



## wwPDB EM Validation Summary Report ⓘ

Apr 1, 2025 – 07:57 pm BST

PDB ID : 6YLH / pdb\_00006ylh  
EMDB ID : EMD-10839  
Title : Rix1-Rea1 pre-60S particle - full composite structure  
Authors : Kater, L.; Beckmann, R.  
Deposited on : 2020-04-07  
Resolution : 3.10 Å (reported)  
Based on initial models : 6N8J, 6QTA, 6HYP, 6OR5, 3JCT, 6HYD

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:

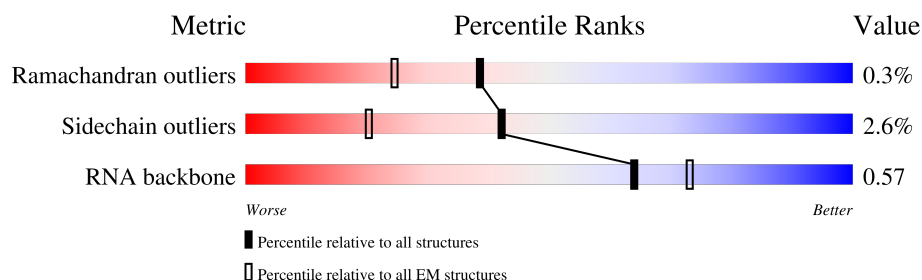
EMDB validation analysis : 0.0.1.dev117  
Mogul : 1.8.4, CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.42

# 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 3.10 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	1	3396	<div> <div>8%</div> <div>71%</div> <div>18%</div> <div>11%</div> </div>
2	2	158	<div> <div>80%</div> <div>17%</div> <div>.</div> </div>
3	3	121	<div> <div>7%</div> <div>80%</div> <div>17%</div> <div>.</div> </div>
4	4	593	<div> <div>63%</div> <div>81%</div> <div>14%</div> </div>
5	5	120	<div> <div>50%</div> <div>61%</div> <div>35%</div> </div>
6	A	254	<div> <div>94%</div> <div>.</div> <div>.</div> </div>
7	B	387	<div> <div>10%</div> <div>96%</div> <div>.</div> </div>
8	C	362	<div> <div>8%</div> <div>98%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
9	D	297	
10	E	176	
11	F	244	
12	G	256	
13	H	191	
14	I	166	
15	J	174	
16	K	334	
17	L	199	
18	M	138	
19	N	204	
20	O	199	
21	P	184	
22	Q	186	
23	R	189	
24	S	172	
25	T	160	
26	U	121	
27	V	137	
28	W	236	
29	X	142	
30	Y	127	
31	Z	136	
32	a	149	
33	b	647	

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Mol	Chain	Length	Quality of chain
34	c	175	
35	d	113	
36	e	130	
37	f	107	
38	g	121	
39	h	120	
40	i	100	
41	j	88	
42	k	78	
43	l	51	
44	m	486	
45	n	105	
46	o	217	
47	p	92	
48	q	165	
49	r	261	
50	s	520	
51	t	767	
52	u	199	
53	x	515	
54	y	245	
55	z	106	
56	v	4910	
57	0	555	
57	w	555	

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Mol	Chain	Length	Quality of chain
58	6	763	<div><div></div><div>19%</div><div>69%</div><div></div><div>29%</div></div>
58	7	763	<div><div></div><div>21%</div><div>71%</div><div></div><div>28%</div></div>

## 2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 180897 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	3039	Total	C	N	O	P	0	0
			65028	29041	11740	21208	3039		

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	154	Total	C	N	O	P	0	0
			3273	1464	576	1079	154		

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	117	Total	C	N	O	P	0	0
			2494	1114	446	817	117		

- Molecule 4 is a protein called Probable metalloprotease ARX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	509	Total	C	N	O	S	0	0
			3945	2503	673	754	15		

- Molecule 5 is a protein called rRNA-processing protein CGR1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	78	Total	C	N	O	S	0	0
			681	419	140	119	3		

- Molecule 6 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	245	Total	C	N	O	S	0	0
			1863	1162	376	324	1		

- Molecule 7 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	386	Total	C	N	O	S	0	0
			3081	1956	584	533	8		

- Molecule 8 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	361	Total	C	N	O	S	0	0
			2749	1730	522	494	3		

- Molecule 9 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	D	243	Total	C	N	O	S	0	0
			1969	1250	344	373	2		

- Molecule 10 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	156	Total	C	N	O	S	0	0
			1239	800	222	216	1		

- Molecule 11 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	216	Total	C	N	O	S	0	0
			1744	1127	317	299	1		

- Molecule 12 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	228	Total	C	N	O	S	0	0
			1784	1142	320	319	3		

- Molecule 13 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	H	187	Total	C	N	O	S	0	0
			1486	944	270	268	4		

- Molecule 14 is a protein called Bud site selection protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	I	130	Total	C	N	O	S	0	0
			1051	657	194	197	3		

- Molecule 15 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	168	Total	C	N	O	S	0	0
			1344	841	251	248	4		

- Molecule 16 is a protein called Pre-rRNA-processing protein IPI1.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	258	Total	C	N	O	S	0	0
			2089	1346	367	368	8		

- Molecule 17 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	181	Total	C	N	O	S	0	0
			1456	907	301	248			

- Molecule 18 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	134	Total	C	N	O	S	0	0
			1040	666	196	176	2		

- Molecule 19 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 20 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 21 is a protein called 60S ribosomal protein L17-A.



Mol	Chain	Residues	Atoms				AltConf	Trace
21	P	171	Total	C	N	O	0	0
			1360	845	272	243		

- Molecule 22 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	Q	144	Total	C	N	O	S	0
			1110	704	213	192	1	0

- Molecule 23 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	R	151	Total	C	N	O		0
			1219	757	258	204		0

- Molecule 24 is a protein called 60S ribosomal protein L20-A.

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

- Molecule 25 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	T	124	Total	C	N	O	S	0
			983	619	188	173	3	0

- Molecule 26 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	U	101	Total	C	N	O		0
			800	518	131	151		0

- Molecule 27 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	V	134	Total	C	N	O	S	0
			993	623	187	176	7	0

- Molecule 28 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	W	233	Total	C	N	O	S	0	0
			1877	1189	322	361	5		

- Molecule 29 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	X	140	Total	C	N	O	S	0	0
			1092	699	195	196	2		

- Molecule 30 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Y	125	Total	C	N	O		0	0
			984	620	191	173			

- Molecule 31 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 32 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	a	93	Total	C	N	O	S	0	0
			735	479	130	125	1		

- Molecule 33 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	b	613	Total	C	N	O	S	0	0
			4953	3110	892	926	25		

- Molecule 34 is a protein called Ribosome biogenesis protein ALB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	c	109	Total	C	N	O		0	0
			872	543	171	158			

- Molecule 35 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	d	105	Total	C	N	O	S	0	0
			856	544	163	148	1		

- Molecule 36 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	e	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 37 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 38 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	g	107	Total	C	N	O	S	0	0
			846	525	173	144	4		

- Molecule 39 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	h	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 40 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	i	96	Total	C	N	O	S	0	0
			743	465	148	128	2		

- Molecule 41 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	j	84	Total	C	N	O	S	0	0
			665	405	145	110	5		

- Molecule 42 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	k	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 43 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	l	49	Total	C	N	O	S	0	0
			428	266	96	64	2		

- Molecule 44 is a protein called Nucleolar GTP-binding protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	m	439	Total	C	N	O	S	0	0
			3546	2249	647	641	9		

- Molecule 45 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	n	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 46 is a protein called 60S ribosomal protein L1-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	o	177	Total	C	N	O	0	0
			877	523	177	177		

- Molecule 47 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	p	89	Total	C	N	O	S	0	0
			680	421	136	117	6		

- Molecule 48 is a protein called 60S ribosomal protein L12-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	q	126	Total	C	N	O	S	0	0
			961	606	171	182	2		

- Molecule 49 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	r	225	Total	C	N	O	S	0	0
			1818	1152	345	314	7		

- Molecule 50 is a protein called Nuclear GTP-binding protein NUG1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	s	56	Total	C	N	O	S	0	0
			463	291	94	77	1		

- Molecule 51 is a protein called Protein SDA1.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	t	431	Total	C	N	O	S	0	0
			3395	2156	587	629	23		

- Molecule 52 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	u	148	Total	C	N	O	S	0	0
			1247	783	250	205	9		

- Molecule 53 is a protein called Ribosome assembly protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	x	459	Total	C	N	O	S	0	0
			3385	2110	620	635	20		

- Molecule 54 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	y	243	Total	C	N	O	S	0	0
			1841	1141	318	376	6		

- Molecule 55 is a protein called UPF0642 protein YBL028C.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	z	77	Total	C	N	O	S	0	0
			643	403	130	109	1		

- Molecule 56 is a protein called Midasin.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	v	3629	Total	C	N	O	0	0
			18010	10752	3629	3629		

- Molecule 57 is a protein called Pre-rRNA-processing protein IPI3.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	w	399	Total	C	N	O	S	0	0
			3139	2004	520	601	14		
57	0	415	Total	C	N	O	S	0	0
			3260	2077	548	621	14		

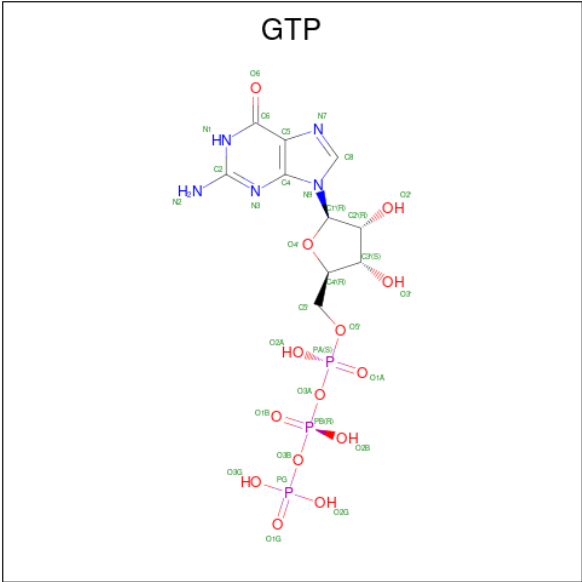
- Molecule 58 is a protein called Pre-rRNA-processing protein RIX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	6	545	Total	C	N	O	S	0	0
			4352	2847	711	777	17		
58	7	547	Total	C	N	O	S	0	0
			4380	2862	720	782	16		

- Molecule 59 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
59	I	1	Total	Zn	0
			1	1	
59	j	1	Total	Zn	0
			1	1	
59	p	1	Total	Zn	0
			1	1	
59	u	1	Total	Zn	0
			1	1	

- Molecule 60 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C<sub>10</sub>H<sub>16</sub>N<sub>5</sub>O<sub>14</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					AltConf
60	b	1	Total	C	N	O	P	0
			32	10	5	14	3	
60	m	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 61 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
61	b	1	Total	Mg	0
			1	1	
61	m	1	Total	Mg	0
			1	1	

