wwPDB EM Validation Summary Report ⓘ

Oct 6, 2024 – 08:49 pm BST

PDB ID	:	5APN
EMDB ID	:	EMD-3152
Title	:	Structure of the yeast 60S ribosomal subunit in complex with Arx1, Alb1 and N-terminally tagged Rei1
Authors	:	Greber, B.J.; Gerhardy, S.; Leitner, A.; Leibundgut, M.; Salem, M.; Boehringer, D.; Leulliot, N.; Aebersold, R.; Panse, V.G.; Ban, V.
Deposited on	:	2015-09-17
Resolution	:	3.91 Å(reported)

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

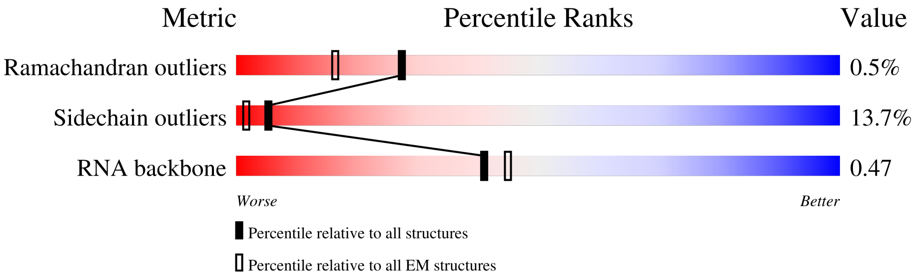
EMDB validation analysis	:	0.0.1.dev113
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

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 3.91 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 >=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	5	3396	
2	7	121	
3	8	158	
4	A	254	
5	B	387	
6	C	362	
7	D	297	
8	E	176	

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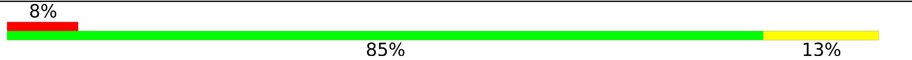
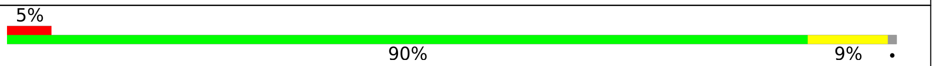
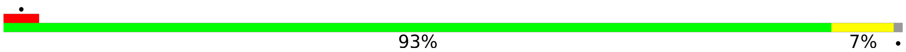
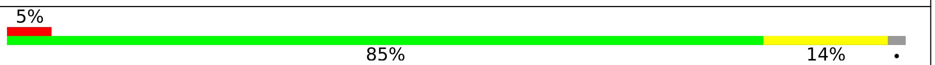
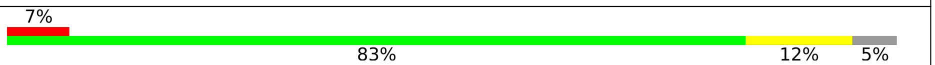
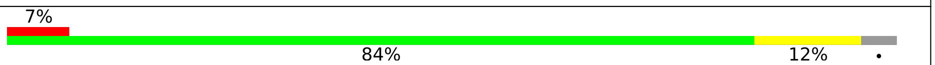
Mol	Chain	Length	Quality of chain
9	F	244	
10	G	256	
11	H	191	
12	I	221	
13	J	174	
14	L	199	
15	M	138	
16	N	204	
17	O	199	
18	P	184	
19	Q	186	
20	R	189	
21	S	172	
22	T	160	
23	U	121	
24	V	137	
25	W	155	
26	X	142	
27	Y	127	
28	Z	136	
29	a	149	
30	b	59	
31	c	105	
32	d	113	
33	e	130	

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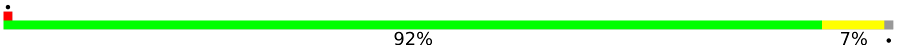
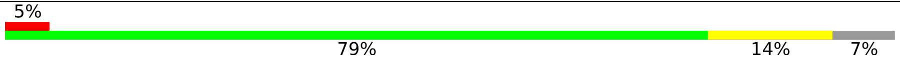
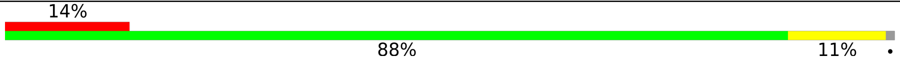
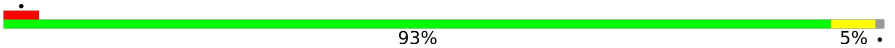
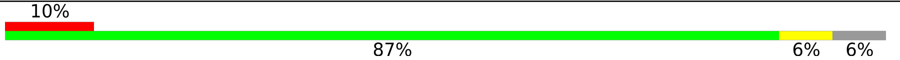
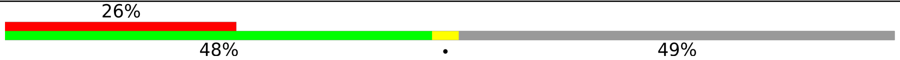
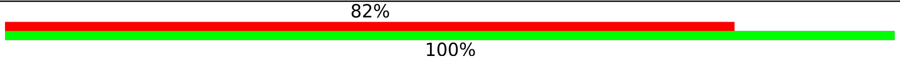
Mol	Chain	Length	Quality of chain
34	f	107	
35	g	121	
36	h	120	
37	i	100	
38	j	88	
39	k	78	
40	l	51	
41	m	128	
42	o	106	
43	p	92	
44	q	312	
45	x	616	
46	y	414	
47	z	85	

2 Entry composition (i)

There are 49 unique types of molecules in this entry. The entry contains 129324 atoms, of which 3 are hydrogens and 0 are deuteriums.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	175	Total	C	N	O	S	0	0
			1355	877	242	235	1		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 45 is a protein called Probable metalloprotease ARX1.

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

There are 23 discrepancies between the modelled and reference sequences:

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

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

- Molecule 46 is a protein called Cytoplasmic 60S subunit biogenesis factor REI1.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
46	y	211	1727	1095	3	307	314	8	0	0

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
y	-20	HIS	-	expression tag	UNP P38344
y	-19	HIS	-	expression tag	UNP P38344
y	-18	HIS	-	expression tag	UNP P38344
y	-17	HIS	-	expression tag	UNP P38344
y	-16	HIS	-	expression tag	UNP P38344
y	-15	HIS	-	expression tag	UNP P38344
y	-14	ASP	-	expression tag	UNP P38344
y	-13	TYR	-	expression tag	UNP P38344
y	-12	ASP	-	expression tag	UNP P38344
y	-11	ILE	-	expression tag	UNP P38344
y	-10	PRO	-	expression tag	UNP P38344
y	-9	THR	-	expression tag	UNP P38344
y	-8	THR	-	expression tag	UNP P38344
y	-7	GLU	-	expression tag	UNP P38344
y	-6	ASN	-	expression tag	UNP P38344
y	-5	LEU	-	expression tag	UNP P38344
y	-4	TYR	-	expression tag	UNP P38344
y	-3	PHE	-	expression tag	UNP P38344
y	-2	GLN	-	expression tag	UNP P38344
y	-1	GLY	-	expression tag	UNP P38344
y	0	ALA	-	expression tag	UNP P38344

- Molecule 47 is a protein called ALB1.

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

- Molecule 48 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 49 is ZINC ION (three-letter code: ZN) (formula: Zn).

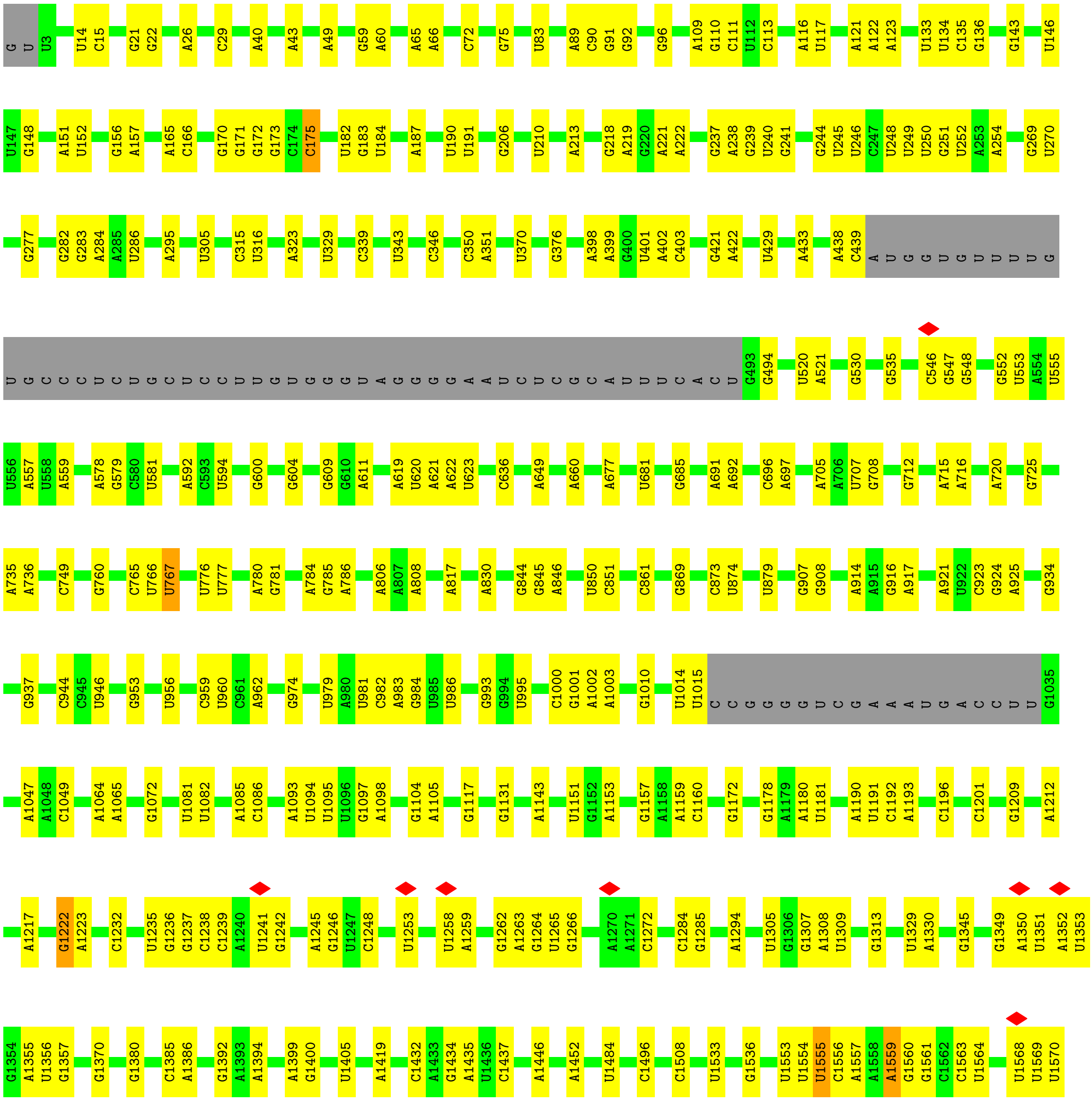
Mol	Chain	Residues	Atoms		AltConf
49	j	1	Total 1	Zn 1	0
49	m	1	Total 1	Zn 1	0
49	o	1	Total 1	Zn 1	0
49	p	1	Total 1	Zn 1	0
49	y	2	Total 2	Zn 2	0

