1%)	59	70
49	2	53/59 (90%)	51 (96%)	2 (4%)	29	53
50	3	26/74 (35%)	25 (96%)	1 (4%)	29	53
51	4	183/186 (98%)	177 (97%)	6 (3%)	33	56
52	5	438/475 (92%)	415 (95%)	23 (5%)	20	46
53	7	261/436 (60%)	253 (97%)	8 (3%)	35	57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
54	6	154/164 (94%)	149 (97%)	5 (3%)	34 56
All	All	6839/7818 (88%)	6742 (99%)	97 (1%)	57 70

5 of 97 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
51	4	145	HIS
52	5	234	LEU
51	4	172	LEU
52	5	89	LEU
52	5	264	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 52 such sidechains are listed below:

Mol	Chain	Res	Type
26	Z	20	ASN
32	f	107	ASN
53	7	422	HIS
26	Z	65	GLN
29	c	10	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	D	156/157 (99%)	60 (38%)	20 (12%)
44	t	3495/3579 (97%)	849 (24%)	0
45	u	74/76 (97%)	30 (40%)	0
46	v	75/76 (98%)	32 (42%)	0
5	E	118/119 (99%)	14 (11%)	0
All	All	3918/4007 (97%)	985 (25%)	20 (0%)

5 of 985 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	D	2	G
4	D	13	G
4	D	34	U
4	D	35	C
4	D	39	G

5 of 20 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	D	86	U
4	D	125	C
4	D	129	C
4	D	126	C
4	D	78	G

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 31 ligands modelled in this entry, 31 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
44	t	11

The worst 5 of 11 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	t	750:G	O3'	890:C	P	20.30
1	t	3919:C	O3'	4035:G	P	19.55
1	t	976:U	O3'	1047:G	P	16.16
1	t	1680:C	O3'	1699:C	P	15.85
1	t	1089:A	O3'	1145:G	P	15.56

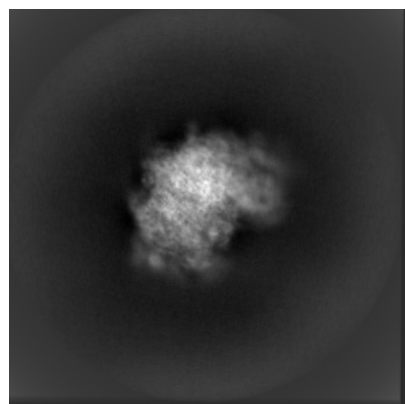
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21435. These allow visual inspection of the internal detail of the map and identification of artifacts.

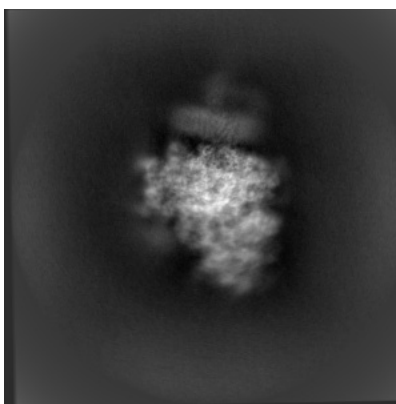
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

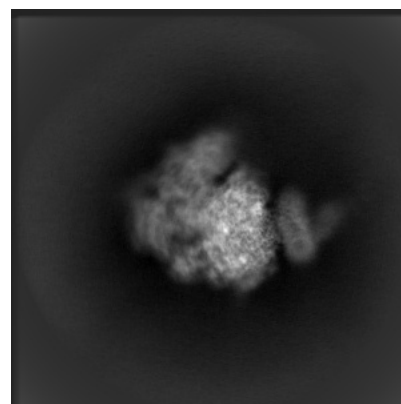
6.1.1 Primary map



X

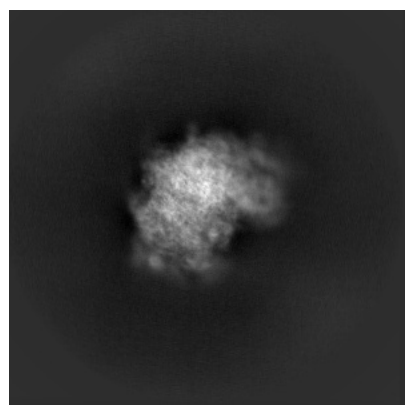


Y

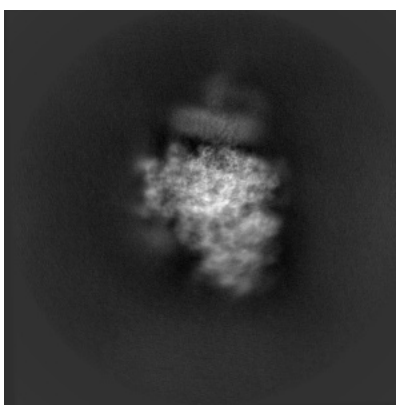


Z

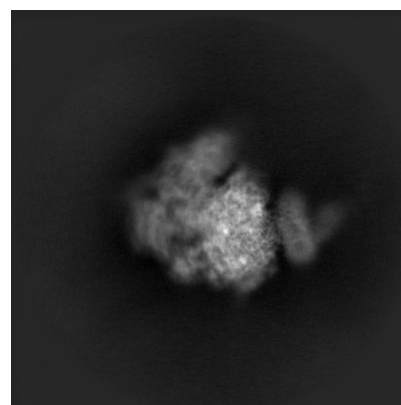
6.1.2 Raw map



X



Y

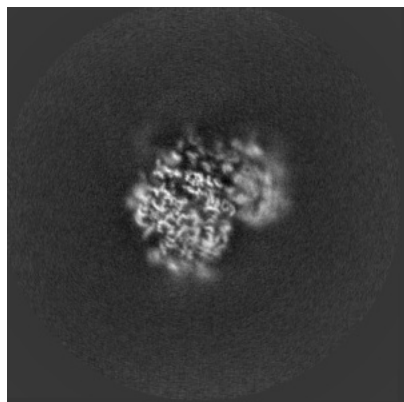


Z

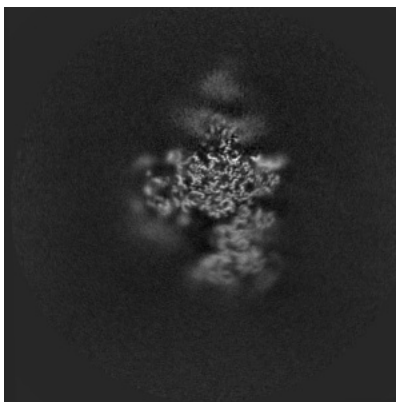
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

