wwPDB EM Validation Summary Report ⓘ

Nov 21, 2022 – 03:08 PM EST

PDB ID	:	8EUG
EMDB ID	:	EMD-24412
Title	:	Ytm1 associated nascent 60S ribosome State 3
Authors	:	Zhou, X.; Bilokapic, S.; Deshmukh, A.A.; Halic, M.
Deposited on	:	2022-10-18
Resolution	:	2.80 Å(reported)

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

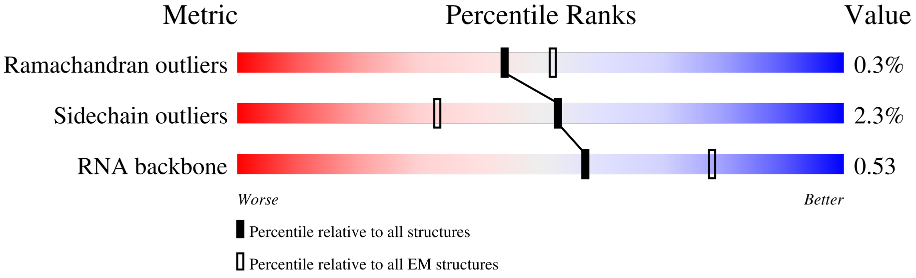
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance ⓘ

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

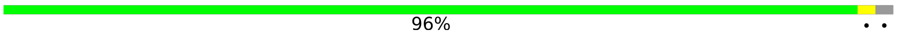
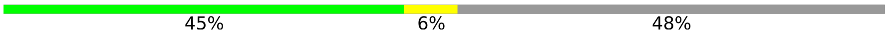
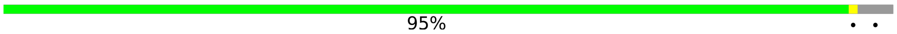
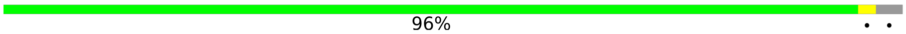
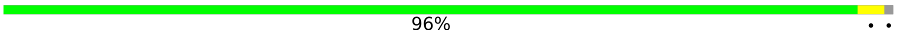
The reported resolution of this entry is 2.80 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	3498	
2	2	165	
3	3	302	
4	8	51	
5	9	229	
6	A	253	
7	B	388	
8	C	363	

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Mol	Chain	Length	Quality of chain
9	D	294	• 97% • •
10	E	195	85% • 12%
11	F	250	84% • 14%
12	G	259	• 87% • 11%
13	H	190	• 92% • 6%
14	I	221	• 76% • 23%
15	J	174	• 89% • 10%
16	K	94	93% • •
17	L	208	95% • •
18	M	134	93% • 7%
19	N	201	98% •
20	O	197	98% • •
21	P	187	• 88% • 9%
22	Q	187	96% • •
23	R	193	• 75% • 23%
24	S	176	93% • 5%
25	T	160	• 98% • •
26	U	117	• 80% • 16%
27	V	139	96% • •
28	X	141	83% • 15%
29	Y	126	95% • •
30	Z	136	• 96% • •
31	a	148	99% • •
32	b	61	89% 11%
33	c	117	• 76% 5% 19%

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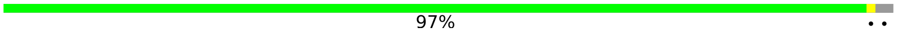
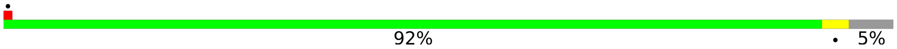
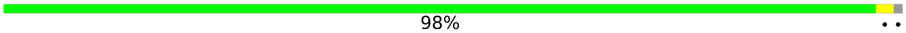
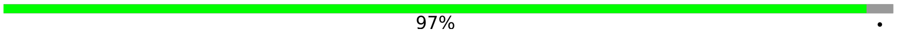
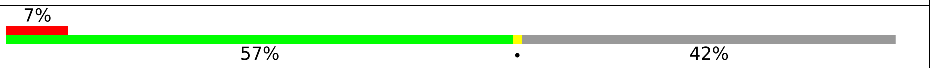
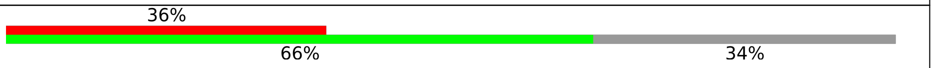
Mol	Chain	Length	Quality of chain
34	d	113	
35	e	127	
36	f	108	
37	g	112	
38	h	122	
39	i	99	
40	j	91	
41	k	74	
42	m	740	
43	n	607	
44	o	106	
45	p	440	
46	u	192	

2 Entry composition (i)

There are 47 unique types of molecules in this entry. The entry contains 123162 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 RNA (2863-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	2869	61386	27430	11112	19975	2869	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	1746	C	U	conflict	GB 157310483
1	2185	U	C	conflict	GB 157310483

- Molecule 2 is a RNA chain called RNA (152-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	151	3211	1437	569	1054	151	0	0

- Molecule 3 is a protein called Protein mak16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	3	119	1006	637	188	175	6	0	0

- Molecule 4 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	8	50	437	273	98	65	1	0	0

- Molecule 5 is a RNA chain called RNA (118-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	9	118	2519	1124	452	825	118	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	A	244	1847	1152	370	320	5	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	B	377	3003	1901	567	525	10	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	C	359	2795	1765	536	491	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	D	287	2305	1457	409	435	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	E	172	1338	860	245	230	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	F	214	1745	1124	320	298	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	G	230	1817	1161	334	319	3	1	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	H	178	Total	C	N	O	S	0	0
			1415	892	260	257	6		

- Molecule 14 is a protein called 60S ribosomal protein L10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	I	170	Total	C	N	O	S	0	0
			1372	869	256	242	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	157	Total	C	N	O	S	0	0
			1276	806	242	223	5		

- Molecule 16 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	90	Total	C	N	O	S	0	0
			695	428	144	117	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	202	Total	C	N	O	S	0	0
			1612	1008	321	282	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	125	Total	C	N	O	S	0	0
			1007	644	191	168	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	200	Total	C	N	O	S	0	0
			1676	1050	348	275	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	O	196	1557	999	297	257	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	P	171	1357	857	262	235	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	Q	186	1486	933	300	252	1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	R	148	1220	759	259	197	5	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	S	167	1388	896	259	228	5	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	T	158	1282	807	247	225	3	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
26	U	98	791	513	137	141	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	V	137	1026	644	193	181	8	0	0

- Molecule 28 is a protein called 60S ribosomal protein L25-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	X	120	962	614	178	169	1	0	0

- Molecule 29 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	Y	125	998	622	201	173	2	0	0

- Molecule 30 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	Z	134	1072	693	199	178	2	0	0

- Molecule 31 is a protein called 60S ribosomal protein L28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	a	147	1169	740	235	192	2	0	0

- Molecule 32 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
32	b	54	463	281	106	76	0	0

- Molecule 33 is a protein called 60S ribosomal protein L30-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	c	95	714	454	124	132	4	0	0

- Molecule 34 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d	102	Total	C	N	O	S	0	0
			849	534	165	147	3		

- Molecule 35 is a protein called 60S ribosomal protein L32-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	117	Total	C	N	O	S	0	0
			939	588	190	156	5		

- Molecule 36 is a protein called 60S ribosomal protein L33-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	f	106	Total	C	N	O	S	0	0
			839	534	162	140	3		

- Molecule 37 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g	106	Total	C	N	O	S	0	0
			861	540	177	142	2		

- Molecule 38 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	h	121	Total	C	N	O	0	0
			999	629	194	176		

- Molecule 39 is a protein called 60S ribosomal protein L36-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	96	Total	C	N	O	S	0	0
			767	478	160	128	1		

- Molecule 40 is a protein called 60S ribosomal protein L37-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	83	Total	C	N	O	S	0	0
			657	402	141	107	7		

- Molecule 41 is a protein called 60S ribosomal protein L38-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	k	69	560	355	103	101	1	0	0

- Molecule 42 is a protein called Ribosome biogenesis protein erb1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	m	398	3127	2001	557	558	11	0	0

- Molecule 43 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	n	354	2903	1892	496	503	12	0	0

- Molecule 44 is a protein called 60S ribosomal protein L42.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	o	97	789	498	158	128	5	0	0

- Molecule 45 is a protein called Ribosome biogenesis protein ytm1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
45	p	290	1431	851	290	290	0	0

- Molecule 46 is a protein called Ribosome biogenesis protein rlp24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	u	59	493	315	100	72	6	0	0

- Molecule 47 is ZINC ION (three-letter code: ZN) (formula: Zn).

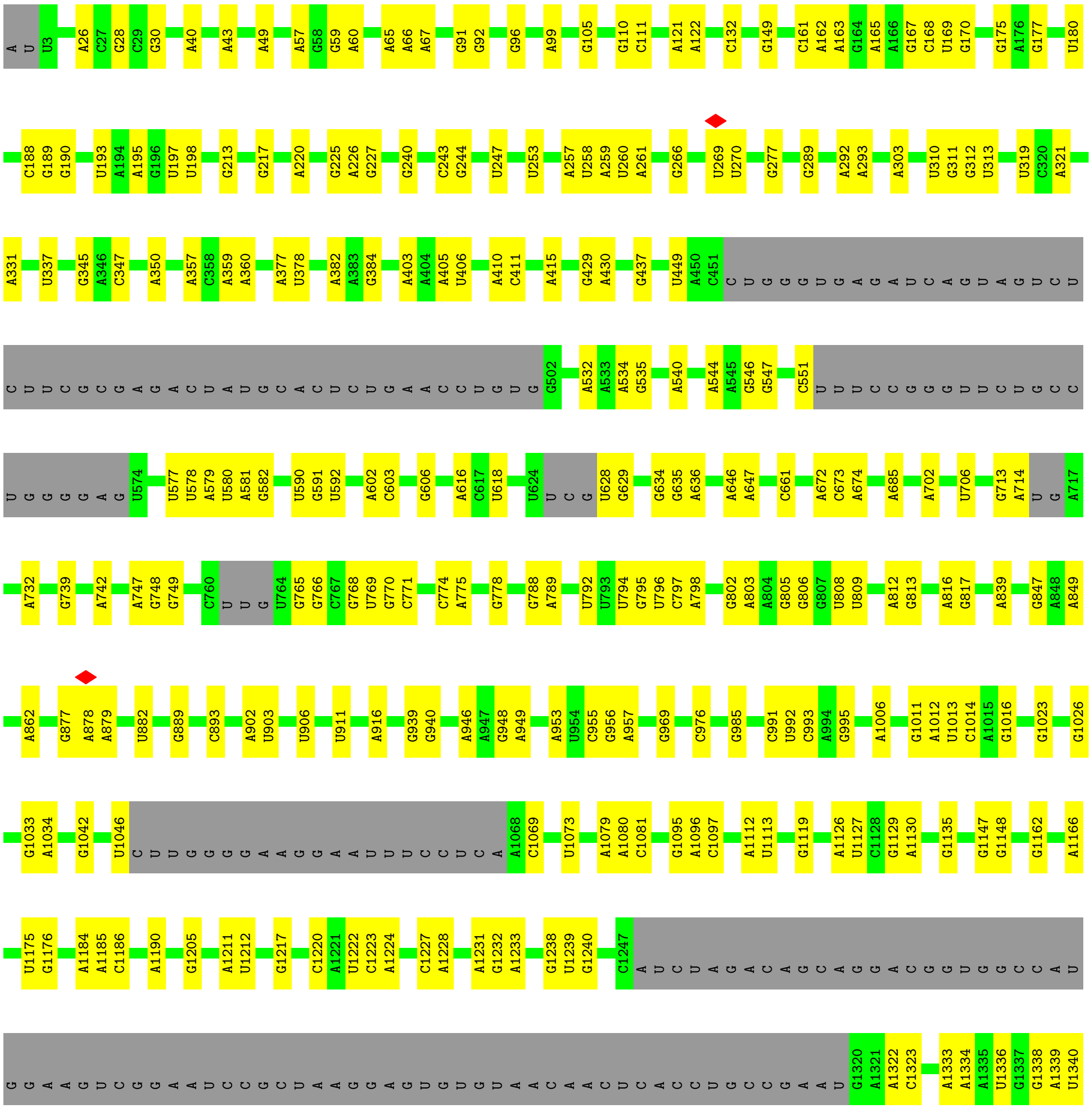
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
47	j	1	1	1	0

