



## wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 03:16 PM UTC

PDB ID : 5APO / pdb\_00005apo  
EMDB ID : EMD-3151  
Title : Structure of the yeast 60S ribosomal subunit in complex with Arx1, Alb1 and C-terminally tagged Rei1  
Authors : Greber, B.J.; Gerhardy, S.; Leitner, A.; Leibundgut, M.; Salem, M.; Boehringer, D.; Leulliot, N.; Aebersold, R.; Panse, V.G.; Ban, N.  
Deposited on : 2015-09-17  
Resolution : 3.41 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](mailto: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>.

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

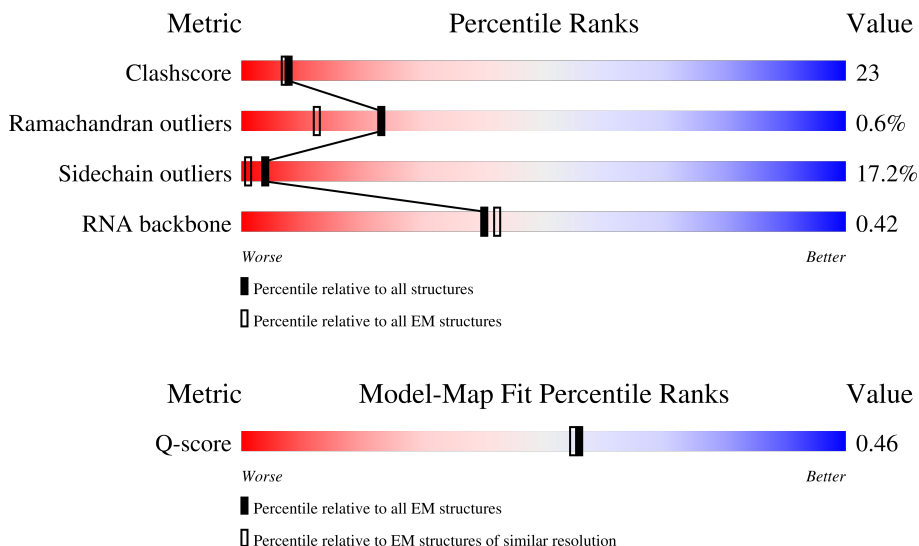
EMDB validation analysis : 0.0.1.dev132  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 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 i

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

The reported resolution of this entry is 3.41 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	14717 ( 2.90 - 3.90 )

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  $\geq 3$ , 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	5	3396	
2	7	121	
3	8	158	








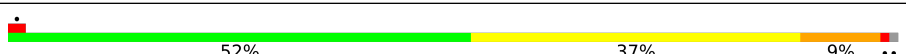
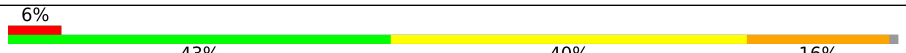







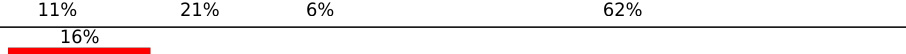


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Mol	Chain	Length	Quality of chain
4	A	254	35% 35% 13% 17%
5	B	387	47% 42% 11%
6	C	362	46% 42% 11%
7	D	297	53% 37% 10%
8	E	176	6% 53% 40% 7%
9	F	244	46% 35% 10% 9%
10	G	256	39% 41% 10% 10%
11	H	191	50% 41% 8%
12	I	221	52% 36% 8%
13	J	174	8% 43% 42% 11%
14	L	199	55% 29% 14%
15	M	138	57% 35% 7%
16	N	204	7% 50% 40% 9%
17	O	199	47% 41% 11%
18	P	184	5% 50% 39% 10%
19	Q	186	52% 36% 11%
20	R	189	41% 33% 9% 17%
21	S	172	51% 39% 9%
22	T	160	49% 40% 10%
23	U	121	45% 34% 6% 16%
24	V	137	47% 45% 7%
25	W	155	23% 14% 59%
26	X	142	35% 39% 11% 15%
27	Y	127	42% 47% 9%
28	Z	136	39% 45% 12%

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Mol	Chain	Length	Quality of chain
29	a	149	
30	b	59	
31	c	105	
32	d	113	
33	e	130	
34	f	107	
35	g	121	
36	h	120	
37	i	100	
38	j	88	
39	k	78	
40	l	51	
41	m	128	
42	o	106	
43	p	92	
44	q	312	
45	x	616	
46	y	401	
47	z	95	

## 2 Entry composition

There are 49 unique types of molecules in this entry. The entry contains 129386 atoms, of which 3 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 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	5	3112	66537	29736	11996	21694	3111	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	7	121	2579	1152	461	845	121	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	8	158	3353	1500	586	1109	158	0	0

- Molecule 4 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	A	212	1630	1021	325	283	1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	B	386	3075	1950	584	533	8	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	C	361	2748	1729	522	494	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	D	294	2359	1489	412	456	2	0	0

- Molecule 8 is a protein called 60S RIBOSOMAL PROTEIN EL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	E	175	1356	878	242	235	1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	F	223	1791	1155	325	310	1	0	0

- Molecule 10 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	G	231	1763	1130	316	314	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	H	191	1518	963	274	277	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	I	213	1722	1094	325	297	6	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	J	169	1353	847	253	249	4	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
14	L	194	Total	C	N	O	0	0
			1548	965	316	267		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	M	137	Total	C	N	O	S	0	0
			1059	678	200	179	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	N	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 17 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	O	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
18	P	183	Total	C	N	O	0	0
			1442	896	287	259		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Q	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
20	R	156	Total	C	N	O	0	0
			1258	781	265	212		

- Molecule 21 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	S	171	1437	925	266	243	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	T	159	1276	805	246	221	4	0	0

- Molecule 23 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
23	U	102	808	524	132	152	0	0

- Molecule 24 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	V	136	1003	628	189	179	7	0	0

- Molecule 25 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	W	63	521	336	102	82	1	0	0

- Molecule 26 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	X	120	959	617	168	172	2	0	0

- Molecule 27 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
27	Y	126	993	625	192	176	0	0

- Molecule 28 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
28	Z	135	1092	710	202	180	0	0

- Molecule 29 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	a	148	1173	749	231	190	3	0	0

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
30	b	58	462	289	100	73	0	0

- Molecule 31 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	c	100	767	492	128	146	1	0	0

- Molecule 32 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	d	109	883	559	167	156	1	0	0

- Molecule 33 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	e	129	1034	655	207	171	1	0	0

- Molecule 34 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	f	106	850	540	165	144	1	0	0

- Molecule 35 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 36 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	h	119	Total	C	N	O	S	0	0
			965	612	185	167	1		

- Molecule 37 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	i	99	Total	C	N	O	S	0	0
			770	481	156	131	2		

- Molecule 38 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	j	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 39 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	k	77	Total	C	N	O	0	0
			608	388	114	106		

- Molecule 40 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	l	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 41 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	m	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 42 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	o	105	847	534	170	138	5	0	0

- Molecule 43 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	p	91	694	429	138	121	6	0	0

- Molecule 44 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	q	120	962	618	169	172	3	0	0

- Molecule 45 is a protein called Probable metalloprotease ARX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	x	579	4477	2823	772	867	15	0	0

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
x	-22	MET	-	initiating methionine	UNP Q03862
x	-21	GLY	-	expression tag	UNP Q03862
x	-20	SER	-	expression tag	UNP Q03862
x	-19	SER	-	expression tag	UNP Q03862
x	-18	HIS	-	expression tag	UNP Q03862
x	-17	HIS	-	expression tag	UNP Q03862
x	-16	HIS	-	expression tag	UNP Q03862
x	-15	HIS	-	expression tag	UNP Q03862
x	-14	HIS	-	expression tag	UNP Q03862
x	-13	HIS	-	expression tag	UNP Q03862
x	-12	SER	-	expression tag	UNP Q03862
x	-11	SER	-	expression tag	UNP Q03862
x	-10	GLY	-	expression tag	UNP Q03862
x	-9	LEU	-	expression tag	UNP Q03862
x	-8	VAL	-	expression tag	UNP Q03862
x	-7	PRO	-	expression tag	UNP Q03862
x	-6	ARG	-	expression tag	UNP Q03862
x	-5	GLY	-	expression tag	UNP Q03862
x	-4	SER	-	expression tag	UNP Q03862

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Chain	Residue	Modelled	Actual	Comment	Reference
x	-3	HIS	-	expression tag	UNP Q03862
x	-2	MET	-	expression tag	UNP Q03862
x	-1	LEU	-	expression tag	UNP Q03862
x	0	GLU	-	expression tag	UNP Q03862

- Molecule 46 is a protein called CYTOPLASMIC 60S SUBUNIT BIOGENESIS FACTOR REI1.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
46	y	217	1788	1131	3	324	322	8	0	0

- Molecule 47 is a protein called ALB1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
47	z	85	510	340	85	85	0	0

- Molecule 48 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
48	5	259	Total	Mg	0
			259	259	
48	7	6	Total	Mg	0
			6	6	
48	8	7	Total	Mg	0
			7	7	
48	B	2	Total	Mg	0
			2	2	
48	C	1	Total	Mg	0
			1	1	
48	N	1	Total	Mg	0
			1	1	
48	P	1	Total	Mg	0
			1	1	
48	R	1	Total	Mg	0
			1	1	
48	V	1	Total	Mg	0
			1	1	
48	y	1	Total	Mg	0
			1	1	

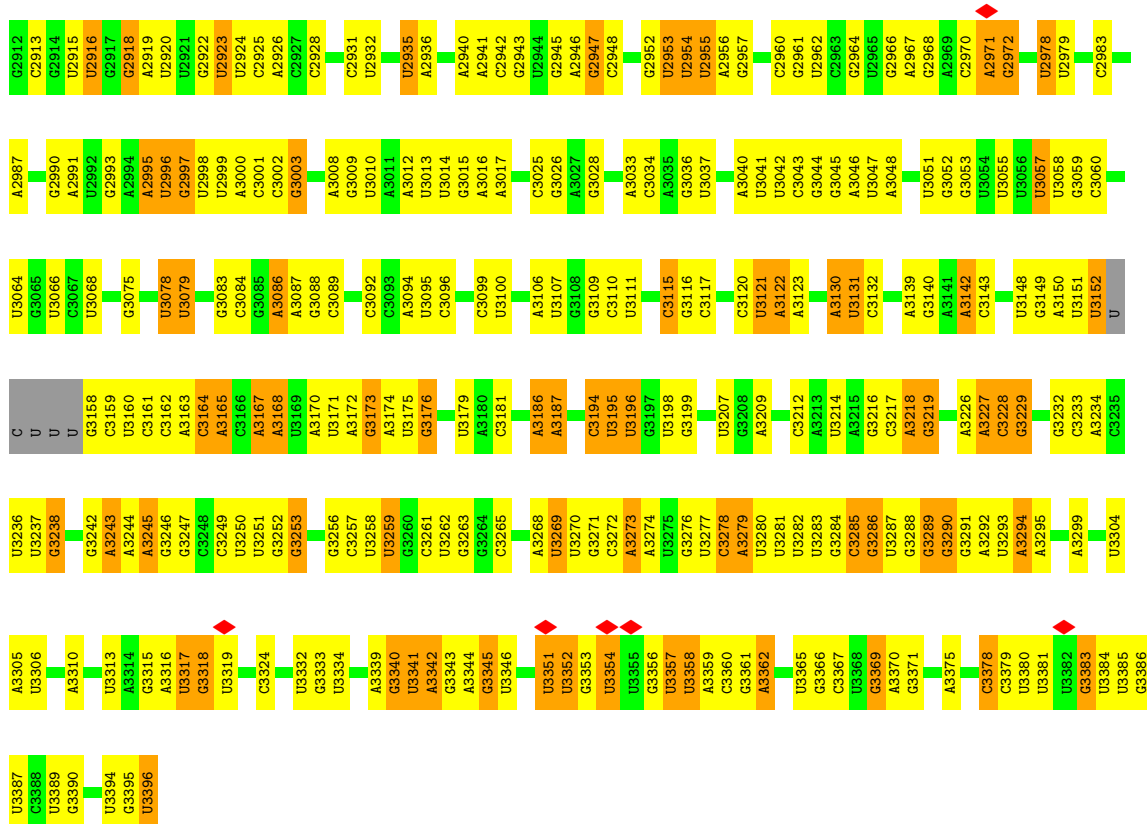
- Molecule 49 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
49	j	1	Total 1	Zn 1	0
49	m	1	Total 1	Zn 1	0
49	o	1	Total 1	Zn 1	0
49	p	1	Total 1	Zn 1	0
49	y	2	Total 2	Zn 2	0

