



wwPDB EM Validation Summary Report ⓘ

Dec 10, 2022 – 09:30 am GMT

PDB ID : 5APN
EMDB ID : EMD-3152
Title : Structure of the yeast 60S ribosomal subunit in complex with Arx1, Alb1 and N-terminally tagged Re1
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)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.4, CSD as541be (2020)
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) : 2.31.3

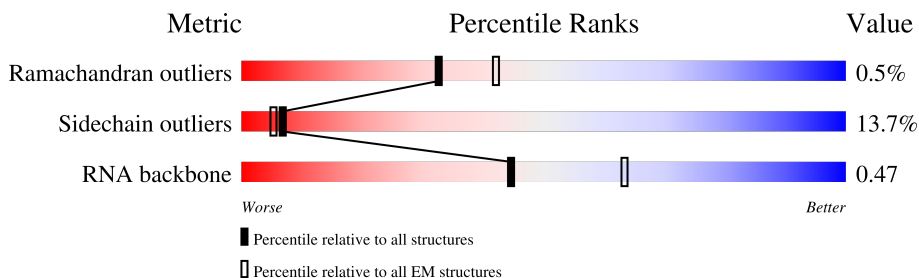
1 Overall quality at a glance

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.




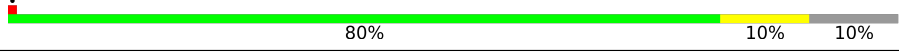

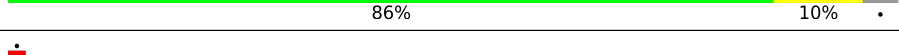
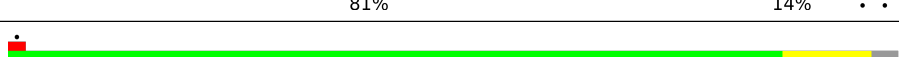
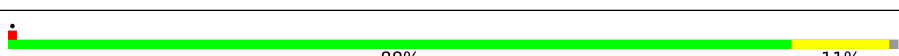


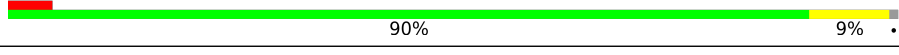




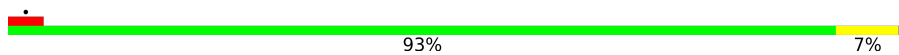




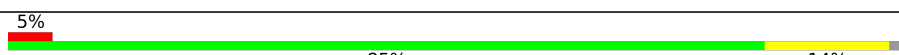
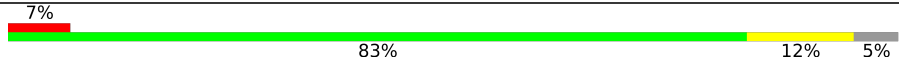





Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	5	3396	
2	7	121	
3	8	158	
4	A	254	
5	B	387	
6	C	362	
7	D	297	
8	E	176	

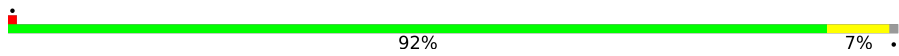


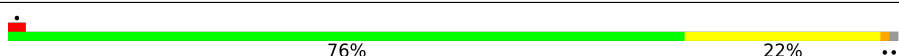
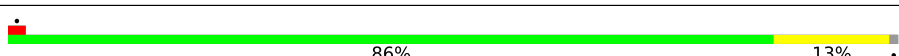
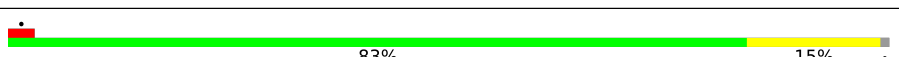
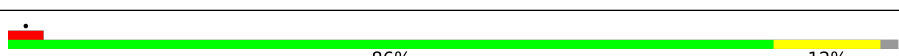

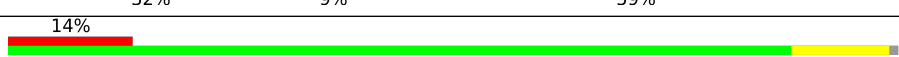

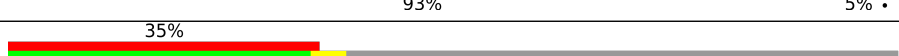
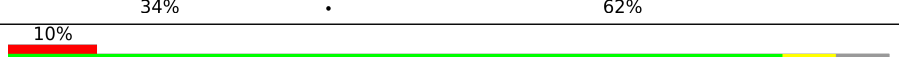


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Mol	Chain	Length	Quality of chain
9	F	244	 82% 9% 9%
10	G	256	 80% 10% 10%
11	H	191	 85% 15%
12	I	221	 86% 10% .
13	J	174	 81% 14% . .
14	L	199	 87% 10% .
15	M	138	 88% 11% .
16	N	204	 85% 13% 8%
17	O	199	 87% 12% .
18	P	184	 90% 9% .
19	Q	186	 85% 15% .
20	R	189	 73% 10% 17%
21	S	172	 84% 15% .
22	T	160	 83% 16% .
23	U	121	 74% 11% 16%
24	V	137	 93% 7% .
25	W	155	 37% 59%
26	X	142	 71% 13% 15%
27	Y	127	 83% 16% .
28	Z	136	 85% 12% . .
29	a	149	 89% 11% .
30	b	59	 85% 14% .
31	c	105	 83% 12% 7% 5%
32	d	113	 84% 12% .
33	e	130	 88% 12% .

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Mol	Chain	Length	Quality of chain
34	f	107	 92% 7%
35	g	121	 79% 14% 5% 7%
36	h	120	 84% 15%
37	i	100	 76% 22%
38	j	88	 86% 13%
39	k	78	 83% 15%
40	l	51	 86% 12%
41	m	128	 32% 9% 59%
42	o	106	 14% 88% 11%
43	p	92	 93% 5%
44	q	312	 35% 34% 62%
45	x	616	 10% 87% 6% 6%
46	y	414	 26% 48% 49%
47	z	85	 82% 100%

2 Entry composition

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
			Total	C	N	O	S		
7	D	294	2359	1489	412	456	2	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 45 is a protein called Probable metalloprotease ARX1.

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

There are 23 discrepancies between the modelled and reference sequences:

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

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

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

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
46	y	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

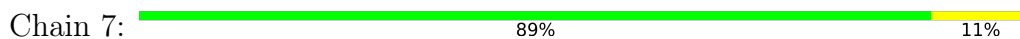
- Molecule 48 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

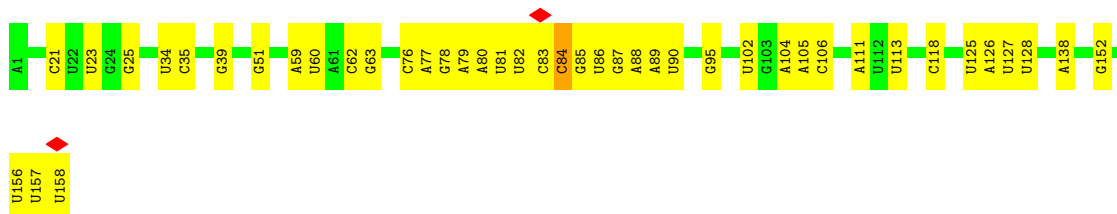
- Molecule 49 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

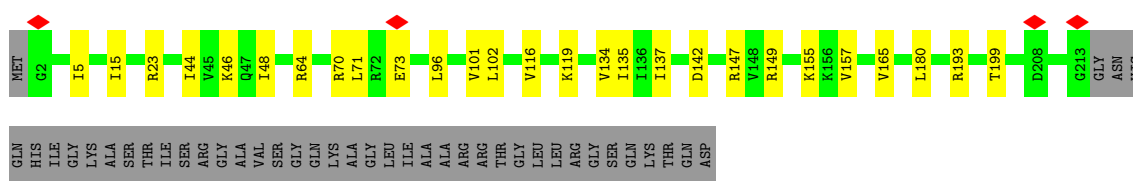
• Molecule 2: 5S rRNA



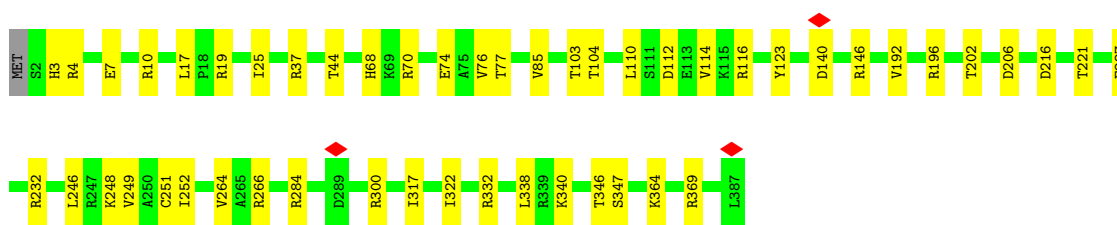
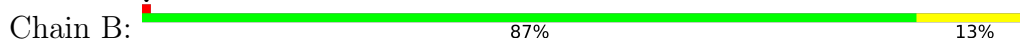
• Molecule 3: 5.8S rRNA