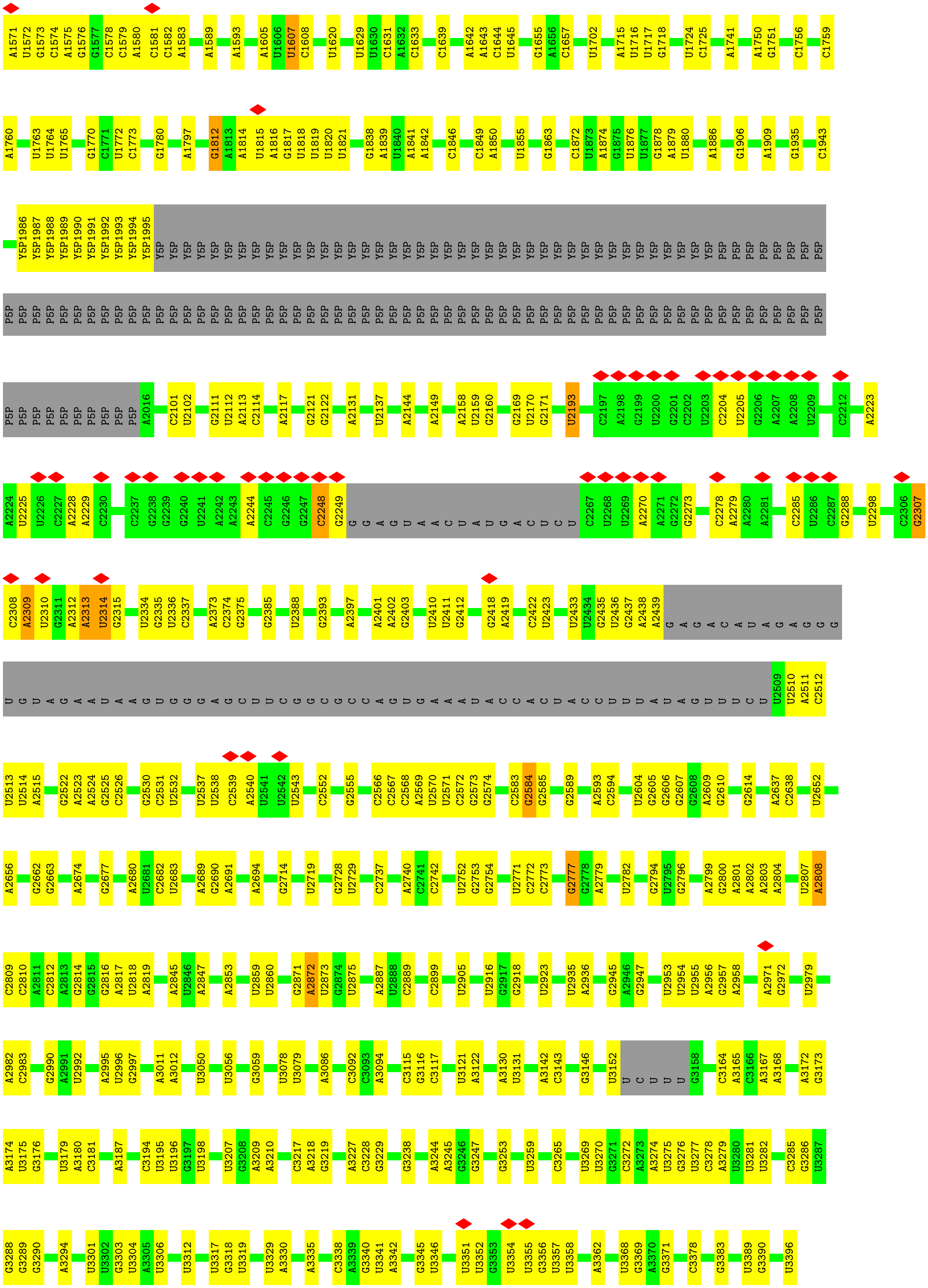
3 Residue-property plots ⓘ

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

Chain 5:




A1571 U1572 G1573 C1574 A1575 G1576 G1577 C1578 C1579 A1580 C1581 C1582 A1583 A1589 A1593 A1605 U1606 U1607 C1608 U1620 U1629 U1630 C1631 A1632 C1633 C1639 A1642 A1643 C1644 U1645 G1655 A1656 C1657 U1702 A1715 U1716 U1717 G1718 U1724 C1725 A1741 A1750 G1751 C1756 C1759
A1760 U1763 U1764 U1765 G1770 C1771 U1772 C1773 G1780 A1797 G1812 A1813 A1814 U1815 A1816 G1817 U1818 U1819 U1820 U1821 G1838 A1839 U1840 A1841 A1842 C1846 C1849 A1850 U1855 G1863 C1872 U1873 A1874 G1875 U1876 U1877 G1878 A1879 U1880 A1886 G1906 A1909 G1935 C1943
Y5P1986 Y5P1987 Y5P1988 Y5P1989 Y5P1990 Y5P1991 Y5P1992 Y5P1993 Y5P1994 Y5P1995 Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P Y5P P5P P5P P5P P5P P5P P5P P5P P5P
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A2224 U2225 U2226 C2227 A2228 A2229 C2230 C2237 G2238 G2239 G2240 U2241 A2242 A2243 A2244 C2245 G2246 G2247 C2248 G2249 G G A G U A A C U A U G A C U C U C2267 U2268 U2269 A2270 A2271 G2272 G2273 C2278 A2279 A2280 A2281 C2285 U2286 C2287 G2288 U2298 C2306 G2307
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U G U A G A A U A A G U G G G A G C U U C G G C G C C A G U G A A A U A C C A C U A C C U U U A U A G U U U C U U2509 U2510 A2511 C2512
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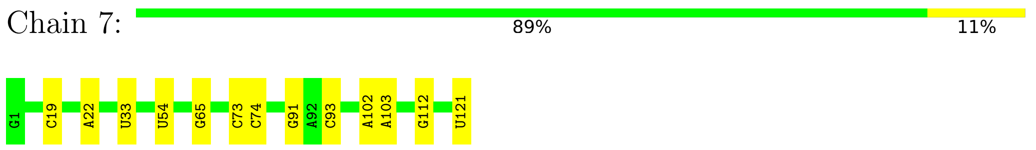
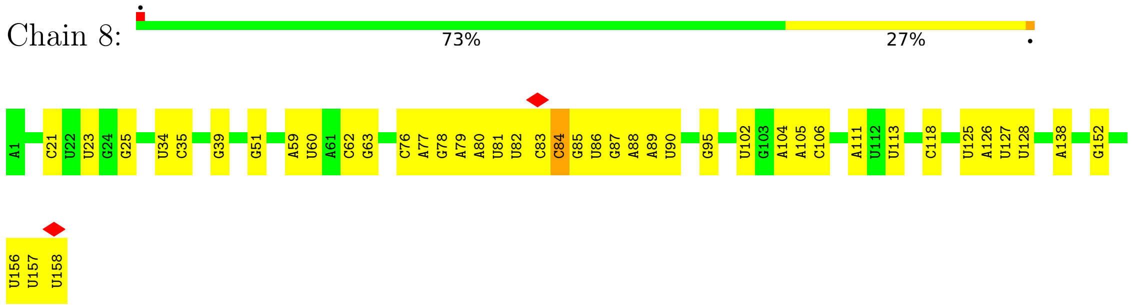
C2809 C2810 A2811 C2812 A2813 G2814 G2815 G2816 A2817 U2818 A2819 A2845 U2846 A2847 A2853 U2859 U2860 G2871 A2872 U2873 G2874 U2875 A2887 U2888 C2889 C2899 U2905 U2916 G2917 G2918 U2923 U2935 A2936 G2945 A2946 G2947 U2953 U2954 U2955 A2956 G2957 A2958 A2971 G2972 U2979
A2982 C2983 G2990 A2991 U2992 A2995 U2996 G2997 A3011 A3012 U3050 U3056 G3059 U3078 U3079 A3086 C3092 C3093 A3094 C3115 G3116 C3117 U3121 A3122 A3130 U3131 A3142 C3143 G3146 U3152 U C U U U G3158 C3164 A3165 C3166 A3167 A3168 A3172 G3173
A3174 U3175 G3176 U3179 A3180 C3181 A3187 C3194 U3195 U3196 G3197 U3198 U3207 G3208 A3209 A3210 C3217 A3218 G3219 A3227 C3228 G3229 G3238 A3244 A3245 G3246 G3247 G3253 U3259 C3265 U3269 U3270 G3271 C3272 A3273 A3274 U3275 G3276 C3277 C3278 A3279 U3280 U3281 U3282 C3285 G3286 U3287
G3288 G3289 G3290 A3294 U3301 U3302 G3303 U3304 A3305 U3306 U3312 U3317 G3318 U3319 U3329 A3330 A3335 C3338 A3339 G3340 U3341 A3342 G3345 U3346 U3351 U3352 G3353 U3354 U3355 G3356 U3357 C3358 A3362 U3368 G3369 A3370 G3371 C3378 G3383 U3389 G3390 U3396

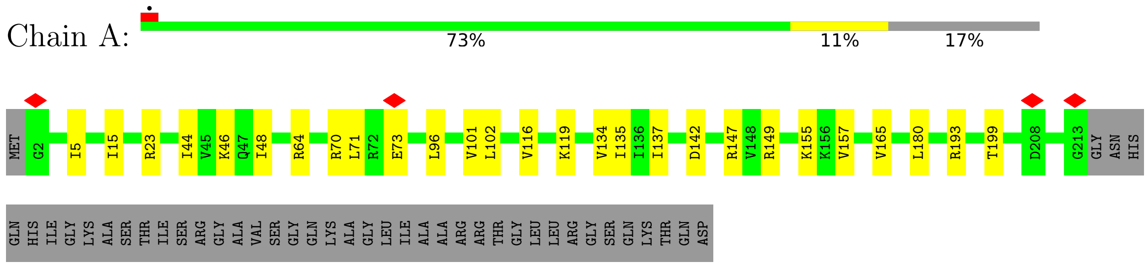
- Molecule 2: 5S rRNA



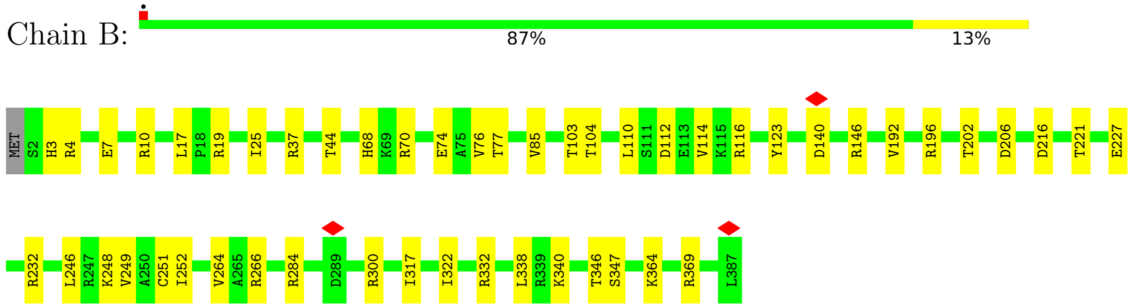
- Molecule 3: 5.8S rRNA



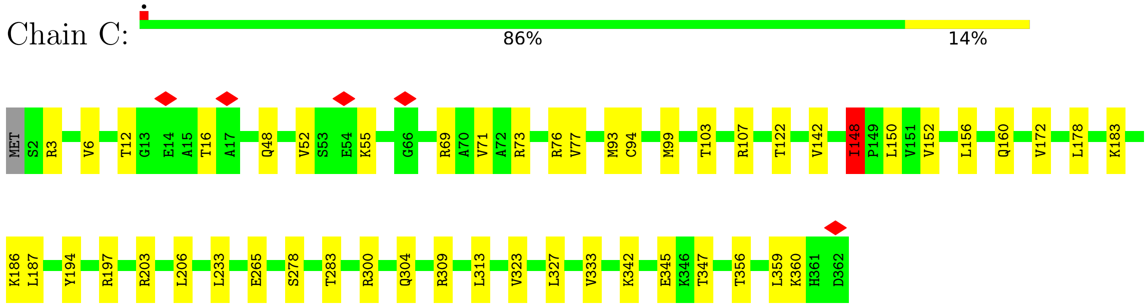
- Molecule 4: 60S ribosomal protein L2-A



