



## wwPDB EM Validation Summary Report ⓘ

Apr 22, 2024 – 08:48 pm BST

PDB ID : 6ZXE  
EMDB ID : EMD-11518  
Title : Cryo-EM structure of a late human pre-40S ribosomal subunit - State F2  
Authors : Ameismeier, M.; Zemp, I.; van den Heuvel, J.; Thoms, M.; Berninghausen, O.;  
Kutay, U.; Beckmann, R.  
Deposited on : 2020-07-29  
Resolution : 3.00 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:

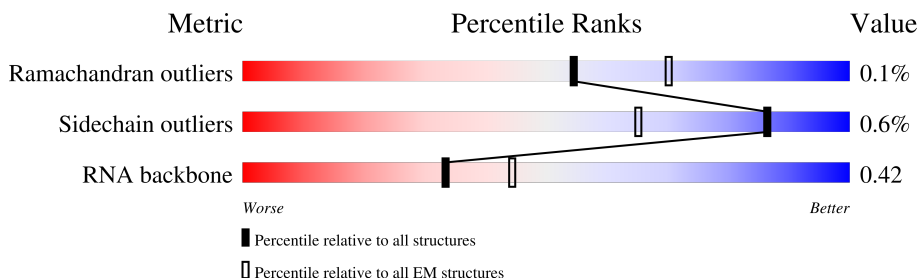
EMDB validation analysis : 0.0.1.dev92  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 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 3.00 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	2	1873	
2	R	135	
3	A	295	
4	B	264	
5	C	293	
6	E	263	
7	G	249	
8	H	194	

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Mol	Chain	Length	Quality of chain
9	I	208	5% 98%
10	J	194	91% 7%
11	L	158	7% 94%
12	N	151	99%
13	O	151	5% 89% 11%
14	V	83	99%
15	W	130	99%
16	X	143	97%
17	Y	133	92% 7%
18	b	84	98%
19	e	59	80% 20%
20	x	252	70% 29%
21	y	412	8% 78% 21%
22	d	56	11% 98%
23	D	243	32% 92% 7%
24	F	204	53% 90% 7%
25	K	165	38% 58% 42%
26	M	132	91% 92% 7%
27	P	145	62% 81% 17%
28	Q	146	34% 94% 5%
29	S	152	78% 91% 9%
30	T	145	70% 99%
31	U	119	33% 85% 15%
32	Z	125	53% 55% 45%
33	c	69	68% 87% 12%

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Mol	Chain	Length	Quality of chain
34	f	156	
35	g	317	
36	k	583	
37	z	568	

## 2 Entry composition [i](#)

There are 38 unique types of molecules in this entry. The entry contains 80500 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 pre-18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	2	1645	35125	15677	6304	11499	1645	0	0

- Molecule 2 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	R	122	990	621	184	182	3	0	0

- Molecule 3 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	A	216	1705	1083	299	315	8	0	0

- Molecule 4 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	B	213	1729	1098	309	308	14	0	0

- Molecule 5 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	C	218	1690	1094	289	297	10	0	0

- Molecule 6 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	E	262	2076	1324	386	358	8	0	0

- Molecule 7 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	230	1862	1164	371	320	7	0	0

- Molecule 8 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H	186	1501	957	276	267	1	0	0

- Molecule 9 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	I	205	1682	1056	331	290	5	0	0

- Molecule 10 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	J	180	1499	955	300	242	2	0	0

- Molecule 11 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	L	151	1229	782	230	211	6	0	0

- Molecule 12 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	N	149	1202	770	228	203	1	0	0

- Molecule 13 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	O	135	1009	618	198	187	6	0	0

- Molecule 14 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	V	82	625	384	116	120	5	0	0

- Molecule 15 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	W	129	1034	659	193	176	6	0	0

- Molecule 16 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	X	141	1098	693	219	183	3	0	0

- Molecule 17 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	Y	124	1014	641	198	170	5	0	0

- Molecule 18 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	b	82	640	402	118	113	7	0	0

- Molecule 19 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	e	47	375	228	84	62	1	0	0

- Molecule 20 is a protein called RNA-binding protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	x	178	1391	891	252	244	4	0	0

- Molecule 21 is a protein called RNA-binding protein NOB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	y	325	Total	C	N	O	S	0	0
			2246	1398	422	418	8		

- Molecule 22 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	d	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 23 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	D	225	Total	C	N	O	S	0	0
			1752	1117	315	313	7		

- Molecule 24 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	F	189	Total	C	N	O	S	0	0
			1495	934	284	270	7		

- Molecule 25 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	K	95	Total	C	N	O	S	0	0
			800	522	142	131	5		

- Molecule 26 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	M	123	Total	C	N	O	S	0	0
			953	598	169	177	9		

- Molecule 27 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	P	120	Total	C	N	O	S	0	0
			984	625	184	168	7		

- Molecule 28 is a protein called 40S ribosomal protein S16.



Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	Q	139	1109	704	210	192	3	0	0

- Molecule 29 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	S	139	1151	725	230	195	1	0	0

- Molecule 30 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	T	144	1122	703	217	199	3	0	0

- Molecule 31 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	U	101	803	504	153	142	4	0	0

- Molecule 32 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	Z	69	549	352	100	96	1	0	0

- Molecule 33 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	c	61	479	292	95	90	2	0	0

- Molecule 34 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	f	59	478	299	91	81	7	0	0

- Molecule 35 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	g	314	2439	1537	425	465	12	0	0

- Molecule 36 is a protein called Leucine-rich repeat-containing protein 47.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	k	430	2886	1788	555	536	7	0	0

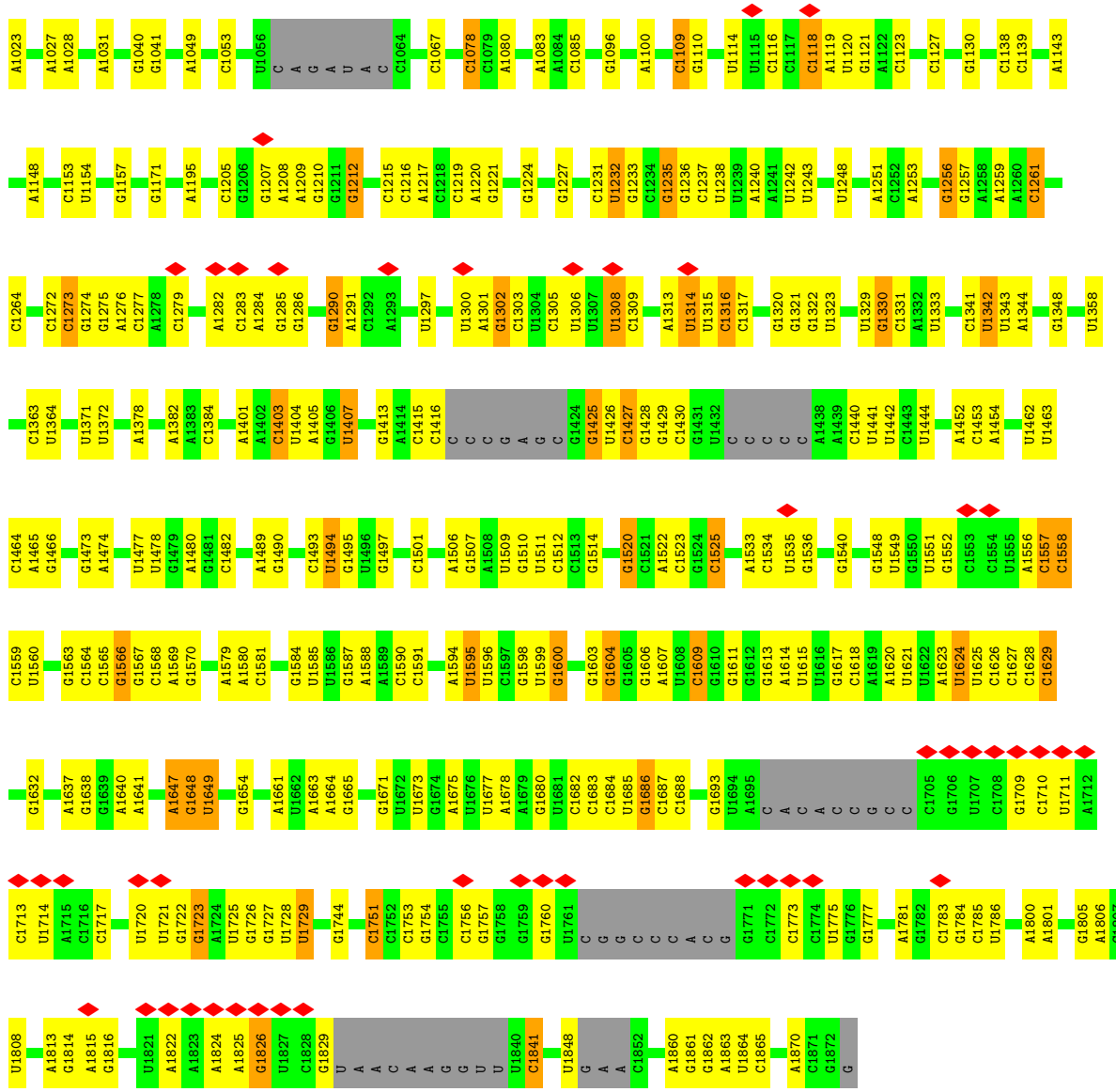
- Molecule 37 is a protein called Serine/threonine-protein kinase RIO1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
37	z	265	1317	787	265	265	0	0