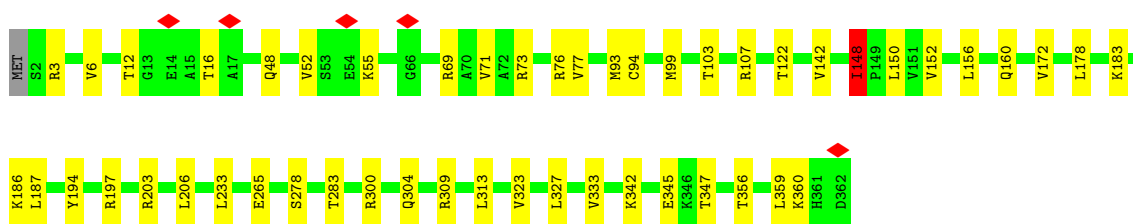
• Molecule 4: 60S ribosomal protein L2-A



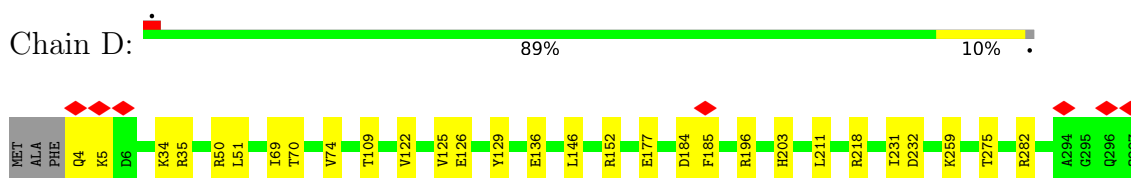
• Molecule 5: 60S ribosomal protein L3



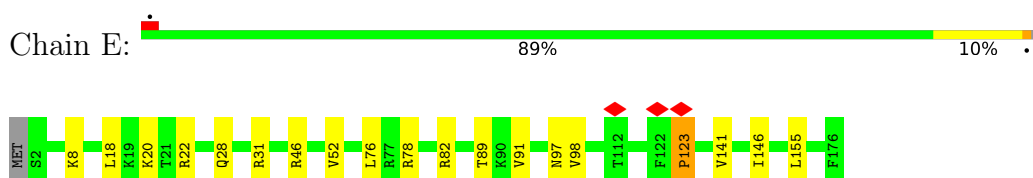
• Molecule 6: 60S ribosomal protein L4-A



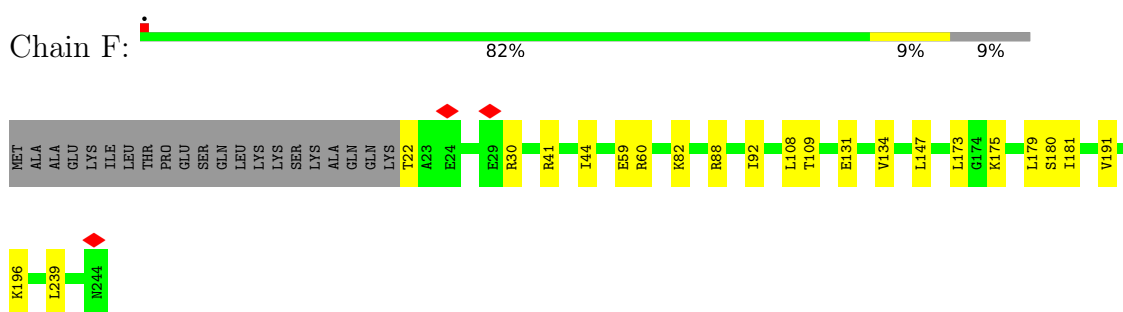
- Molecule 7: 60S ribosomal protein L5



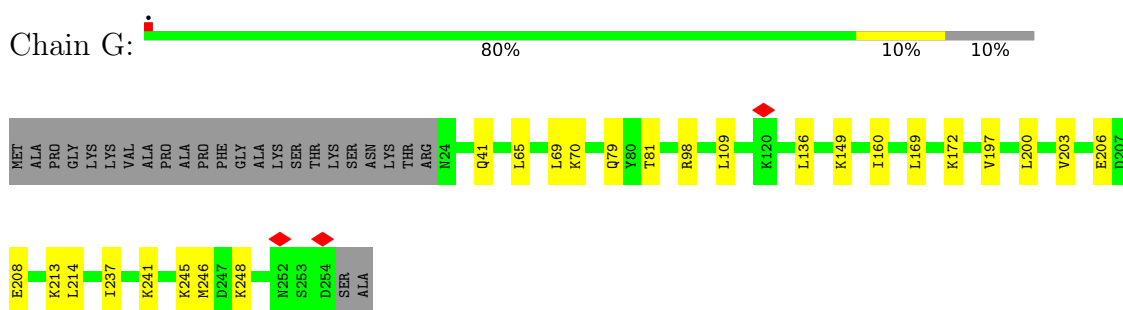
- Molecule 8: 60S ribosomal protein L6-A



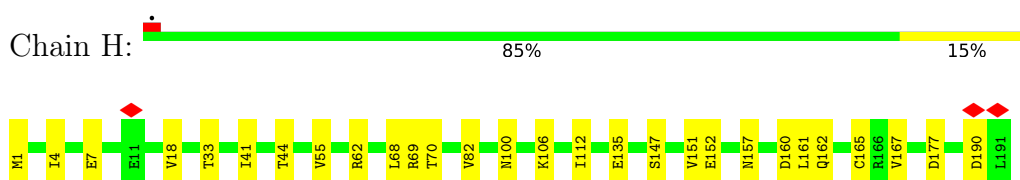
- Molecule 9: 60S ribosomal protein L7-A



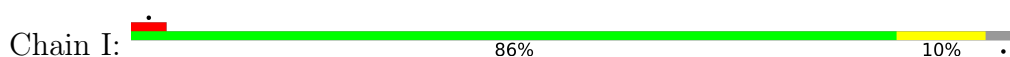
- Molecule 10: 60S ribosomal protein L8-A

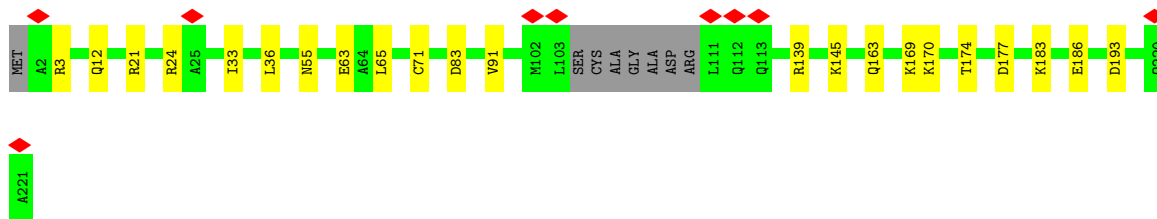


- Molecule 11: 60S ribosomal protein L9-A

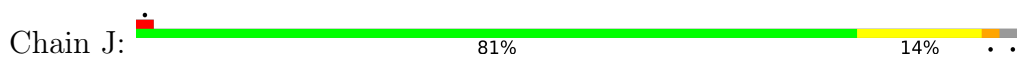


- Molecule 12: 60S ribosomal protein L10

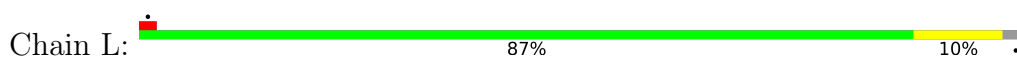




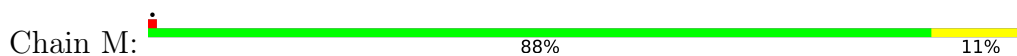
- Molecule 13: 60S ribosomal protein L11-A



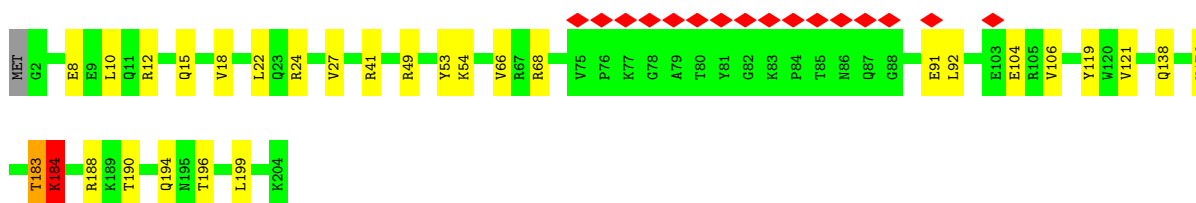
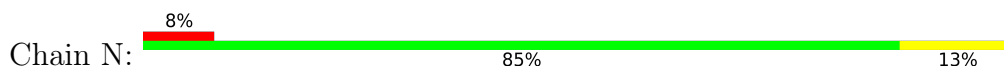
- Molecule 14: 60S ribosomal protein L13-A