### 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.

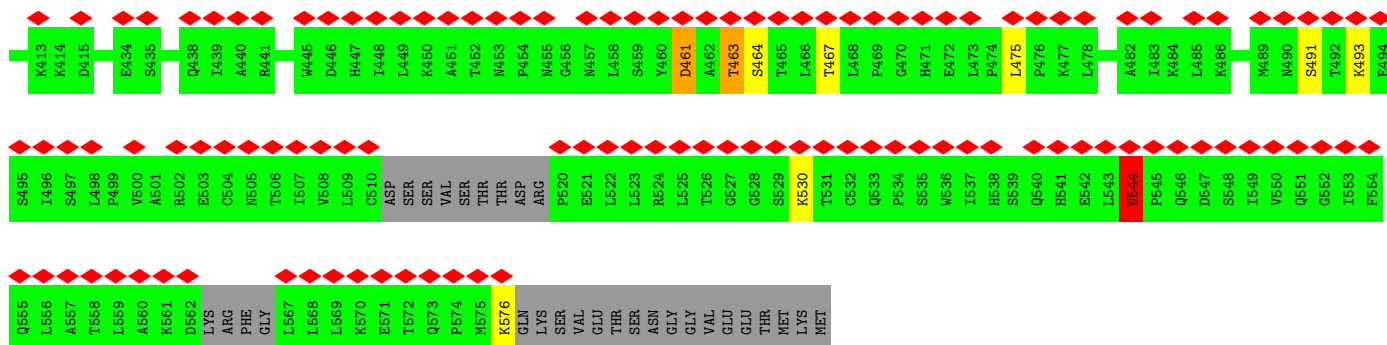
#### • Molecule 1: 25S rRNA



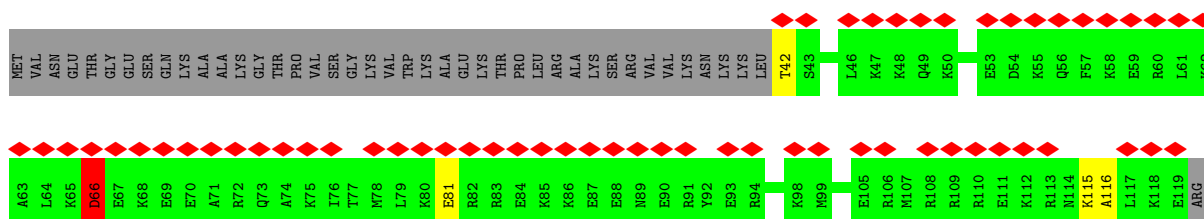


A1302	A1303	A1304	U1305	G1306	G1307	A1308	U1309	G1313	U1329	A1330	G1345	U1348	G	A	U	A	U	U	U	A	G	A1355	U1356	A1386	G1392	A1399	G1400	U1405	G1434	U1435	U1436	C1437	G1443	U1455	G1483	U1484	G1487	C1496	A1503	C1508	U1522	U1523	A1524							
G1525	U1533	G1536	A1539	U1555	C1556	A1557	G1560	G1561	C1562	G1565	A	U	U	U	U	U	U	U	U	U	G1573	C1574	A1575	A1588	A1589	U1629	U1630	C1639	A1642	A1643	C1644	C1657	A1683	U1717	U1724	C1725	U1742	A1750	G1751	A1760										
C1761	C1762	U1763	U1764	U1765	U1766	G1775	G1780	G1794	A1797	A1810	A1813	A1814	U1815	A1816	U1820	U1821	A1839	A1842	C1849	A1850	G1851	G1878	A1879	U1880	G1889	A1896	G1897	G1898	G1899	A1900	A1901	G1906	U1925	C1926	C1951	G1952	G1953	G	U	A	G	U	G							
A	G	G	G	C	C	U	U	A	C	U	C	C	C	C	U	C	C	C	C	C	C	U	C	U	C	U	C	U	C	U	C	U	C	U	C	U	C	U	C	U	C	C	U	G						
C	U	U	U	G	C	U	A	A	A	C2094	C2101	U2102	U2112	G2121	G2122	A2126	A2131	G2134	A2149	G2169	U2170	U2184	G2194	C2195	U2205	G2239	A2244	C2245	G2246	G2247	C2248	G2249	U2254	A	C	C	U	A	U	G	A2262									
C2267	U2268	A2270	A2271	C2272	G2273	C2276	C	C	A	A	C	C	U	C	U	C	U	C	U	A	U	U	A	U	C	U	G	A	A	A	U	G2315	U2318	U2319	A2320	U2334	G2335	U2336	C2337	C2338	C2339									
U2340	A2373	C2374	G2375	C2376	G2377	U2388	G2391	G2394	A2397	A2398	A2399	G	A	G2403	U2410	U2411	G2412	G2418	A2419	G2435	U2436	G2437	G2442	A2443	C2444	A2445	U2446	A2447	G2448	A2449	G2450	G2451	G2452	U2453	A2459	A2462	G2463	U2464	G2465	G2466	G2467	A2468	G2469	U2471	U2472	C2473				
G2474	G2475	C2476	G2477	A2480	U2487	C2490	A2491	C2492	U2493	A2494	C2495	A2500	U2501	A2502	U2504	U2505	U2506	U2507	U2508	U2514	A2515	G2522	A2523	A2524	G2530	C2531	U2532	G2533	G2534	A2535	A2536	U2537	U2538	C2539	A2540	U2541	U2542	U2543	U2544	C2545	C2546	A2547	C2548	G2549	U2550	U2551	C2552	U2553	A2554	C2560
A2561	A2569	U2570	U2571	C2572	G2573	G2586	A2593	C2594	A2595	G2606	G2607	U2613	G	C	U	G	G	G	G	G	C	U	U	U	G	C2625	A2626	C2627	A2628	U2629	C2630	U2631	G2632	U2633	U2634	A	A	A	C	C2645	C2646	A2647	G2648	A2649	U2650	G2651	U2652	C	U2655	
A2656	A2657	G2660	G2661	A2674	G2677	U2681	A2689	A2694	A	A2696	A2697	G2698	A2704	G2714	A2715	U2716	U2717	U2718	U2719	G2720	A2721	U2722	U2723	U2724	U2725	C	A	G	U2729	G2730	U2731	G2732	A2733	U2734	U2735	U2736	U2737	U2738	C2741	C2742	U2752	G2753	G2754	C2755	C2756	U	A	U	C	
G	A	U	C2764	C2765	U2766	U2771	C2772	C2773	G2777	U2778	A2779	A2780	G2791	G2794	U	G	C	C	A	A	A2802	A2803	A2804	C2810	G2814	G2815	G2816	A	U	A	A	C	U2822	G2823	G2824	C2825	U2826	G2831	G2834	U2835	C2837	A2838	G2841	U2842	U2843	C2844	A2845	U2846		
A2847	U2859	U2860	U2861	A2864	U2865	U2866	C2867	U2868	U2869	C2870	C2871	A2872	U2873	G	U	C2876	G2877	G2878	U2880	A2887	U2888	C2889	G2898	C2899	U3041	U3042	A3048	U3058	G3059	U3078	U3079	G3080	A3086	C3092	C3093	U3095	A2936	G2937	G2938	A2941	C2942	G2943	U2944	C2947	C2948	U2949	G2950	G2951		
G	U	U	U2955	C2970	A2971	G2972	U2978	U2979	U2980	U2981	A2982	C2983	U2996	G2997	A3011	A3012	G3022	U3023	G3028	A3032	C3039	A3040	U3041	U3042	A3048	U3058	G3059	U3078	U3079	G3080	A3086	C3092	C3093	U3100	G3101	C3115	G3116	A3129	C2942	G2943	U2944	C2947	C2948	U2949	G2950	G2951				

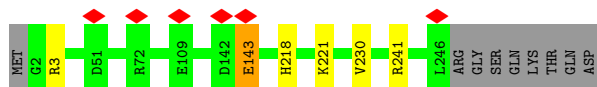




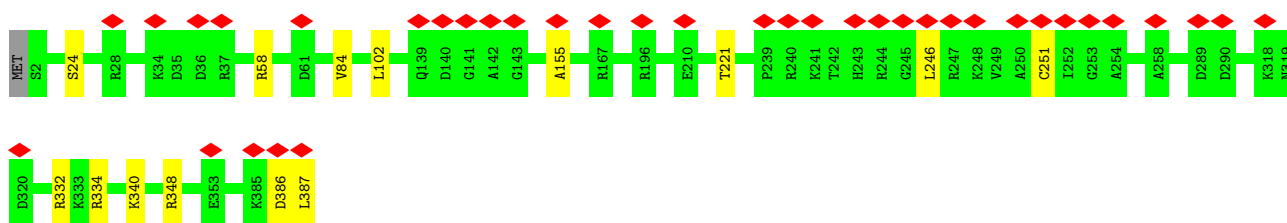
• Molecule 5: rRNA-processing protein CGR1



• Molecule 6: 60S ribosomal protein L2-A



• Molecule 7: 60S ribosomal protein L3

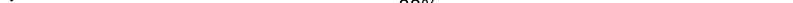


• Molecule 8: 60S ribosomal protein L4-A

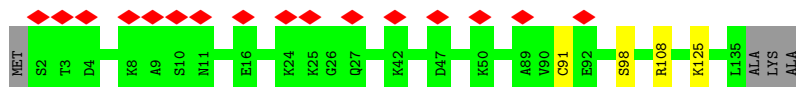


• Molecule 9: 60S ribosomal protein L5

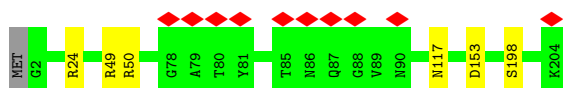


- Chain L:  14% 88% 9%

- Molecule 18: 60S ribosomal protein L14-A



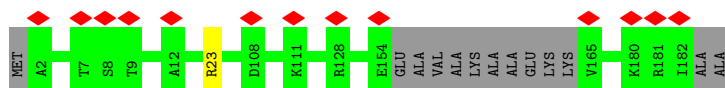
- Molecule 19: 60S ribosomal protein L15-A



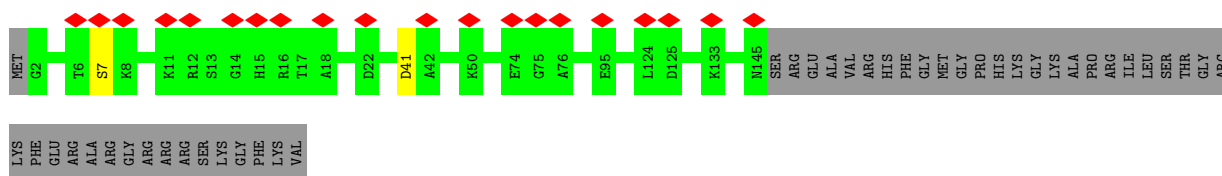
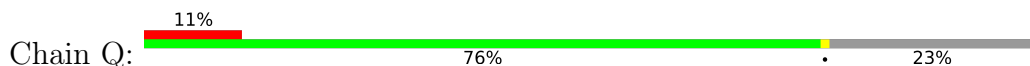
- Molecule 20: 60S ribosomal protein L16-A



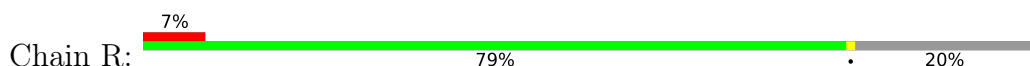
- Molecule 21: 60S ribosomal protein L17-A

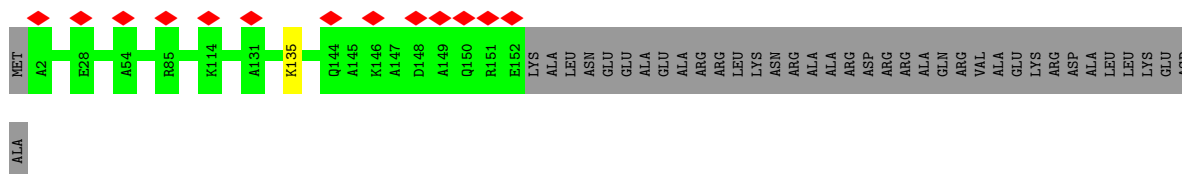


- Molecule 22: 60S ribosomal protein L18-A

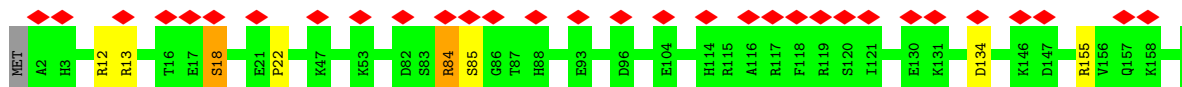


- Molecule 23: 60S ribosomal protein L19-A

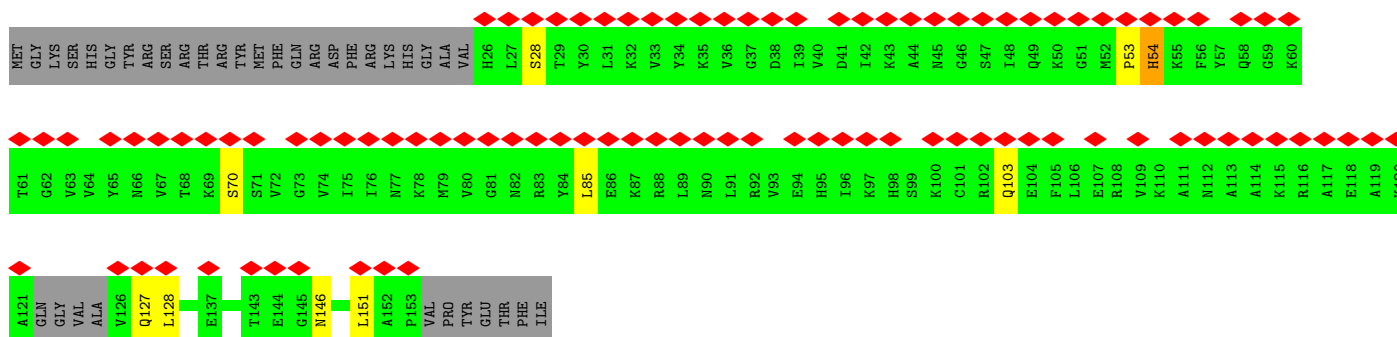
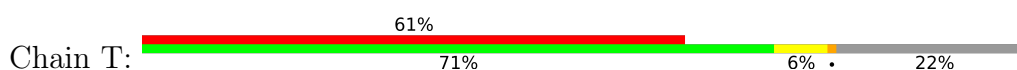




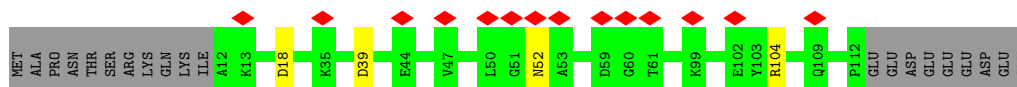
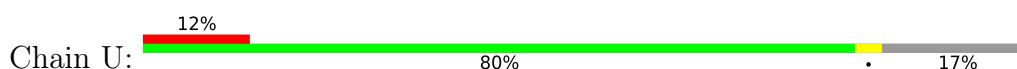
- Molecule 24: 60S ribosomal protein L20-A



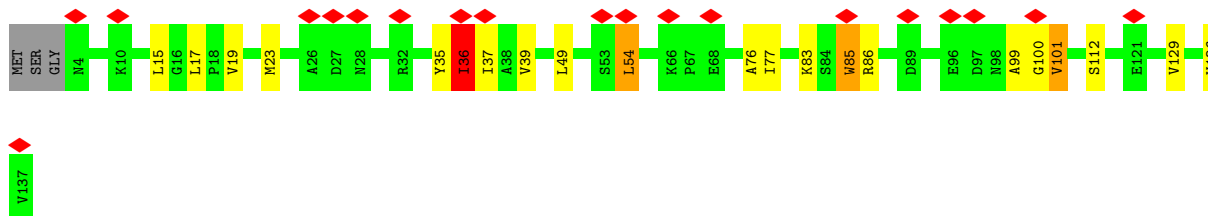
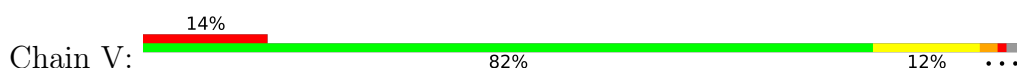
- Molecule 25: 60S ribosomal protein L21-A



- Molecule 26: 60S ribosomal protein L22-A

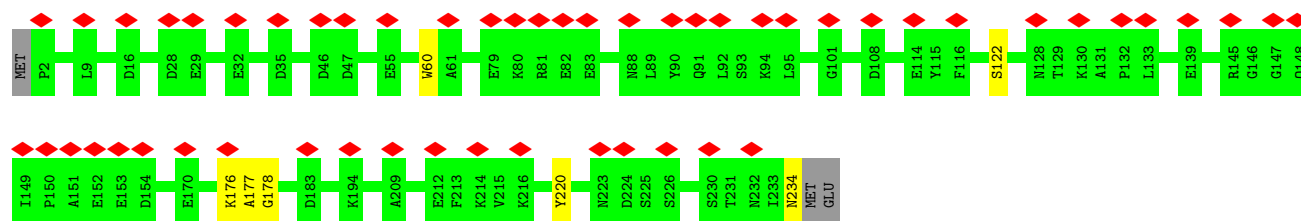


- Molecule 27: 60S ribosomal protein L23-A

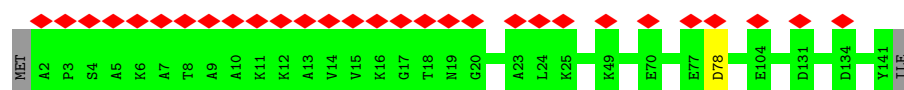


- Molecule 28: Ribosome assembly factor MRT4





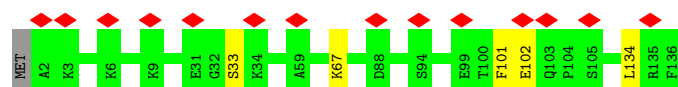
- Molecule 29: 60S ribosomal protein L25



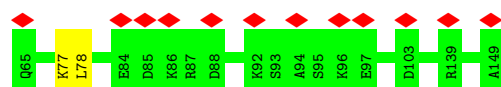
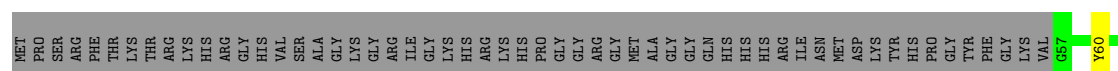
- Molecule 30: 60S ribosomal protein L26-A



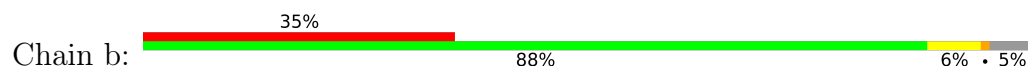
- Molecule 31: 60S ribosomal protein L27-A



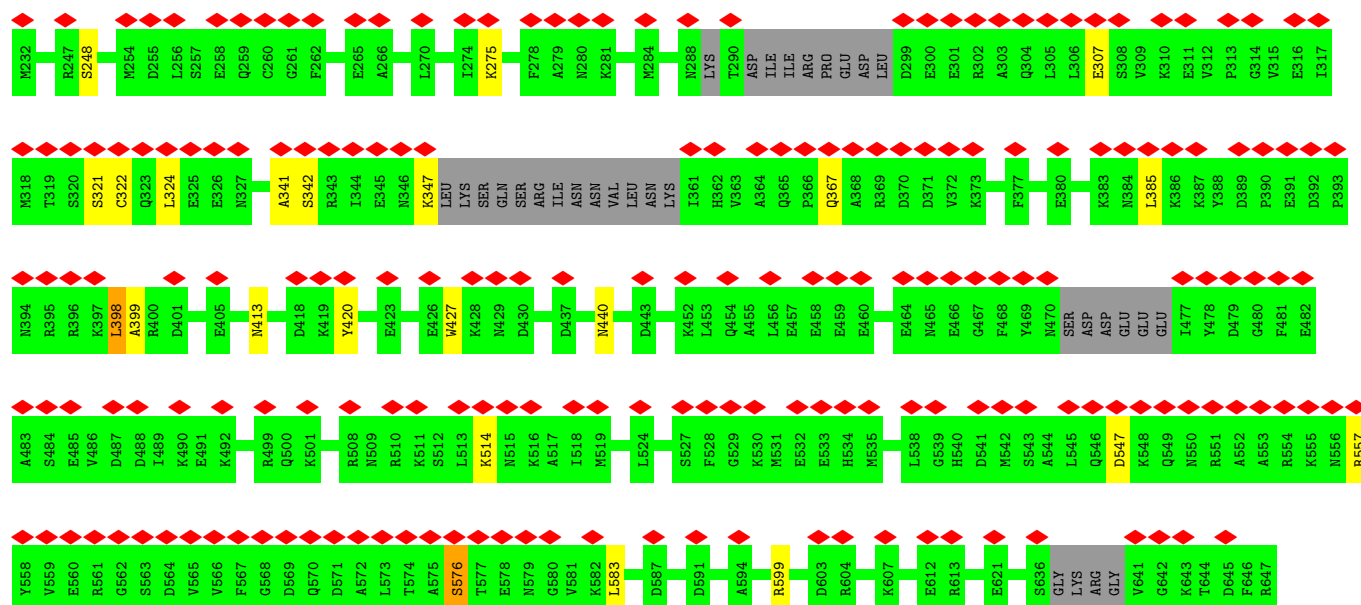
- Molecule 32: 60S ribosomal protein L28