- Molecule 5: 60S ribosomal protein L3

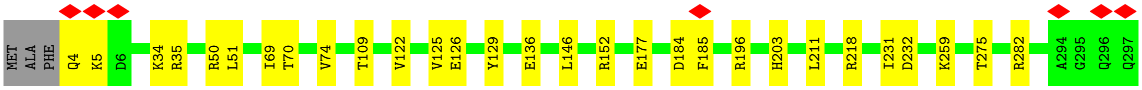


- Molecule 6: 60S ribosomal protein L4-A



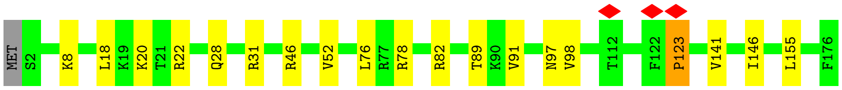
- Molecule 7: 60S ribosomal protein L5

Chain D:



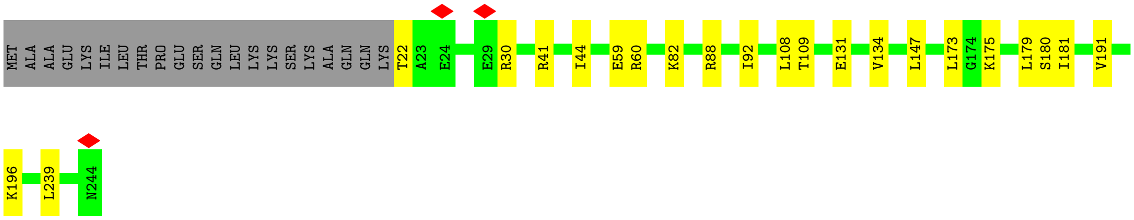
- Molecule 8: 60S ribosomal protein L6-A

Chain E:



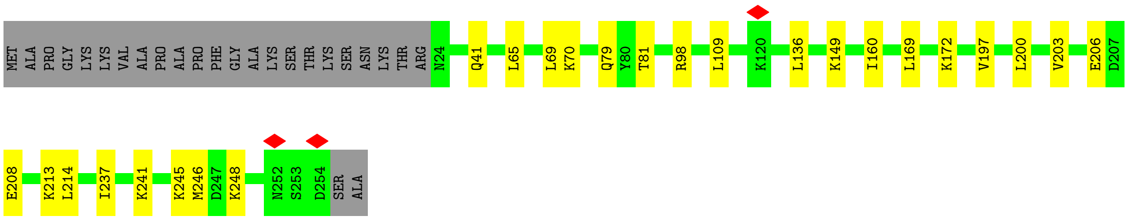
- Molecule 9: 60S ribosomal protein L7-A

Chain F:



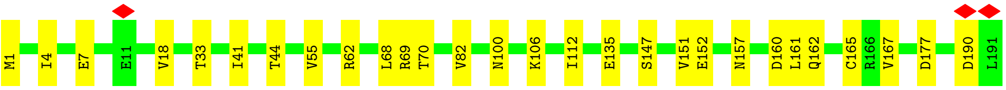
- Molecule 10: 60S ribosomal protein L8-A

Chain G:



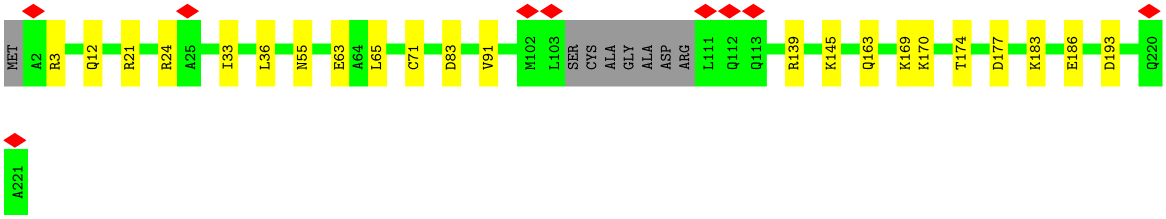
- Molecule 11: 60S ribosomal protein L9-A

Chain H:



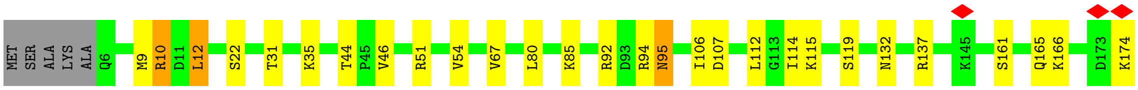
- Molecule 12: 60S ribosomal protein L10

Chain I:



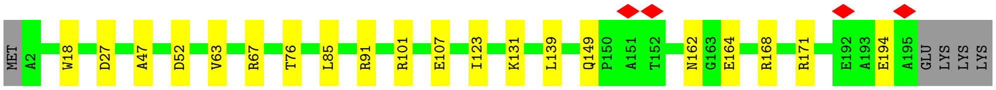
- Molecule 13: 60S ribosomal protein L11-A

Chain J:



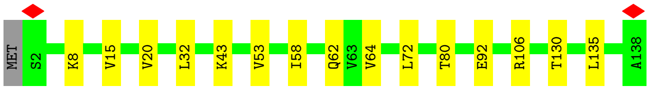
- Molecule 14: 60S ribosomal protein L13-A

Chain L:



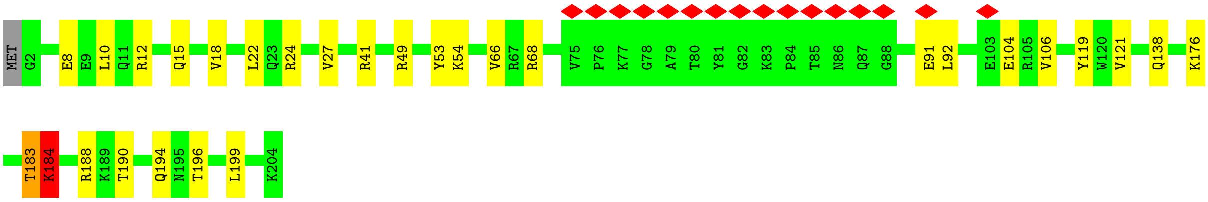
- Molecule 15: 60S ribosomal protein L14-A

Chain M:



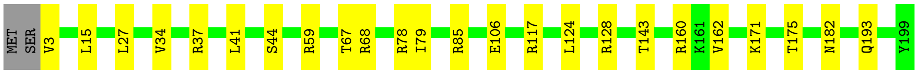
- Molecule 16: 60S ribosomal protein L15-A

Chain N:



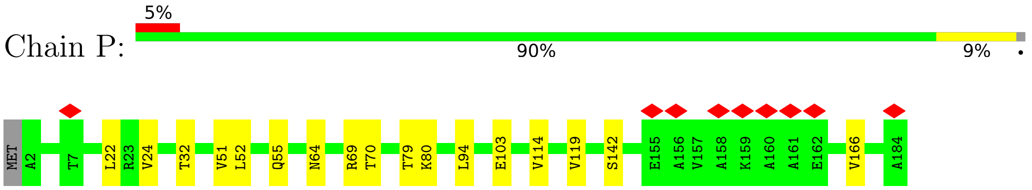
- Molecule 17: 60S ribosomal protein L16-A

Chain O:



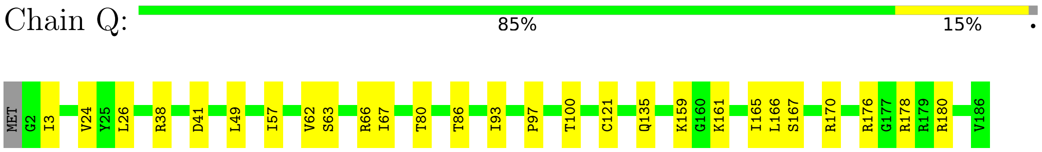
- Molecule 18: 60S ribosomal protein L17-A

Chain P:



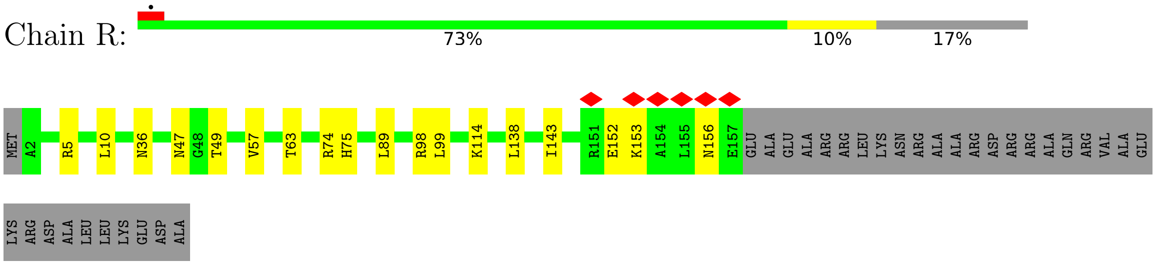
- Molecule 19: 60S ribosomal protein L18-A

Chain Q:



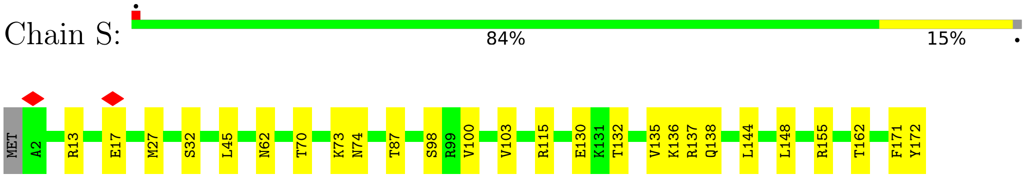
- Molecule 20: 60S ribosomal protein L19-A

Chain R:



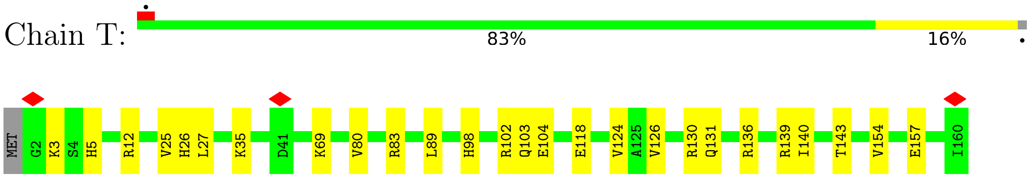
- Molecule 21: 60S ribosomal protein L20-A

Chain S:



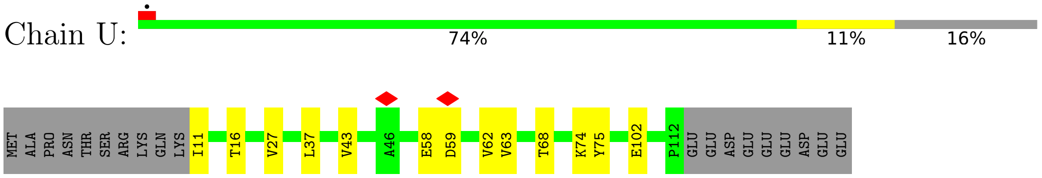
- Molecule 22: 60S ribosomal protein L21-A

Chain T:



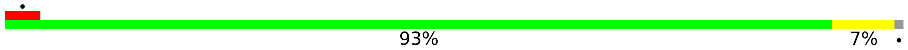
- Molecule 23: 60S ribosomal protein L22-A

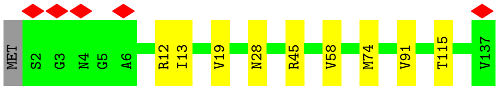
Chain U:



- Molecule 24: 60S ribosomal protein L23-A

Chain V:



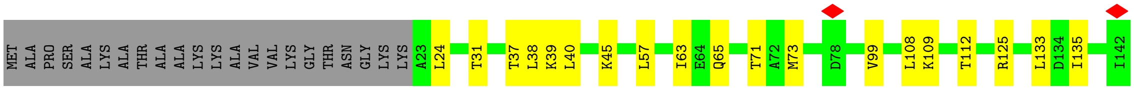


- Molecule 25: 60S ribosomal protein L24-A

Chain W:

- Molecule 26: 60S ribosomal protein L25

Chain X:

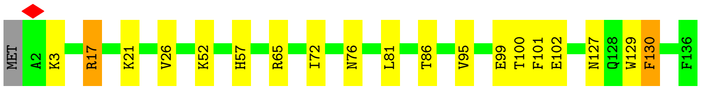


- Molecule 27: 60S ribosomal protein L26-A

Chain Y:

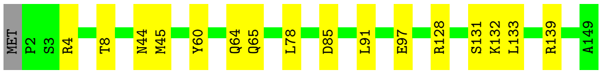
- Molecule 28: 60S ribosomal protein L27-A

Chain Z:



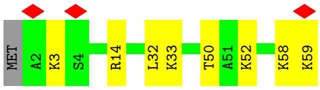
- Molecule 29: 60S ribosomal protein L28

Chain a:



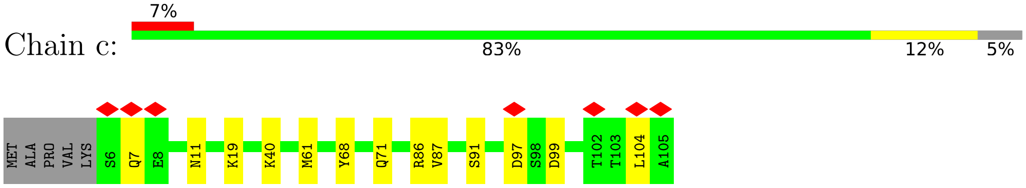
- Molecule 30: 60S ribosomal protein L29

Chain b:



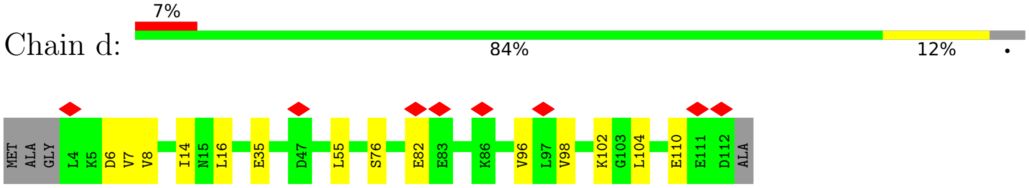
- Molecule 31: 60S ribosomal protein L30

Chain c:



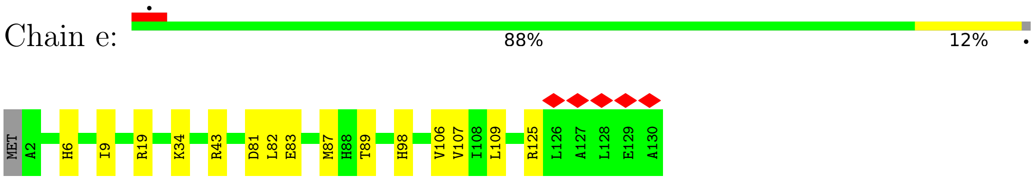
- Molecule 32: 60S ribosomal protein L31-A

Chain d:



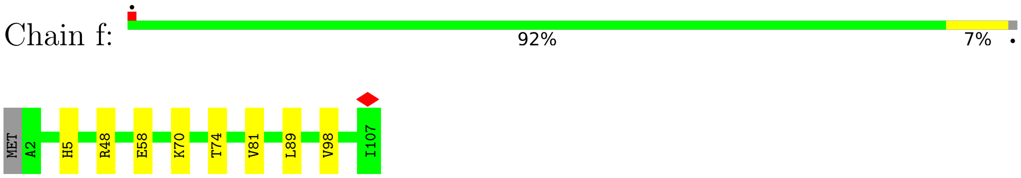
- Molecule 33: 60S ribosomal protein L32

Chain e:



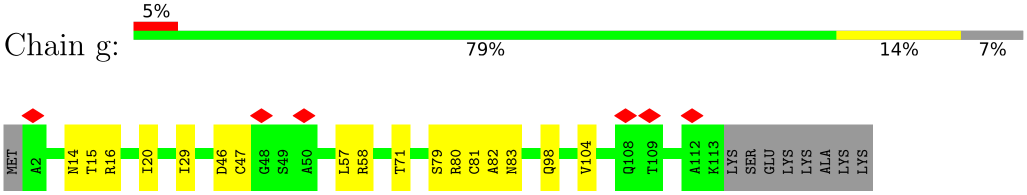
- Molecule 34: 60S ribosomal protein L33-A

Chain f:



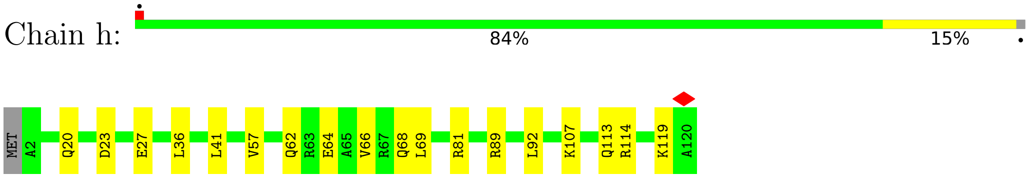
- Molecule 35: 60S ribosomal protein L34-A

Chain g:



- Molecule 36: 60S ribosomal protein L35-A

Chain h:

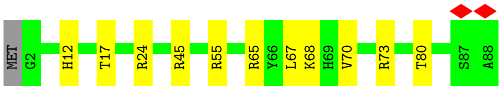


- Molecule 37: 60S ribosomal protein L36-A

Chain i:

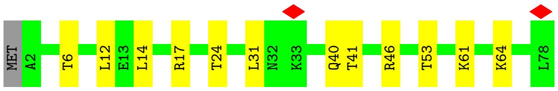
- Molecule 38: 60S ribosomal protein L37-A

Chain j:



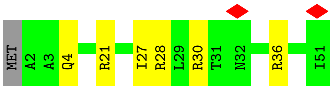
- Molecule 39: 60S ribosomal protein L38

Chain k:



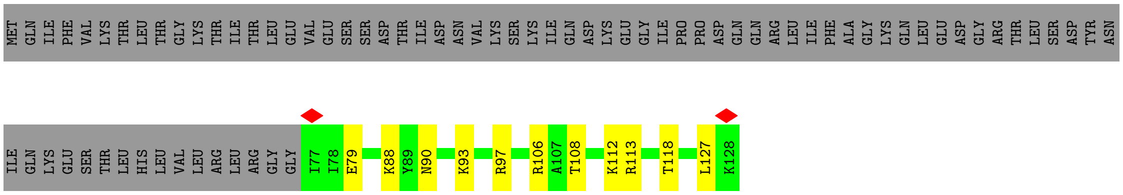
- Molecule 40: 60S ribosomal protein L39

Chain l:



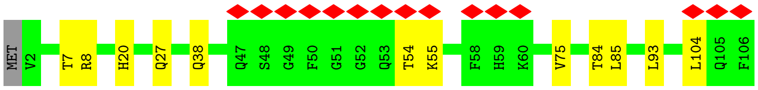
- Molecule 41: Ubiquitin-60S ribosomal protein L40

Chain m:



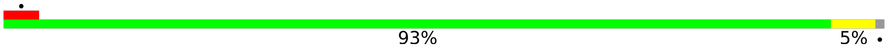
- Molecule 42: 60S ribosomal protein L42-A

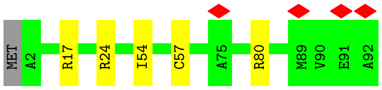
Chain o:



- Molecule 43: 60S ribosomal protein L43-A

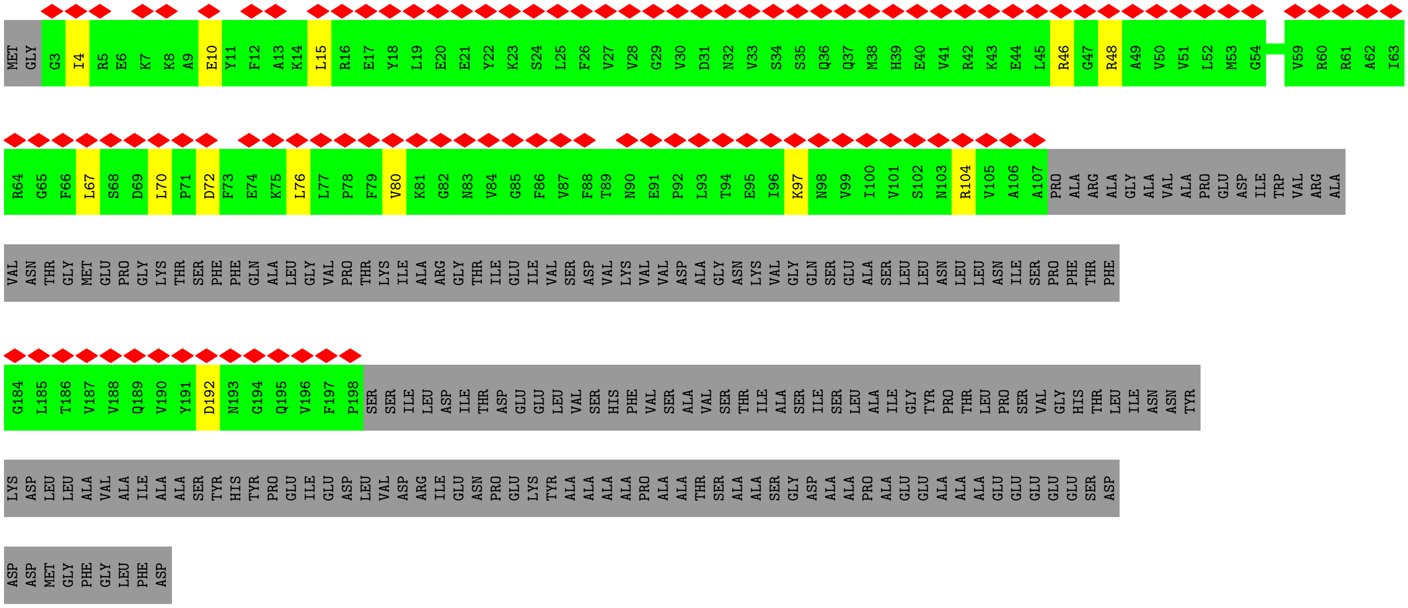
Chain p:





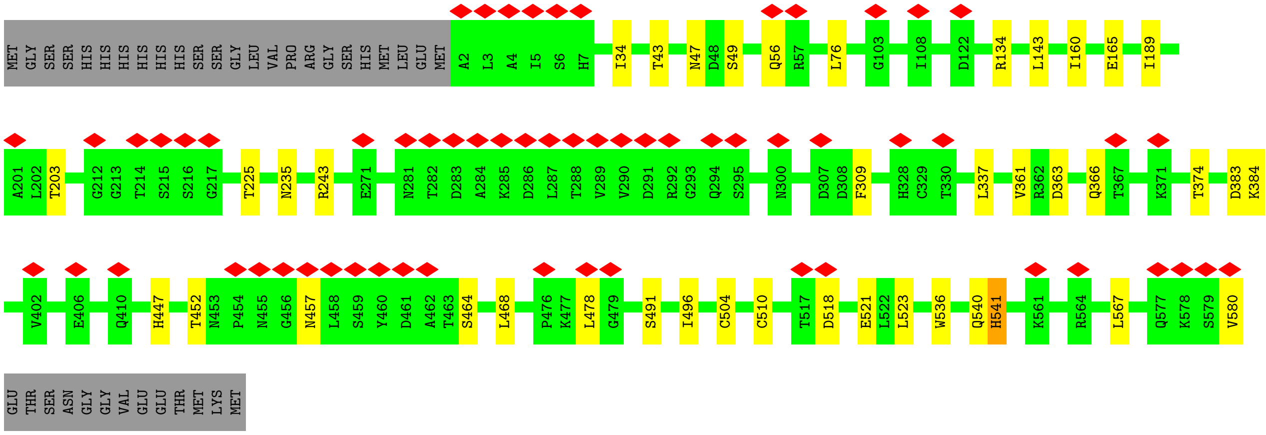
- Molecule 44: 60S acidic ribosomal protein P0