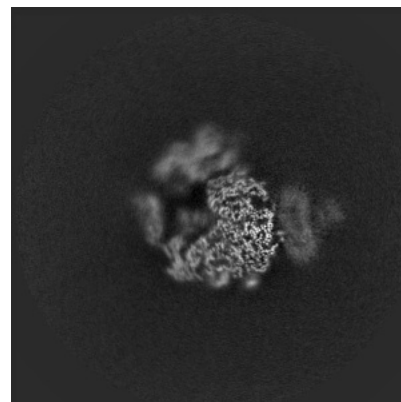
6.2.1 Primary map



X Index: 250

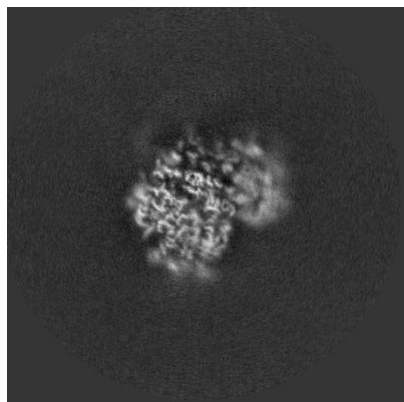


Y Index: 250

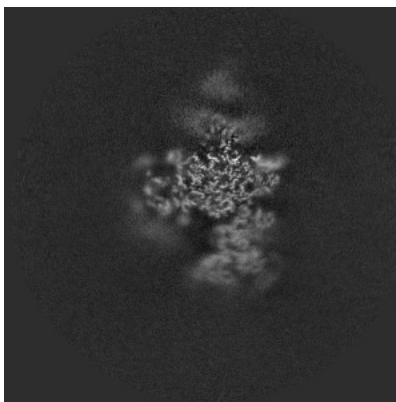


Z Index: 250

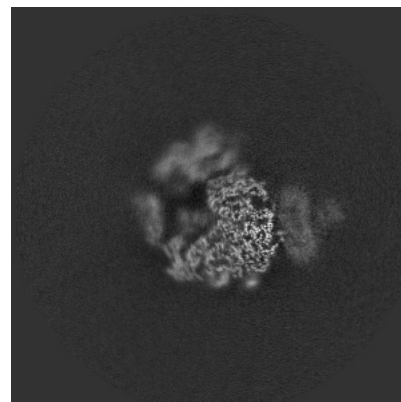
6.2.2 Raw map



X Index: 250



Y Index: 250

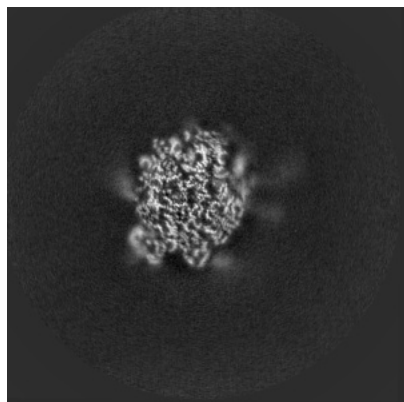


Z Index: 250

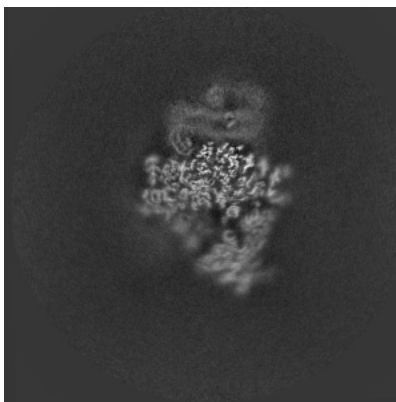
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

