



## wwPDB EM Validation Summary Report ⓘ

Apr 22, 2024 – 04:26 PM EDT

PDB ID : 8V84  
EMDB ID : EMD-43021  
Title : 60S ribosome biogenesis intermediate (Dbp10 catalytic structure - Overall map)  
Authors : Cruz, V.E.; Weirich, C.S.; Peddada, N.; Erzberger, J.P.  
Deposited on : 2023-12-04  
Resolution : 2.70 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev92  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36.2

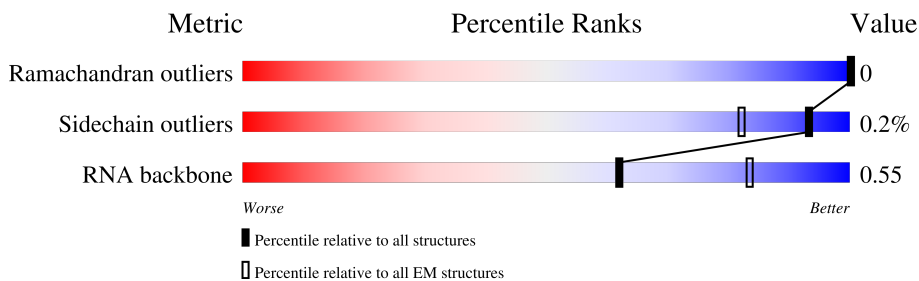
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.70 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.



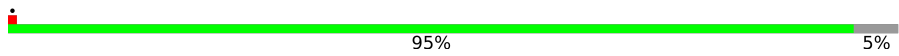


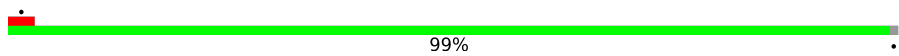

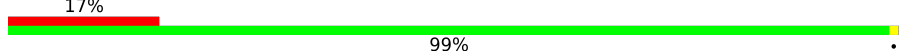




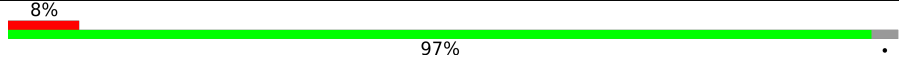

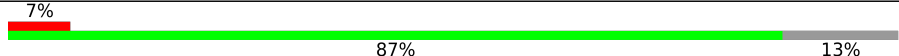
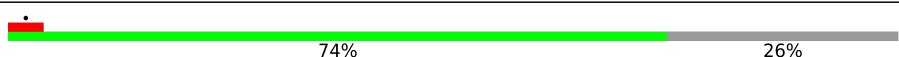
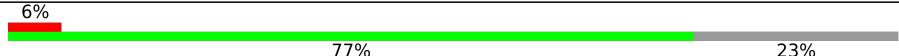

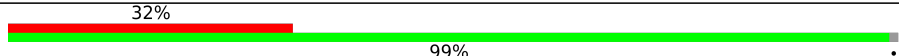


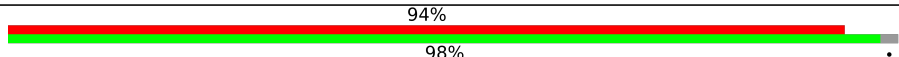
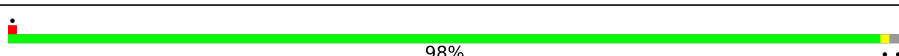

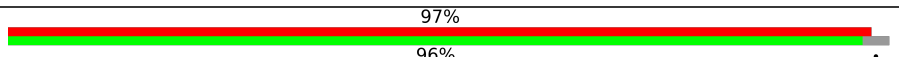

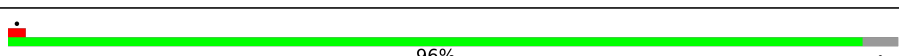
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	3396	
2	2	158	
3	3	995	
4	6	232	
5	7	204	
6	8	434	
7	A	291	
8	B	387	

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Mol	Chain	Length	Quality of chain
9	C	362	
10	D	505	
11	E	176	
12	F	244	
13	G	256	
14	H	191	
15	I	463	
16	J	427	
17	K	376	
18	L	199	
19	M	138	
20	N	204	
21	O	199	
22	P	184	
23	Q	186	
24	R	306	
25	S	172	
26	T	250	
27	V	137	
28	W	236	
29	Y	127	
30	Z	453	
31	a	217	
32	b	647	
33	e	130	

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Mol	Chain	Length	Quality of chain
34	f	107	99%
35	h	120	32% 99%
36	i	100	25% 84% 16%
37	j	88	82% 18%
38	l	181	97% 97%
39	m	807	20% 26% 74%
40	n	605	52% 56% 44%
41	o	220	41% 60% 40%
42	q	618	58% 57% 42%
43	r	261	61% 76% 23%
44	t	322	70% 77% 23%
45	u	199	49% 56% 44%
46	v	231	13% 64% 35%
47	w	278	8% 87% 13%
48	x	295	5% 95% 5%
49	y	245	73% 92% 8%

## 2 Entry composition [i](#)

There are 52 unique types of molecules in this entry. The entry contains 121244 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 *Saccharomyces cerevisiae* 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	1970	42190	18840	7647	13733	1970	0	0

- Molecule 2 is a RNA chain called *Saccharomyces cerevisiae* 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	150	3189	1426	563	1050	150	0	0

- Molecule 3 is a protein called ATP-dependent RNA helicase DBP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	3	355	2884	1842	508	523	11	0	0

- Molecule 4 is a RNA chain called ITS2 RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	6	58	1227	550	210	409	58	0	0

- Molecule 5 is a protein called 60S ribosomal subunit assembly/export protein LOC1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
5	7	11	87	56	15	16	0	0

- Molecule 6 is a protein called Ribosomal RNA-processing protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	8	143	1203	743	240	216	4	0	0

- Molecule 7 is a protein called Ribosome biogenesis protein BRX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	A	255	2080	1326	372	376	6	0	0

- Molecule 8 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	B	331	2626	1669	484	467	6	0	0

- Molecule 9 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	C	343	2611	1643	499	466	3	0	0

- Molecule 10 is a protein called ATP-dependent RNA helicase HAS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	D	423	3377	2183	573	609	12	0	0

- Molecule 11 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	E	151	1205	780	215	209	1	0	0

- Molecule 12 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	F	241	1936	1246	351	338	1	0	0

- Molecule 13 is a protein called Large ribosomal subunit protein eL8A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	G	164	1272	818	217	235	2	0	0

- Molecule 14 is a protein called Large ribosomal subunit protein uL6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	H	190	Total	C	N	O	S	0	0
			1510	957	273	276	4		

- Molecule 15 is a protein called Ribosome biogenesis protein NSA1.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	I	394	Total	C	N	O	S	0	0
			3126	1997	525	593	11		

- Molecule 16 is a protein called rRNA-processing protein EBP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	J	151	Total	C	N	O	S	0	0
			1271	793	240	235	3		

- Molecule 17 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	K	265	Total	C	N	O	S	0	0
			2135	1375	351	405	4		

- Molecule 18 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	L	110	Total	C	N	O	0	0
			884	552	185	147		

- Molecule 19 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	M	134	Total	C	N	O	S	0	0
			1041	668	197	174	2		

- Molecule 20 is a protein called Large ribosomal subunit protein eL15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	N	177	Total	C	N	O	S	0	0
			1513	948	320	244	1		

- Molecule 21 is a protein called Large ribosomal subunit protein uL13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	O	174	1386	897	259	229	1	0	0

- Molecule 22 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	P	137	1062	666	198	198		0	0

- Molecule 23 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 24 is a protein called Protein MAK16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	R	190	1578	996	297	275	10	0	0

- Molecule 25 is a protein called Large ribosomal subunit protein eL20A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	S	170	1432	922	265	242	3	0	0

- Molecule 26 is a protein called Ribosomal RNA-processing protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	T	79	625	390	109	126		0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	V	122	903	567	169	160	7	0	0

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



Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	W	232	1870	1184	321	360	5	0	0

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

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

- Molecule 30 is a protein called Ribosome biogenesis protein SSF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	Z	253	2020	1280	361	370	9	0	0

- Molecule 31 is a protein called Large ribosomal subunit protein uL1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	a	210	1668	1067	291	301	9	0	0

- Molecule 32 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	b	423	3429	2193	586	632	18	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	125	1010	640	203	166	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 L35-A.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	i	84	665	413	136	114	2	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	j	72	571	347	124	95	5	0	0

- Molecule 38 is a protein called 60S ribosome subunit biogenesis protein NIP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	l	176	1394	896	244	247	7	0	0

- Molecule 39 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	m	211	1759	1116	305	333	5	0	0

- Molecule 40 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	n	337	2760	1804	462	486	8	0	0

- Molecule 41 is a protein called Ribosome biogenesis protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	o	133	1107	716	198	189	4	0	0

- Molecule 42 is a protein called 25S rRNA (cytosine(2870)-C(5))-methyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	q	358	2799	1779	490	518	12	0	0

- Molecule 43 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	r	200	1615	1018	306	285	6	0	0

- Molecule 44 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	t	249	1973	1258	352	360	3	0	0

- Molecule 45 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	u	112	944	594	191	150	9	0	0

- Molecule 46 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	v	149	1242	778	242	219	3	0	0

- Molecule 47 is a protein called Ribosomal RNA-processing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	w	243	2058	1334	353	366	5	0	0

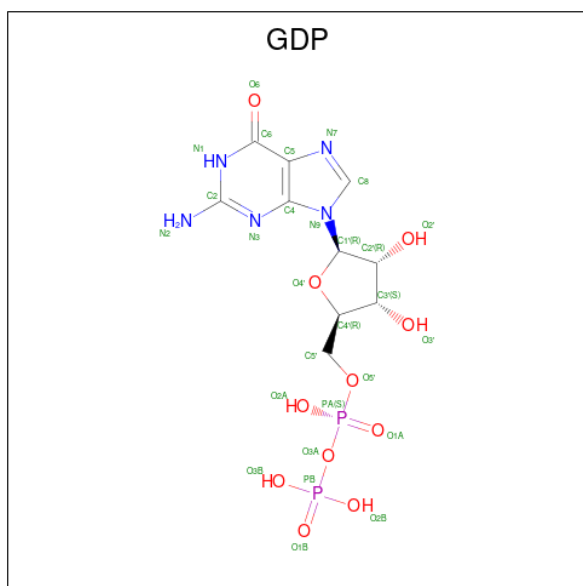
- Molecule 48 is a protein called Ribosome production factor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	x	279	2362	1500	427	431	4	0	0

- Molecule 49 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	y	225	1701	1056	295	343	7	0	0

- Molecule 50 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula:  $C_{10}H_{15}N_5O_{11}P_2$ ).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
50	b	1	28	10	5	11	2	0

- Molecule 51 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
51	b	1	1	1	0

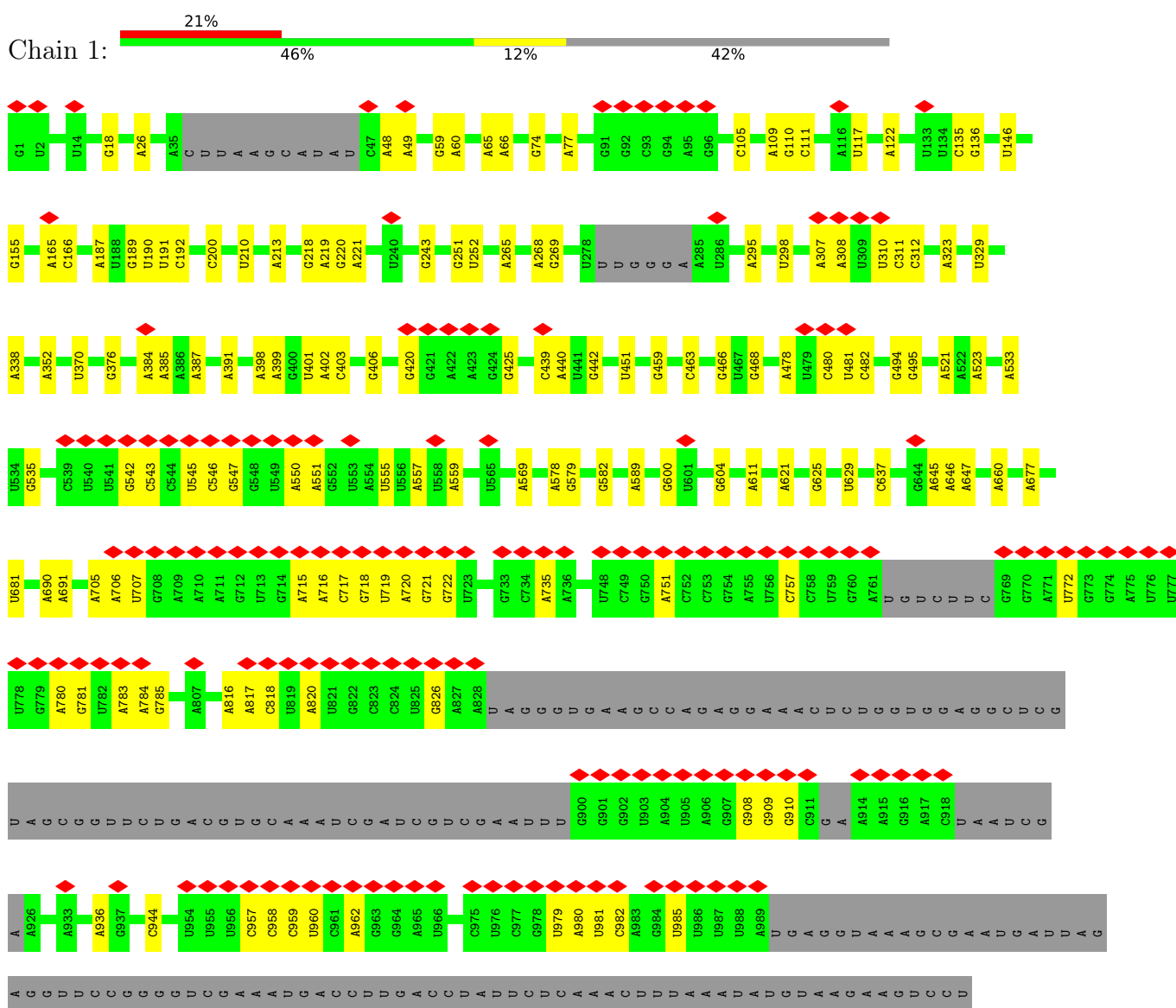
- Molecule 52 is ZINC ION (three-letter code: ZN) (formula: Zn).