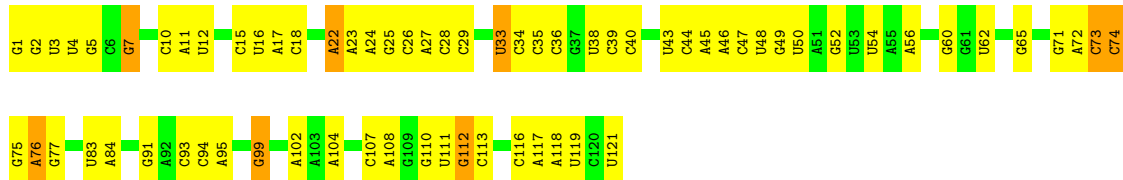




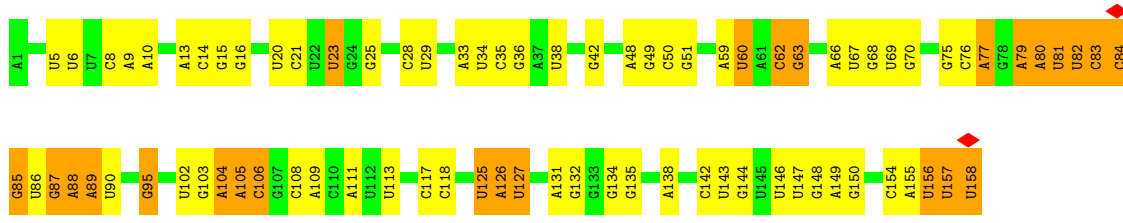
U2835	A2746	A2657	G2573	C	G2376	G2283	A2223	A2145	P5P	A2019	G1949	C1846
C2836	A2747	G2661	G2574	U	G2377	C2284	A2234	C2146	P5P	A2020	U1950	C1849
A2837	A2748	G2662	G2575	U2509	C2378	C2285	A2225	A2147	P5P	A2021	C1951	A1850
G2838	G2749	G2663	G2576	A	G2385	U2286	U2226	U2148	P5P	A2022	G1952	G1862
G2839	G2750	G2664	G2577	G	G2386	G2287	U2227	C2156	P5P	A2023	G1953	U1862
C2840	U2752	U2665	U2513	U	U2388	G2288	C2227	G2157	P5P	A2024	Y5P	G1863
G2841	G2753	C2666	U2514	U	C2389	U2289	A2228	A2158	P5P	A2025	Y5P	A1864
U2842	U2757	A2667	A2515	U	A2390	C2290	A2229	G2163	P5P	P5P	Y5P	C1866
U2843	U2758	U2668	A2519	A	G2391	U2291	C2230	C2164	P5P	P5P	Y5P	U1870
C2844	G2761	G2669	U2521	A	G2392	U2292	C2231	A2168	P5P	P5P	Y5P	A1874
A2845	U2674	U2670	U2522	U	G2393	G2293	A2232	G2169	P5P	P5P	Y5P	U1875
A2847	C2675	C2671	G2522	A	A2394	U2294	A2233	G2180	P5P	P5P	Y5P	G1876
C2850	A2676	A2676	A2523	A	A2397	A2295	A2234	U2175	P5P	P5P	Y5P	U1877
A2853	U2766	G2677	A2524	A	A2398	C2235	G2235	G2176	P5P	P5P	Y5P	U1878
U2854	U2767	A2678	G2525	U	A2399	U2298	G2236	G2177	P5P	P5P	Y5P	G1878
U2855	U2768	A2679	G2526	U	G2400	A2299	G2237	A2178	P5P	P5P	Y5P	A1879
G2856	A2769	U2680	G2527	G	A2401	G2304	C2237	G2179	P5P	P5P	Y5P	U1880
C2867	G2770	U2681	G2530	G	A2402	C2305	G2238	G2186	P5P	P5P	Y5P	A1887
G2871	U2771	C2682	C2531	G	G2403	G2306	G2239	G2187	P5P	P5P	Y5P	A1891
A2872	C2772	U2683	U2532	A	A2404	G2307	G2240	U2190	P5P	P5P	Y5P	A1892
U2873	C2773	C2684	G2533	G	U2407	C2308	U2241	U2191	P5P	P5P	Y5P	A1893
U2875	G2774	U2685	G2534	U	G2409	A2309	A2242	U2193	P5P	P5P	Y5P	A1894
C2880	A2691	G2686	A2535	C	U2410	U2310	A2244	G2199	P5P	P5P	Y5P	A1895
U2881	A2694	A2694	U2536	C	U2411	G2311	C2245	G2199	P5P	P5P	Y5P	G1898
G2882	U2701	U2687	U2537	G	U2416	G2312	G2246	U2200	P5P	P5P	Y5P	G1899
U2883	A2702	U2688	U2538	C	U2417	A2313	G2247	G2201	P5P	P5P	Y5P	A1900
C2884	A2703	U2689	C2539	C	G2418	U2314	C2248	U2202	P5P	P5P	Y5P	A1901
C2885	A2704	U2690	A2540	C	A2419	G2315	G2249	G2196	P5P	P5P	Y5P	G1906
U2886	G2705	U2691	U2541	A	C2420	G2316	G	G2197	P5P	P5P	Y5P	C1907
U2887	U2712	U2692	U2542	G	C2422	A2317	G	A2198	P5P	P5P	Y5P	A1908
A2888	U2713	U2693	U2543	U	U2423	C2322	G	G2199	P5P	P5P	Y5P	A1913
C2889	G2714	A2694	C2544	A	A2424	G2323	A	G2199	P5P	P5P	Y5P	G1914
U2890	U2717	U2695	A2545	U	U2426	A2332	A	U2200	P5P	P5P	Y5P	A1915
G2891	U2718	U2696	G2546	U	U2427	C2333	C	G2201	P5P	P5P	Y5P	U1916
U2892	U2719	U2697	G2547	U	U2428	U2334	A	U2202	P5P	P5P	Y5P	C1917
C2893	U2724	U2698	G2548	C	G2429	G2335	U	G2203	P5P	P5P	Y5P	C1918
C2894	U2725	U2699	U2550	C	A2430	U2336	U	C2204	P5P	P5P	Y5P	G1928
A2897	U2726	U2700	U2551	U	C2431	C2337	G	U2205	P5P	P5P	Y5P	G1929
G2898	A2727	U2701	U2552	U	A2432	C2338	A	G2206	P5P	P5P	Y5P	A1930
C2899	G2728	U2702	A2553	U	U2433	C2339	C	A2207	P5P	P5P	Y5P	Y5P1986
C2900	U2729	U2703	C2554	C	U2434	U2340	U	Y5P1987	P5P	P5P	Y5P	Y5P1988
G2901	G2730	U2704	U2555	C	G2435	A2341	C	Y5P1989	P5P	P5P	Y5P	Y5P1989
U2904	U2731	U2705	U2556	U	U2436	U2342	U	Y5P1990	P5P	P5P	Y5P	Y5P1991
U2905	A2736	U2706	U2557	U	G2437	A2343	A	G1940	P5P	P5P	Y5P	C1941
C2906	A2737	U2707	U2558	U	A2438	A2344	A	Y5P1992	P5P	P5P	Y5P	U1942
G2907	C2737	U2708	U2559	U	A2439	U2345	U	Y5P1994	P5P	P5P	Y5P	C1943
U2908	A2740	U2709	C2560	U	G	U2346	U	Y5P1995	P5P	P5P	Y5P	A1946
C2909	G2741	U2710	A2561	A	A	G2437	C2267	A2016	P5P	P5P	Y5P	A1947
G2910	C2742	U2711	U2562	G	A	A2357	U2268	A2017	P5P	P5P	Y5P	G1948
C2911	U2742	U2712	U2563	U	A	A2358	U2269	A2018	P5P	P5P	Y5P	
G2912	G2743	U2713	C2564	U	A	C2362	A2270					
U2913	C2744	U2714	A2565	U	A	A2363	U2269					
C2914	U2745	U2715	U2566	U	A	C2366	A2271					
G2915	G2745	U2716	C2567	U	U	A2372	A2272					
U2916	U2910	U2717	U2568	U	U	A2373	G2272					
A2911	G2828	U2718	A2569	U	U	C2374	G2273					
		U2719	U2570	U	U	G2375	U2274					
		U2720	U2571	U	U		A2275					
		U2721	C2572	U	U		G2276					
		U2722		U	U		A2220					
		U2723		U	U		C2277					
		U2724		U	U		C2278					
		U2725		U	U		A2279					
		U2726		U	U		A2280					
		U2727		U	U		A2281					
		U2728		U	U		U2282					



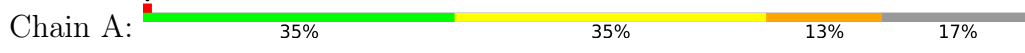
• Molecule 2: 5S ribosomal RNA



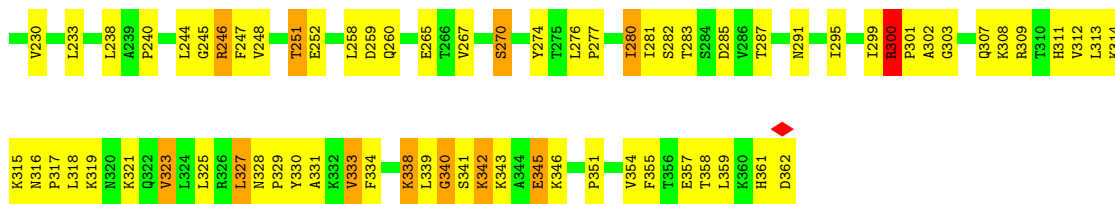
• Molecule 3: 5.8S ribosomal RNA



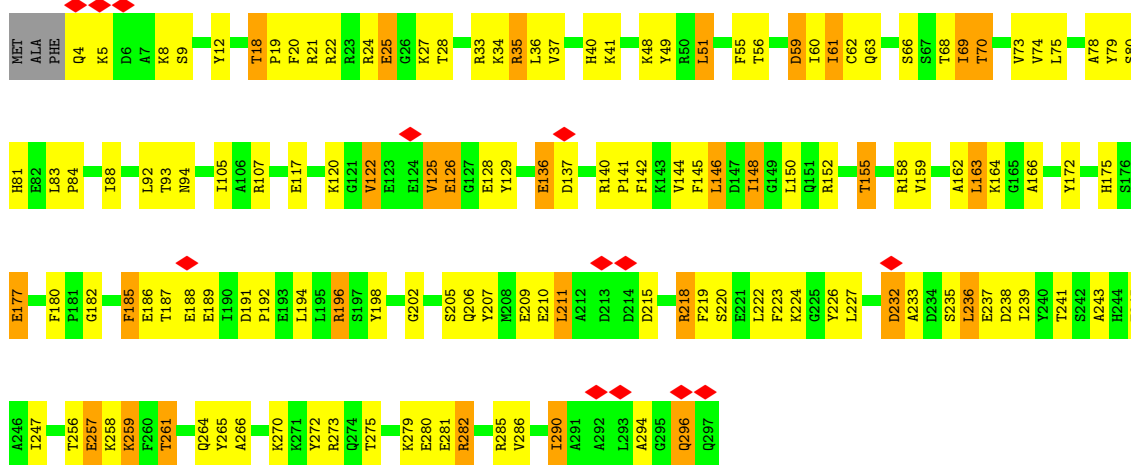
• Molecule 4: 60S ribosomal protein L2-A