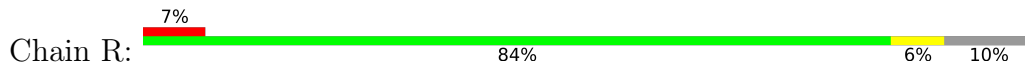
- Molecule 38 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
38	y	1	1	1	0
38	f	1	1	1	0

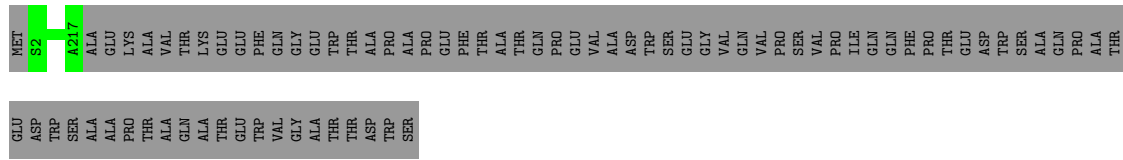




- Molecule 2: 40S ribosomal protein S17



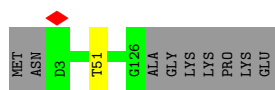
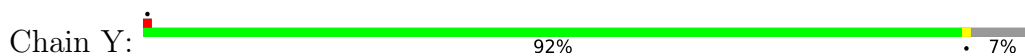
- Molecule 3: 40S ribosomal protein SA







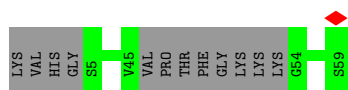
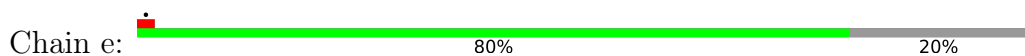
- Molecule 17: 40S ribosomal protein S24



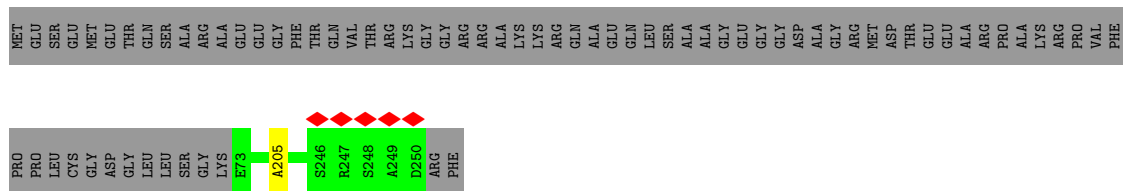
- Molecule 18: 40S ribosomal protein S27



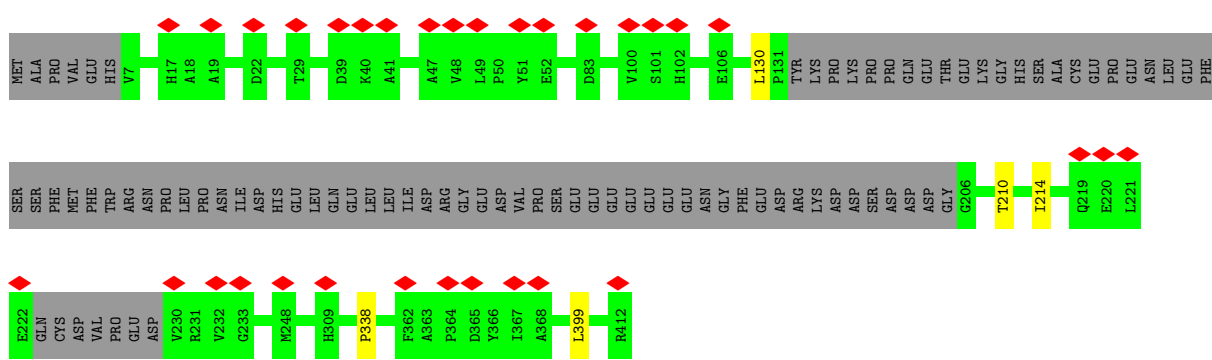
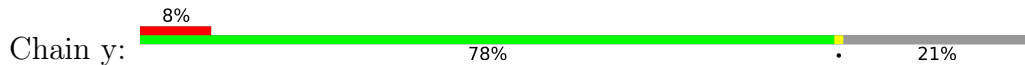
- Molecule 19: 40S ribosomal protein S30



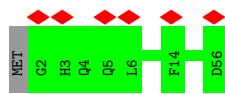
- Molecule 20: RNA-binding protein PNO1



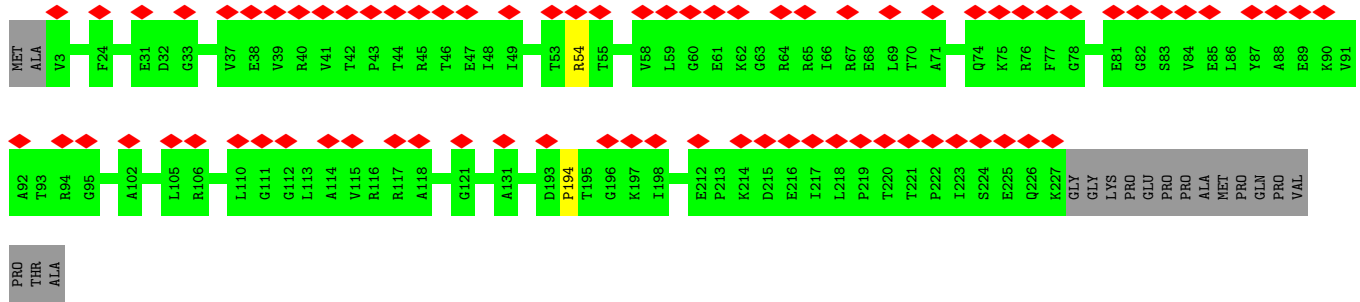
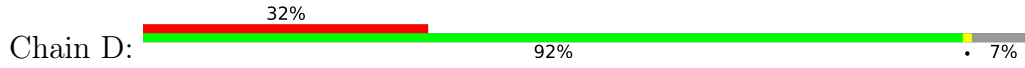
- Molecule 21: RNA-binding protein NOB1



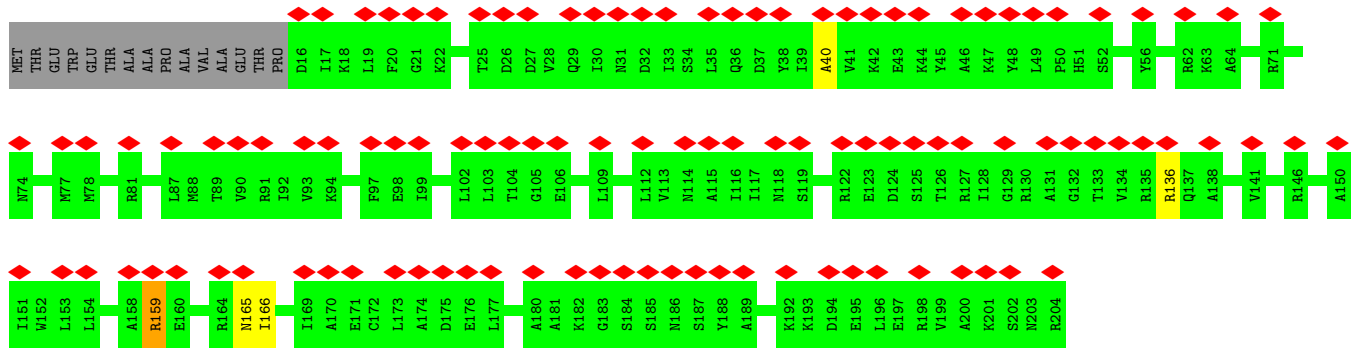
- Molecule 22: 40S ribosomal protein S29



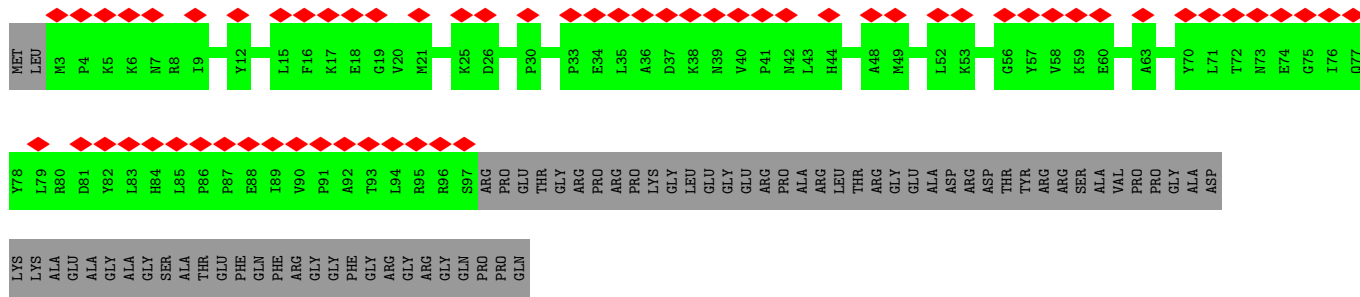
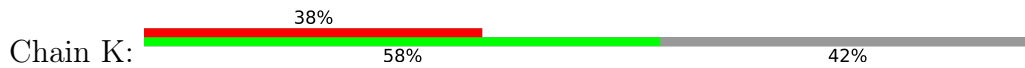
• Molecule 23: 40S ribosomal protein S3