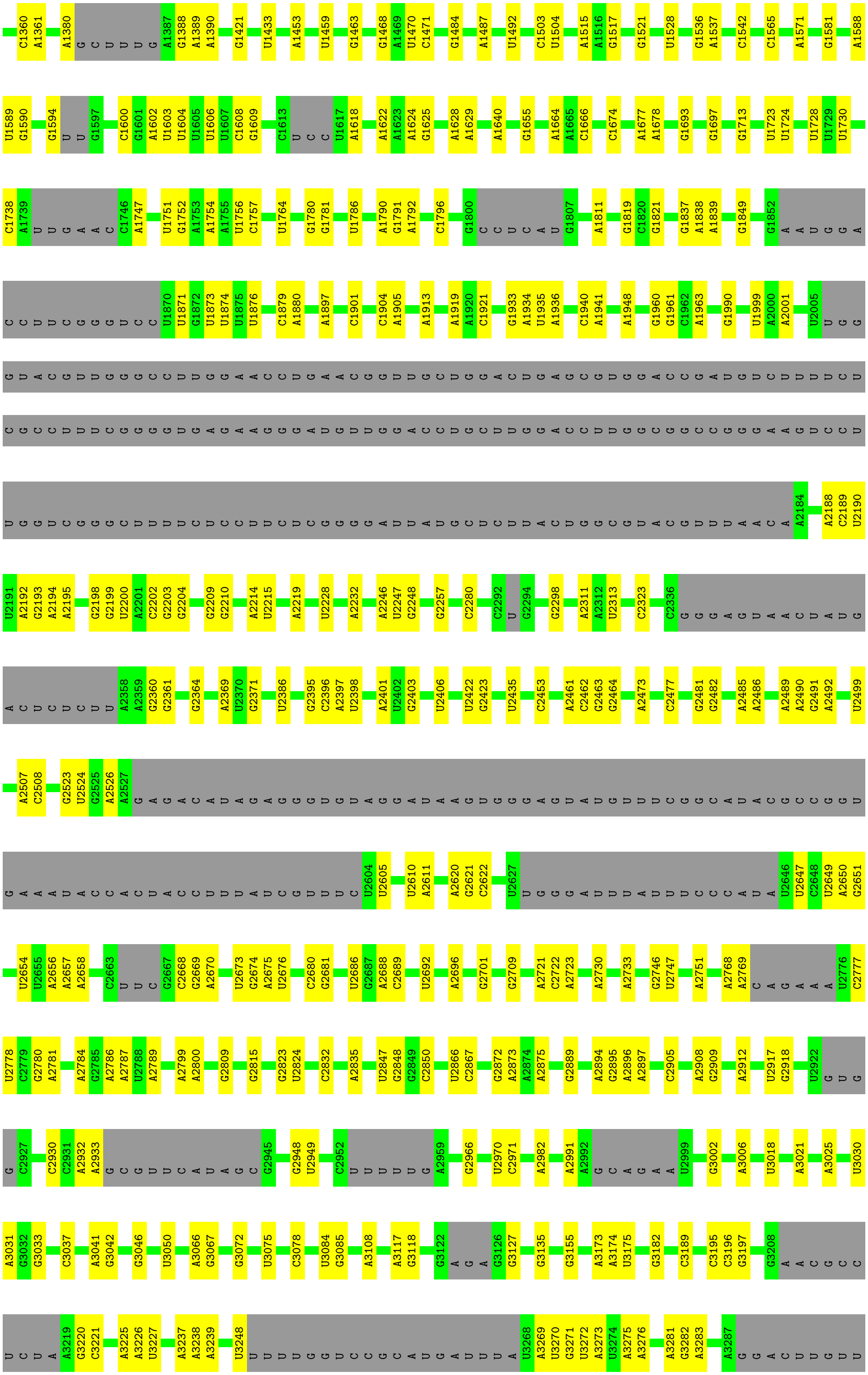
3 Residue-property plots ⓘ

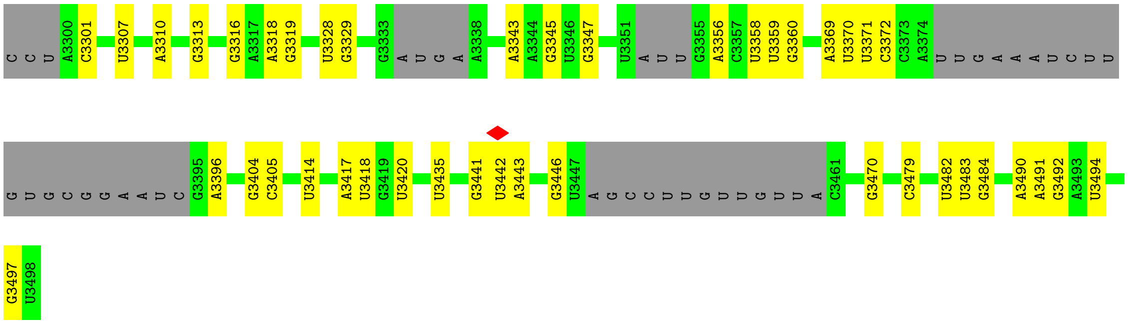
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: RNA (2863-MER)

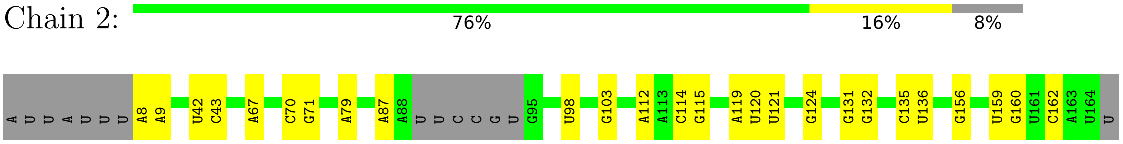
Chain 1:



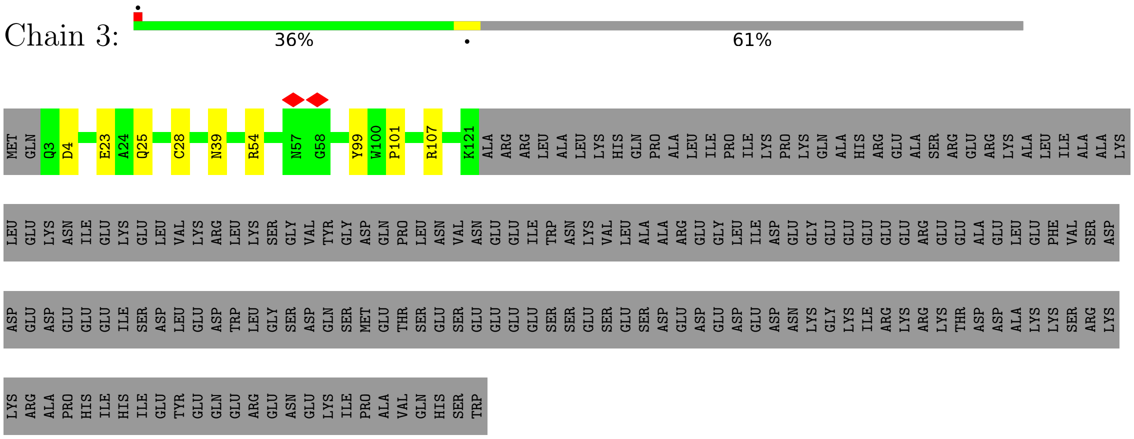

C1360 A1361 A1380 G C U U U G A1387 G1388 A1389 A1390 G1421 U1433 A1453 U1459 G1463 G1468 A1469 U1470 C1471 G1484 A1487 U1492 C1503 U1504 A1515 A1516 G1517 G1521 U1528 G1536 A1537 C1542 C1565 A1571 G1581 A1588
U1589 G1590 G1594 U U G1597 C1600 G1601 A1602 U1603 U1604 U1605 U1606 U1607 C1608 G1609 C1613 U C C U1617 A1618 A1622 A1623 A1624 G1625 A1628 A1629 A1640 G1655 A1664 A1665 C1666 C1674 A1677 A1678 G1693 G1697 G1713 U1723 U1724 U1728 U1729 U1730
C1738 A1739 U U G A A C C1746 A1747 U1751 G1752 A1753 A1754 A1755 U1756 C1757 U1764 G1780 G1781 U1786 A1790 G1791 A1792 C1796 G1800 C C U C A U G1807 A1811 G1819 C1820 G1821 G1837 A1838 A1839 G1849 G1852 A A U G G A
C C U U C G G G U C C U1870 U1871 G1872 U1873 U1874 U1875 U1876 C1879 A1880 A1897 C1901 C1904 A1905 A1913 A1919 A1920 C1921 G1933 A1934 U1935 A1936 C1940 A1941 A1948 G1960 G1961 C1962 A1963 G1990 U1999 A2000 A2001 U2005 U G G
G U A C G U U G G G C C U U G G A A C C U G A A C G G U U G C U G G A C U G A G C G U G G A C C G A U G U C U U U U C U
C G C C U U U C G G G G G U G A G A A G G G A U G U U G G G A C C U G G C U U G G A C C U U G G C G G C C G G G A A G U C C U
U G G U C G G G C U U U U C U C C C U U C U C C G G G G A U U A U G C U C U U A C U U G G C G U A C G U U U A A C A A2184 A2188 C2189 U2190
U2191 A2192 G2193 A2194 A2195 G2198 G2199 U2200 A2201 C2202 G2203 G2204 G2209 G2210 A2214 U2215 A2219 U2228 A2232 A2246 U2247 G2248 G2257 C2280 C2292 U G2294 G2298 A2311 A2312 U2313 C2323 C2336 G G G A G U A A C U A U G
A C U C U C U U A2358 A2359 G2360 G2361 G2364 A2369 U2370 G2371 U2386 G2395 C2396 A2397 U2398 A2401 U2402 G2403 U2406 U2422 G2423 U2435 C2453 A2461 C2462 G2463 G2464 A2473 C2477 G2481 G2482 A2485 A2486 A2489 A2490 G2491 A2492 U2499
A2507 C2508 G2523 U2524 G2525 A2526 A2527 G A G A C A U A G A G G G U G U A G G A U A A G U G G G A G U A U G G U U U C G G G C A U A C G C C G G U
G A A A U A C C A C U A C C U U U A U C G U U U C U2604 U2605 U2610 A2611 A2620 G2621 C2622 U2627 U G G G A U U U A U U U C C C A U A U2646 U2647 C2648 U2649 A2650 G2651
U2654 U2655 A2656 A2657 A2658 C2663 U U C G2667 C2668 G2669 A2670 U2673 G2674 A2675 U2676 C2680 G2681 U2686 G2687 A2688 C2689 U2692 A2696 G2701 G2709 A2721 C2722 A2723 A2730 A2733 G2746 U2747 A2751 A2768 A2769 C A G A A A U2776 C2777
U2778 C2779 G2780 A2781 A2784 G2785 A2786 A2787 U2788 A2789 A2799 A2800 G2809 G2815 G2823 U2824 C2832 A2835 U2847 G2848 G2849 C2850 U2866 C2867 G2872 A2873 A2874 A2875 G2889 A2894 G2895 A2896 A2897 C2905 A2908 G2909 A2912 U2917 G2918 U2922 G U G
G C2927 C2930 C2931 A2932 A2933 G C G U U C A U A G C G2945 G2948 U2949 C2952 U U U U U G A2959 G2966 U2970 C2971 A2982 A2991 A2992 G C A G A A U2999 G3002 A3006 U3018 A3021 A3025 U3030
A3031 G3032 G3033 C3037 A3041 G3042 G3046 U3050 A3066 G3067 G3072 U3075 C3078 U3084 G3085 A3108 A3117 G3118 G3122 A G A G3126 C3127 G3135 G3155 A3173 A3174 U3175 G3182 C3189 C3195 C3196 G3197 G3208 A A C G C C
U C U A A3219 G3220 C3221 A3225 A3226 U3227 A3237 A3238 A3239 U3248 U U U U G G U C C G C A U U G A U U U A U3268 A3269 U3270 G3271 U3272 A3273 U3274 A3275 A3276 A3281 G3282 A3283 A3287 G G A C U U G U U



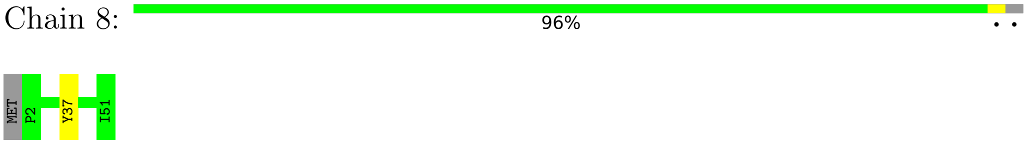
- Molecule 2: RNA (152-MER)