- Molecule 15: 60S ribosomal protein L14-A



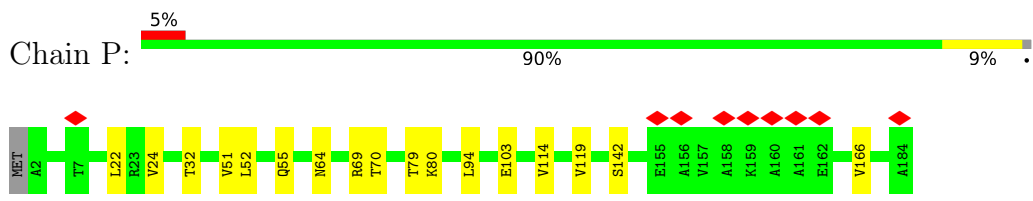
- Molecule 16: 60S ribosomal protein L15-A



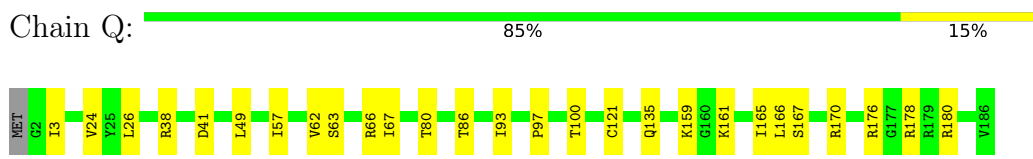
- Molecule 17: 60S ribosomal protein L16-A



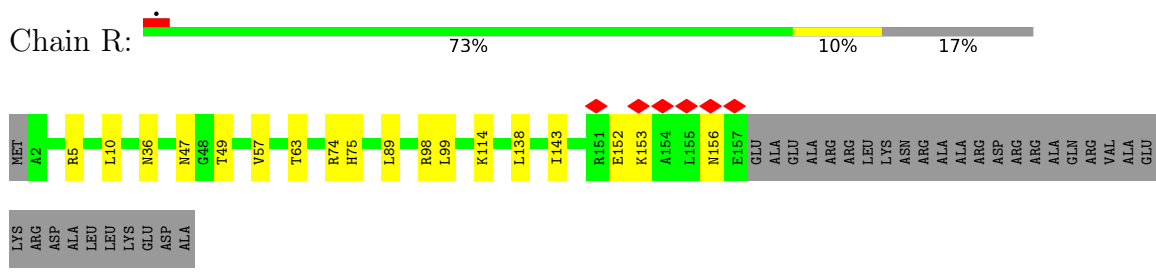
- Molecule 18: 60S ribosomal protein L17-A



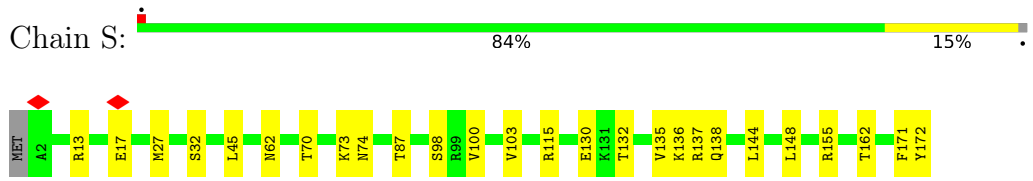
• Molecule 19: 60S ribosomal protein L18-A



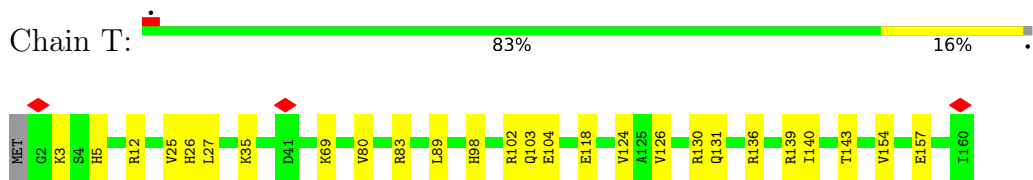
• Molecule 20: 60S ribosomal protein L19-A



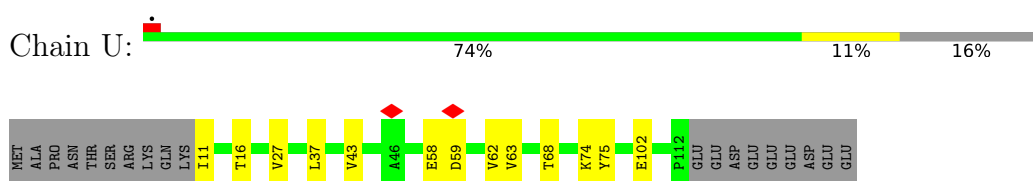
• Molecule 21: 60S ribosomal protein L20-A



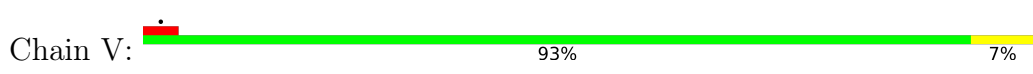
• Molecule 22: 60S ribosomal protein L21-A

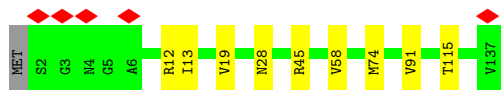


• Molecule 23: 60S ribosomal protein L22-A

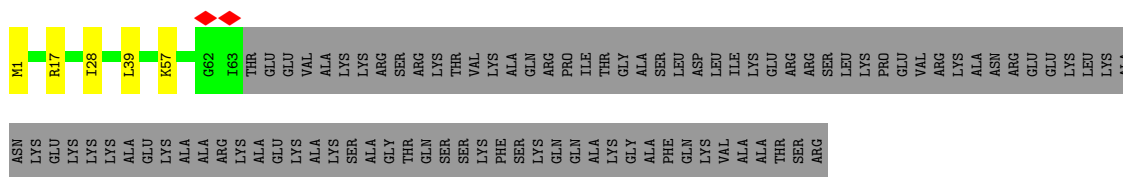


• Molecule 24: 60S ribosomal protein L23-A

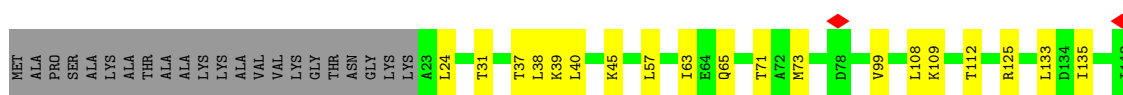




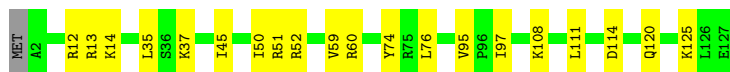
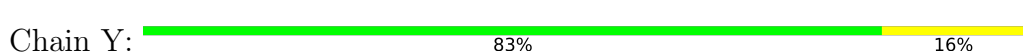
• Molecule 25: 60S ribosomal protein L24-A



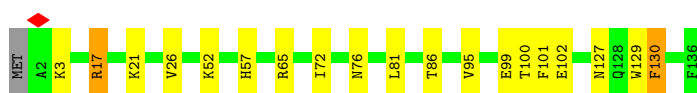
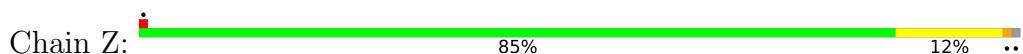
• Molecule 26: 60S ribosomal protein L25



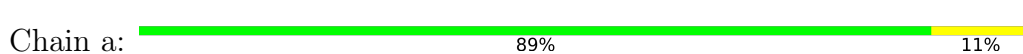
• Molecule 27: 60S ribosomal protein L26-A



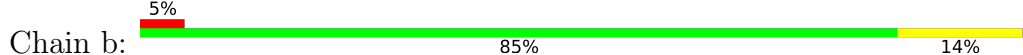
• Molecule 28: 60S ribosomal protein L27-A



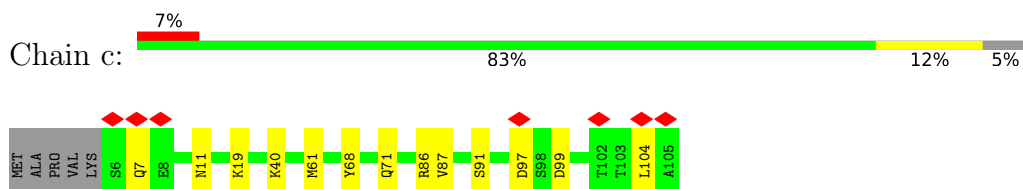
• Molecule 29: 60S ribosomal protein L28



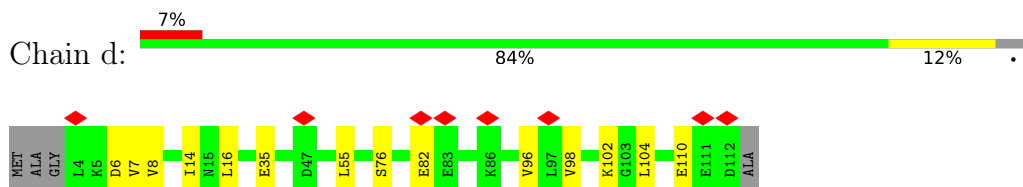
• Molecule 30: 60S ribosomal protein L29