Chain q:



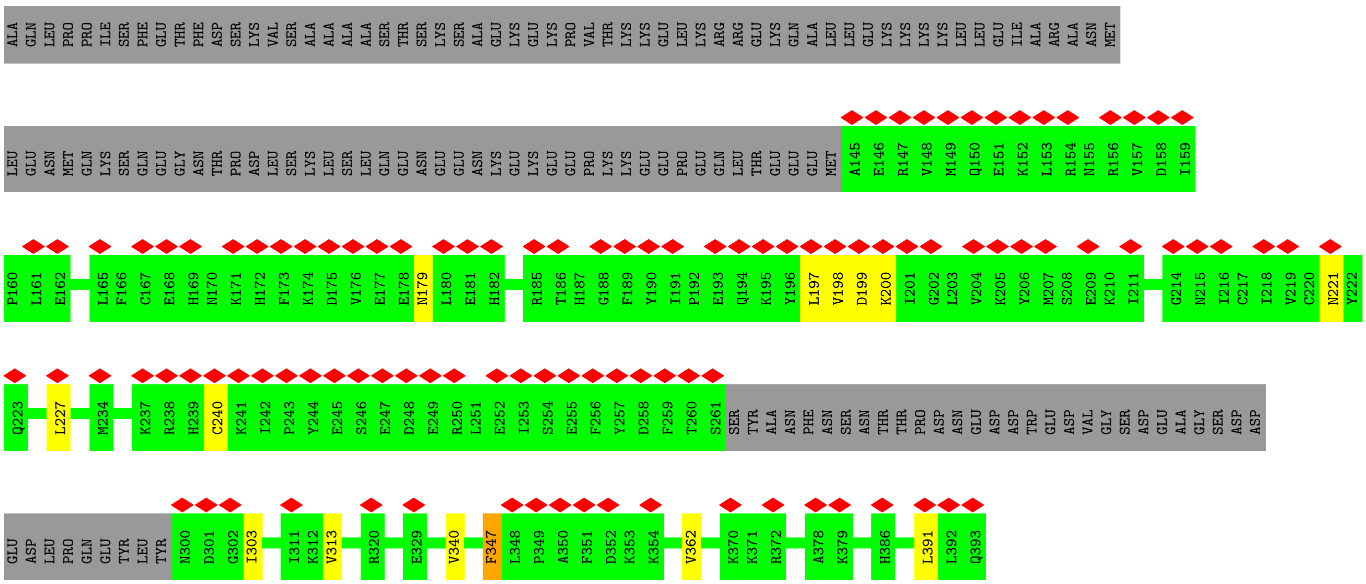
- Molecule 45: Probable metalloprotease ARX1

Chain x:



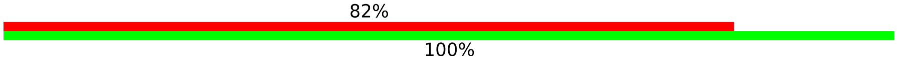
- Molecule 46: Cytoplasmic 60S subunit biogenesis factor REI1

Chain y:



- Molecule 47: ALB1

Chain z:



4 Experimental information

Property	**Value**	**Source**
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	22040	Depositor
Resolution determination method	Not provided	
CTF correction method	PER DETECTOR FRAME	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{Å}^2)$	20	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	100720	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.352	Depositor
Minimum map value	-0.140	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.028	Depositor
Recommended contour level	0.06	Depositor
Map size (Å)	300.24, 300.24, 300.24	wwPDB
Map dimensions	216, 216, 216	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.39, 1.39, 1.39	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: P5P, ZN, MG, Y5P

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| >5$	RMSZ	$\#\|Z\| >5$
1	5	0.45	1/74039 (0.0%)	0.94	44/115426 (0.0%)
2	7	0.33	0/2883	0.85	0/4491
3	8	0.47	0/3746	0.97	1/5832 (0.0%)
4	A	0.34	0/1662	0.55	0/2236
5	B	0.36	0/3146	0.55	0/4228
6	C	0.37	0/2800	0.58	0/3790
7	D	0.34	0/2408	0.51	0/3248
8	E	0.34	0/1377	0.58	0/1851
9	F	0.36	0/1828	0.54	0/2461
10	G	0.34	0/1795	0.55	0/2429
11	H	0.34	0/1539	0.50	0/2073
12	I	0.34	0/1758	0.57	0/2358
13	J	0.33	0/1374	0.54	0/1842
14	L	0.35	0/1573	0.59	0/2113
15	M	0.34	0/1074	0.54	0/1446
16	N	0.43	0/1757	0.57	0/2354
17	O	0.37	0/1585	0.52	0/2128
18	P	0.39	0/1465	0.55	0/1968
19	Q	0.35	0/1465	0.56	0/1965
20	R	0.34	0/1275	0.48	0/1702
21	S	0.37	0/1473	0.54	0/1980
22	T	0.36	0/1300	0.51	0/1743
23	U	0.34	0/825	0.54	0/1120
24	V	0.33	0/1018	0.52	0/1369
25	W	0.36	0/533	0.47	0/707
26	X	0.35	0/974	0.60	0/1314
27	Y	0.33	0/1004	0.52	0/1341
28	Z	0.36	0/1118	0.59	0/1497
29	a	0.38	0/1204	0.57	0/1612
30	b	0.33	0/473	0.53	0/629
31	c	0.35	0/775	0.53	0/1040
32	d	0.38	0/897	0.58	0/1205

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	e	0.37	0/1055	0.54	0/1413
34	f	0.39	0/868	0.55	0/1168
35	g	0.35	0/890	0.57	0/1189
36	h	0.37	0/974	0.55	0/1297
37	i	0.33	0/777	0.53	0/1033
38	j	0.39	0/696	0.58	0/923
39	k	0.35	0/614	0.58	0/822
40	l	0.37	0/443	0.53	0/588
41	m	0.33	0/423	0.53	0/562
42	o	0.38	0/860	0.59	0/1136
43	p	0.34	0/701	0.53	0/934
44	q	0.55	0/977	0.63	0/1313
45	x	0.37	0/4557	0.57	0/6189
46	y	0.41	0/1759	0.55	0/2363
All	All	0.41	1/137737 (0.0%)	0.82	45/202428 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	C	0	2
13	J	0	1
16	N	0	2
28	Z	0	1
32	d	0	2
35	g	0	1
45	x	0	2
46	y	0	1
All	All	0	12

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	5	1394	A	N9-C4	-5.33	1.34	1.37

The worst 5 of 45 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	5	2307	G	C4-N9-C1’	-8.80	115.06	126.50
1	5	2307	G	C8-N9-C1’	8.09	137.51	127.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	1555	U	N3-C2-O2	-8.00	116.60	122.20
1	5	1812	G	N3-C4-N9	-7.42	121.55	126.00
1	5	2309	A	C8-N9-C4	-6.81	103.08	105.80

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	C	148	ILE	Peptide
6	C	197	ARG	Peptide
13	J	9	MET	Peptide
16	N	183	THR	Peptide
16	N	184	LYS	Peptide

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	
4	A	210/254 (83%)	193 (92%)	17 (8%)	0	100	100
5	B	384/387 (99%)	359 (94%)	25 (6%)	0	100	100
6	C	359/362 (99%)	330 (92%)	27 (8%)	2 (1%)	22	57
7	D	292/297 (98%)	283 (97%)	7 (2%)	2 (1%)	19	54
8	E	173/176 (98%)	160 (92%)	10 (6%)	3 (2%)	7	35
9	F	221/244 (91%)	211 (96%)	9 (4%)	1 (0%)	25	60
10	G	229/256 (90%)	201 (88%)	26 (11%)	2 (1%)	14	48
11	H	189/191 (99%)	178 (94%)	10 (5%)	1 (0%)	25	60

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	I	209/221 (95%)	193 (92%)	16 (8%)	0	100	100
13	J	167/174 (96%)	143 (86%)	19 (11%)	5 (3%)	3	26
14	L	192/199 (96%)	169 (88%)	21 (11%)	2 (1%)	13	46
15	M	135/138 (98%)	131 (97%)	4 (3%)	0	100	100
16	N	201/204 (98%)	189 (94%)	10 (5%)	2 (1%)	13	46
17	O	195/199 (98%)	190 (97%)	5 (3%)	0	100	100
18	P	181/184 (98%)	176 (97%)	5 (3%)	0	100	100
19	Q	183/186 (98%)	173 (94%)	9 (5%)	1 (0%)	25	60
20	R	154/189 (82%)	148 (96%)	6 (4%)	0	100	100
21	S	169/172 (98%)	161 (95%)	8 (5%)	0	100	100
22	T	157/160 (98%)	153 (98%)	2 (1%)	2 (1%)	10	41
23	U	100/121 (83%)	95 (95%)	5 (5%)	0	100	100
24	V	134/137 (98%)	130 (97%)	4 (3%)	0	100	100
25	W	61/155 (39%)	57 (93%)	4 (7%)	0	100	100
26	X	118/142 (83%)	108 (92%)	10 (8%)	0	100	100
27	Y	124/127 (98%)	118 (95%)	5 (4%)	1 (1%)	16	51
28	Z	133/136 (98%)	114 (86%)	16 (12%)	3 (2%)	5	31
29	a	146/149 (98%)	131 (90%)	14 (10%)	1 (1%)	19	54
30	b	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
31	c	98/105 (93%)	91 (93%)	7 (7%)	0	100	100
32	d	107/113 (95%)	97 (91%)	9 (8%)	1 (1%)	14	48
33	e	127/130 (98%)	119 (94%)	7 (6%)	1 (1%)	16	51
34	f	104/107 (97%)	98 (94%)	6 (6%)	0	100	100
35	g	110/121 (91%)	100 (91%)	8 (7%)	2 (2%)	7	35
36	h	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
37	i	97/100 (97%)	87 (90%)	7 (7%)	3 (3%)	3	26
38	j	85/88 (97%)	78 (92%)	7 (8%)	0	100	100
39	k	75/78 (96%)	68 (91%)	6 (8%)	1 (1%)	10	41
40	l	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
41	m	50/128 (39%)	46 (92%)	4 (8%)	0	100	100
42	o	103/106 (97%)	96 (93%)	7 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	p	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
44	q	116/312 (37%)	109 (94%)	7 (6%)	0	100	100
45	x	577/616 (94%)	540 (94%)	37 (6%)	0	100	100
46	y	207/414 (50%)	192 (93%)	15 (7%)	0	100	100
All	All	6982/7900 (88%)	6509 (93%)	437 (6%)	36 (0%)	27	60

5 of 36 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	E	98	VAL
13	J	10	ARG
13	J	95	ASN
16	N	184	LYS
13	J	115	LYS