• Molecule 24: 40S ribosomal protein S5

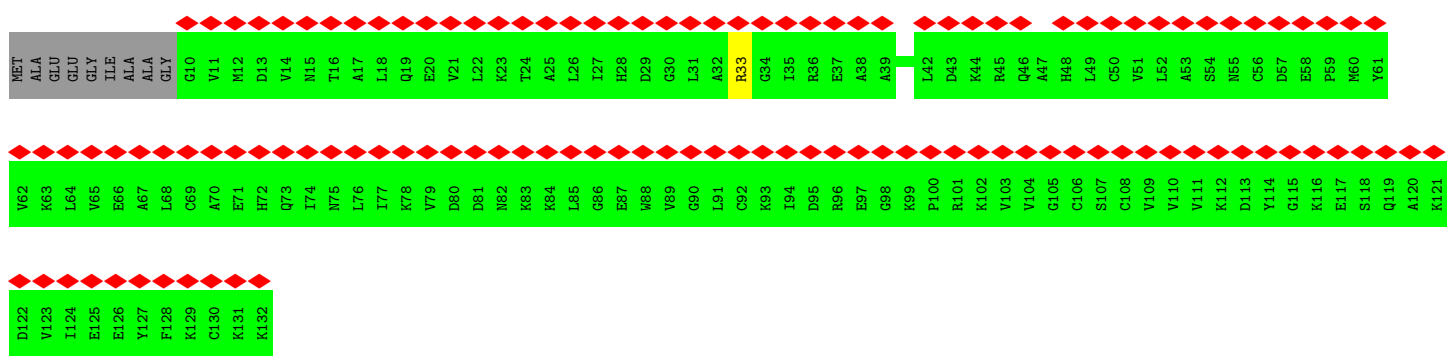
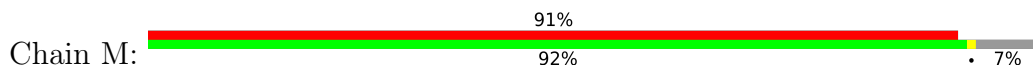


• Molecule 25: 40S ribosomal protein S10

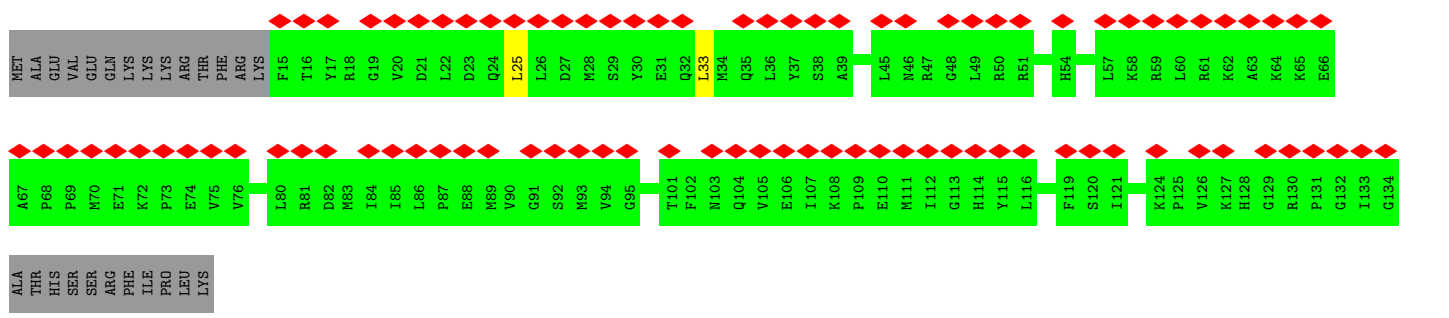
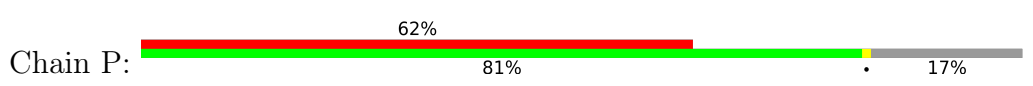


• Molecule 26: 40S ribosomal protein S12

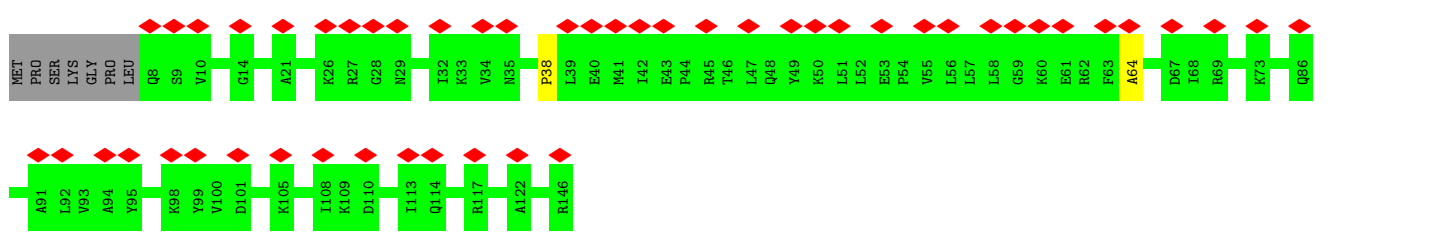
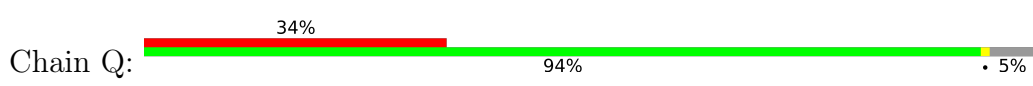




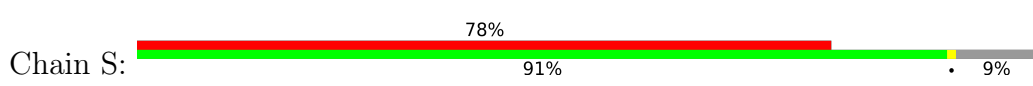
• Molecule 27: 40S ribosomal protein S15

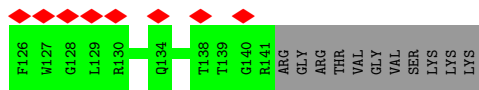


• Molecule 28: 40S ribosomal protein S16

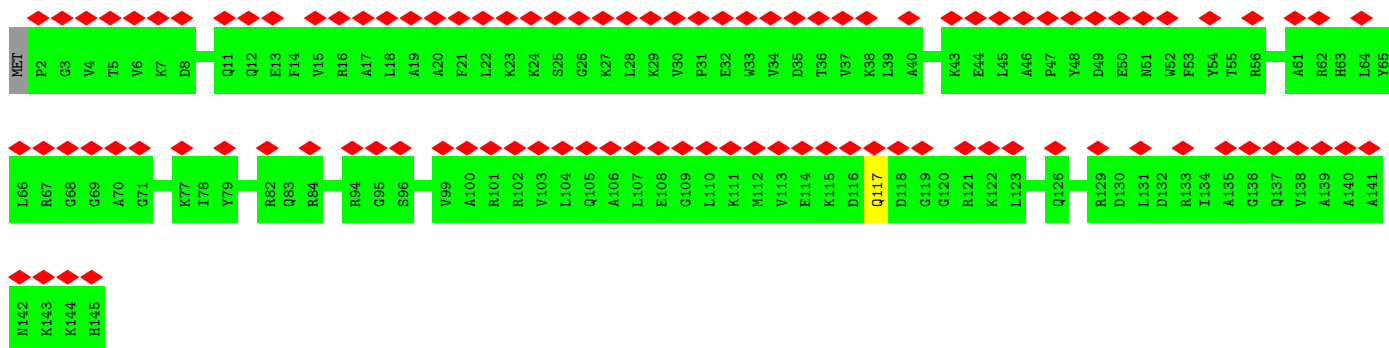


• Molecule 29: 40S ribosomal protein S18

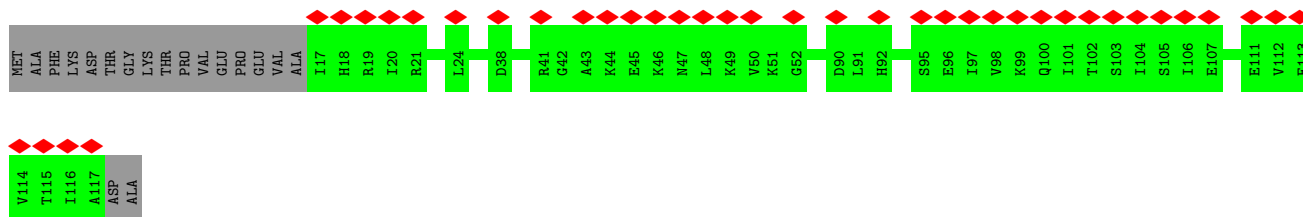
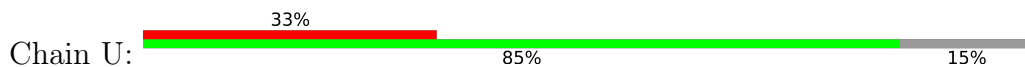




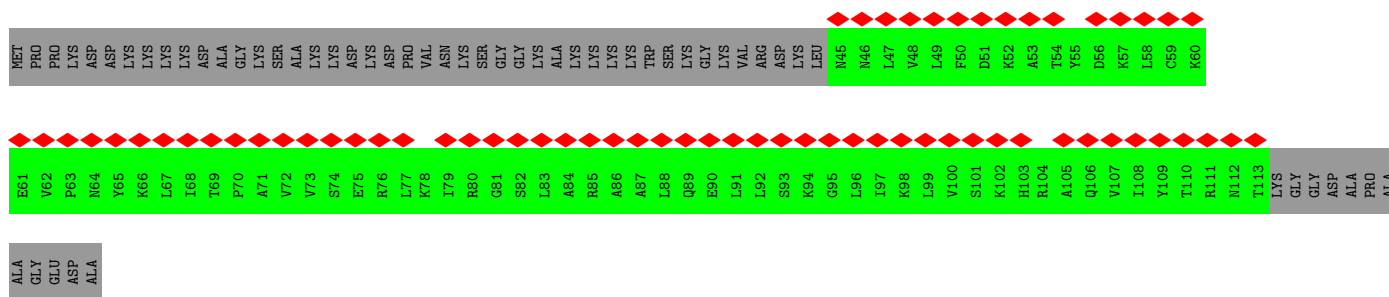
• Molecule 30: 40S ribosomal protein S19