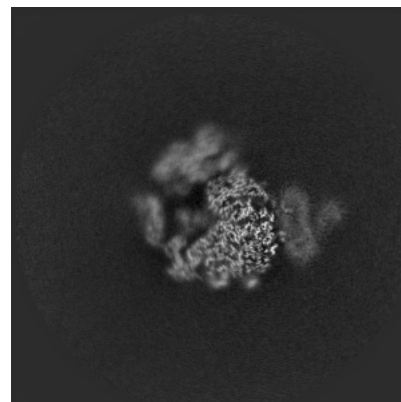
6.3.1 Primary map



X Index: 285

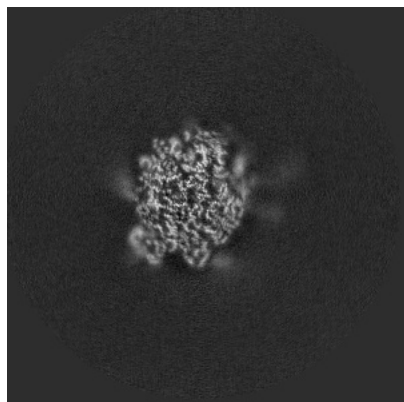


Y Index: 225

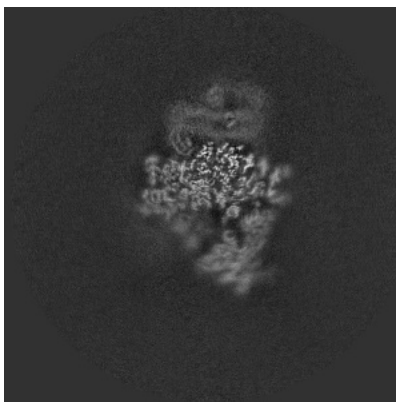


Z Index: 252

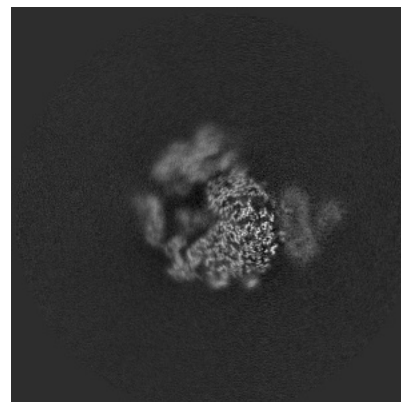
6.3.2 Raw map



X Index: 285



Y Index: 225

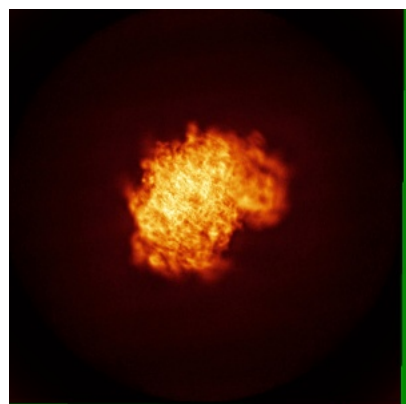


Z Index: 252

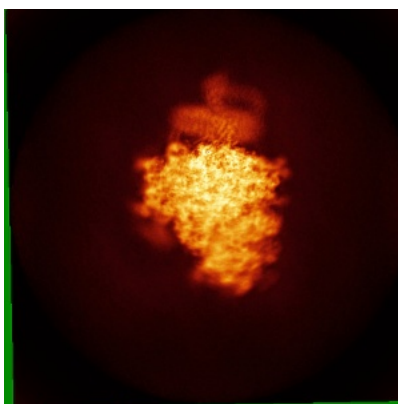
The images above show the largest variance slices of the map in three orthogonal directions.

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

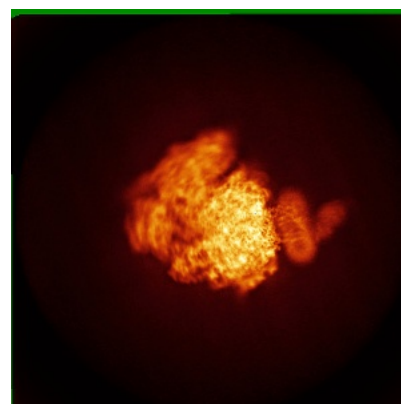
6.4.1 Primary map



X

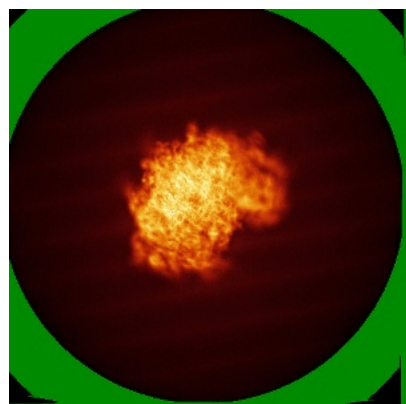


Y

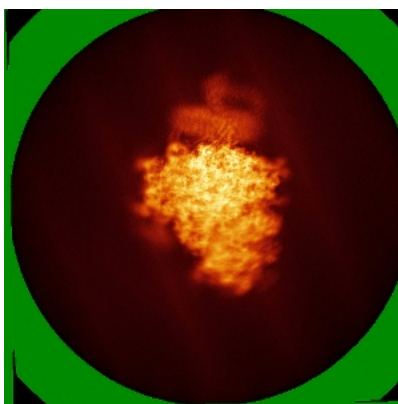


Z

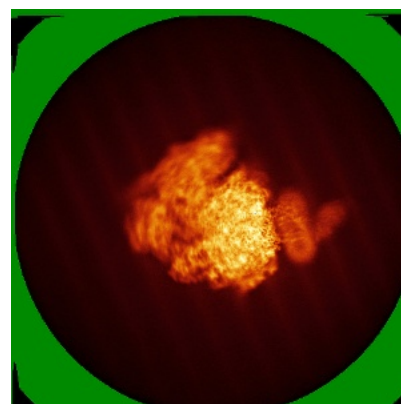
6.4.2 Raw map



X



Y

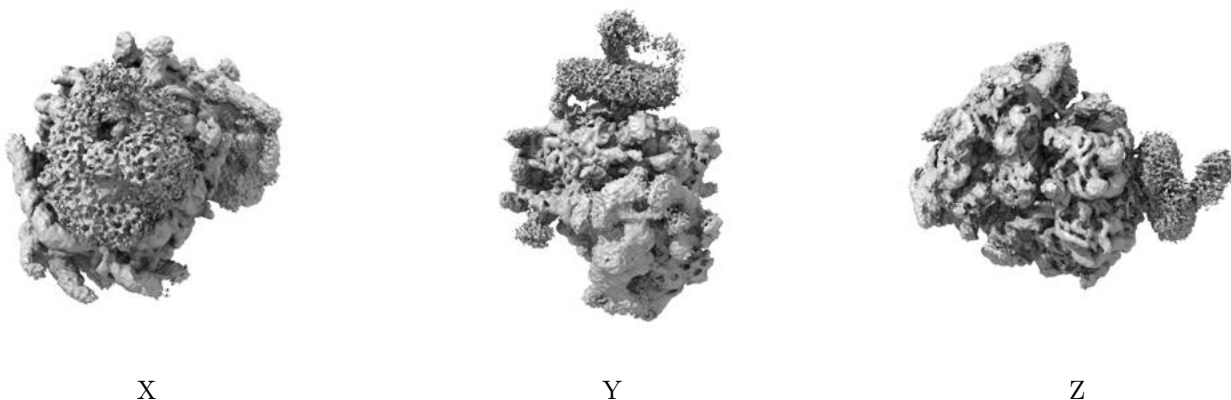


Z

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.