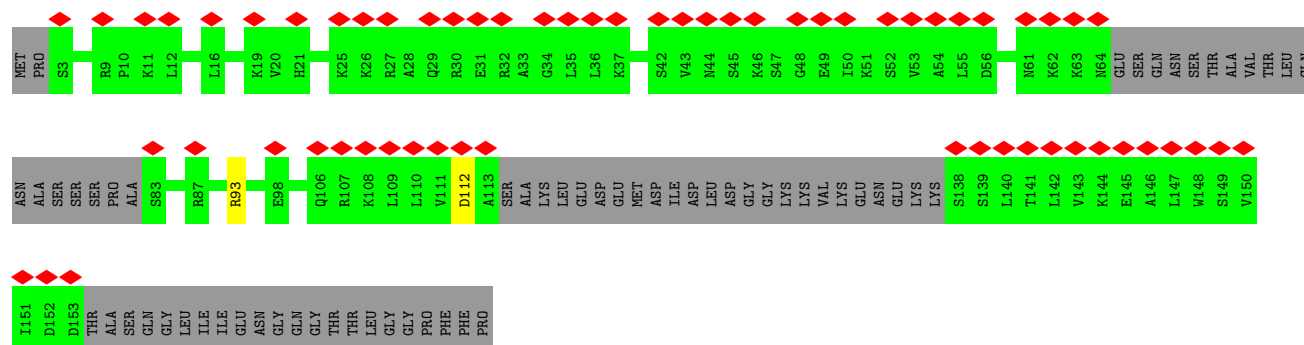
- Molecule 33: Nucleolar GTP-binding protein 1



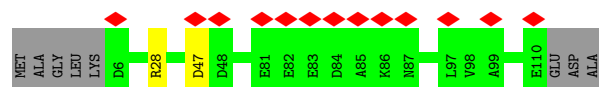
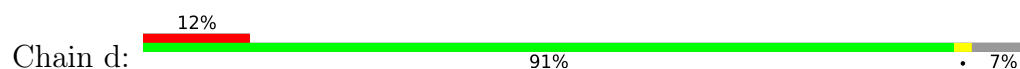




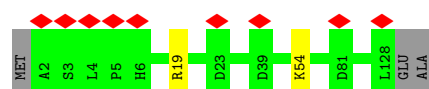
• Molecule 34: Ribosome biogenesis protein ALB1



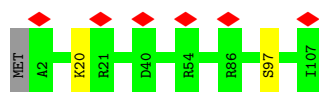
• Molecule 35: 60S ribosomal protein L31-A



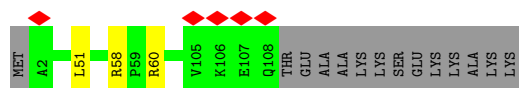
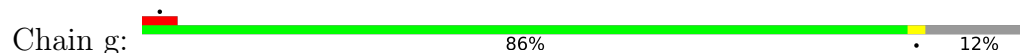
• Molecule 36: 60S ribosomal protein L32



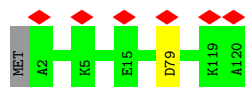
• Molecule 37: 60S ribosomal protein L33-A



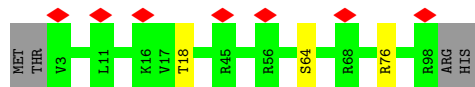
- Molecule 38: 60S ribosomal protein L34-A



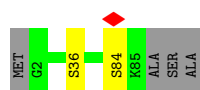
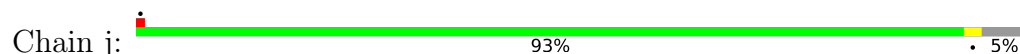
- Molecule 39: 60S ribosomal protein L35-A



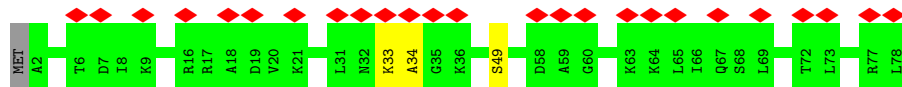
- Molecule 40: 60S ribosomal protein L36-A



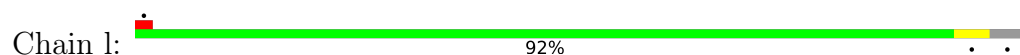
- Molecule 41: 60S ribosomal protein L37-A

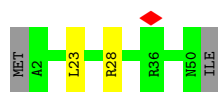


- Molecule 42: 60S ribosomal protein L38



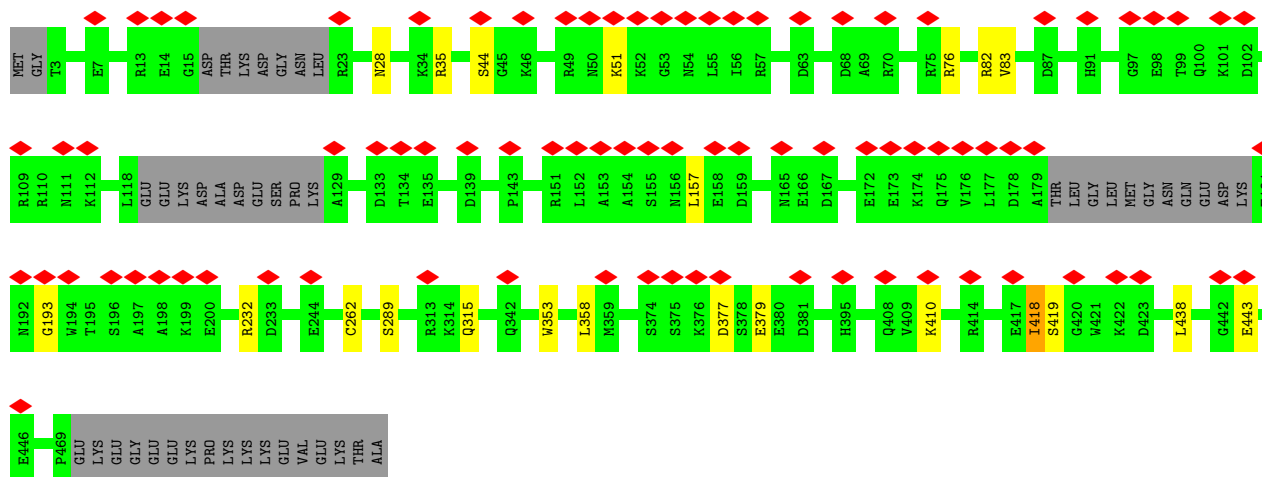
- Molecule 43: 60S ribosomal protein L39





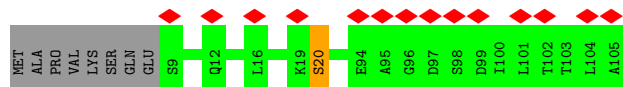
- Molecule 44: Nucleolar GTP-binding protein 2

Chain m: 17% 86% 10%



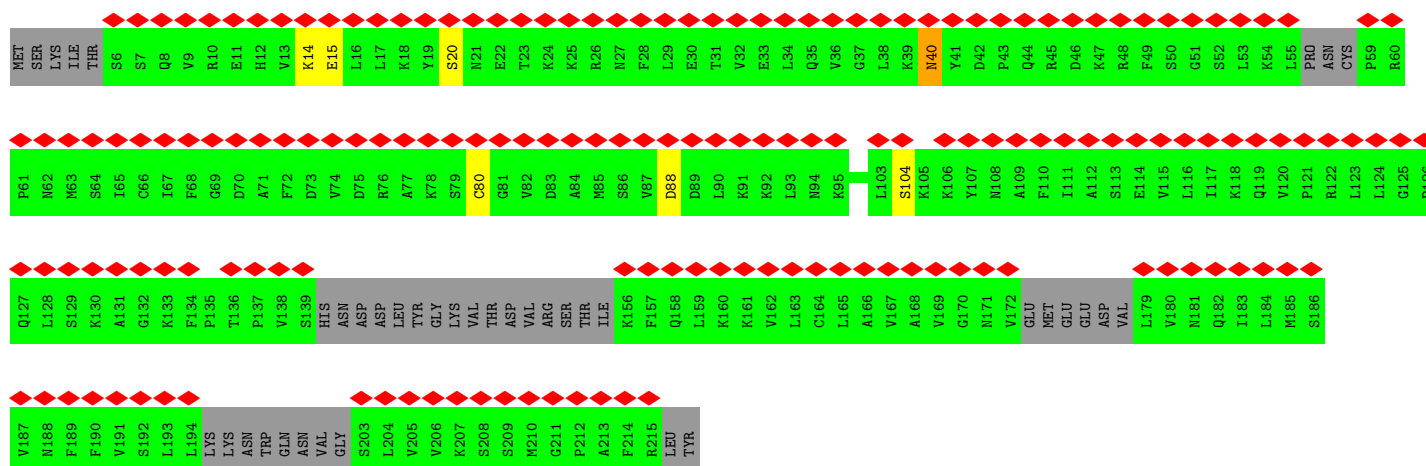
- Molecule 45: 60S ribosomal protein L30

Chain n: 13% 91% 8%

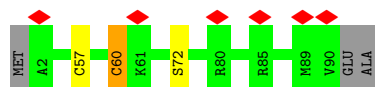
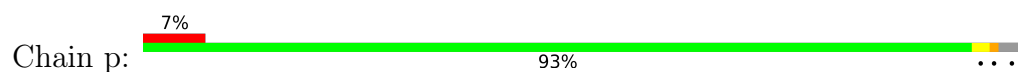


- Molecule 46: 60S ribosomal protein L1-A

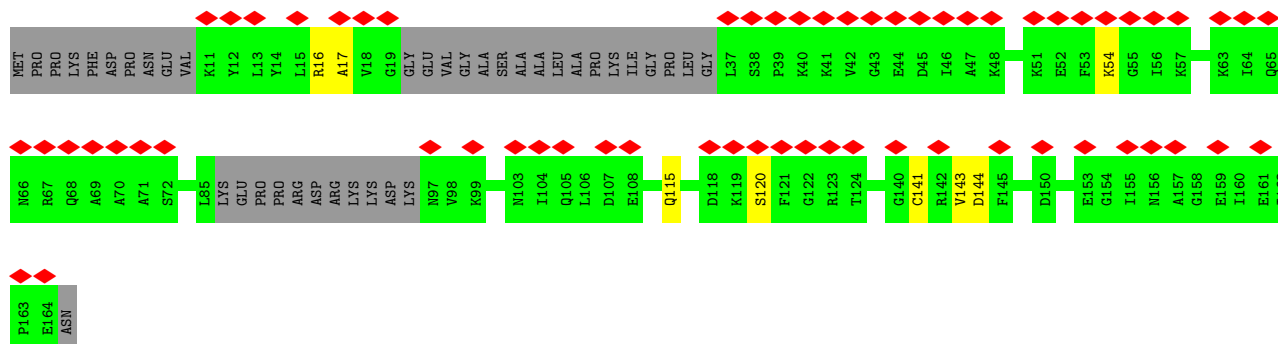
Chain o: 77% 78% 18%



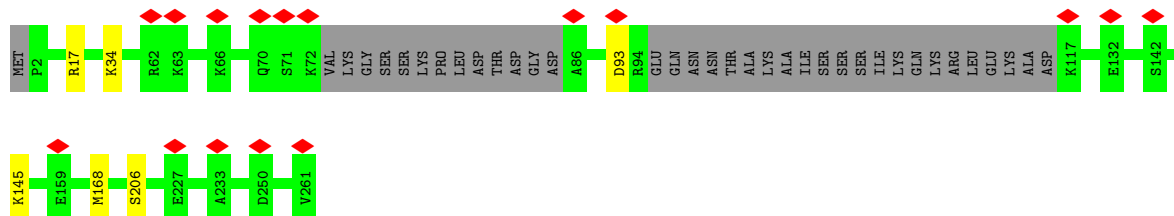
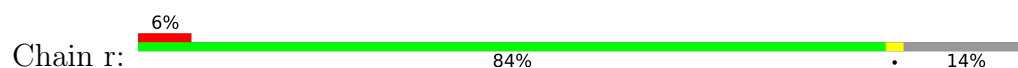
- Molecule 47: 60S ribosomal protein L43-A



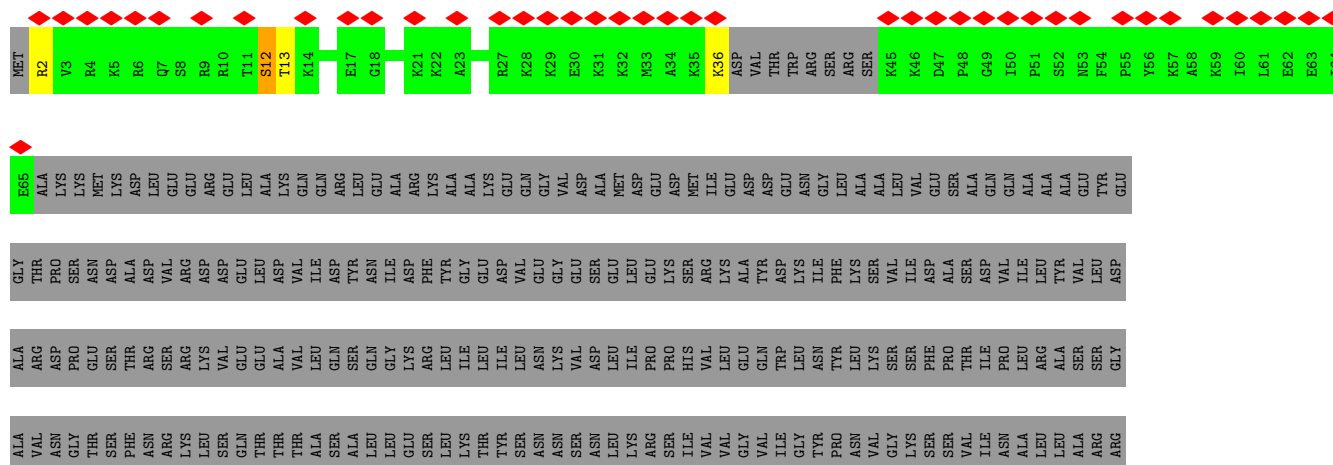
• Molecule 48: 60S ribosomal protein L12-A