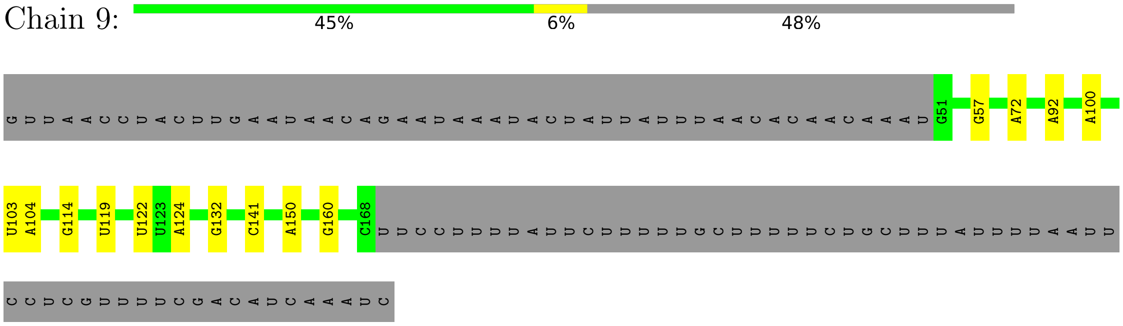
- Molecule 3: Protein mak16



- Molecule 4: 60S ribosomal protein L39

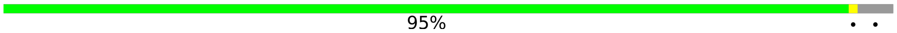


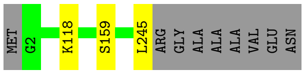
- Molecule 5: RNA (118-MER)



- Molecule 6: 60S ribosomal protein L2-A

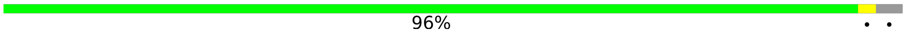
Chain A:

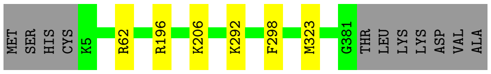




- Molecule 7: 60S ribosomal protein L3-A

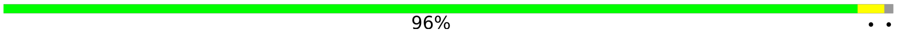
Chain B:

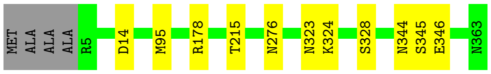




- Molecule 8: 60S ribosomal protein L4-B

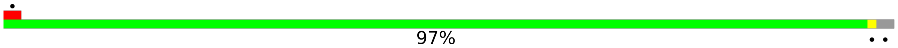
Chain C:

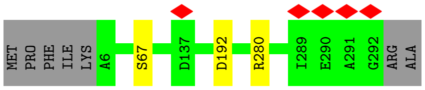




- Molecule 9: 60S ribosomal protein L5-A

Chain D:



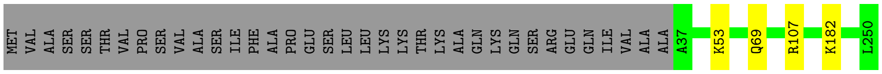


- Molecule 10: 60S ribosomal protein L6

Chain E:

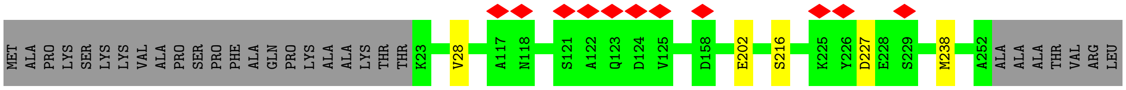
- Molecule 11: 60S ribosomal protein L7-B

Chain F:

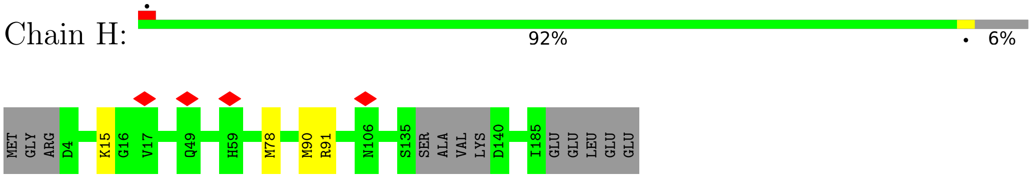


- Molecule 12: 60S ribosomal protein L8

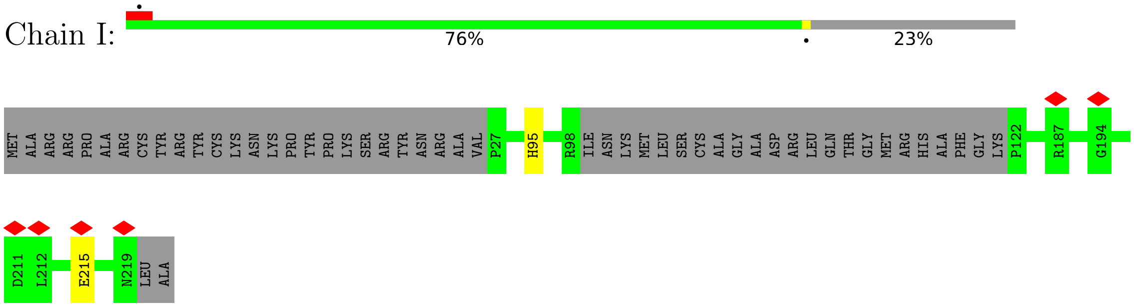
Chain G:



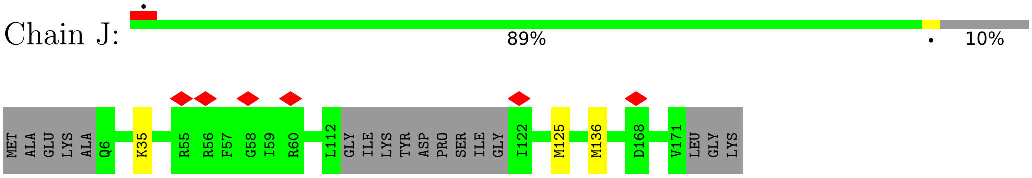
- Molecule 13: 60S ribosomal protein L9-A



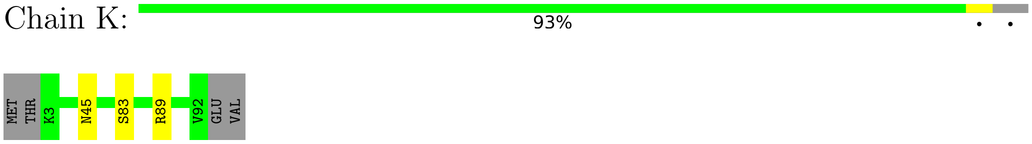
- Molecule 14: 60S ribosomal protein L10-A



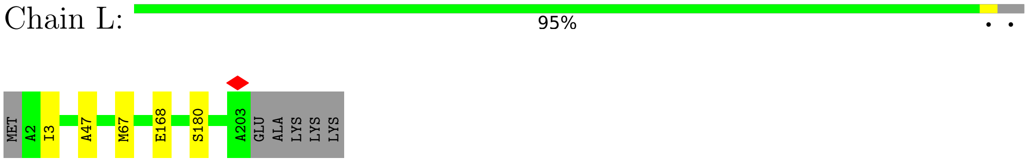
- Molecule 15: 60S ribosomal protein L11-A



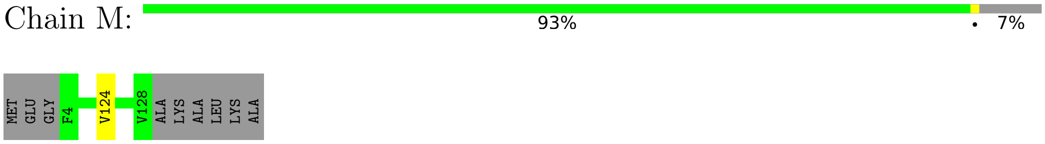
- Molecule 16: 60S ribosomal protein L43-A



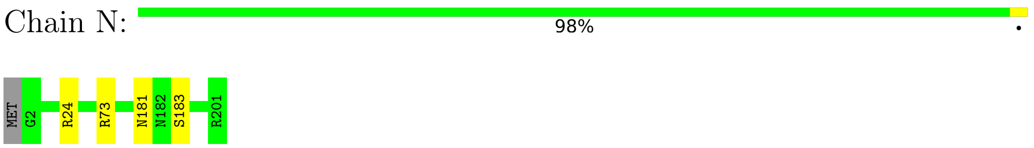
- Molecule 17: 60S ribosomal protein L13



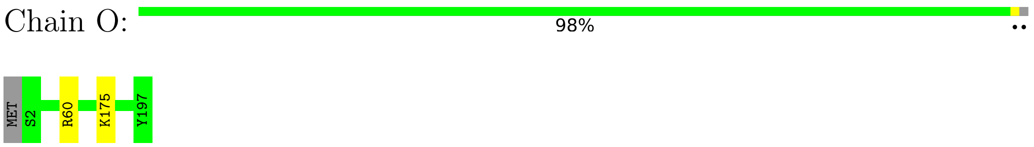
- Molecule 18: 60S ribosomal protein L14



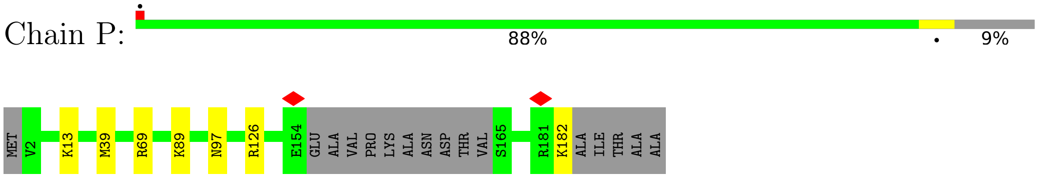
- Molecule 19: 60S ribosomal protein L15-A



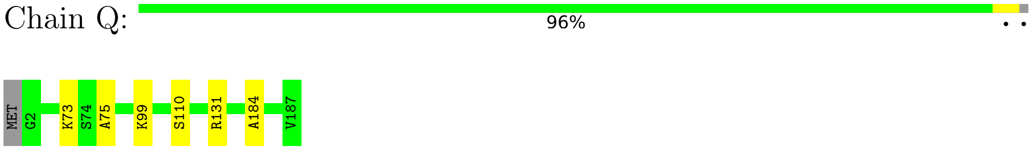
- Molecule 20: 60S ribosomal protein L16-B



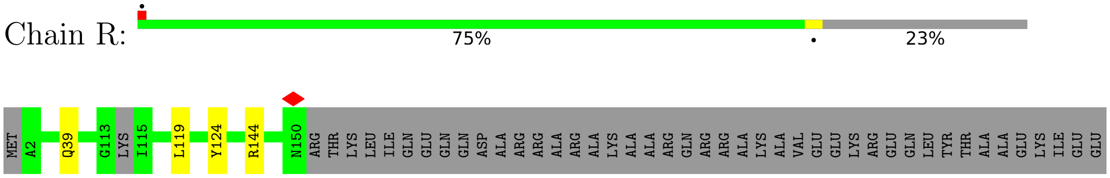
- Molecule 21: 60S ribosomal protein L17-A



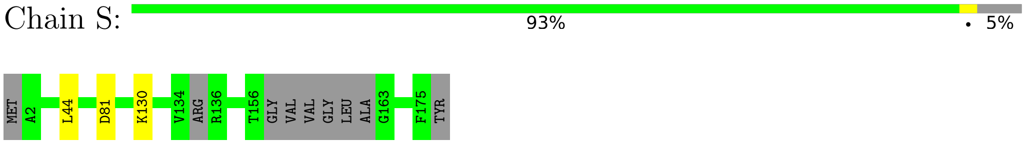
- Molecule 22: 60S ribosomal protein L18-A



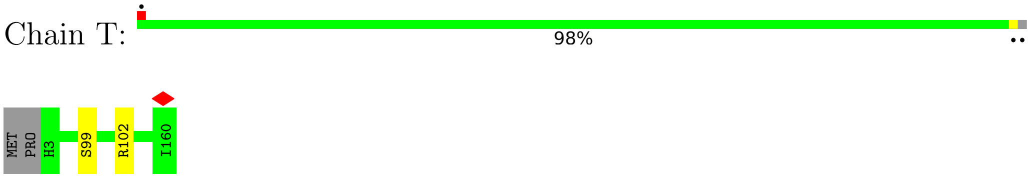
- Molecule 23: 60S ribosomal protein L19-A