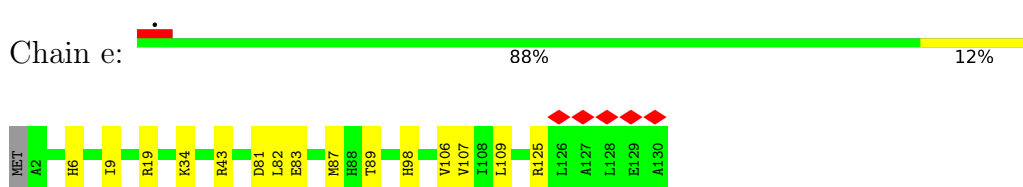
- Molecule 31: 60S ribosomal protein L30



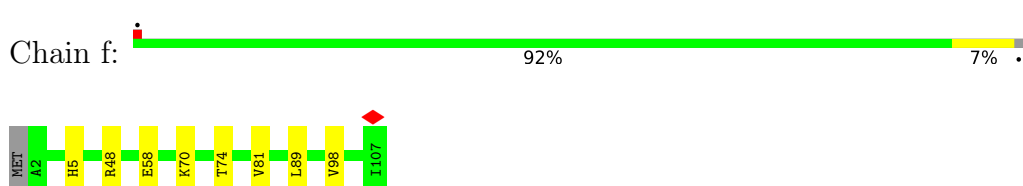
- Molecule 32: 60S ribosomal protein L31-A



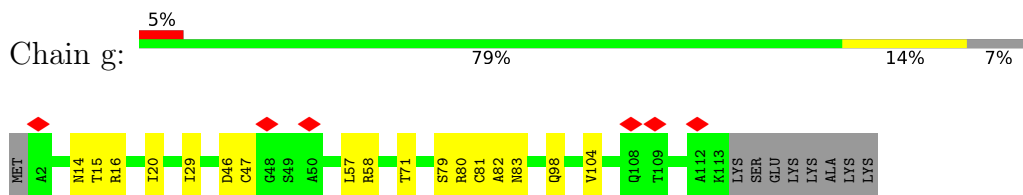
- Molecule 33: 60S ribosomal protein L32



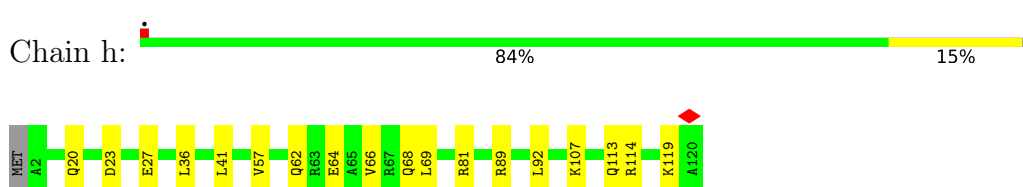
- Molecule 34: 60S ribosomal protein L33-A



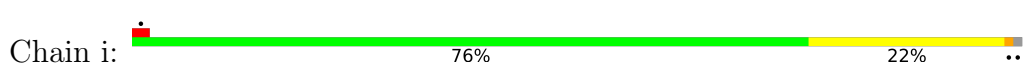
- Molecule 35: 60S ribosomal protein L34-A

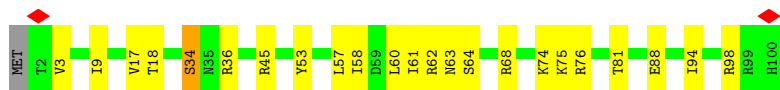


- Molecule 36: 60S ribosomal protein L35-A

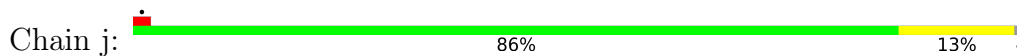


- Molecule 37: 60S ribosomal protein L36-A

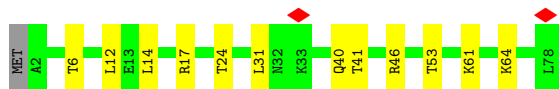
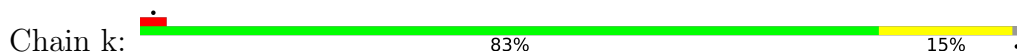




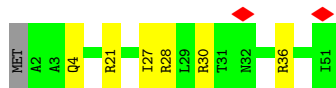
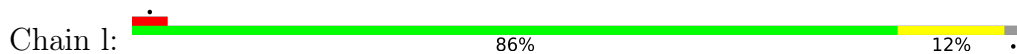
- Molecule 38: 60S ribosomal protein L37-A



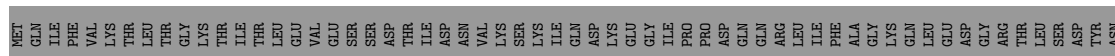
- Molecule 39: 60S ribosomal protein L38



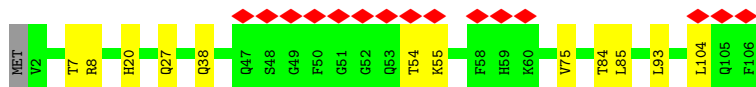
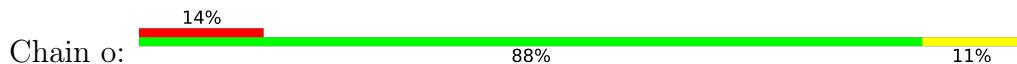
- Molecule 40: 60S ribosomal protein L39



- Molecule 41: Ubiquitin-60S ribosomal protein L40

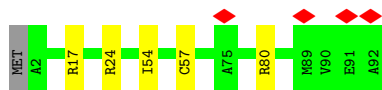


- Molecule 42: 60S ribosomal protein L42-A

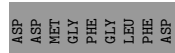
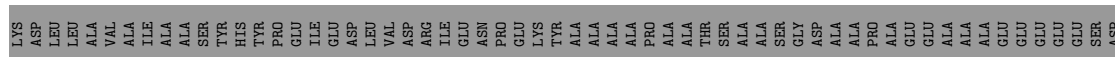
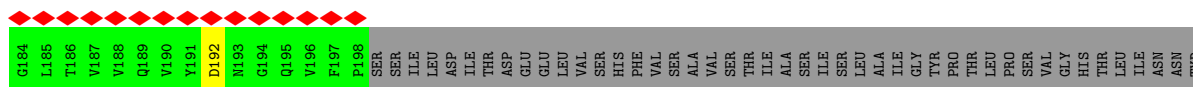
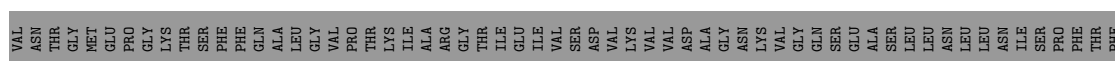
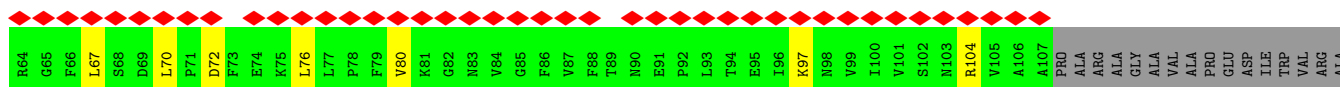
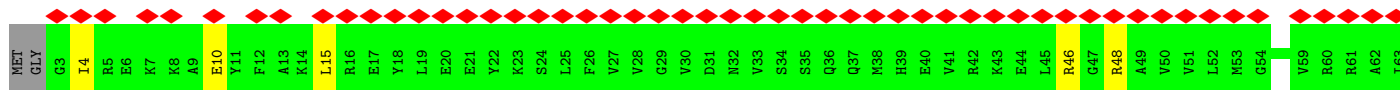


- Molecule 43: 60S ribosomal protein L43-A

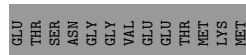
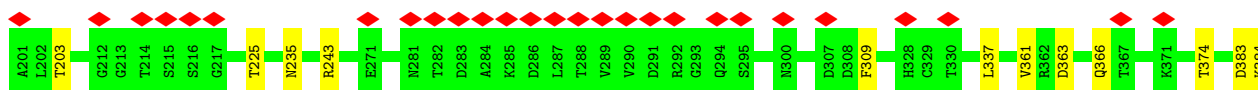
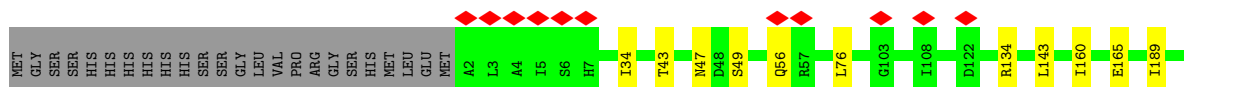
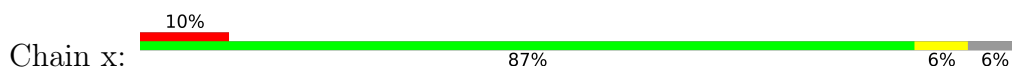