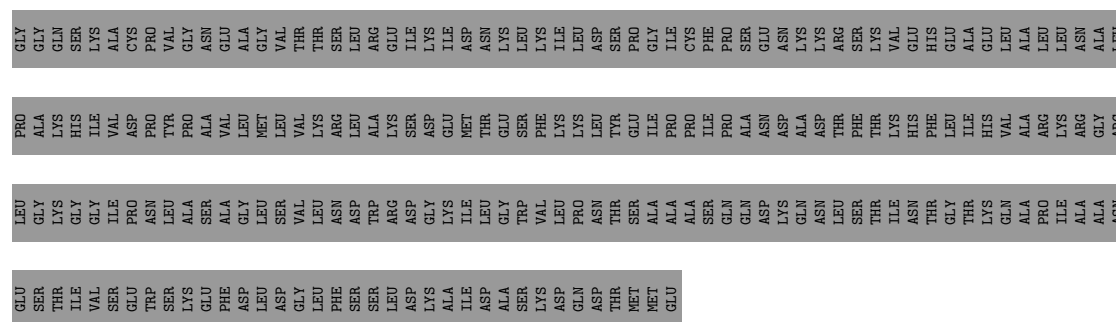


• Molecule 49: Ribosome biogenesis protein NSA2

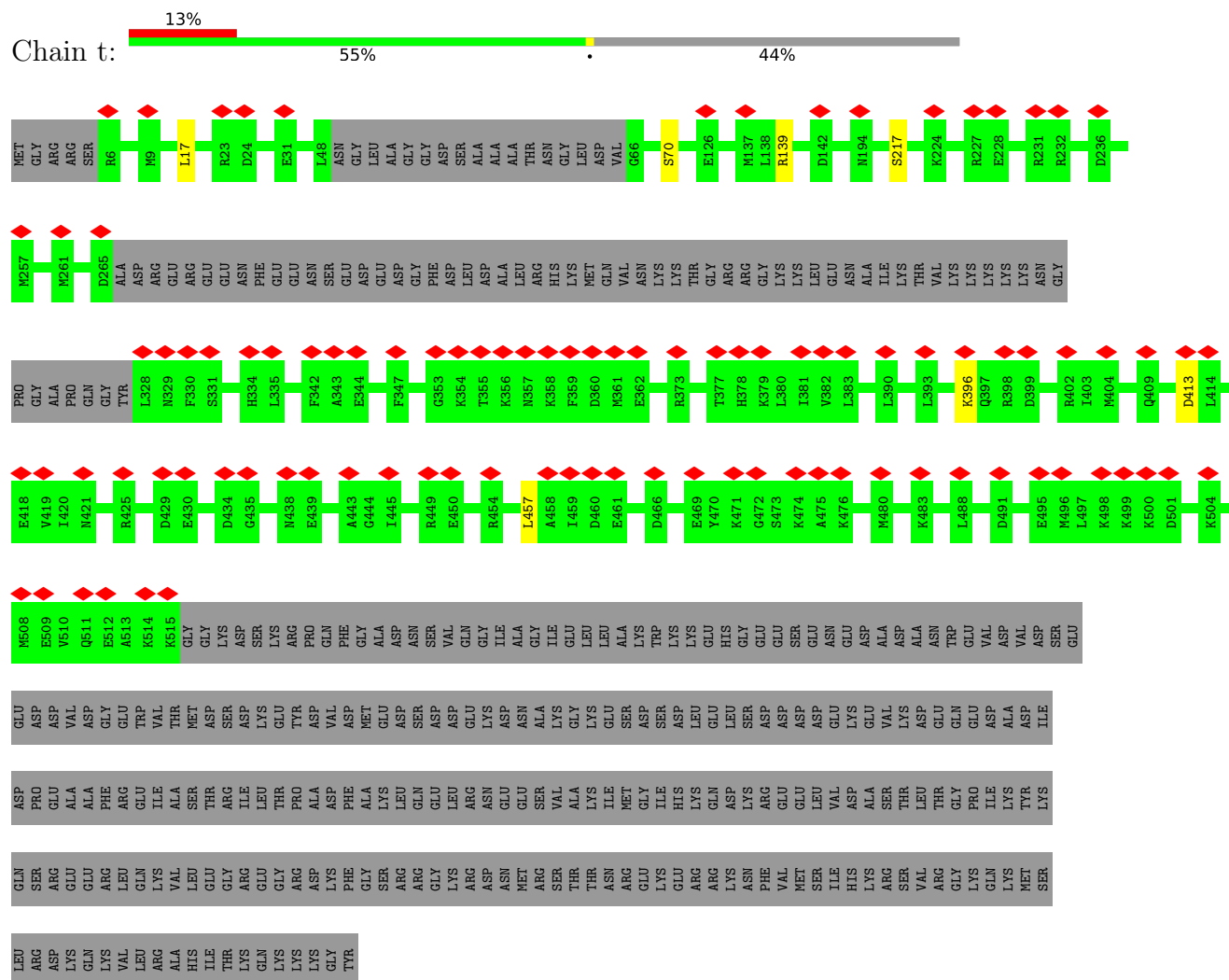


• Molecule 50: Nuclear GTP-binding protein NUG1

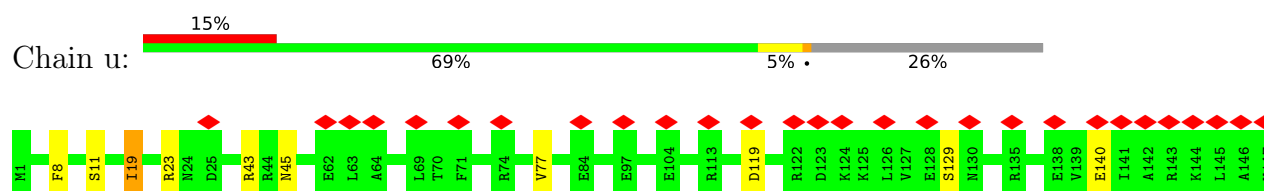


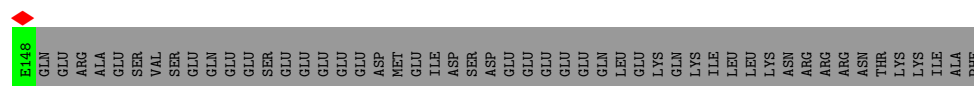


- Molecule 51: Protein SDA1



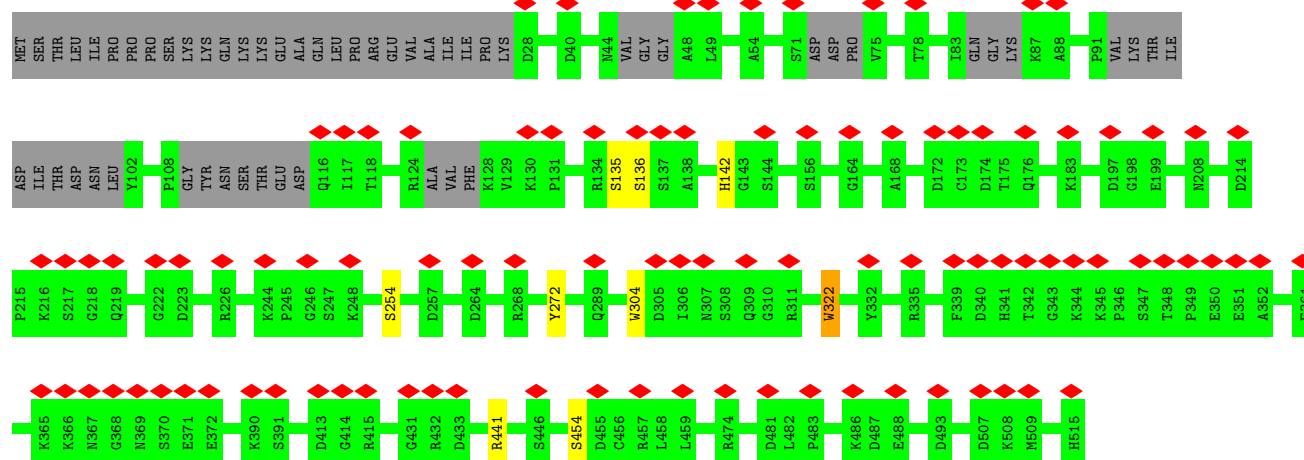
- Molecule 52: Ribosome biogenesis protein RLP24





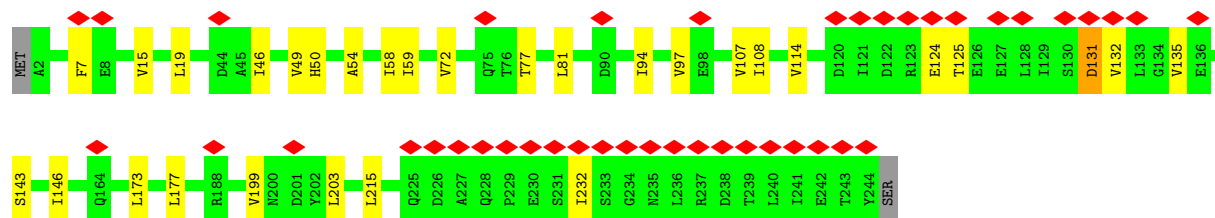
• Molecule 53: Ribosome assembly protein 4

Chain x: 19% 87% 11%



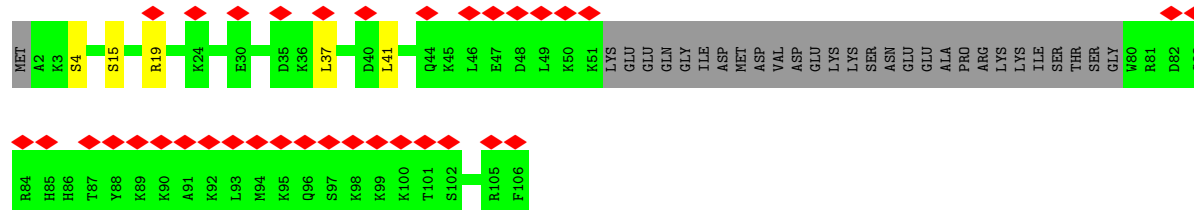
• Molecule 54: Eukaryotic translation initiation factor 6