- Molecule 24: 60S ribosomal protein L20-A

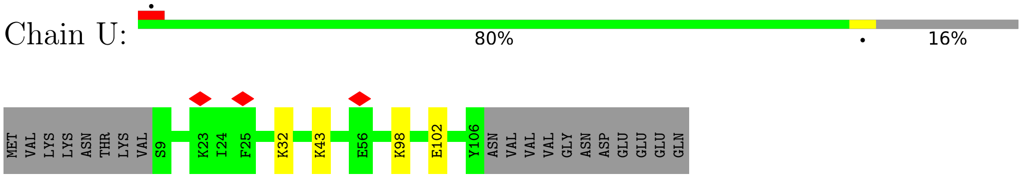


- Molecule 25: 60S ribosomal protein L21-A



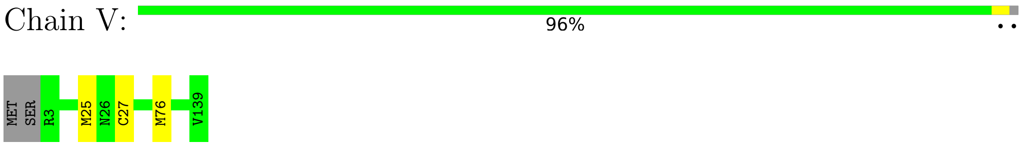
- Molecule 26: 60S ribosomal protein L22

Chain U:



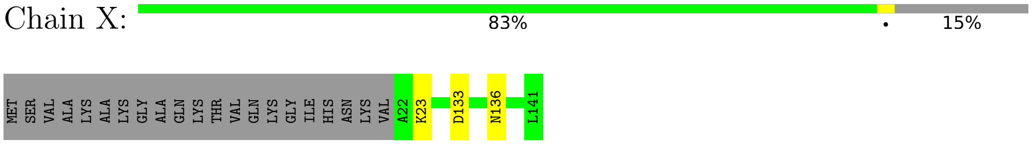
- Molecule 27: 60S ribosomal protein L23-A

Chain V:



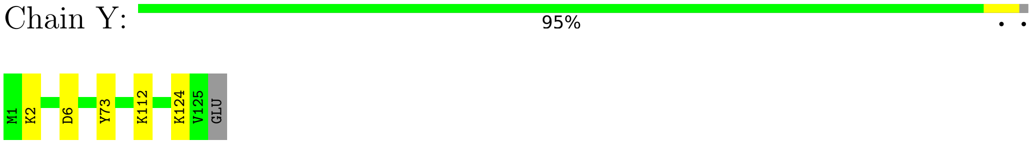
- Molecule 28: 60S ribosomal protein L25-A

Chain X:



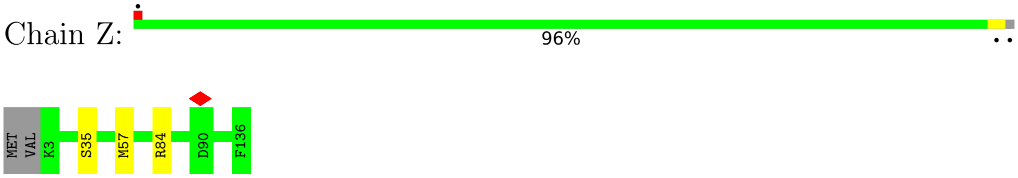
- Molecule 29: 60S ribosomal protein L26

Chain Y:



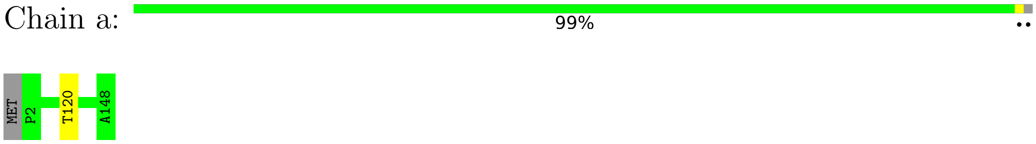
- Molecule 30: 60S ribosomal protein L27-A

Chain Z:



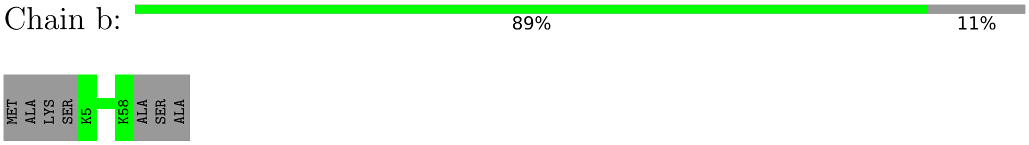
- Molecule 31: 60S ribosomal protein L28-A

Chain a:



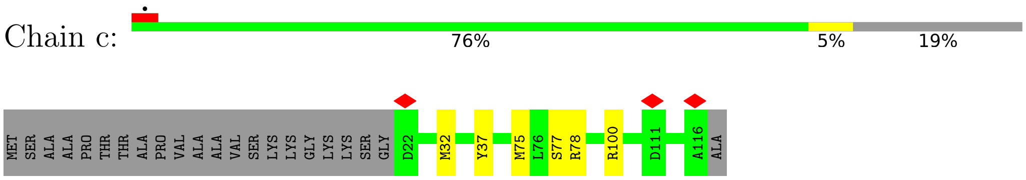
- Molecule 32: 60S ribosomal protein L29

Chain b:



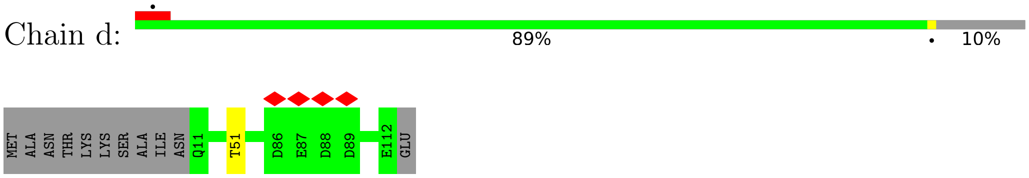
- Molecule 33: 60S ribosomal protein L30-2

Chain c:



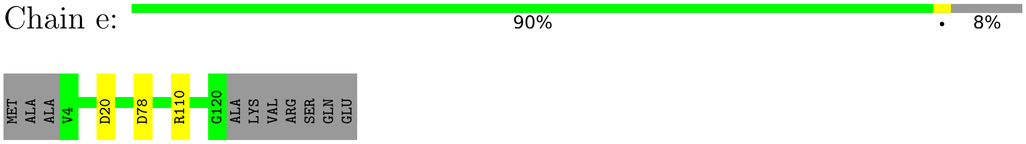
- Molecule 34: 60S ribosomal protein L31

Chain d:



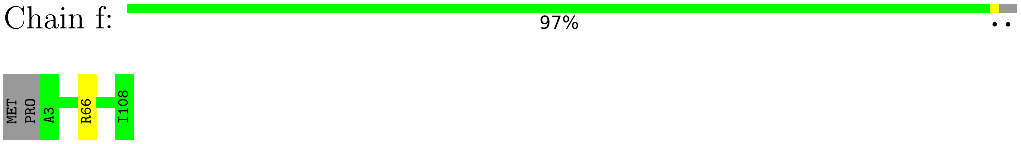
- Molecule 35: 60S ribosomal protein L32-A

Chain e:



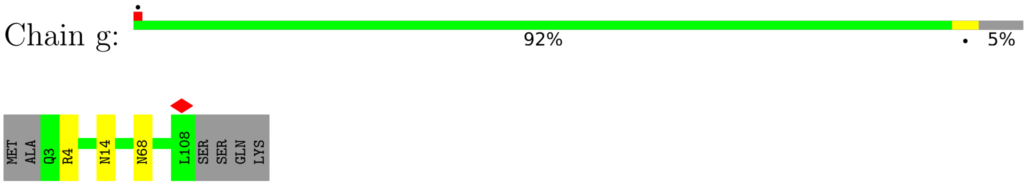
- Molecule 36: 60S ribosomal protein L33-B

Chain f:



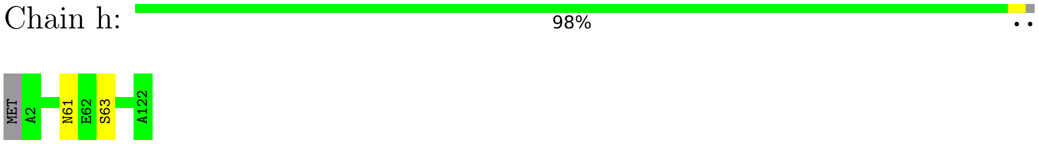
- Molecule 37: 60S ribosomal protein L34-A

Chain g:



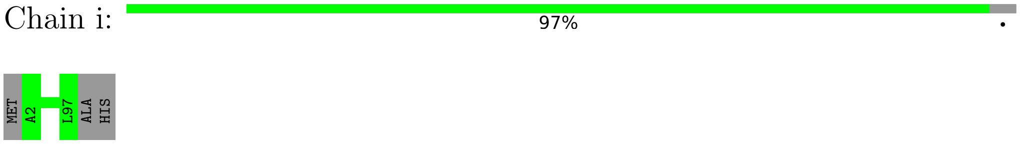
- Molecule 38: 60S ribosomal protein L35

Chain h:

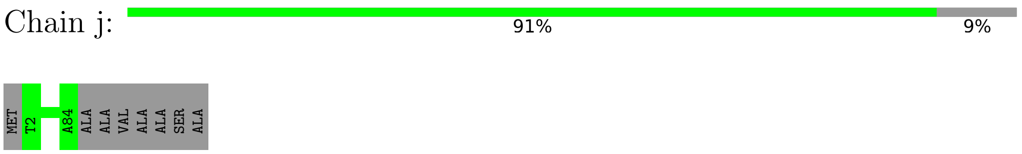


- Molecule 39: 60S ribosomal protein L36-B

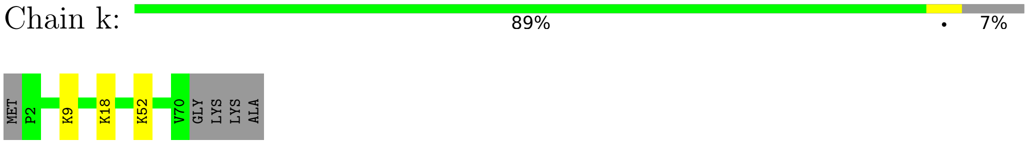
Chain i:



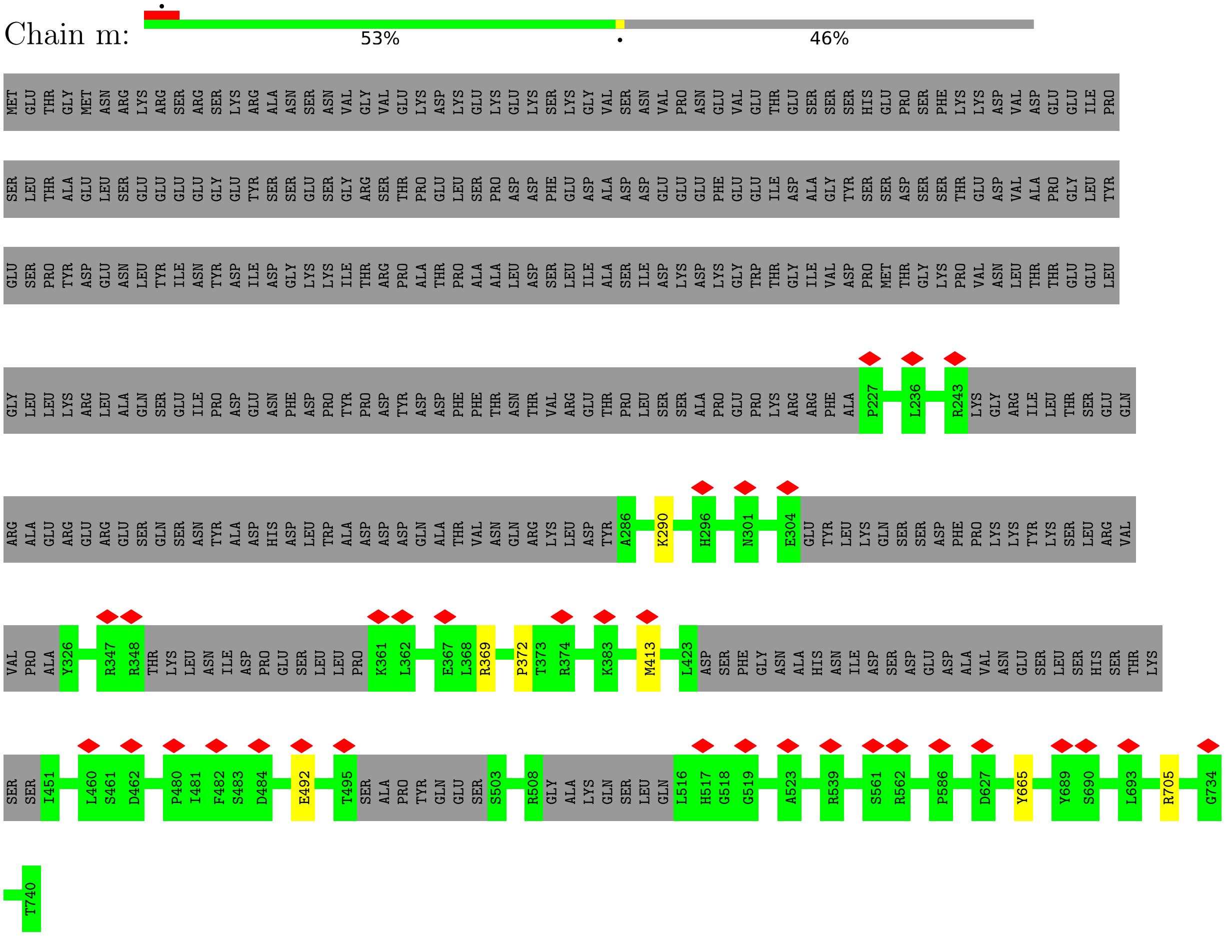
- Molecule 40: 60S ribosomal protein L37-B



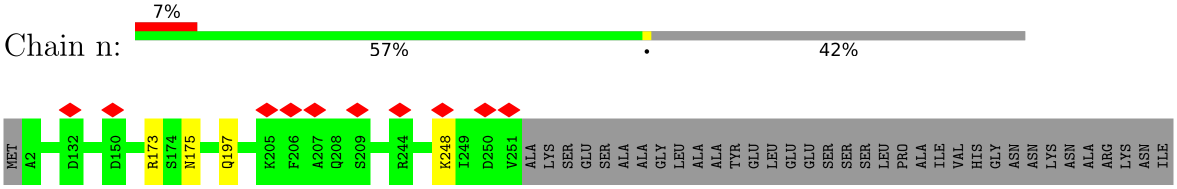
- Molecule 41: 60S ribosomal protein L38-1

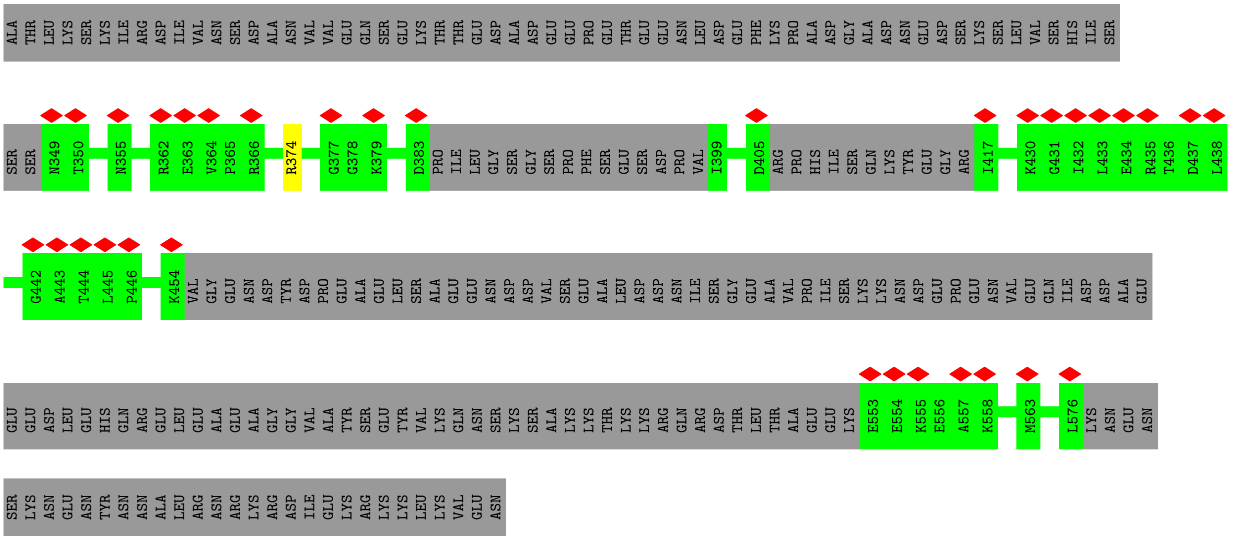


- Molecule 42: Ribosome biogenesis protein erb1

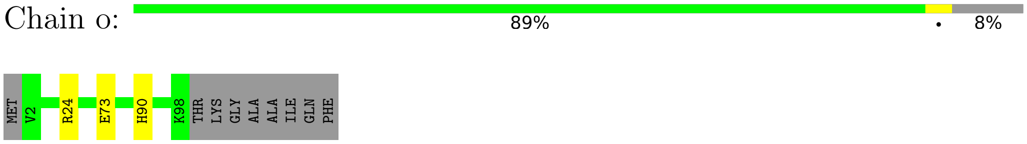


- Molecule 43: Pescadillo homolog

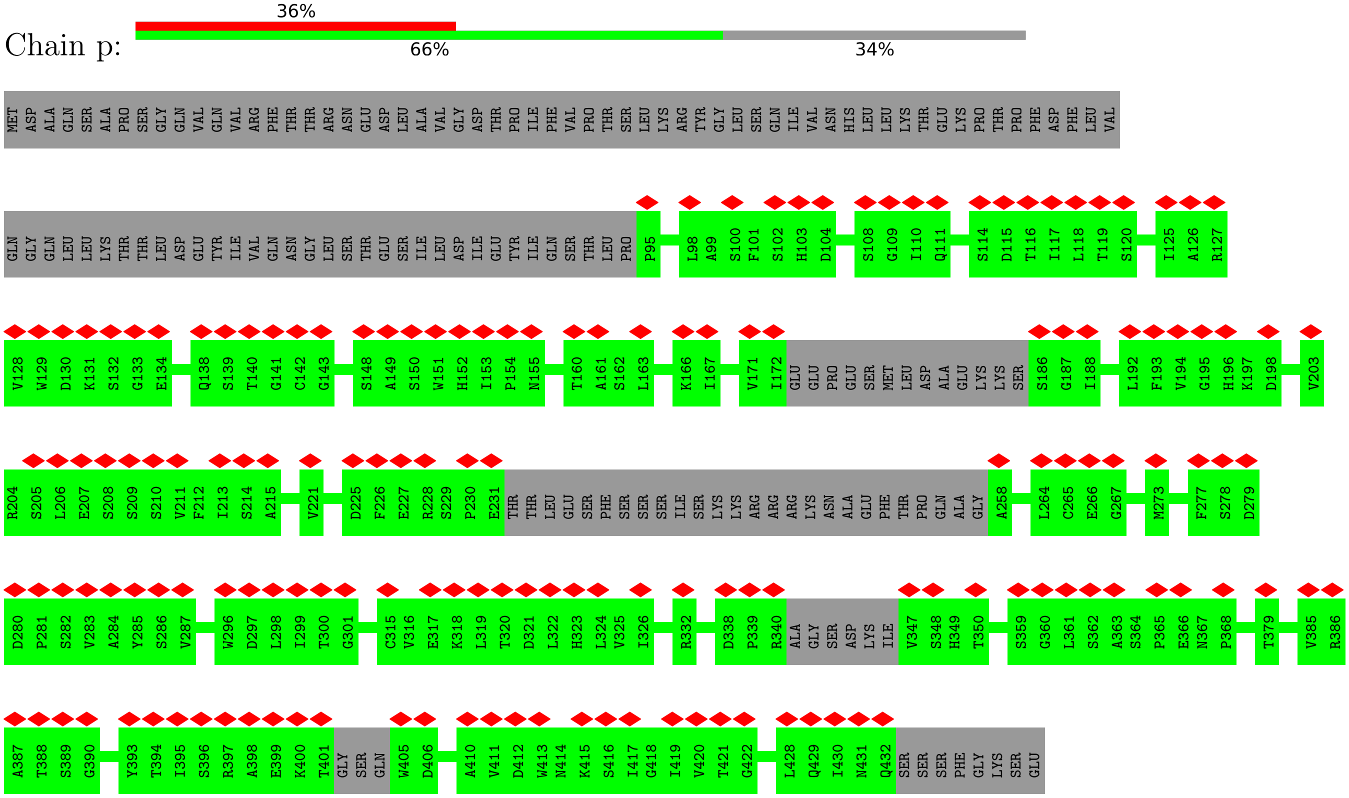




- Molecule 44: 60S ribosomal protein L42



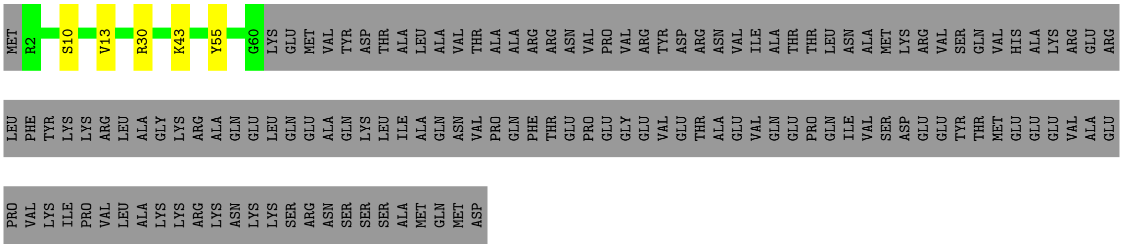
- Molecule 45: Ribosome biogenesis protein ytm1



- Molecule 46: Ribosome biogenesis protein rlp24

Chain u:


28%
•
69%


MET
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V13
R30
K43
Y55
G60
LYS
GLU
MET
VAL
TYR
ASP
THR
ALA
LEU
ALA
VAL
THR
ALA
ALA
ARG
ARG
ASN
VAL
PRO
VAL
ARG
TYR
ASP
ARG
ASN
VAL
ILE
ALA
THR
THR
LEU
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ARG
LYS
ASN
LYS
LYS
SER
ARG
ASN
SER
SER
SER
ALA
MET
GLN
MET
ASP

4 Experimental information ⓘ

Property	**Value**	**Source**
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	35000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{Å}^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.870	Depositor
Minimum map value	-0.492	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.015	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	542.72, 542.72, 542.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	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: ZN

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	0.22	0/68700	0.73	0/107035
2	2	0.22	0/3589	0.72	0/5586
3	3	0.31	0/1028	0.64	0/1384
4	8	0.25	0/448	0.58	0/597
5	9	0.17	0/2816	0.70	0/4388
6	A	0.26	0/1885	0.57	0/2542
7	B	0.26	0/3069	0.54	0/4130
8	C	0.26	0/2848	0.52	0/3842
9	D	0.25	0/2354	0.49	0/3166
10	E	0.27	0/1366	0.54	0/1843
11	F	0.26	0/1781	0.49	0/2389
12	G	0.26	0/1846	0.50	0/2485
13	H	0.24	0/1433	0.54	0/1931
14	I	0.26	0/1398	0.55	0/1873
15	J	0.25	0/1296	0.59	0/1732
16	K	0.25	0/704	0.58	0/941
17	L	0.26	0/1644	0.53	0/2215
18	M	0.24	0/1024	0.52	0/1375
19	N	0.26	0/1717	0.57	0/2304
20	O	0.26	0/1588	0.51	0/2128
21	P	0.27	0/1381	0.54	0/1849
22	Q	0.25	0/1510	0.57	0/2017
23	R	0.24	0/1238	0.56	0/1647
24	S	0.25	0/1422	0.52	0/1909
25	T	0.27	0/1309	0.52	0/1761
26	U	0.26	0/805	0.57	0/1080
27	V	0.27	0/1042	0.55	0/1402
28	X	0.26	0/978	0.51	0/1314
29	Y	0.25	0/1008	0.61	0/1341
30	Z	0.27	0/1095	0.52	0/1467
31	a	0.26	0/1198	0.56	0/1608
32	b	0.29	0/471	0.55	0/623