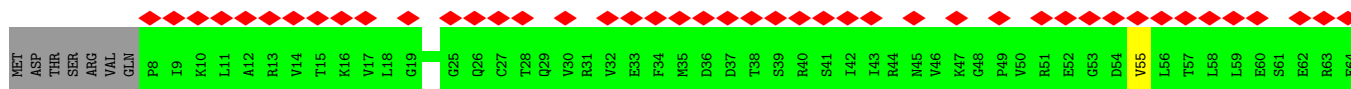
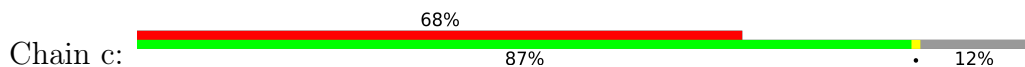
• Molecule 31: 40S ribosomal protein S20

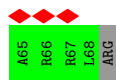


• Molecule 32: 40S ribosomal protein S25

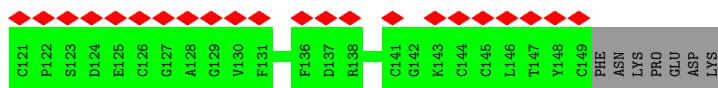
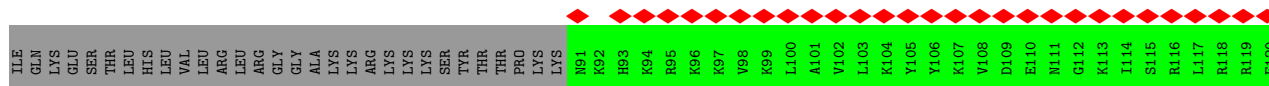


• Molecule 33: 40S ribosomal protein S28

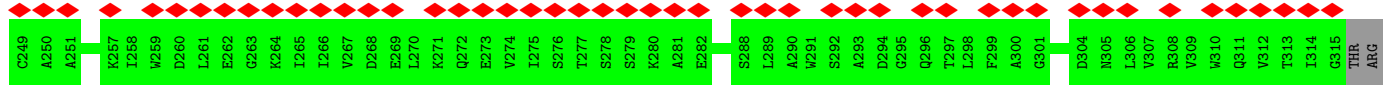
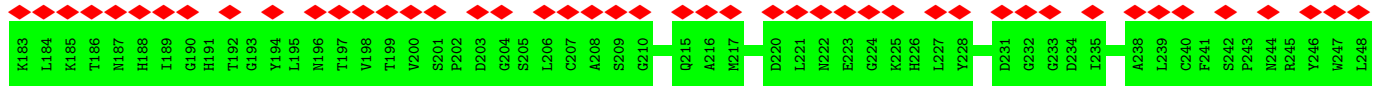
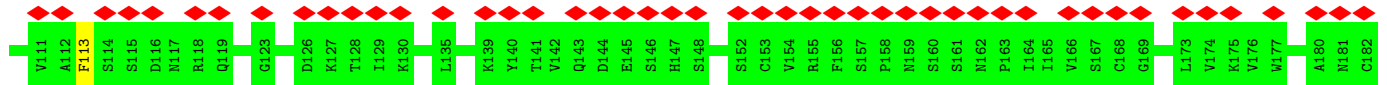
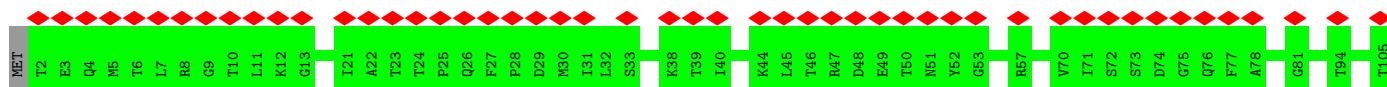




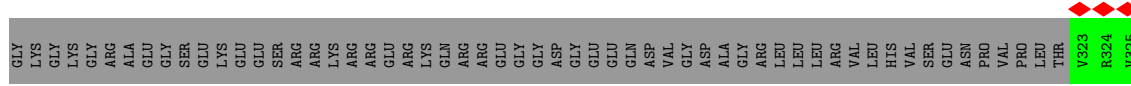
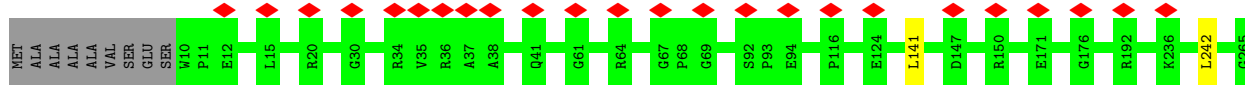
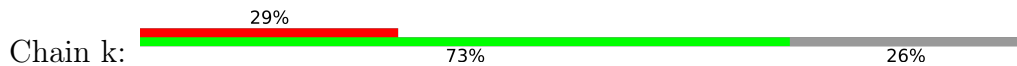
• Molecule 34: Ubiquitin-40S ribosomal protein S27a

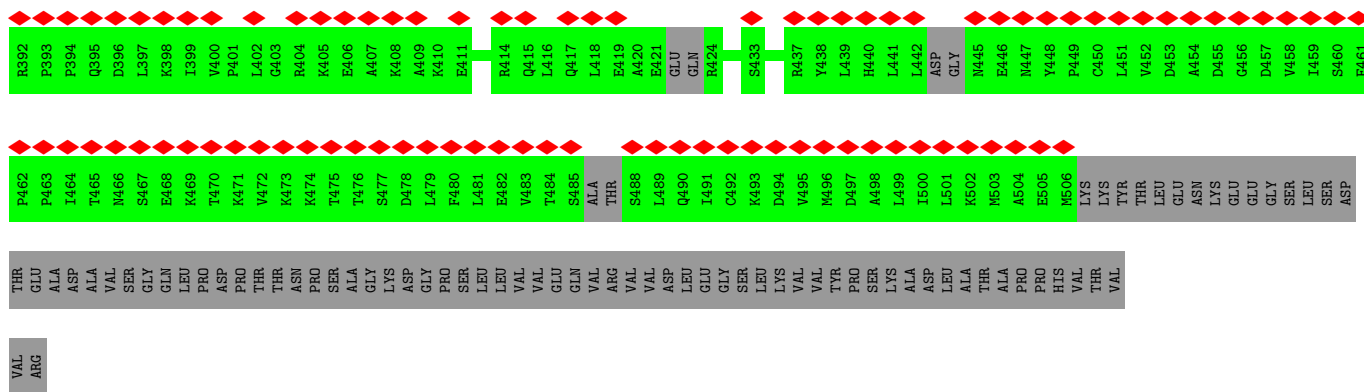


• Molecule 35: Receptor of activated protein C kinase 1

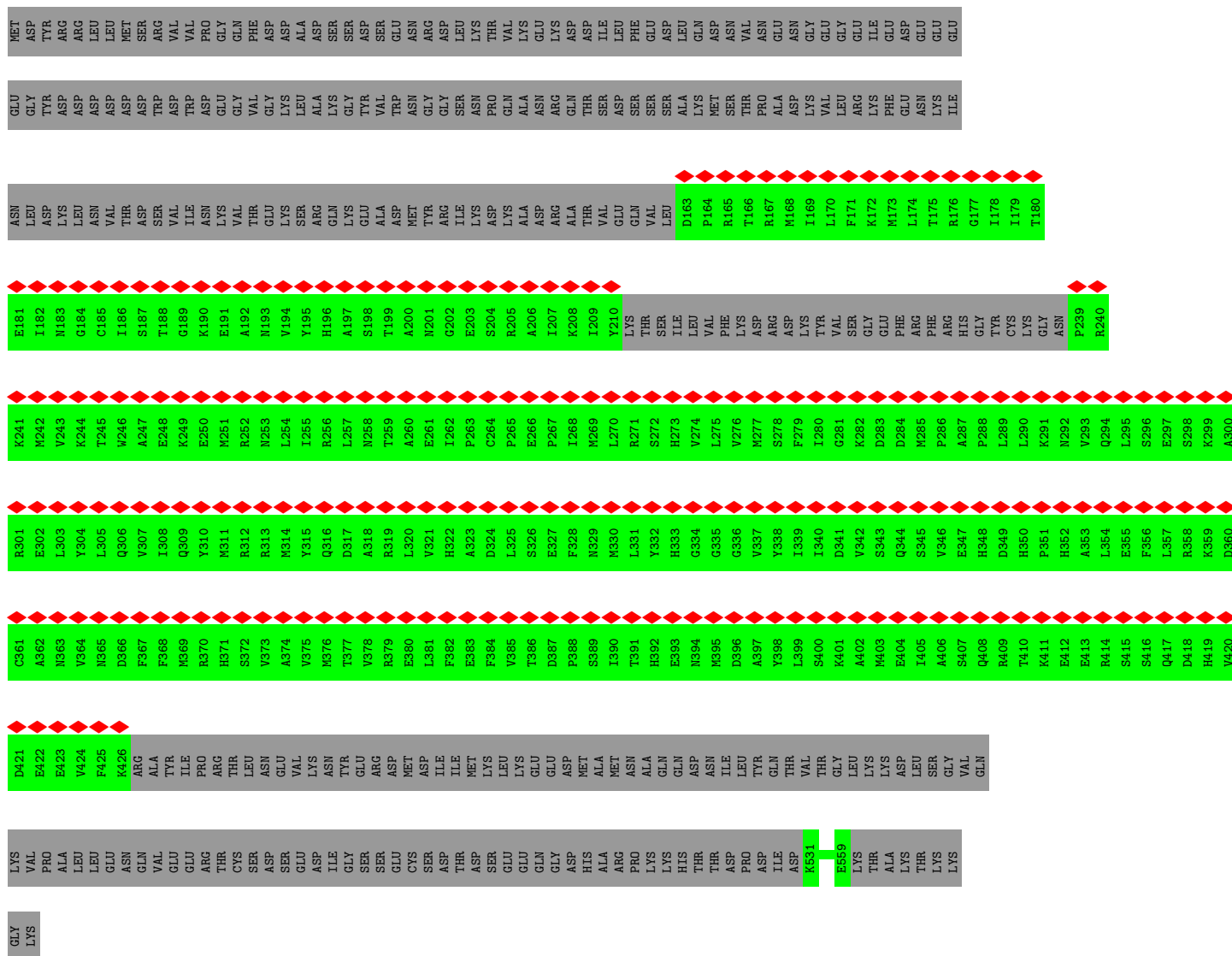
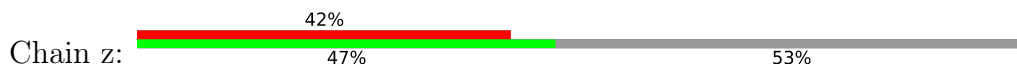