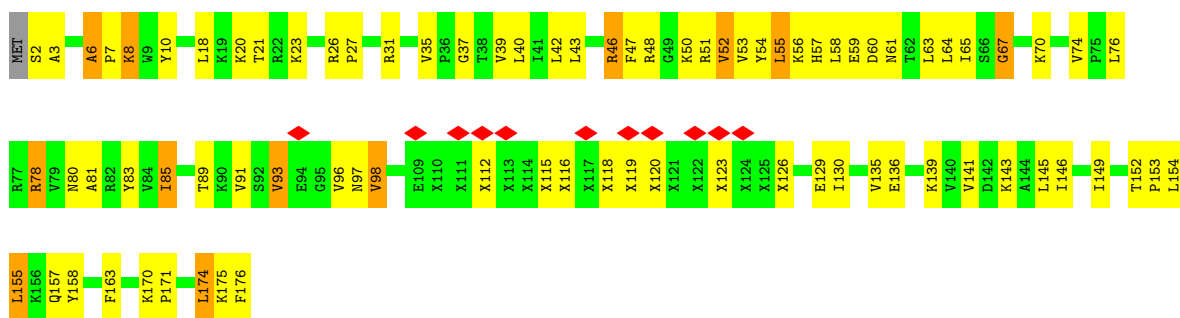




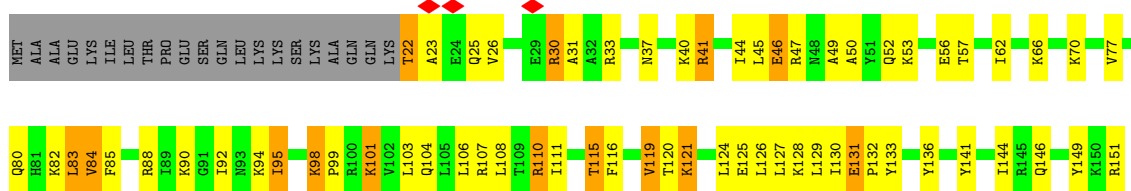
• Molecule 7: 60S ribosomal protein L5

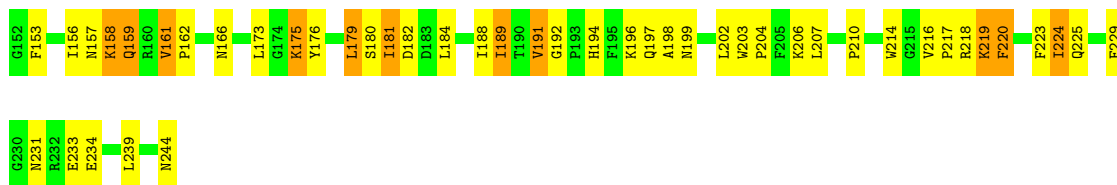


• Molecule 8: 60S RIBOSOMAL PROTEIN EL6

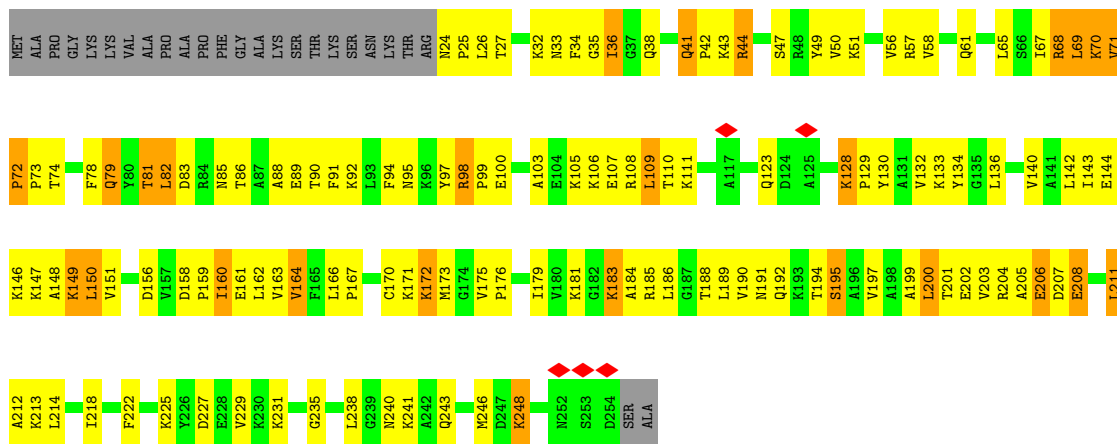


• Molecule 9: 60S ribosomal protein L7-A





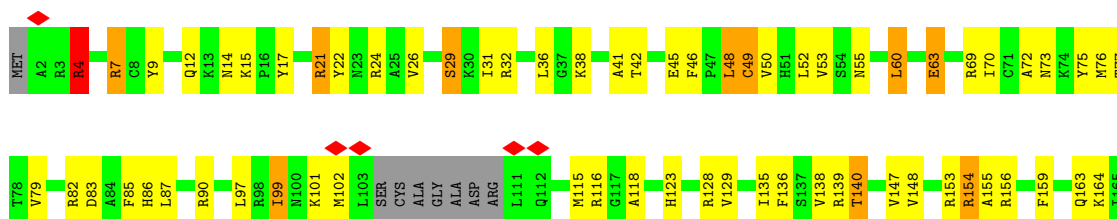
• Molecule 10: 60S ribosomal protein L8-A



• Molecule 11: 60S ribosomal protein L9-A

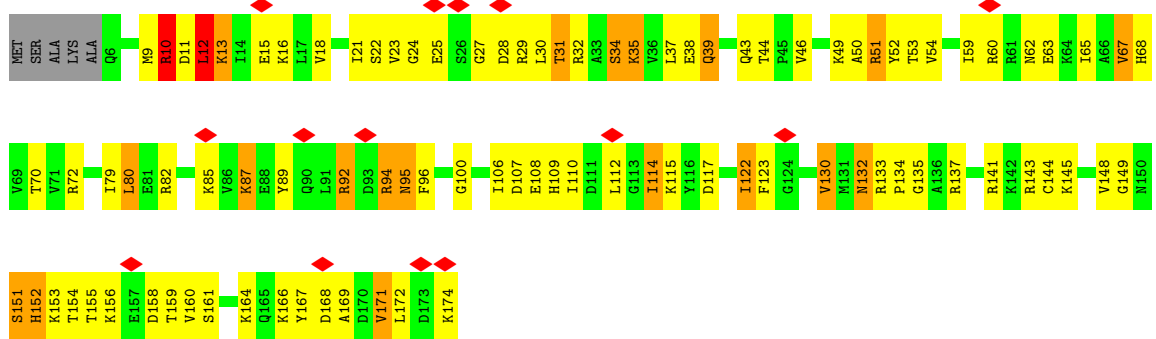


• Molecule 12: 60S ribosomal protein L10

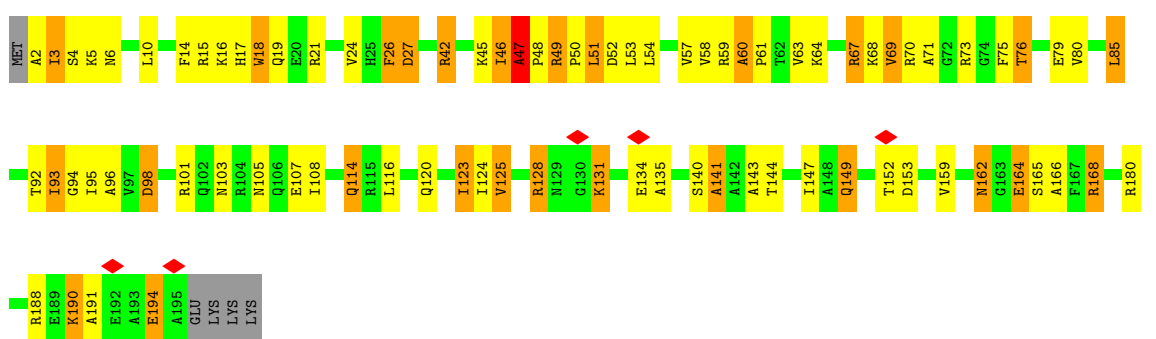




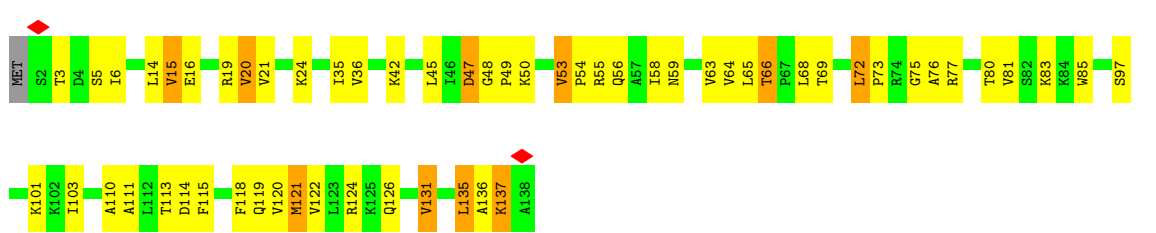
• Molecule 13: 60S ribosomal protein L11-A



• Molecule 14: 60S ribosomal protein L13-A

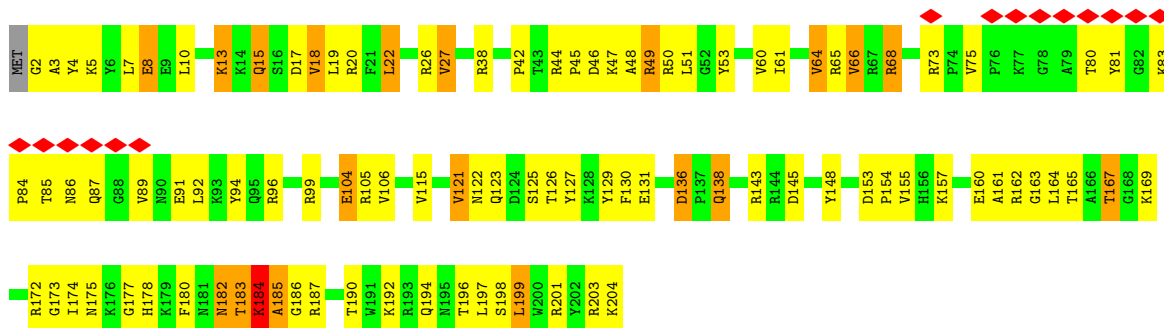


• Molecule 15: 60S ribosomal protein L14-A

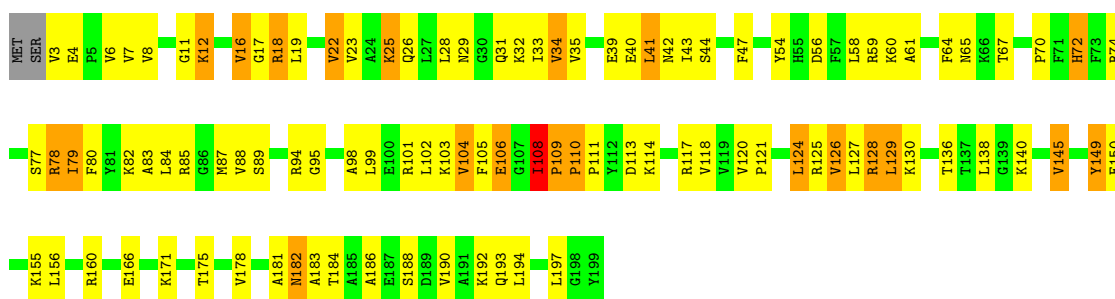


• Molecule 16: 60S ribosomal protein L15-A

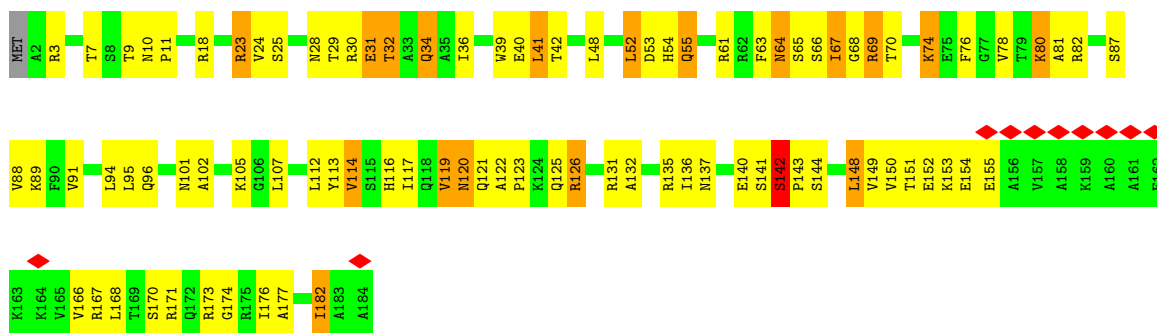




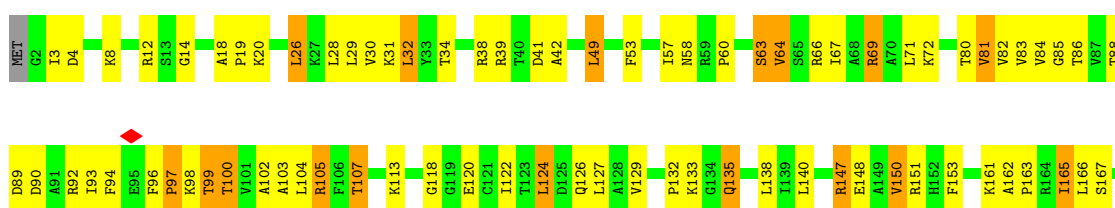
• Molecule 17: 60S ribosomal protein L16-A