- Molecule 44: 60S acidic ribosomal protein P0

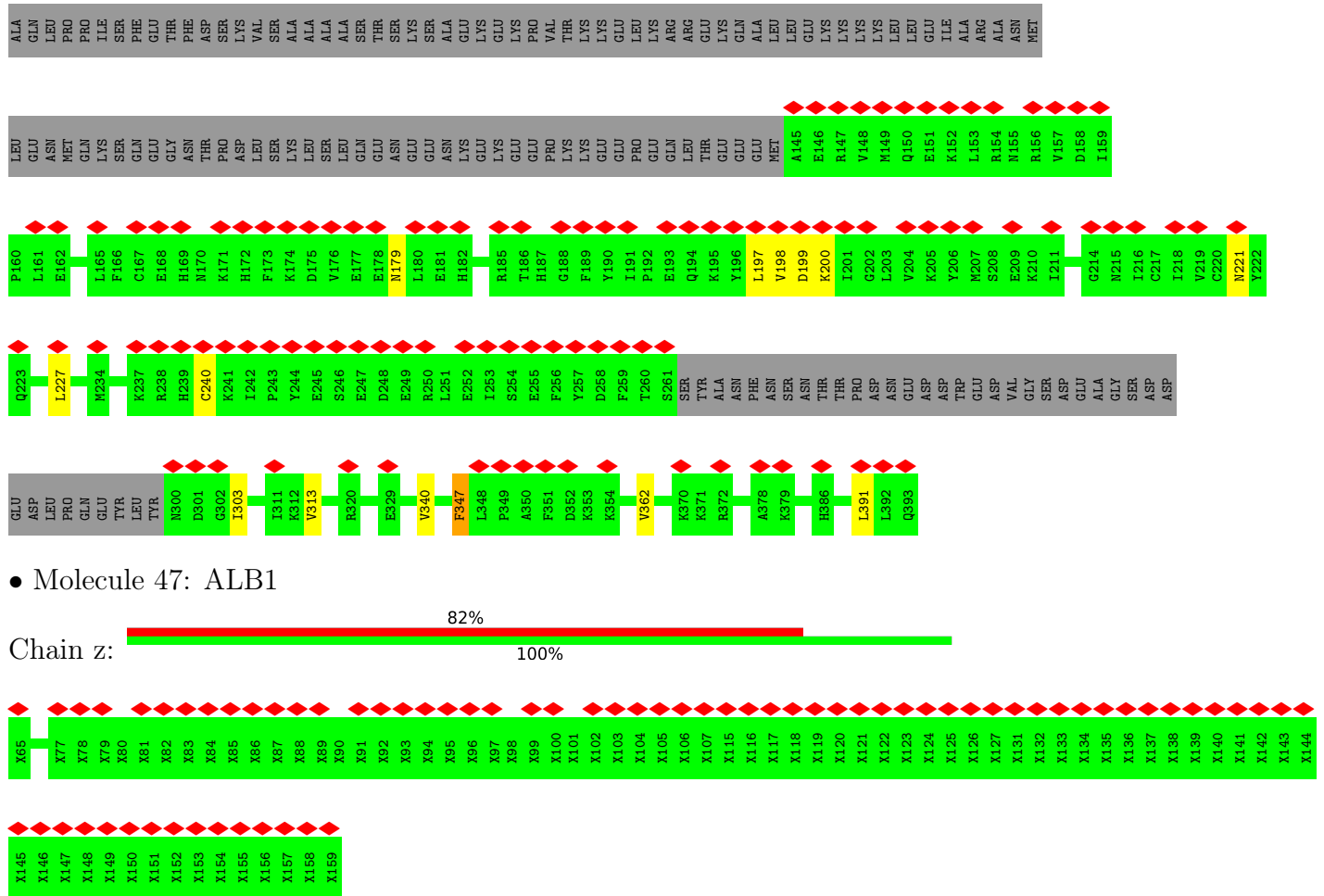


- Molecule 45: Probable metalloprotease ARX1



- Molecule 46: Cytoplasmic 60S subunit biogenesis factor REI1





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 ($e^-/\text{\AA}^2$)	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 (\AA)	300.24, 300.24, 300.24	wwPDB
Map dimensions	216, 216, 216	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.39, 1.39, 1.39	Depositor

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, P5P, 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(°)	Ideal(°)
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 [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	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%)	25	63
7	D	292/297 (98%)	283 (97%)	7 (2%)	2 (1%)	22	60
8	E	173/176 (98%)	160 (92%)	10 (6%)	3 (2%)	9	43
9	F	221/244 (91%)	211 (96%)	9 (4%)	1 (0%)	29	67
10	G	229/256 (90%)	201 (88%)	26 (11%)	2 (1%)	17	54
11	H	189/191 (99%)	178 (94%)	10 (5%)	1 (0%)	29	67

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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%)	4	32
14	L	192/199 (96%)	169 (88%)	21 (11%)	2 (1%)	15	52
15	M	135/138 (98%)	131 (97%)	4 (3%)	0	100	100
16	N	201/204 (98%)	189 (94%)	10 (5%)	2 (1%)	15	52
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%)	29	67
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%)	12	48
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%)	19	57
28	Z	133/136 (98%)	114 (86%)	16 (12%)	3 (2%)	6	37
29	a	146/149 (98%)	131 (90%)	14 (10%)	1 (1%)	22	60
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%)	17	54
33	e	127/130 (98%)	119 (94%)	7 (6%)	1 (1%)	19	57
34	f	104/107 (97%)	98 (94%)	6 (6%)	0	100	100
35	g	110/121 (91%)	100 (91%)	8 (7%)	2 (2%)	8	41
36	h	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
37	i	97/100 (97%)	87 (90%)	7 (7%)	3 (3%)	4	32
38	j	85/88 (97%)	78 (92%)	7 (8%)	0	100	100
39	k	75/78 (96%)	68 (91%)	6 (8%)	1 (1%)	12	48
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%)	32	67

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 [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	A	166/196 (85%)	139 (84%)	27 (16%)	2	16
5	B	319/323 (99%)	269 (84%)	50 (16%)	2	17
6	C	288/289 (100%)	240 (83%)	48 (17%)	2	15
7	D	243/245 (99%)	216 (89%)	27 (11%)	6	27
8	E	136/153 (89%)	119 (88%)	17 (12%)	4	23
9	F	187/205 (91%)	166 (89%)	21 (11%)	6	27
10	G	177/208 (85%)	154 (87%)	23 (13%)	4	22
11	H	171/171 (100%)	144 (84%)	27 (16%)	2	17
12	I	179/187 (96%)	157 (88%)	22 (12%)	4	24
13	J	147/150 (98%)	122 (83%)	25 (17%)	2	14
14	L	154/159 (97%)	136 (88%)	18 (12%)	5	25
15	M	108/109 (99%)	93 (86%)	15 (14%)	3	21

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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	5906/6642 (89%)	5096 (86%)	810 (14%)	7 21

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 [i](#)

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 [i](#)

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

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

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

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	P5P	5	2022	1	-	0/3/25/26	0/3/3/3
1	Y5P	5	1986	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	1993	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	1990	1	-	1/7/33/34	0/2/2/2
1	Y5P	5	1994	1	-	1/7/33/34	0/2/2/2
1	P5P	5	2019	1	-	0/3/25/26	0/3/3/3
1	P5P	5	2018	1	-	0/3/25/26	0/3/3/3
1	P5P	5	2023	1	-	0/3/25/26	0/3/3/3
1	P5P	5	2016	1	-	0/3/25/26	0/3/3/3
1	P5P	5	2020	1	-	0/3/25/26	0/3/3/3
1	Y5P	5	1987	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	2021	1	-	0/3/25/26	0/3/3/3
1	P5P	5	2017	1	-	0/3/25/26	0/3/3/3
1	Y5P	5	1995	1	-	1/7/33/34	0/2/2/2
1	Y5P	5	1992	1	-	1/7/33/34	0/2/2/2
1	Y5P	5	1988	1	-	1/7/33/34	0/2/2/2
1	Y5P	5	1991	1	-	1/7/33/34	0/2/2/2

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(°)	Ideal(°)
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 [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
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

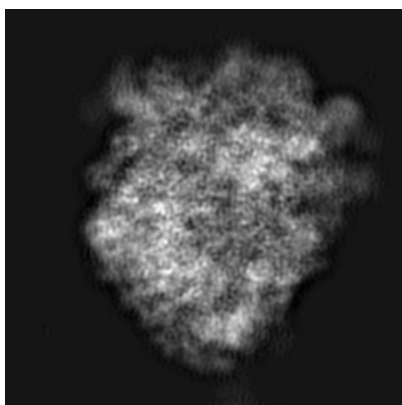
6 Map visualisation [i](#)

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.