• Molecule 36: Leucine-rich repeat-containing protein 47





● Molecule 37: Serine/threonine-protein kinase RIO1



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	32535	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 ( $e^-/\text{\AA}^2$ )	48	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.501	Depositor
Minimum map value	-0.258	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.035	Depositor
Map size (Å)	381.24, 381.24, 381.24	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.059, 1.059, 1.059	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z  > 5$	RMSZ	# $ Z  > 5$
1	2	1.06	1/39273 (0.0%)	1.21	296/61196 (0.5%)
2	R	0.44	0/1002	0.62	0/1345
3	A	0.57	0/1742	0.60	0/2367
4	B	0.50	0/1756	0.60	0/2350
5	C	0.59	0/1726	0.66	0/2332
6	E	0.56	0/2118	0.61	1/2849 (0.0%)
7	G	0.48	0/1885	0.55	0/2510
8	H	0.44	0/1524	0.58	1/2042 (0.0%)
9	I	0.55	0/1711	0.60	0/2282
10	J	0.58	0/1524	0.60	1/2035 (0.0%)
11	L	0.63	0/1250	0.62	0/1673
12	N	0.51	0/1226	0.57	0/1649
13	O	0.48	0/1022	0.59	0/1372
14	V	0.54	0/631	0.59	0/844
15	W	0.61	0/1051	0.63	0/1406
16	X	0.58	0/1116	0.60	0/1490
17	Y	0.58	0/1031	0.57	0/1370
18	b	0.52	0/653	0.59	0/876
19	e	0.50	0/377	0.52	0/493
20	x	0.48	0/1413	0.61	0/1906
21	y	0.44	0/2283	0.60	2/3106 (0.1%)
22	d	0.38	0/470	0.59	0/623
23	D	0.38	0/1780	0.60	0/2397
24	F	0.35	0/1516	0.64	1/2037 (0.0%)
25	K	0.36	0/824	0.60	0/1112
26	M	0.32	0/963	0.58	0/1291
27	P	0.34	0/1003	0.63	2/1341 (0.1%)
28	Q	0.36	0/1126	0.62	0/1506
29	S	0.32	0/1169	0.61	1/1567 (0.1%)
30	T	0.33	0/1142	0.54	0/1530
31	U	0.36	0/813	0.55	0/1092
32	Z	0.33	0/555	0.65	0/747

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	c	0.34	0/481	0.74	0/643
34	f	0.31	0/487	0.58	0/646
35	g	0.33	0/2496	0.58	0/3398
36	k	0.35	0/2920	0.60	1/3977 (0.0%)
37	z	0.27	0/1314	0.52	0/1830
All	All	0.80	1/85373 (0.0%)	0.95	306/123230 (0.2%)

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
23	D	0	1
24	F	0	2
28	Q	0	1
All	All	0	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2	64	A	N9-C4	-5.32	1.34	1.37

The worst 5 of 306 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	501	C	N1-C2-O2	14.44	127.56	118.90
1	2	293	C	N1-C2-O2	13.16	126.79	118.90
1	2	501	C	C2-N1-C1'	13.00	133.10	118.80
1	2	72	C	N1-C2-O2	12.19	126.22	118.90
1	2	501	C	N3-C2-O2	-11.89	113.58	121.90

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
23	D	194	PRO	Peptide
24	F	165	ASN	Peptide
24	F	40	ALA	Peptide
28	Q	38	PRO	Peptide

## 5.2 Too-close contacts [i](#)

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

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	R	120/135 (89%)	109 (91%)	10 (8%)	1 (1%)	19	57
3	A	214/295 (72%)	204 (95%)	10 (5%)	0	100	100
4	B	211/264 (80%)	193 (92%)	18 (8%)	0	100	100
5	C	216/293 (74%)	203 (94%)	13 (6%)	0	100	100
6	E	260/263 (99%)	247 (95%)	13 (5%)	0	100	100
7	G	228/249 (92%)	218 (96%)	10 (4%)	0	100	100
8	H	184/194 (95%)	172 (94%)	12 (6%)	0	100	100
9	I	203/208 (98%)	192 (95%)	11 (5%)	0	100	100
10	J	178/194 (92%)	162 (91%)	15 (8%)	1 (1%)	25	64
11	L	149/158 (94%)	142 (95%)	7 (5%)	0	100	100
12	N	147/151 (97%)	143 (97%)	4 (3%)	0	100	100
13	O	133/151 (88%)	122 (92%)	11 (8%)	0	100	100
14	V	80/83 (96%)	78 (98%)	2 (2%)	0	100	100
15	W	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
16	X	139/143 (97%)	132 (95%)	6 (4%)	1 (1%)	22	60
17	Y	122/133 (92%)	114 (93%)	8 (7%)	0	100	100
18	b	80/84 (95%)	71 (89%)	9 (11%)	0	100	100
19	e	43/59 (73%)	40 (93%)	3 (7%)	0	100	100
20	x	176/252 (70%)	166 (94%)	9 (5%)	1 (1%)	25	64
21	y	319/412 (77%)	293 (92%)	25 (8%)	1 (0%)	41	76
22	d	53/56 (95%)	48 (91%)	5 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	D	223/243 (92%)	210 (94%)	13 (6%)	0	100	100
24	F	187/204 (92%)	162 (87%)	24 (13%)	1 (0%)	29	68
25	K	93/165 (56%)	89 (96%)	4 (4%)	0	100	100
26	M	121/132 (92%)	107 (88%)	14 (12%)	0	100	100
27	P	118/145 (81%)	104 (88%)	14 (12%)	0	100	100
28	Q	137/146 (94%)	124 (90%)	12 (9%)	1 (1%)	22	60
29	S	137/152 (90%)	119 (87%)	18 (13%)	0	100	100
30	T	142/145 (98%)	132 (93%)	10 (7%)	0	100	100
31	U	99/119 (83%)	88 (89%)	11 (11%)	0	100	100
32	Z	67/125 (54%)	61 (91%)	6 (9%)	0	100	100
33	c	59/69 (86%)	48 (81%)	11 (19%)	0	100	100
34	f	57/156 (36%)	44 (77%)	13 (23%)	0	100	100
35	g	312/317 (98%)	282 (90%)	30 (10%)	0	100	100
36	k	418/583 (72%)	378 (90%)	40 (10%)	0	100	100
37	z	259/568 (46%)	234 (90%)	25 (10%)	0	100	100
All	All	5811/7176 (81%)	5352 (92%)	452 (8%)	7 (0%)	54	85

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	J	161	LEU
24	F	166	ILE
21	y	338	PRO
2	R	76	GLU
28	Q	64	ALA