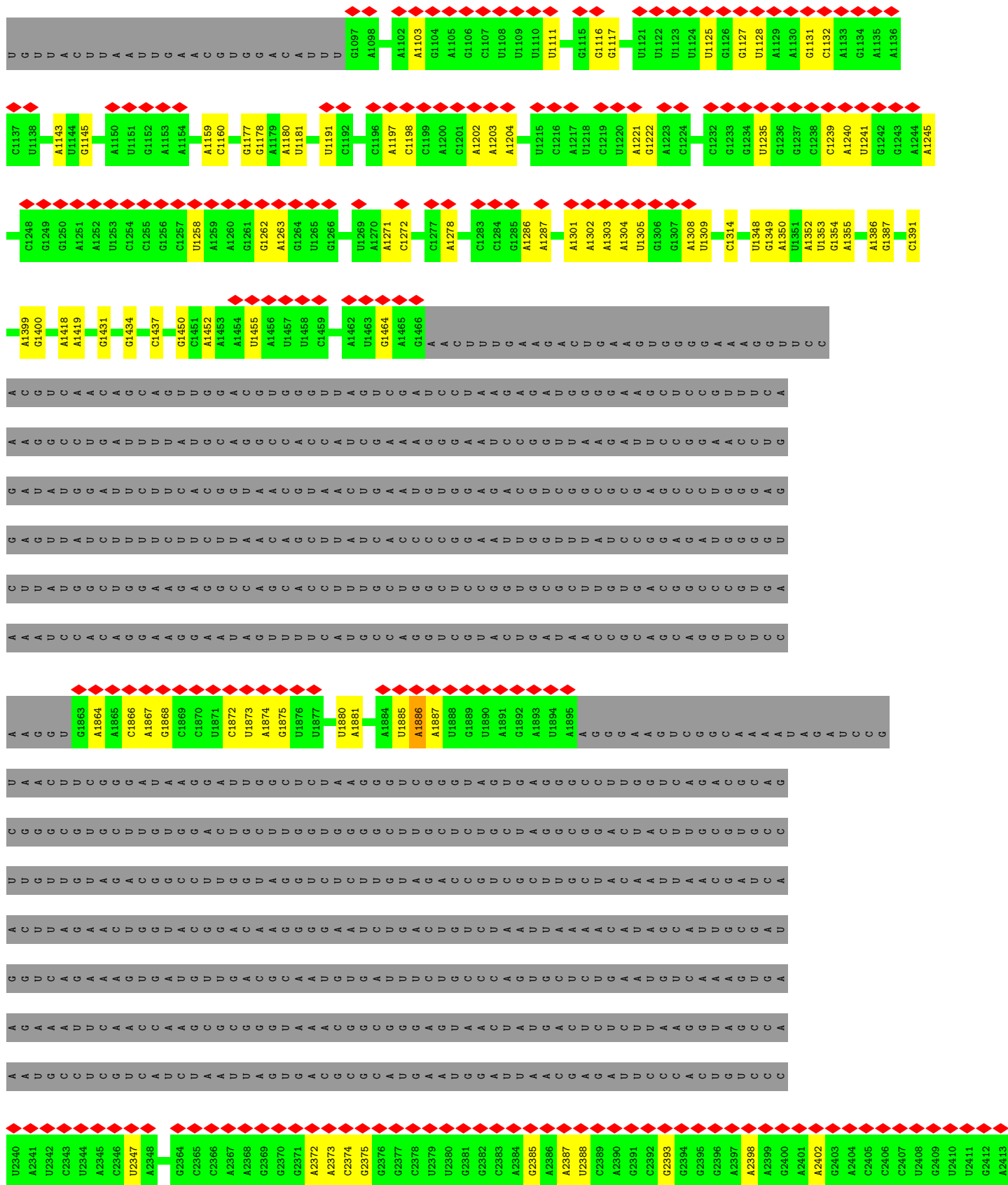
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
52	j	1	1	1	0
52	u	1	1	1	0

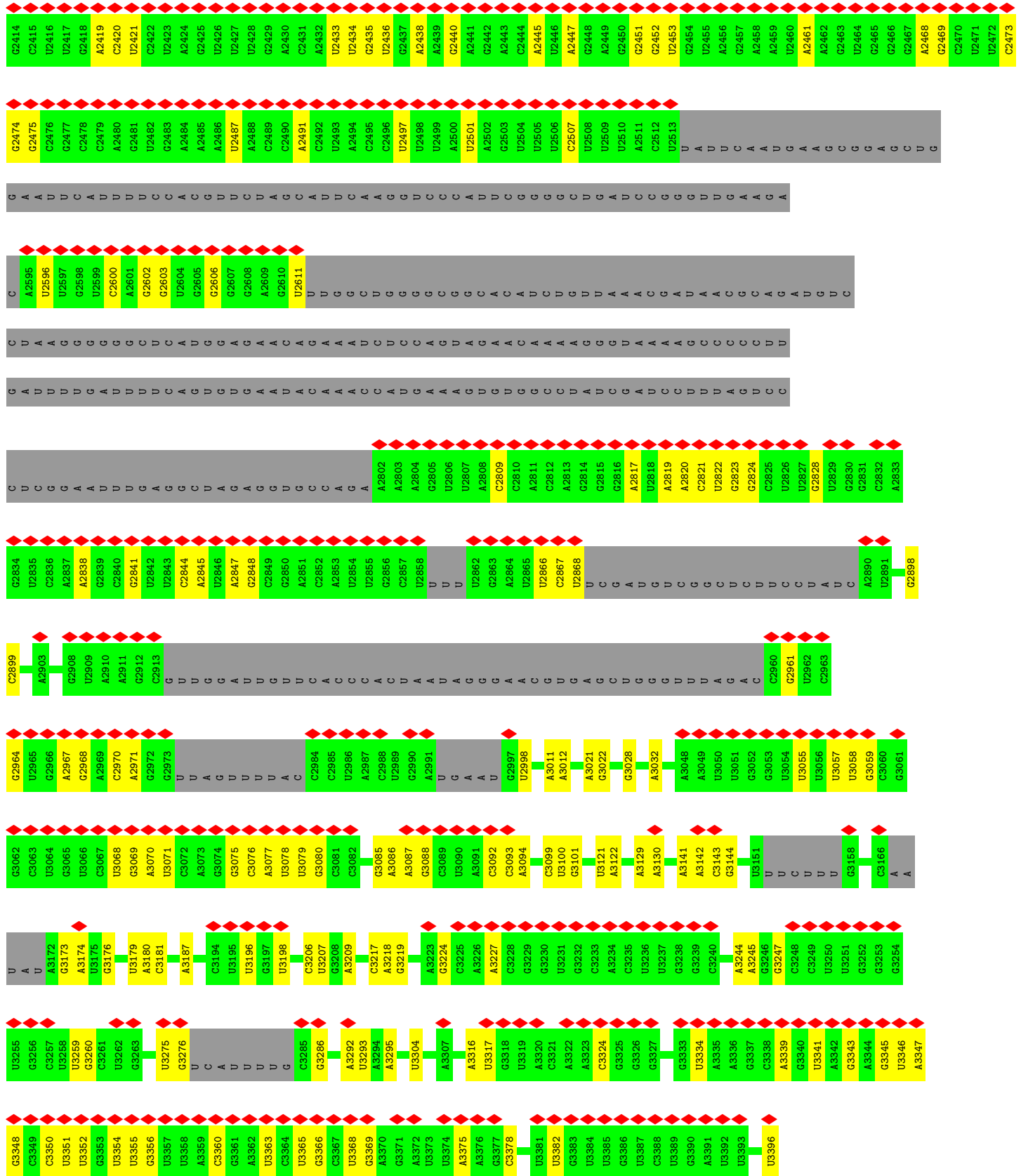
### 3 Residue-property plots i

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: *Saccharomyces cerevisiae* 25S ribosomal RNA



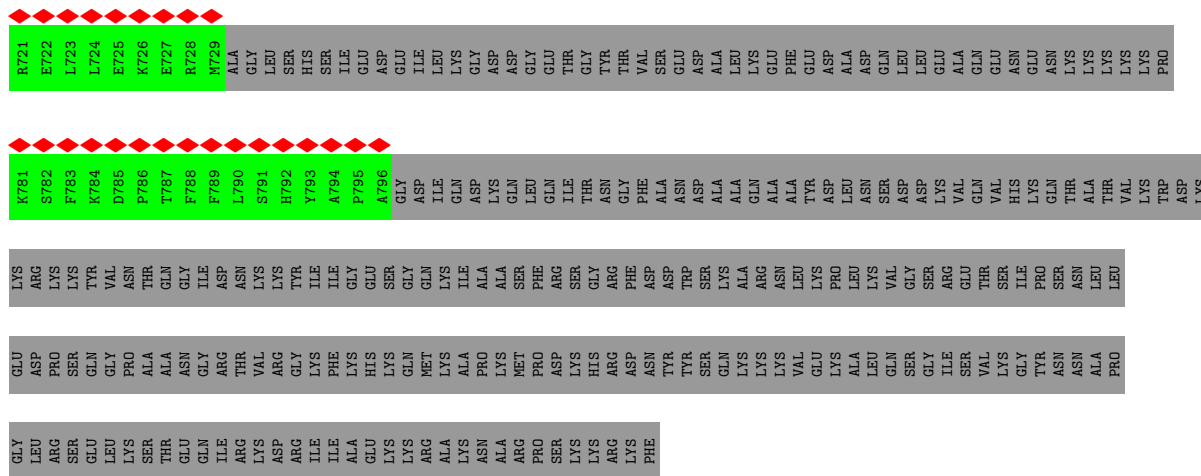




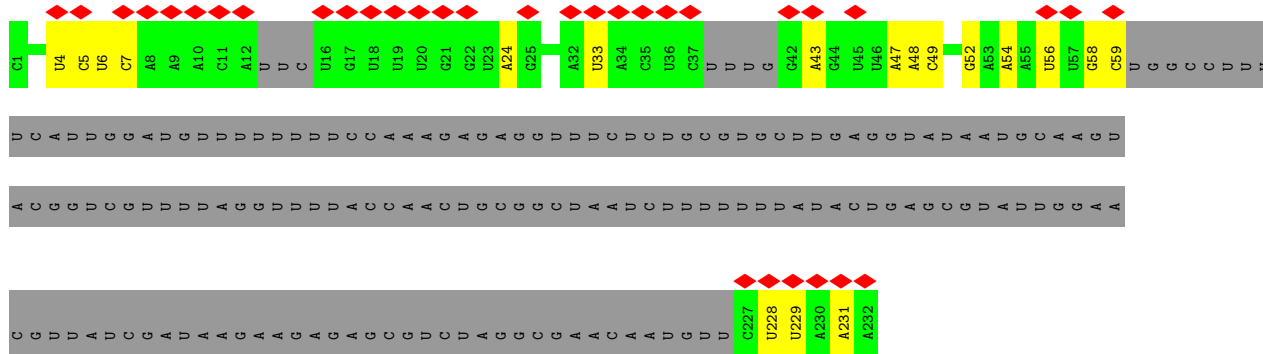
• Molecule 2: Saccharomyces cerevisiae 5.8S ribosomal RNA



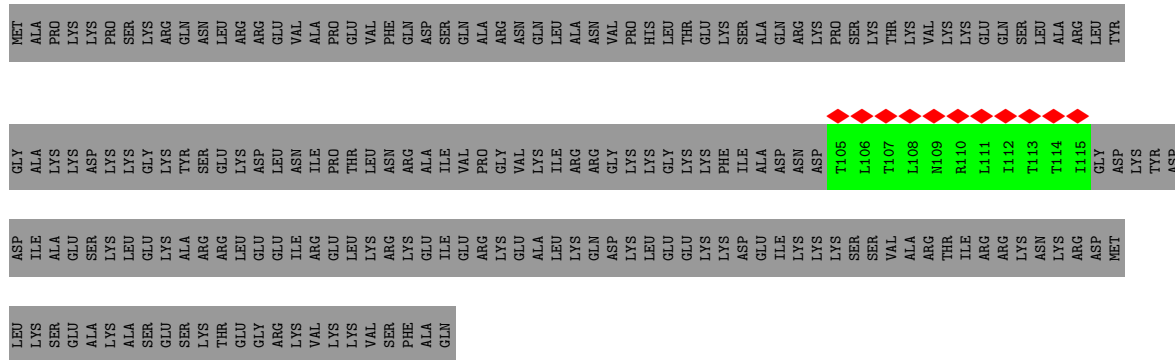




• Molecule 4: ITS2 RNA

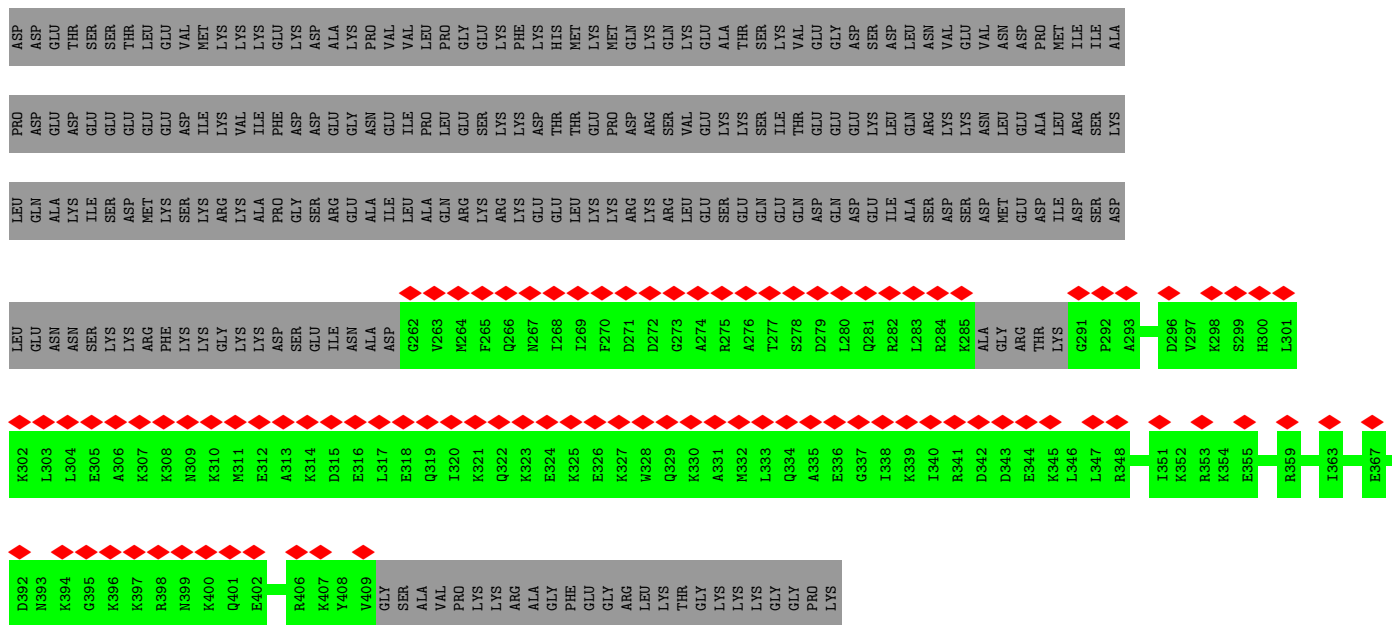


• Molecule 5: 60S ribosomal subunit assembly/export protein LOC1

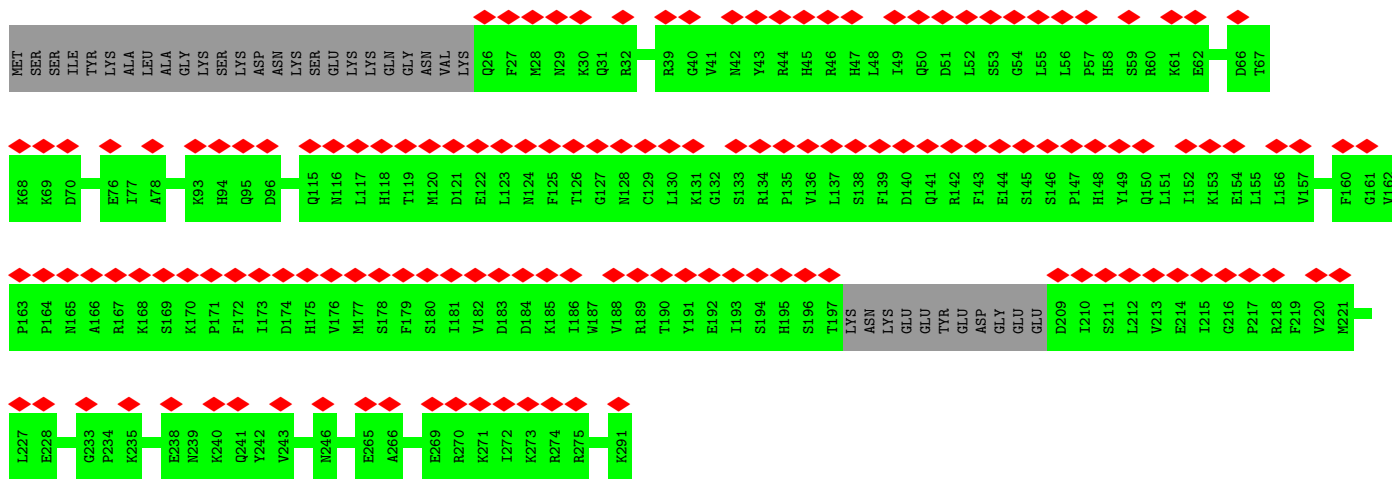
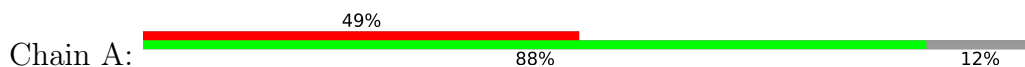