• Molecule 18: 60S ribosomal protein L17-A

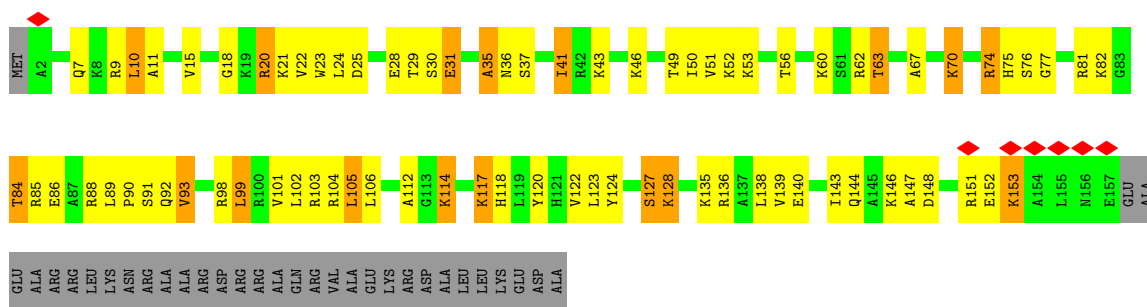


• Molecule 19: 60S ribosomal protein L18-A

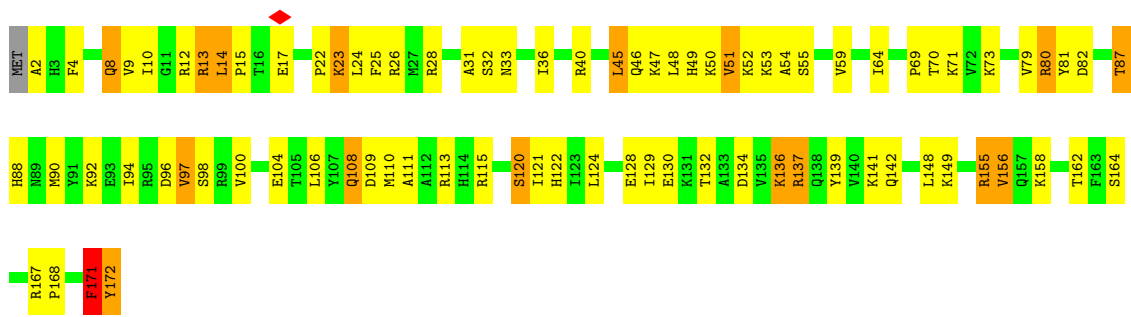




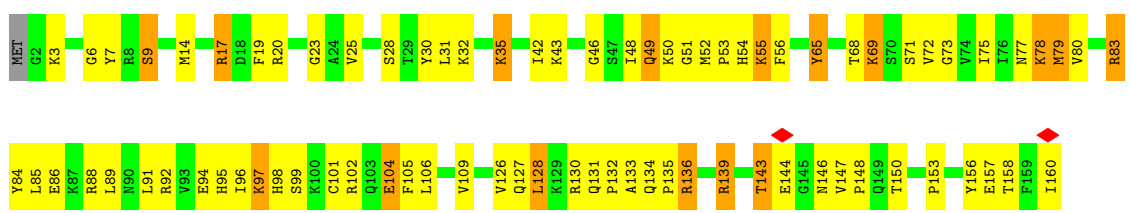
• Molecule 20: 60S ribosomal protein L19-A



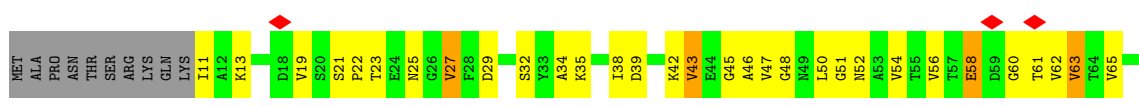
• Molecule 21: 60S ribosomal protein L20-A



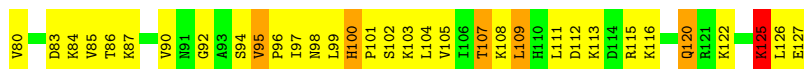
• Molecule 22: 60S ribosomal protein L21-A



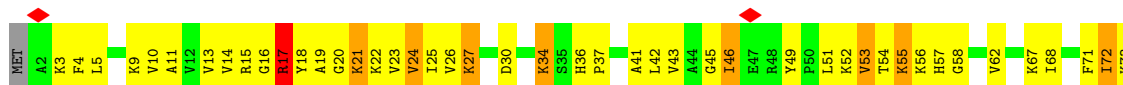
• Molecule 23: 60S ribosomal protein L22-A







- Molecule 28: 60S ribosomal protein L27-A



- Molecule 29: 60S ribosomal protein L28



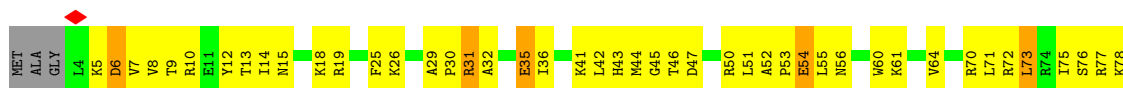
- Molecule 30: 60S ribosomal protein L29



- Molecule 31: 60S ribosomal protein L30

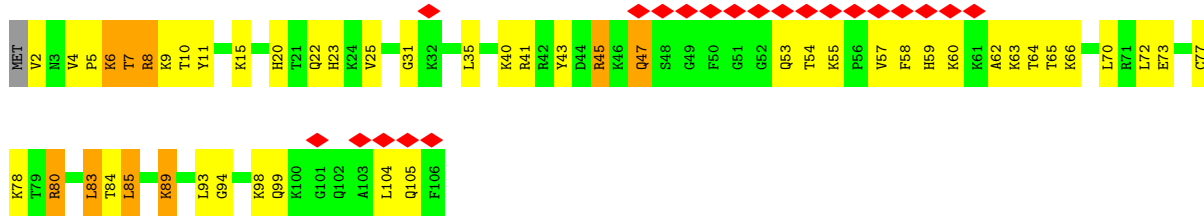


- Molecule 32: 60S ribosomal protein L31-A

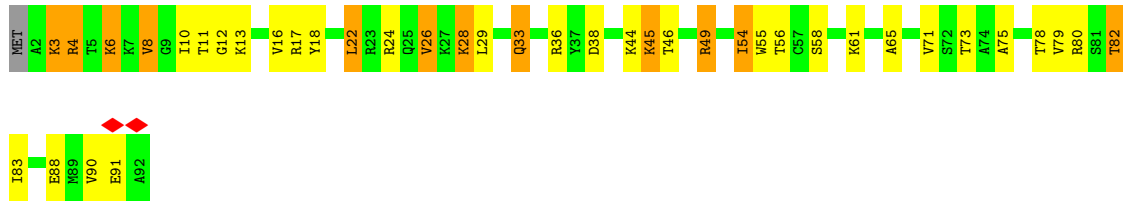




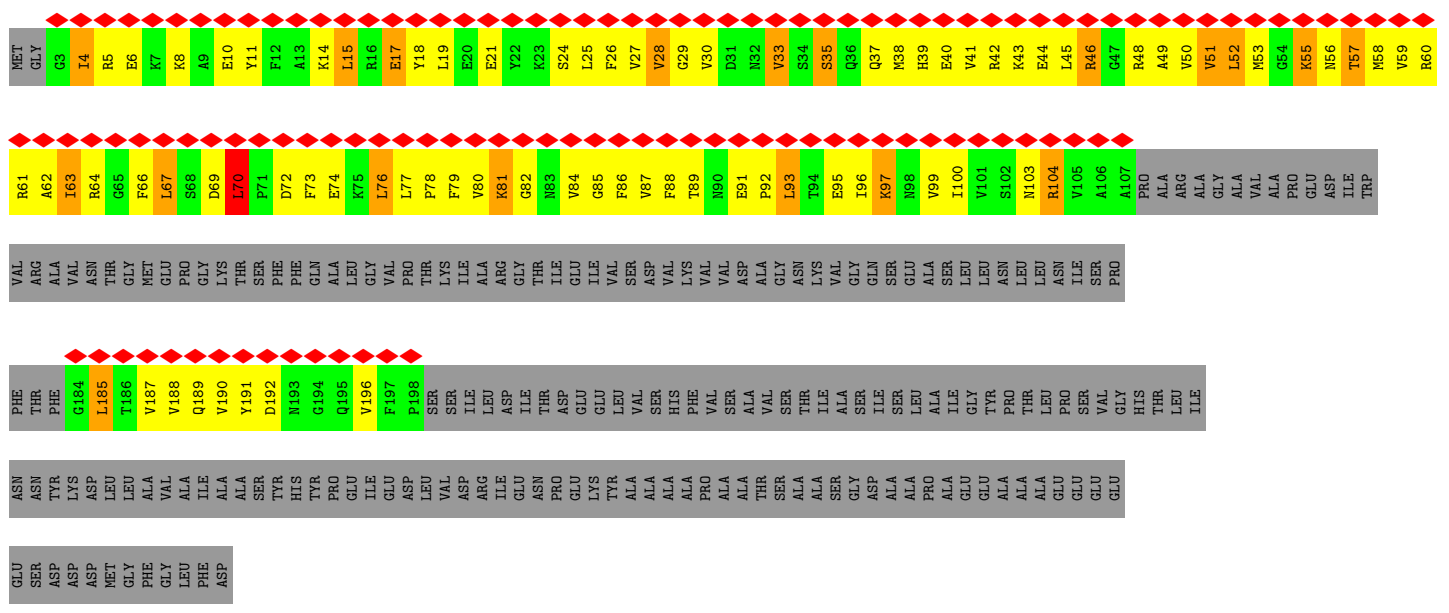




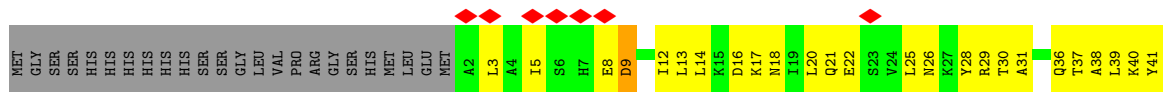
• Molecule 43: 60S ribosomal protein L43-A



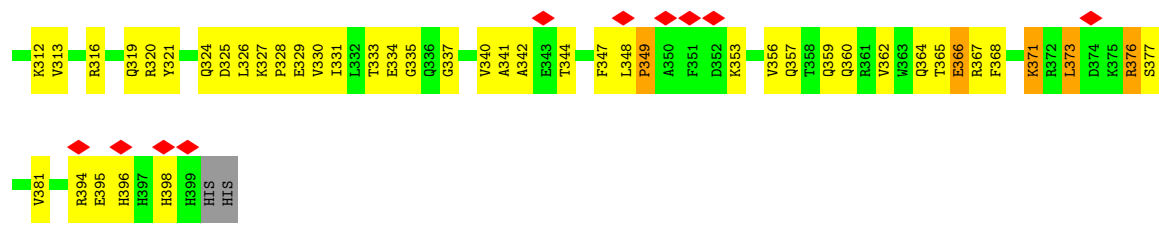
• Molecule 44: 60S acidic ribosomal protein P0



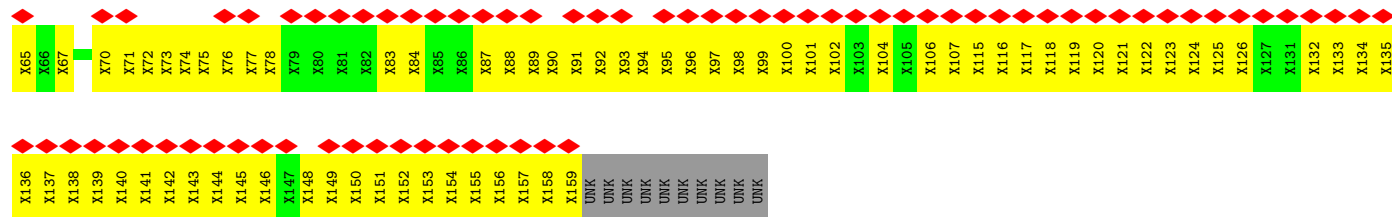
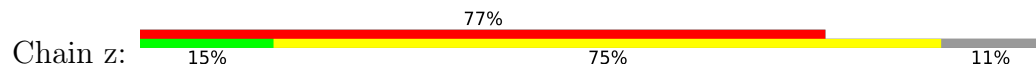
• Molecule 45: Probable metalloprotease ARX1