Chain y: 17% 87% 12%



• Molecule 55: UPF0642 protein YBL028C

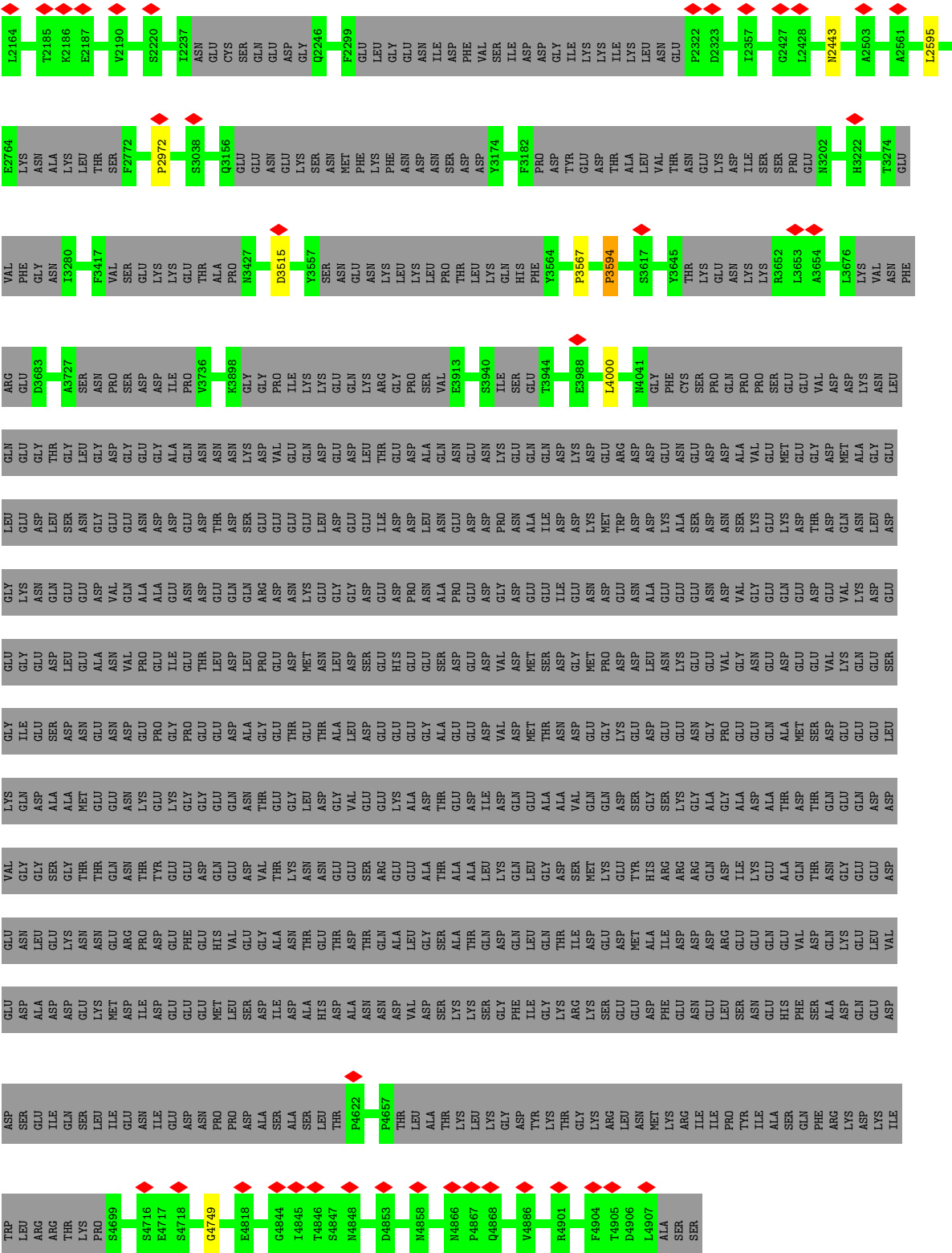
Chain z: 33% 68% 5% 27%



• Molecule 56: Midasin

Chain v: 74% 26%

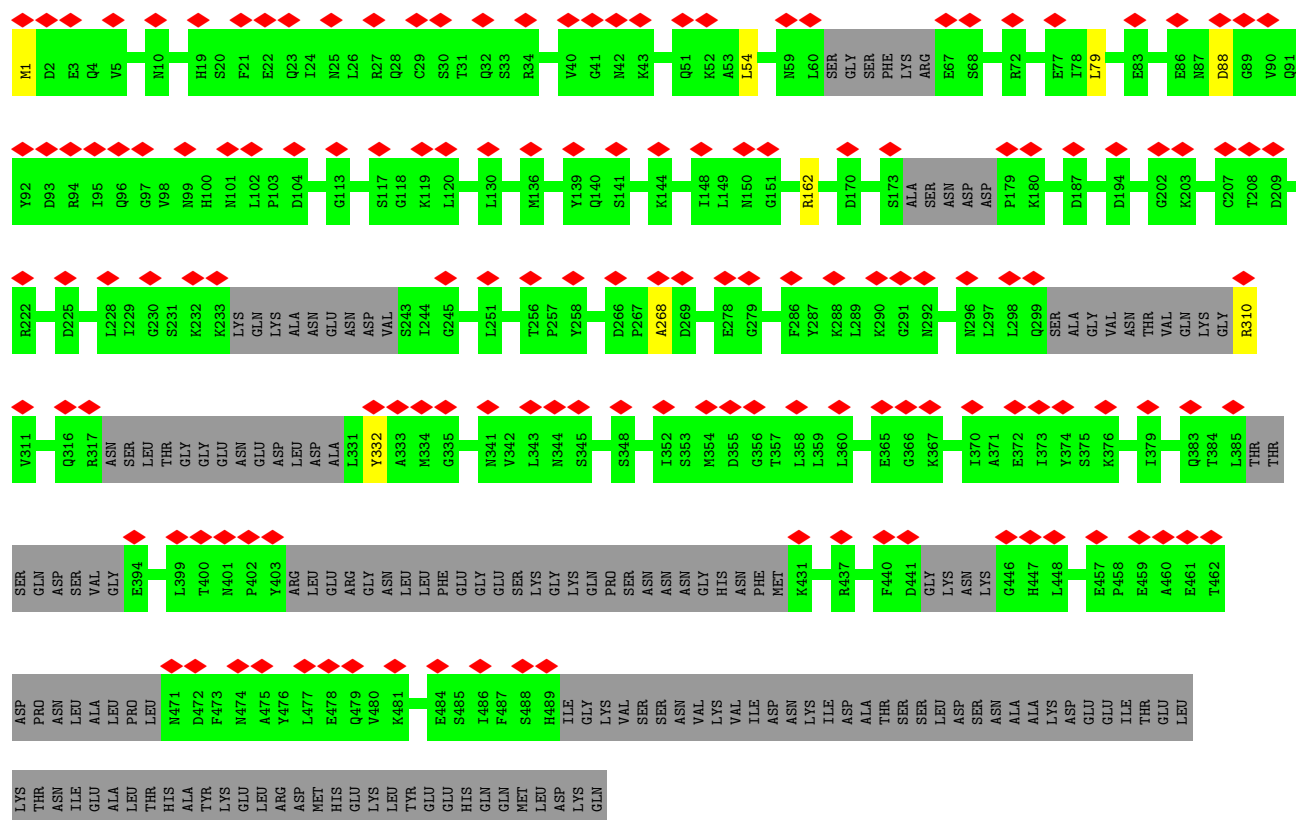




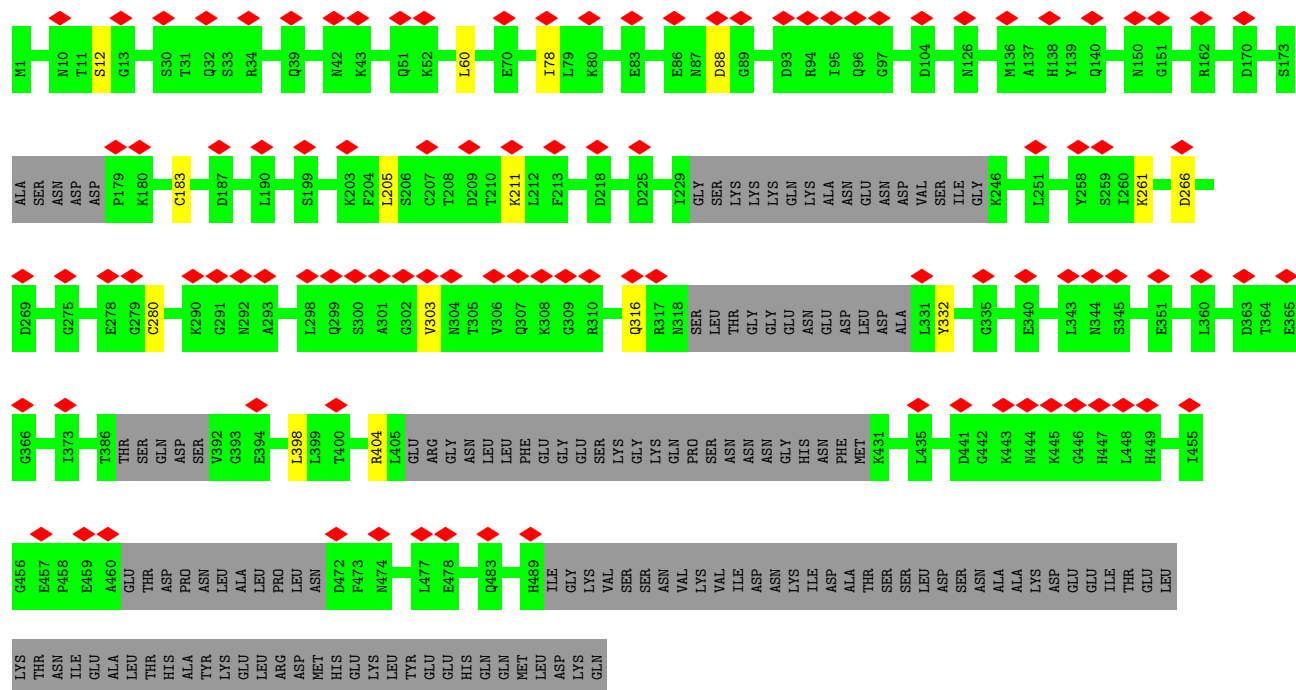
● Molecule 57: Pre-rRNA-processing protein IPI3



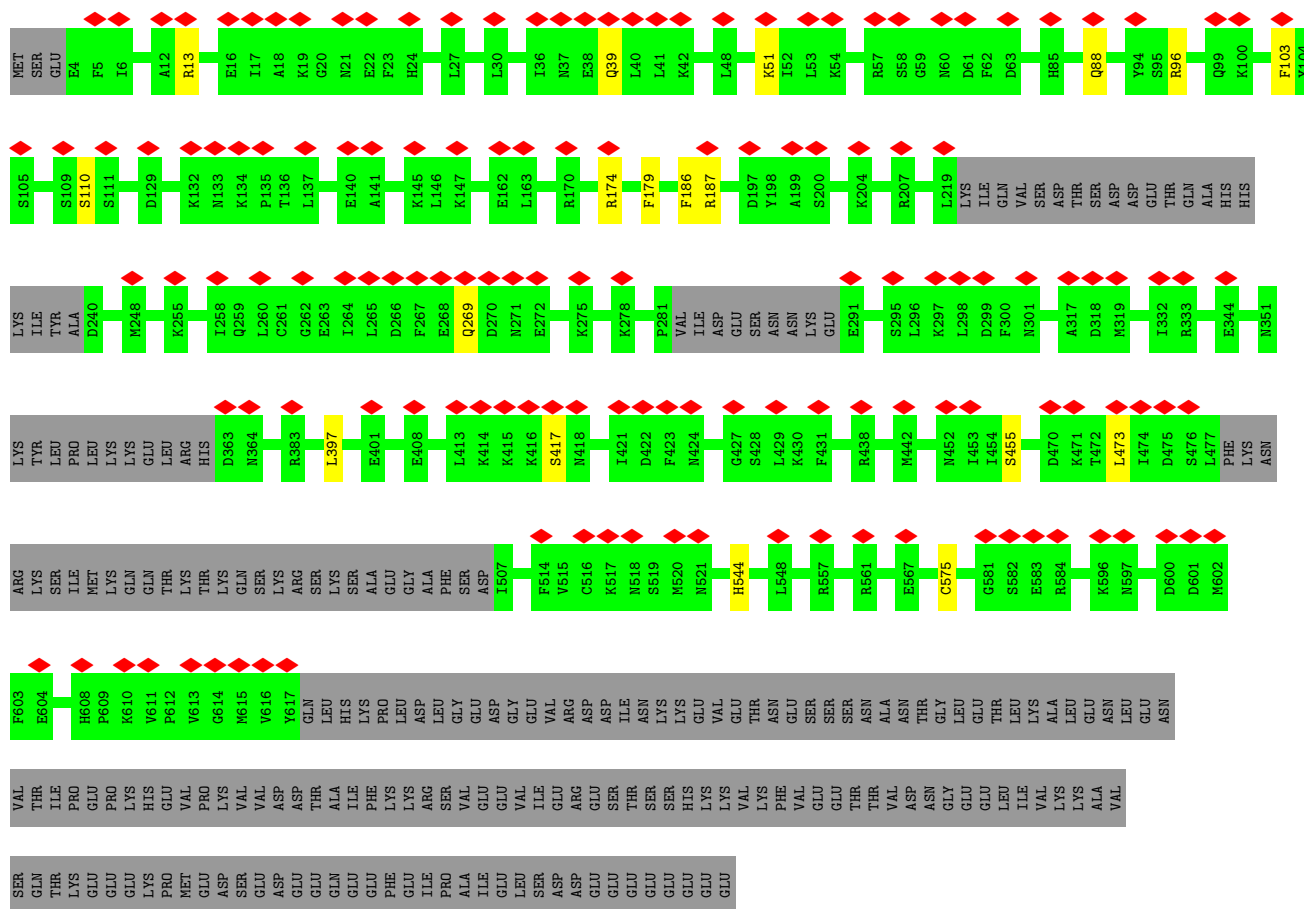




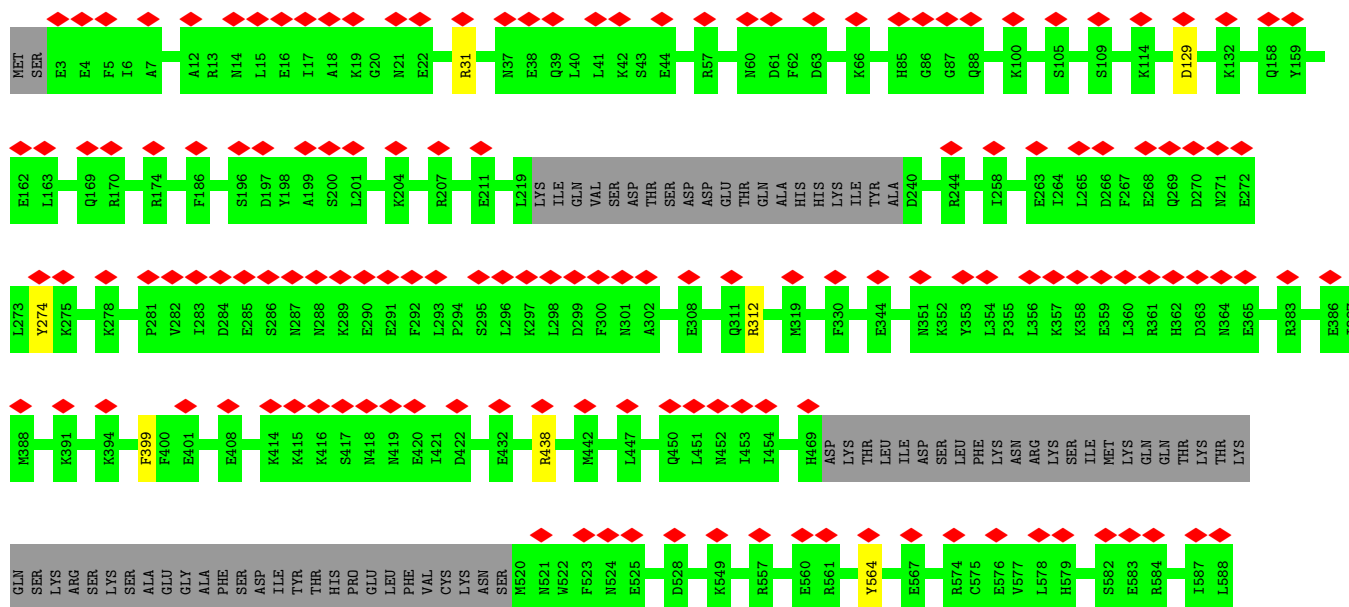
• Molecule 57: Pre-rRNA-processing protein IPI3



• Molecule 58: Pre-rRNA-processing protein RIX1



• Molecule 58: Pre-rRNA-processing protein RIX1





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	114398	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	75	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.138	Depositor
Minimum map value	-0.036	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.025	Depositor
Map size ( $\text{\AA}$ )	635.4, 635.4, 635.4	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.059, 1.059, 1.059	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, GTP, 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	1	0.37	5/72767 (0.0%)	0.91	87/113396 (0.1%)
2	2	0.36	0/3657	0.85	0/5692
3	3	0.27	0/2787	0.83	2/4339 (0.0%)
4	4	0.28	0/4015	0.63	3/5447 (0.1%)
5	5	0.31	0/685	0.69	1/895 (0.1%)
6	A	0.31	0/1897	0.65	1/2550 (0.0%)
7	B	0.31	0/3152	0.67	2/4239 (0.0%)
8	C	0.29	0/2801	0.58	0/3792
9	D	0.28	0/2013	0.62	0/2715
10	E	0.30	0/1260	0.63	1/1694 (0.1%)
11	F	0.31	0/1781	0.60	0/2396
12	G	0.31	0/1816	0.58	0/2450
13	H	0.29	0/1507	0.56	0/2029
14	I	0.28	0/1067	0.61	1/1433 (0.1%)
15	J	0.27	0/1365	0.66	1/1831 (0.1%)
16	K	0.29	0/2125	0.60	1/2862 (0.0%)
17	L	0.31	0/1480	0.69	2/1986 (0.1%)
18	M	0.28	0/1055	0.58	0/1421
19	N	0.32	0/1757	0.67	0/2354
20	O	0.31	0/1585	0.60	0/2128
21	P	0.32	0/1382	0.64	0/1856
22	Q	0.29	0/1127	0.63	0/1521
23	R	0.29	0/1236	0.66	0/1650
24	S	0.31	0/1473	0.63	1/1980 (0.1%)
25	T	0.29	0/997	0.67	1/1336 (0.1%)
26	U	0.30	0/817	0.52	0/1109
27	V	0.40	0/1008	1.18	18/1356 (1.3%)
28	W	0.28	0/1910	0.57	0/2575
29	X	0.29	0/1108	0.55	0/1492
30	Y	0.28	0/995	0.59	0/1329
31	Z	0.31	0/1118	0.61	0/1497
32	a	0.29	0/751	0.55	0/1013

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	b	0.29	0/5032	0.68	9/6756 (0.1%)
34	c	0.28	0/879	0.64	1/1171 (0.1%)
35	d	0.29	0/870	0.64	0/1168
36	e	0.28	0/1041	0.60	0/1394
37	f	0.31	0/868	0.58	0/1168
38	g	0.31	0/856	0.67	0/1144
39	h	0.30	0/978	0.56	0/1301
40	i	0.28	0/749	0.65	0/995
41	j	0.31	0/680	0.68	0/901
42	k	0.30	0/618	0.61	0/826
43	l	0.29	0/435	0.63	0/577
44	m	0.30	0/3617	0.63	1/4870 (0.0%)
45	n	0.28	0/751	0.63	2/1008 (0.2%)
46	o	0.24	0/872	0.70	2/1208 (0.2%)
47	p	0.31	0/687	0.65	0/915
48	q	0.27	0/969	0.59	0/1301
49	r	0.31	0/1850	0.62	0/2472
50	s	0.27	0/467	0.69	2/609 (0.3%)
51	t	0.27	0/3447	0.54	0/4643
52	u	0.31	0/1269	0.72	3/1687 (0.2%)
53	x	0.27	0/3457	0.60	2/4691 (0.0%)
54	y	0.34	0/1864	1.11	27/2538 (1.1%)
55	z	0.26	0/650	0.60	0/854
56	v	0.27	0/17970	0.50	2/25013 (0.0%)
57	0	0.44	0/3312	0.71	4/4487 (0.1%)
57	w	0.41	0/3187	0.70	2/4316 (0.0%)
58	6	0.41	0/4443	0.67	4/6029 (0.1%)
58	7	0.40	0/4472	0.65	2/6067 (0.0%)
All	All	0.33	5/190784 (0.0%)	0.76	185/274472 (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
4	4	0	4
5	5	0	3
6	A	0	4
7	B	0	3
9	D	0	3
10	E	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
11	F	0	2
12	G	0	2
13	H	0	1
14	I	0	1
15	J	0	3
16	K	0	3
17	L	0	1
18	M	0	1
24	S	0	4
25	T	0	4
27	V	0	7
28	W	0	1
30	Y	0	1
31	Z	0	2
33	b	0	11
34	c	0	1
40	i	0	1
42	k	0	2
44	m	0	1
45	n	0	1
46	o	0	6
47	p	0	1
48	q	0	2
49	r	0	1
52	u	0	1
54	y	0	5
56	v	0	14
57	0	0	1
57	w	0	1
58	6	0	2
All	All	0	102

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	3093	C	C4-C5	10.73	1.51	1.43
1	1	3093	C	N1-C2	9.40	1.49	1.40
1	1	3093	C	N3-C4	9.07	1.40	1.33
1	1	3093	C	C2-N3	8.52	1.42	1.35
1	1	2318	U	C1'-N1	5.87	1.57	1.48

The worst 5 of 185 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	3048	A	O4'-C1'-N9	12.94	118.55	108.20
1	1	3093	C	C5-C6-N1	10.67	126.34	121.00
1	1	2335	G	O4'-C1'-N9	10.03	116.22	108.20
1	1	3093	C	C6-N1-C2	-9.96	116.31	120.30
1	1	2531	C	C2-N1-C1'	9.73	129.51	118.80

There are no chirality outliers.