• Molecule 6: Ribosomal RNA-processing protein 14

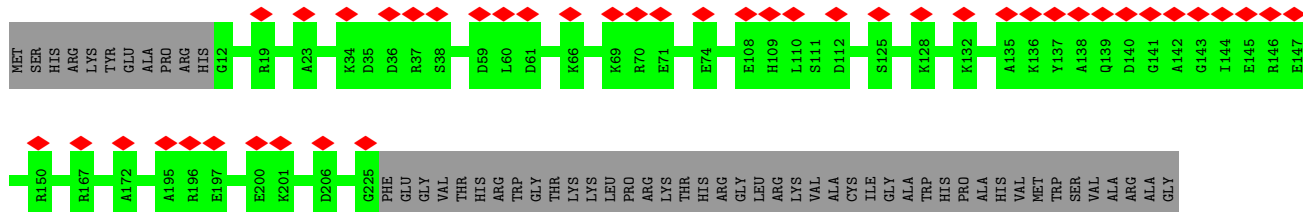
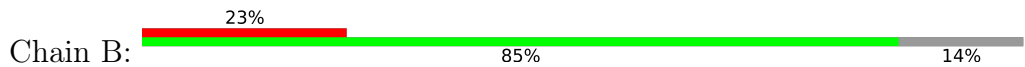


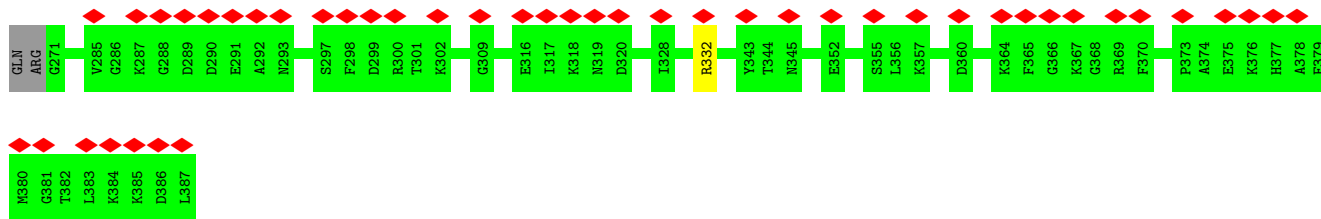


• Molecule 7: Ribosome biogenesis protein BRX1

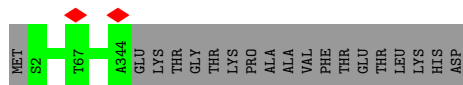


• Molecule 8: Large ribosomal subunit protein uL3

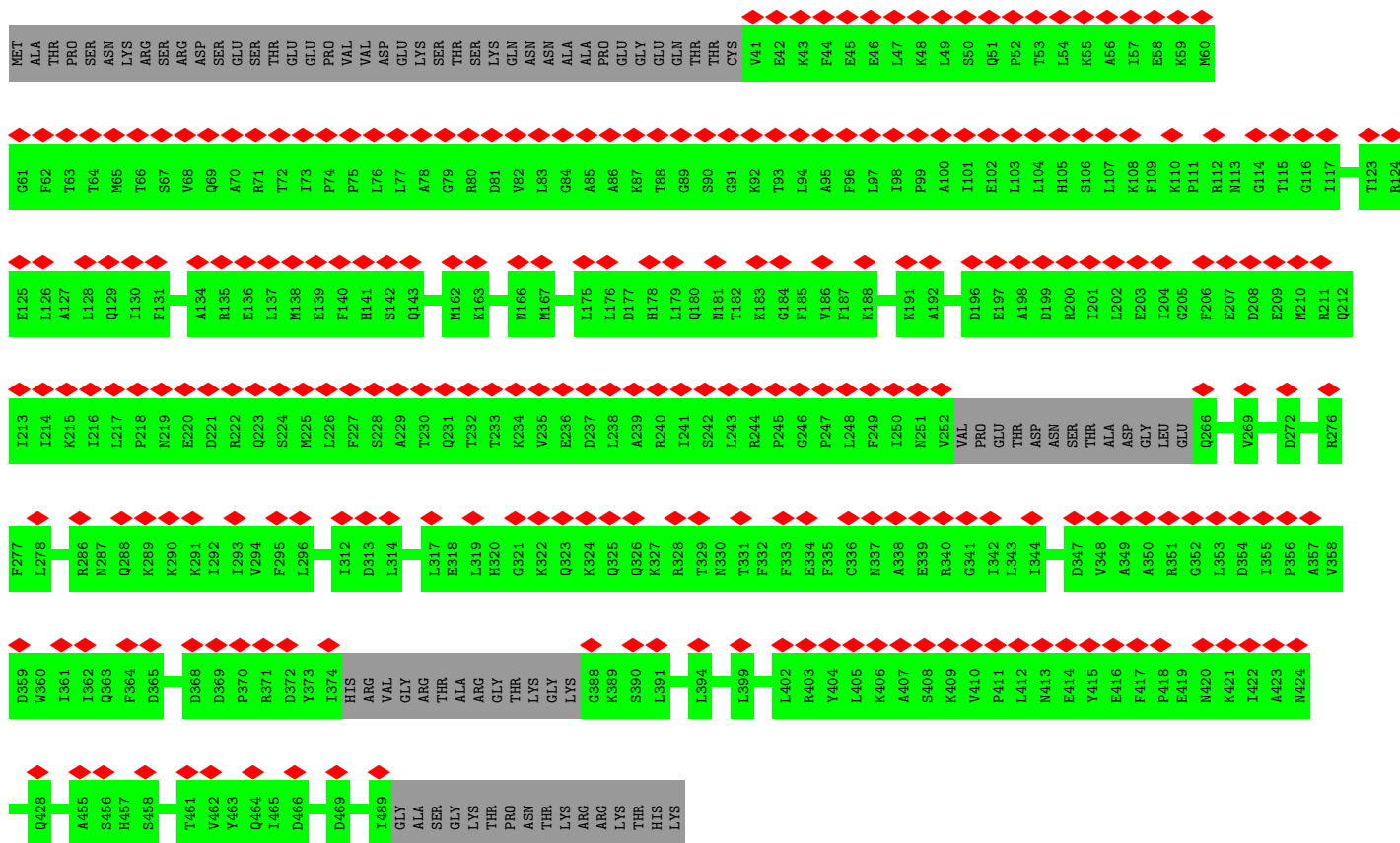
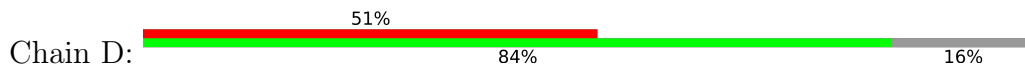




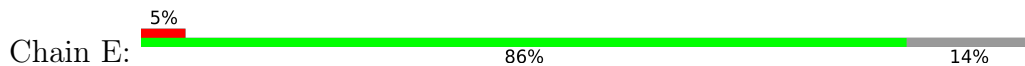
- Molecule 9: 60S ribosomal protein L4-A



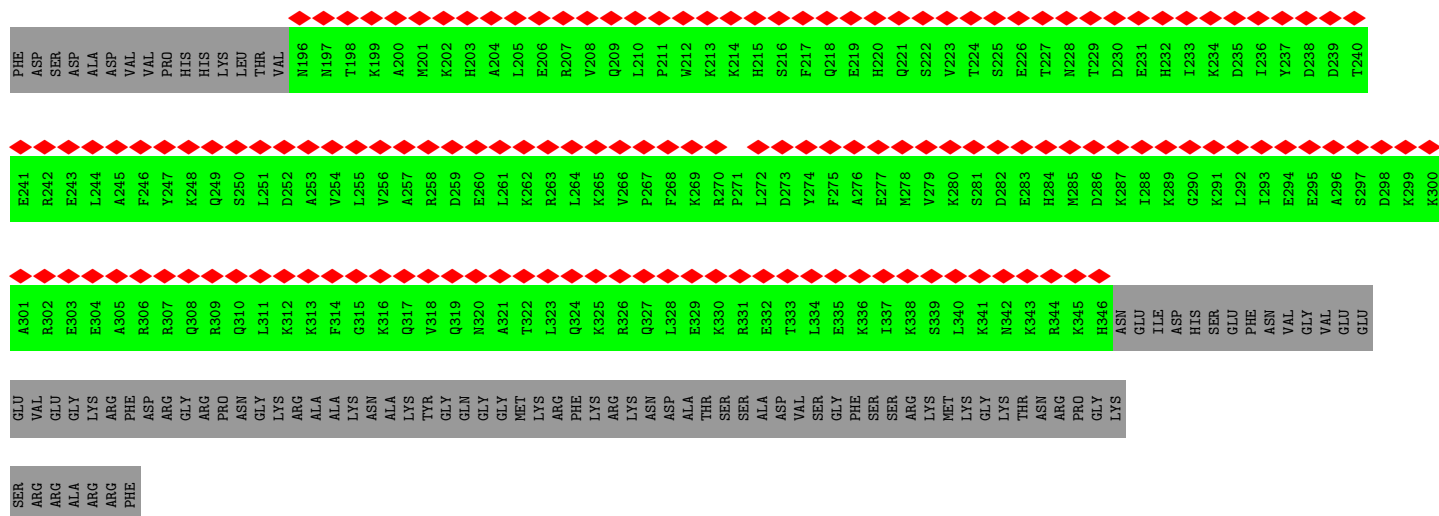
- Molecule 10: ATP-dependent RNA helicase HAS1



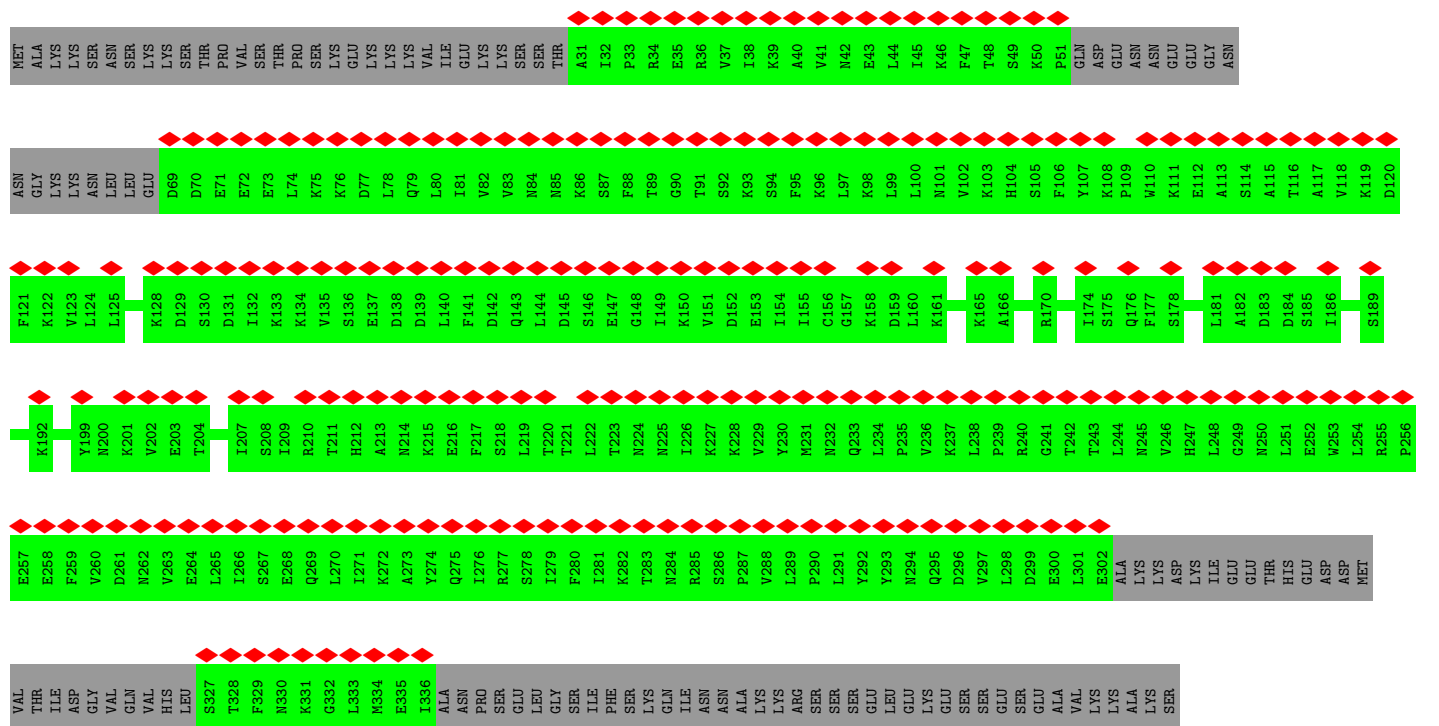
- Molecule 11: 60S ribosomal protein L6-A



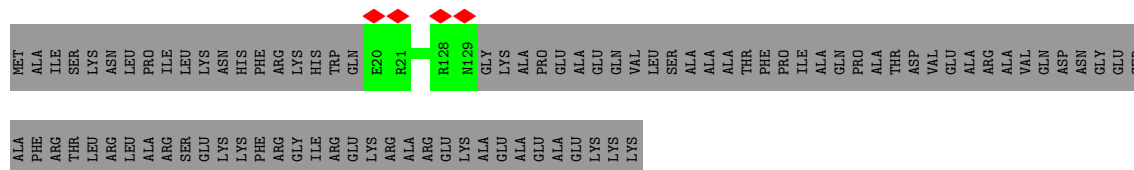




● Molecule 17: Proteasome-interacting protein CIC1



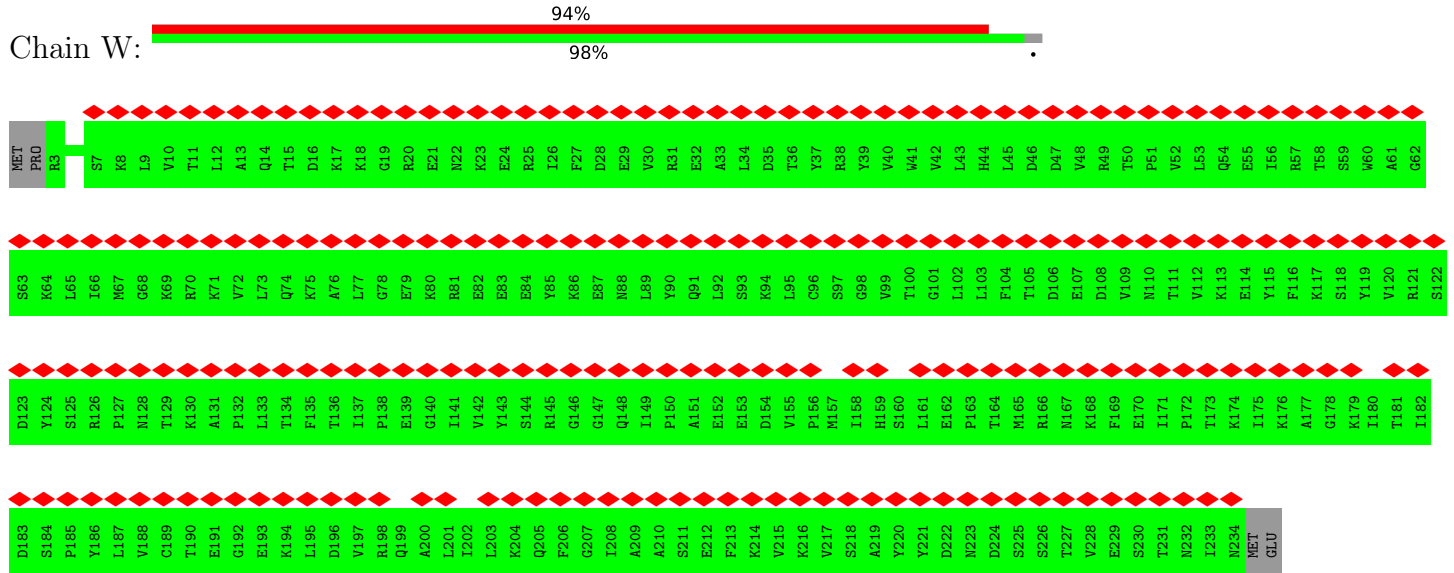
● Molecule 18: 60S ribosomal protein L13-A