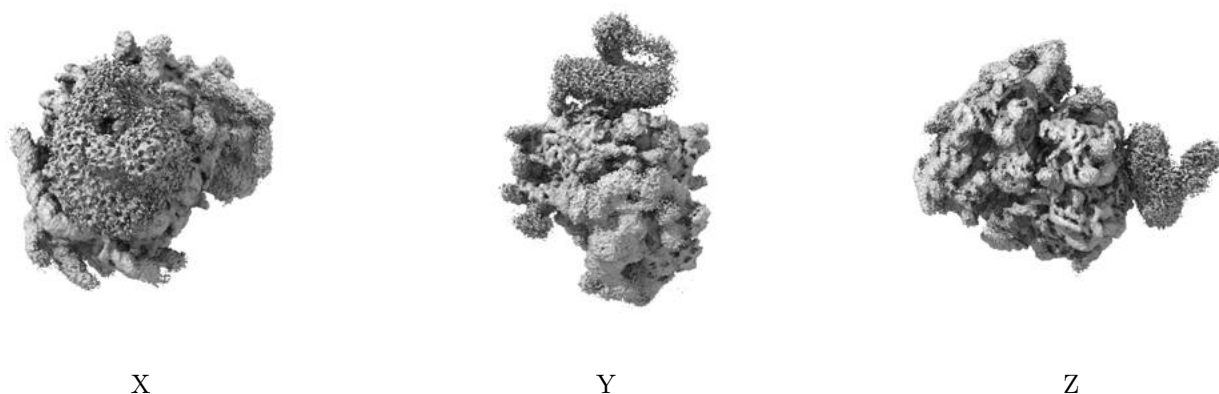
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0073. 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



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.

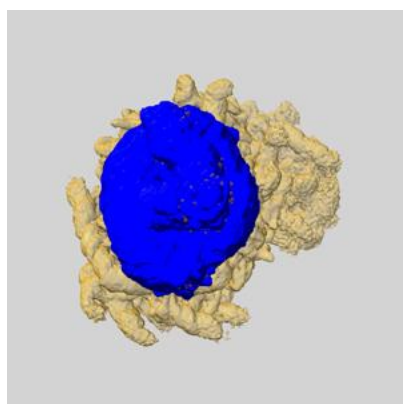
6.6 Mask visualisation [i](#)

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

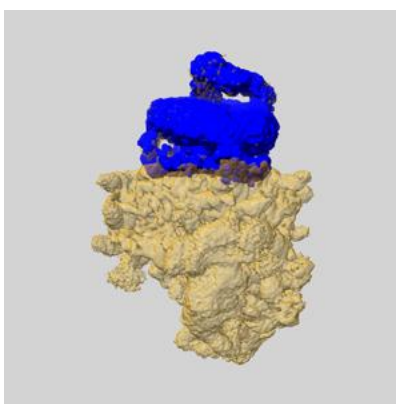
A mask typically either:

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

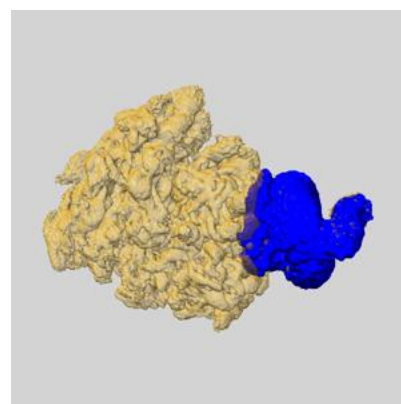
6.6.1 emd_21435_msk_1.map [i](#)



