



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 08:17 PM UTC

PDB ID : 8BIP / pdb_00008bip
EMDB ID : EMD-16086
Title : Structure of a yeast 80S ribosome-bound N-Acetyltransferase B complex
Authors : Knorr, A.G.; Mackens-Kiani, T.; Musial, J.; Berninghausen, O.; Becker, T.;
Beatrix, B.; Beckmann, R.
Deposited on : 2022-11-02
Resolution : 3.10 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.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

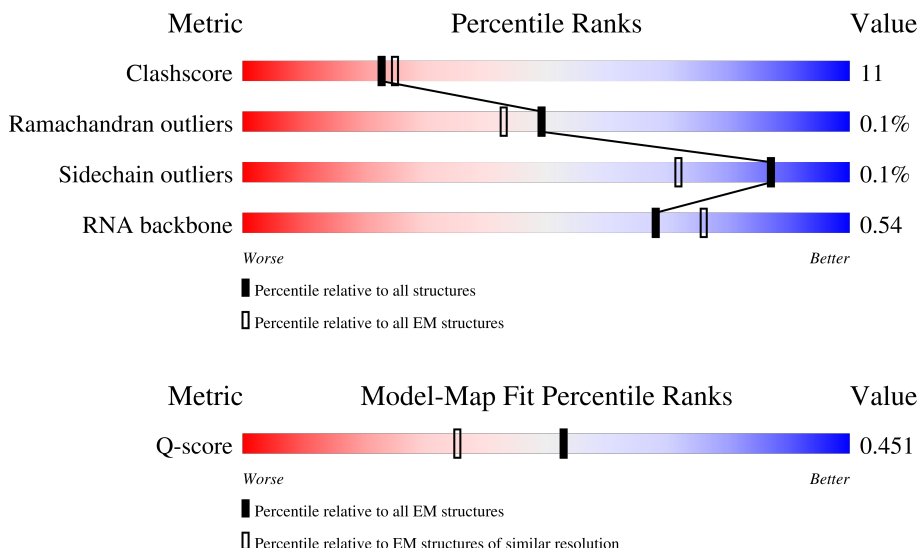
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 Å.

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



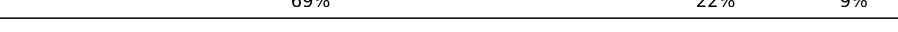
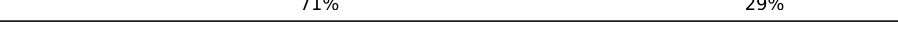
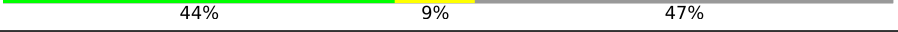
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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	C4	121	
2	C3	158	
3	LA	251	

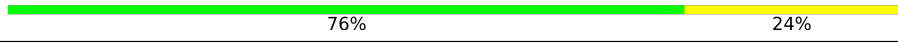
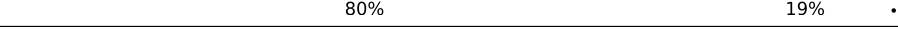
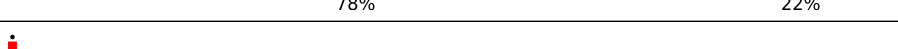
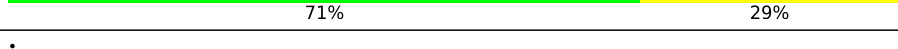
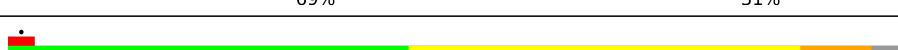
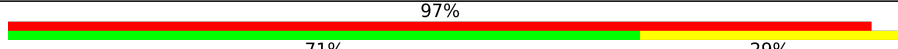
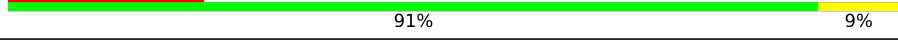
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	LB	386	 75%25%
5	LC	361	 81%19%
6	LD	294	 72%27%
7	LE	175	 71%25%5%
8	LF	222	 73%27%
9	LG	233	 75%24%
10	LH	191	 75%25%
11	LI	218	 74%26%
12	LJ	169	 67%33%
13	LL	193	 72%28%
14	LM	136	 72%28%
15	LN	203	 72%28%
16	LO	197	 77%22%
17	LP	183	 6%83%17%
18	LQ	185	 77%23%
19	LR	188	 69%22%9%
20	LS	171	 71%29%
21	LT	159	 63%37%
22	LU	100	 79%21%
23	LV	136	 77%23%
24	LW	126	 44%9%47%
25	LX	121	 83%17%
26	LY	125	 78%22%
27	LZ	135	 70%30%
28	La	148	 72%28%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	Lb	58	
30	Lc	96	
31	Ld	109	
32	Le	127	
33	Lf	106	
34	Lg	112	
35	Lh	119	
36	Li	99	
37	Lj	85	
38	Lk	77	
39	Ll	50	
40	Lm	52	
41	Ln	25	
42	Lo	103	
43	Lp	91	
44	1	3395	
45	A	195	
46	B	796	
47	8	23	

2 Entry composition

There are 49 unique types of molecules in this entry. The entry contains 134392 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C4	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C3	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 3 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	LA	251	Total	C	N	O	S	0	0
			1899	1182	385	331	1		

- Molecule 4 is a protein called 60S ribosomal protein L3.

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

- Molecule 5 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 6 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LD	294	Total	C	N	O	S	0	0
			2351	1484	410	455	2		

- Molecule 7 is a protein called 60S ribosomal protein L6-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LE	167	Total	C	N	O	S	0	0
			1305	841	234	229	1		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LE	132	ALA	THR	conflict	UNP P05739
LE	146	ILE	LEU	conflict	UNP P05739
LE	173	MET	LEU	conflict	UNP P05739

- Molecule 8 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LF	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 9 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LG	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 10 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LH	191	Total	C	N	O	S	0	0
			1508	957	274	273	4		

- Molecule 11 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LI	218	Total	C	N	O	S	0	0
			1764	1117	334	306	7		

- Molecule 12 is a protein called 60S ribosomal protein L11-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LJ	169	Total	C	N	O	S	0	0
			1350	846	253	247	4		

- Molecule 13 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	LL	193	Total	C	N	O	0	0
			1543	962	315	266		

- Molecule 14 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LM	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 15 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 16 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 17 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	LP	183	Total	C	N	O	0	0
			1416	879	284	253		

- Molecule 18 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 19 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	LR	171	Total	C	N	O	0	0
			1378	850	294	234		

- Molecule 20 is a protein called 60S ribosomal protein L20-A.

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

- Molecule 21 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 22 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LU	100	Total	C	N	O	S	0	0
			796	516	131	149			

- Molecule 23 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 24 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LW	67	Total	C	N	O	S	0	0
			538	345	106	86	1		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LW	104	GLN	ASN	conflict	UNP P04449
LW	109	GLN	LEU	conflict	UNP P04449
LW	112	ASP	ASN	conflict	UNP P04449
LW	119	ALA	GLU	conflict	UNP P04449

- Molecule 25 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LX	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 26 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 27 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 28 is a protein called 60S ribosomal protein L28.

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

- Molecule 29 is a protein called 60S ribosomal protein L29.

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

- Molecule 30 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Lc	96	Total	C	N	O	S	0	0
			737	476	123	137	1		

- Molecule 31 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Ld	109	Total	C	N	O	S	0	0
			880	559	168	152	1		

- Molecule 32 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Le	127	Total	C	N	O	S	0	0
			1017	644	205	167	1		

- Molecule 33 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 34 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 35 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 36 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Li	99	Total	C	N	O	S	0	0
			766	478	154	132	2		

- Molecule 37 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lj	85	Total	C	N	O	S	0	0
			670	408	146	111	5		

- Molecule 38 is a protein called 60S ribosomal protein L38.

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

- Molecule 39 is a protein called 60S ribosomal protein L39.

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

- Molecule 40 is a protein called 60S ribosomal protein L40-A.

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

- Molecule 41 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Ln	25	Total	C	N	O	S	0	0
			229	139	62	27	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lo	103	Total	C	N	O	S	0	0
			824	517	167	135	5		

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

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

- Molecule 44 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	1	3301	Total	C	N	O	P	0	0
			70586	31525	12690	23070	3301		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	?	-	G	deletion	GB 1262303
1	1962	A	G	conflict	GB 1262303

- Molecule 45 is a protein called N-terminal acetyltransferase B complex catalytic subunit NAT3.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	A	195	Total	C	N	O	S	0	0
			1612	1030	273	297	12		

- Molecule 46 is a protein called N-terminal acetyltransferase B complex subunit MDM20.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	B	796	Total	C	N	O	S	0	0
			6536	4195	1080	1231	30		

- Molecule 47 is a protein called Nascent peptide chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	8	23	Total	C	N	O	0	0
			115	69	23	23		

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

Mol	Chain	Residues	Atoms		AltConf
48	C4	1	Total	Mg	0
			1	1	
48	C3	1	Total	Mg	0
			1	1	
48	LA	2	Total	Mg	0
			2	2	
48	LB	1	Total	Mg	0
			1	1	
48	LN	1	Total	Mg	0
			1	1	
48	LP	1	Total	Mg	0
			1	1	
48	LR	1	Total	Mg	0
			1	1	
48	LV	1	Total	Mg	0
			1	1	
48	Le	1	Total	Mg	0
			1	1	
48	1	196	Total	Mg	0
			196	196	

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

Mol	Chain	Residues	Atoms		AltConf
49	Lg	1	Total	Zn	0
			1	1	
49	Lj	1	Total	Zn	0
			1	1	
49	Lm	1	Total	Zn	0
			1	1	

Continued on next page...

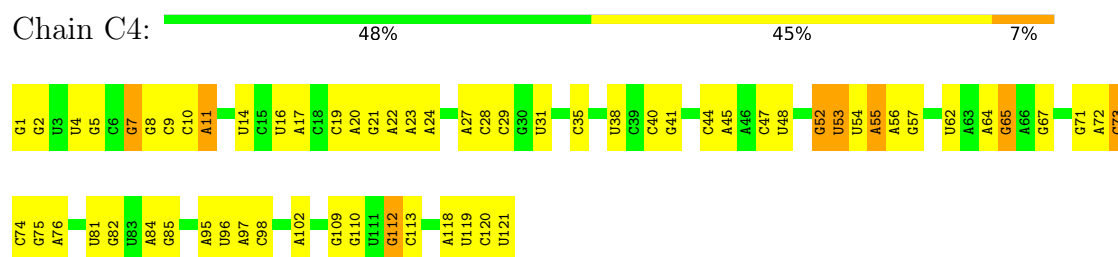
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
49	Lo	1	Total 1	Zn 1	0
49	Lp	1	Total 1	Zn 1	0

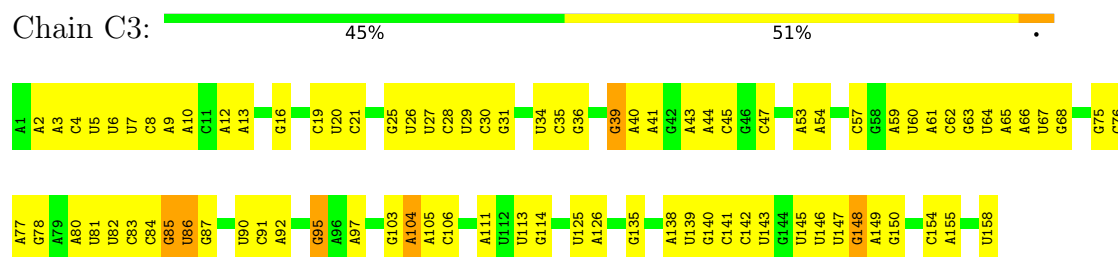
3 Residue-property plots

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

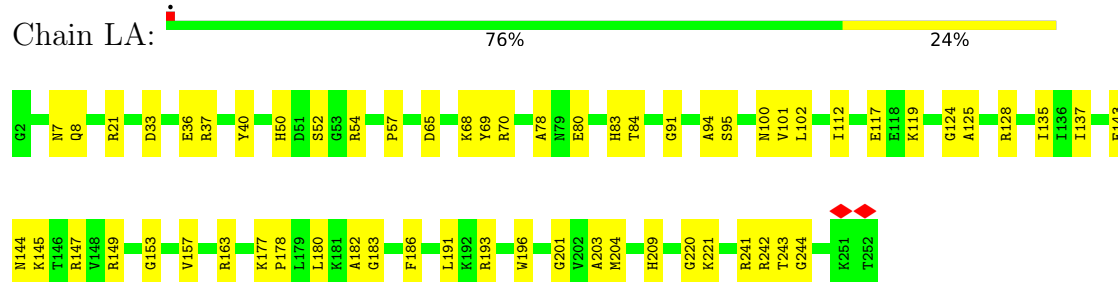
• Molecule 1: 5S rRNA



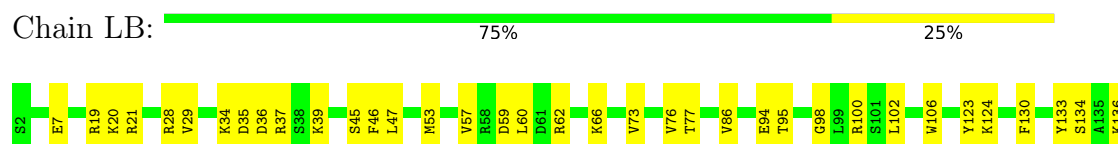
• Molecule 2: 5.8S rRNA

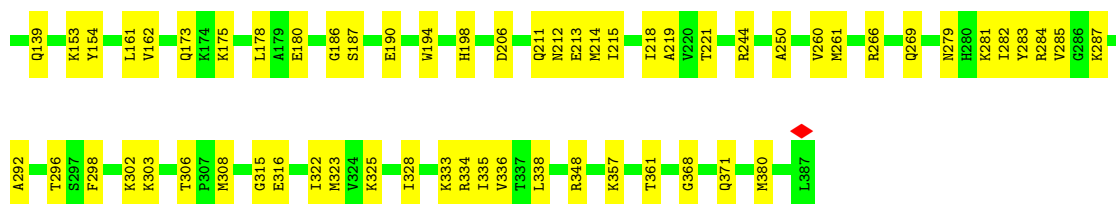


• Molecule 3: 60S ribosomal protein L2-A



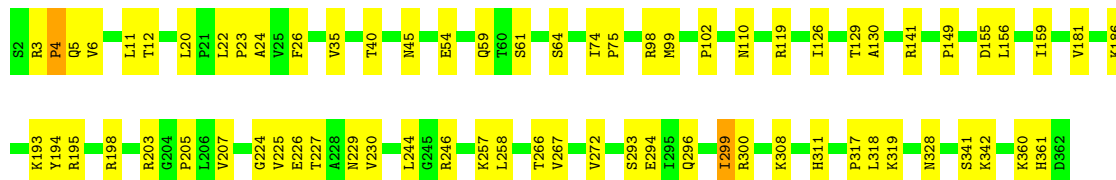
• Molecule 4: 60S ribosomal protein L3





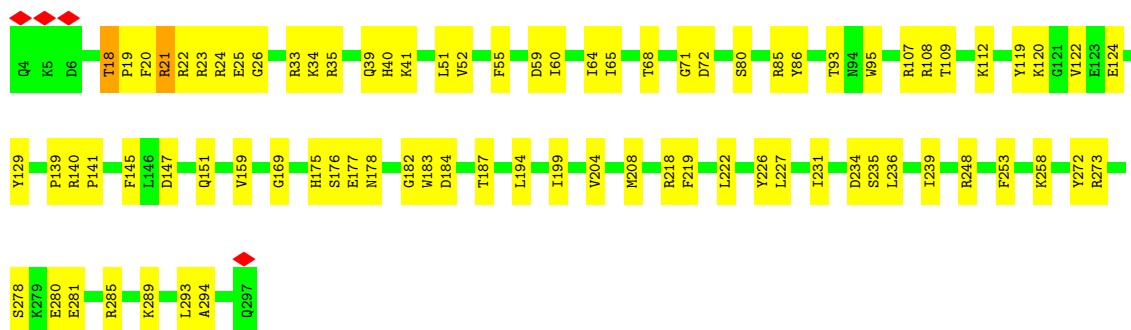
• Molecule 5: 60S ribosomal protein L4-A