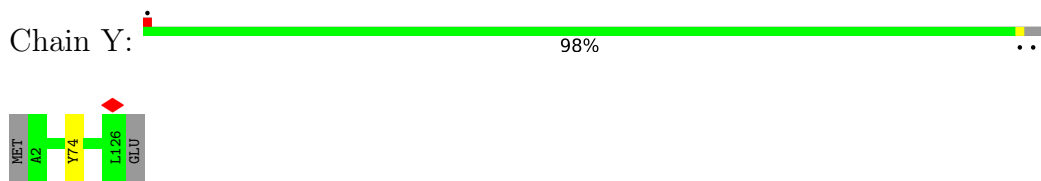




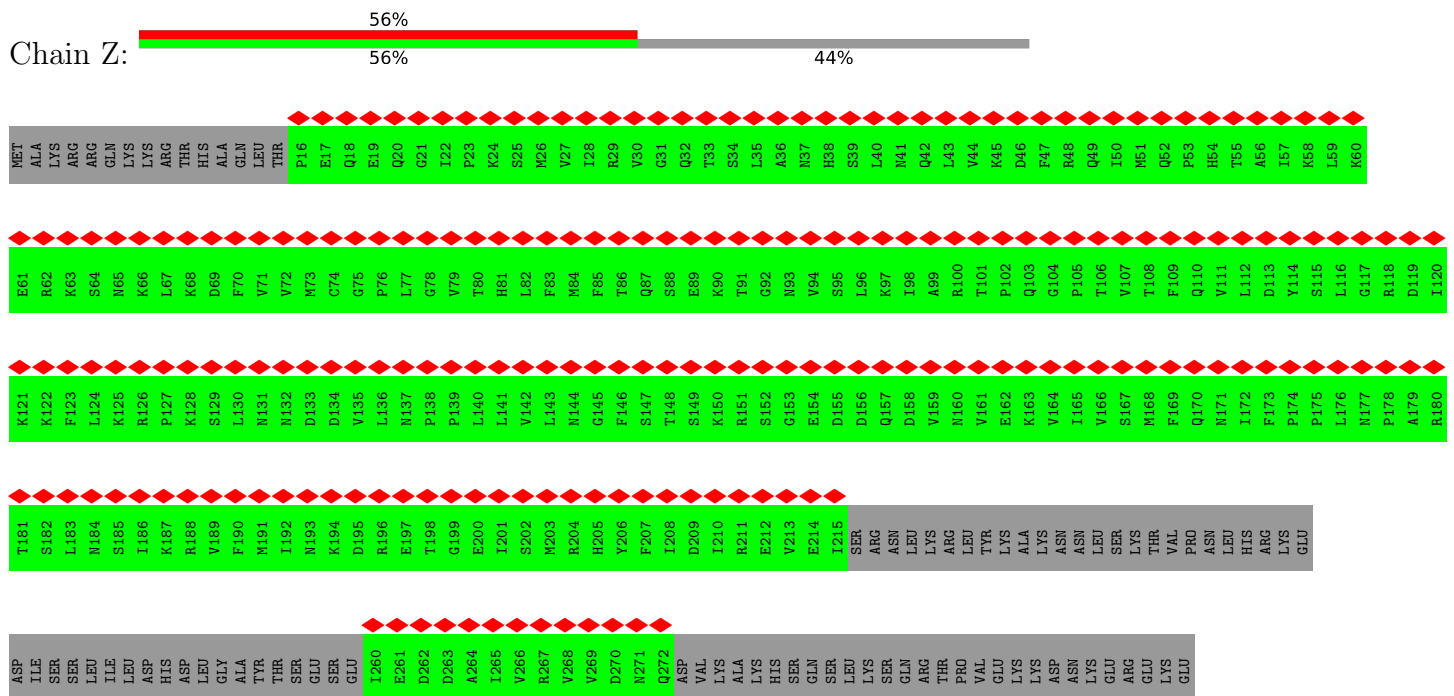
• Molecule 28: Ribosome assembly factor MRT4



• Molecule 29: 60S ribosomal protein L26-A



• Molecule 30: Ribosome biogenesis protein SSF1





THR	GLU	GLU	GLU	ASP	VAL	GLU	MET	GLU	PRO	PRO	T320	P321	R322	K323	K324	A325	I326	K327	L328	T329	E330	L331	G332	P333	R334	L335	T336	L337	K338	L339	V340	K341	I342	E343	E344	G345	I346	C347	S348	G349	K350	V351	L352	H353	H354	E355	F356	V357	Q358	K359	SER									
SER	GLU	GLU	ILE	ASP	ALA	LEU	GLU	LYS	LYS	HIS	PRO	ALA	ALA	LYS	MET	ARG	GLY	TYR	HIS	ASN	GLN	VAL	PRO	ARG	GLU	LYS	LEU	LEU	ASN	ILE	ALA	LYS	GLN	ARG	LYS	ALA	ALA	ALA	ALA	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LYS													
ASP	ASP	ALA	MET	THR	SER	ASP	GLU	SER	SER	SER	ARG	R10	E11	H12	V13	K14	E15	L16	G17	K18	Y19	N21	E22	T23	K24	D25	R26	N27	F28	L29	E30	T31	V32	E33	L34	Q35	V36	L38	K39	M40	Y41	D42	P43	Q44	R45	D46	K47	R48	F49	S50	G51	S52	L53	K54	L55	P56	N57	C58	P59	R60
P61	M62	M63	S64	I65	I67	F68	G69	D70	A71	F72	D73	V74	D75	R76	A77	K78	S79	C80	G81	V82	D83	A84	M85	S86	V87	D88	D89	K91	K92	L93	N94	K95	N96	K97	K98	L99	I100	K101	K102	L103	S104	K105	K106	Y107	N108	A109	F110	I111	A112	E113	S114	V115	L116	I117	K118	Q119	V120			
P121	R122	L123	L124	G125	P126	Q127	L128	K130	A131	G132	K133	F134	P135	T136	P137	V138	S139	H140	N141	D142	D143	L144	Y145	G146	K147	V148	T149	D150	V151	R152	S153	T154	I155	K156	F157	Q158	L159	K160	V161	L163	C164	L165	A166	V167	A168	V169	G170	N171	V172	E173	M174	E175	E176	D177	L179	V180				
M181	Q182	I183	L184	M185	S186	V187	N188	F189	V191	S192	L193	L194	K195	K196	N197	V198	Q199	N200	V201	G202	S203	L204	V205	V206	K207	S208	S209	M210	G211	P212	A213	F214	R215	L216	Y217																									

● Molecule 31: Large ribosomal subunit protein uL1A

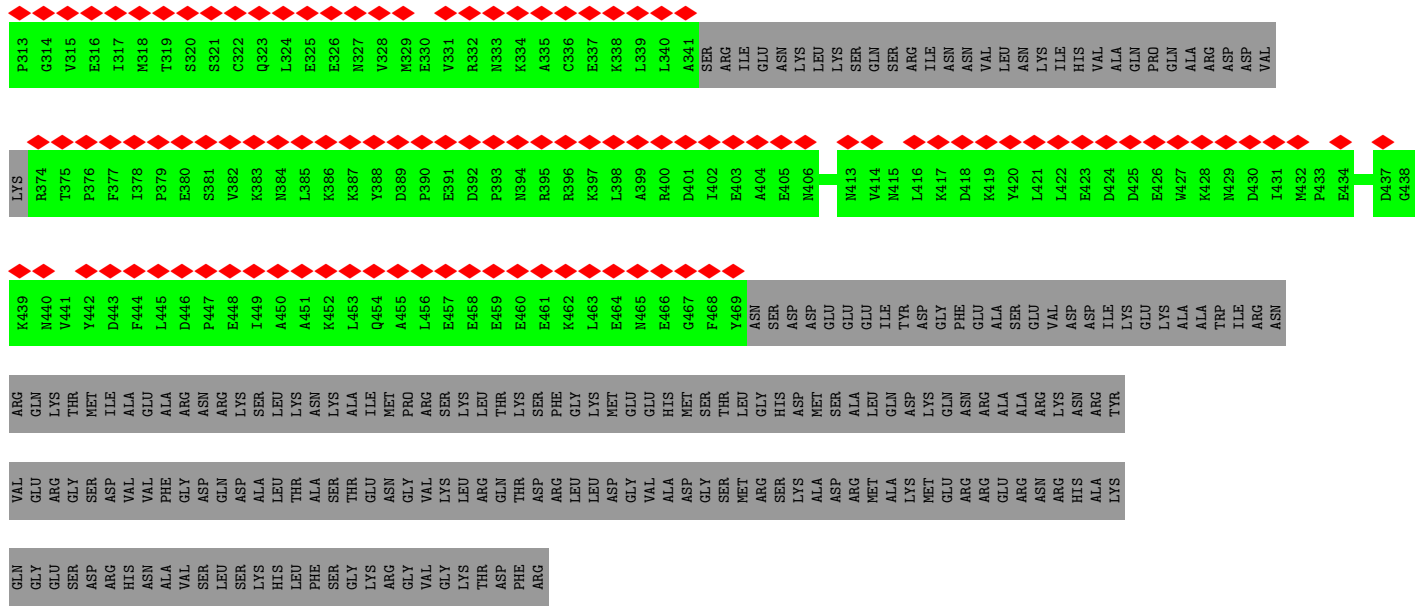


MET	SER	LYS	ILE	THR	SER	Q8	V9	E11	H12	V13	K14	E15	L16	L17	K18	Y19	N21	E22	T23	K24	D25	R26	N27	F28	L29	E30	T31	V32	E33	L34	Q35	V36	L38	K39	M40	Y41	D42	P43	Q44	R45	D46	K47	R48	F49	S50	G51	S52	L53	K54	L55	P56	N57	C58	P59	R60		
P61	M62	M63	S64	I65	I67	F68	G69	D70	A71	F72	D73	V74	D75	R76	A77	K78	S79	C80	G81	V82	D83	A84	M85	S86	V87	D88	D89	K91	K92	L93	N94	K95	N96	K97	K98	L99	I100	K101	K102	L103	S104	K105	K106	Y107	N108	A109	F110	I111	A112	E113	S114	V115	L116	I117	K118	Q119	V120
P121	R122	L123	L124	G125	P126	Q127	L128	K130	A131	G132	K133	F134	P135	T136	P137	V138	S139	H140	N141	D142	D143	L144	Y145	G146	K147	V148	T149	D150	V151	R152	S153	T154	I155	K156	F157	Q158	L159	K160	V161	L163	C164	L165	A166	V167	A168	V169	G170	N171	V172	E173	M174	E175	E176	D177	L179	V180	
M181	Q182	I183	L184	M185	S186	V187	N188	F189	V191	S192	L193	L194	K195	K196	N197	V198	Q199	N200	V201	G202	S203	L204	V205	V206	K207	S208	S209	M210	G211	P212	A213	F214	R215	L216	Y217																						

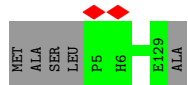
● Molecule 32: Nucleolar GTP-binding protein 1



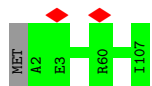
M1	Q2	L3	S4	W5	K6	D7	T8	P9	T10	V11	A12	P13	A14	M15	D16	L17	D19	L20	V21	L22	N23	R24	T25	Q26	R27	K28	T29	P30	T31	V32	I33	K34	P35	G36	F37	K38	I39	T40	R41	L42	R43	A44	F45	Y46	M47	R48	K49	V50	K51	Y52	T53	G54	E55	G56	F57	V58	E59	K60	
F61	E62	D63	I64	L65	K66	G67	F68	N69	N70	I71	N72	D73	V74	H75	F76	F77	H78	R79	D80	L81	R82	D83	T84	L85	Y86	E87	K88	M89	H90	Y91	K92	I93	S94	L95	A96	A97	I98	S99	R100	A101	K102	S103	L104	V105	E106	Q107	V108	A109	R110	D111	V112	V113	R114	L115	L116	K117	F118	G119	Q120
S121	L122	F123	Q124	C125	K126	Q127	K129	R130	A131	A132	L133	G134	R135	F136	A137	T138	I139	V140	K141	K142	L143	R144	D145	P146	L147	A148	Y149	L150	E151	Q152	V153	R154	Q155	L160	I163	D164	P165	M166	T167	R168	T169	L170	L171	I172	C173	G174	Y175	P176	M177	V178	G179	K180	S181	S182	F183	L184			
R185	C186	I187	T188	K189	S190	D191	D193	V194	Q195	F196	I197	A198	F199	T200	T201	K202	F209	D210	Y211	K212	Y213	P214	R215	D220	T221	P222	G223	T224	L225	D226	R227	P228	T229	E230	E231	M232	N233	I234	L235	N237	L238	Q238	S239	G240	Y241	A242	I243	A244	H245	L246	R247	S248	C249	V250	L251	Y252			
F253	M254	D255	L256	S257	E258	Q259	C260	G261	T263	I264	E265	A266	Q267	V268	K269	L270	F271	H272	S273	I274	K275	P276	L277	A279	M280	K281	S282	V283	M284	V285	V286	I287	M288	K289	T290	ASP	ILE	ILE	ARG	PRO	GLU	ASP	LEU	ASP	GLU	ARG	GLU	ARG	ALA	GLN	L305	L306	E307	S308	V309	K310	E311	V312	



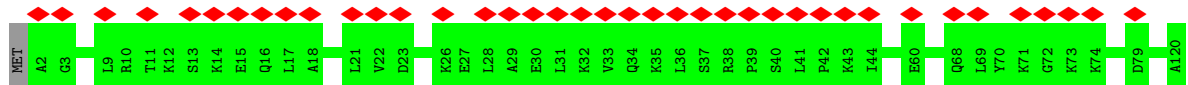
• Molecule 33: 60S ribosomal protein L32



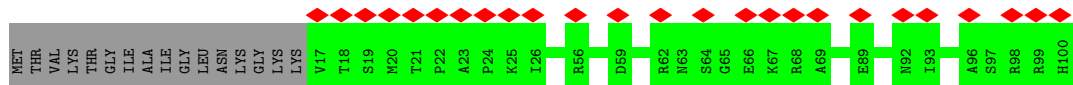
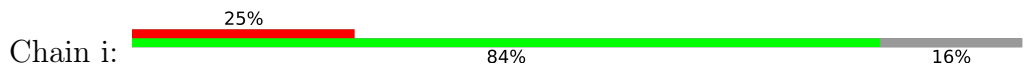
• Molecule 34: 60S ribosomal protein L33-A



• Molecule 35: 60S ribosomal protein L35-A



• Molecule 36: 60S ribosomal protein L36-A

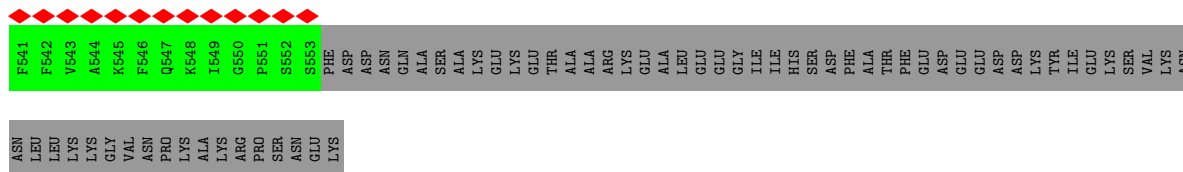


• Molecule 37: 60S ribosomal protein L37-A

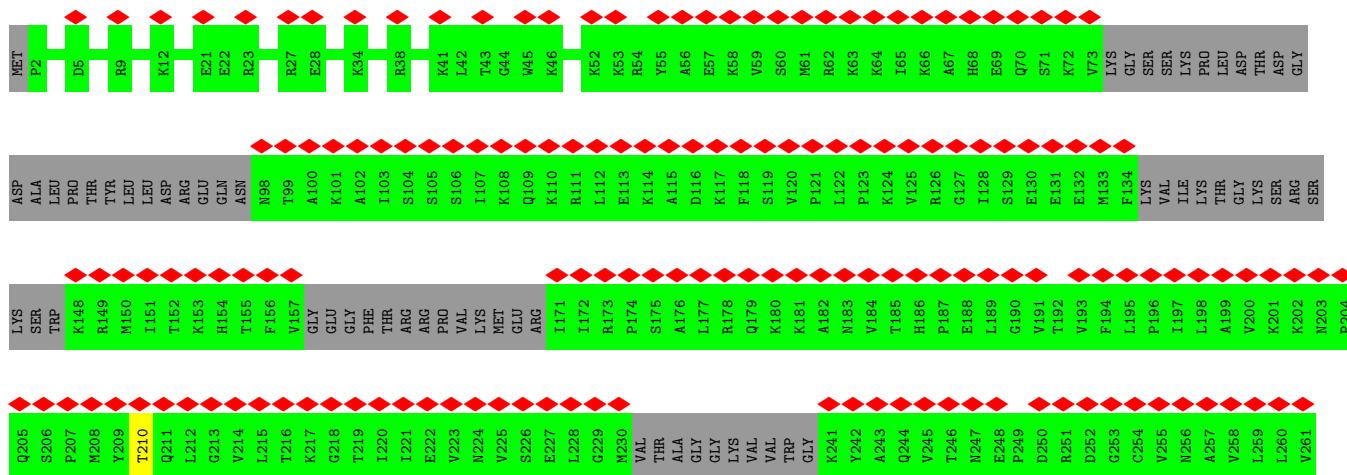
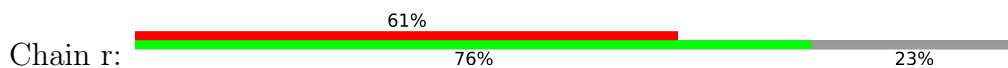