• Molecule 47: ALB1



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	134701	Depositor
Resolution determination method	Not provided	
CTF correction method	PER DETECTOR FRAME	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	20	Depositor
Minimum defocus (nm)	800.00	Depositor
Maximum defocus (nm)	3000.00	Depositor
Magnification	100720	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	1.020	Depositor
Minimum map value	-0.642	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.055	Depositor
Recommended contour level	0.1	Depositor
Map size ( $\text{\AA}$ )	300.24, 300.24, 300.24	wwPDB
Map dimensions	216, 216, 216	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.39, 1.39, 1.39	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: Y5P, P5P, 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	5	0.32	0/74039	0.44	3/115426 (0.0%)
2	7	0.21	0/2883	0.32	0/4491
3	8	0.34	0/3746	0.45	0/5832
4	A	0.52	0/1662	0.99	3/2236 (0.1%)
5	B	0.57	1/3146 (0.0%)	0.96	10/4228 (0.2%)
6	C	0.61	0/2800	1.06	14/3790 (0.4%)
7	D	0.41	0/2408	0.85	3/3248 (0.1%)
8	E	0.48	0/1269	0.94	4/1705 (0.2%)
9	F	0.57	0/1828	0.96	5/2461 (0.2%)
10	G	0.49	0/1795	1.02	10/2429 (0.4%)
11	H	0.50	0/1539	0.88	1/2073 (0.0%)
12	I	0.45	0/1758	0.95	8/2358 (0.3%)
13	J	0.42	0/1374	0.88	3/1842 (0.2%)
14	L	0.60	0/1573	1.02	8/2113 (0.4%)
15	M	0.49	0/1074	0.91	0/1446
16	N	0.66	0/1757	1.07	8/2354 (0.3%)
17	O	0.61	0/1585	1.00	6/2128 (0.3%)
18	P	0.67	0/1465	0.98	4/1968 (0.2%)
19	Q	0.54	0/1465	0.99	2/1965 (0.1%)
20	R	0.51	0/1275	0.85	0/1702
21	S	0.58	0/1473	0.95	4/1980 (0.2%)
22	T	0.49	0/1300	0.87	1/1743 (0.1%)
23	U	0.44	0/825	0.88	0/1120
24	V	0.56	0/1018	0.98	3/1369 (0.2%)
25	W	0.47	0/533	0.90	3/707 (0.4%)
26	X	0.54	0/974	0.99	5/1314 (0.4%)
27	Y	0.55	0/1004	1.03	6/1341 (0.4%)
28	Z	0.47	0/1118	1.04	8/1497 (0.5%)
29	a	0.60	0/1204	0.99	2/1612 (0.1%)
30	b	0.48	0/473	0.93	3/629 (0.5%)
31	c	0.44	0/775	0.77	0/1040
32	d	0.60	0/897	0.96	2/1205 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	e	0.69	1/1055 (0.1%)	0.96	0/1413
34	f	0.64	0/868	1.10	4/1168 (0.3%)
35	g	0.54	0/890	1.04	4/1189 (0.3%)
36	h	0.54	0/974	1.02	4/1297 (0.3%)
37	i	0.47	0/777	0.88	0/1033
38	j	0.66	0/696	0.95	3/923 (0.3%)
39	k	0.41	0/614	0.87	2/822 (0.2%)
40	l	0.57	0/443	0.92	0/588
41	m	0.52	0/423	1.04	5/562 (0.9%)
42	o	0.49	0/860	0.90	1/1136 (0.1%)
43	p	0.55	0/701	0.96	3/934 (0.3%)
44	q	0.89	1/977 (0.1%)	0.91	2/1313 (0.2%)
45	x	0.49	0/4557	0.96	13/6189 (0.2%)
46	y	0.49	0/1746	0.93	5/2346 (0.2%)
All	All	0.43	3/137616 (0.0%)	0.69	175/202265 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	C	0	3
8	E	0	1
14	L	0	1
16	N	0	1
27	Y	0	1
28	Z	0	1
32	d	0	3
37	i	0	1
45	x	0	3
46	y	0	1
All	All	0	16

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	e	21	HIS	CG-ND1	5.77	1.44	1.38
5	B	220	VAL	CA-CB	-5.51	1.47	1.54
44	q	28	VAL	CA-CB	5.10	1.59	1.53

The worst 5 of 175 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	h	41	LEU	CA-C-N	10.07	129.73	119.56
36	h	41	LEU	C-N-CA	10.07	129.73	119.56
34	f	89	LEU	CA-C-N	9.72	131.99	119.84
34	f	89	LEU	C-N-CA	9.72	131.99	119.84
28	Z	27	LYS	CA-C-N	9.50	130.15	119.32

There are no chirality outliers.

5 of 16 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	C	145	ILE	Peptide
6	C	148	ILE	Peptide
6	C	300	ARG	Peptide
8	E	67	GLY	Peptide
14	L	141	ALA	Peptide

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	5	66537	0	33466	1633	0
2	7	2579	0	1304	70	0
3	8	3353	0	1695	86	0
4	A	1630	0	1682	127	0
5	B	3075	0	3142	191	0
6	C	2748	0	2859	178	0
7	D	2359	0	2311	134	0
8	E	1356	0	1448	94	0
9	F	1791	0	1869	115	0
10	G	1763	0	1819	121	0
11	H	1518	0	1587	84	0
12	I	1722	0	1755	98	0
13	J	1353	0	1383	89	0
14	L	1548	0	1613	109	0
15	M	1059	0	1154	55	0
16	N	1720	0	1779	95	0
17	O	1555	0	1659	95	0
18	P	1442	0	1485	77	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	Q	1441	0	1543	83	0
20	R	1258	0	1342	75	0
21	S	1437	0	1475	79	0
22	T	1276	0	1323	87	0
23	U	808	0	822	42	0
24	V	1003	0	1048	78	0
25	W	521	0	551	28	0
26	X	959	0	1023	76	0
27	Y	993	0	1081	87	0
28	Z	1092	0	1155	79	0
29	a	1173	0	1215	88	0
30	b	462	0	491	25	0
31	c	767	0	816	67	0
32	d	883	0	918	67	0
33	e	1034	0	1101	70	0
34	f	850	0	880	55	0
35	g	880	0	945	53	0
36	h	965	0	1067	60	0
37	i	770	0	846	51	0
38	j	681	0	683	36	0
39	k	608	0	671	35	0
40	l	436	0	475	27	0
41	m	417	0	455	27	0
42	o	847	0	914	48	0
43	p	694	0	734	41	0
44	q	962	0	989	140	0
45	x	4477	0	4559	399	0
46	y	1785	3	1755	133	0
47	z	510	0	517	100	0
48	5	259	0	0	0	0
48	7	6	0	0	0	0
48	8	7	0	0	0	0
48	B	2	0	0	0	0
48	C	1	0	0	0	0
48	N	1	0	0	0	0
48	P	1	0	0	0	0
48	R	1	0	0	0	0
48	V	1	0	0	0	0
48	y	1	0	0	0	0
49	j	1	0	0	0	0
49	m	1	0	0	0	0
49	o	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
49	p	1	0	0	0	0
49	y	2	0	0	0	0
All	All	129383	3	95404	5040	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 23.

The worst 5 of 5040 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)
15:M:48:GLY:HA3	15:M:53:VAL:HG13	1.25	1.18
45:x:279:LEU:HD11	47:z:98:UNK:HB1	1.24	1.18
4:A:149:ARG:HH12	4:A:155:LYS:HE3	1.06	1.18
8:E:78:ARG:HG3	8:E:78:ARG:HH11	1.03	1.14
1:5:1221:A:H5'	44:q:57:THR:HB	1.13	1.12

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	A	210/254 (83%)	195 (93%)	14 (7%)	1 (0%)	24	54
5	B	384/387 (99%)	367 (96%)	17 (4%)	0	100	100
6	C	359/362 (99%)	329 (92%)	28 (8%)	2 (1%)	21	49
7	D	292/297 (98%)	282 (97%)	8 (3%)	2 (1%)	18	47
8	E	155/176 (88%)	143 (92%)	9 (6%)	3 (2%)	6	26
9	F	221/244 (91%)	210 (95%)	10 (4%)	1 (0%)	24	54
10	G	229/256 (90%)	200 (87%)	28 (12%)	1 (0%)	30	59
11	H	189/191 (99%)	178 (94%)	10 (5%)	1 (0%)	24	54

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	I	209/221 (95%)	193 (92%)	16 (8%)	0	100	100
13	J	167/174 (96%)	143 (86%)	18 (11%)	6 (4%)	2	16
14	L	192/199 (96%)	170 (88%)	20 (10%)	2 (1%)	12	39
15	M	135/138 (98%)	133 (98%)	2 (2%)	0	100	100
16	N	201/204 (98%)	187 (93%)	13 (6%)	1 (0%)	24	54
17	O	195/199 (98%)	193 (99%)	2 (1%)	0	100	100
18	P	181/184 (98%)	176 (97%)	5 (3%)	0	100	100
19	Q	183/186 (98%)	174 (95%)	8 (4%)	1 (0%)	24	54
20	R	154/189 (82%)	148 (96%)	5 (3%)	1 (1%)	21	49
21	S	169/172 (98%)	163 (96%)	6 (4%)	0	100	100
22	T	157/160 (98%)	151 (96%)	4 (2%)	2 (1%)	9	33
23	U	100/121 (83%)	95 (95%)	5 (5%)	0	100	100
24	V	134/137 (98%)	130 (97%)	4 (3%)	0	100	100
25	W	61/155 (39%)	57 (93%)	3 (5%)	1 (2%)	7	29
26	X	118/142 (83%)	109 (92%)	9 (8%)	0	100	100
27	Y	124/127 (98%)	118 (95%)	5 (4%)	1 (1%)	16	44
28	Z	133/136 (98%)	112 (84%)	18 (14%)	3 (2%)	5	23
29	a	146/149 (98%)	132 (90%)	13 (9%)	1 (1%)	18	47
30	b	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
31	c	98/105 (93%)	92 (94%)	6 (6%)	0	100	100
32	d	107/113 (95%)	97 (91%)	8 (8%)	2 (2%)	6	26
33	e	127/130 (98%)	120 (94%)	7 (6%)	0	100	100
34	f	104/107 (97%)	100 (96%)	4 (4%)	0	100	100
35	g	110/121 (91%)	104 (94%)	5 (4%)	1 (1%)	14	41
36	h	117/120 (98%)	109 (93%)	8 (7%)	0	100	100
37	i	97/100 (97%)	86 (89%)	8 (8%)	3 (3%)	3	18
38	j	85/88 (97%)	77 (91%)	8 (9%)	0	100	100
39	k	75/78 (96%)	70 (93%)	4 (5%)	1 (1%)	9	33
40	l	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
41	m	50/128 (39%)	46 (92%)	3 (6%)	1 (2%)	6	24
42	o	103/106 (97%)	94 (91%)	9 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	p	89/92 (97%)	82 (92%)	7 (8%)	0	100	100
44	q	116/312 (37%)	111 (96%)	4 (3%)	1 (1%)	14	41
45	x	577/616 (94%)	544 (94%)	32 (6%)	1 (0%)	43	71
46	y	201/401 (50%)	191 (95%)	10 (5%)	0	100	100
All	All	6958/7887 (88%)	6511 (94%)	407 (6%)	40 (1%)	23	49

5 of 40 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	E	98	VAL
13	J	10	ARG
13	J	95	ASN
16	N	184	LYS
25	W	25	ASP

### 5.3.2 Protein sidechains [i](#)

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	A	166/196 (85%)	126 (76%)	40 (24%)	1	2
5	B	321/323 (99%)	254 (79%)	67 (21%)	1	4
6	C	288/289 (100%)	229 (80%)	59 (20%)	1	4
7	D	243/245 (99%)	204 (84%)	39 (16%)	2	10
8	E	135/136 (99%)	120 (89%)	15 (11%)	6	21
9	F	187/205 (91%)	158 (84%)	29 (16%)	2	10
10	G	177/208 (85%)	142 (80%)	35 (20%)	1	5
11	H	171/171 (100%)	140 (82%)	31 (18%)	2	7
12	I	179/187 (96%)	150 (84%)	29 (16%)	2	10
13	J	147/150 (98%)	123 (84%)	24 (16%)	2	10
14	L	154/159 (97%)	125 (81%)	29 (19%)	1	6
15	M	108/109 (99%)	90 (83%)	18 (17%)	2	9

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	N	175/176 (99%)	145 (83%)	30 (17%)	2	9
17	O	160/162 (99%)	122 (76%)	38 (24%)	1	2
18	P	145/146 (99%)	115 (79%)	30 (21%)	1	4
19	Q	150/151 (99%)	120 (80%)	30 (20%)	1	5
20	R	129/154 (84%)	100 (78%)	29 (22%)	1	3
21	S	155/156 (99%)	127 (82%)	28 (18%)	2	7
22	T	136/137 (99%)	115 (85%)	21 (15%)	2	10
23	U	89/107 (83%)	76 (85%)	13 (15%)	3	12
24	V	104/105 (99%)	91 (88%)	13 (12%)	4	17
25	W	55/129 (43%)	50 (91%)	5 (9%)	9	29
26	X	104/118 (88%)	83 (80%)	21 (20%)	1	4
27	Y	109/110 (99%)	93 (85%)	16 (15%)	3	12
28	Z	115/116 (99%)	91 (79%)	24 (21%)	1	4
29	a	118/119 (99%)	102 (86%)	16 (14%)	3	14
30	b	46/47 (98%)	35 (76%)	11 (24%)	1	2
31	c	84/88 (96%)	69 (82%)	15 (18%)	2	7
32	d	94/97 (97%)	84 (89%)	10 (11%)	6	23
33	e	110/111 (99%)	91 (83%)	19 (17%)	2	8
34	f	90/91 (99%)	81 (90%)	9 (10%)	7	25
35	g	95/103 (92%)	79 (83%)	16 (17%)	2	9
36	h	103/105 (98%)	82 (80%)	21 (20%)	1	4
37	i	80/82 (98%)	57 (71%)	23 (29%)	0	1
38	j	70/71 (99%)	58 (83%)	12 (17%)	2	9
39	k	67/69 (97%)	56 (84%)	11 (16%)	2	10
40	l	45/46 (98%)	35 (78%)	10 (22%)	1	3
41	m	47/116 (40%)	40 (85%)	7 (15%)	3	12
42	o	90/91 (99%)	74 (82%)	16 (18%)	2	7
43	p	71/72 (99%)	52 (73%)	19 (27%)	0	1
44	q	105/254 (41%)	85 (81%)	20 (19%)	1	6
45	x	508/540 (94%)	461 (91%)	47 (9%)	8	29
46	y	187/355 (53%)	168 (90%)	19 (10%)	7	24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	5912/6602 (90%)	4898 (83%)	1014 (17%)	<b>4</b> <b>9</b>