Chain LC: 81% 19%



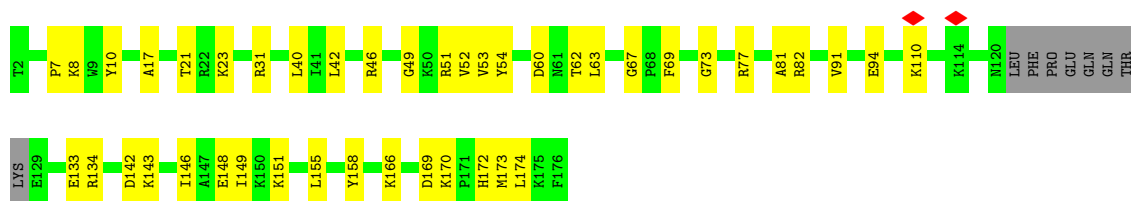
• Molecule 6: 60S ribosomal protein L5

Chain LD: 72% 27%



• Molecule 7: 60S ribosomal protein L6-B

Chain LE: 71% 25% 5%



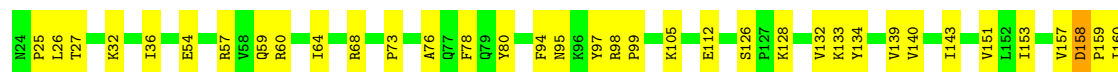
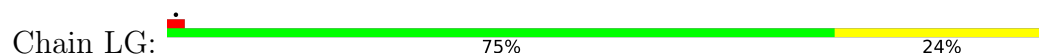
• Molecule 8: 60S ribosomal protein L7-A

Chain LF: 73% 27%

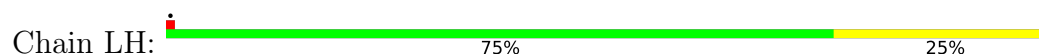




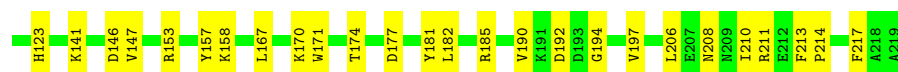
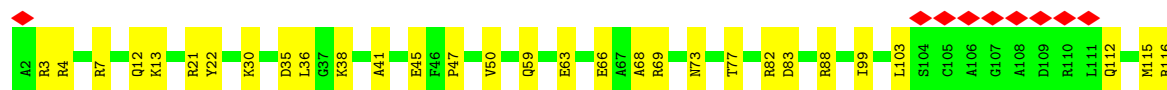
- Molecule 9: 60S ribosomal protein L8-A



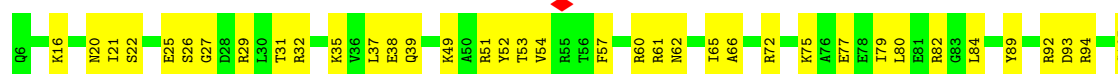
- Molecule 10: 60S ribosomal protein L9-A



- Molecule 11: 60S ribosomal protein L10

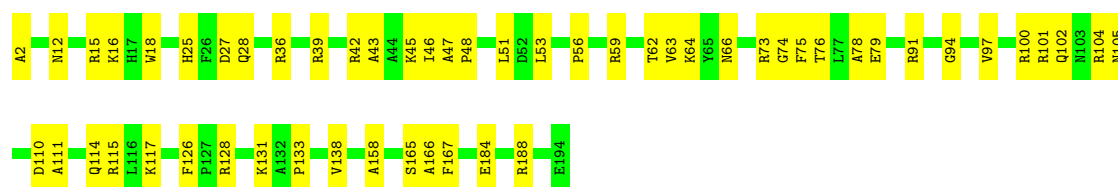


- Molecule 12: 60S ribosomal protein L11-B

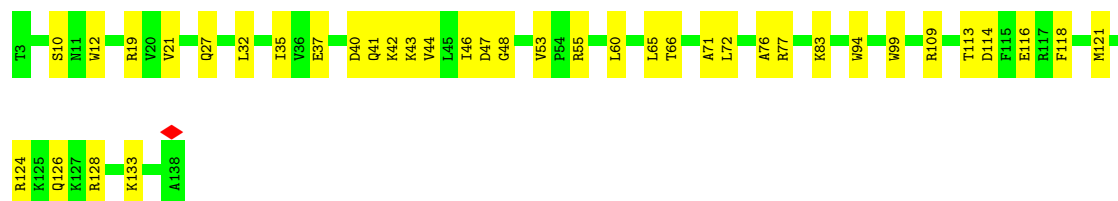
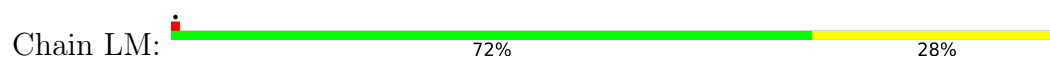


- Molecule 13: 60S ribosomal protein L13-A

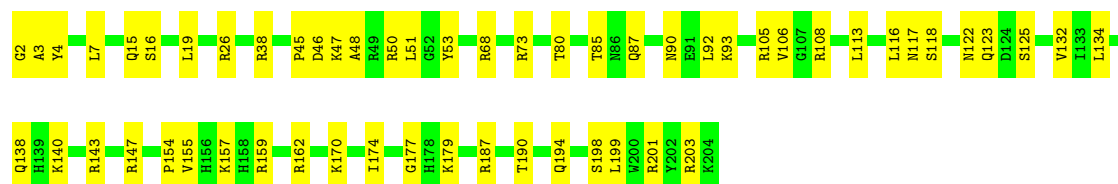




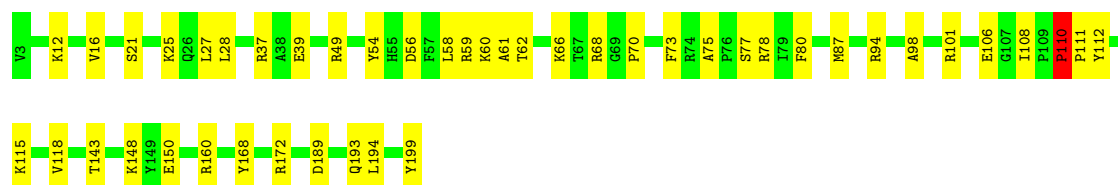
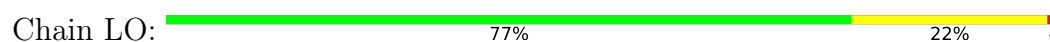
- Molecule 14: 60S ribosomal protein L14-A



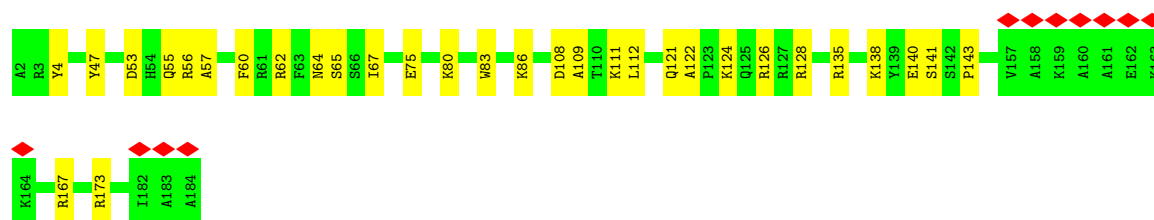
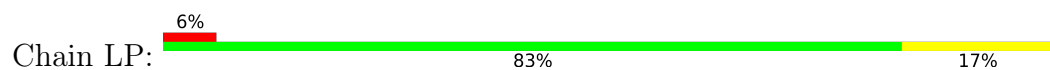
- Molecule 15: 60S ribosomal protein L15-A



- Molecule 16: 60S ribosomal protein L16-A

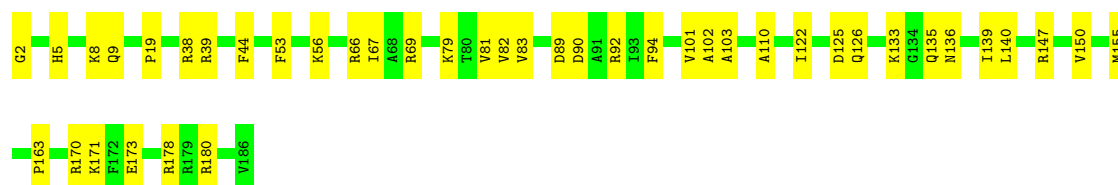


- Molecule 17: 60S ribosomal protein L17-A



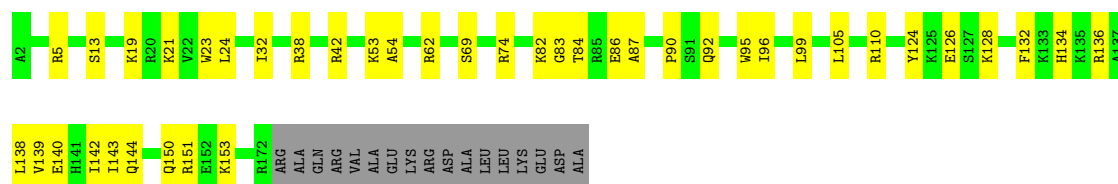
- Molecule 18: 60S ribosomal protein L18-A

Chain LQ:  77% 23%



- Molecule 19: 60S ribosomal protein L19-A

Chain LR:  69% 22% 9%



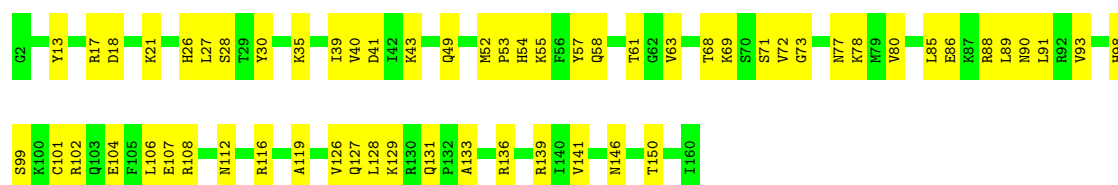
- Molecule 20: 60S ribosomal protein L20-A

Chain LS:  71% 29%



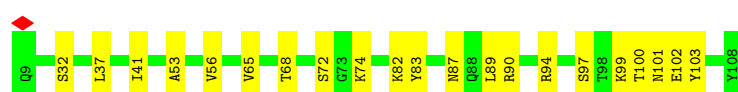
- Molecule 21: 60S ribosomal protein L21-A

Chain LT:  63% 37%



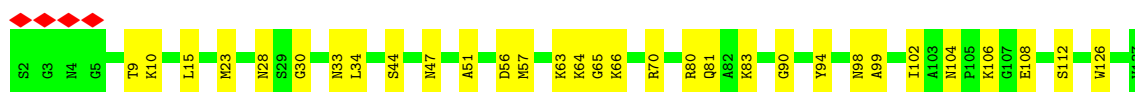
- Molecule 22: 60S ribosomal protein L22-A

Chain LU:  79% 21%



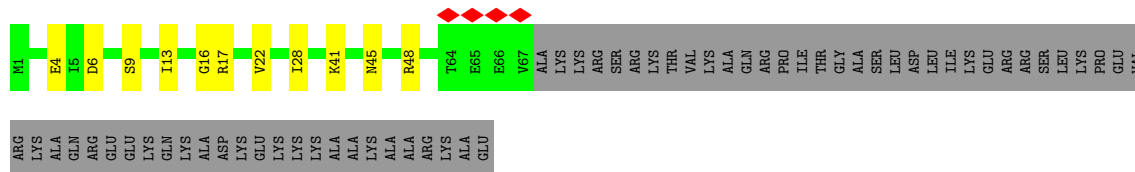
- Molecule 23: 60S ribosomal protein L23-A

Chain LV:  77% 23%



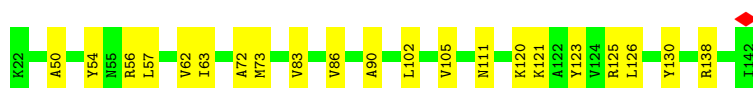
- Molecule 24: 60S ribosomal protein L24-A

Chain LW: 44% 9% 47%



- Molecule 25: 60S ribosomal protein L25

Chain LX: 83% 17%



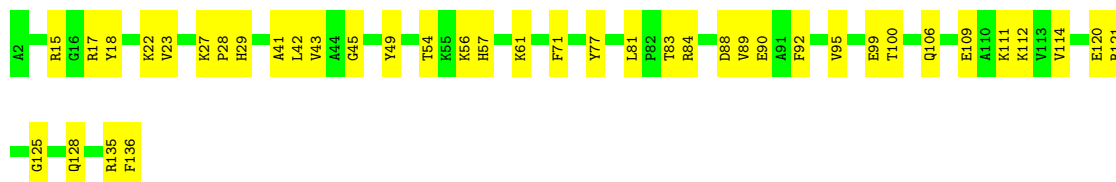
- Molecule 26: 60S ribosomal protein L26-A