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	c	0.26	0/723	0.50	0/973
34	d	0.24	0/864	0.55	0/1161
35	e	0.25	0/953	0.54	0/1271
36	f	0.26	0/859	0.52	0/1152
37	g	0.27	0/873	0.58	0/1170
38	h	0.25	0/1008	0.52	0/1340
39	i	0.25	0/774	0.56	0/1028
40	j	0.26	0/671	0.57	0/888
41	k	0.28	0/566	0.59	0/757
42	m	0.25	0/3209	0.51	0/4357
43	n	0.26	0/2971	0.48	0/3997
44	o	0.25	0/803	0.54	0/1064
45	p	0.24	0/1426	0.44	0/1977
46	u	0.28	0/509	0.54	0/678
All	All	0.23	0/132200	0.66	0/193717

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	
3	3	117/302 (39%)	102 (87%)	13 (11%)	2 (2%)	9	29
4	8	48/51 (94%)	47 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	A	242/253 (96%)	235 (97%)	7 (3%)	0	100	100
7	B	375/388 (97%)	365 (97%)	10 (3%)	0	100	100
8	C	357/363 (98%)	336 (94%)	20 (6%)	1 (0%)	41	72
9	D	285/294 (97%)	279 (98%)	6 (2%)	0	100	100
10	E	170/195 (87%)	160 (94%)	9 (5%)	1 (1%)	25	56
11	F	212/250 (85%)	209 (99%)	3 (1%)	0	100	100
12	G	229/259 (88%)	219 (96%)	7 (3%)	3 (1%)	12	36
13	H	174/190 (92%)	168 (97%)	6 (3%)	0	100	100
14	I	166/221 (75%)	162 (98%)	4 (2%)	0	100	100
15	J	153/174 (88%)	151 (99%)	2 (1%)	0	100	100
16	K	88/94 (94%)	85 (97%)	3 (3%)	0	100	100
17	L	200/208 (96%)	194 (97%)	4 (2%)	2 (1%)	15	44
18	M	123/134 (92%)	118 (96%)	4 (3%)	1 (1%)	19	49
19	N	198/201 (98%)	184 (93%)	12 (6%)	2 (1%)	15	44
20	O	194/197 (98%)	190 (98%)	4 (2%)	0	100	100
21	P	167/187 (89%)	161 (96%)	5 (3%)	1 (1%)	25	56
22	Q	184/187 (98%)	173 (94%)	8 (4%)	3 (2%)	9	31
23	R	144/193 (75%)	139 (96%)	4 (3%)	1 (1%)	22	53
24	S	161/176 (92%)	157 (98%)	4 (2%)	0	100	100
25	T	156/160 (98%)	154 (99%)	2 (1%)	0	100	100
26	U	96/117 (82%)	91 (95%)	5 (5%)	0	100	100
27	V	135/139 (97%)	133 (98%)	2 (2%)	0	100	100
28	X	118/141 (84%)	116 (98%)	2 (2%)	0	100	100
29	Y	123/126 (98%)	122 (99%)	1 (1%)	0	100	100
30	Z	132/136 (97%)	123 (93%)	8 (6%)	1 (1%)	19	49
31	a	145/148 (98%)	139 (96%)	6 (4%)	0	100	100
32	b	52/61 (85%)	50 (96%)	2 (4%)	0	100	100
33	c	93/117 (80%)	91 (98%)	2 (2%)	0	100	100
34	d	100/113 (88%)	95 (95%)	5 (5%)	0	100	100
35	e	115/127 (91%)	114 (99%)	1 (1%)	0	100	100
36	f	104/108 (96%)	97 (93%)	7 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	g	104/112 (93%)	99 (95%)	5 (5%)	0	100	100
38	h	119/122 (98%)	118 (99%)	1 (1%)	0	100	100
39	i	94/99 (95%)	88 (94%)	6 (6%)	0	100	100
40	j	81/91 (89%)	78 (96%)	3 (4%)	0	100	100
41	k	67/74 (90%)	67 (100%)	0	0	100	100
42	m	384/740 (52%)	361 (94%)	21 (6%)	2 (0%)	29	61
43	n	344/607 (57%)	329 (96%)	15 (4%)	0	100	100
44	o	95/106 (90%)	92 (97%)	3 (3%)	0	100	100
45	p	280/440 (64%)	271 (97%)	9 (3%)	0	100	100
46	u	57/192 (30%)	55 (96%)	2 (4%)	0	100	100
All	All	6981/8593 (81%)	6717 (96%)	244 (4%)	20 (0%)	44	72

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	G	28	VAL
12	G	227[A]	ASP
12	G	227[B]	ASP
42	m	369	ARG
17	L	47	ALA

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	
3	3	108/271 (40%)	101 (94%)	7 (6%)	17	44
4	8	46/47 (98%)	45 (98%)	1 (2%)	52	83
6	A	187/192 (97%)	184 (98%)	3 (2%)	62	88
7	B	316/326 (97%)	310 (98%)	6 (2%)	57	85
8	C	296/297 (100%)	286 (97%)	10 (3%)	37	71
9	D	235/241 (98%)	232 (99%)	3 (1%)	69	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	E	139/155 (90%)	134 (96%)	5 (4%)	35	69
11	F	180/210 (86%)	176 (98%)	4 (2%)	52	83
12	G	192/212 (91%)	189 (98%)	3 (2%)	62	88
13	H	160/170 (94%)	156 (98%)	4 (2%)	47	80
14	I	146/187 (78%)	144 (99%)	2 (1%)	67	90
15	J	134/146 (92%)	131 (98%)	3 (2%)	52	83
16	K	71/75 (95%)	68 (96%)	3 (4%)	30	63
17	L	162/167 (97%)	159 (98%)	3 (2%)	57	85
18	M	108/113 (96%)	108 (100%)	0	100	100
19	N	175/176 (99%)	173 (99%)	2 (1%)	73	92
20	O	161/162 (99%)	159 (99%)	2 (1%)	71	92
21	P	138/149 (93%)	132 (96%)	6 (4%)	29	62
22	Q	158/159 (99%)	155 (98%)	3 (2%)	57	85
23	R	126/162 (78%)	123 (98%)	3 (2%)	49	81
24	S	148/154 (96%)	145 (98%)	3 (2%)	55	84
25	T	137/139 (99%)	135 (98%)	2 (2%)	65	89
26	U	85/103 (82%)	81 (95%)	4 (5%)	26	59
27	V	105/107 (98%)	102 (97%)	3 (3%)	42	76
28	X	106/122 (87%)	103 (97%)	3 (3%)	43	77
29	Y	110/111 (99%)	105 (96%)	5 (4%)	27	60
30	Z	113/115 (98%)	111 (98%)	2 (2%)	59	86
31	a	121/122 (99%)	120 (99%)	1 (1%)	81	94
32	b	47/51 (92%)	47 (100%)	0	100	100
33	c	77/91 (85%)	71 (92%)	6 (8%)	12	35
34	d	93/102 (91%)	92 (99%)	1 (1%)	73	92
35	e	100/107 (94%)	97 (97%)	3 (3%)	41	75
36	f	89/91 (98%)	88 (99%)	1 (1%)	73	92
37	g	92/97 (95%)	89 (97%)	3 (3%)	38	72
38	h	106/107 (99%)	104 (98%)	2 (2%)	57	85
39	i	82/84 (98%)	82 (100%)	0	100	100
40	j	68/71 (96%)	68 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	k	63/66 (96%)	60 (95%)	3 (5%)	25	58
42	m	344/659 (52%)	339 (98%)	5 (2%)	65	89
43	n	312/532 (59%)	307 (98%)	5 (2%)	62	88
44	o	87/93 (94%)	84 (97%)	3 (3%)	37	71
46	u	52/168 (31%)	47 (90%)	5 (10%)	8	24
All	All	5775/6909 (84%)	5642 (98%)	133 (2%)	53	82

5 of 133 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
42	m	290	LYS
42	m	705	ARG
46	u	30	ARG
15	J	35	LYS
14	I	215	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
27	V	134	ASN
28	X	67	ASN
43	n	349	ASN
30	Z	91	ASN
12	G	95	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2837/3498 (81%)	600 (21%)	19 (0%)
2	2	150/165 (90%)	24 (16%)	2 (1%)
5	9	117/229 (51%)	14 (11%)	0
All	All	3104/3892 (79%)	638 (20%)	21 (0%)

5 of 638 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	26	A
1	1	28	G

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Mol	Chain	Res	Type
1	1	30	G
1	1	40	A
1	1	43	A

5 of 21 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	2657	A
1	1	3358	U
2	2	131	G
1	1	3441	G
1	1	3174	A

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 1 ligands modelled in this entry, 1 is 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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

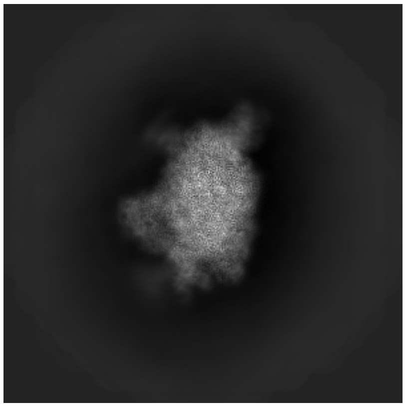
6 Map visualisation ⓘ

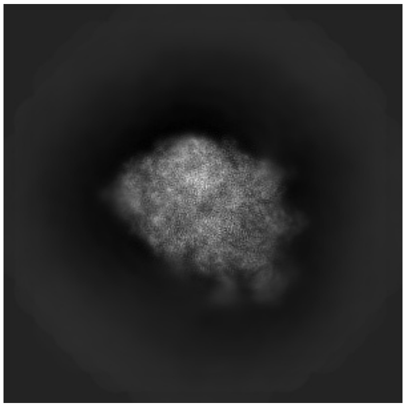
This section contains visualisations of the EMDB entry EMD-24412. These allow visual inspection of the internal detail of the map and identification of artifacts.

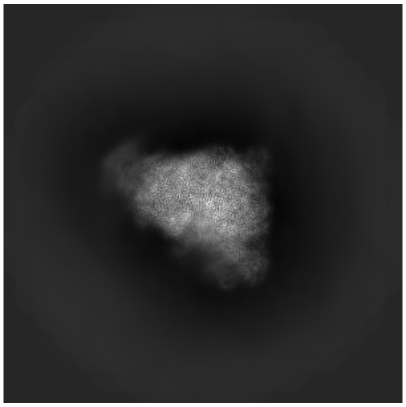
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections ⓘ

6.1.1 Primary map


X

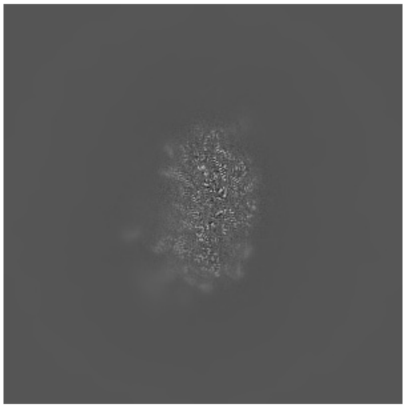

Y

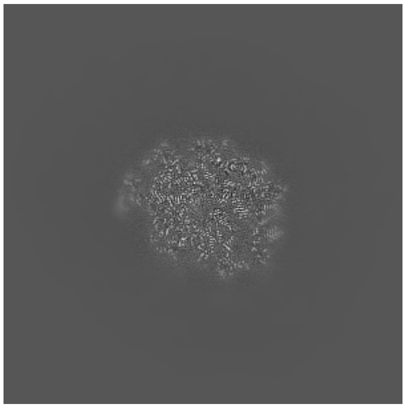

Z

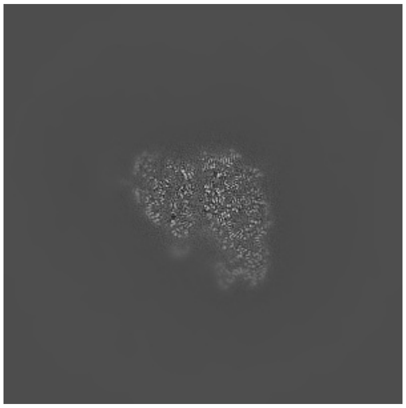
The images above show the map projected in three orthogonal directions.