X



Y

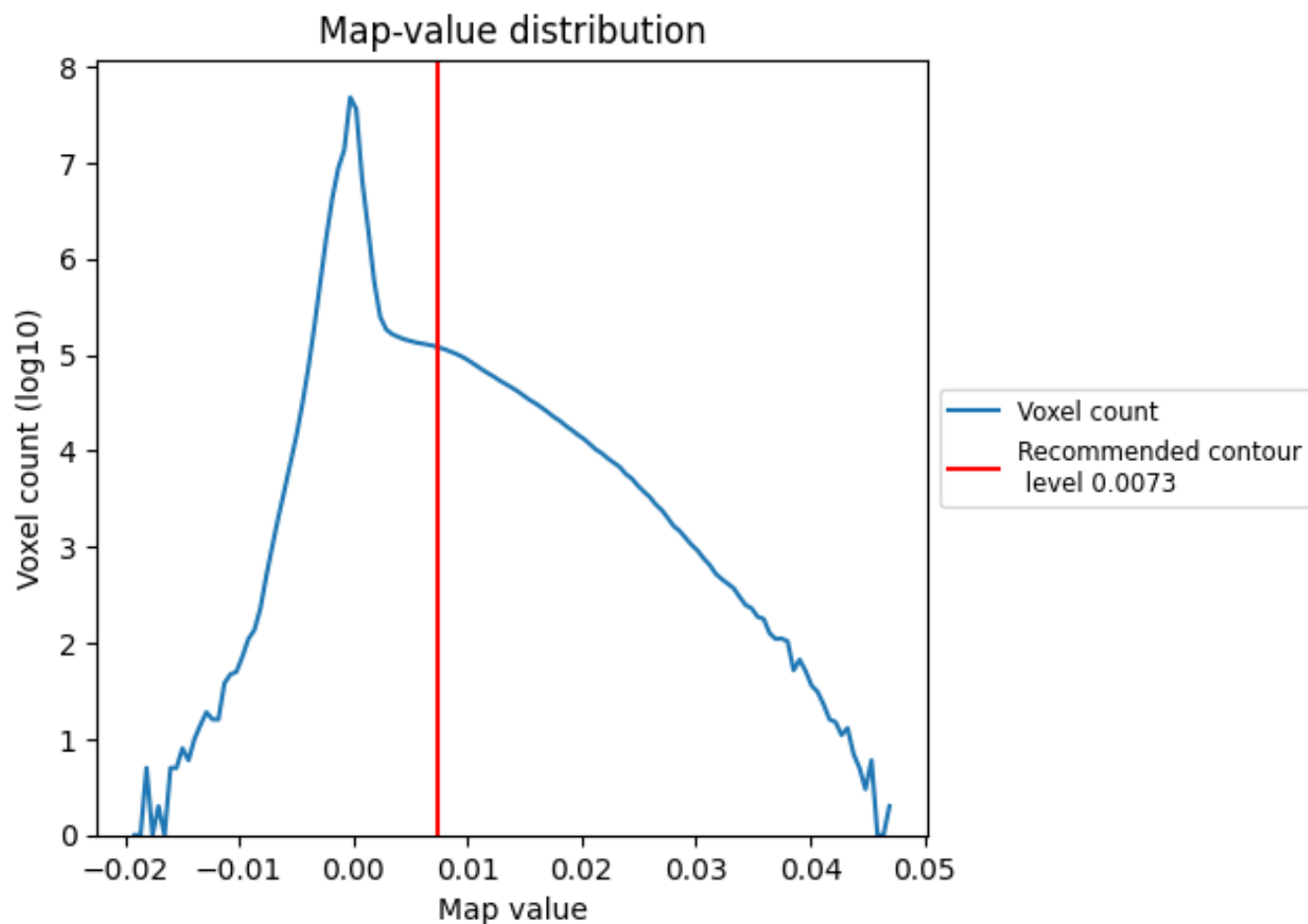


Z

7 Map analysis [i](#)

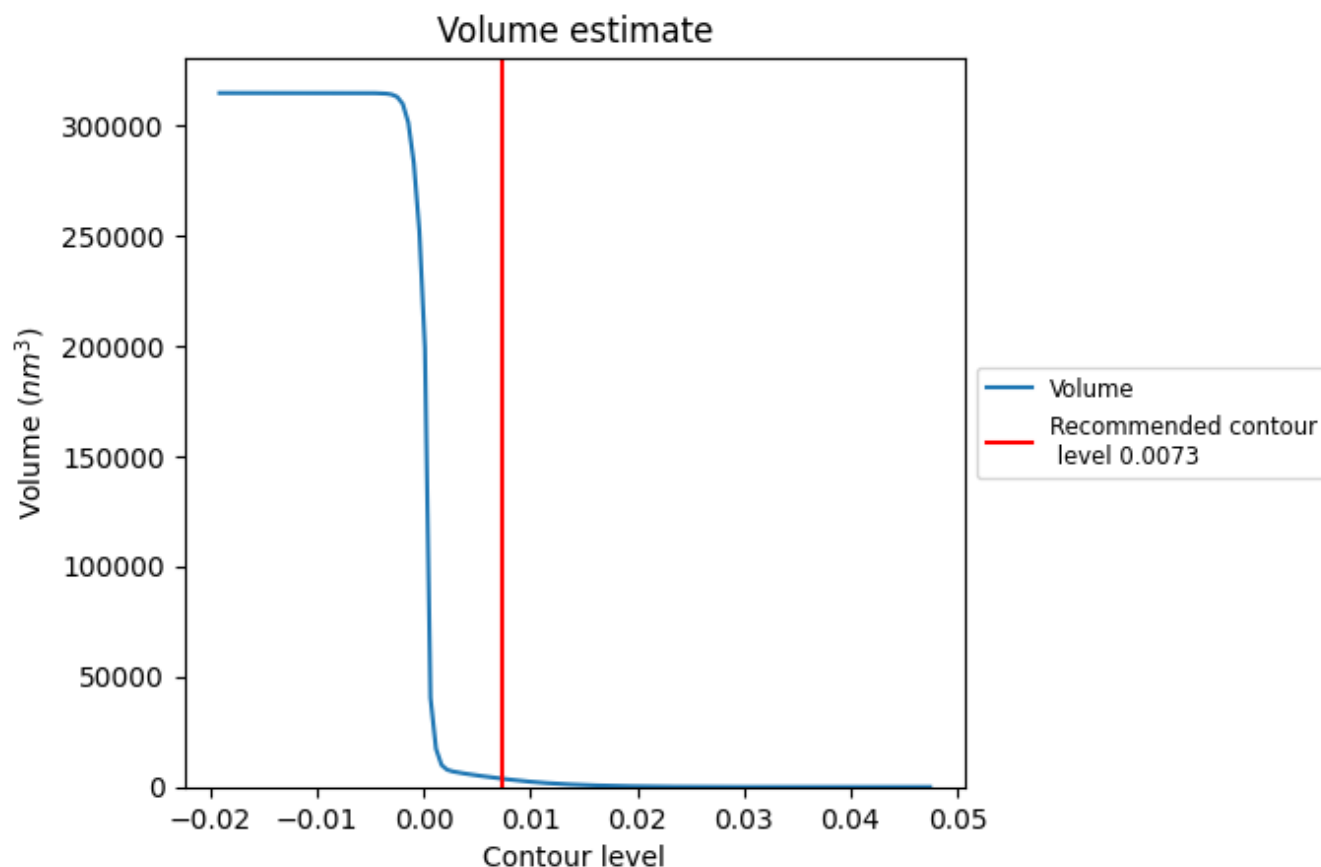
This section contains the results of statistical analysis of the map.

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.