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	A	166/196 (85%)	139 (84%)	27 (16%)	2	12
5	B	319/323 (99%)	269 (84%)	50 (16%)	2	13
6	C	288/289 (100%)	240 (83%)	48 (17%)	2	12
7	D	243/245 (99%)	216 (89%)	27 (11%)	5	21
8	E	136/153 (89%)	119 (88%)	17 (12%)	3	18
9	F	187/205 (91%)	166 (89%)	21 (11%)	5	21
10	G	177/208 (85%)	154 (87%)	23 (13%)	3	18
11	H	171/171 (100%)	144 (84%)	27 (16%)	2	13
12	I	179/187 (96%)	157 (88%)	22 (12%)	4	19
13	J	147/150 (98%)	122 (83%)	25 (17%)	1	11
14	L	154/159 (97%)	136 (88%)	18 (12%)	4	20
15	M	108/109 (99%)	93 (86%)	15 (14%)	3	17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	N	175/176 (99%)	147 (84%)	28 (16%)	2	13
17	O	160/162 (99%)	136 (85%)	24 (15%)	2	14
18	P	145/146 (99%)	128 (88%)	17 (12%)	4	20
19	Q	150/151 (99%)	124 (83%)	26 (17%)	1	10
20	R	129/154 (84%)	111 (86%)	18 (14%)	3	16
21	S	155/156 (99%)	129 (83%)	26 (17%)	1	11
22	T	136/137 (99%)	112 (82%)	24 (18%)	1	10
23	U	89/107 (83%)	76 (85%)	13 (15%)	2	15
24	V	104/105 (99%)	95 (91%)	9 (9%)	8	30
25	W	55/129 (43%)	50 (91%)	5 (9%)	7	28
26	X	104/118 (88%)	85 (82%)	19 (18%)	1	9
27	Y	109/110 (99%)	90 (83%)	19 (17%)	1	10
28	Z	115/116 (99%)	98 (85%)	17 (15%)	2	15
29	a	118/119 (99%)	103 (87%)	15 (13%)	3	18
30	b	46/47 (98%)	38 (83%)	8 (17%)	1	10
31	c	84/88 (96%)	71 (84%)	13 (16%)	2	13
32	d	94/97 (97%)	83 (88%)	11 (12%)	4	20
33	e	110/111 (99%)	96 (87%)	14 (13%)	3	18
34	f	90/91 (99%)	82 (91%)	8 (9%)	8	29
35	g	95/103 (92%)	81 (85%)	14 (15%)	2	15
36	h	103/105 (98%)	85 (82%)	18 (18%)	1	10
37	i	80/82 (98%)	59 (74%)	21 (26%)	0	3
38	j	70/71 (99%)	59 (84%)	11 (16%)	2	13
39	k	67/69 (97%)	56 (84%)	11 (16%)	2	12
40	l	45/46 (98%)	39 (87%)	6 (13%)	3	17
41	m	47/116 (40%)	36 (77%)	11 (23%)	0	4
42	o	90/91 (99%)	78 (87%)	12 (13%)	3	17
43	p	71/72 (99%)	66 (93%)	5 (7%)	12	36
44	q	105/254 (41%)	92 (88%)	13 (12%)	4	18
45	x	508/540 (94%)	468 (92%)	40 (8%)	10	33
46	y	182/378 (48%)	168 (92%)	14 (8%)	10	34

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	5906/6642 (89%)	5096 (86%)	810 (14%)	5 17

5 of 810 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
22	T	26	HIS
29	a	91	LEU
46	y	199	ASP
22	T	130	ARG
22	T	25	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 98 such sidechains are listed below:

Mol	Chain	Res	Type
26	X	137	ASN
31	c	75	ASN
27	Y	100	HIS
29	a	44	ASN
35	g	52	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3084/3396 (90%)	666 (21%)	79 (2%)
2	7	120/121 (99%)	13 (10%)	0
3	8	157/158 (99%)	42 (26%)	6 (3%)
All	All	3361/3675 (91%)	721 (21%)	85 (2%)

5 of 721 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	14	U
1	5	15	C
1	5	21	G
1	5	22	G
1	5	26	A

5 of 85 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5	2662	G
1	5	3228	C
1	5	2772	C
1	5	3078	U
1	5	3317	U

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

20 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	Y5P	5	1992	1	14,19,20	2.23	1 (7%)	18,26,29	1.04	1 (5%)
1	Y5P	5	1990	1	14,19,20	2.27	1 (7%)	18,26,29	1.07	1 (5%)
1	P5P	5	2022	1	16,23,24	0.79	0	14,33,36	0.79	0
1	P5P	5	2019	1	16,23,24	0.80	0	14,33,36	0.80	0
1	Y5P	5	1994	1	14,19,20	2.30	1 (7%)	18,26,29	1.07	1 (5%)
1	Y5P	5	1988	1	14,19,20	2.26	1 (7%)	18,26,29	1.03	1 (5%)
1	P5P	5	2017	1	16,23,24	0.78	0	14,33,36	0.76	0
1	P5P	5	2020	1	16,23,24	0.78	0	14,33,36	0.78	0
1	P5P	5	2021	1	16,23,24	0.77	0	14,33,36	0.75	0
1	P5P	5	2016	1	16,23,24	0.78	0	14,33,36	0.77	0
1	Y5P	5	1995	1	14,19,20	2.29	1 (7%)	18,26,29	0.97	1 (5%)
1	P5P	5	2025	1	16,23,24	0.78	0	14,33,36	0.74	0
1	Y5P	5	1987	1	14,19,20	2.32	1 (7%)	18,26,29	1.02	1 (5%)
1	P5P	5	2024	1	16,23,24	0.79	0	14,33,36	0.76	0
1	Y5P	5	1991	1	14,19,20	2.35	1 (7%)	18,26,29	1.01	1 (5%)
1	P5P	5	2018	1	16,23,24	0.78	0	14,33,36	0.77	0
1	Y5P	5	1986	1	14,19,20	2.24	1 (7%)	18,26,29	1.02	1 (5%)
1	Y5P	5	1993	1	14,19,20	2.36	1 (7%)	18,26,29	1.01	1 (5%)
1	Y5P	5	1989	1	14,19,20	2.31	1 (7%)	18,26,29	0.97	1 (5%)
1	P5P	5	2023	1	16,23,24	0.81	0	14,33,36	0.83	0

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

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

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	5	1991	Y5P	C4-N3	-8.61	1.38	1.46
1	5	1993	Y5P	C4-N3	-8.61	1.38	1.46
1	5	1987	Y5P	C4-N3	-8.48	1.38	1.46
1	5	1989	Y5P	C4-N3	-8.47	1.38	1.46
1	5	1994	Y5P	C4-N3	-8.44	1.38	1.46

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	5	1994	Y5P	N1-C2-N3	-3.75	114.34	125.33
1	5	1986	Y5P	N1-C2-N3	-3.73	114.38	125.33
1	5	1992	Y5P	N1-C2-N3	-3.70	114.47	125.33
1	5	1990	Y5P	N1-C2-N3	-3.69	114.52	125.33
1	5	1988	Y5P	N1-C2-N3	-3.64	114.67	125.33

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

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

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 286 ligands modelled in this entry, 286 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	5	2
47	z	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	1953:G	O3'	1986:Y5P	P	107.33
1	5	2025:P5P	O3'	2093:A	P	105.65
1	z	107:UNK	C	115:UNK	N	20.22
1	z	127:UNK	C	131:UNK	N	9.70

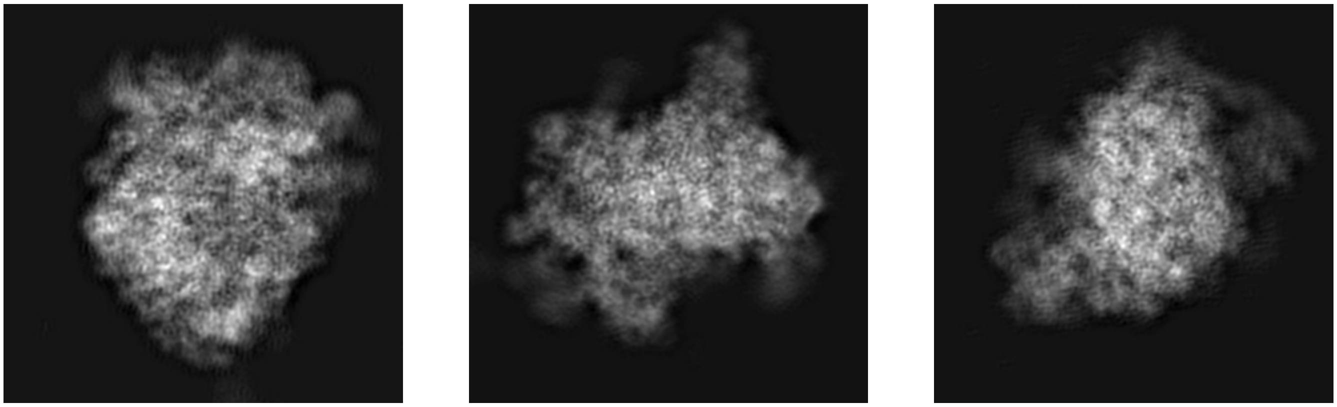
6 Map visualisation ⓘ

This section contains visualisations of the EMDB entry EMD-3152. 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

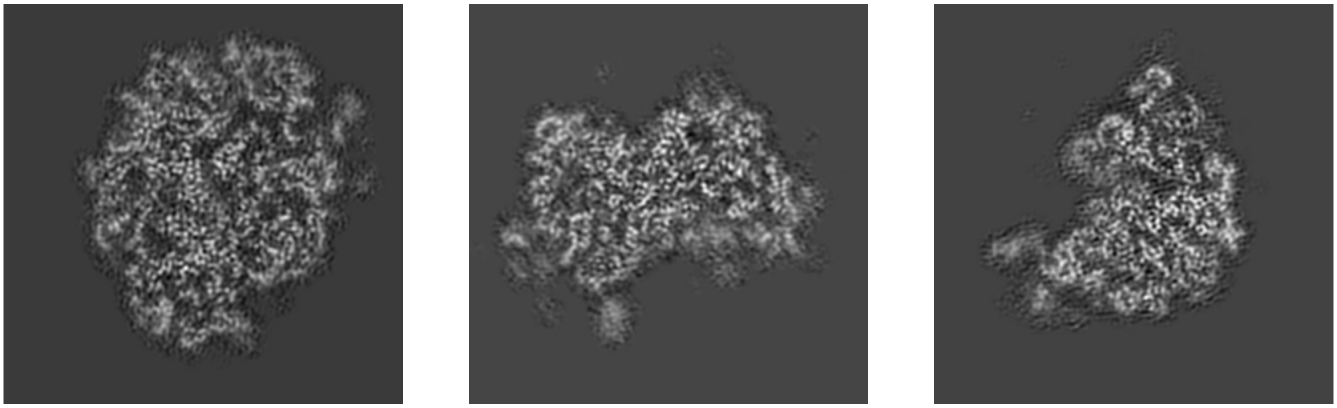


X Y Z

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

6.2 Central slices ⓘ

6.2.1 Primary map

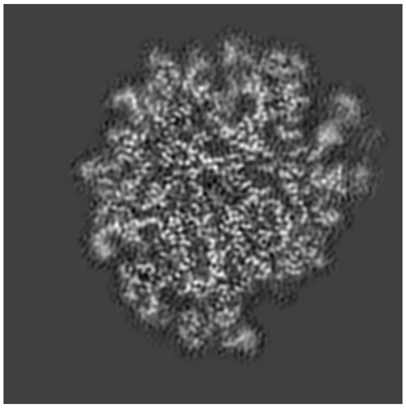


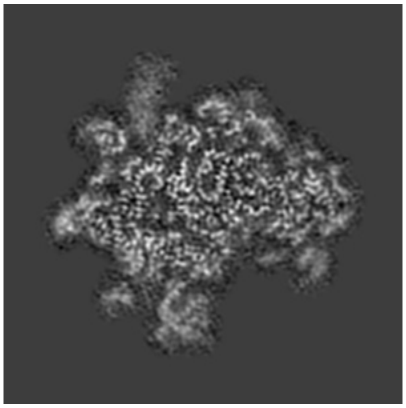
X Index: 108 Y Index: 108 Z Index: 108

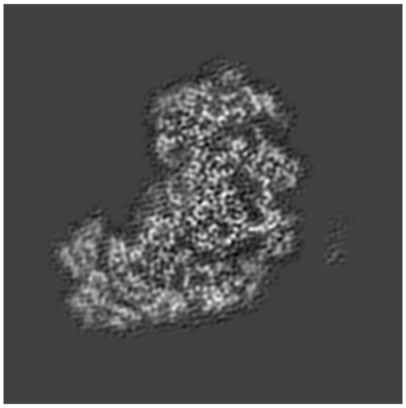
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices

6.3.1 Primary map


X Index: 113

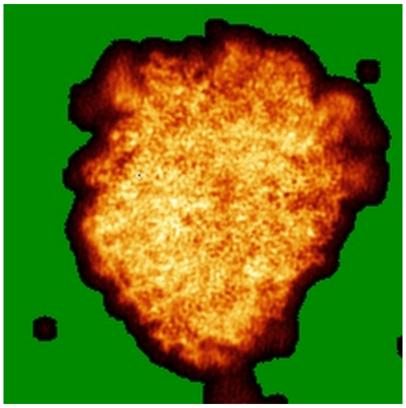

Y Index: 87

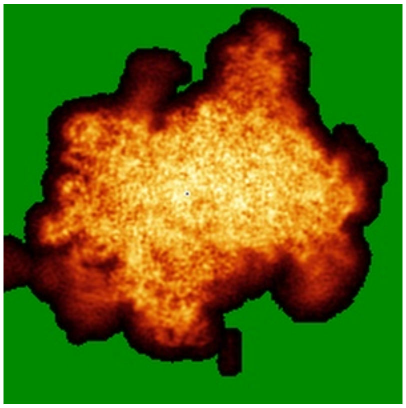

Z Index: 94

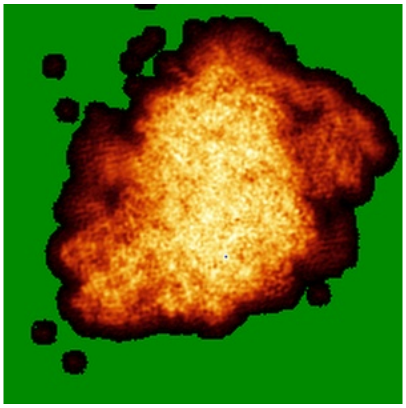
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color)

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 ⓘ

6.5.1 Primary map

X

Y

Z

The images above show the 3D surface view of the map at the recommended contour level 0.06. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

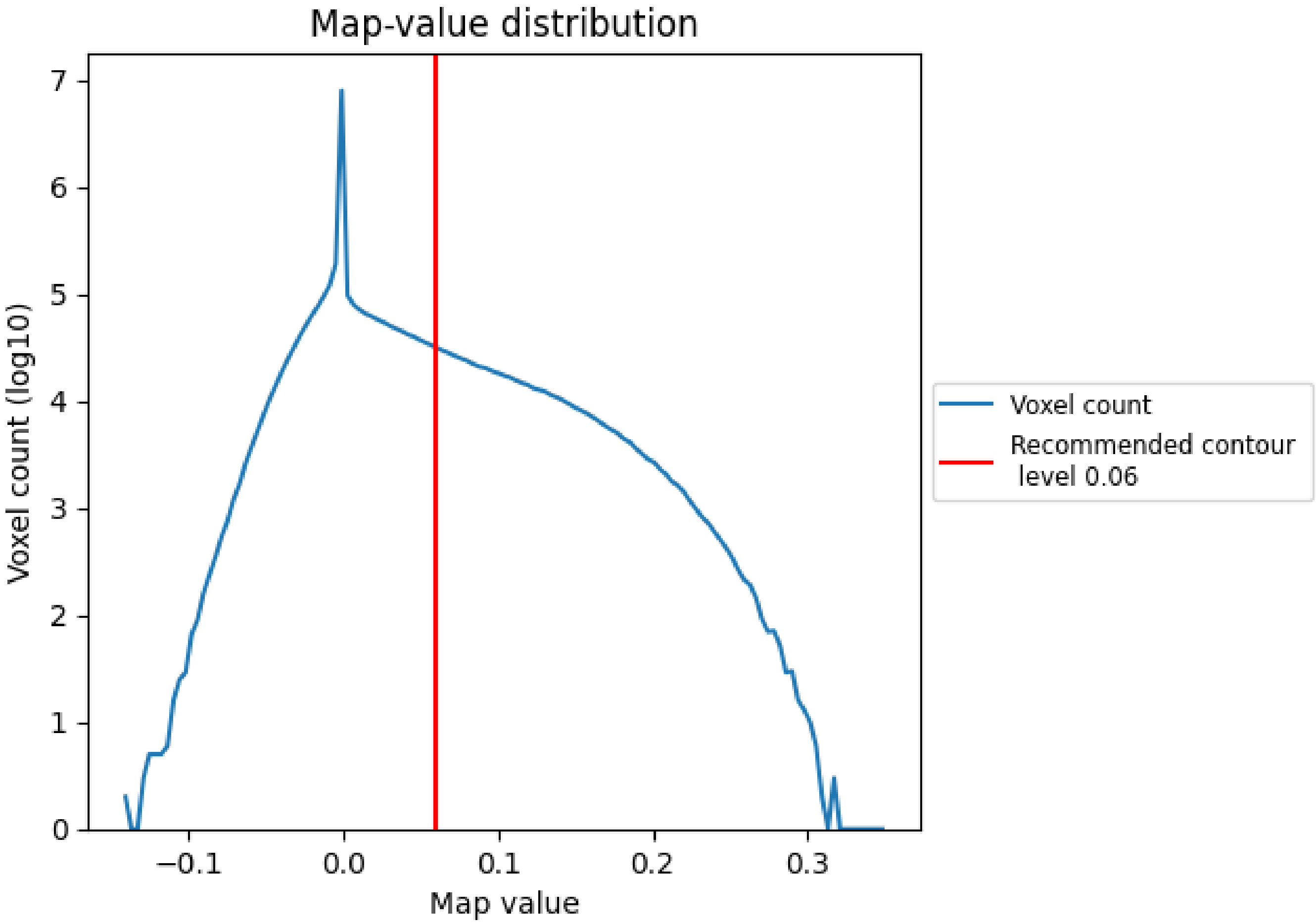
6.6 Mask visualisation ⓘ

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

7 Map analysis (i)

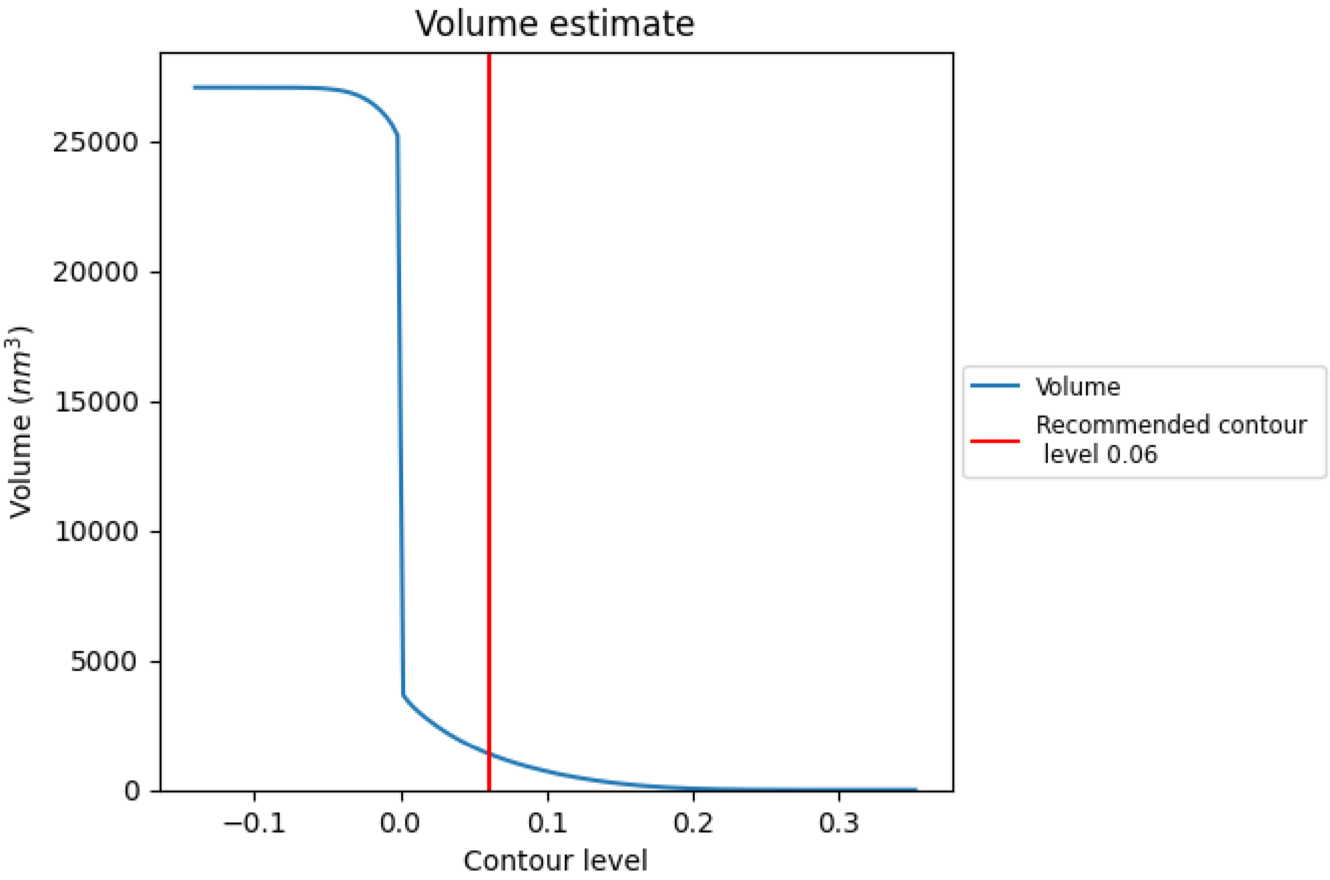
This section contains the results of statistical analysis of the map.

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.

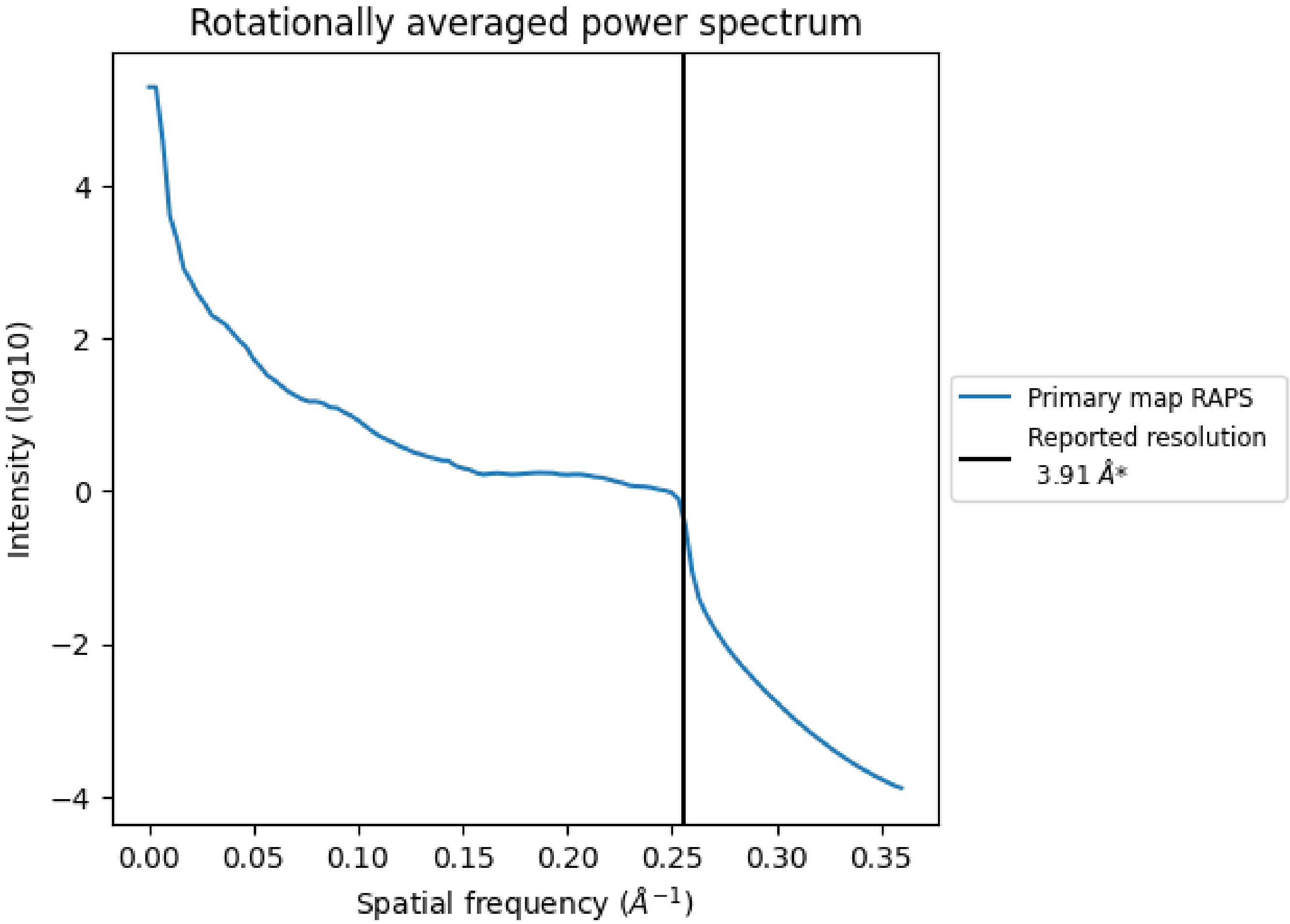
7.2 Volume estimate ⓘ



The volume at the recommended contour level is 1406 nm^3; this corresponds to an approximate mass of 1270 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 0.256 Å^{-1}