5 of 1014 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	O	94	ARG
41	m	85	LEU
21	S	9	VAL
40	l	12	LYS
44	q	104	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 149 such sidechains are listed below:

Mol	Chain	Res	Type
36	h	104	GLN
46	y	170	ASN
40	l	38	ASN
45	x	146	HIS
14	L	25	HIS

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3102/3396 (91%)	669 (21%)	73 (2%)
2	7	120/121 (99%)	14 (11%)	0
3	8	157/158 (99%)	36 (22%)	5 (3%)
All	All	3379/3675 (91%)	719 (21%)	78 (2%)

5 of 719 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	14	U
1	5	15	C
1	5	22	G
1	5	26	A
1	5	40	A

5 of 78 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5	2872	A
1	5	3341	U
1	5	2971	A
1	5	3195	U
3	8	88	A

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

20 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	Y5P	5	1991	1	14,19,20	4.20	2 (14%)	18,26,29	1.03	1 (5%)
1	P5P	5	2021	1	20,23,24	0.66	1 (5%)	27,33,36	0.70	1 (3%)
1	P5P	5	2016	1	20,23,24	0.74	1 (5%)	27,33,36	0.73	1 (3%)
1	P5P	5	2020	1	20,23,24	0.74	1 (5%)	27,33,36	0.74	1 (3%)
1	Y5P	5	1989	1	14,19,20	4.22	2 (14%)	18,26,29	1.01	1 (5%)
1	Y5P	5	1988	1	14,19,20	4.35	2 (14%)	18,26,29	1.07	1 (5%)
1	Y5P	5	1994	1	14,19,20	4.34	2 (14%)	18,26,29	1.09	1 (5%)
1	P5P	5	2022	1	20,23,24	0.77	1 (5%)	27,33,36	0.75	1 (3%)
1	Y5P	5	1992	1	14,19,20	4.41	2 (14%)	18,26,29	1.08	1 (5%)
1	Y5P	5	1993	1	14,19,20	4.36	2 (14%)	18,26,29	1.04	1 (5%)
1	P5P	5	2017	1	20,23,24	0.65	1 (5%)	27,33,36	0.71	1 (3%)
1	P5P	5	2019	1	20,23,24	0.68	1 (5%)	27,33,36	0.75	1 (3%)
1	P5P	5	2018	1	20,23,24	0.71	1 (5%)	27,33,36	0.74	1 (3%)
1	P5P	5	2025	1	20,23,24	0.65	1 (5%)	27,33,36	0.70	1 (3%)
1	Y5P	5	1995	1	14,19,20	4.20	2 (14%)	18,26,29	1.00	1 (5%)
1	Y5P	5	1987	1	14,19,20	4.19	2 (14%)	18,26,29	1.05	1 (5%)
1	Y5P	5	1986	1	14,19,20	4.38	2 (14%)	18,26,29	1.06	1 (5%)
1	P5P	5	2023	1	20,23,24	0.66	1 (5%)	27,33,36	0.75	1 (3%)
1	Y5P	5	1990	1	14,19,20	4.33	2 (14%)	18,26,29	1.10	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	P5P	5	2024	1	20,23,24	0.74	1 (5%)	27,33,36	0.73	1 (3%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	Y5P	5	1991	1	-	1/7/33/34	0/2/2/2
1	P5P	5	2021	1	-	0/7/25/26	0/3/3/3
1	P5P	5	2016	1	-	0/7/25/26	0/3/3/3
1	P5P	5	2020	1	-	0/7/25/26	0/3/3/3
1	Y5P	5	1989	1	-	1/7/33/34	0/2/2/2
1	Y5P	5	1988	1	-	1/7/33/34	0/2/2/2
1	Y5P	5	1994	1	-	1/7/33/34	0/2/2/2
1	P5P	5	2022	1	-	0/7/25/26	0/3/3/3
1	Y5P	5	1992	1	-	1/7/33/34	0/2/2/2
1	Y5P	5	1993	1	-	1/7/33/34	0/2/2/2
1	P5P	5	2017	1	-	0/7/25/26	0/3/3/3
1	P5P	5	2019	1	-	0/7/25/26	0/3/3/3
1	P5P	5	2018	1	-	0/7/25/26	0/3/3/3
1	P5P	5	2025	1	-	0/7/25/26	0/3/3/3
1	Y5P	5	1995	1	-	1/7/33/34	0/2/2/2
1	Y5P	5	1987	1	-	1/7/33/34	0/2/2/2
1	Y5P	5	1986	1	-	1/7/33/34	0/2/2/2
1	P5P	5	2023	1	-	0/7/25/26	0/3/3/3
1	Y5P	5	1990	1	-	1/7/33/34	0/2/2/2
1	P5P	5	2024	1	-	0/7/25/26	0/3/3/3

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	5	1992	Y5P	C2-N3	14.39	1.38	1.27
1	5	1986	Y5P	C2-N3	14.18	1.38	1.27
1	5	1988	Y5P	C2-N3	14.04	1.38	1.27
1	5	1993	Y5P	C2-N3	13.96	1.38	1.27
1	5	1994	Y5P	C2-N3	13.95	1.38	1.27

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	1986	Y5P	N1-C2-N3	-3.99	114.34	125.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	1994	Y5P	N1-C2-N3	-3.97	114.37	125.39
1	5	1992	Y5P	N1-C2-N3	-3.93	114.50	125.39
1	5	1990	Y5P	N1-C2-N3	-3.92	114.53	125.39
1	5	1988	Y5P	N1-C2-N3	-3.89	114.61	125.39

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	5	1987	Y5P	O4'-C1'-N1-C2
1	5	1989	Y5P	O4'-C1'-N1-C2
1	5	1990	Y5P	O4'-C1'-N1-C2
1	5	1991	Y5P	O4'-C1'-N1-C2
1	5	1993	Y5P	O4'-C1'-N1-C2

There are no ring outliers.

13 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	5	1991	Y5P	1	0
1	5	1989	Y5P	2	0
1	5	1988	Y5P	1	0
1	5	1994	Y5P	1	0
1	5	2022	P5P	1	0
1	5	1992	Y5P	1	0
1	5	1993	Y5P	1	0
1	5	2017	P5P	1	0
1	5	2018	P5P	1	0
1	5	1987	Y5P	1	0
1	5	2023	P5P	2	0
1	5	1990	Y5P	2	0
1	5	2024	P5P	1	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 286 ligands modelled in this entry, 286 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
47	<i>z</i>	2
1	5	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	<i>z</i>	107:UNK	C	115:UNK	N	20.22
1	5	1995:Y5P	O3'	2016:P5P	P	17.42
1	<i>z</i>	127:UNK	C	131:UNK	N	9.67

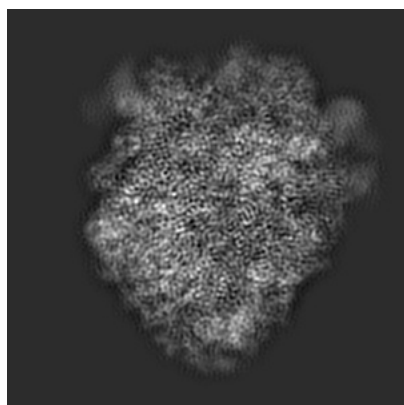
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3151. These allow visual inspection of the internal detail of the map and identification of artifacts.

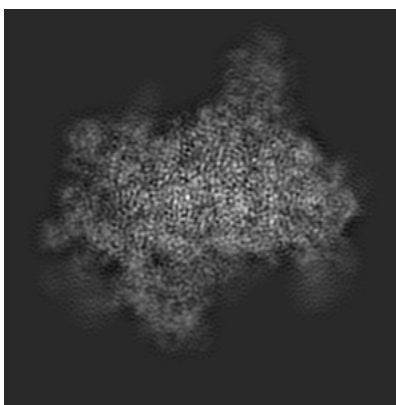
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

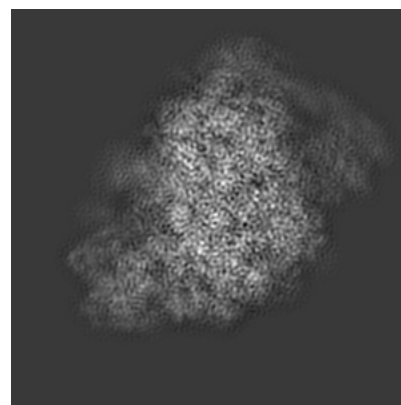
#### 6.1.1 Primary map



X



Y

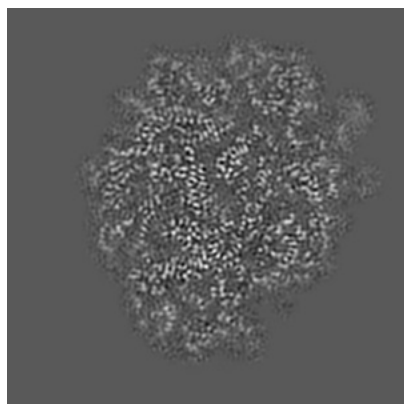


Z

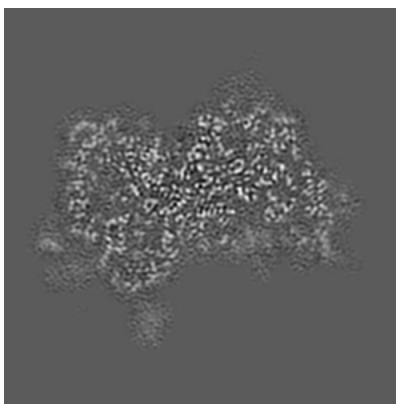
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

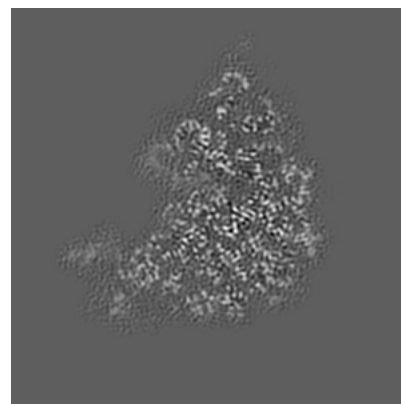
#### 6.2.1 Primary map



X Index: 108



Y Index: 108

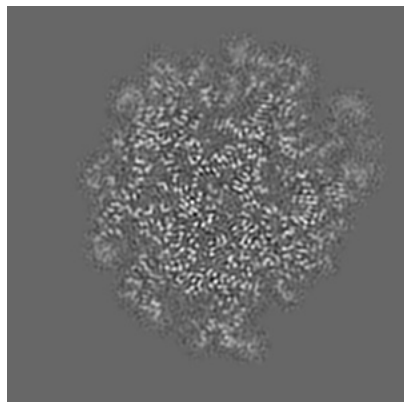


Z Index: 108

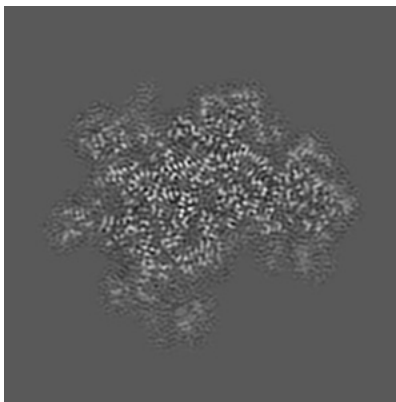
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

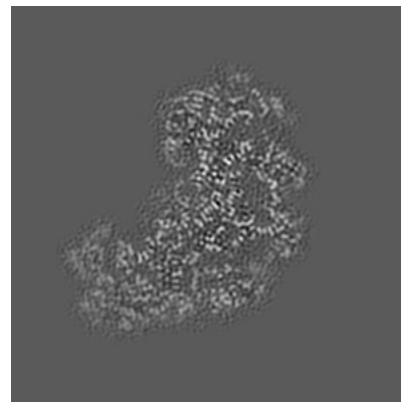
### 6.3.1 Primary map



X Index: 116



Y Index: 91

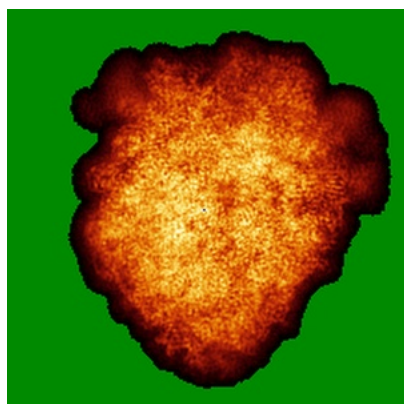


Z Index: 94

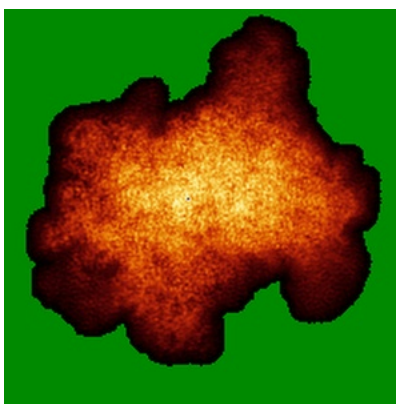
The images above show the largest variance slices of the map in three orthogonal directions.