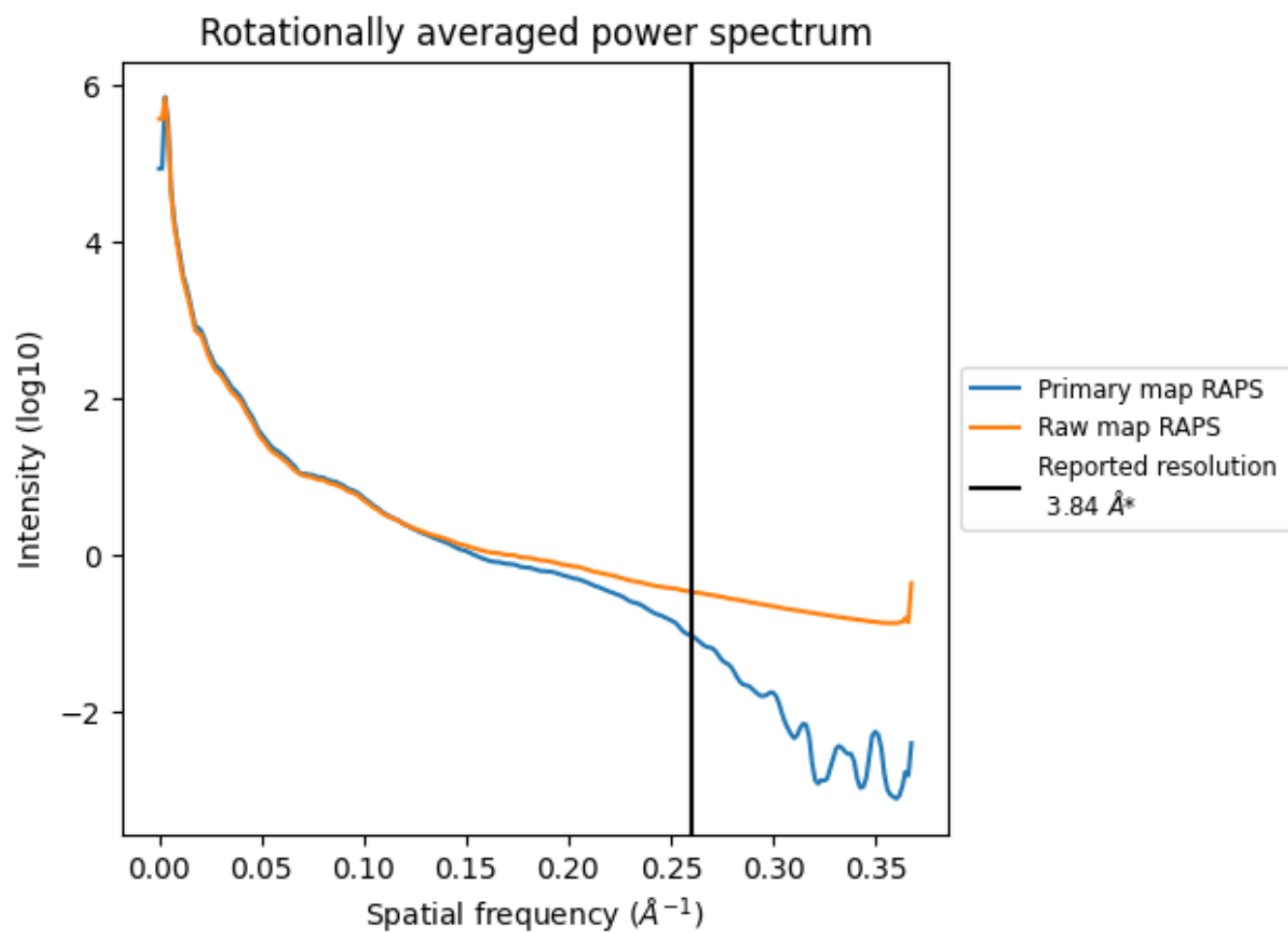
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3776 nm^3 ; this corresponds to an approximate mass of 3411 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 ⓘ