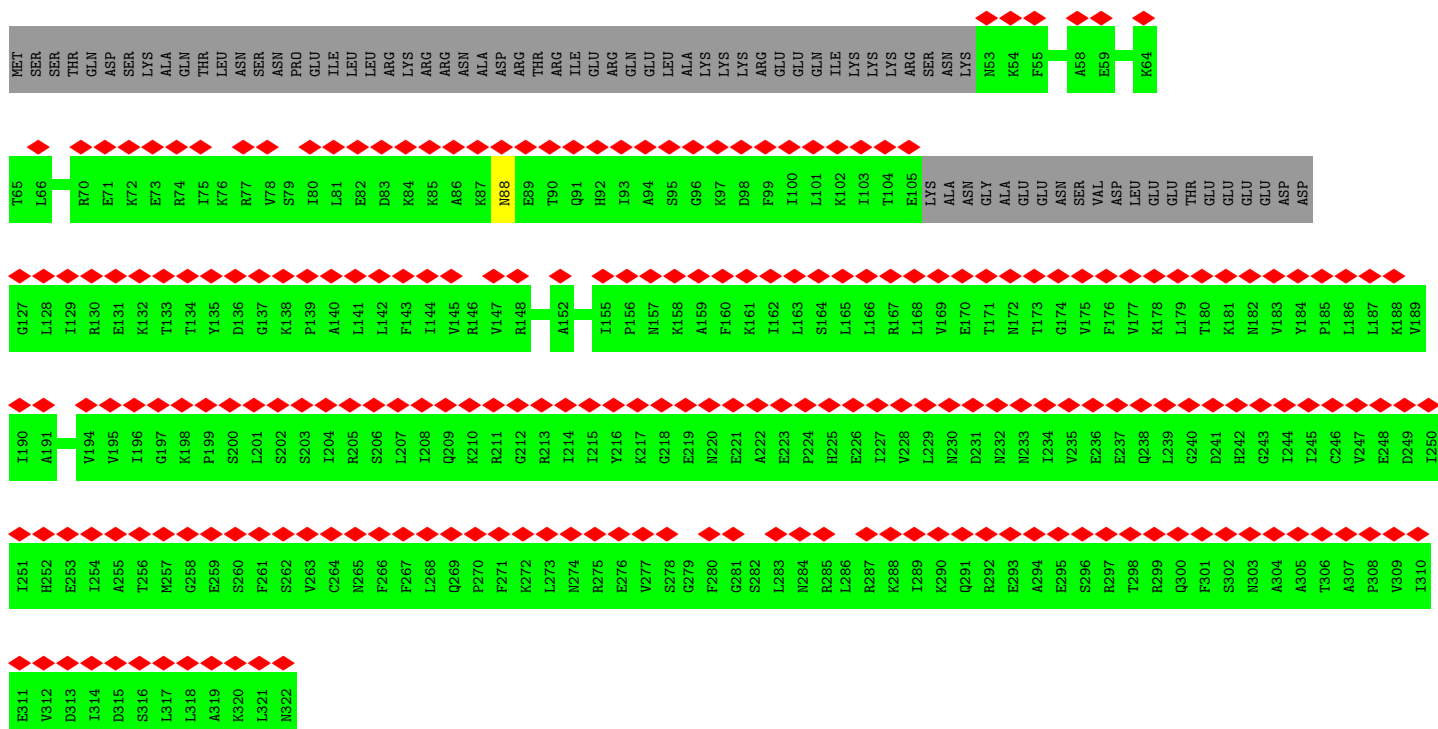
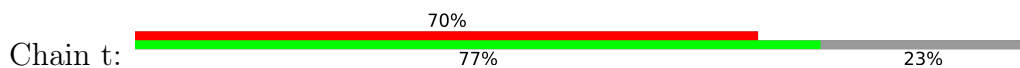




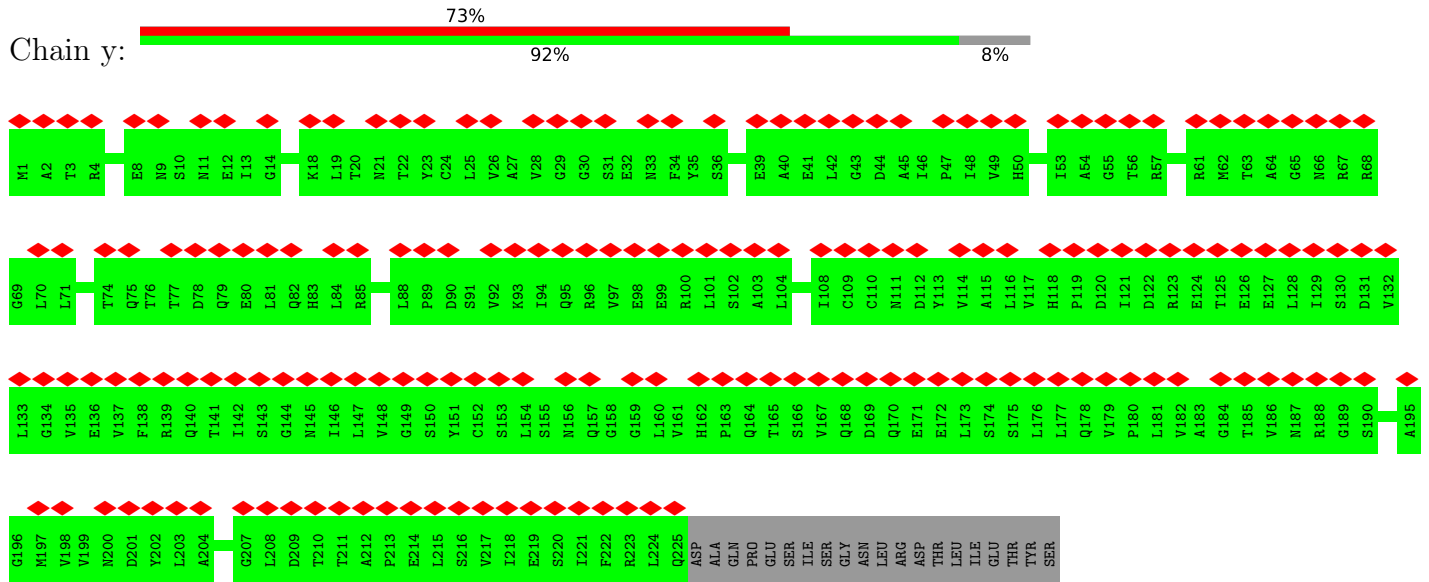
• Molecule 43: Ribosome biogenesis protein NSA2



• Molecule 44: Ribosome biogenesis protein RLP7









## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	195000	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 ( $e^-/\text{\AA}^2$ )	39.3	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.197	Depositor
Minimum map value	-0.106	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.017	Depositor
Map size (Å)	432.00003, 432.00003, 432.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	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, GDP

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	1	0.32	0/47220	0.77	3/73589 (0.0%)
2	2	0.34	0/3562	0.76	0/5542
3	3	0.24	0/2935	0.47	0/3945
4	6	0.21	0/1367	0.81	0/2118
5	7	0.21	0/86	0.49	0/117
6	8	0.24	0/1210	0.49	0/1590
7	A	0.25	0/2126	0.46	0/2868
8	B	0.25	0/2679	0.51	0/3600
9	C	0.28	0/2660	0.52	0/3601
10	D	0.25	0/3441	0.45	0/4642
11	E	0.27	0/1226	0.49	0/1648
12	F	0.28	0/1974	0.48	0/2654
13	G	0.27	0/1294	0.45	0/1751
14	H	0.26	0/1531	0.50	0/2062
15	I	0.26	0/3182	0.49	0/4288
16	J	0.24	0/1289	0.44	0/1715
17	K	0.24	0/2169	0.44	0/2925
18	L	0.28	0/897	0.56	0/1205
19	M	0.25	0/1056	0.50	0/1421
20	N	0.28	0/1544	0.57	0/2065
21	O	0.28	0/1412	0.50	0/1892
22	P	0.26	0/1080	0.49	0/1455
23	Q	0.27	0/1127	0.52	0/1521
24	R	0.29	0/1609	0.49	0/2157
25	S	0.26	0/1468	0.49	0/1973
26	T	0.23	0/626	0.39	0/831
27	V	0.25	0/917	0.50	0/1235
28	W	0.24	0/1902	0.48	0/2564
29	Y	0.27	0/995	0.54	0/1329
30	Z	0.24	0/2051	0.46	0/2758
31	a	0.24	0/1695	0.46	0/2276
32	b	0.24	0/3495	0.46	0/4714

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	e	0.28	0/1031	0.55	0/1379
34	f	0.30	0/868	0.54	0/1168
35	h	0.26	0/978	0.48	0/1301
36	i	0.25	0/672	0.55	0/894
37	j	0.27	0/583	0.57	0/774
38	l	0.24	0/1425	0.46	0/1922
39	m	0.24	0/1806	0.47	0/2443
40	n	0.24	0/2828	0.44	0/3825
41	o	0.24	0/1129	0.46	0/1502
42	q	0.24	0/2854	0.46	0/3860
43	r	0.24	0/1637	0.46	0/2181
44	t	0.24	0/1999	0.47	0/2690
45	u	0.24	0/964	0.53	0/1283
46	v	0.25	0/1258	0.50	0/1670
47	w	0.26	0/2104	0.45	0/2832
48	x	0.27	0/2408	0.51	0/3230
49	y	0.24	0/1722	0.51	0/2343
All	All	0.28	0/128091	0.63	3/183348 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	406	G	O4'-C1'-N9	8.42	114.94	108.20
1	1	1886	A	O4'-C1'-N9	5.63	112.71	108.20
1	1	1314	C	C2-N1-C1'	5.29	124.62	118.80

There are no chirality outliers.

There are no planarity outliers.

## 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	
3	3	347/995 (35%)	338 (97%)	9 (3%)	0	100	100
5	7	9/204 (4%)	9 (100%)	0	0	100	100
6	8	139/434 (32%)	135 (97%)	4 (3%)	0	100	100
7	A	251/291 (86%)	244 (97%)	7 (3%)	0	100	100
8	B	327/387 (84%)	319 (98%)	8 (2%)	0	100	100
9	C	341/362 (94%)	334 (98%)	7 (2%)	0	100	100
10	D	417/505 (83%)	408 (98%)	9 (2%)	0	100	100
11	E	147/176 (84%)	144 (98%)	3 (2%)	0	100	100
12	F	239/244 (98%)	236 (99%)	3 (1%)	0	100	100
13	G	162/256 (63%)	156 (96%)	6 (4%)	0	100	100
14	H	188/191 (98%)	183 (97%)	5 (3%)	0	100	100
15	I	390/463 (84%)	382 (98%)	8 (2%)	0	100	100
16	J	149/427 (35%)	147 (99%)	2 (1%)	0	100	100
17	K	259/376 (69%)	255 (98%)	4 (2%)	0	100	100
18	L	108/199 (54%)	107 (99%)	1 (1%)	0	100	100
19	M	132/138 (96%)	128 (97%)	4 (3%)	0	100	100
20	N	173/204 (85%)	171 (99%)	2 (1%)	0	100	100
21	O	170/199 (85%)	169 (99%)	1 (1%)	0	100	100
22	P	133/184 (72%)	126 (95%)	7 (5%)	0	100	100
23	Q	142/186 (76%)	141 (99%)	1 (1%)	0	100	100
24	R	188/306 (61%)	186 (99%)	2 (1%)	0	100	100
25	S	168/172 (98%)	164 (98%)	4 (2%)	0	100	100
26	T	77/250 (31%)	77 (100%)	0	0	100	100
27	V	120/137 (88%)	120 (100%)	0	0	100	100
28	W	230/236 (98%)	226 (98%)	4 (2%)	0	100	100
29	Y	123/127 (97%)	122 (99%)	1 (1%)	0	100	100
30	Z	247/453 (54%)	245 (99%)	2 (1%)	0	100	100
31	a	208/217 (96%)	198 (95%)	10 (5%)	0	100	100
32	b	417/647 (64%)	406 (97%)	11 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	e	123/130 (95%)	123 (100%)	0	0	100	100
34	f	104/107 (97%)	102 (98%)	2 (2%)	0	100	100
35	h	117/120 (98%)	116 (99%)	1 (1%)	0	100	100
36	i	82/100 (82%)	78 (95%)	4 (5%)	0	100	100
37	j	70/88 (80%)	67 (96%)	3 (4%)	0	100	100
38	l	174/181 (96%)	171 (98%)	3 (2%)	0	100	100
39	m	205/807 (25%)	196 (96%)	9 (4%)	0	100	100
40	n	329/605 (54%)	321 (98%)	8 (2%)	0	100	100
41	o	131/220 (60%)	131 (100%)	0	0	100	100
42	q	356/618 (58%)	347 (98%)	9 (2%)	0	100	100
43	r	190/261 (73%)	184 (97%)	6 (3%)	0	100	100
44	t	245/322 (76%)	241 (98%)	4 (2%)	0	100	100
45	u	110/199 (55%)	110 (100%)	0	0	100	100
46	v	145/231 (63%)	143 (99%)	2 (1%)	0	100	100
47	w	239/278 (86%)	233 (98%)	6 (2%)	0	100	100
48	x	275/295 (93%)	264 (96%)	11 (4%)	0	100	100
49	y	223/245 (91%)	216 (97%)	7 (3%)	0	100	100
All	All	9119/13773 (66%)	8919 (98%)	200 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	3	316/870 (36%)	316 (100%)	0	100	100
5	7	11/181 (6%)	11 (100%)	0	100	100
6	8	128/388 (33%)	128 (100%)	0	100	100
7	A	232/263 (88%)	232 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	B	278/323 (86%)	277 (100%)	1 (0%)	91	97
9	C	273/289 (94%)	273 (100%)	0	100	100
10	D	371/440 (84%)	371 (100%)	0	100	100
11	E	131/153 (86%)	131 (100%)	0	100	100
12	F	204/205 (100%)	204 (100%)	0	100	100
13	G	133/208 (64%)	133 (100%)	0	100	100
14	H	170/171 (99%)	169 (99%)	1 (1%)	86	95
15	I	352/410 (86%)	352 (100%)	0	100	100
16	J	139/383 (36%)	139 (100%)	0	100	100
17	K	245/346 (71%)	245 (100%)	0	100	100
18	L	89/159 (56%)	89 (100%)	0	100	100
19	M	106/109 (97%)	106 (100%)	0	100	100
20	N	153/176 (87%)	152 (99%)	1 (1%)	84	94
21	O	144/162 (89%)	144 (100%)	0	100	100
22	P	109/146 (75%)	109 (100%)	0	100	100
23	Q	118/151 (78%)	118 (100%)	0	100	100
24	R	171/274 (62%)	171 (100%)	0	100	100
25	S	155/156 (99%)	155 (100%)	0	100	100
26	T	69/219 (32%)	69 (100%)	0	100	100
27	V	94/105 (90%)	94 (100%)	0	100	100
28	W	209/213 (98%)	209 (100%)	0	100	100
29	Y	108/110 (98%)	107 (99%)	1 (1%)	78	92
30	Z	234/413 (57%)	234 (100%)	0	100	100
31	a	191/198 (96%)	190 (100%)	1 (0%)	88	96
32	b	380/573 (66%)	379 (100%)	1 (0%)	92	98
33	e	108/111 (97%)	108 (100%)	0	100	100
34	f	90/91 (99%)	90 (100%)	0	100	100
35	h	104/105 (99%)	104 (100%)	0	100	100
36	i	70/82 (85%)	70 (100%)	0	100	100
37	j	59/71 (83%)	59 (100%)	0	100	100
38	l	151/156 (97%)	151 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	m	193/723 (27%)	193 (100%)	0	100	100
40	n	305/548 (56%)	304 (100%)	1 (0%)	92	98
41	o	118/199 (59%)	117 (99%)	1 (1%)	81	93
42	q	304/535 (57%)	301 (99%)	3 (1%)	76	91
43	r	178/229 (78%)	177 (99%)	1 (1%)	86	95
44	t	220/287 (77%)	219 (100%)	1 (0%)	88	96
45	u	98/180 (54%)	98 (100%)	0	100	100
46	v	134/205 (65%)	133 (99%)	1 (1%)	84	94
47	w	225/257 (88%)	224 (100%)	1 (0%)	91	97
48	x	263/276 (95%)	263 (100%)	0	100	100
49	y	193/211 (92%)	193 (100%)	0	100	100
All	All	8126/12060 (67%)	8111 (100%)	15 (0%)	93	98

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
41	o	102	PHE
46	v	21	ASN
42	q	362	TYR
47	w	6	PHE
43	r	210	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
39	m	170	HIS
48	x	208	GLN
49	y	170	GLN
43	r	40	GLN
19	M	41	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1950/3396 (57%)	392 (20%)	6 (0%)
2	2	147/158 (93%)	27 (18%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	6	54/232 (23%)	18 (33%)	0
All	All	2151/3786 (56%)	437 (20%)	6 (0%)

5 of 437 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	18	G
1	1	26	A
1	1	48	A
1	1	49	A
1	1	59	G

5 of 6 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	1886	A
1	1	2420	C
1	1	3121	U
1	1	1240	A
1	1	720	A

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 for Mogul analysis.