6.2 Central slices ⓘ

6.2.1 Primary map


X Index: 256

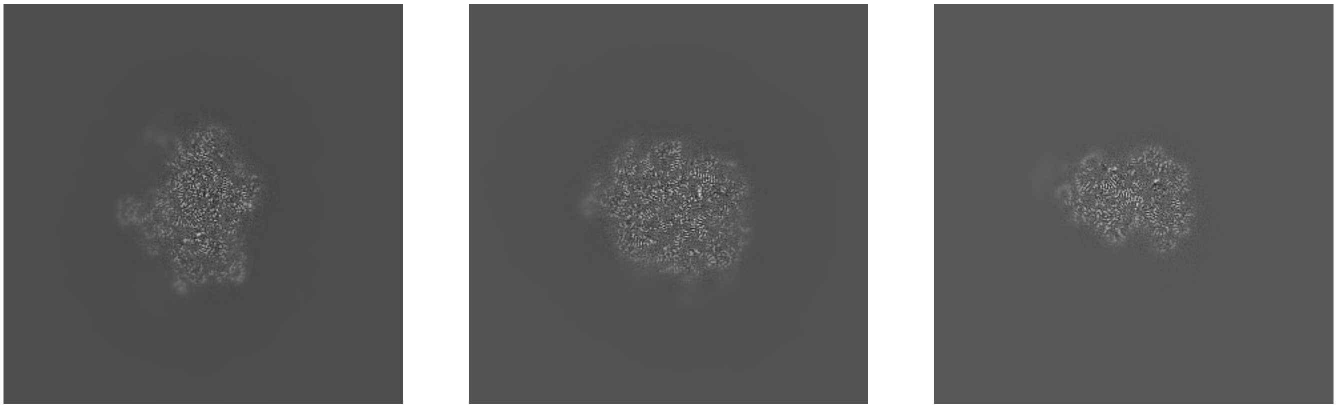

Y Index: 256


Z Index: 256

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

6.3 Largest variance slices

6.3.1 Primary map

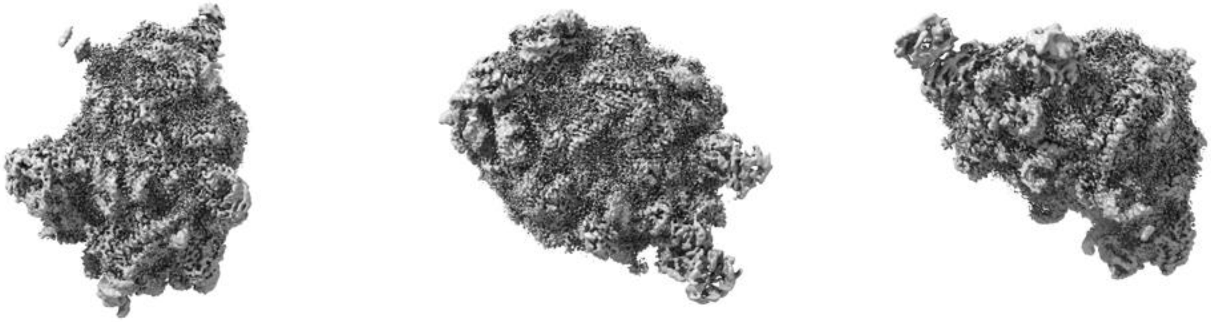


X Index: 283 Y Index: 263 Z Index: 276

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

6.4 Orthogonal surface views

6.4.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

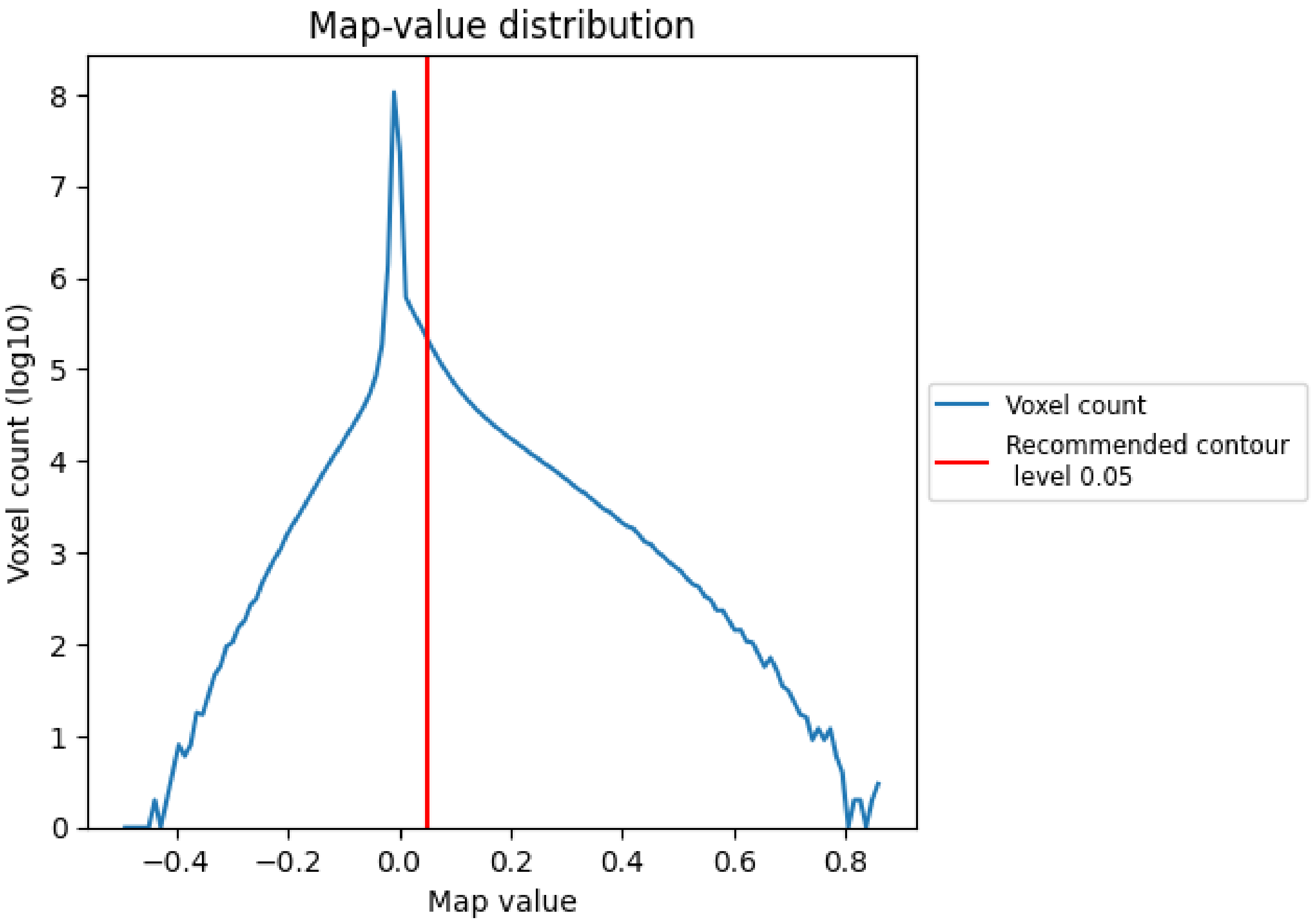
6.5 Mask visualisation ⓘ

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

7 Map analysis ⓘ

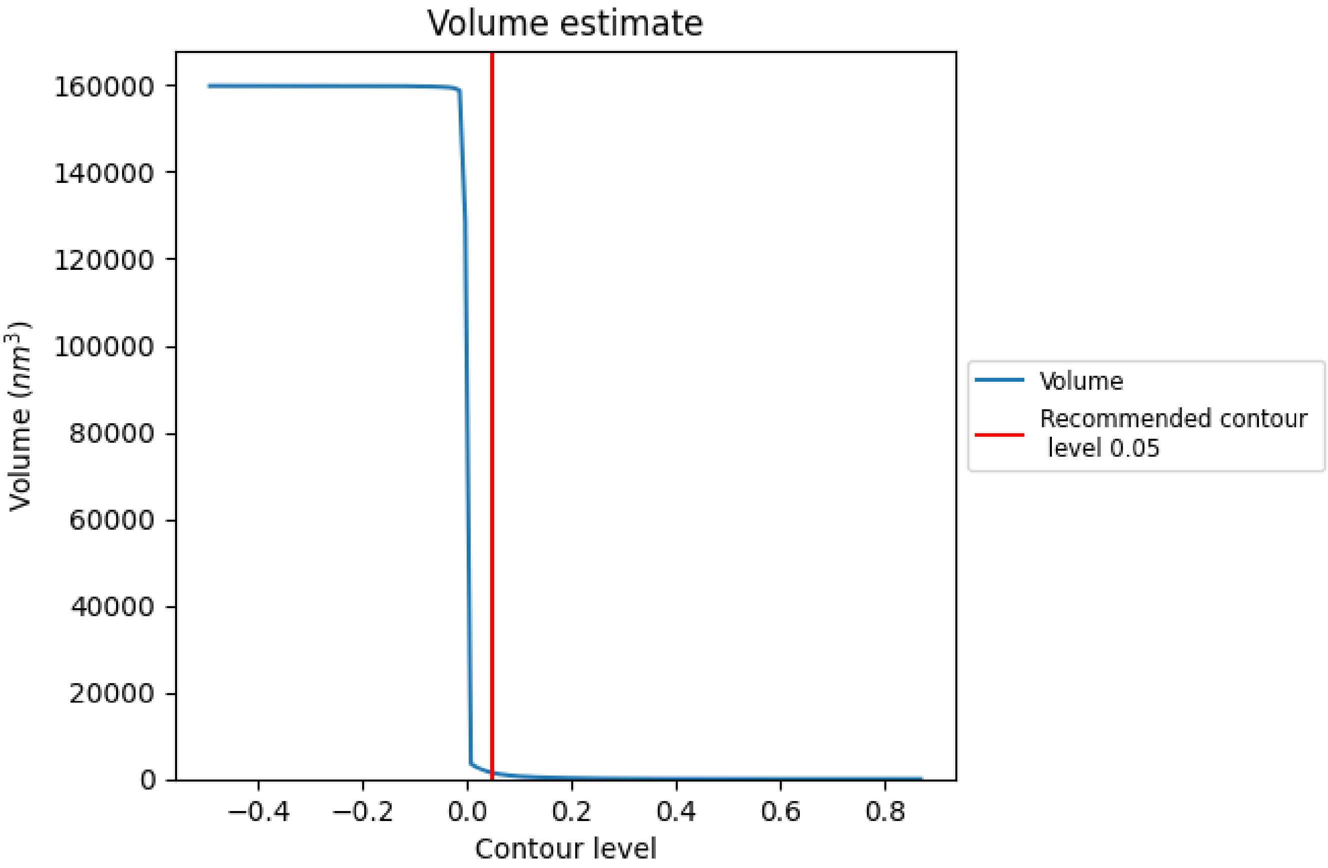
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ



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.