5 of 102 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	4	329	CYS	Mainchain
4	4	362	ARG	Peptide
4	4	461	ASP	Mainchain
4	4	463	THR	Peptide
5	5	42	THR	Mainchain

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

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

## 5.3 Torsion angles [i](#)

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

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	4	495/593 (84%)	456 (92%)	34 (7%)	5 (1%)	13	42
5	5	76/120 (63%)	71 (93%)	5 (7%)	0	100	100
6	A	243/254 (96%)	227 (93%)	16 (7%)	0	100	100
7	B	384/387 (99%)	342 (89%)	41 (11%)	1 (0%)	37	68
8	C	359/362 (99%)	336 (94%)	21 (6%)	2 (1%)	22	53
9	D	239/297 (80%)	218 (91%)	21 (9%)	0	100	100
10	E	152/176 (86%)	148 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	F	214/244 (88%)	195 (91%)	19 (9%)	0	100	100
12	G	226/256 (88%)	209 (92%)	17 (8%)	0	100	100
13	H	185/191 (97%)	172 (93%)	13 (7%)	0	100	100
14	I	128/166 (77%)	113 (88%)	13 (10%)	2 (2%)	8	31
15	J	166/174 (95%)	145 (87%)	20 (12%)	1 (1%)	22	53
16	K	248/334 (74%)	231 (93%)	15 (6%)	2 (1%)	16	48
17	L	179/199 (90%)	165 (92%)	12 (7%)	2 (1%)	12	39
18	M	132/138 (96%)	126 (96%)	6 (4%)	0	100	100
19	N	201/204 (98%)	187 (93%)	14 (7%)	0	100	100
20	O	195/199 (98%)	194 (100%)	1 (0%)	0	100	100
21	P	167/184 (91%)	155 (93%)	12 (7%)	0	100	100
22	Q	142/186 (76%)	131 (92%)	11 (8%)	0	100	100
23	R	149/189 (79%)	142 (95%)	7 (5%)	0	100	100
24	S	169/172 (98%)	156 (92%)	10 (6%)	3 (2%)	7	29
25	T	120/160 (75%)	115 (96%)	5 (4%)	0	100	100
26	U	99/121 (82%)	95 (96%)	4 (4%)	0	100	100
27	V	132/137 (96%)	120 (91%)	10 (8%)	2 (2%)	8	33
28	W	231/236 (98%)	225 (97%)	4 (2%)	2 (1%)	14	45
29	X	138/142 (97%)	130 (94%)	8 (6%)	0	100	100
30	Y	123/127 (97%)	119 (97%)	4 (3%)	0	100	100
31	Z	133/136 (98%)	118 (89%)	15 (11%)	0	100	100
32	a	91/149 (61%)	84 (92%)	5 (6%)	2 (2%)	5	24
33	b	600/647 (93%)	538 (90%)	58 (10%)	4 (1%)	19	51
34	c	103/175 (59%)	99 (96%)	4 (4%)	0	100	100
35	d	103/113 (91%)	100 (97%)	3 (3%)	0	100	100
36	e	125/130 (96%)	122 (98%)	3 (2%)	0	100	100
37	f	104/107 (97%)	103 (99%)	1 (1%)	0	100	100
38	g	105/121 (87%)	104 (99%)	1 (1%)	0	100	100
39	h	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
40	i	94/100 (94%)	85 (90%)	8 (8%)	1 (1%)	12	39
41	j	82/88 (93%)	80 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	k	75/78 (96%)	71 (95%)	4 (5%)	0	100	100
43	l	47/51 (92%)	44 (94%)	3 (6%)	0	100	100
44	m	431/486 (89%)	390 (90%)	38 (9%)	3 (1%)	19	51
45	n	95/105 (90%)	92 (97%)	3 (3%)	0	100	100
46	o	167/217 (77%)	145 (87%)	22 (13%)	0	100	100
47	p	87/92 (95%)	84 (97%)	2 (2%)	1 (1%)	12	39
48	q	120/165 (73%)	101 (84%)	16 (13%)	3 (2%)	4	22
49	r	219/261 (84%)	197 (90%)	20 (9%)	2 (1%)	14	45
50	s	52/520 (10%)	47 (90%)	3 (6%)	2 (4%)	2	15
51	t	425/767 (55%)	399 (94%)	26 (6%)	0	100	100
52	u	146/199 (73%)	139 (95%)	7 (5%)	0	100	100
53	x	445/515 (86%)	417 (94%)	28 (6%)	0	100	100
54	y	241/245 (98%)	220 (91%)	20 (8%)	1 (0%)	30	63
55	z	73/106 (69%)	67 (92%)	6 (8%)	0	100	100
56	v	3549/4910 (72%)	3232 (91%)	313 (9%)	4 (0%)	48	79
57	0	401/555 (72%)	393 (98%)	8 (2%)	0	100	100
57	w	379/555 (68%)	375 (99%)	4 (1%)	0	100	100
58	6	535/763 (70%)	527 (98%)	8 (2%)	0	100	100
58	7	541/763 (71%)	533 (98%)	8 (2%)	0	100	100
All	All	14977/19187 (78%)	13942 (93%)	990 (7%)	45 (0%)	38	68

5 of 45 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	C	339	LEU
28	W	177	ALA
33	b	398	LEU
33	b	399	ALA
56	v	241	PRO

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	4	445/520 (86%)	425 (96%)	20 (4%)	23	53
5	5	70/106 (66%)	67 (96%)	3 (4%)	25	55
6	A	188/196 (96%)	185 (98%)	3 (2%)	58	79
7	B	322/323 (100%)	314 (98%)	8 (2%)	42	69
8	C	288/289 (100%)	284 (99%)	4 (1%)	62	81
9	D	205/245 (84%)	199 (97%)	6 (3%)	37	65
10	E	134/153 (88%)	129 (96%)	5 (4%)	29	59
11	F	183/205 (89%)	180 (98%)	3 (2%)	58	79
12	G	187/208 (90%)	179 (96%)	8 (4%)	25	55
13	H	167/171 (98%)	165 (99%)	2 (1%)	67	83
14	I	116/141 (82%)	108 (93%)	8 (7%)	13	39
15	J	146/150 (97%)	143 (98%)	3 (2%)	48	72
16	K	238/302 (79%)	232 (98%)	6 (2%)	42	69
17	L	145/159 (91%)	142 (98%)	3 (2%)	48	72
18	M	107/109 (98%)	104 (97%)	3 (3%)	38	66
19	N	175/176 (99%)	169 (97%)	6 (3%)	32	62
20	O	160/162 (99%)	156 (98%)	4 (2%)	42	69
21	P	139/146 (95%)	138 (99%)	1 (1%)	81	90
22	Q	118/151 (78%)	116 (98%)	2 (2%)	56	78
23	R	125/154 (81%)	124 (99%)	1 (1%)	79	89
24	S	155/156 (99%)	153 (99%)	2 (1%)	65	82
25	T	107/137 (78%)	100 (94%)	7 (6%)	14	41
26	U	88/107 (82%)	84 (96%)	4 (4%)	23	53
27	V	103/105 (98%)	99 (96%)	4 (4%)	27	58
28	W	210/213 (99%)	206 (98%)	4 (2%)	52	75
29	X	116/118 (98%)	115 (99%)	1 (1%)	75	88
30	Y	108/110 (98%)	104 (96%)	4 (4%)	29	59
31	Z	115/116 (99%)	112 (97%)	3 (3%)	41	68
32	a	76/119 (64%)	75 (99%)	1 (1%)	65	82
33	b	541/573 (94%)	519 (96%)	22 (4%)	26	57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	c	99/153 (65%)	99 (100%)	0	100	100
35	d	92/97 (95%)	90 (98%)	2 (2%)	47	71
36	e	109/111 (98%)	107 (98%)	2 (2%)	54	76
37	f	90/91 (99%)	88 (98%)	2 (2%)	47	71
38	g	92/103 (89%)	89 (97%)	3 (3%)	33	62
39	h	104/105 (99%)	103 (99%)	1 (1%)	73	86
40	i	78/82 (95%)	77 (99%)	1 (1%)	65	82
41	j	69/71 (97%)	67 (97%)	2 (3%)	37	65
42	k	68/69 (99%)	67 (98%)	1 (2%)	60	80
43	l	44/46 (96%)	42 (96%)	2 (4%)	23	53
44	m	388/428 (91%)	370 (95%)	18 (5%)	23	52
45	n	81/88 (92%)	81 (100%)	0	100	100
47	p	70/72 (97%)	68 (97%)	2 (3%)	37	65
48	q	105/136 (77%)	102 (97%)	3 (3%)	37	65
49	r	198/229 (86%)	195 (98%)	3 (2%)	60	80
50	s	50/445 (11%)	48 (96%)	2 (4%)	27	58
51	t	379/665 (57%)	372 (98%)	7 (2%)	54	76
52	u	131/180 (73%)	124 (95%)	7 (5%)	19	48
53	x	338/451 (75%)	330 (98%)	8 (2%)	44	70
54	y	209/211 (99%)	208 (100%)	1 (0%)	86	92
55	z	69/95 (73%)	64 (93%)	5 (7%)	12	38
57	0	375/497 (76%)	364 (97%)	11 (3%)	37	65
57	w	362/497 (73%)	357 (99%)	5 (1%)	62	81
58	6	503/707 (71%)	491 (98%)	12 (2%)	44	70
58	7	505/707 (71%)	500 (99%)	5 (1%)	73	86
All	All	9885/12156 (81%)	9629 (97%)	256 (3%)	42	68

5 of 256 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
57	0	183	CYS
57	0	398	LEU
22	Q	41	ASP

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Mol	Chain	Res	Type
20	O	148	LYS
58	6	179	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
34	c	61	ASN
52	u	110	ASN
34	c	64	ASN
43	l	20	ASN
53	x	424	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3010/3396 (88%)	598 (19%)	26 (0%)
2	2	152/158 (96%)	27 (17%)	1 (0%)
3	3	115/121 (95%)	19 (16%)	1 (0%)
All	All	3277/3675 (89%)	644 (19%)	28 (0%)

5 of 644 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	13	A
1	1	14	U
1	1	18	G
1	1	26	A
1	1	30	G

5 of 28 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	2318	U
3	3	52	G
1	1	2444	C
1	1	3042	U
1	1	2339	C

## 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 8 ligands modelled in this entry, 6 are monoatomic - leaving 2 for Mogul analysis.

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	$\# Z  > 2$
60	GTP	m	501	61	26,34,34	1.14	1 (3%)	32,54,54	1.59	7 (21%)
60	GTP	b	701	61,33	26,34,34	1.14	2 (7%)	32,54,54	1.70	7 (21%)

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
60	GTP	m	501	61	-	6/18/38/38	0/3/3/3
60	GTP	b	701	61,33	-	2/18/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	b	701	GTP	C5-C6	-4.09	1.39	1.47
60	m	501	GTP	C5-C6	-4.06	1.39	1.47
60	b	701	GTP	C2-N3	2.28	1.38	1.33

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	b	701	GTP	PA-O3A-PB	-4.29	118.11	132.83
60	m	501	GTP	PA-O3A-PB	-3.93	119.34	132.83
60	m	501	GTP	PB-O3B-PG	-3.63	120.36	132.83
60	b	701	GTP	PB-O3B-PG	-3.53	120.70	132.83
60	b	701	GTP	C5-C6-N1	3.37	119.91	113.95

There are no chirality outliers.

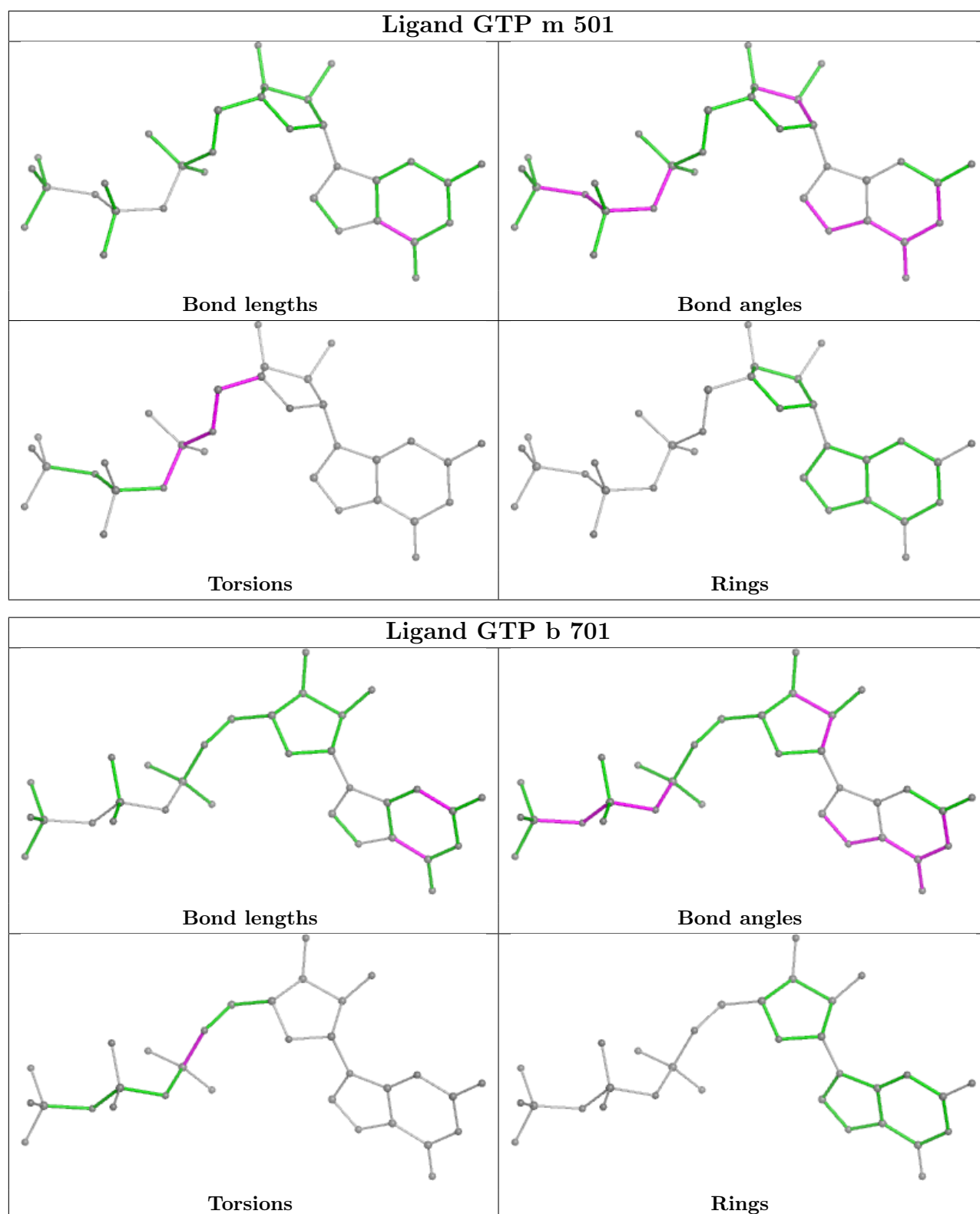
5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
60	b	701	GTP	C5'-O5'-PA-O1A
60	m	501	GTP	C5'-O5'-PA-O3A
60	m	501	GTP	C5'-O5'-PA-O2A
60	m	501	GTP	O4'-C4'-C5'-O5'
60	m	501	GTP	C4'-C5'-O5'-PA

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 5.7 Other polymers ⓘ

There are no such residues in this entry.