Chain LY: 78% 22%



- Molecule 27: 60S ribosomal protein L27-A

Chain LZ: 70% 30%

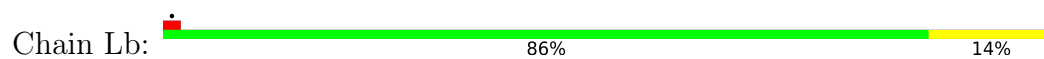


- Molecule 28: 60S ribosomal protein L28

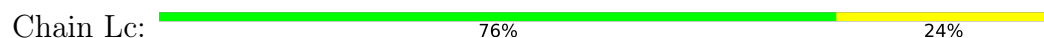
Chain La: 72% 28%



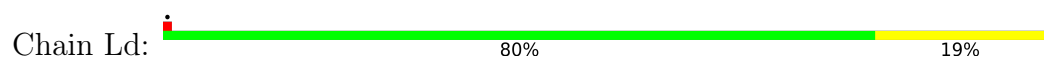
- Molecule 29: 60S ribosomal protein L29



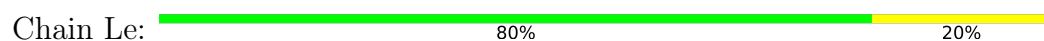
- Molecule 30: 60S ribosomal protein L30



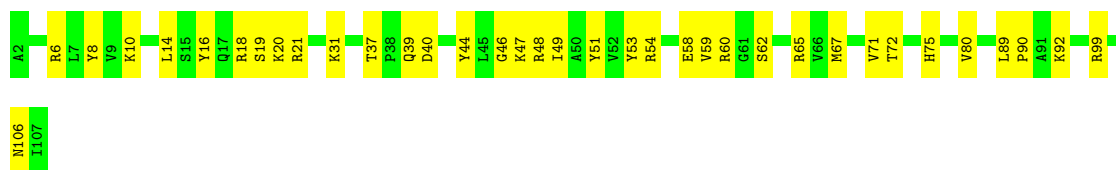
- Molecule 31: 60S ribosomal protein L31-A



- Molecule 32: 60S ribosomal protein L32



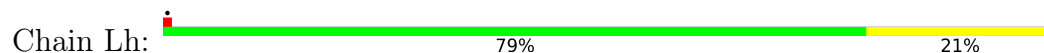
- Molecule 33: 60S ribosomal protein L33-A



- Molecule 34: 60S ribosomal protein L34-A

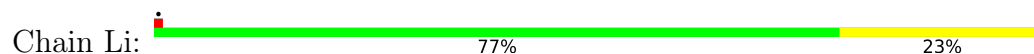


- Molecule 35: 60S ribosomal protein L35-A

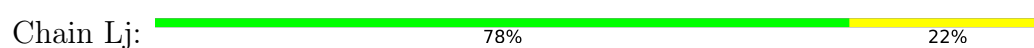




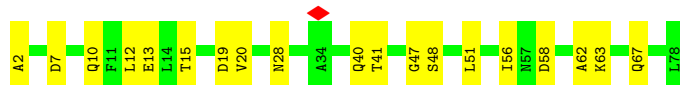
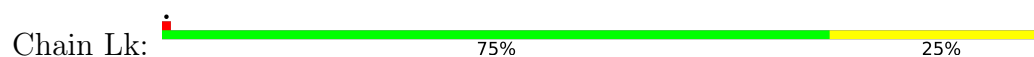
- Molecule 36: 60S ribosomal protein L36-A



- Molecule 37: 60S ribosomal protein L37-A



- Molecule 38: 60S ribosomal protein L38



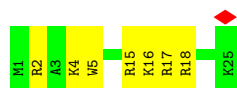
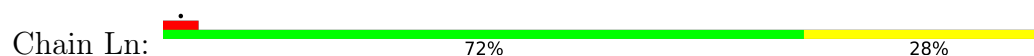
- Molecule 39: 60S ribosomal protein L39



- Molecule 40: 60S ribosomal protein L40-A

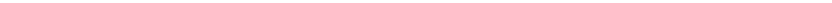


- Molecule 41: 60S ribosomal protein L41-A

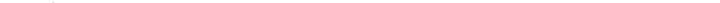


- Molecule 42: 60S ribosomal protein L42-A

V2	K6	K15	R18	V25	A30	S34	Q38	R41	R42	K46	Q47	Q53	K61	A62	K63	T64	T65	V68	V69	L70	R71	L72	E73	C77	K78	T79	R80	T84	R87	F91	G94	Q99	Q102	A103	I104
----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------

- Chain Lp:  69% 31%

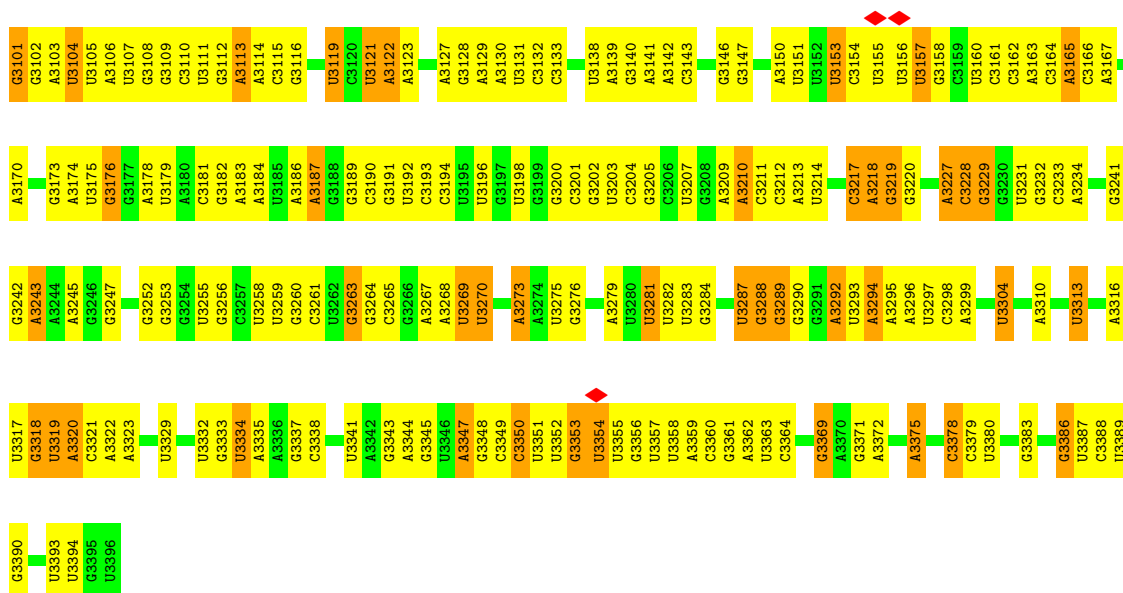
A2	K3	R4	V16	R17	Y18	L29	D38	C39	C42	K45	T46	V47	K48	R49	W55	T56	C57	S58	C59	C60	K61	R62	T63	V64	A68	Y69	T73	V79	T83	R84	R85	E88	E91	A92
----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Chain 1:  45% 44% 8% .

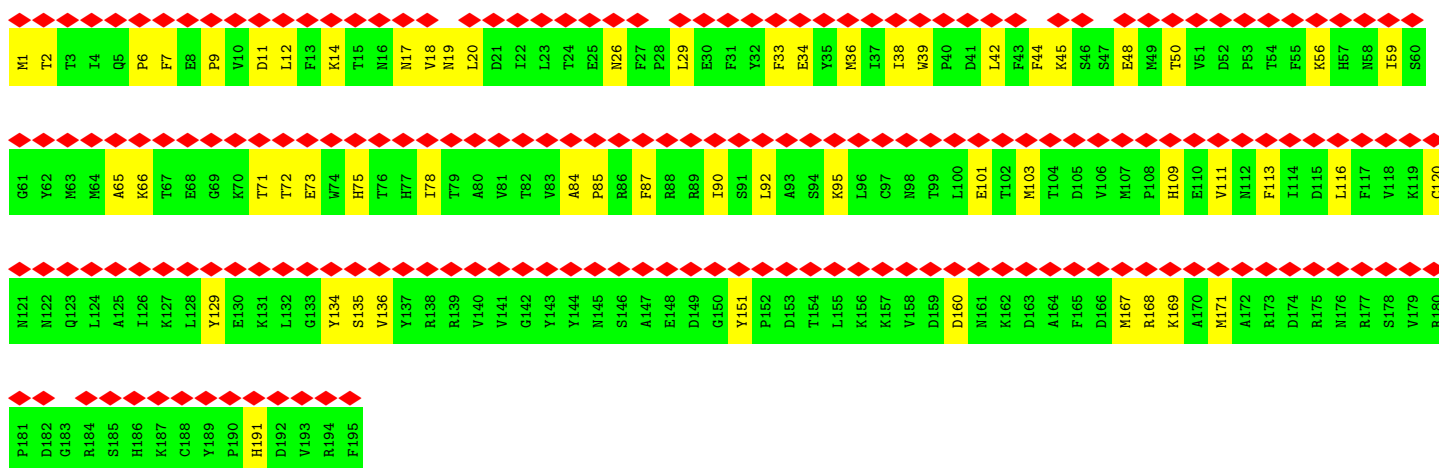
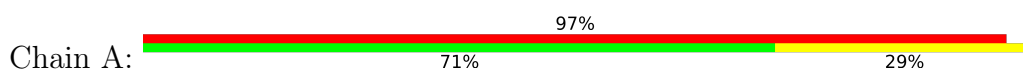
G700	A628	U549	C	U322	U250	G176	U97
G701	A550	U		A323	U251		G98
C702	A630	C		A421	U252		C99
G703	G631	G		A423	A325	C179	A99
U704	G632	C		G424	A254	C180	A100
A705	C633			G425	A255	U181	G101
U706	C634	A486		U328	A256		
U707	U556	U487		U329	G256	U184	G104
U708	U557	U488		G427	U257	U185	C105
A709	C638	U489		G337	G258	A186	A106
G639	A558	C490		A338	C259	U187	A107
A559	G639	A491		C339	C260	A188	A108
U640	C640	C492		C340	U261	U190	A109
C641	C641	U493		G341	U262	U191	G110
U713	C562	G494		A342			C111
U714	U563	U495		C346	A265	U194	U112
A715	A647	U496		G347	G267	U195	C113
U716	C648	C497		A348	A268	G196	
C717	A649	A498		C349	G269	A199	A116
U718	C650	U501		C350		C200	U117
U719	G651	U502		A351	U274	A201	U119
A720	G575	C503		G353	U276	G202	G120
		A504			G277		A121
G655	G579	G442			U207	U207	A122
A656		G443			C208		A123
A657		U444			A209		
G658	G583	U506			U278		G127
G726	G584	U507			U279		G128
G727	A660	U508			U280		A211
C728	C586	U509			G281		A212
U730	G661	U447			G282		U129
U731	U662	U448			C283		A130
C732	C663	U449			G214		
	U664	G450			U286		U133
U742	A665	A516			G287		C134
C743	A666	G517			C288		C135
U744	C667	U518			G217		G136
C745	G595	A519			C218		A219
U746	C596	U520			G219		G137
A747	C670	A521			C220		U138
U748	U671	A522			U291		G139
C749	A672	C523			C292		
	U673	G600			A222		A222
C752	G674	U601			U293		U147
U753	A677	A602			G394		A148
G754	A608	U528			U223		G149
U755	C609	A529			C224		A150
U756	G610	G530			G225		
C757	C611	A531			U228		G155
U758	G684	A611			G229		G156
U759	U687	U612			U230		A157
G760		G613			G301		U158
U761		A537			U302		A159
U762	A690	U615			C403		
C763	A691	U540			U305		G239
U764	A692	G617			A306		U240
A693	C618	U541			A307		C81
C694	A619	G542			C242		A165
C695	U620	C543			G243		C166
C696	A621	C544			G244		
U697	C697	U545			U245		U169
C698	A622	C546			U246		G171
U699		G547			C247		G172
		C549			U248		G173
U776		U637			U249		
					C251		