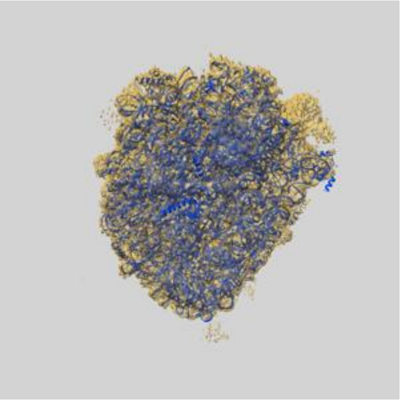
8 Fourier-Shell correlation

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

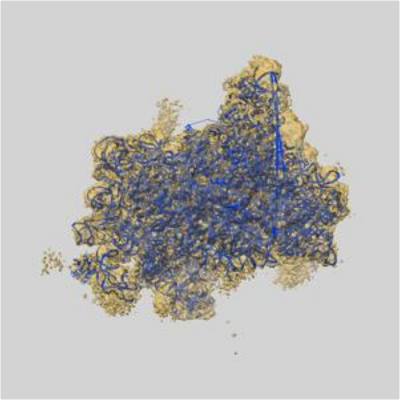
9 Map-model fit ⓘ

This section contains information regarding the fit between EMDB map EMD-3152 and PDB model 5APN. Per-residue inclusion information can be found in section 3 on page 14.

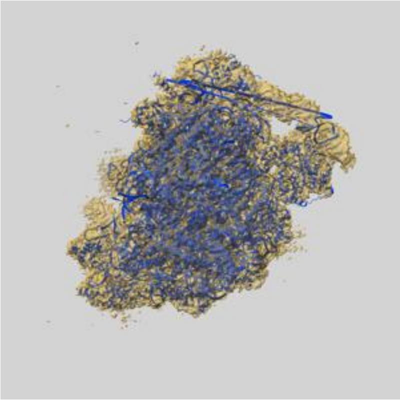
9.1 Map-model overlay ⓘ



X



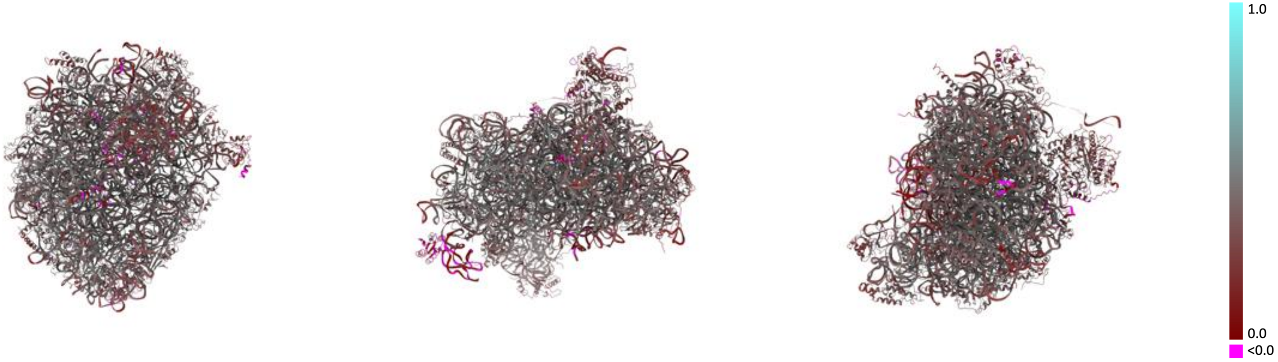
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.06 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.

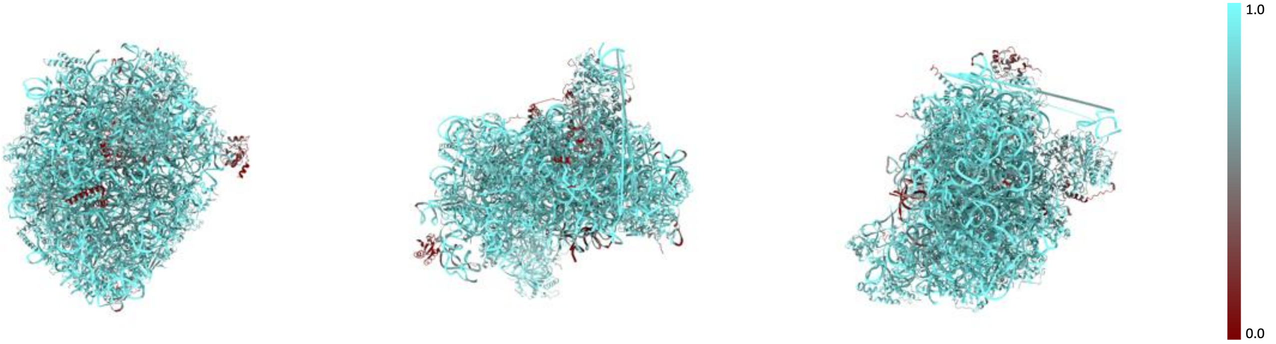
9.2 Q-score mapped to coordinate model ⓘ



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.

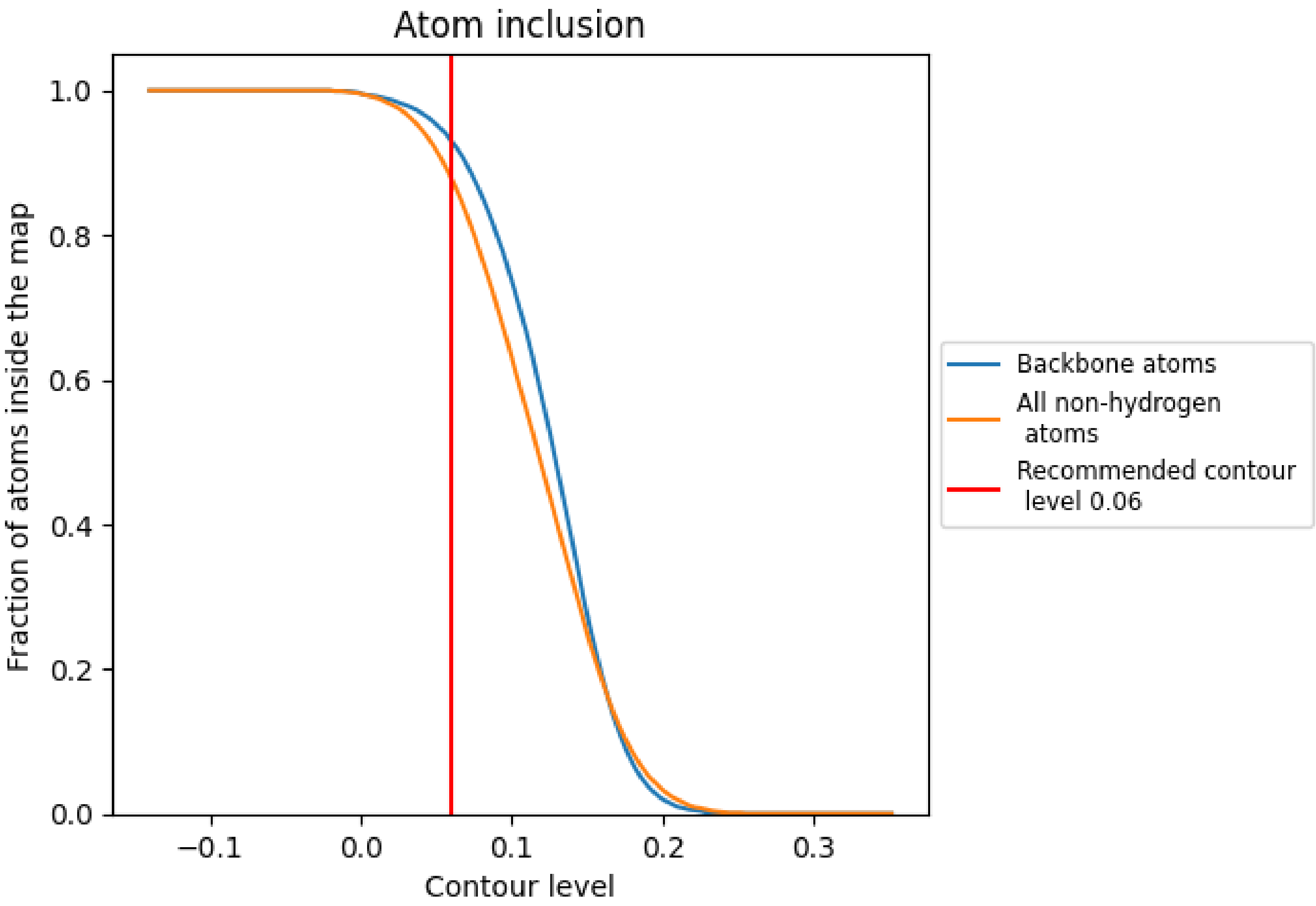
9.3 Atom inclusion mapped to coordinate model ⓘ



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 (0.06).

9.4 Atom inclusion ⓘ



At the recommended contour level, 93% of all backbone atoms, 88% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8780	0.3890
5	0.9420	0.3900
7	0.9870	0.3860
8	0.9580	0.4110
A	0.8140	0.4210
B	0.8650	0.4260
C	0.8610	0.4350
D	0.8470	0.3440
E	0.8500	0.3920
F	0.8400	0.4230
G	0.8500	0.3660
H	0.8500	0.4020
I	0.8290	0.4030
J	0.8310	0.3050
L	0.8480	0.4110
M	0.8670	0.4080
N	0.7920	0.4200
O	0.8620	0.4310
P	0.8190	0.4360
Q	0.8510	0.4350
R	0.8300	0.4090
S	0.8570	0.4310
T	0.8350	0.4310
U	0.7800	0.3730
V	0.8170	0.4070
W	0.8300	0.4050
X	0.8070	0.4340
Y	0.8460	0.4160
Z	0.8500	0.3590
a	0.8690	0.4330
b	0.7810	0.4000
c	0.7620	0.3400
d	0.7760	0.4280
e	0.8150	0.4370
f	0.8560	0.4520

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Chain	Atom inclusion	Q-score
g	0.7940	0.4070
h	0.8330	0.3990
i	0.7840	0.3800
j	0.8490	0.4430
k	0.7900	0.3690
l	0.7830	0.4430
m	0.8190	0.3980
o	0.7230	0.3430
p	0.8000	0.3950
q	0.1230	0.0770
x	0.7050	0.3040
y	0.4140	0.2860
z	0.1510	0.0910