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

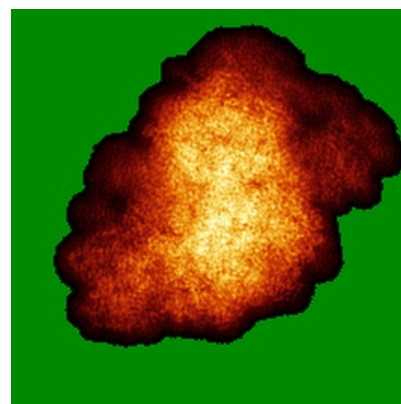
### 6.4.1 Primary map



X



Y

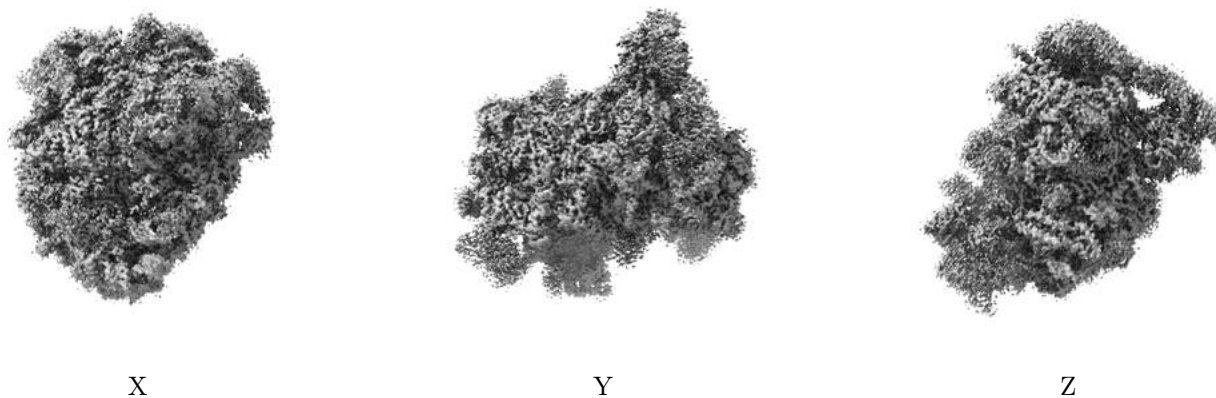


Z

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

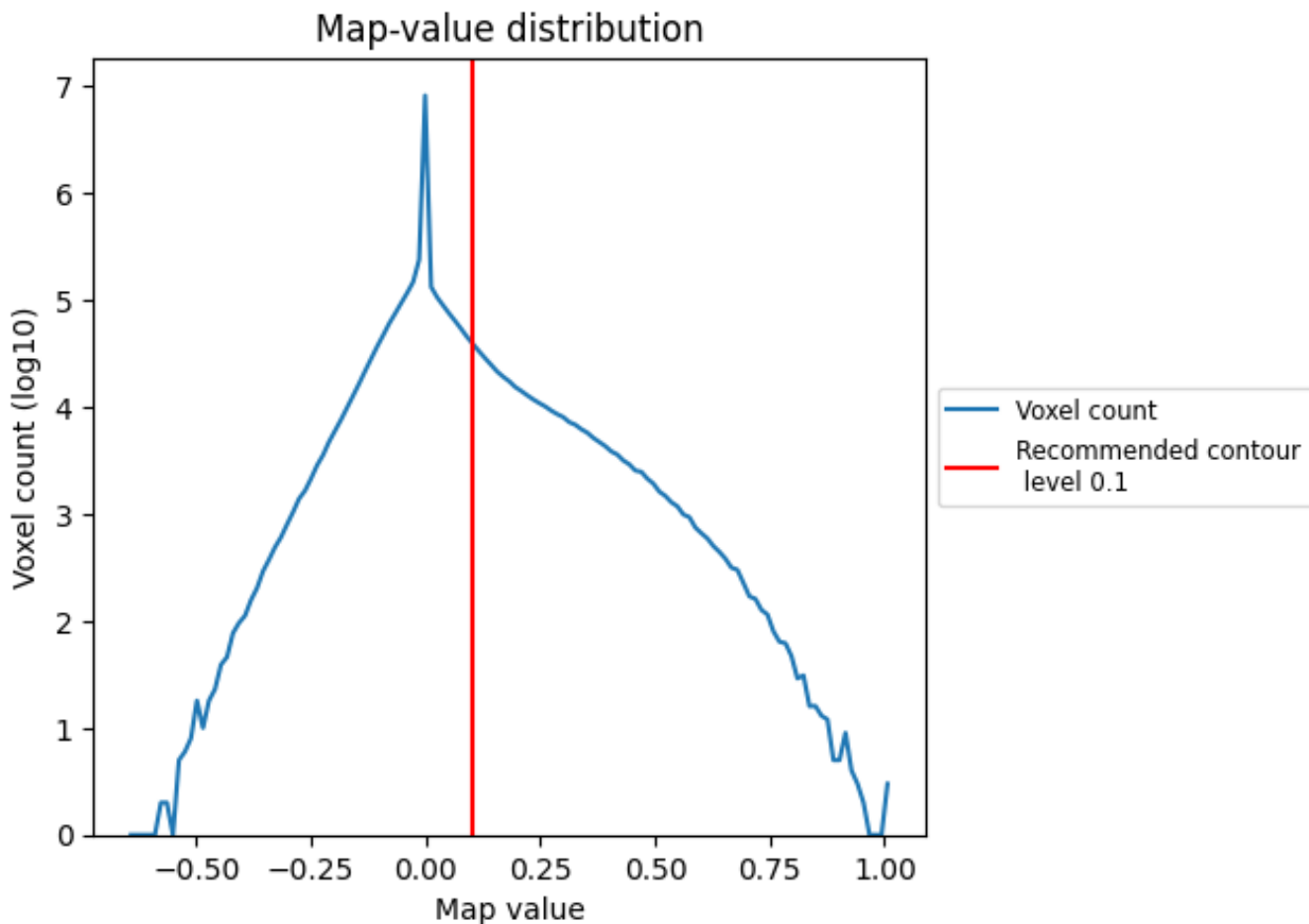
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

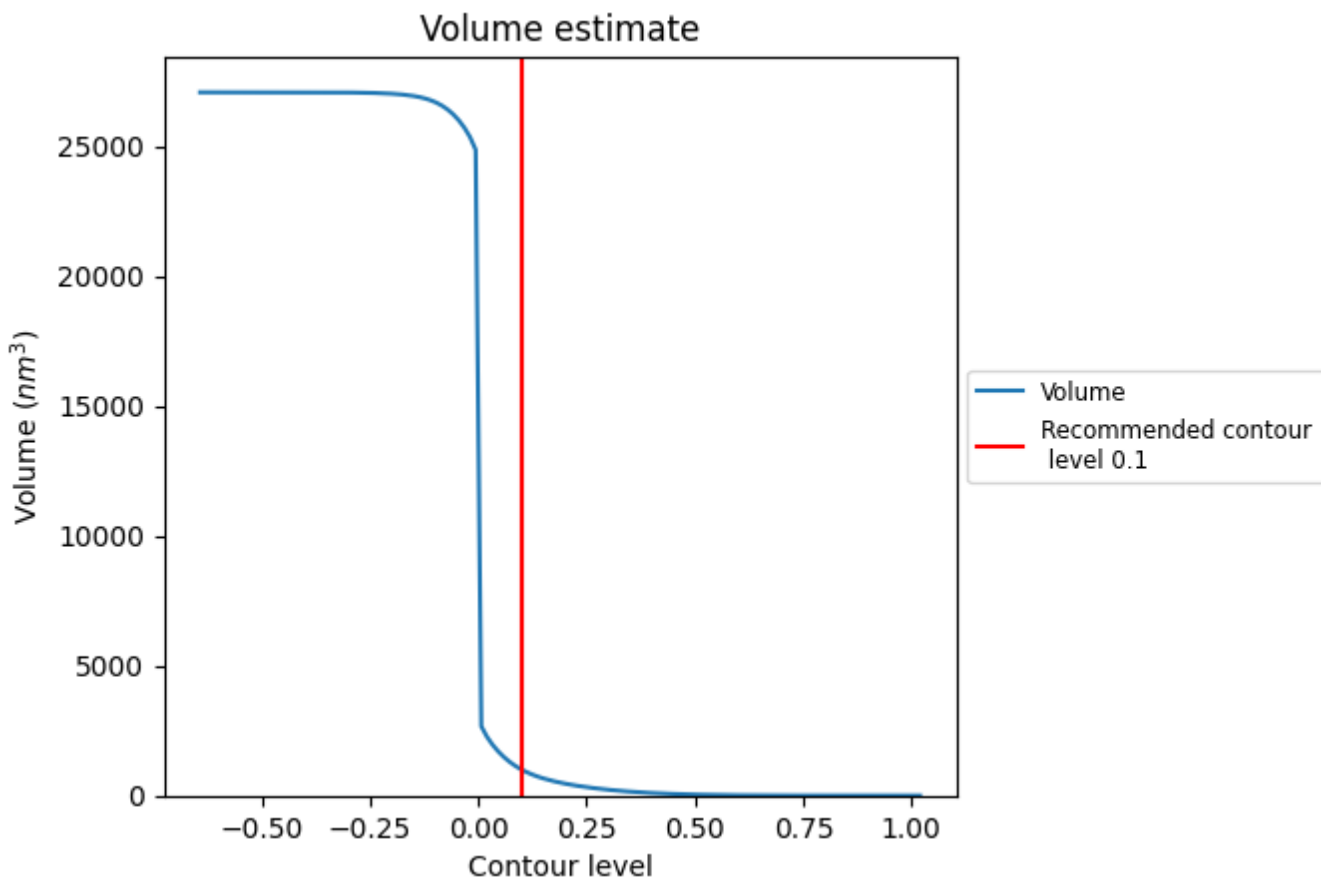
This section contains the results of statistical analysis of the map.

### 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.

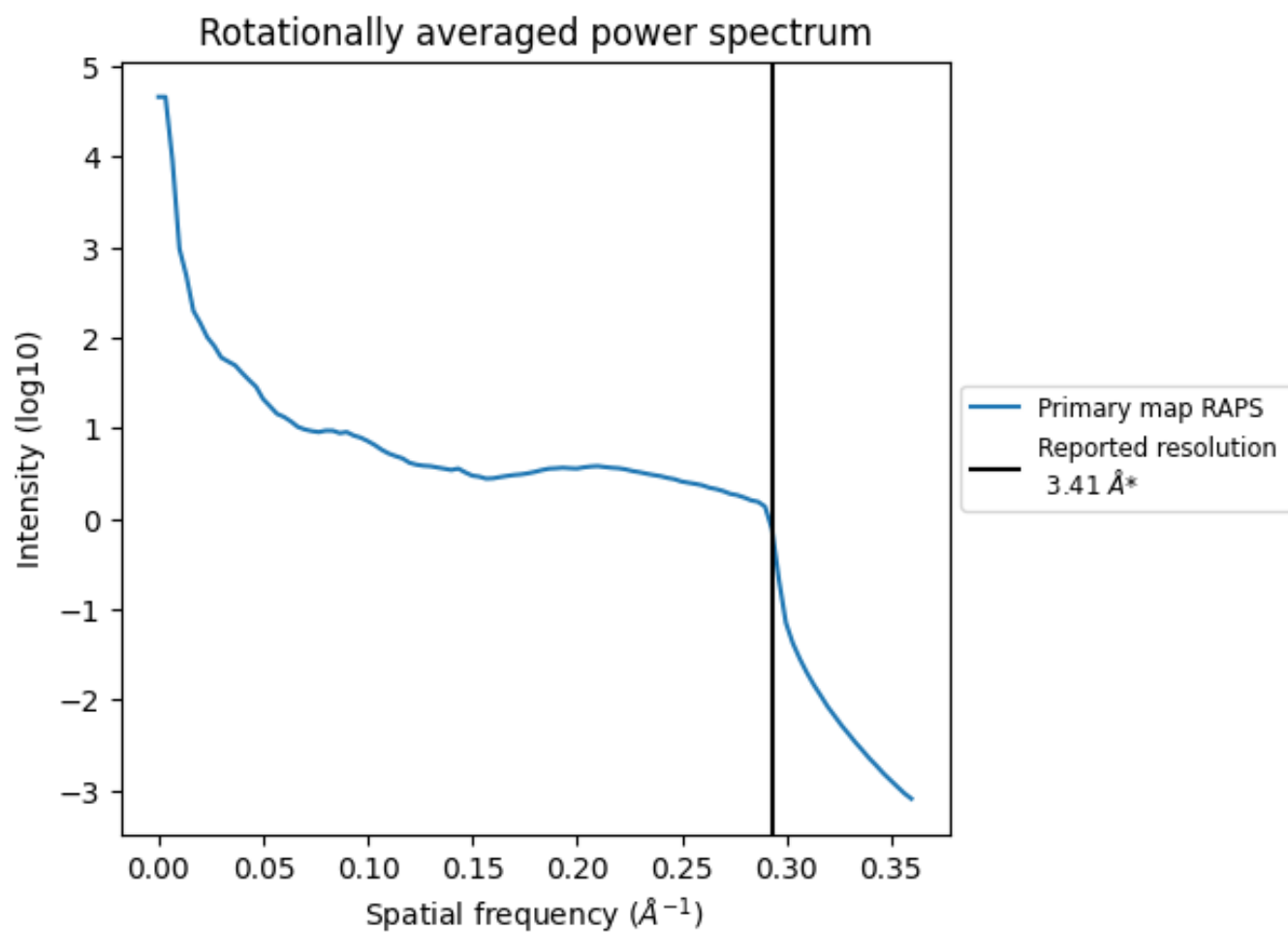
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1001 nm<sup>3</sup>; this corresponds to an approximate mass of 904 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 [i](#)