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



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
50	GDP	b	801	51	24,30,30	0.95	1 (4%)	30,47,47	1.31	4 (13%)

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
50	GDP	b	801	51	-	5/12/32/32	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	b	801	GDP	C6-N1	-2.41	1.34	1.37

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	b	801	GDP	PA-O3A-PB	-3.91	119.40	132.83
50	b	801	GDP	C3'-C2'-C1'	2.74	105.11	100.98
50	b	801	GDP	C8-N7-C5	2.37	107.51	102.99
50	b	801	GDP	C5-C6-N1	2.36	118.12	113.95

There are no chirality outliers.

All (5) torsion outliers are listed below:

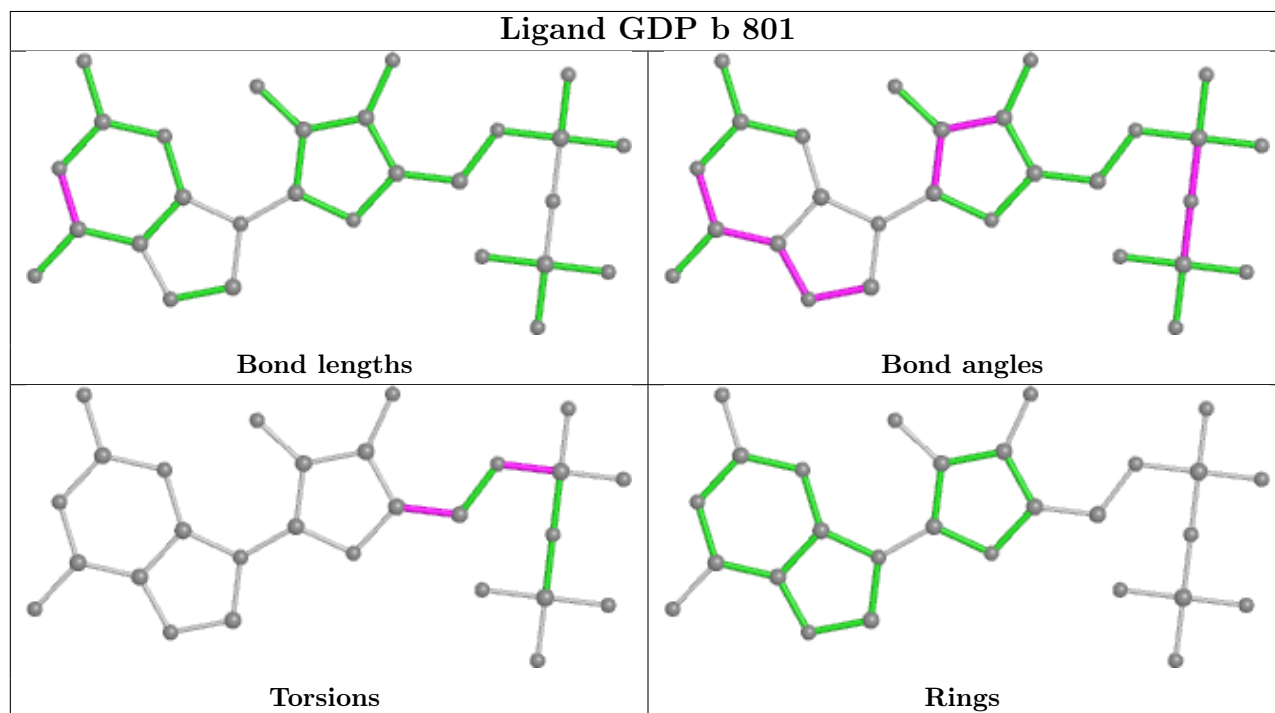
Mol	Chain	Res	Type	Atoms
50	b	801	GDP	C5'-O5'-PA-O3A
50	b	801	GDP	C5'-O5'-PA-O2A
50	b	801	GDP	O4'-C4'-C5'-O5'
50	b	801	GDP	C3'-C4'-C5'-O5'
50	b	801	GDP	C5'-O5'-PA-O1A

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier.

Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

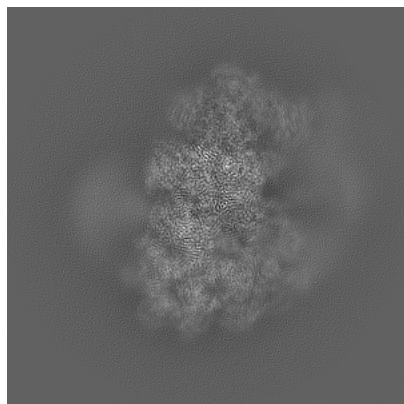
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43021. These allow visual inspection of the internal detail of the map and identification of artifacts.

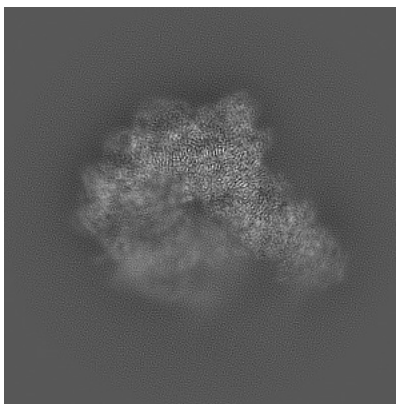
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

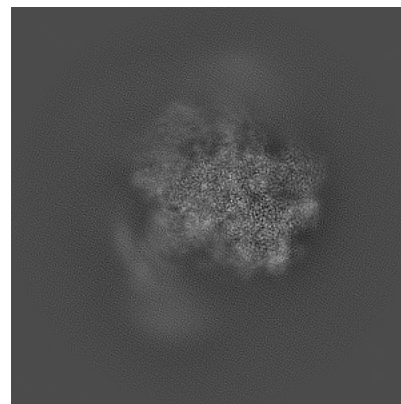
#### 6.1.1 Primary map



X

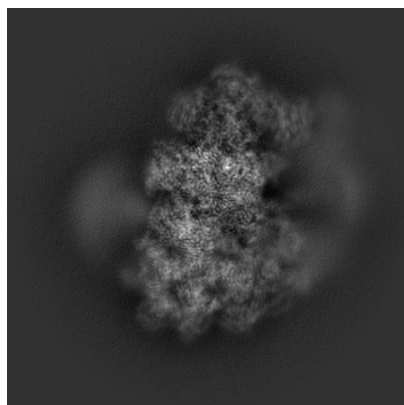


Y

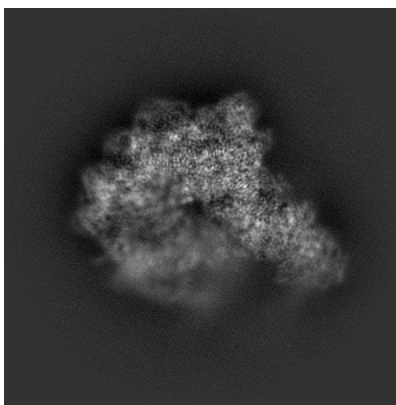


Z

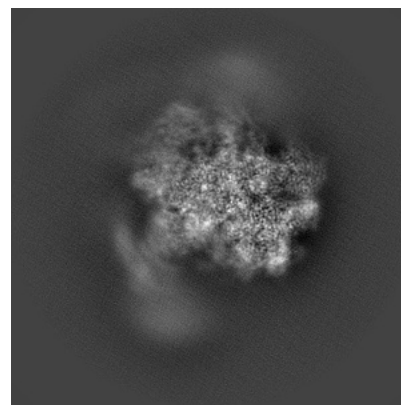
#### 6.1.2 Raw map



X



Y

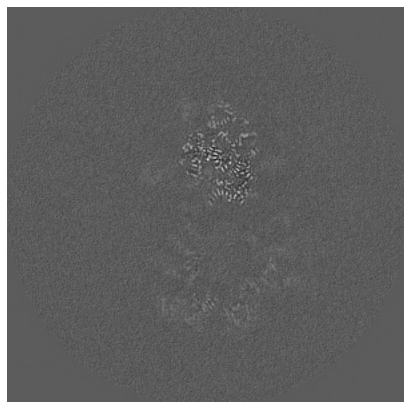


Z

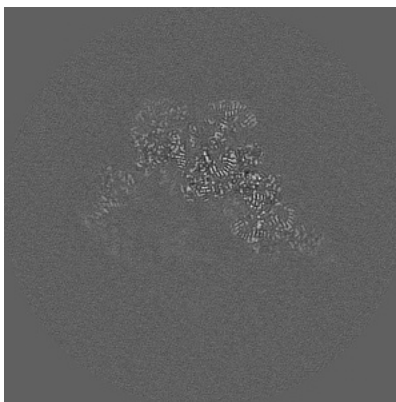
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

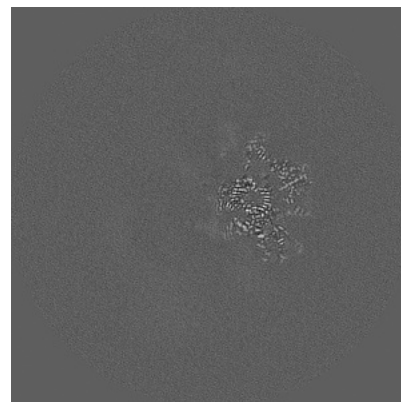
### 6.2.1 Primary map



X Index: 200

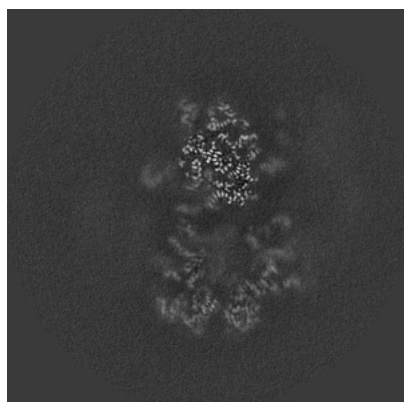


Y Index: 200

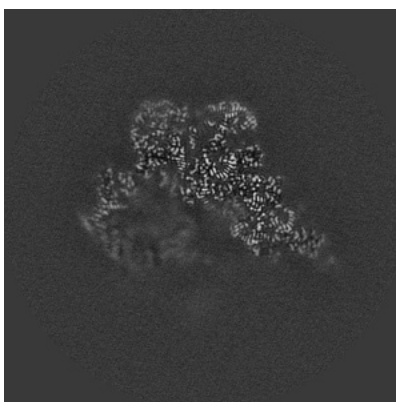


Z Index: 200

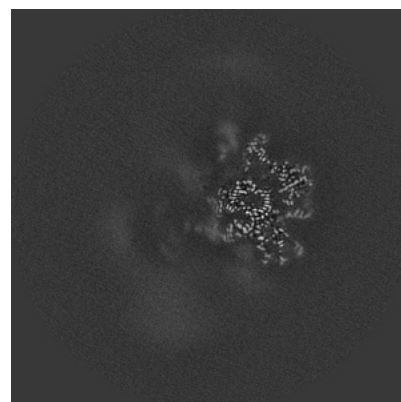
### 6.2.2 Raw map



X Index: 200



Y Index: 200

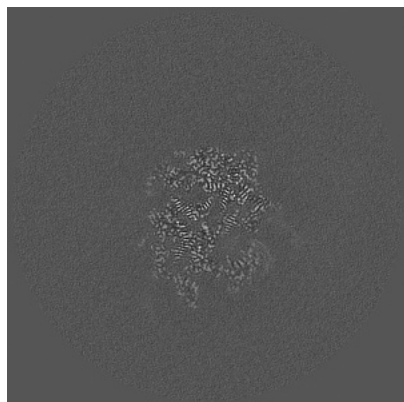


Z Index: 200

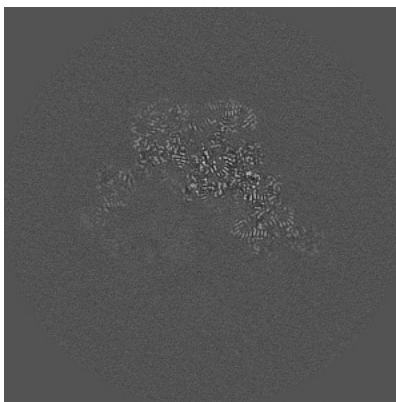
The images above show central slices of the map in three orthogonal directions.