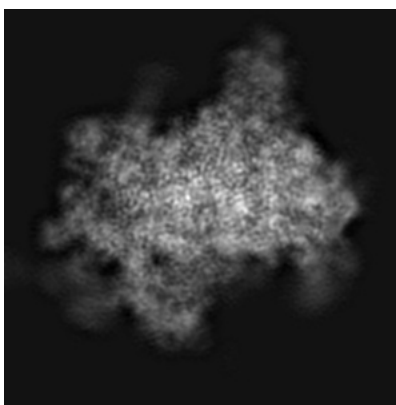
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

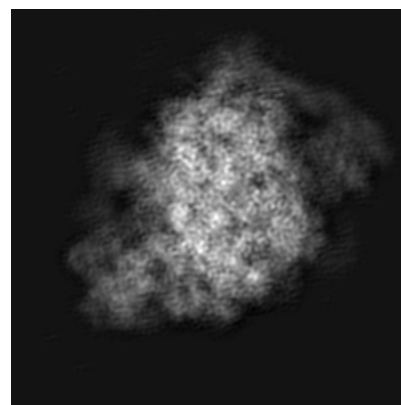
6.1.1 Primary map



X



Y

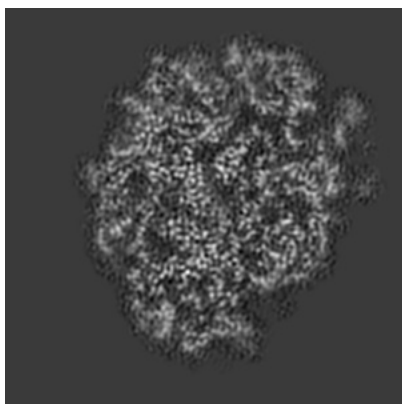


Z

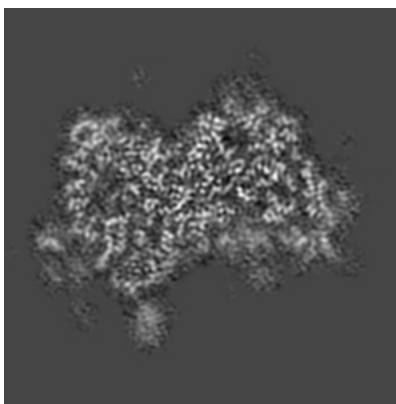
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

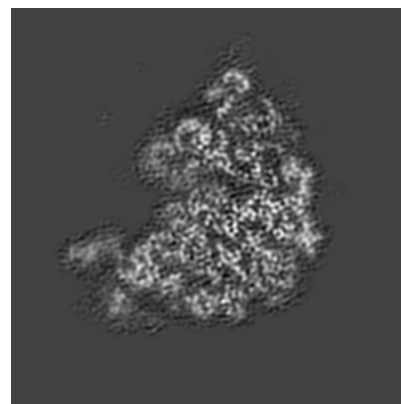
6.2.1 Primary map



X Index: 108



Y Index: 108

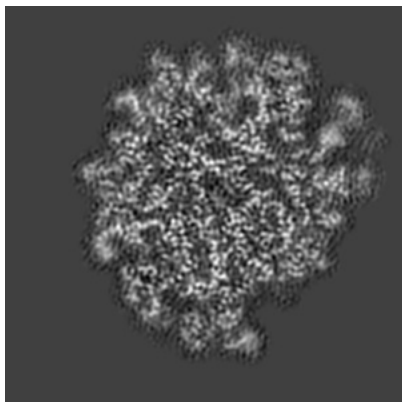


Z Index: 108

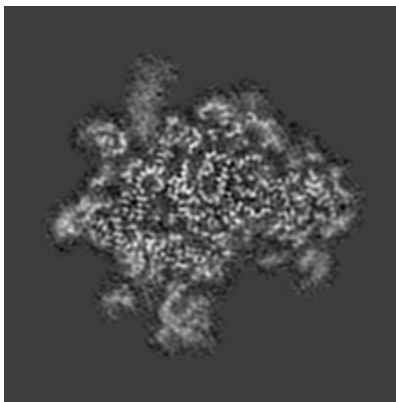
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

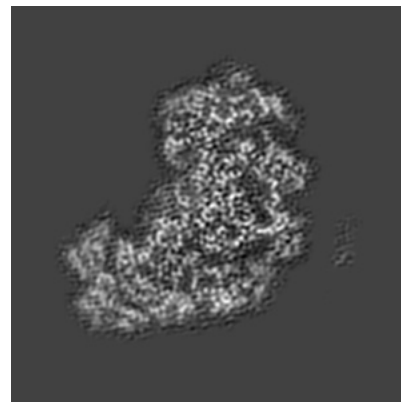
6.3.1 Primary map



X Index: 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 surface views [i](#)