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

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	R	110/122 (90%)	103 (94%)	7 (6%)	17	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	A	180/243 (74%)	180 (100%)	0	100	100
4	B	194/231 (84%)	193 (100%)	1 (0%)	88	96
5	C	184/225 (82%)	183 (100%)	1 (0%)	88	96
6	E	224/225 (100%)	223 (100%)	1 (0%)	91	97
7	G	200/218 (92%)	198 (99%)	2 (1%)	76	91
8	H	167/174 (96%)	167 (100%)	0	100	100
9	I	178/180 (99%)	177 (99%)	1 (1%)	86	95
10	J	160/168 (95%)	159 (99%)	1 (1%)	86	95
11	L	135/142 (95%)	133 (98%)	2 (2%)	65	87
12	N	130/131 (99%)	130 (100%)	0	100	100
13	O	105/119 (88%)	105 (100%)	0	100	100
14	V	66/67 (98%)	66 (100%)	0	100	100
15	W	112/113 (99%)	112 (100%)	0	100	100
16	X	113/115 (98%)	111 (98%)	2 (2%)	59	85
17	Y	108/115 (94%)	107 (99%)	1 (1%)	78	92
18	b	74/76 (97%)	74 (100%)	0	100	100
19	e	38/48 (79%)	38 (100%)	0	100	100
20	x	150/208 (72%)	150 (100%)	0	100	100
21	y	194/367 (53%)	192 (99%)	2 (1%)	76	91
22	d	48/49 (98%)	48 (100%)	0	100	100
23	D	189/202 (94%)	188 (100%)	1 (0%)	88	96
24	F	159/170 (94%)	157 (99%)	2 (1%)	69	89
25	K	86/136 (63%)	86 (100%)	0	100	100
26	M	104/108 (96%)	103 (99%)	1 (1%)	76	91
27	P	107/130 (82%)	107 (100%)	0	100	100
28	Q	115/121 (95%)	115 (100%)	0	100	100
29	S	121/132 (92%)	121 (100%)	0	100	100
30	T	114/115 (99%)	113 (99%)	1 (1%)	78	92
31	U	93/107 (87%)	93 (100%)	0	100	100
32	Z	61/103 (59%)	61 (100%)	0	100	100
33	c	54/62 (87%)	53 (98%)	1 (2%)	57	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	f	52/140 (37%)	52 (100%)	0	100	100
35	g	271/275 (98%)	270 (100%)	1 (0%)	91	97
36	k	231/487 (47%)	230 (100%)	1 (0%)	91	97
All	All	4627/5624 (82%)	4598 (99%)	29 (1%)	86	95

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	L	69	ARG
35	g	113	PHE
16	X	105	PHE
26	M	33	ARG
16	X	9	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 64 such sidechains are listed below:

Mol	Chain	Res	Type
36	k	78	HIS
36	k	109	ASN
16	X	61	GLN
14	V	33	GLN
36	k	139	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1631/1873 (87%)	492 (30%)	42 (2%)

5 of 492 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	3	C
1	2	4	C
1	2	5	U
1	2	10	G

5 of 42 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	1425	G
1	2	1580	A
1	2	1440	C
1	2	1511	U
1	2	1606	G

#### 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 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

#### 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

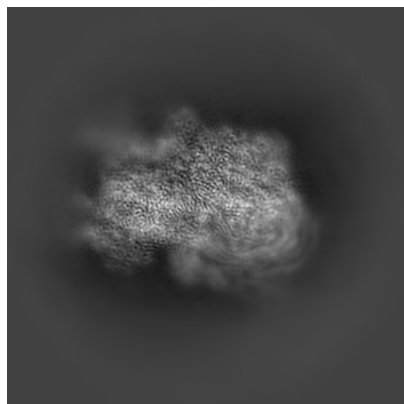
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11518. These allow visual inspection of the internal detail of the map and identification of artifacts.

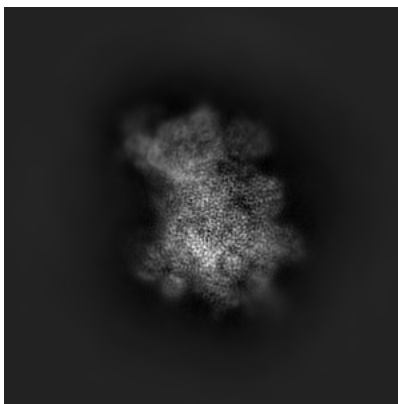
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

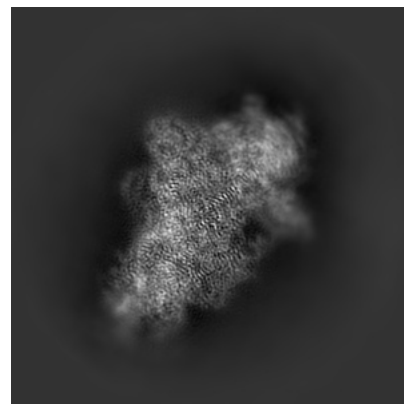
#### 6.1.1 Primary map



X

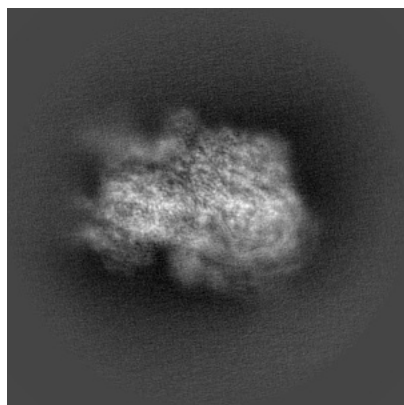


Y

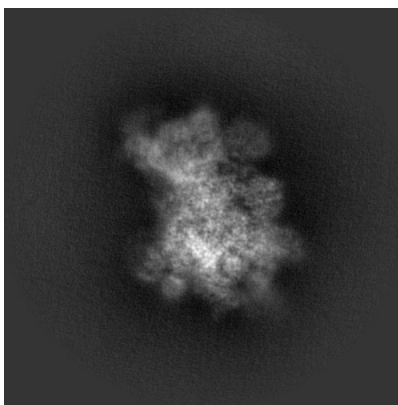


Z

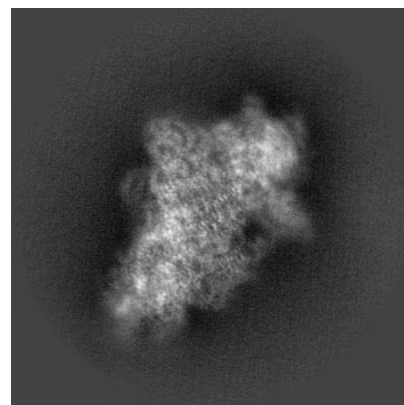
#### 6.1.2 Raw map



X



Y

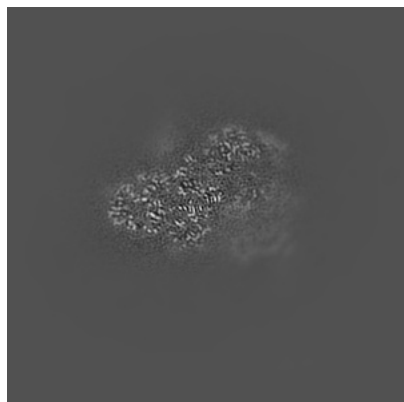


Z

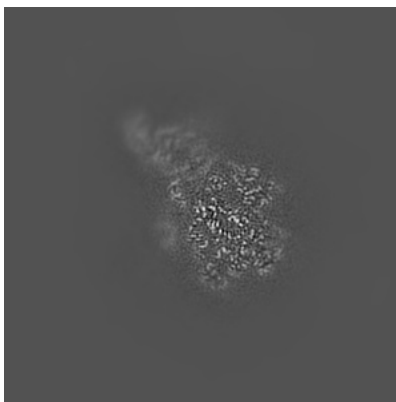
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

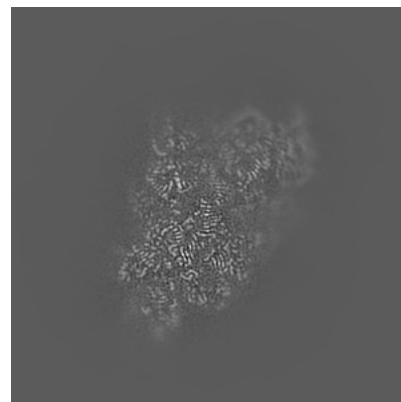
### 6.2.1 Primary map



X Index: 180

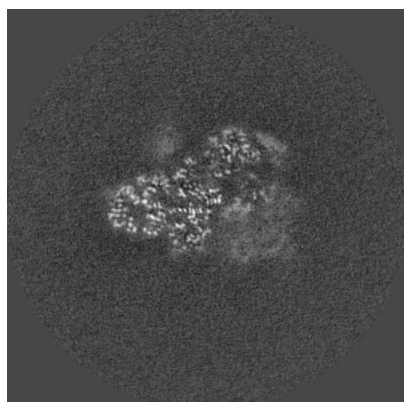


Y Index: 180

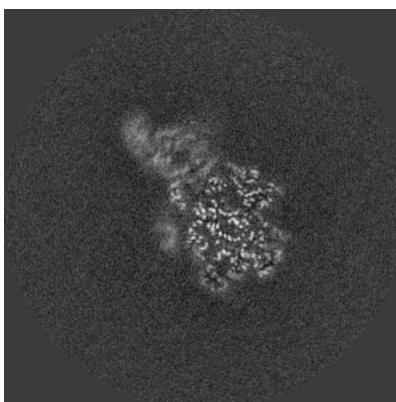


Z Index: 180

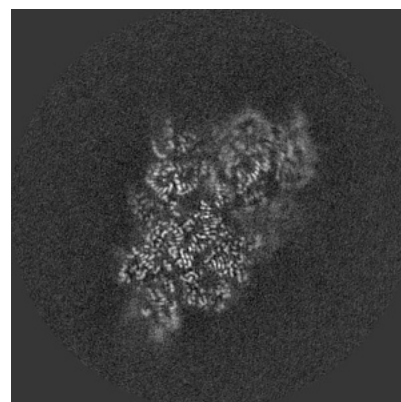
### 6.2.2 Raw map



X Index: 180



Y Index: 180

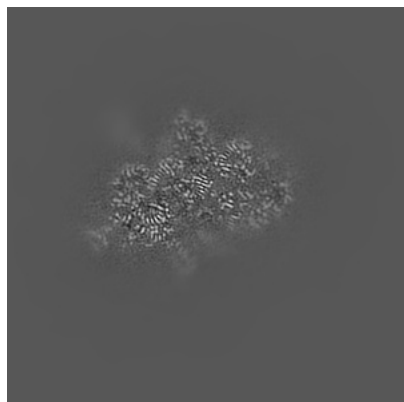


Z Index: 180

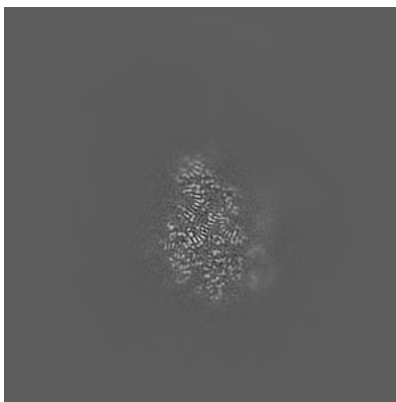
The images above show central slices of the map in three orthogonal directions.