U777	U865	C959	A1046	A1143	A1231	A1302	A1381	A1477	U1570	A1638	A1741	A1814	A1909
A780	U871	U960	A1047	U1144	C1233	G1306	G1382	C1478	U1571	C1639	U1742	U1815	A1910
G781	U872	U966	A1049	G1152	G1234	G1307	G1383	G1480	U1572	A1642	U1743	A1816	A1911
A784	C873	U967	C1049	U1235	U1236	A1308	A1386	A1481	G1573	A1643	G1744	G1817	A1913
G785	U874	U968	U1050	A1154	G1237	U1309	G1387	A1482	C1574	A1644	G1745	U1818	A1914
A786	U875	C969	A1061	C1155	G1238	U1315	G1388	G1483	A1575	U1645	U1746	U1819	U1920
G787	U876	A970	A1062	C1156	C1239	C1320	A1389	G1486	A1580	G1646	G1747	U1820	U1921
C788	U877	A972	G1063	U1157	A1240	G1321	C1397	G1487	C1582	G1650	A1750	A1821	A1922
A789	A884	A973	A1064	A1158	U1241	U1322	U1398	G1488	A1583	U1651	G1751	G1825	A1923
U790	G887	G974	A1065	A1159	A1244	U1323	A1399	A1489	A1586	A1656	A1757	C1826	G1927
A791	A888	U979	U1071	U1167	A1245	U1324	G1400	A1491	G1586	C1657	G1758	A1828	A1932
G792	C792	A980	G1072	U1168	U1247	U1328	G1404	G1492	A1587	U1658	C1761	G1829	G1935
C793	U794	A896	U1073	A1169	A1251	U1329	G1407	G1493	A1588	U1659	U1765	G1830	A1936
G795	U899	U985	A1078	G1174	U1252	A1330	A1407	U1494	A1589	G1660	C1762	U1831	
U796	G900	U986	C1175	G1175	U1253	C1333	C1411	U1495	G1590	G1661	U1763	A1835	G1940
U797	U900	U987	A1079	A1177	C1254	U1334	G1412	C1496	G1591	G1662	U1764	U1836	C1941
G798	U903	U988	A1080	G1178	C1255	C1335	G1413	A1497	U1592	G1666	C1765	U1837	U1942
G799	A904	A992	U1081	A1179	G1256	U1336	G1414	A1498	G1593	A1667	U1766	G1838	
C804	U907	G993	A1084	A1179	G1257	A1337	U1415	C1499	U1596	G1668	G1770	A1839	A1945
G805	G908	A998	A1085	A1181	U1258	C1338	U1416	U1507	C1596	U1675	G1775	A1841	A1946
A806	U908	G999	C1086	U1181	U1259	G1339	G1417	G1508	C1597	A1676	U1776	A1842	G1947
A817	C911	G999	G1087	U1188	A1259	G1340	A1418	C1508	G1598	G1677	U1777	A1948	G1948
U821	G912	U1000	A1093	C1189	G1260	U1341	A1419	U1522	U1601	G1678	U1778	C1846	G1952
U822	A913	G1001	A1094	A1190	G1261	U1342	U1420	U1523	A1602	A1679	G1779	G1847	G1953
G823	A914	A1002	U1095	U1191	G1262	C1342	G1421	A1524	A1603	G1680	C1780	G1848	G1954
C824	A915	A1003	C1192	C1192	U1263	U1347	G1422	G1525	G1604	U1681	G1781	C1849	U1955
A830	G916	G1010	A1096	A1193	G1264	U1348	C1426	G1529	U1606	U1682	U1782	A1850	A1956
U837	A917	A1011	A1097	G1194	U1265	G1349	U1427	A1530	U1607	A1683	U1783	U1862	U1957
G838	A921	U1014	A1103	C1196	G1266	U1351	G1432	C1531	C1608	U1688	U1784	G1863	U1958
C839	U922	U1015	A1105	C1201	A1270	A1352	U1433	U1532	G1609	U1688	G1785	G1864	G1959
C840	G923	C1016	G1106	A1202	A1271	U1353	A1434	U1533	C1610	A1596	G1786	A1864	A1960
A841	A926	C1017	C1107	A1203	U1274	G1354	G1435	A1534	A1613	A1697	C1787	A1865	G1961
C842	C927	G1018	C1108	A1204	C1274	A1355	U1436	A1535	C1614	A1697	G1788	C1866	A1962
A844	C928	G1019	U1109	A1204	C1275	U1356	U1437	A1536	C1615	C1709	G1789	C1867	G1963
U849	A841	G1020	U1110	U1208	U1276	U1357	C1437	G1544	U1616	C1710	G1790	A1867	C1964
A842	U930	G1021	U1111	U1210	C1277	C1358	G1443	G1547	U1617	G1713	C1791	A1868	U1965
G844	G937	G1024	U1114	U1214	A1276	C1359	U1444	G1547	G1618	G1713	C1792	U1869	U1966
G845	U943	A1025	G1117	U1215	C1280	C1360	U1445	U1553	A1619	U1717	G1793	U1877	U1967
A846	C944	A1026	C1118	C1216	G1281	U1361	A1446	U1554	A1620	U1718	U1795	G1878	A1972
A847	C945	A1027	C1119	A1217	G1281	G1362	U1447	U1555	A1621	G1719	G1796	A1879	G1973
C849	U946	U1028	A1120	U1218	G1286	A1363	G1450	C1556	U1622	U1720	A1797	U1880	A1974
U855	C949	G1029	U1121	C1219	U1287	C1364		A1557	G1623	U1721	A1798	A1881	C1975
G856	G950	A1030	U1128	G1222	A1288	U1368	A1460	G1560	G1624	U1724	A1799	A1883	G1976
G857	A951	G1031	U1129	A1223	U1289	A1369	A1461	U1561	U1625	U1725	U1801	A1884	C1977
A952	G952	C1032	A1130	C1224	A1290	G1370	A1462	C1562	U1629	C1725	A1802	U1884	A1978
G860	G953	U1033	G1131	A1225	A1291	G1371	U1463	C1563	U1630	A1729	G1803	U1884	C1979
C861	U954	U1034	G1132	G1226	C1292	C1372	U1470	U1564	U1631	G1730	A1804	U1884	C1980
U862	U955	A1035	A1133	C1227	U1293	A1373	U1471	U1565	A1632	G1733	C1805	U1884	G1981
G864	U956	A1036	G1134	C1228	U1299	G1374	A1472	A1566	C1633	U1734	A1806	U1884	G1982
		U1039	G1142	G1230	A1301	U1378	G1473	U1567	G1634	G1735	G1807	U1884	G1983
		A1040				U1379	G1473	U1568	U1635	G1736	A1809	U1884	G1984
						G1380		U1569	U1636		A1810	U1884	G1985
									U1637			U1884	G1986
													G1987

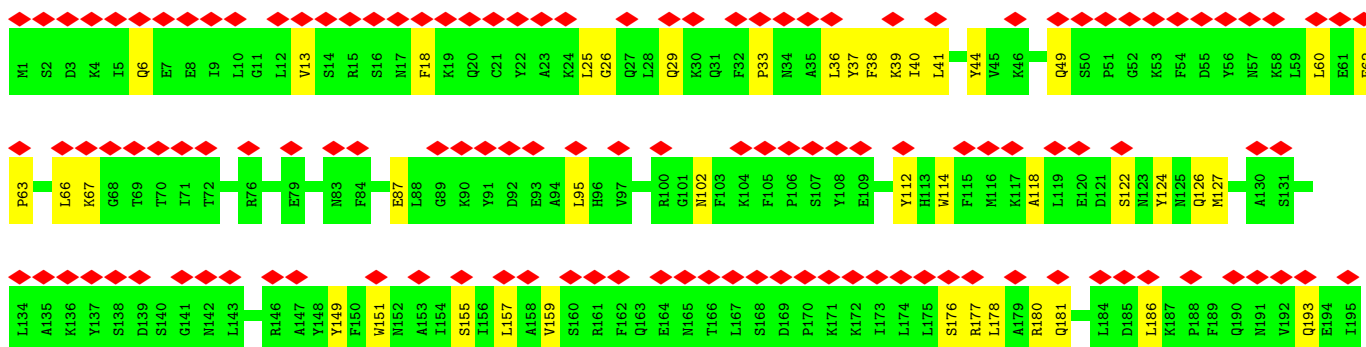
U3023	G2945	G2751	A2673	C2582	U2508	G2448	C2378	G2201	A2113	A2049	C1988
A3024	A2946	U2752	A2674	C2583	U2509	A2449	U2379	C2202	C2114	C2050	U1989
G3025	C2947	G2753	C2675	G2584	U2510	G2450	U2380	U2203	G2115	G2051	U1990
G3026	C2948	G2754	A2676	G2585	A2511	G2451	U2392	G2204	G2116	G2052	G1991
U3029	U2949	C2755	A2677	G2586	C2512	G2452	A2295	U2205	A2117	U2056	U1992
G3030	G2950	A2758	A2678	U2587	G2513	U	G2302	G2206	C2118	U2057	G1993
G3031	U2955	U2759	A2679	U2588	U2514	U	G2303	U2209	A2119	G2058	U1994
A3032	G2956	C2765	A2680	A2593	A2515	U	A2304	G2210	G2120	A2059	A1995
U3037	C2960	U2766	C2682	U2597	G2522	U	G2305	A2213	G2121	A	C1996
U3038	U2961	U2767	U2683	G2598	A2523	G	G2306	A2214	U2129	G	U1997
C3039	C2962	U2768	C2684	G2599	A2524	A	G2307	A2215	G2130	G	G1998
U3042	G2963	A2769	A2685	G2602	G2525	U	C2308	G2216	A2131	U	C1999
G3046	G2964	U2772	A2686	G2603	G2527	U	A2309	U2217	C2132	C	U2000
A3047	A2967	C2773	U2687	G2606	U2531	A	G2396	G2218	U2133	U	U2001
U3050	U2971	C2774	A2689	G2607	C2532	G	A2397	A2219	U2137	C	U2002
G3051	G2972	U2775	A2690	U2611	G2534	U	A2398	A2220	A2138	U	G2003
G3052	C2973	G2776	A2691	U2612	A2535	G	U2402	A2221	G2142	G	U2004
G3053	U2974	G2777	A2694	G2613	A2537	G	G2403	A2222	A2143	A	G2005
U3059	U2975	U2778	A2695	U2614	U2538	A	A2404	A2223	A2144	G	G2006
U3064	A2976	C2788	A2696	G2615	C2539	C	C2405	A2224	A2145	A	G2007
G3065	G2977	U2779	A2697	G2616	U2541	U	U2406	U2225	C2146	C	G2008
G3066	U2978	G2796	U2698	U2617	U2542	U	U2407	A2226	A2147	U	G2009
G3067	U2979	G2797	G2699	G2618	U2543	C	U2408	A2227	U2148	G	U2010
U3068	U2980	U2800	G2700	G2619	U2544	G	U2411	A2228	U2154	C	U2011
G3069	A2981	A2801	U2701	G2622	C2547	C	G2412	A2229	G2155	G	G2012
G3070	U2982	A2802	U2702	G2623	G2548	C	A2413	A2230	A2158	U2081	C2013
U3071	C2983	A2803	A2704	U2632	G2549	C	A2414	A2231	U2159	U2082	G2014
G3072	U2984	U2804	C2707	G2632	C2552	U	G2415	A2232	G2160	G2084	U2015
A3073	G2985	G2805	C2708	U2633	G2555	G	G2416	A2233	G2161	U2085	U2016
G3074	U2986	U2806	U2709	U2634	A2556	A	C2417	A2234	A2167	A2086	G2017
G3075	C2987	U2807	C2710	U2635	A2557	A	U2417	A2235	G2168	C2087	C2018
U3078	U2988	A2808	U2719	G2636	C2558	U	U2423	A2236	G2169	A2088	U2019
G3081	U2989	U2809	A2721	C2637	U2559	A	U2424	A2237	U2170	A2089	A2020
C3082	U2990	G2816	U2722	A2642	C2560	U	U2425	A2238	G2171	U2090	G2021
G3083	U2991	U2817	U2723	A2647	A2561	A	G2426	A2239	G2174	U2091	G2022
C3084	A3000	U2818	U2724	U2648	C2562	C	A2427	A2240	U2175	A2092	C2023
A3086	C3001	A2819	C2725	G2651	G2563	U	C2431	A2241	G2176	G2094	G2024
U3089	C3002	U2820	A2727	U2652	U2564	A	A2432	A2242	G2177	A2095	G2025
U3090	A3006	G2824	U2728	U2655	U2565	U	U2433	A2243	G2180	A2096	U2026
A3091	U3007	U2825	A2736	A2656	C2566	U	U2434	A2244	C2181	U2097	C2027
C3092	U3013	U2826	C2737	G2657	C2567	U	G2435	A2245	G2185	C2098	U2028
C3093	U3014	G2827	A2740	G2658	C2568	U	A2436	A2246	G2188	U2102	U2031
A3094	G3015	U2828	C2741	G2659	A2569	U	A2437	A2247	U2103	U2103	U2032
U3095	C3016	U2829	C2742	G2660	U2570	U	A2438	A2248	G2192	A2104	U2033
A3096	A3016	G2830	U2745	G2661	C2571	U	A2439	A2249	U2193	G2105	G2032
C3097	U3017	G2831	A2746	G2662	C2572	U	A2441	A2250	G2194	A2106	C2034
G3098	C3018	C2832	U2747	G2663	G2573	U	G2442	A2251	U2200	A2107	G2035
U3099	A3021	U2835	A2748	C2666	U2578	U	U2443	A2252	G2036	U2111	G2037
U3099	G3022	C2836	U2749	A2671	G2579	U	C2444	A2253	C2038	U2112	C2039
U3099	U3098	A2837	U2750	G2672	U2581	U	A2445	A2254	U2040	U2040	U2041
U3099	U3098	U2837	U2750	U2581	U2581	U	U2446	A2255	U2042	U2042	U2043
U3099	U3098	U2837	U2750	U2581	U2581	U	U2447	A2256	U2044	U2044	U2044
U3099	U3098	U2837	U2750	U2581	U2581	U	U2447	A2257	U2045	U2045	G2045
U3099	U3098	U2837	U2750	U2581	U2581	U	U2447	A2258	U2046	U2046	A2047
U3099	U3098	U2837	U2750	U2581	U2581	U	U2447	A2259	U2047	U2047	G2048

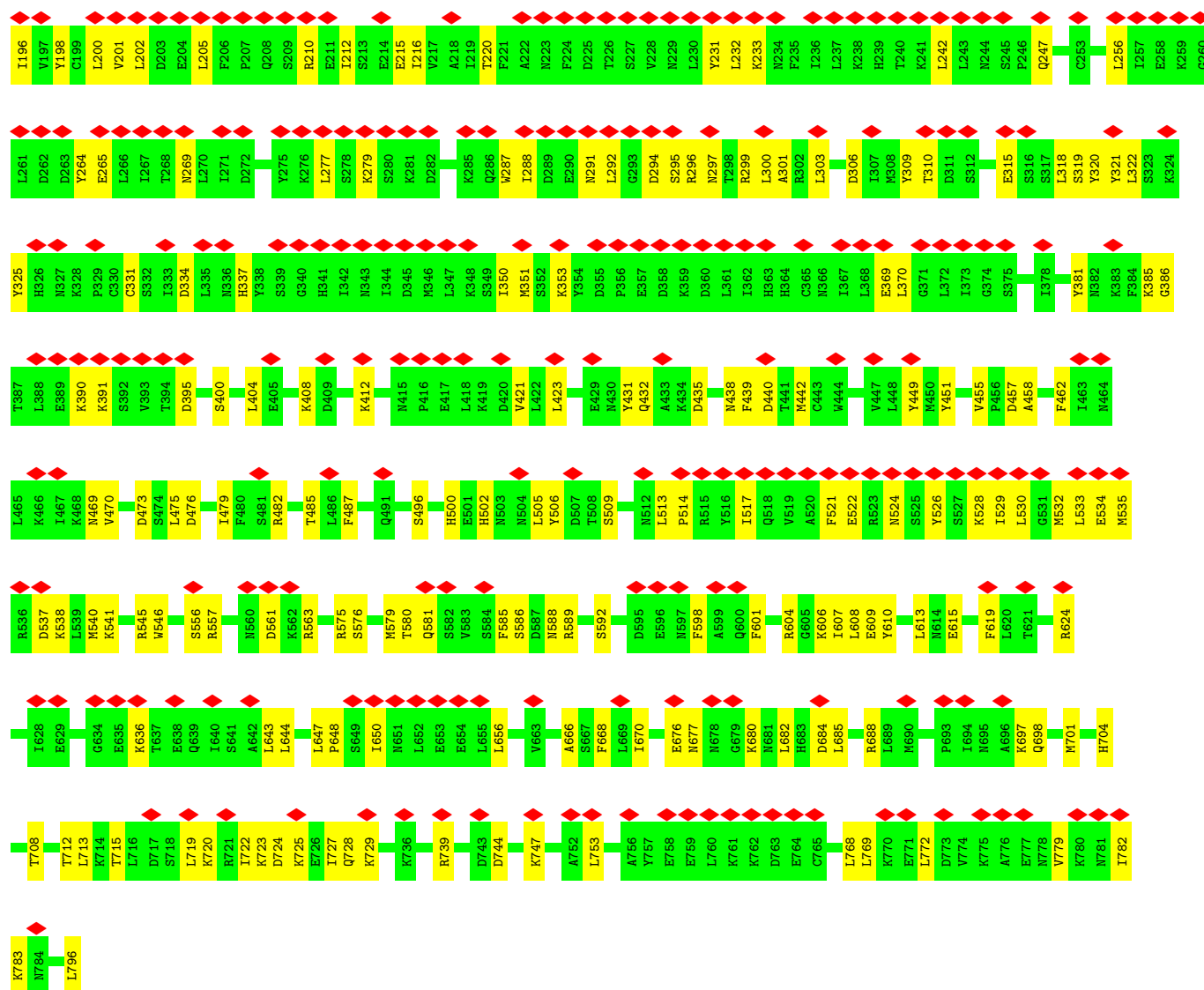


• Molecule 45: N-terminal acetyltransferase B complex catalytic subunit NAT3

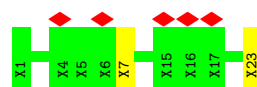
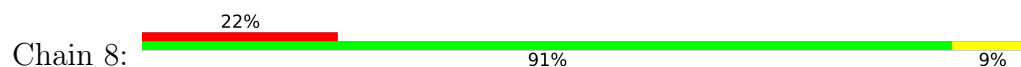