6.4.1 Primary map



X



Y



Z

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

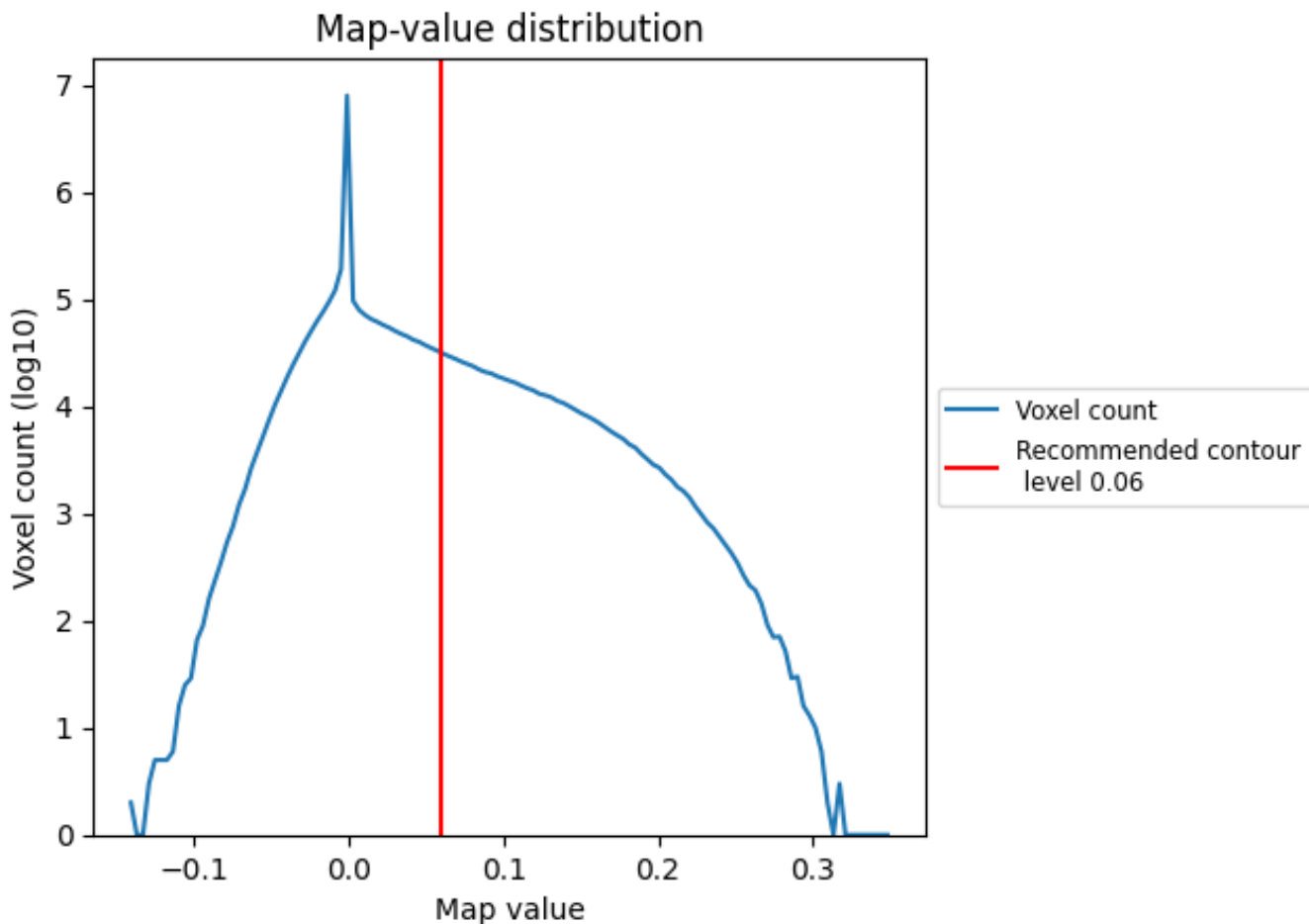
6.5 Mask visualisation

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

7 Map analysis [i](#)

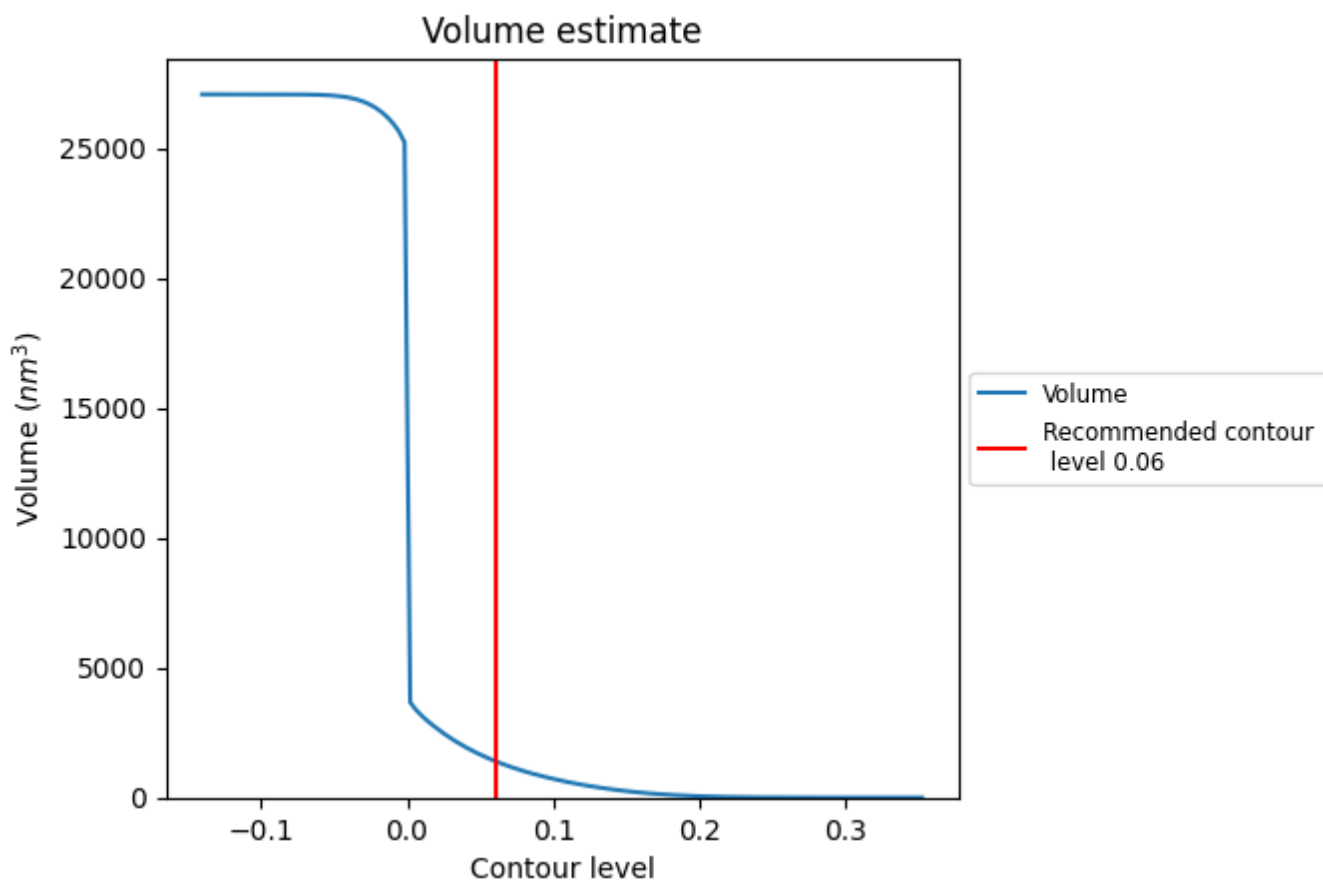
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

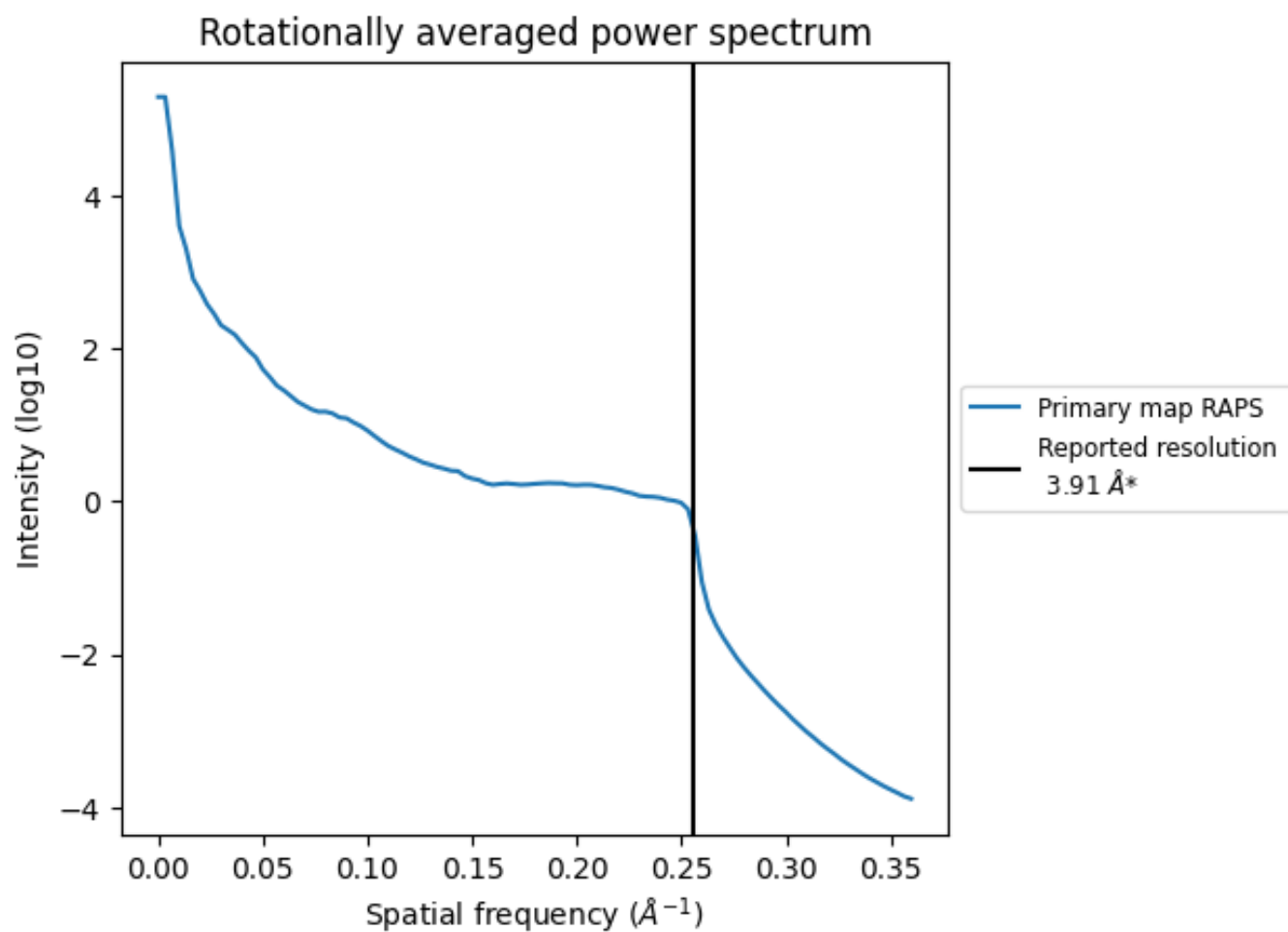
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1406 nm³; 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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.256\AA^{-1}

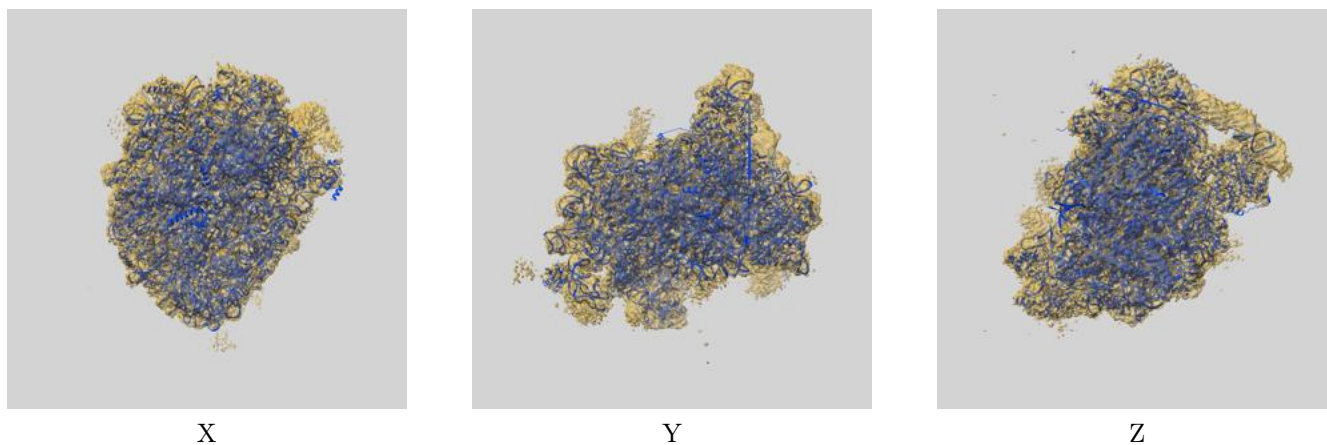
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