## 5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
56	v	3
1	1	3

The worst 5 of 6 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	v	3595:LEU	C	3599:ARG	N	4.97
1	1	3167:A	O3'	3168:A	P	4.92
1	v	3575:LEU	C	3579:VAL	N	3.43
1	v	3587:MET	C	3591:ARG	N	3.23
1	1	1012:G	O3'	1013:G	P	3.13

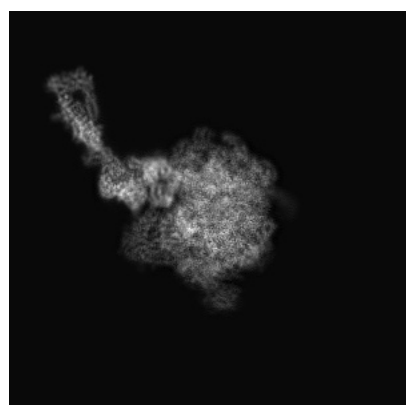
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10839. These allow visual inspection of the internal detail of the map and identification of artifacts.

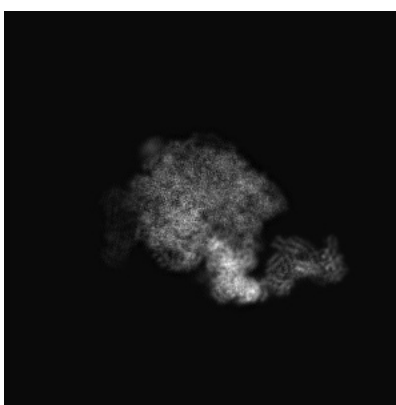
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

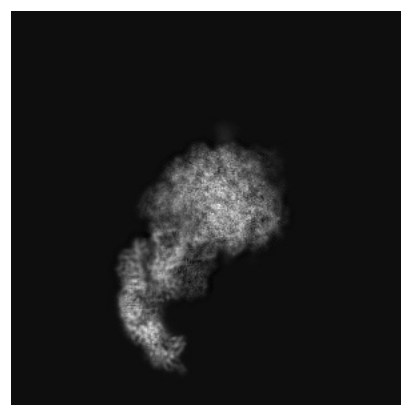
#### 6.1.1 Primary map



X



Y

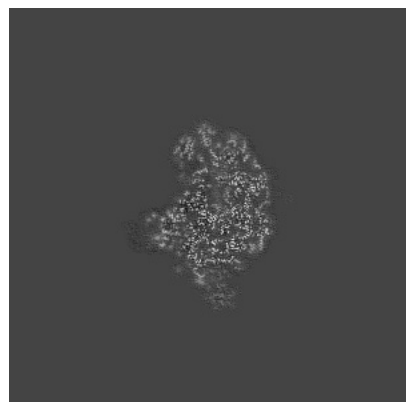


Z

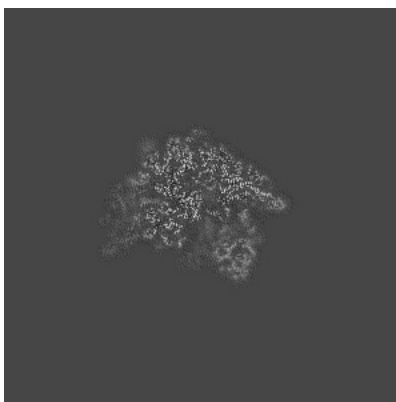
The images above show the map projected in three orthogonal directions.

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

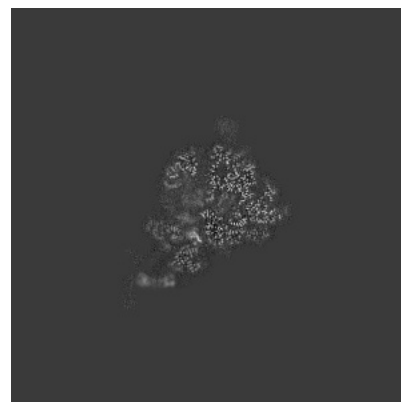
#### 6.2.1 Primary map



X Index: 300



Y Index: 300



Z Index: 300

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

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

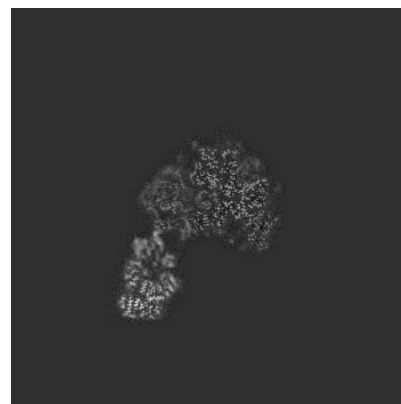
### 6.3.1 Primary map



X Index: 219



Y Index: 303

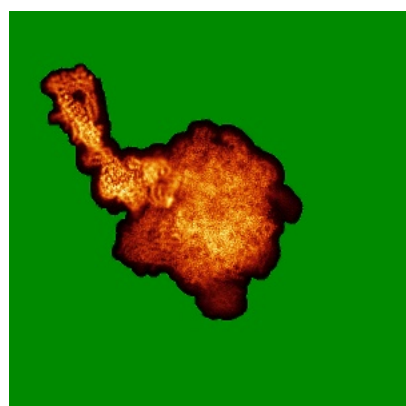


Z Index: 336

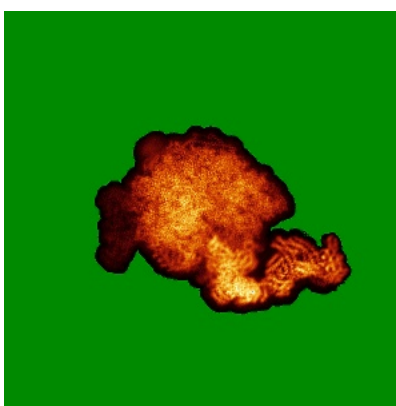
The images above show the largest variance slices of the map in three orthogonal directions.

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

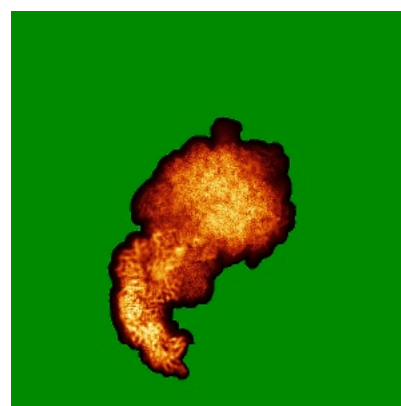
### 6.4.1 Primary map



X



Y

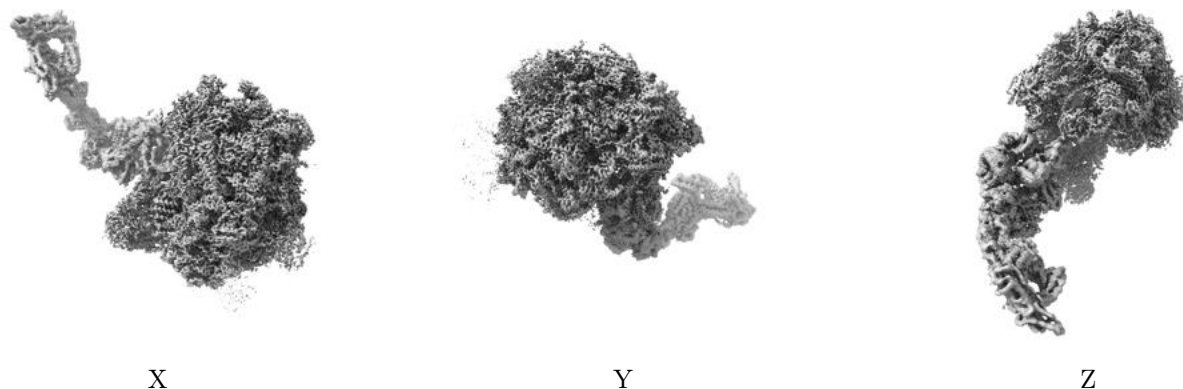


Z

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

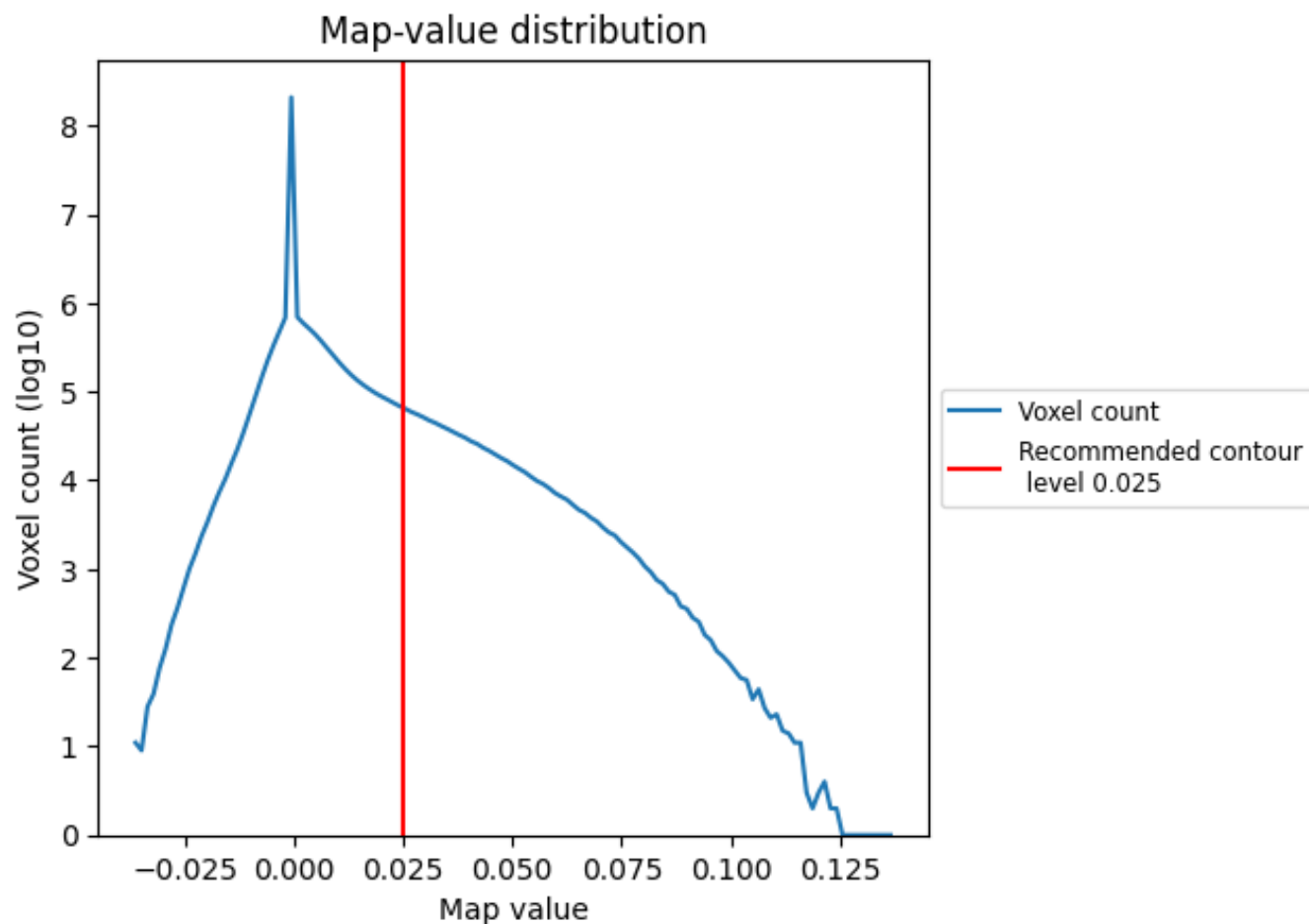
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

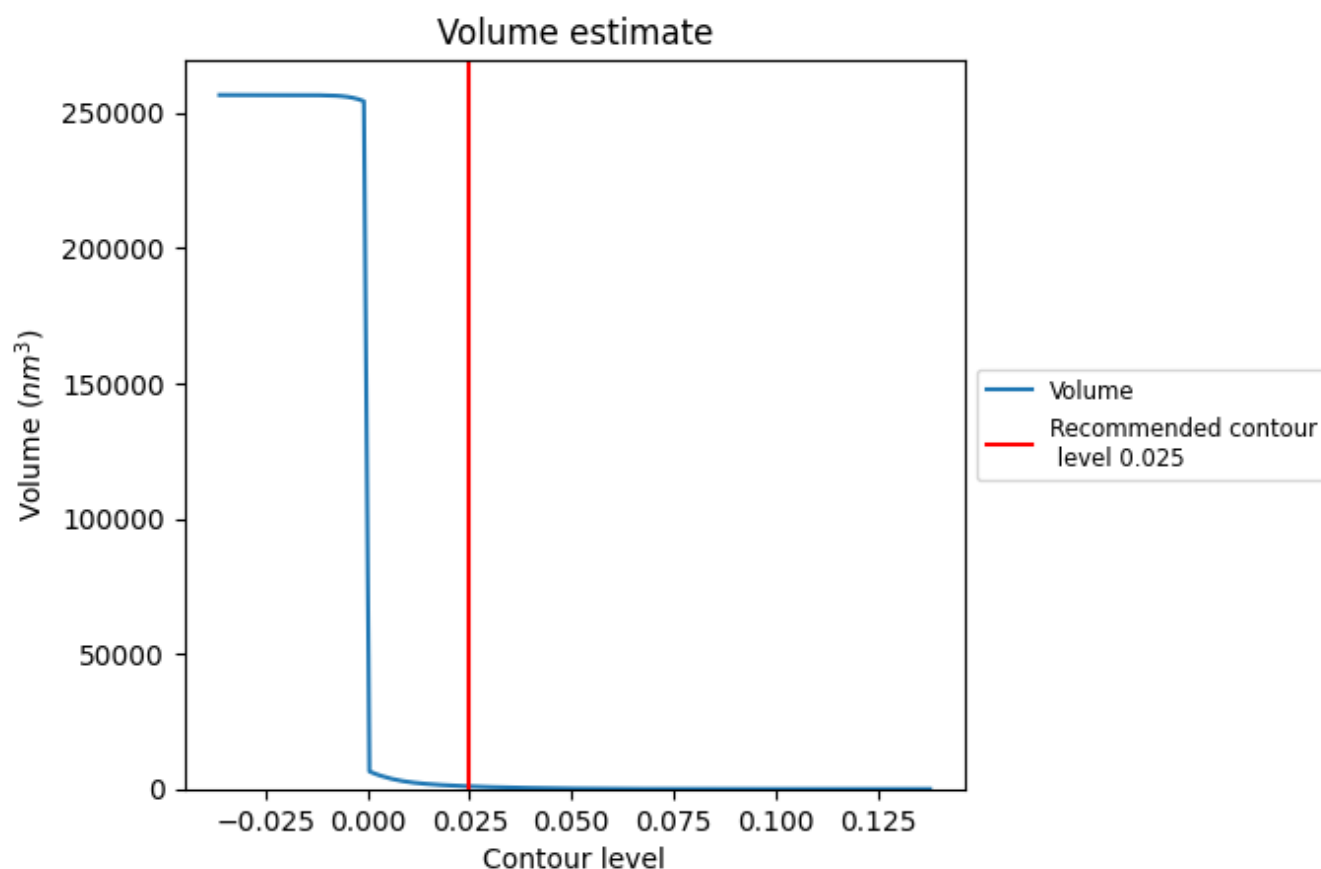
This section contains the results of statistical analysis of the map.