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

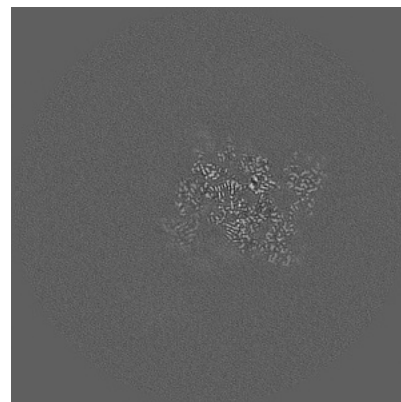
### 6.3.1 Primary map



X Index: 249

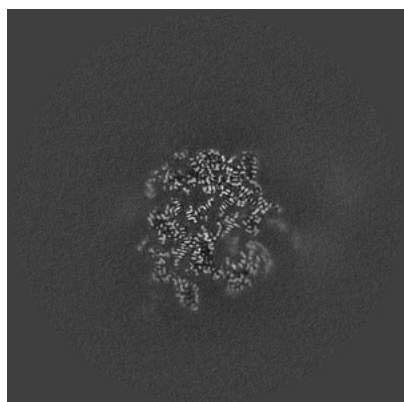


Y Index: 199

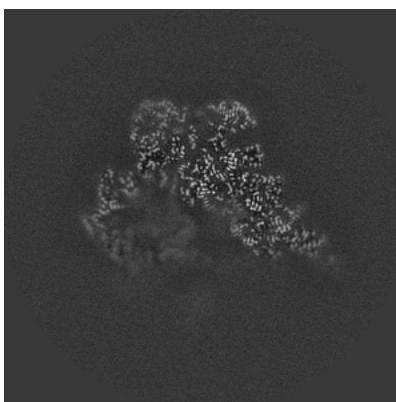


Z Index: 240

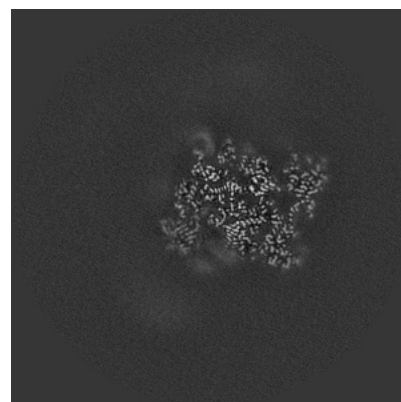
### 6.3.2 Raw map



X Index: 250



Y Index: 201



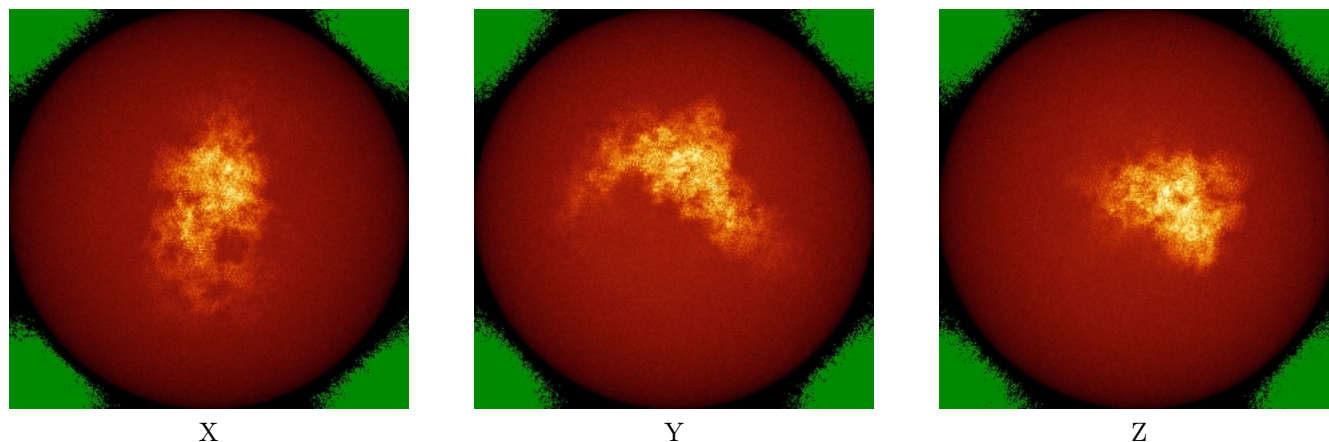
Z Index: 240

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

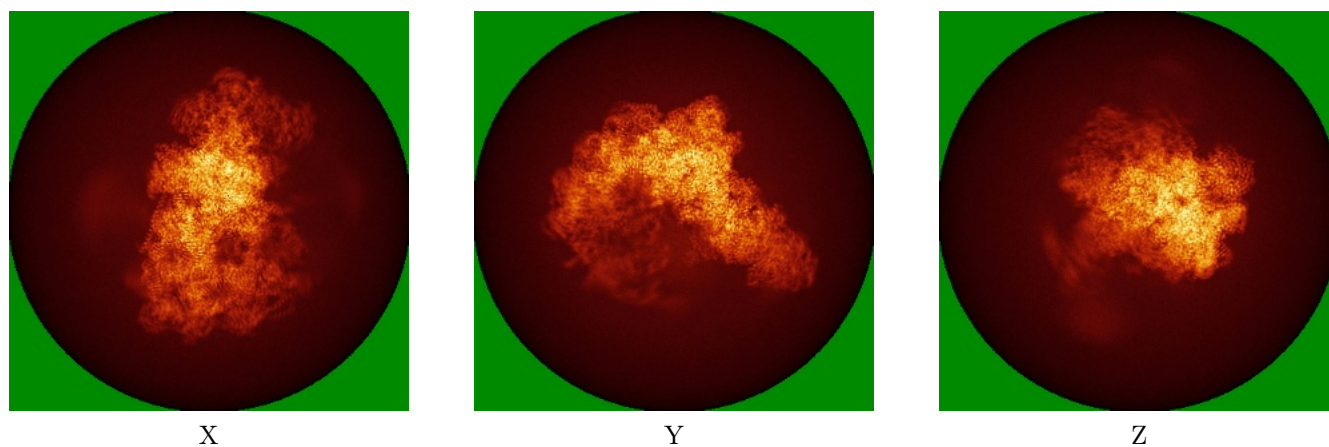


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

### 6.4.1 Primary map



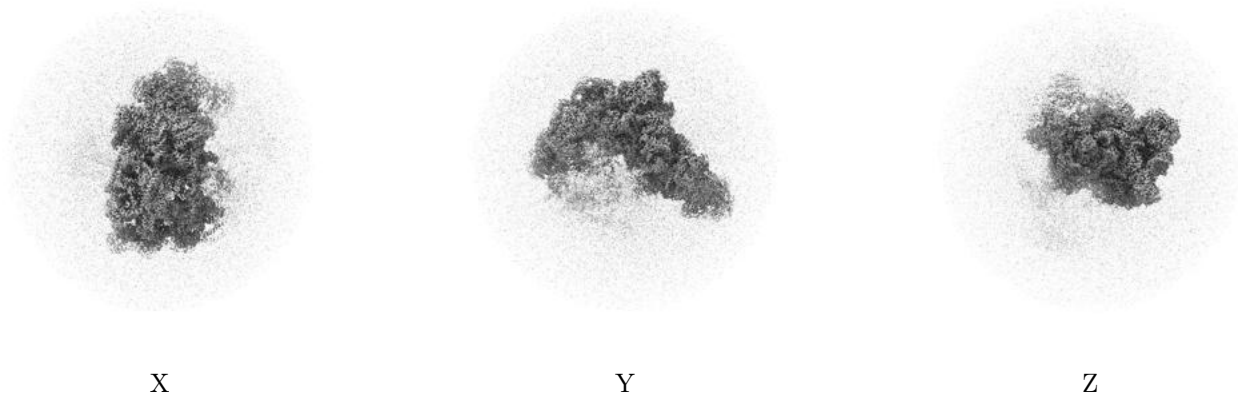
### 6.4.2 Raw map



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 0.017. 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.

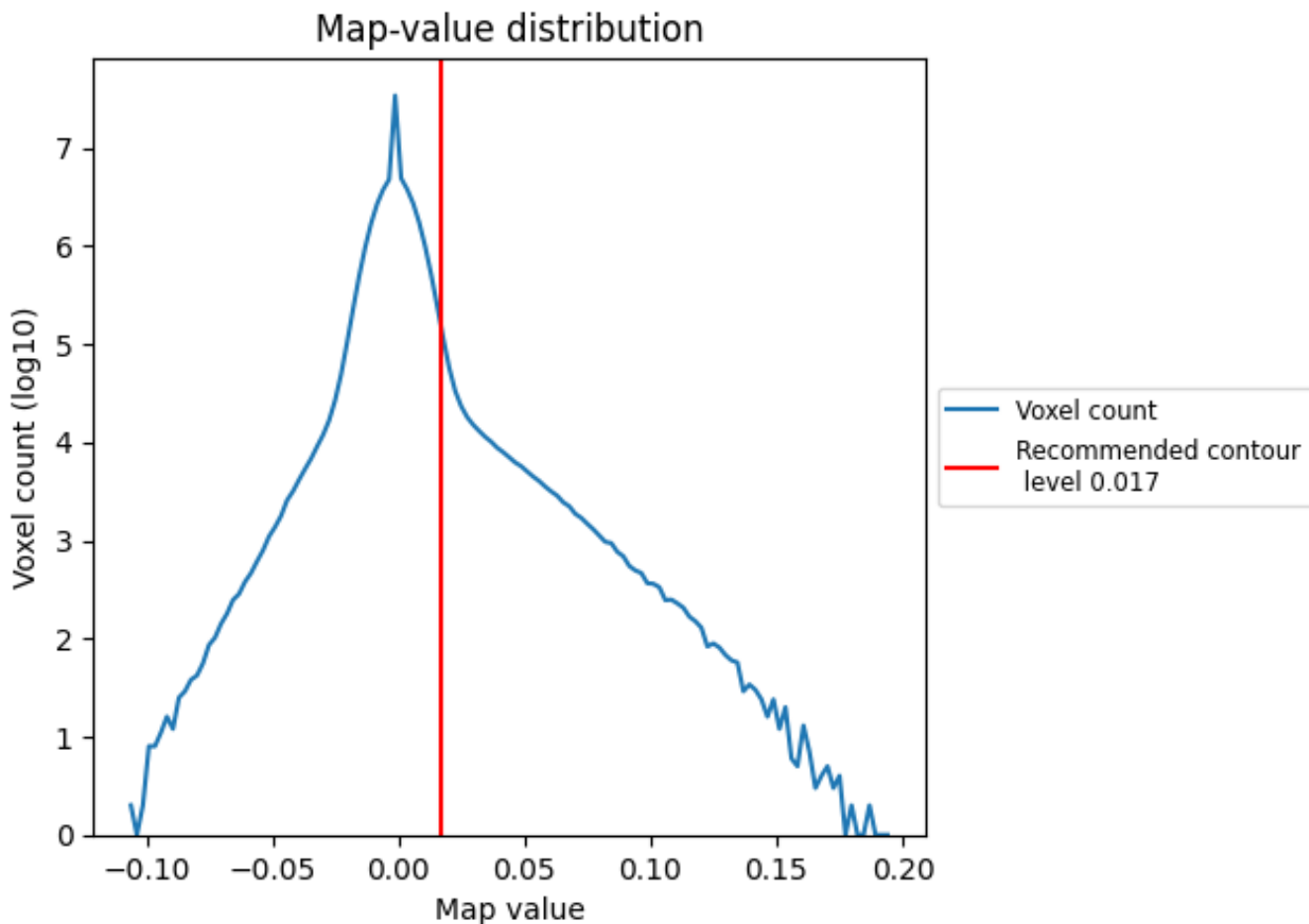
## 6.6 Mask visualisation [i](#)

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.

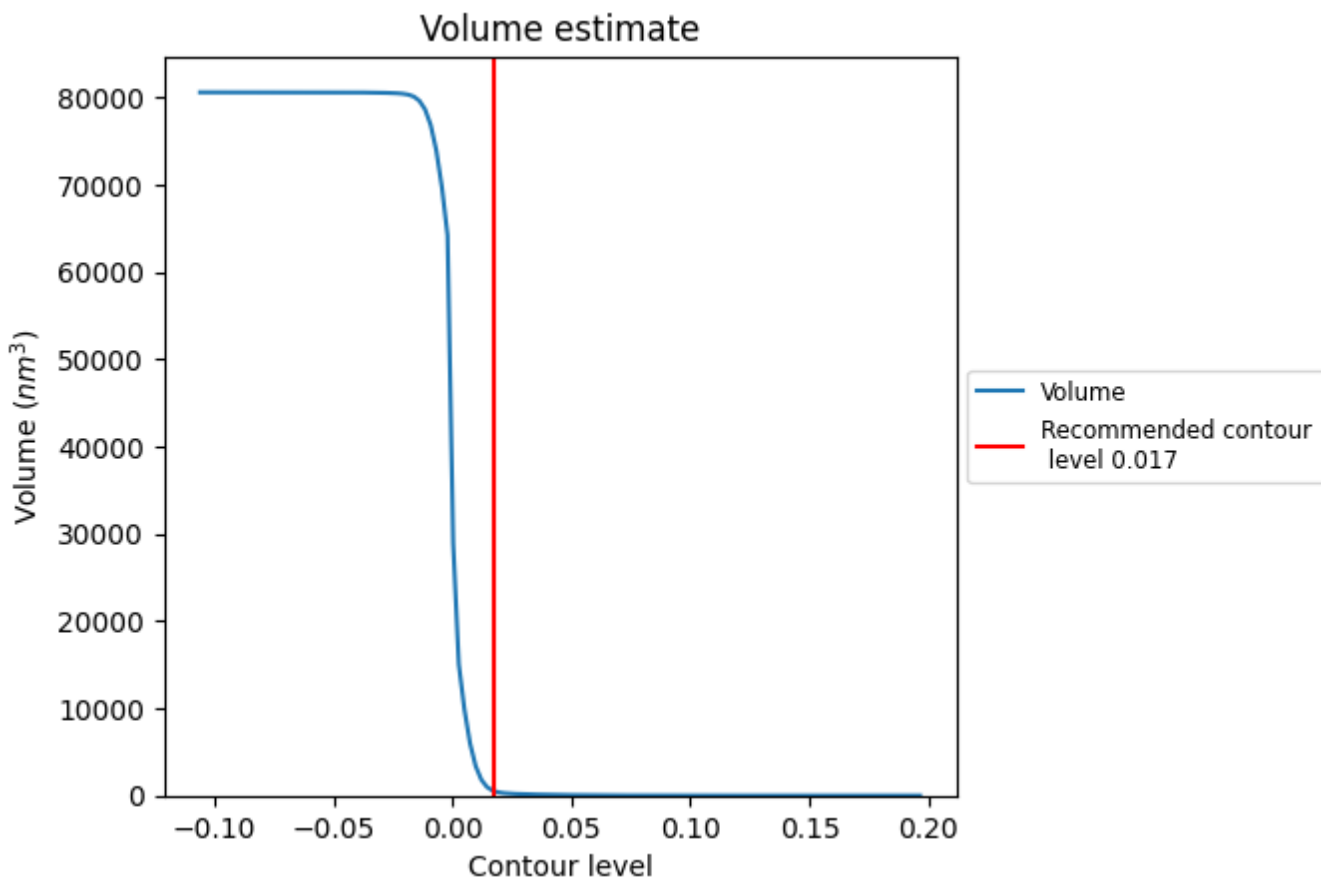
### 7.1 Map-value distribution [i](#)



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.



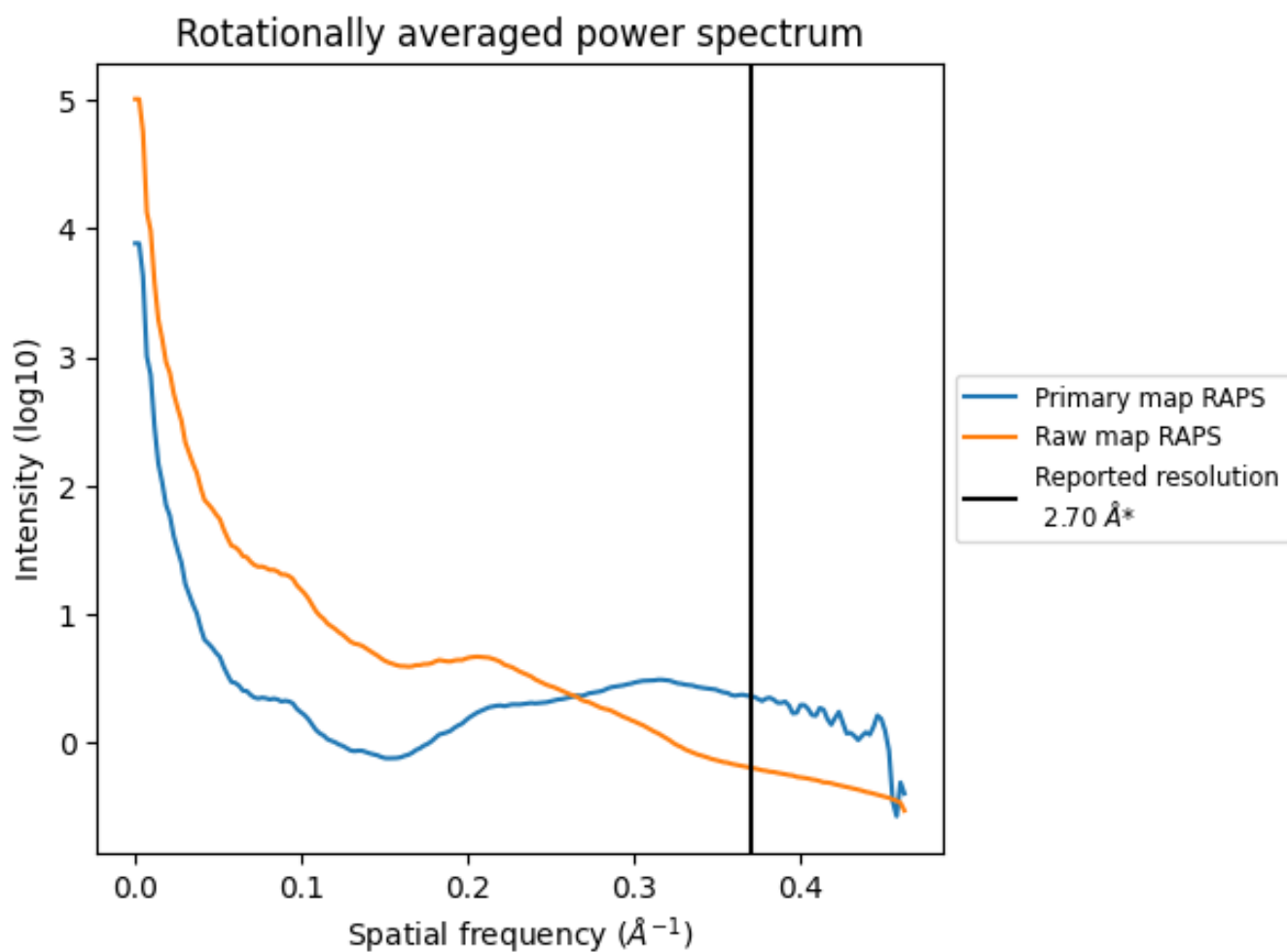
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 554 nm<sup>3</sup>; this corresponds to an approximate mass of 500 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](#)