• Molecule 46: N-terminal acetyltransferase B complex subunit MDM2





• Molecule 47: Nascent peptide chain



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	45530	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45.2	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.563	Depositor
Minimum map value	-0.645	Depositor
Average map value	0.011	Depositor
Map value standard deviation	0.093	Depositor
Recommended contour level	0.215	Depositor
Map size (Å)	417.99997, 417.99997, 417.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	C4	0.16	0/2883	0.22	0/4491
2	C3	0.18	0/3746	0.26	0/5832
3	LA	0.19	0/1933	0.35	0/2598
4	LB	0.17	0/3146	0.31	0/4228
5	LC	0.18	0/2800	0.39	1/3790 (0.0%)
6	LD	0.18	0/2400	0.45	3/3239 (0.1%)
7	LE	0.15	0/1327	0.31	0/1790
8	LF	0.17	0/1821	0.30	0/2451
9	LG	0.16	0/1836	0.35	0/2481
10	LH	0.16	0/1529	0.35	0/2060
11	LI	0.16	0/1801	0.29	0/2416
12	LJ	0.16	0/1371	0.43	0/1838
13	LL	0.16	0/1568	0.36	0/2106
14	LM	0.16	0/1068	0.34	0/1438
15	LN	0.17	0/1757	0.31	0/2354
16	LO	0.17	0/1585	0.29	0/2128
17	LP	0.16	0/1439	0.28	0/1938
18	LQ	0.15	0/1465	0.26	0/1965
19	LR	0.16	0/1395	0.30	0/1861
20	LS	0.18	0/1473	0.37	0/1980
21	LT	0.18	0/1300	0.37	0/1743
22	LU	0.15	0/812	0.36	0/1099
23	LV	0.17	0/1018	0.36	0/1369
24	LW	0.17	0/550	0.30	0/731
25	LX	0.17	0/979	0.27	0/1321
26	LY	0.17	0/995	0.32	0/1329
27	LZ	0.16	0/1118	0.38	0/1497
28	La	0.17	0/1204	0.34	0/1612
29	Lb	0.16	0/473	0.38	0/629
30	Lc	0.16	0/745	0.30	0/1001
31	Ld	0.20	0/894	0.33	0/1200
32	Le	0.16	0/1038	0.29	0/1390

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Lf	0.18	0/868	0.32	0/1168
34	Lg	0.17	0/890	0.33	0/1189
35	Lh	0.15	0/978	0.31	0/1301
36	Li	0.15	0/772	0.34	0/1026
37	Lj	0.17	0/685	0.29	0/908
38	Lk	0.16	0/618	0.32	0/826
39	Ll	0.20	0/443	0.38	0/588
40	Lm	0.17	0/423	0.41	0/562
41	Ln	0.13	0/230	0.32	0/296
42	Lo	0.16	0/836	0.37	0/1104
43	Lp	0.18	0/701	0.37	0/934
44	1	0.17	0/79000	0.27	0/123166
45	A	0.13	0/1654	0.32	0/2237
46	B	0.10	0/6665	0.29	0/8979
All	All	0.17	0/144232	0.29	4/212189 (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
9	LG	0	2
16	LO	0	1
All	All	0	3

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	LC	294	GLU	N-CA-C	-10.71	98.88	112.90
6	LD	18	THR	CA-C-N	10.06	129.87	120.21
6	LD	18	THR	C-N-CA	10.06	129.87	120.21
6	LD	26	GLY	N-CA-C	-5.21	105.03	114.46

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	LG	158	ASP	Peptide
9	LG	76	ALA	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
16	LO	110[A]	PRO	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C4	2579	0	1304	64	0
2	C3	3353	0	1695	74	0
3	LA	1899	0	1956	51	0
4	LB	3075	0	3142	74	0
5	LC	2748	0	2859	74	0
6	LD	2351	0	2294	75	0
7	LE	1305	0	1373	35	0
8	LF	1784	0	1862	46	0
9	LG	1804	0	1877	42	0
10	LH	1508	0	1572	35	0
11	LI	1764	0	1804	39	0
12	LJ	1350	0	1381	50	0
13	LL	1543	0	1608	48	0
14	LM	1053	0	1149	31	0
15	LN	1720	0	1779	48	0
16	LO	1555	0	1659	34	0
17	LP	1416	0	1433	25	0
18	LQ	1441	0	1543	44	0
19	LR	1378	0	1462	34	0
20	LS	1437	0	1475	38	0
21	LT	1276	0	1323	51	0
22	LU	796	0	812	15	0
23	LV	1003	0	1048	21	0
24	LW	538	0	550	8	0
25	LX	964	0	1025	19	0
26	LY	984	0	1075	19	0
27	LZ	1092	0	1155	31	0
28	La	1173	0	1215	32	0
29	Lb	462	0	491	9	0
30	Lc	737	0	792	16	0
31	Ld	880	0	923	26	0
32	Le	1017	0	1081	19	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
33	Lf	850	0	880	27	0
34	Lg	880	0	943	28	0
35	Lh	969	0	1078	24	0
36	Li	766	0	844	17	0
37	Lj	670	0	673	17	0
38	Lk	612	0	682	13	0
39	Ll	436	0	475	21	0
40	Lm	417	0	455	13	0
41	Ln	229	0	273	6	0
42	Lo	824	0	888	25	0
43	Lp	694	0	735	24	0
44	1	70586	0	35467	1382	0
45	A	1612	0	1577	49	0
46	B	6536	0	6588	166	0
47	8	115	0	26	5	0
48	1	196	0	0	0	0
48	C3	1	0	0	0	0
48	C4	1	0	0	0	0
48	LA	2	0	0	0	0
48	LB	1	0	0	0	0
48	LN	1	0	0	0	0
48	LP	1	0	0	0	0
48	LR	1	0	0	0	0
48	LV	1	0	0	0	0
48	Le	1	0	0	0	0
49	Lg	1	0	0	0	0
49	Lj	1	0	0	0	0
49	Lm	1	0	0	0	0
49	Lo	1	0	0	0	0
49	Lp	1	0	0	0	0
All	All	134392	0	98301	2557	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

The worst 5 of 2557 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:LC:299:ILE:HD12	18:LQ:39:ARG:O	1.24	1.30
44:1:2875:U:O4	47:8:23:UNK:C	1.79	1.28
5:LC:299:ILE:CD1	18:LQ:39:ARG:O	1.83	1.25

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:Ld:7:VAL:HG22	31:Ld:77:ARG:O	1.41	1.21
44:1:1257:C:H42	44:1:1261:G:N2	1.45	1.14

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	LA	249/251 (99%)	232 (93%)	17 (7%)	0	100	100
4	LB	384/386 (100%)	357 (93%)	27 (7%)	0	100	100
5	LC	359/361 (99%)	334 (93%)	24 (7%)	1 (0%)	36	67
6	LD	292/294 (99%)	279 (96%)	12 (4%)	1 (0%)	36	67
7	LE	163/175 (93%)	154 (94%)	9 (6%)	0	100	100
8	LF	220/222 (99%)	207 (94%)	13 (6%)	0	100	100
9	LG	231/233 (99%)	220 (95%)	11 (5%)	0	100	100
10	LH	189/191 (99%)	178 (94%)	11 (6%)	0	100	100
11	LI	216/218 (99%)	209 (97%)	7 (3%)	0	100	100
12	LJ	167/169 (99%)	152 (91%)	15 (9%)	0	100	100
13	LL	191/193 (99%)	175 (92%)	15 (8%)	1 (0%)	24	57
14	LM	134/136 (98%)	126 (94%)	8 (6%)	0	100	100
15	LN	201/203 (99%)	188 (94%)	13 (6%)	0	100	100
16	LO	195/197 (99%)	188 (96%)	5 (3%)	2 (1%)	12	41
17	LP	181/183 (99%)	172 (95%)	9 (5%)	0	100	100
18	LQ	183/185 (99%)	176 (96%)	7 (4%)	0	100	100
19	LR	169/188 (90%)	164 (97%)	5 (3%)	0	100	100
20	LS	169/171 (99%)	160 (95%)	9 (5%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	LT	157/159 (99%)	147 (94%)	10 (6%)	0	100	100
22	LU	98/100 (98%)	93 (95%)	5 (5%)	0	100	100
23	LV	134/136 (98%)	133 (99%)	1 (1%)	0	100	100
24	LW	65/126 (52%)	63 (97%)	2 (3%)	0	100	100
25	LX	119/121 (98%)	116 (98%)	3 (2%)	0	100	100
26	LY	123/125 (98%)	117 (95%)	6 (5%)	0	100	100
27	LZ	133/135 (98%)	122 (92%)	11 (8%)	0	100	100
28	La	146/148 (99%)	130 (89%)	16 (11%)	0	100	100
29	Lb	56/58 (97%)	52 (93%)	4 (7%)	0	100	100
30	Lc	94/96 (98%)	94 (100%)	0	0	100	100
31	Ld	107/109 (98%)	101 (94%)	6 (6%)	0	100	100
32	Le	125/127 (98%)	120 (96%)	5 (4%)	0	100	100
33	Lf	104/106 (98%)	98 (94%)	6 (6%)	0	100	100
34	Lg	110/112 (98%)	108 (98%)	2 (2%)	0	100	100
35	Lh	117/119 (98%)	113 (97%)	4 (3%)	0	100	100
36	Li	97/99 (98%)	92 (95%)	5 (5%)	0	100	100
37	Lj	83/85 (98%)	80 (96%)	3 (4%)	0	100	100
38	Lk	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
39	Ll	48/50 (96%)	48 (100%)	0	0	100	100
40	Lm	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
41	Ln	23/25 (92%)	23 (100%)	0	0	100	100
42	Lo	101/103 (98%)	96 (95%)	5 (5%)	0	100	100
43	Lp	89/91 (98%)	85 (96%)	4 (4%)	0	100	100
45	A	193/195 (99%)	189 (98%)	4 (2%)	0	100	100
46	B	794/796 (100%)	784 (99%)	10 (1%)	0	100	100
All	All	7134/7306 (98%)	6797 (95%)	332 (5%)	5 (0%)	49	78

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	LD	21	ARG
16	LO	111[A]	PRO
13	LL	63	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
16	LO	110[A]	PRO
5	LC	4	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	LA	190/193 (98%)	190 (100%)	0	100	100
4	LB	319/322 (99%)	319 (100%)	0	100	100
5	LC	288/288 (100%)	286 (99%)	2 (1%)	76	82
6	LD	241/243 (99%)	241 (100%)	0	100	100
7	LE	138/153 (90%)	138 (100%)	0	100	100
8	LF	186/186 (100%)	186 (100%)	0	100	100
9	LG	187/191 (98%)	187 (100%)	0	100	100
10	LH	168/171 (98%)	168 (100%)	0	100	100
11	LI	185/185 (100%)	185 (100%)	0	100	100
12	LJ	146/147 (99%)	146 (100%)	0	100	100
13	LL	154/154 (100%)	154 (100%)	0	100	100
14	LM	107/107 (100%)	106 (99%)	1 (1%)	70	80
15	LN	175/175 (100%)	175 (100%)	0	100	100
16	LO	160/160 (100%)	160 (100%)	0	100	100
17	LP	138/145 (95%)	138 (100%)	0	100	100
18	LQ	150/150 (100%)	150 (100%)	0	100	100
19	LR	139/153 (91%)	139 (100%)	0	100	100
20	LS	155/155 (100%)	155 (100%)	0	100	100
21	LT	136/136 (100%)	135 (99%)	1 (1%)	76	82
22	LU	87/87 (100%)	87 (100%)	0	100	100
23	LV	104/104 (100%)	104 (100%)	0	100	100
24	LW	54/107 (50%)	54 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	LX	104/105 (99%)	104 (100%)	0	100	100
26	LY	108/108 (100%)	108 (100%)	0	100	100
27	LZ	115/115 (100%)	115 (100%)	0	100	100
28	La	118/118 (100%)	118 (100%)	0	100	100
29	Lb	46/46 (100%)	46 (100%)	0	100	100
30	Lc	81/81 (100%)	81 (100%)	0	100	100
31	Ld	93/96 (97%)	91 (98%)	2 (2%)	45	71
32	Le	108/109 (99%)	108 (100%)	0	100	100
33	Lf	90/90 (100%)	90 (100%)	0	100	100
34	Lg	95/95 (100%)	94 (99%)	1 (1%)	65	78
35	Lh	104/104 (100%)	104 (100%)	0	100	100
36	Li	80/81 (99%)	80 (100%)	0	100	100
37	Lj	69/69 (100%)	69 (100%)	0	100	100
38	Lk	68/68 (100%)	68 (100%)	0	100	100
39	Ll	45/45 (100%)	45 (100%)	0	100	100
40	Lm	47/47 (100%)	47 (100%)	0	100	100
41	Ln	22/23 (96%)	22 (100%)	0	100	100
42	Lo	87/88 (99%)	87 (100%)	0	100	100
43	Lp	71/71 (100%)	71 (100%)	0	100	100
45	A	180/180 (100%)	180 (100%)	0	100	100
46	B	743/743 (100%)	743 (100%)	0	100	100
All	All	6081/6194 (98%)	6074 (100%)	7 (0%)	87	90

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
21	LT	77	ASN
31	Ld	7	VAL
34	Lg	84	CYS
31	Ld	8	VAL
14	LM	27	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 49 such sidechains are listed below:

Mol	Chain	Res	Type
28	La	67	HIS
42	Lo	47	GLN
30	Lc	75	ASN
38	Lk	10	GLN
42	Lo	90	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C4	120/121 (99%)	11 (9%)	1 (0%)
2	C3	157/158 (99%)	25 (15%)	1 (0%)
44	1	3297/3395 (97%)	579 (17%)	34 (1%)
All	All	3574/3674 (97%)	615 (17%)	36 (1%)

5 of 615 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C4	7	G
1	C4	11	A
1	C4	53	U
1	C4	54	U
1	C4	55	A

5 of 36 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
44	1	3121	U
44	1	3351	U
44	1	3218	A
44	1	3275	U
44	1	1355	A

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 211 ligands modelled in this entry, 211 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

There are no chain breaks in this entry.