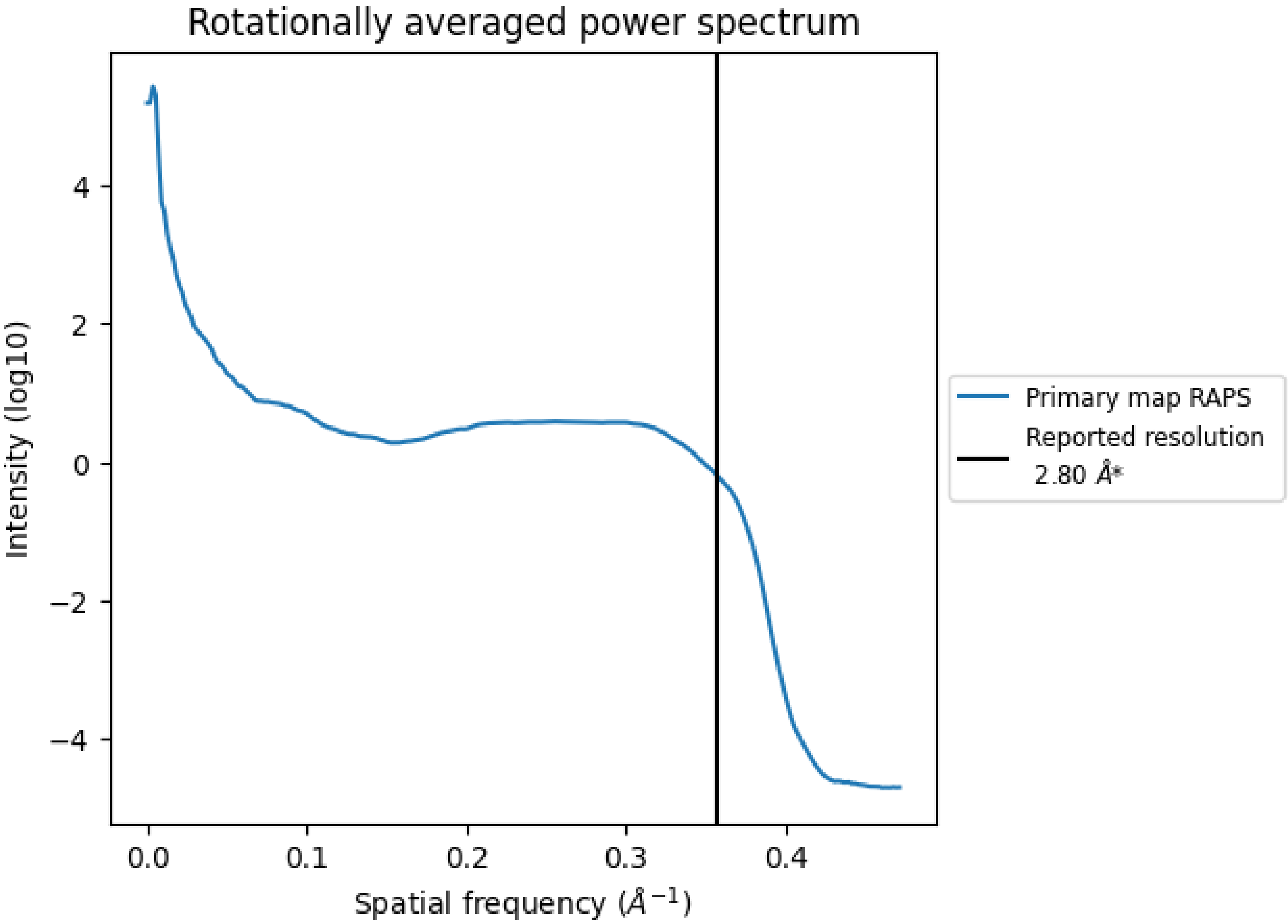
7.2 Volume estimate ⓘ



The volume at the recommended contour level is 1408 nm^3; this corresponds to an approximate mass of 1272 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 0.357 Å^{-1}

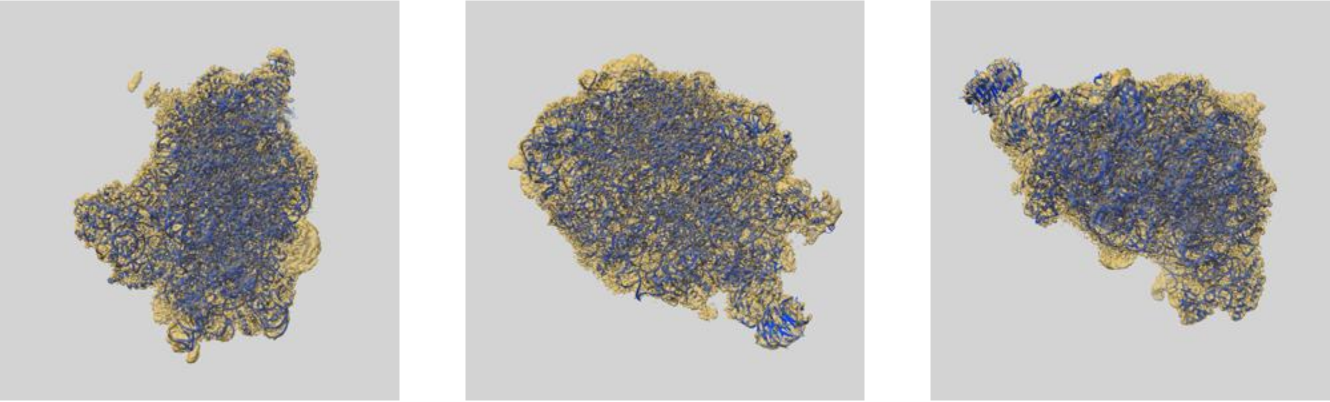
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit ⓘ

This section contains information regarding the fit between EMDB map EMD-24412 and PDB model 8EUG. Per-residue inclusion information can be found in section 3 on page 12.

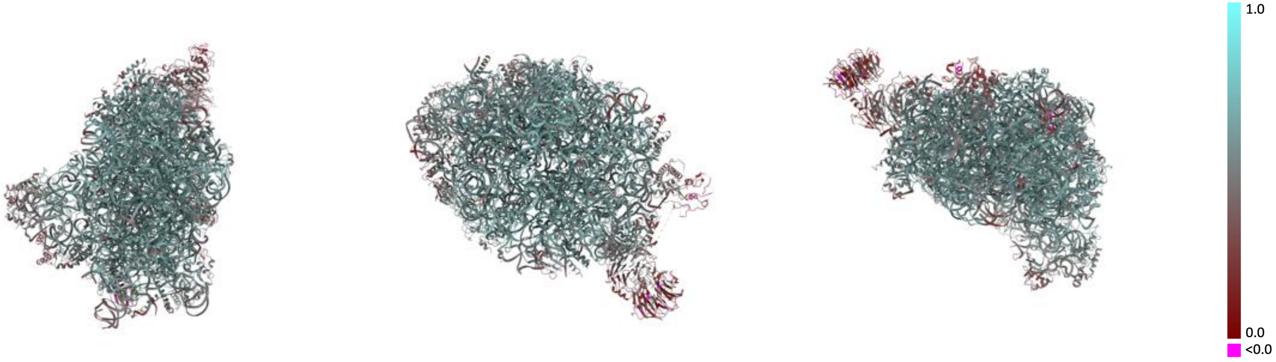
9.1 Map-model overlay ⓘ



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.05 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.

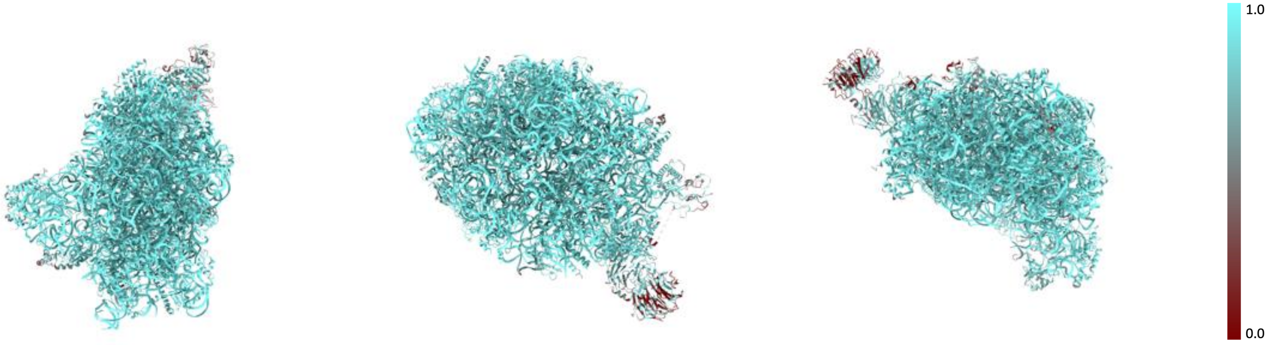
9.2 Q-score mapped to coordinate model



X Y Z

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.

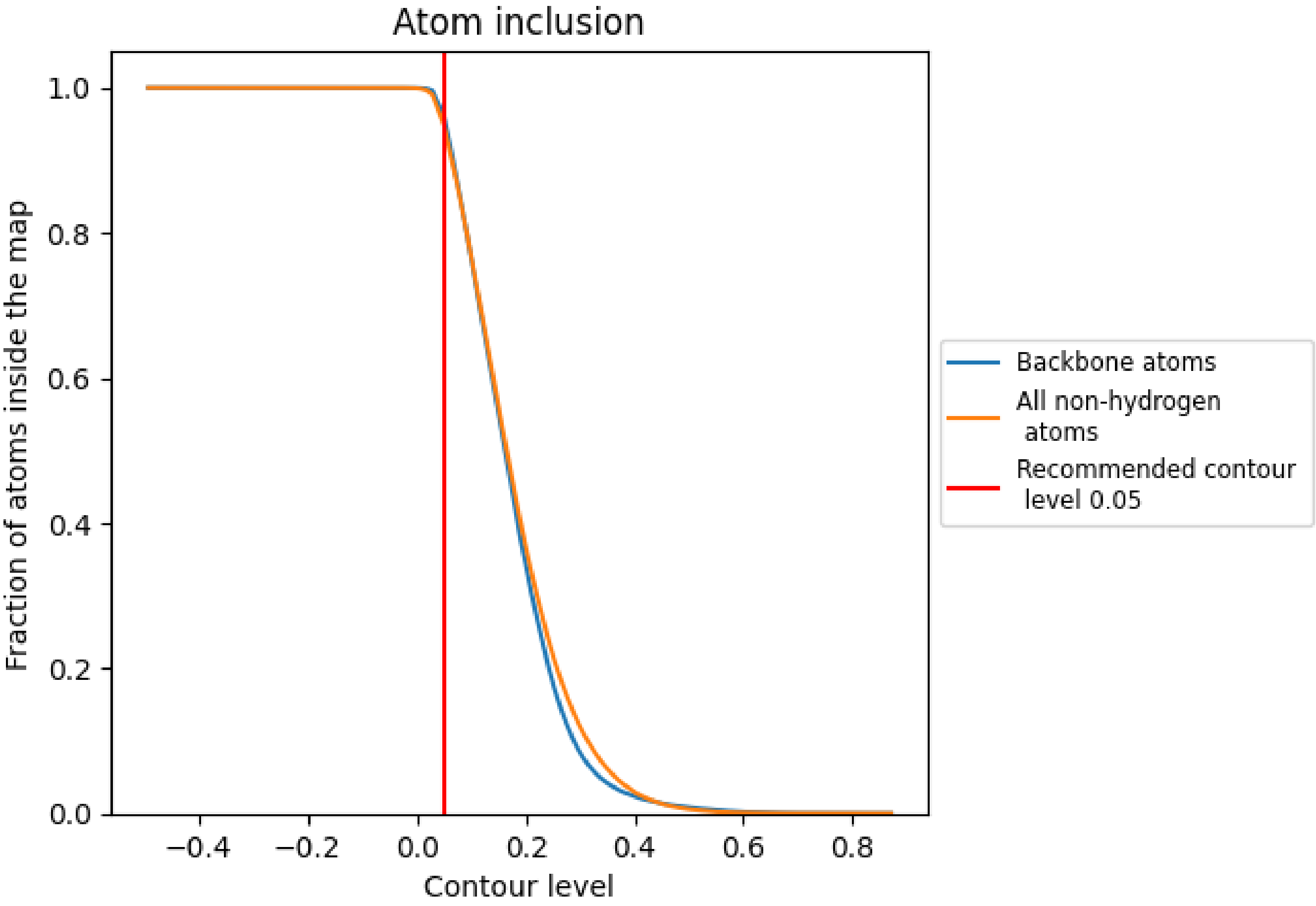
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (0.05).

9.4 Atom inclusion ⓘ



At the recommended contour level, 96% of all backbone atoms, 95% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9491	0.5670
1	0.9863	0.5950
2	0.9907	0.6210
3	0.8356	0.4530
8	0.9904	0.6190
9	0.9921	0.5370
A	0.9821	0.6130
B	0.9726	0.5920
C	0.9743	0.6030
D	0.8878	0.4980
E	0.9280	0.5250
F	0.9624	0.5920
G	0.8954	0.5310
H	0.7751	0.3480
I	0.8445	0.4870
J	0.7798	0.3820
K	0.9580	0.6010
L	0.9576	0.6030
M	0.9488	0.5140
N	0.9894	0.6350
O	0.9617	0.5810
P	0.9500	0.5850
Q	0.9798	0.6020
R	0.9607	0.5850
S	0.9576	0.5600
T	0.9534	0.5770
U	0.7951	0.4340
V	0.9659	0.5790
X	0.9692	0.6000
Y	0.9709	0.5930
Z	0.9321	0.5370
a	0.9655	0.6130
b	0.9483	0.5460
c	0.8944	0.5330
d	0.9305	0.5790

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Chain	Atom inclusion	Q-score
e	0.9823	0.6130
f	0.9816	0.6060
g	0.9661	0.6040
h	0.9586	0.5880
i	0.9538	0.5710
j	0.9905	0.6440
k	0.8846	0.5210
m	0.7330	0.3910
n	0.7601	0.4050
o	0.9389	0.5650
p	0.4403	0.2640
u	0.9474	0.5350