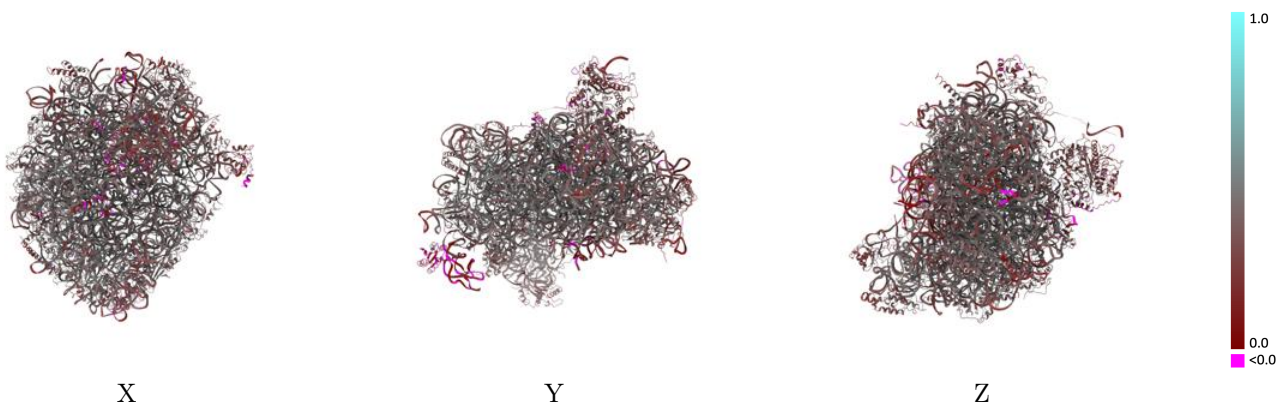
This section contains information regarding the fit between EMDB map EMD-3152 and PDB model 5APN. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay [i](#)



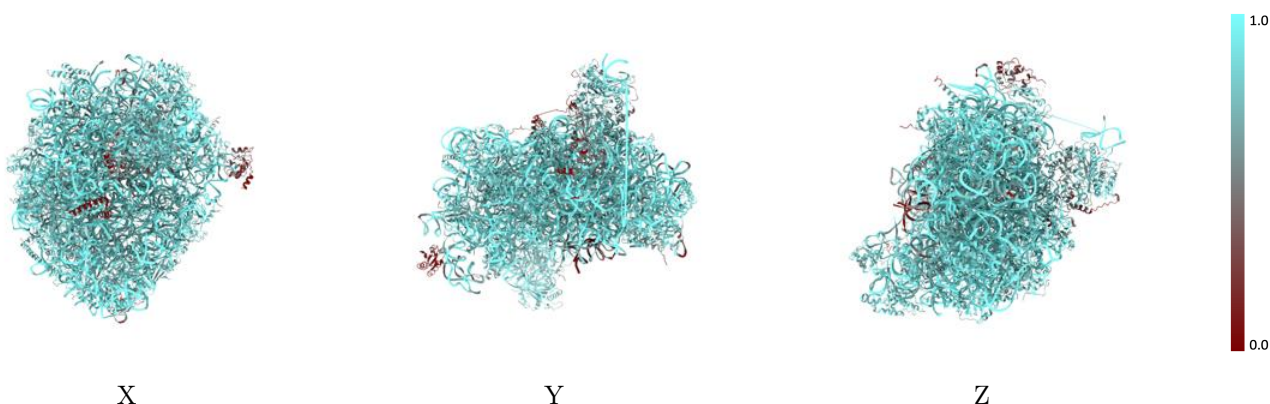
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



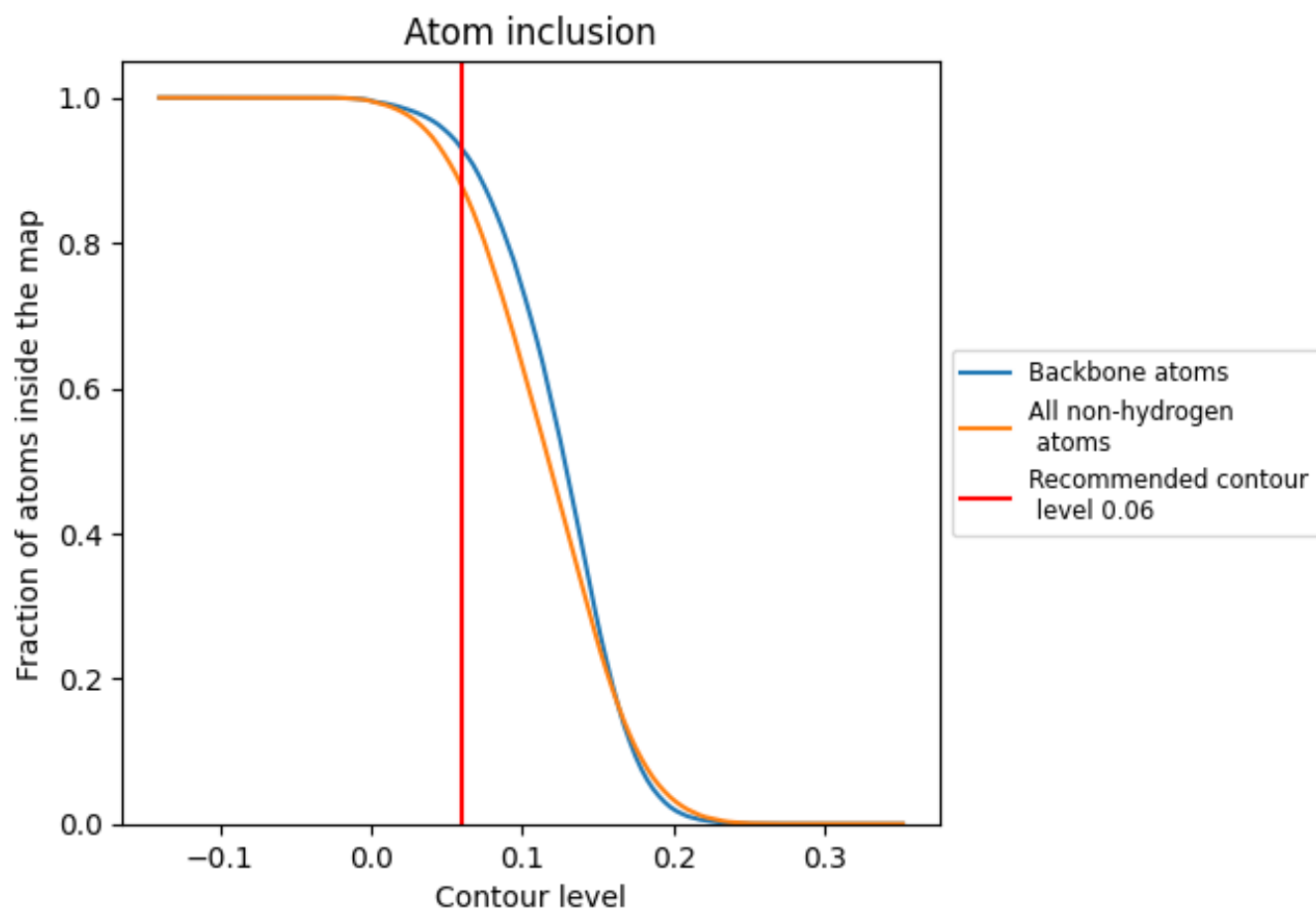
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.06).







































































9.4 Atom inclusion [i](#)



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	 0.8782	 0.3890
5	 0.9424	 0.3900
7	 0.9868	 0.3860
8	 0.9580	 0.4110
A	 0.8143	 0.4210
B	 0.8646	 0.4260
C	 0.8605	 0.4350
D	 0.8467	 0.3440
E	 0.8503	 0.3920
F	 0.8399	 0.4230
G	 0.8500	 0.3660
H	 0.8503	 0.4020
I	 0.8292	 0.4030
J	 0.8312	 0.3050
L	 0.8479	 0.4110
M	 0.8672	 0.4080
N	 0.7924	 0.4200
O	 0.8620	 0.4310
P	 0.8189	 0.4360
Q	 0.8509	 0.4350
R	 0.8300	 0.4090
S	 0.8572	 0.4310
T	 0.8347	 0.4310
U	 0.7796	 0.3730
V	 0.8173	 0.4070
W	 0.8297	 0.4050
X	 0.8068	 0.4340
Y	 0.8458	 0.4160
Z	 0.8497	 0.3590
a	 0.8689	 0.4330
b	 0.7810	 0.4000
c	 0.7616	 0.3400
d	 0.7760	 0.4280
e	 0.8145	 0.4370
f	 0.8563	 0.4520



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Chain	Atom inclusion	Q-score
g	 0.7944	 0.4070
h	 0.8328	 0.3990
i	 0.7836	 0.3800
j	 0.8491	 0.4430
k	 0.7899	 0.3690
l	 0.7831	 0.4430
m	 0.8193	 0.3990
o	 0.7226	 0.3430
p	 0.8000	 0.3950
q	 0.1234	 0.0770
x	 0.7048	 0.3040
y	 0.4136	 0.2860
z	 0.1510	 0.0910