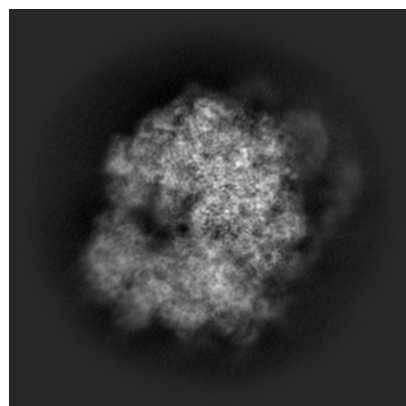
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16086. These allow visual inspection of the internal detail of the map and identification of artifacts.

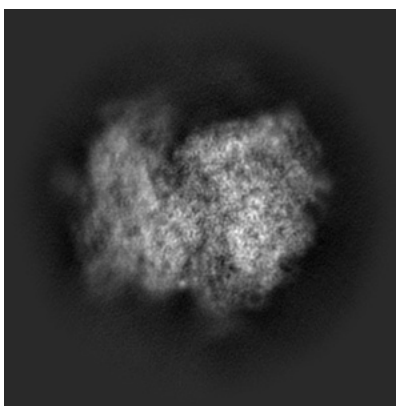
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

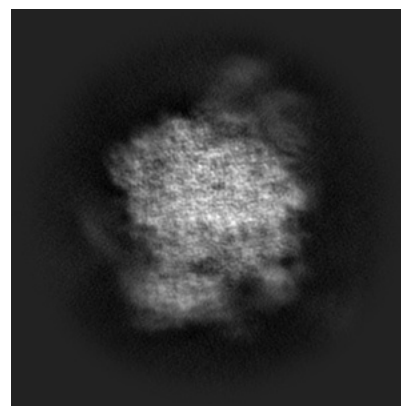
6.1.1 Primary map



X

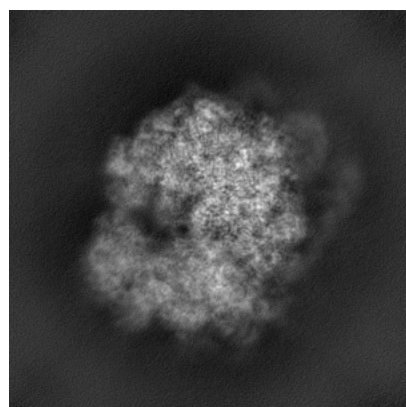


Y

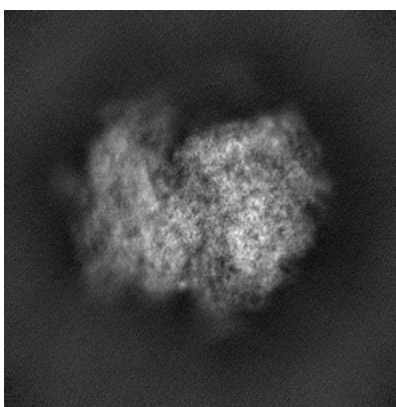


Z

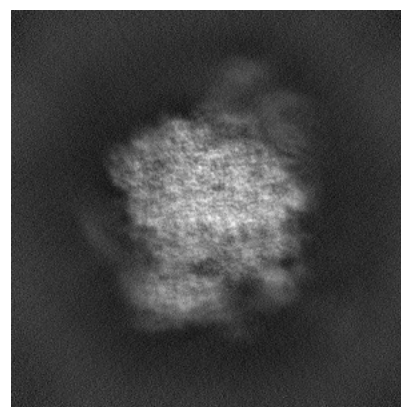
6.1.2 Raw map



X



Y

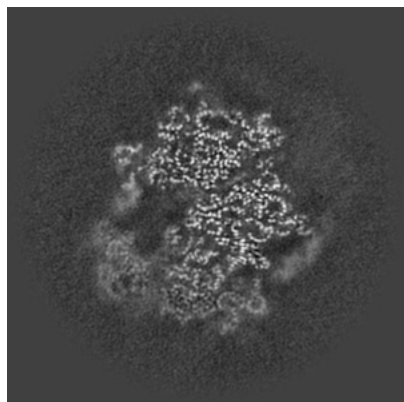


Z

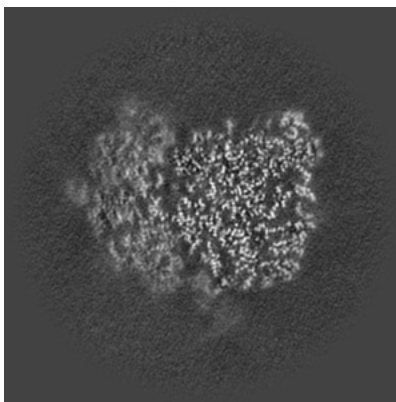
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

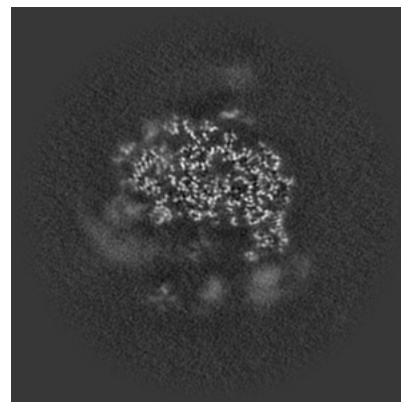
6.2.1 Primary map



X Index: 200

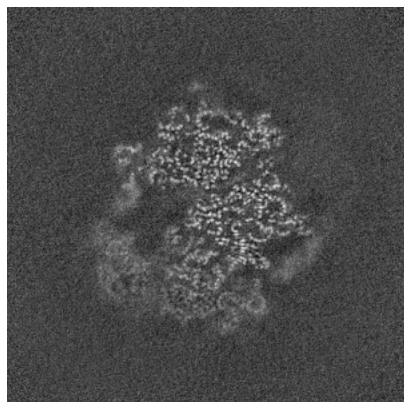


Y Index: 200

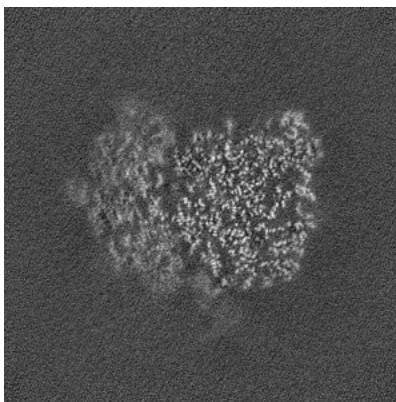


Z Index: 200

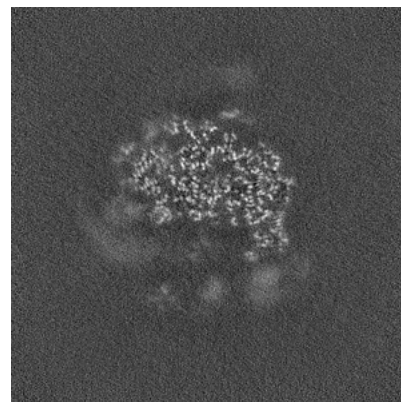
6.2.2 Raw map



X Index: 200



Y Index: 200

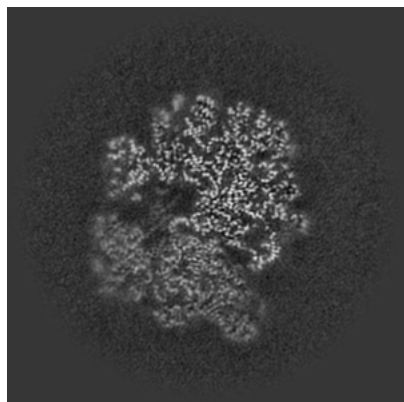


Z Index: 200

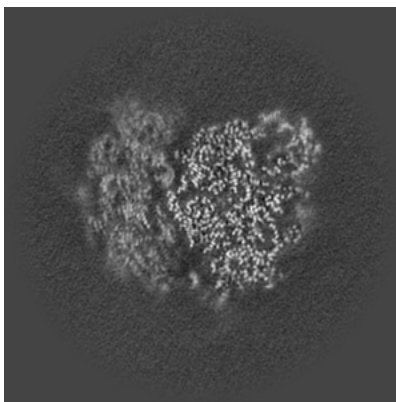
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

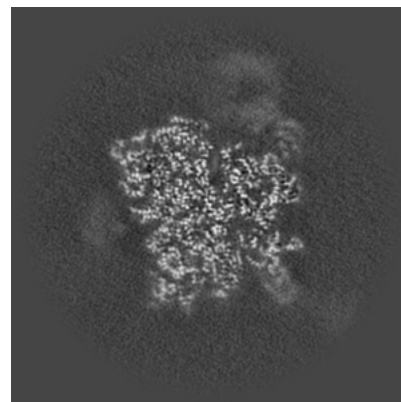
6.3.1 Primary map



X Index: 182

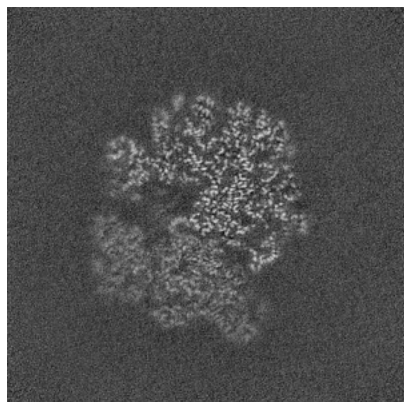


Y Index: 210

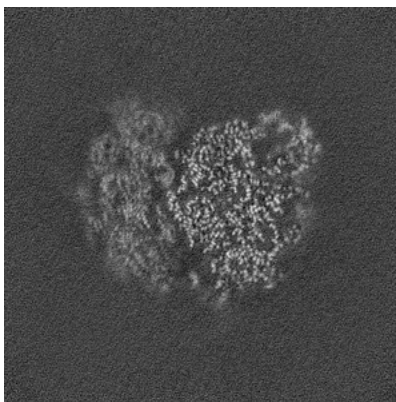


Z Index: 235

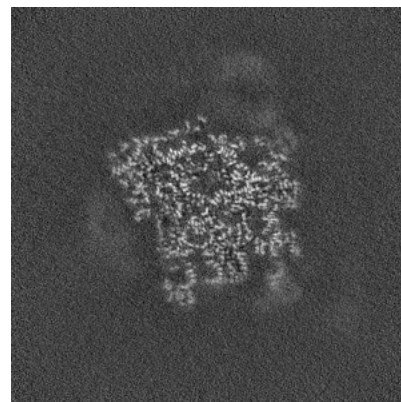
6.3.2 Raw map



X Index: 183



Y Index: 210

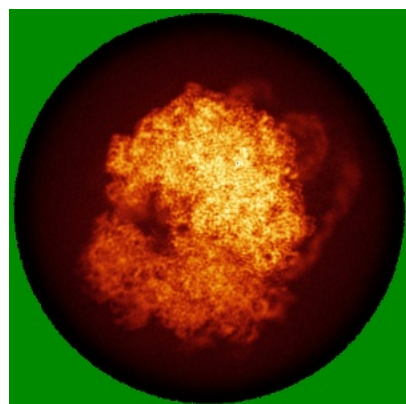


Z Index: 226

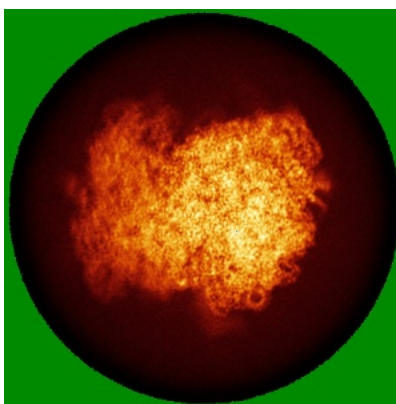
The images above show the largest variance slices of the map in three orthogonal directions.