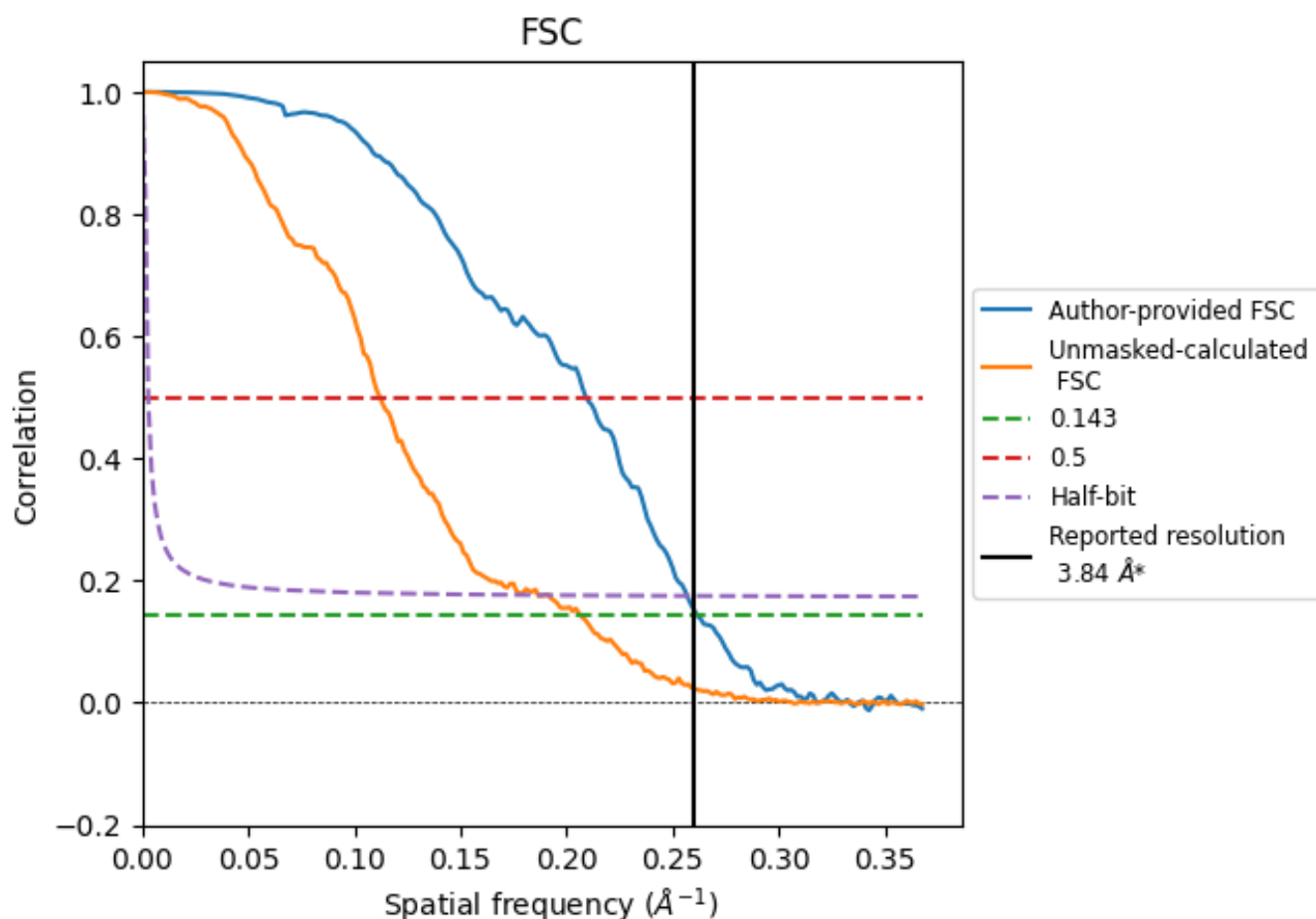


*Reported resolution corresponds to spatial frequency of 0.260 $\text{\AA}^{-1}$

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 0.260 Å⁻¹

8.2 Resolution estimates [i](#)

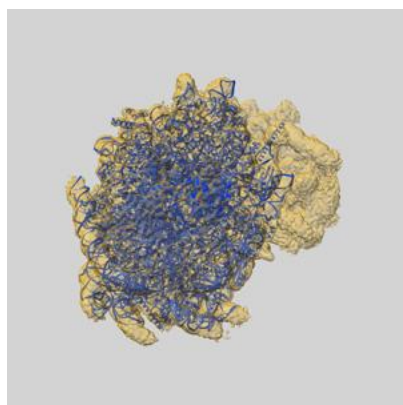
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.84	-	-
Author-provided FSC curve	3.82	4.78	3.89
Unmasked-calculated*	4.84	8.93	5.36

*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 4.84 differs from the reported value 3.84 by more than 10 %

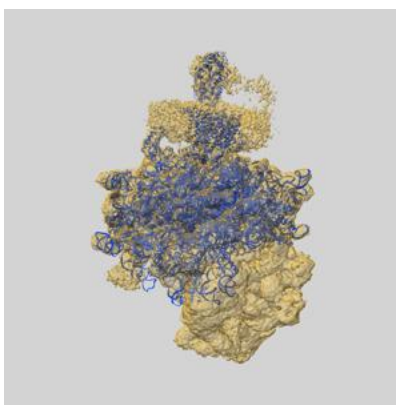
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21435 and PDB model 6W6L. Per-residue inclusion information can be found in section 3 on page 15.

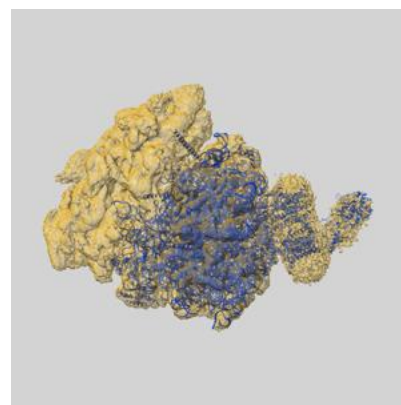
9.1 Map-model overlay [i](#)



X



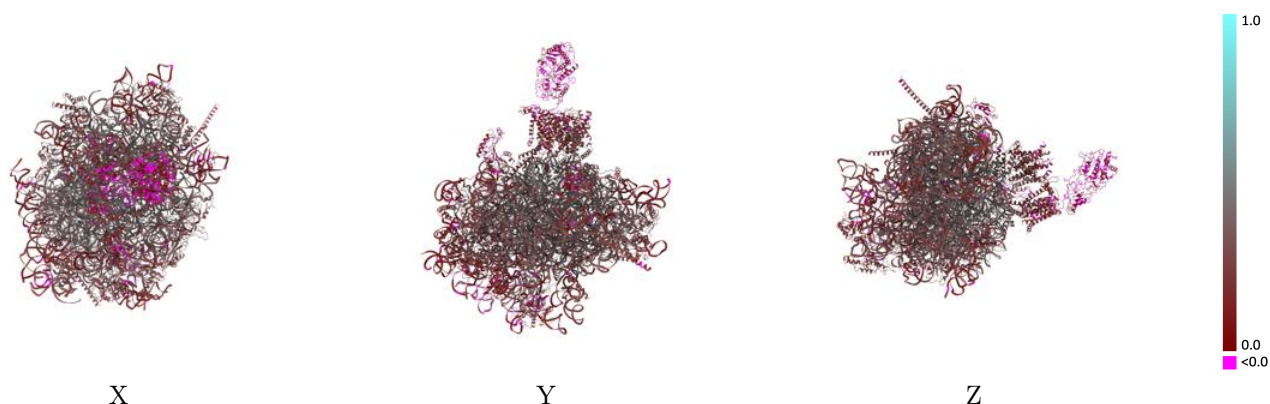
Y



Z

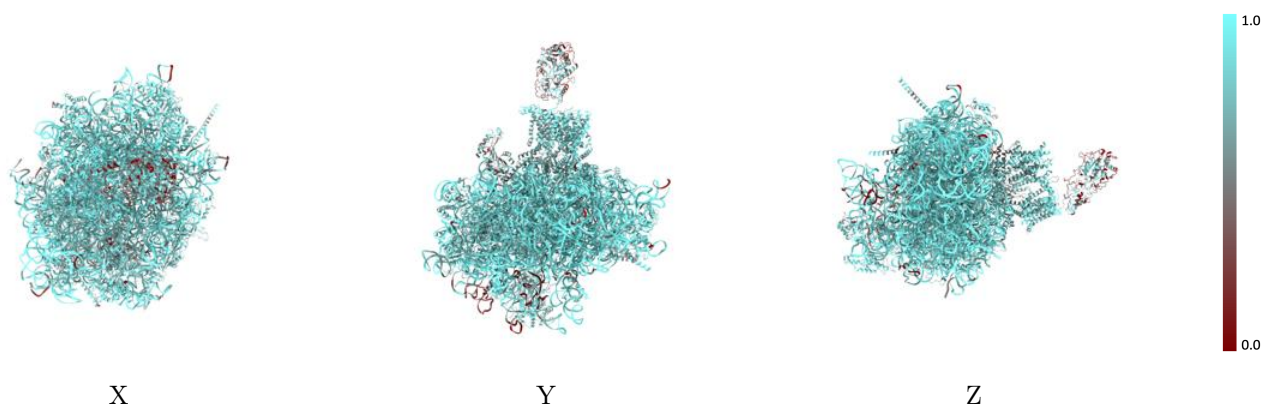
The images above show the 3D surface view of the map at the recommended contour level 0.0073 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