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

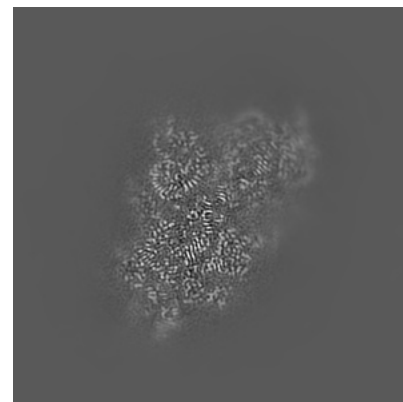
### 6.3.1 Primary map



X Index: 155

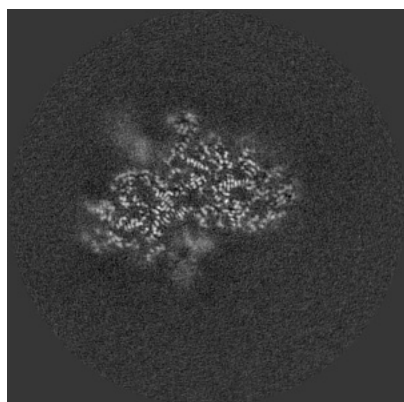


Y Index: 134

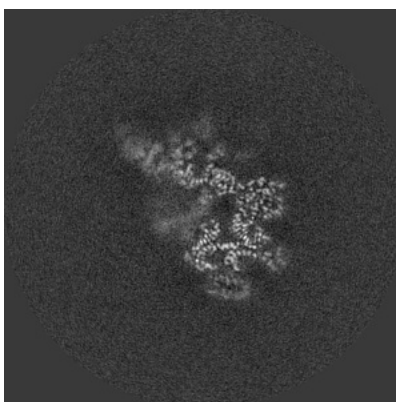


Z Index: 182

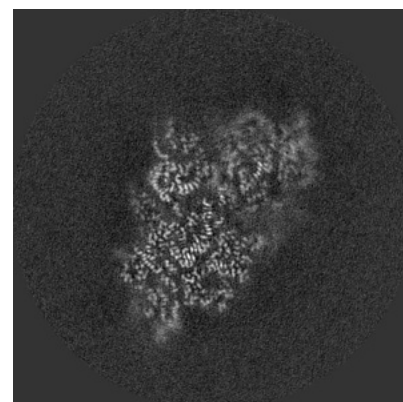
### 6.3.2 Raw map



X Index: 147



Y Index: 199

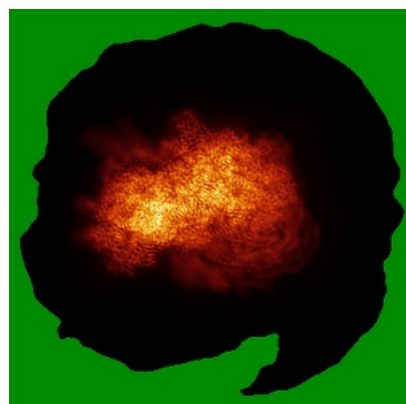


Z Index: 181

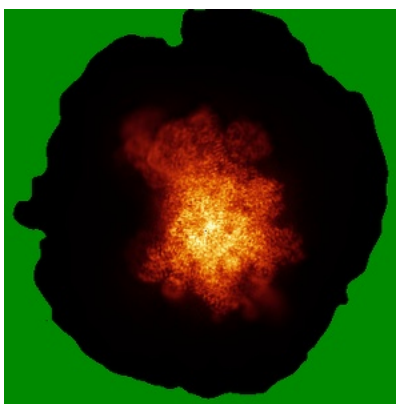
The images above show the largest variance slices of the map in three orthogonal directions.

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

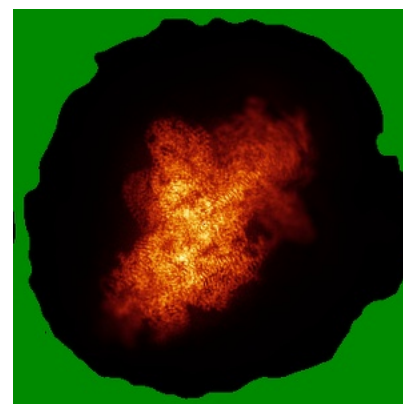
### 6.4.1 Primary map



X

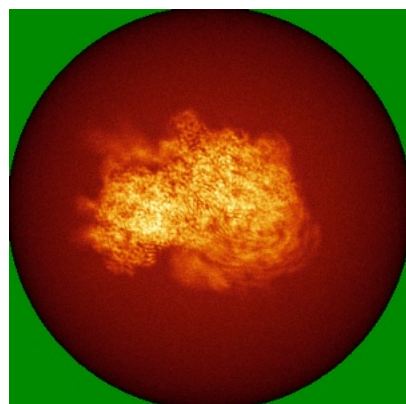


Y

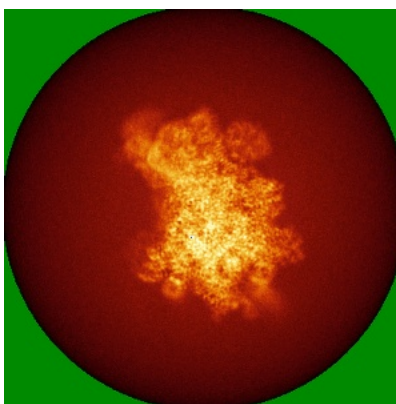


Z

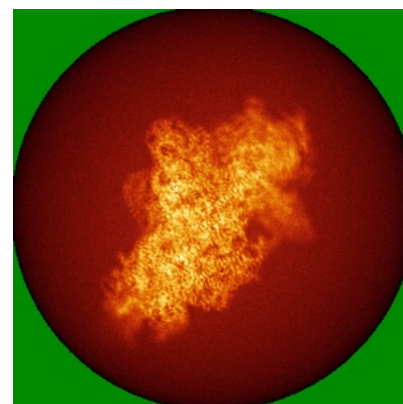
### 6.4.2 Raw map



X



Y



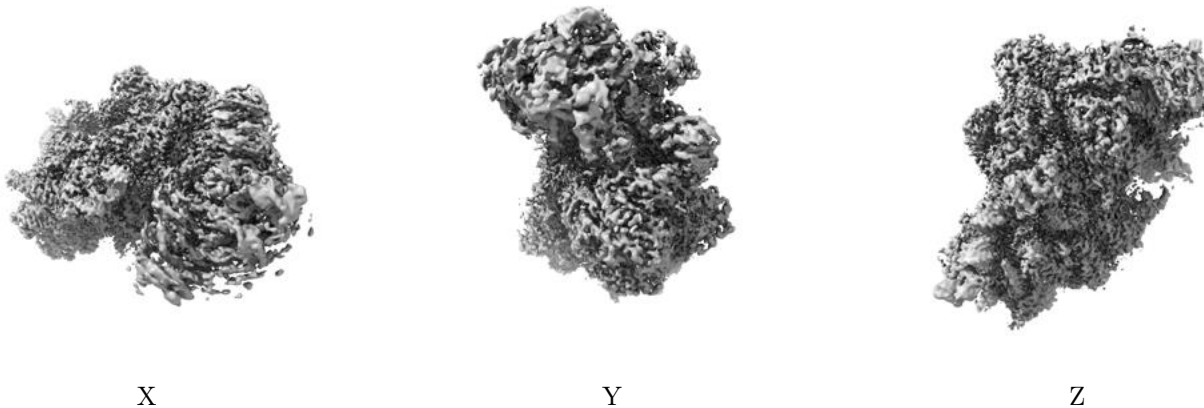
Z

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.



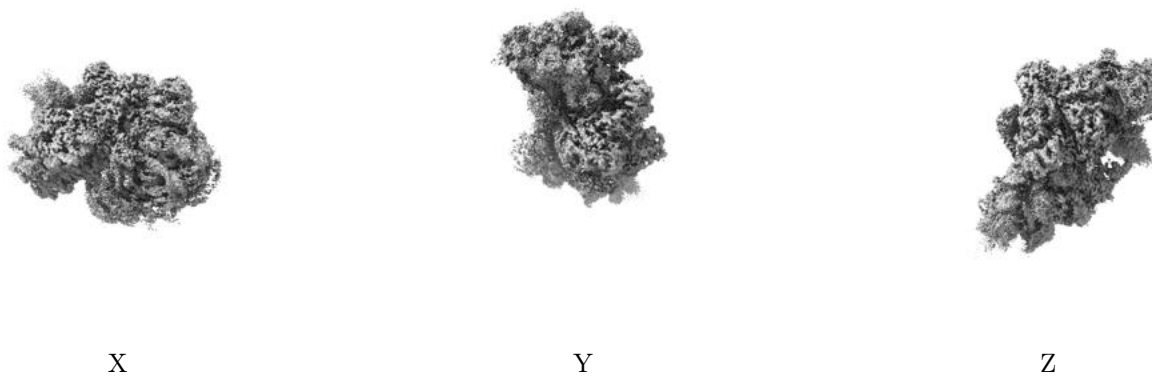
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.035. 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.