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

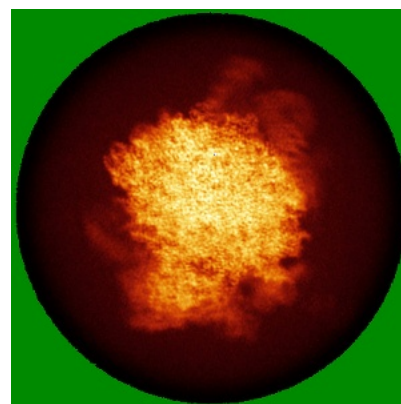
6.4.1 Primary map



X

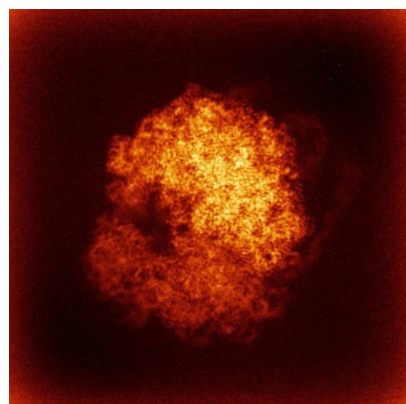


Y

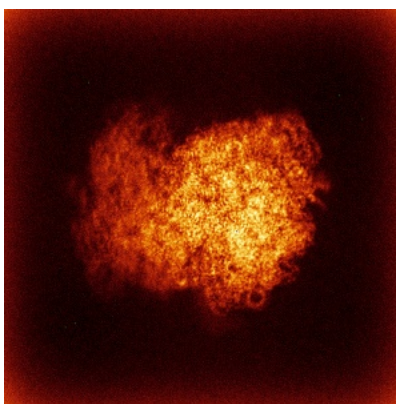


Z

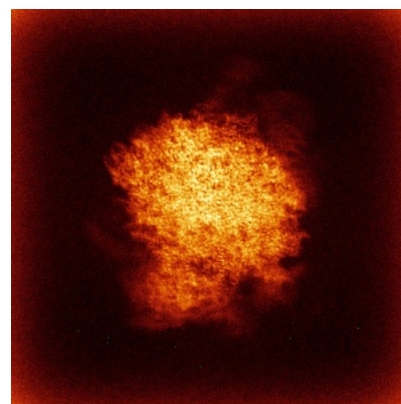
6.4.2 Raw map



X



Y

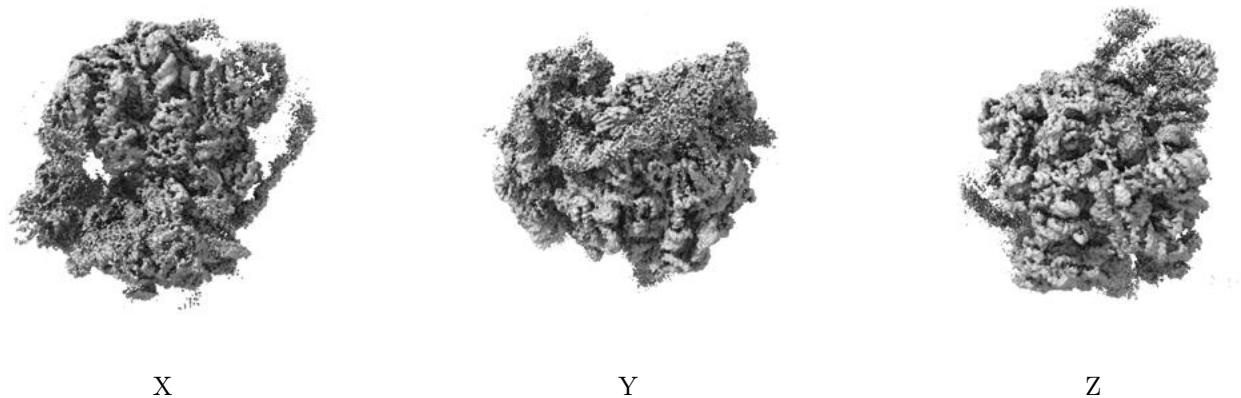


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

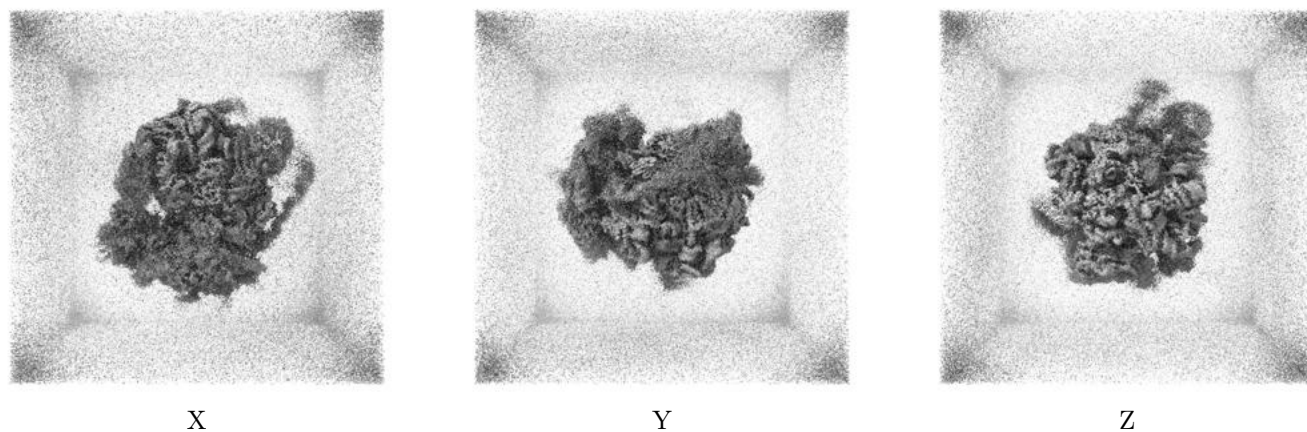
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.215. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

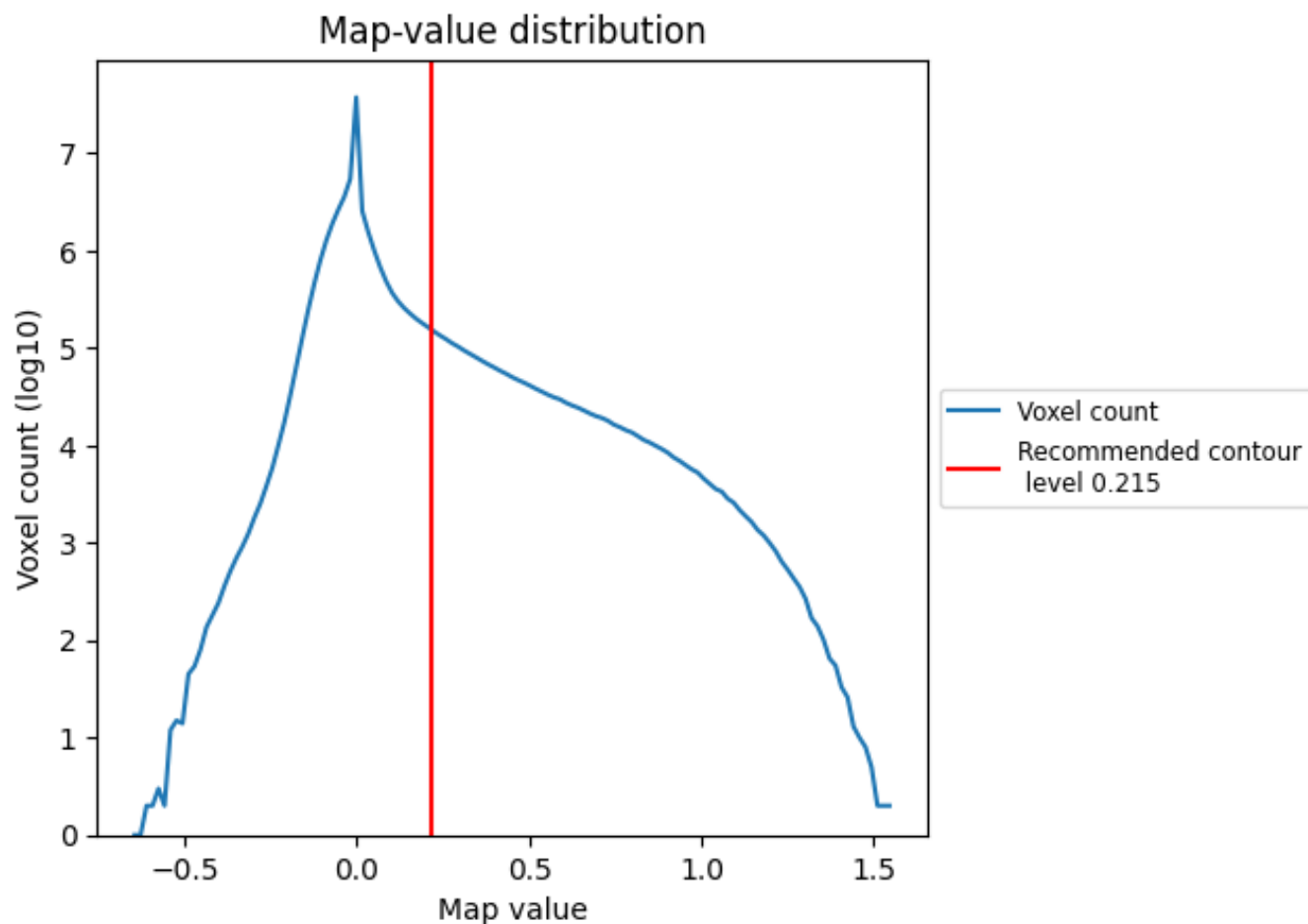
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

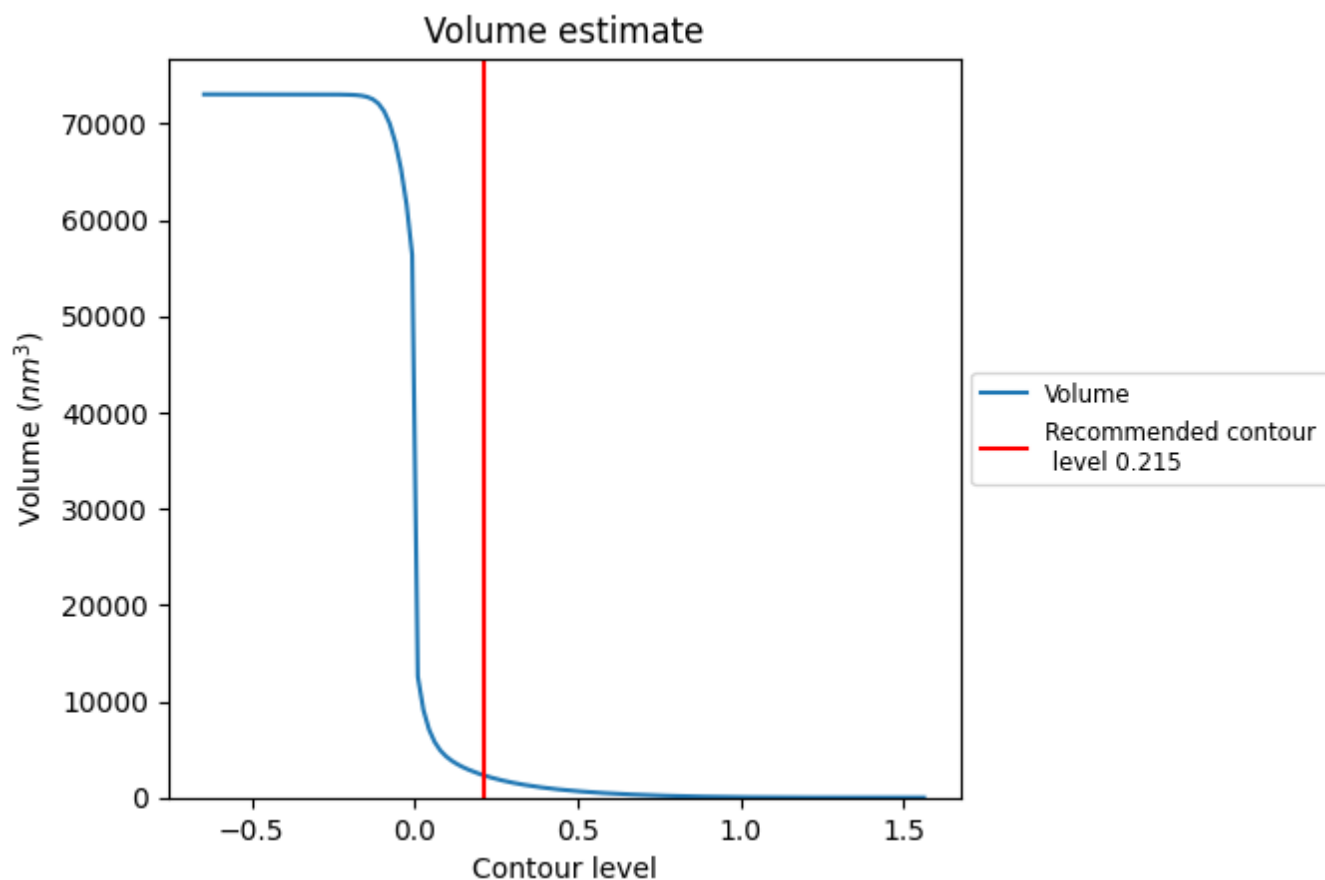
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

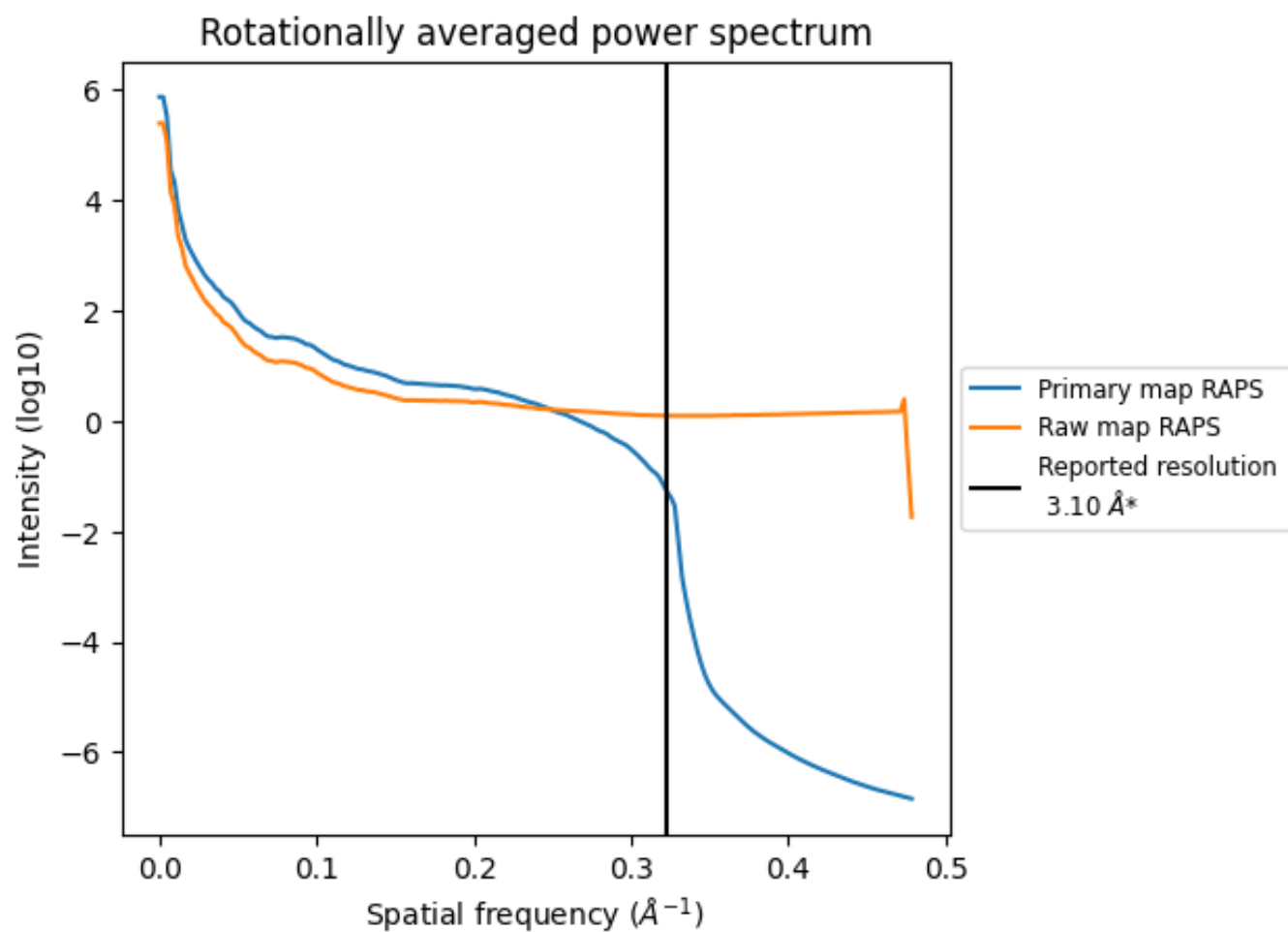
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2283 nm³; this corresponds to an approximate mass of 2062 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