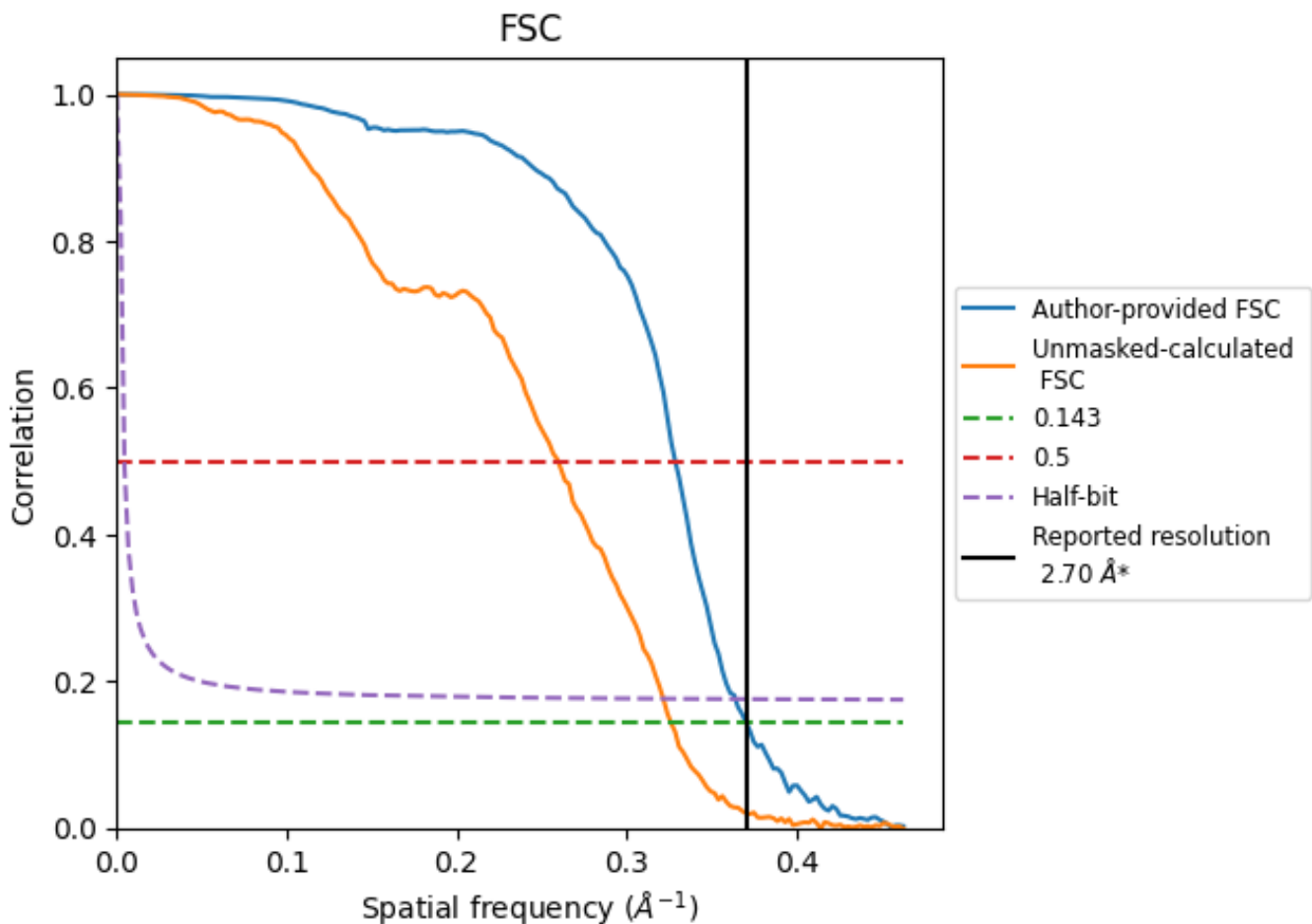


\*Reported resolution corresponds to spatial frequency of 0.370 Å<sup>-1</sup>

## 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 0.370 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

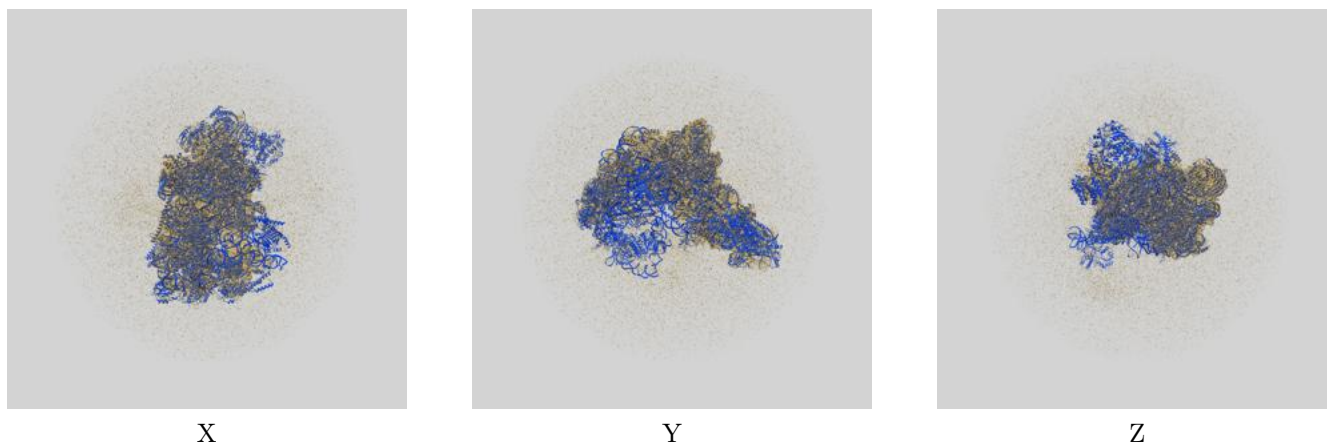
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	2.70	3.04	2.75
Unmasked-calculated*	3.07	3.85	3.11

\*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 3.07 differs from the reported value 2.7 by more than 10 %

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

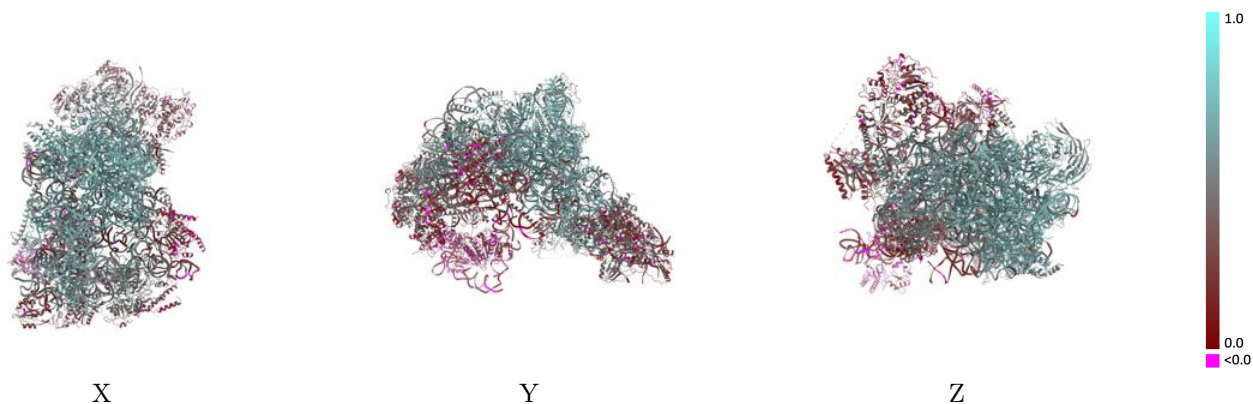
This section contains information regarding the fit between EMDB map EMD-43021 and PDB model 8V84. Per-residue inclusion information can be found in section 3 on page 13.

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



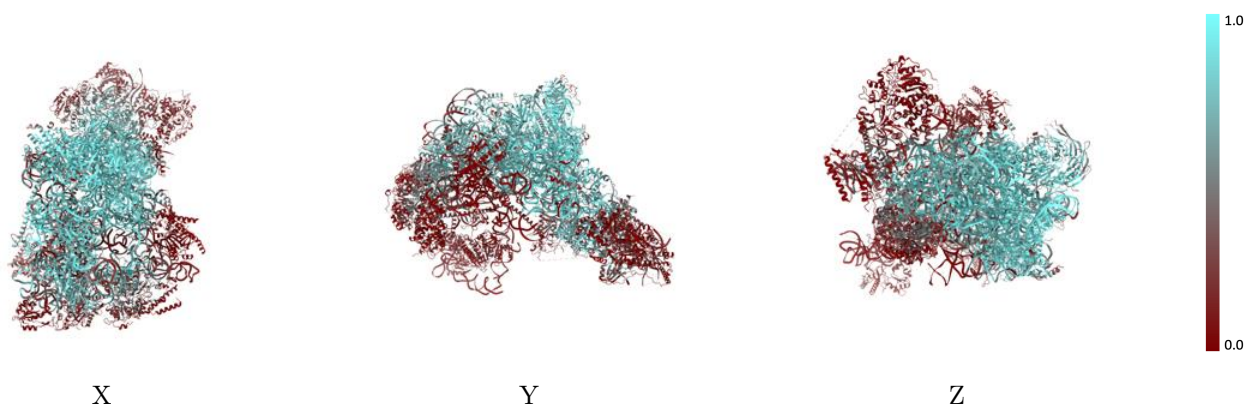
The images above show the 3D surface view of the map at the recommended contour level 0.017 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



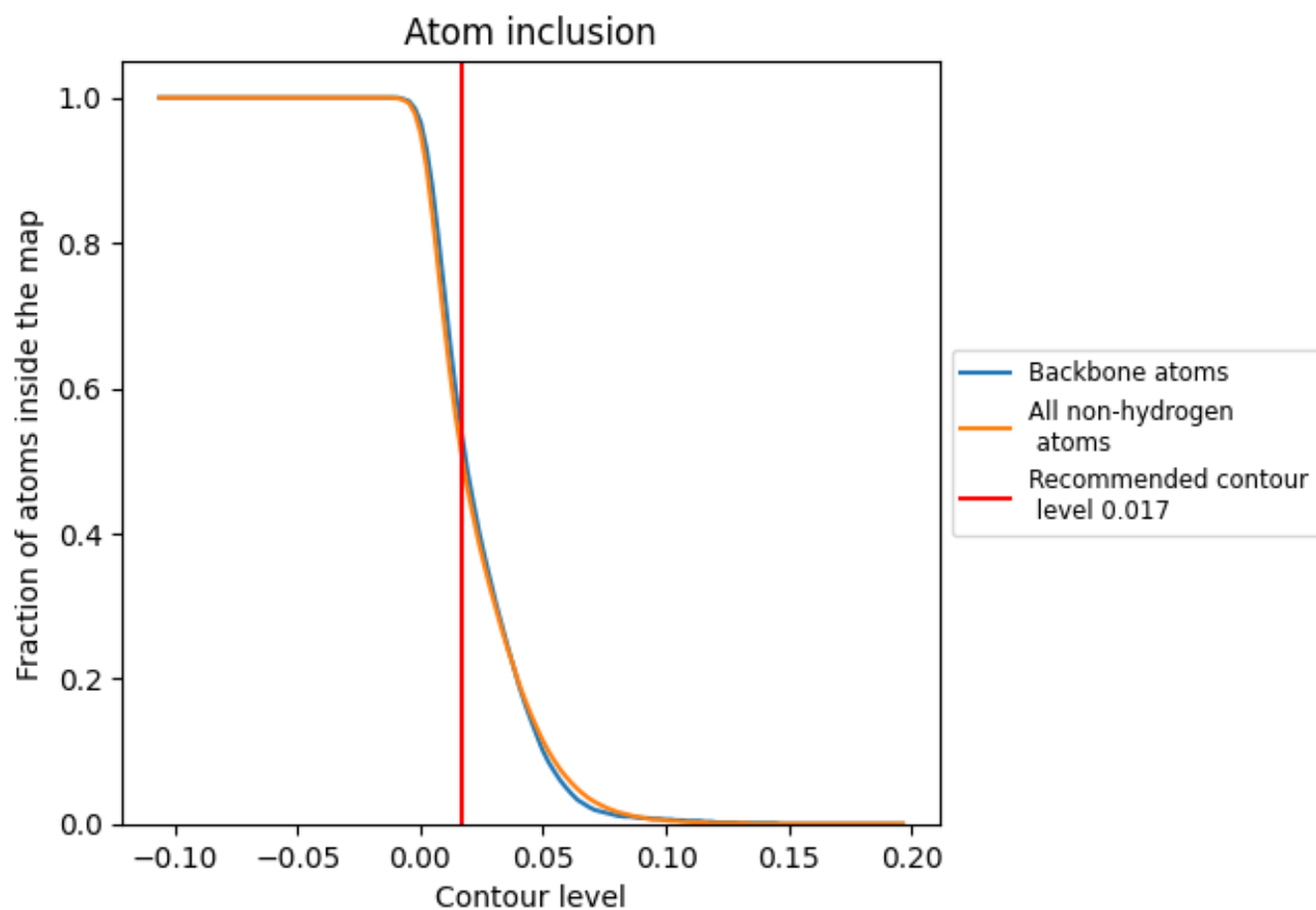
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.017).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 54% of all backbone atoms, 50% 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 (0.017) and Q-score for the entire model and for each chain.































Chain	Atom inclusion	Q-score
All	 0.5050	 0.4610
1	 0.5930	 0.4840
2	 0.7680	 0.5770
3	 0.0400	 0.2020
6	 0.3750	 0.4080
7	 0.0000	 0.0610
8	 0.2940	 0.3920
A	 0.3730	 0.4550
B	 0.5990	 0.5370
C	 0.9320	 0.6810
D	 0.3600	 0.4430
E	 0.7860	 0.6140
F	 0.8360	 0.6280
G	 0.7510	 0.5860
H	 0.6300	 0.5610
I	 0.7720	 0.6080
J	 0.0810	 0.2700
K	 0.1850	 0.3550
L	 0.8800	 0.6470
M	 0.7550	 0.6090
N	 0.8160	 0.6170
O	 0.8030	 0.6240
P	 0.8090	 0.6270
Q	 0.8520	 0.6520
R	 0.8490	 0.6450
S	 0.5760	 0.5380
T	 0.0150	 0.1610
V	 0.1960	 0.3830
W	 0.0970	 0.3140
Y	 0.8800	 0.6540
Z	 0.0200	 0.1950
a	 0.0010	 0.0370
b	 0.1890	 0.3620
e	 0.9100	 0.6770
f	 0.9030	 0.6760



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Chain	Atom inclusion	Q-score
h	 0.5580	 0.5340
i	 0.5990	 0.5490
j	 0.8830	 0.6590
l	 0.0070	 0.1190
m	 0.2230	 0.3350
n	 0.0780	 0.2610
o	 0.2790	 0.3640
q	 0.0080	 0.1190
r	 0.2010	 0.3570
t	 0.1400	 0.3230
u	 0.2160	 0.3700
v	 0.6360	 0.5550
w	 0.7720	 0.5970
x	 0.8100	 0.6170
y	 0.2390	 0.4130