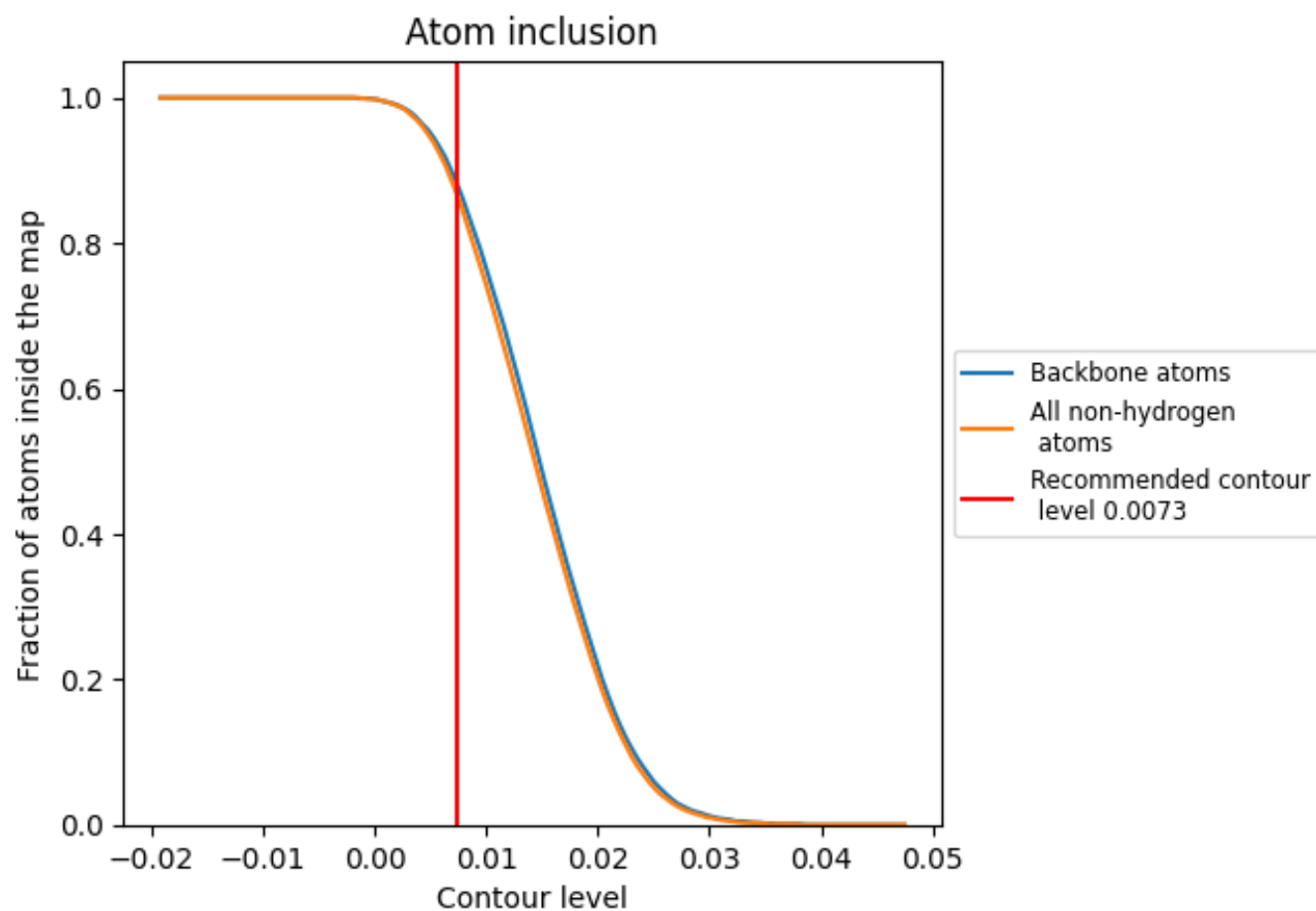
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0073).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 87% 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 (0.0073) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8710	 0.2910
1	 0.7880	 0.2400
2	 0.7820	 0.2730
3	 0.7560	 0.1440
4	 0.8210	 0.1830
5	 0.4940	 0.0340
6	 0.7640	 0.1540
7	 0.5230	 0.1630
A	 0.8390	 0.3420
B	 0.8620	 0.3090
C	 0.8920	 0.3840
D	 0.9840	 0.3990
E	 0.9940	 0.2630
F	 0.8960	 0.1970
G	 0.8860	 0.2800
H	 0.8220	 0.2760
I	 0.8430	 0.2960
J	 0.8310	 0.2060
K	 0.5280	 0.0810
L	 0.7780	 0.1730
M	 0.8340	 0.3220
N	 0.8820	 0.2330
O	 0.9060	 0.3690
P	 0.8450	 0.2920
Q	 0.8950	 0.4140
R	 0.8870	 0.3530
S	 0.8460	 0.3000
T	 0.8750	 0.2450
U	 0.8420	 0.2700
V	 0.7180	 0.1210
W	 0.7900	 0.3020
X	 0.8330	 0.2910
Y	 0.8680	 0.4090
Z	 0.8630	 0.4170
a	 0.8840	 0.2930



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Chain	Atom inclusion	Q-score
b	 0.9230	 0.3400
c	 0.8230	 0.2050
d	 0.8710	 0.2620
e	 0.9020	 0.3670
f	 0.8610	 0.4040
g	 0.8630	 0.3580
h	 0.8640	 0.3570
i	 0.8320	 0.3590
j	 0.8610	 0.2760
k	 0.9220	 0.4330
l	 0.8370	 0.3220
m	 0.8910	 0.4240
o	 0.6640	 0.1890
p	 0.7960	 0.2550
q	 0.8000	 0.3020
r	 0.9110	 0.3860
t	 0.9510	 0.3110
u	 0.3950	 0.1160
v	 0.8300	 0.2100
y	 0.7260	 0.3850