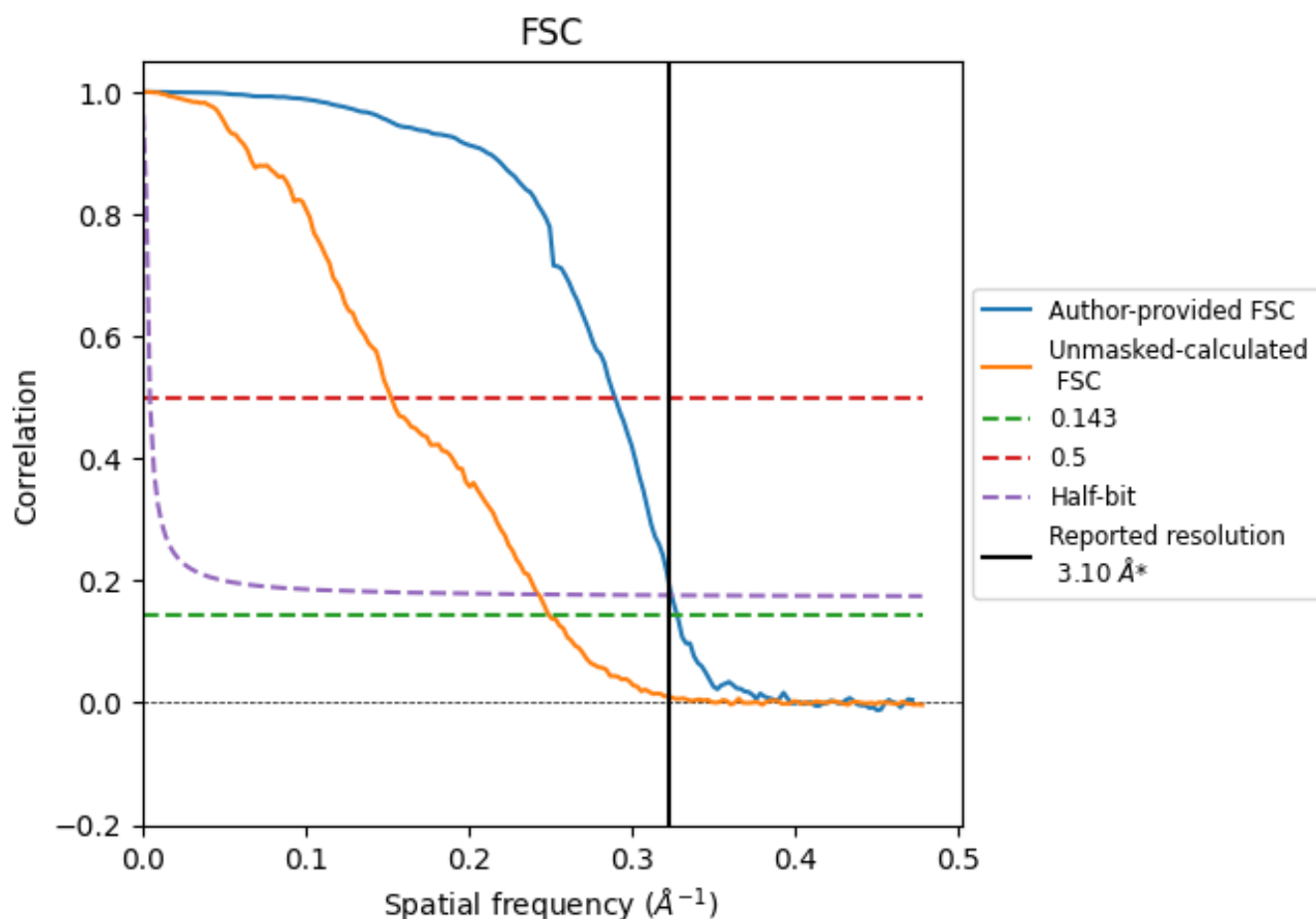


*Reported resolution corresponds to spatial frequency of 0.323 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.323 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

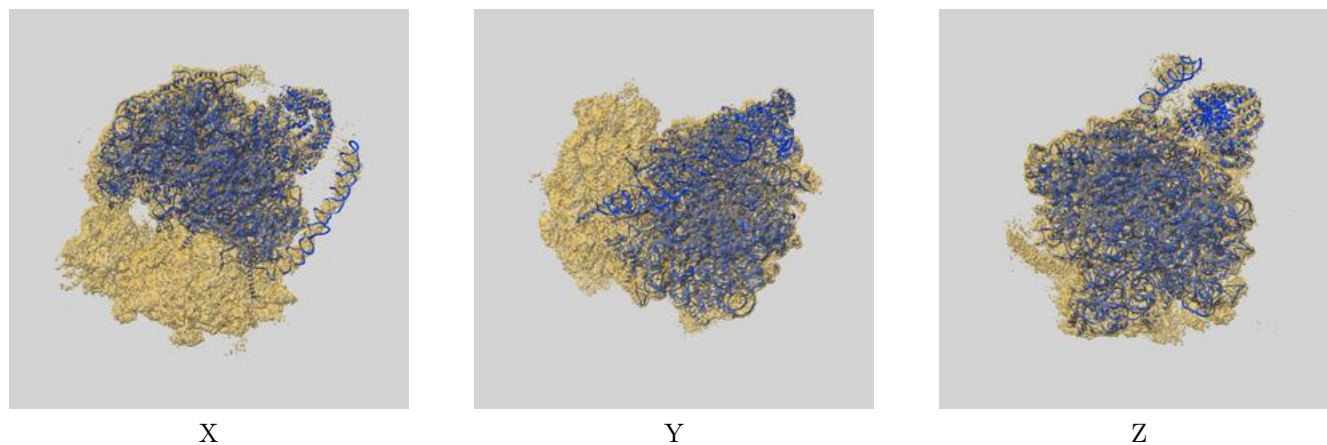
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.05	3.45	3.08
Unmasked-calculated*	4.00	6.55	4.11

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.00 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

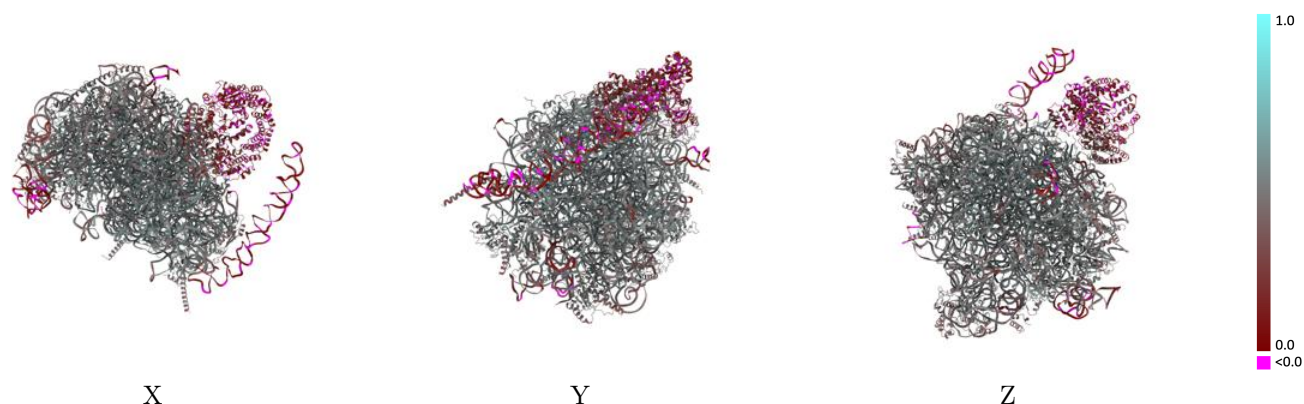
This section contains information regarding the fit between EMDB map EMD-16086 and PDB model 8BIP. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

9.1 Map-model overlay [i](#)



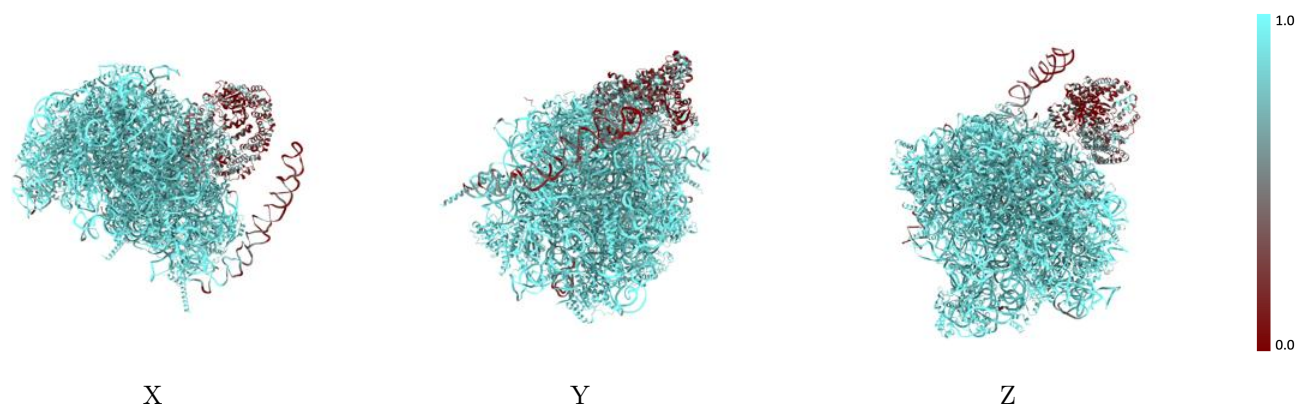
The images above show the 3D surface view of the map at the recommended contour level 0.215 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



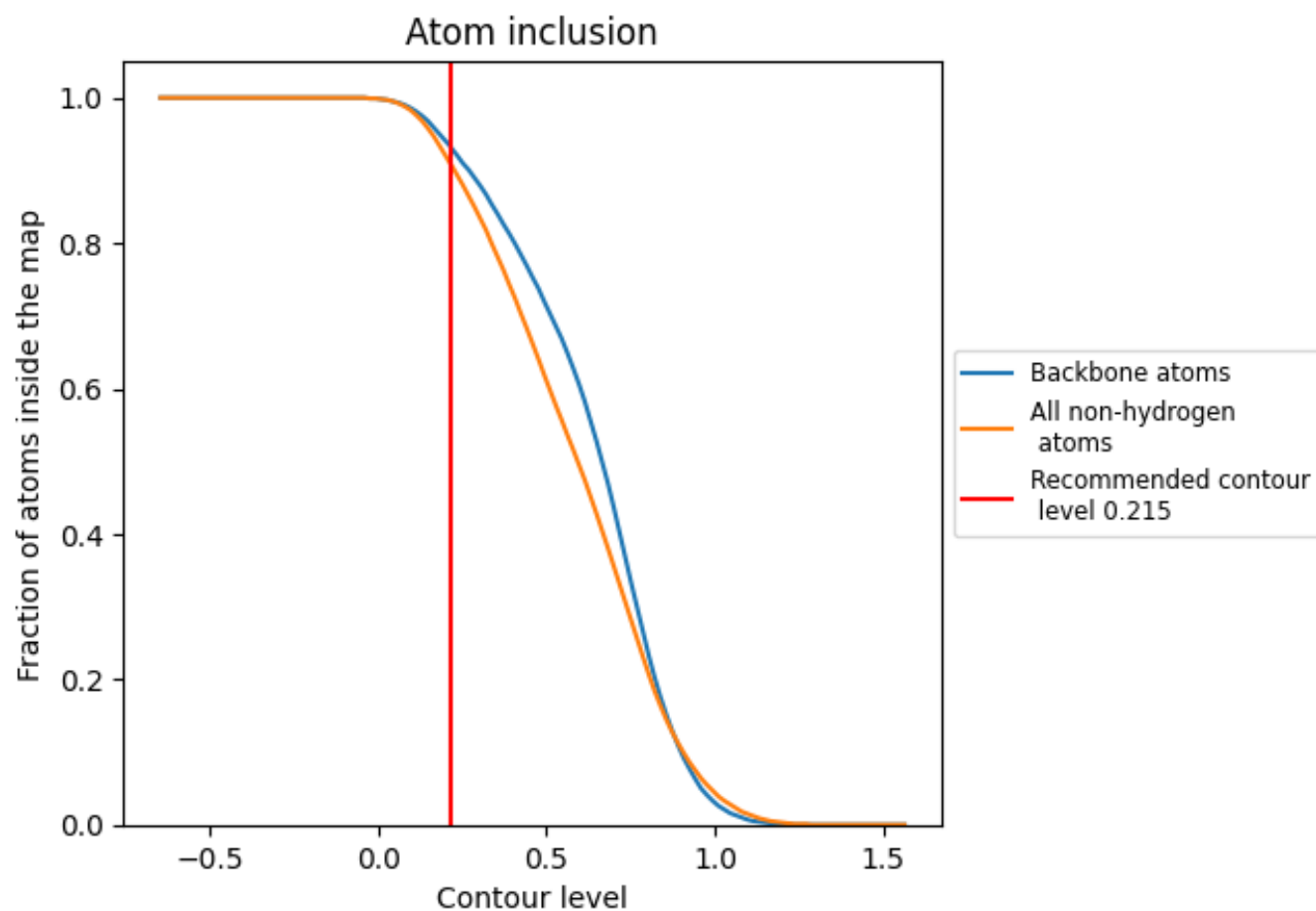
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.215).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 91% 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 (0.215) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9090	 0.4510
1	 0.9540	 0.4550
8	 0.7220	 0.4130
A	 0.0550	 0.0950
B	 0.4360	 0.1860
C3	 0.9930	 0.4860
C4	 0.9980	 0.4740
LA	 0.9140	 0.5230
LB	 0.9420	 0.5050
LC	 0.9430	 0.5040
LD	 0.9270	 0.4260
LE	 0.9280	 0.4510
LF	 0.9450	 0.4930
LG	 0.9090	 0.4540
LH	 0.9280	 0.4700
LI	 0.9030	 0.4810
LJ	 0.8540	 0.4040
LL	 0.9380	 0.4750
LM	 0.9240	 0.4630
LN	 0.9430	 0.5170
LO	 0.9390	 0.4950
LP	 0.9040	 0.5080
LQ	 0.9530	 0.5080
LR	 0.9110	 0.4920
LS	 0.9250	 0.5000
LT	 0.9260	 0.5040
LU	 0.9010	 0.4630
LV	 0.8790	 0.5090
LW	 0.8850	 0.4970
LX	 0.9040	 0.5050
LY	 0.9440	 0.5030
LZ	 0.9390	 0.4740
La	 0.9540	 0.5110
Lb	 0.9140	 0.4700
Lc	 0.9320	 0.4800



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Ld	 0.9170	 0.5130
Le	 0.9300	 0.5220
Lf	 0.9390	 0.5150
Lg	 0.9300	 0.5130
Lh	 0.9400	 0.4760
Li	 0.8920	 0.4520
Lj	 0.9740	 0.5340
Lk	 0.9130	 0.4740
Ll	 0.9420	 0.5140
Lm	 0.9080	 0.4920
Ln	 0.8410	 0.4580
Lo	 0.9340	 0.4970
Lp	 0.9060	 0.5050