\*Reported resolution corresponds to spatial frequency of  $0.293 \text{\AA}^{-1}$

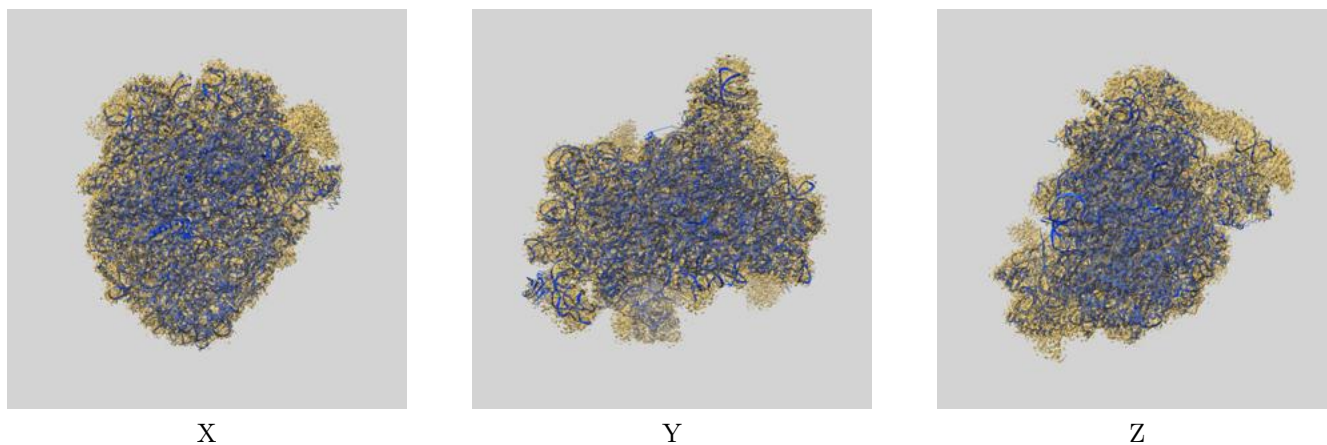
## 8 Fourier-Shell correlation

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

## 9 Map-model fit [i](#)

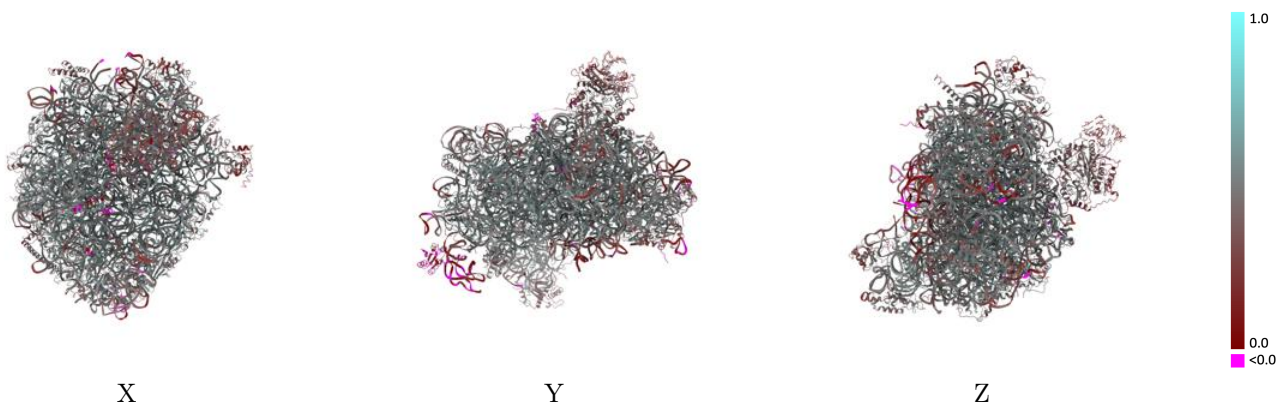
This section contains information regarding the fit between EMDB map EMD-3151 and PDB model 5APO. Per-residue inclusion information can be found in section 3 on page 14.

### 9.1 Map-model overlay [i](#)



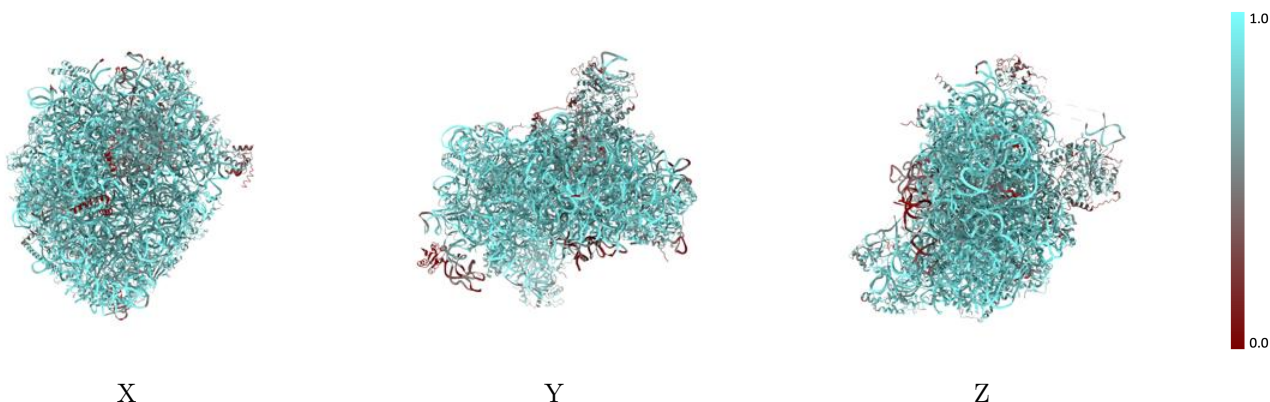
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



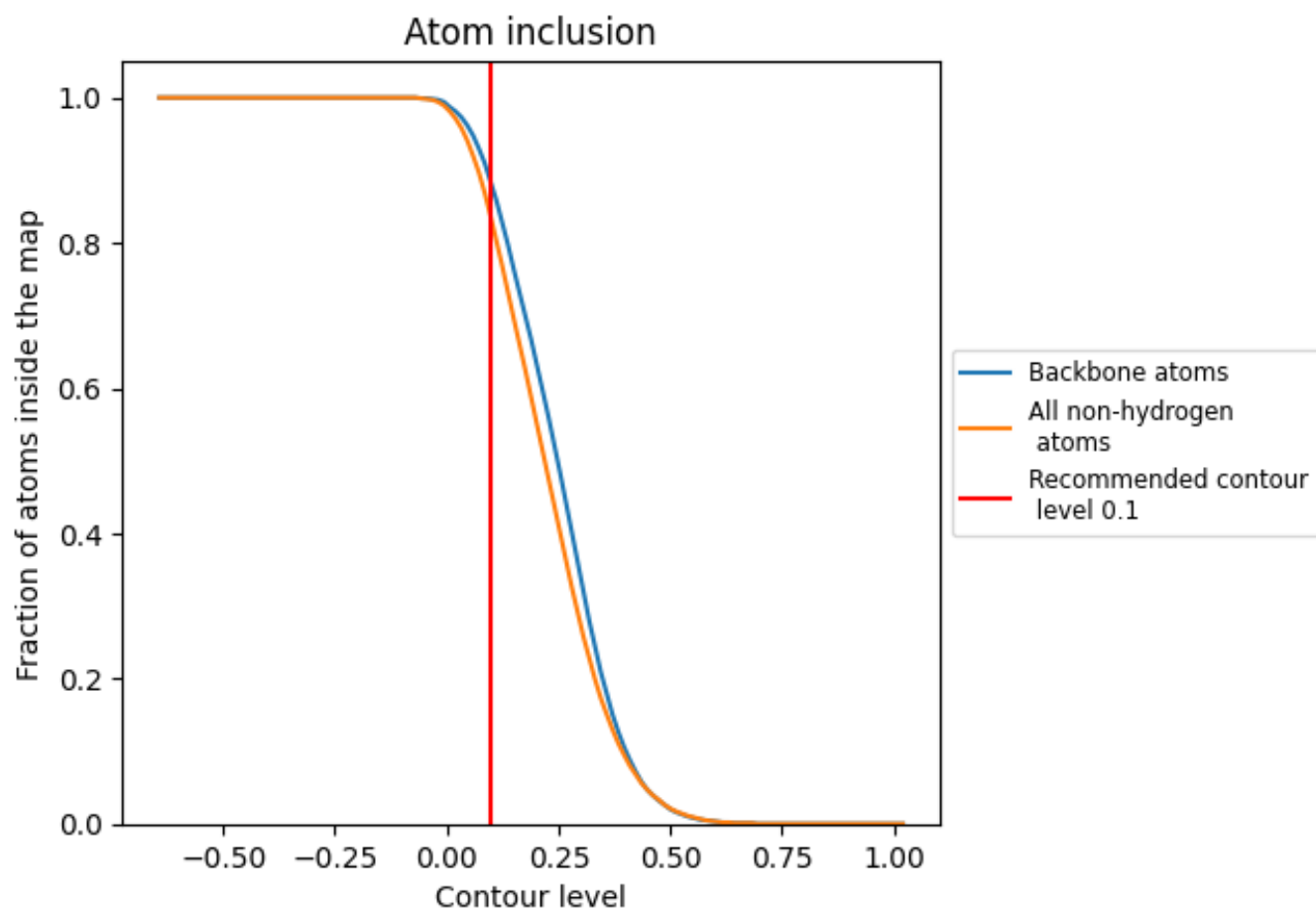
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 83% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary



























The table lists the average atom inclusion at the recommended contour level (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8320	 0.4600
5	 0.8790	 0.4610
7	 0.9300	 0.4640
8	 0.9160	 0.4870
A	 0.8160	 0.5030
B	 0.8610	 0.5040
C	 0.8540	 0.5080
D	 0.7770	 0.4220
E	 0.7700	 0.4440
F	 0.8600	 0.5080
G	 0.7920	 0.4370
H	 0.8090	 0.4780
I	 0.7880	 0.4720
J	 0.7020	 0.3630
L	 0.8340	 0.4890
M	 0.8430	 0.4840
N	 0.8130	 0.5010
O	 0.8650	 0.5110
P	 0.8180	 0.5010
Q	 0.8520	 0.5180
R	 0.8170	 0.4810
S	 0.8480	 0.5050
T	 0.8160	 0.4920
U	 0.7240	 0.4450
V	 0.8220	 0.4870
W	 0.8260	 0.4880
X	 0.8120	 0.4890
Y	 0.8170	 0.4890
Z	 0.7700	 0.4300
a	 0.8570	 0.5030
b	 0.7630	 0.4570
c	 0.7300	 0.4050
d	 0.7670	 0.4720
e	 0.8480	 0.5200
f	 0.8760	 0.5270



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Chain	Atom inclusion	Q-score
g	 0.7980	 0.4900
h	 0.8130	 0.4970
i	 0.7450	 0.4320
j	 0.8830	 0.5260
k	 0.6920	 0.4240
l	 0.8360	 0.5070
m	 0.7850	 0.4820
o	 0.6490	 0.4210
p	 0.8010	 0.4720
q	 0.0520	 0.0480
x	 0.6010	 0.3600
y	 0.5160	 0.3680
z	 0.1490	 0.1320