### 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.

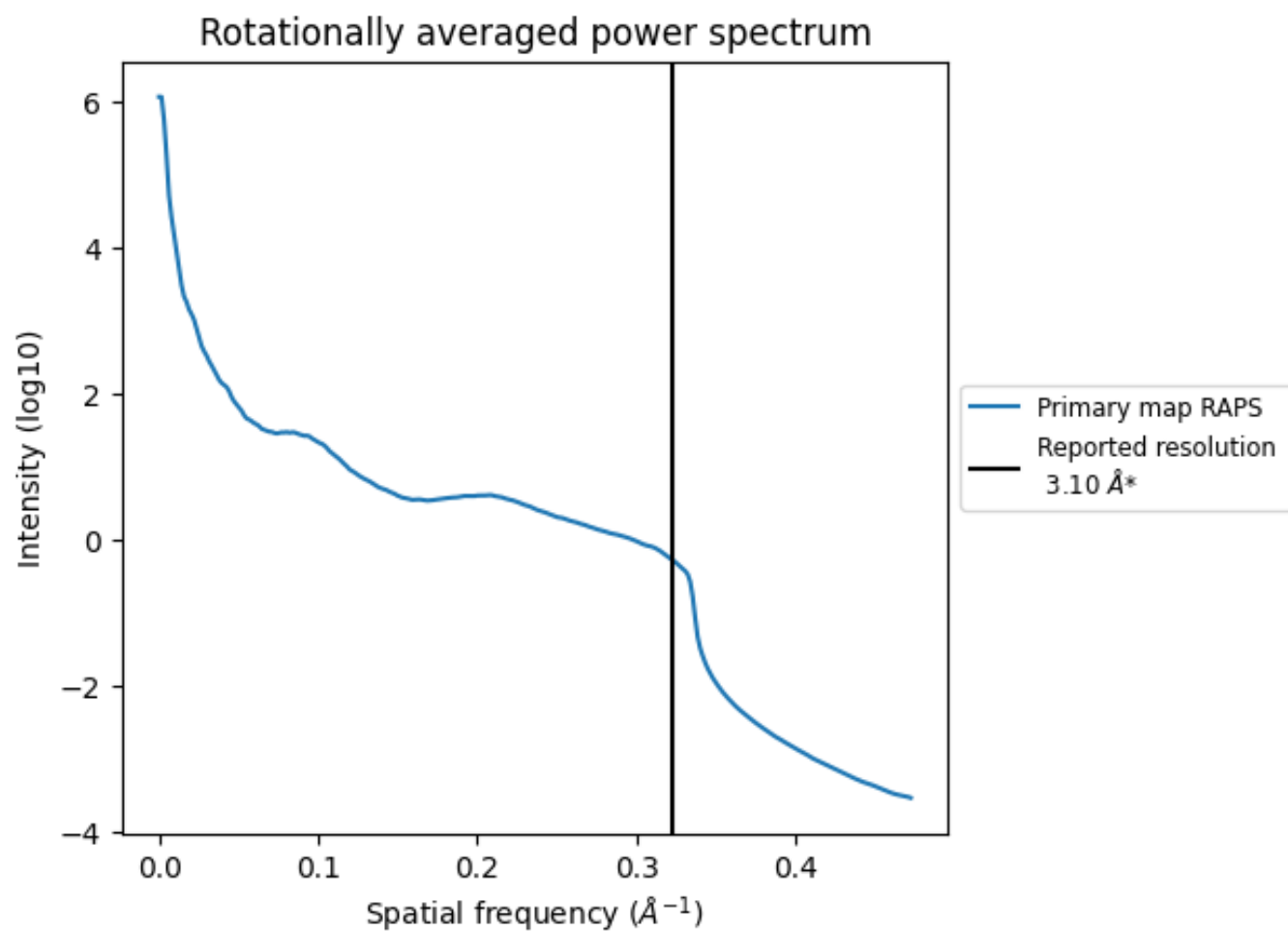
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 970  $\text{nm}^3$ ; this corresponds to an approximate mass of 876 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 0.323 Å<sup>-1</sup>

## 8 Fourier-Shell correlation

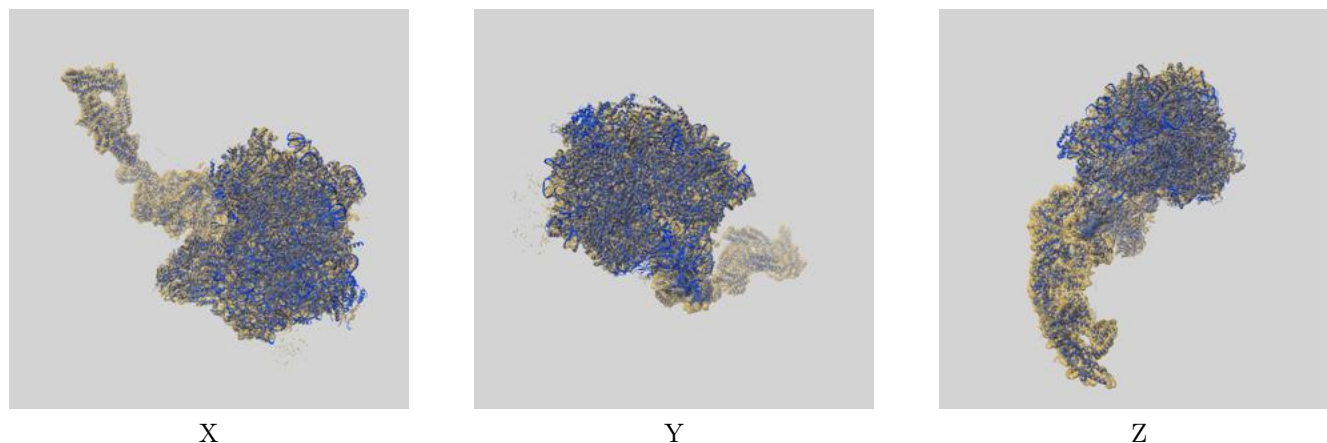
This section was not generated. No FSC curve or half-maps provided.



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

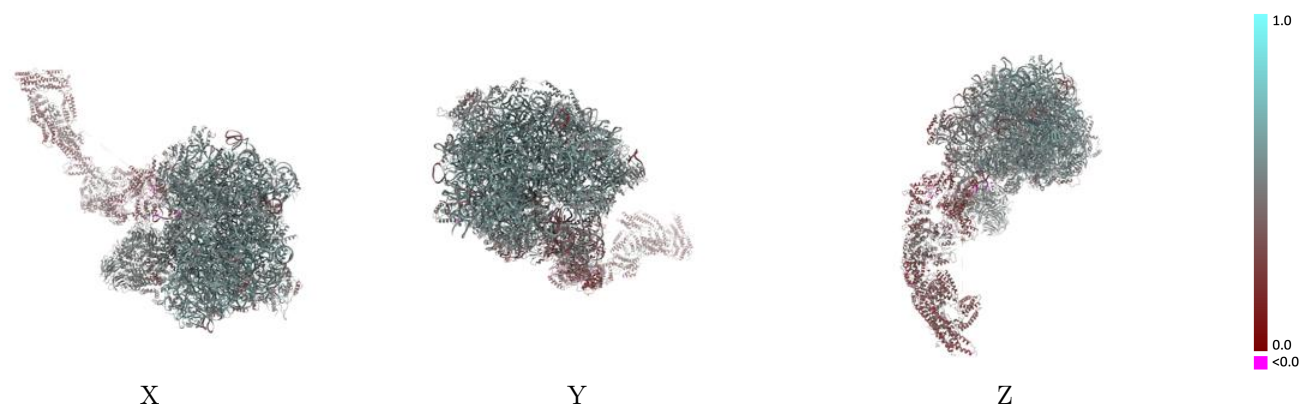
This section contains information regarding the fit between EMDB map EMD-10839 and PDB model 6YLH. Per-residue inclusion information can be found in section 3 on page 16.

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



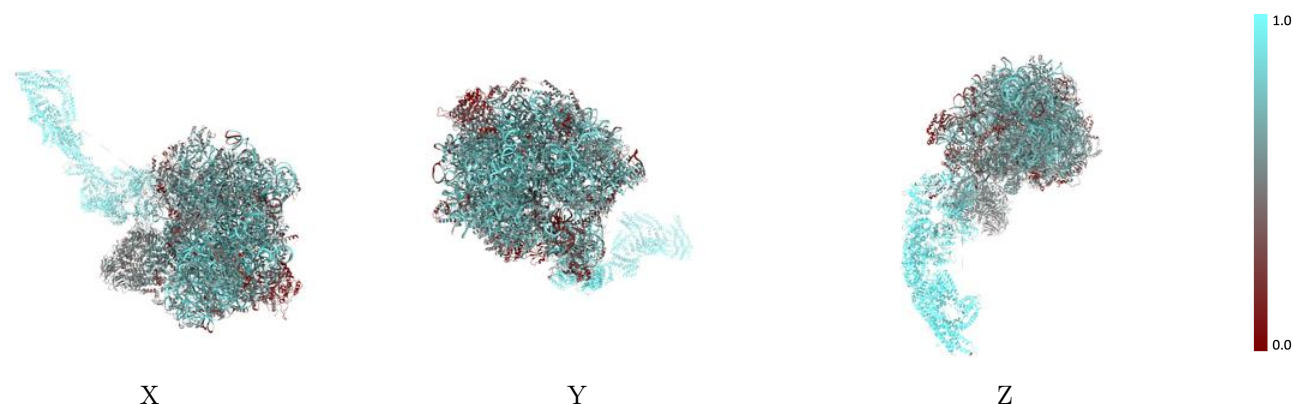
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



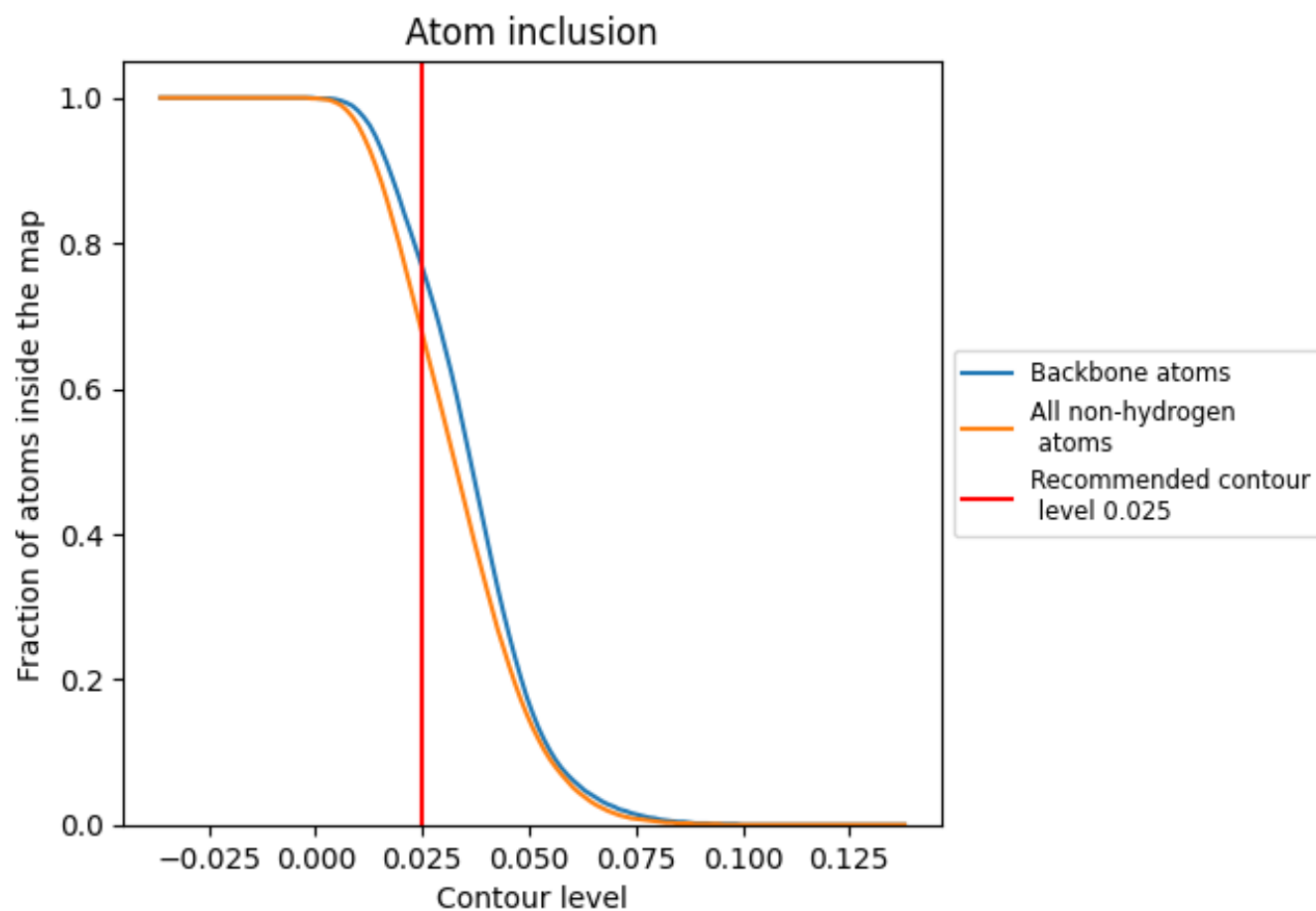
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.025).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 68% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6770	 0.5120
0	 0.5160	 0.4940
1	 0.7870	 0.5480
2	 0.8580	 0.5820
3	 0.6800	 0.4900
4	 0.2700	 0.4940
5	 0.3130	 0.4510
6	 0.4990	 0.4750
7	 0.4880	 0.4760
A	 0.7320	 0.5940
B	 0.6650	 0.5690
C	 0.6460	 0.5630
D	 0.2140	 0.4160
E	 0.5640	 0.5370
F	 0.6510	 0.5490
G	 0.5850	 0.5290
H	 0.6260	 0.5570
I	 0.4290	 0.5260
J	 0.4950	 0.4410
K	 0.5600	 0.4690
L	 0.6300	 0.5460
M	 0.6000	 0.5500
N	 0.7280	 0.5850
O	 0.6880	 0.5710
P	 0.6820	 0.5740
Q	 0.6140	 0.5490
R	 0.6600	 0.5570
S	 0.5720	 0.5370
T	 0.2310	 0.4690
U	 0.5570	 0.5320
V	 0.6040	 0.5070
W	 0.5160	 0.5000
X	 0.5850	 0.5660
Y	 0.6450	 0.5640
Z	 0.6320	 0.5360



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Chain	Atom inclusion	Q-score
a	 0.6440	 0.5570
b	 0.4750	 0.5120
c	 0.3450	 0.5350
d	 0.6370	 0.5660
e	 0.6450	 0.5770
f	 0.7080	 0.5950
g	 0.6760	 0.5700
h	 0.6550	 0.5610
i	 0.5980	 0.5390
j	 0.7640	 0.5940
k	 0.5040	 0.5280
l	 0.7220	 0.5970
m	 0.6000	 0.5450
n	 0.5900	 0.5340
o	 0.0800	 0.3960
p	 0.6690	 0.5750
q	 0.3760	 0.4680
r	 0.6470	 0.5650
s	 0.2710	 0.5010
t	 0.5640	 0.4930
u	 0.5940	 0.5420
v	 0.9180	 0.3230
w	 0.4490	 0.4900
x	 0.5710	 0.4990
y	 0.5480	 0.5020
z	 0.4430	 0.5340