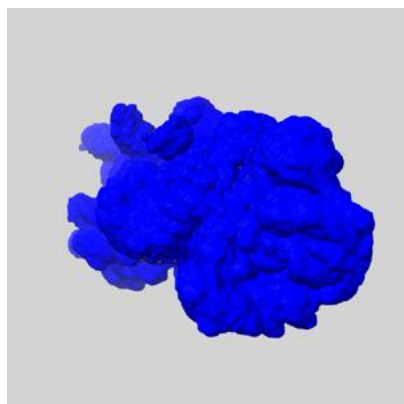
## 6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

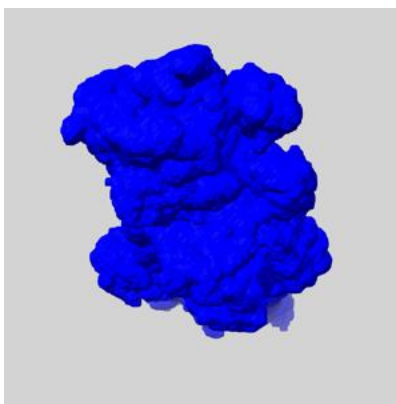
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

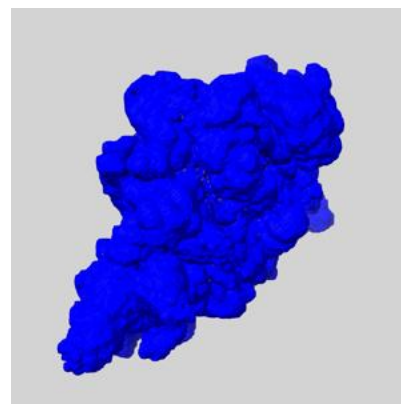
### 6.6.1 emd\_11518\_msk\_1.map [i](#)



X



Y

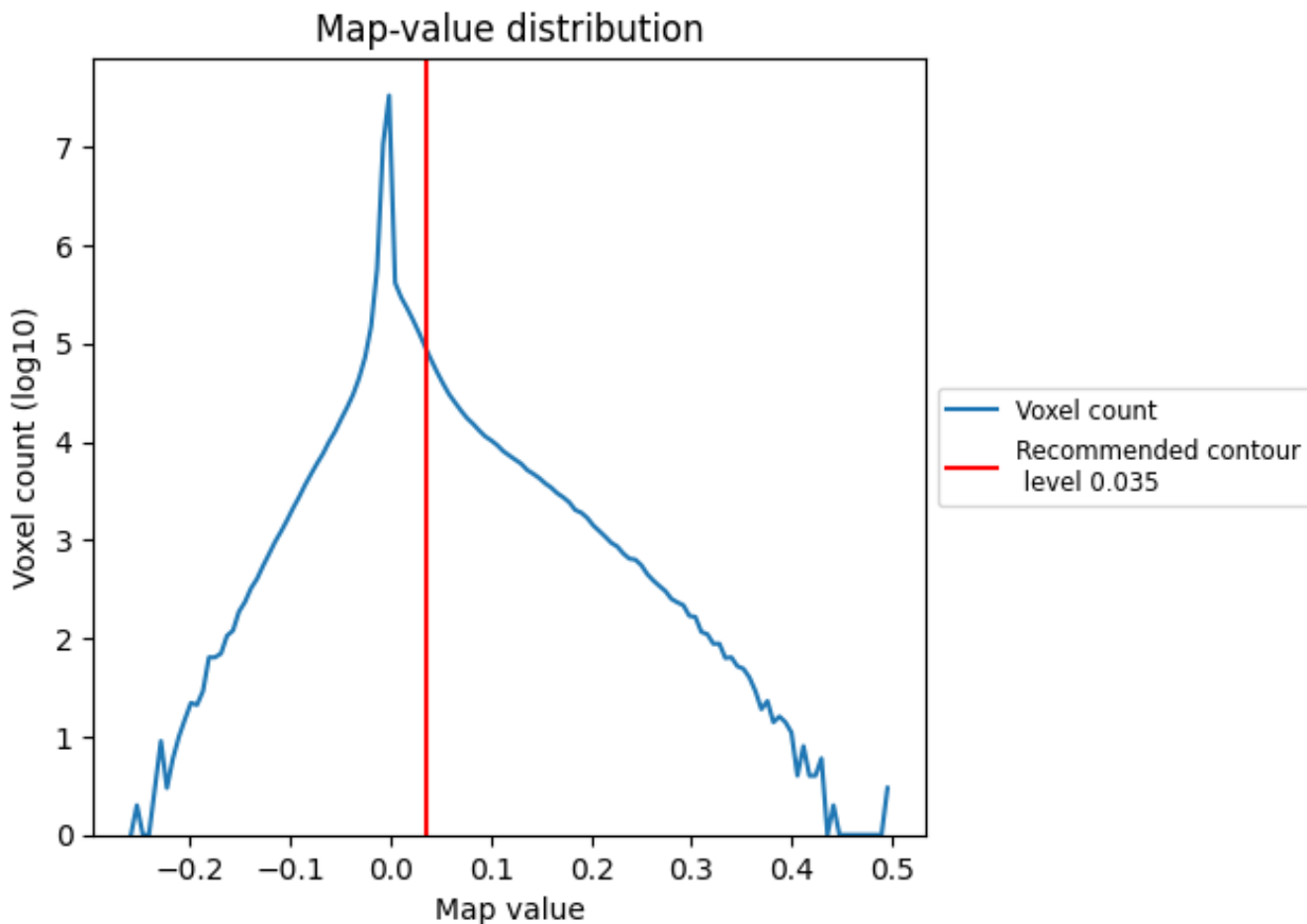


Z

## 7 Map analysis [i](#)

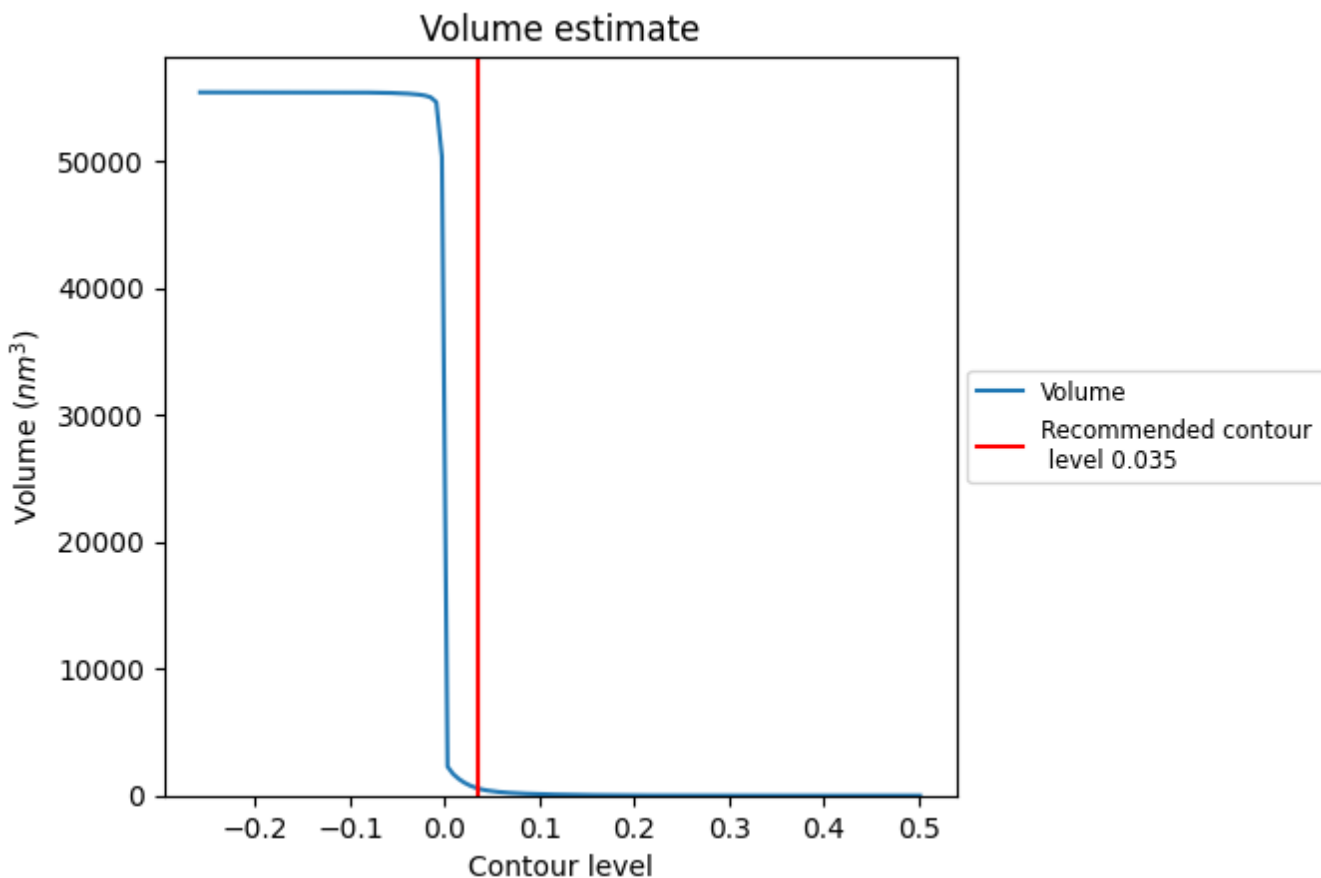
This section contains the results of statistical analysis of the map.

### 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.

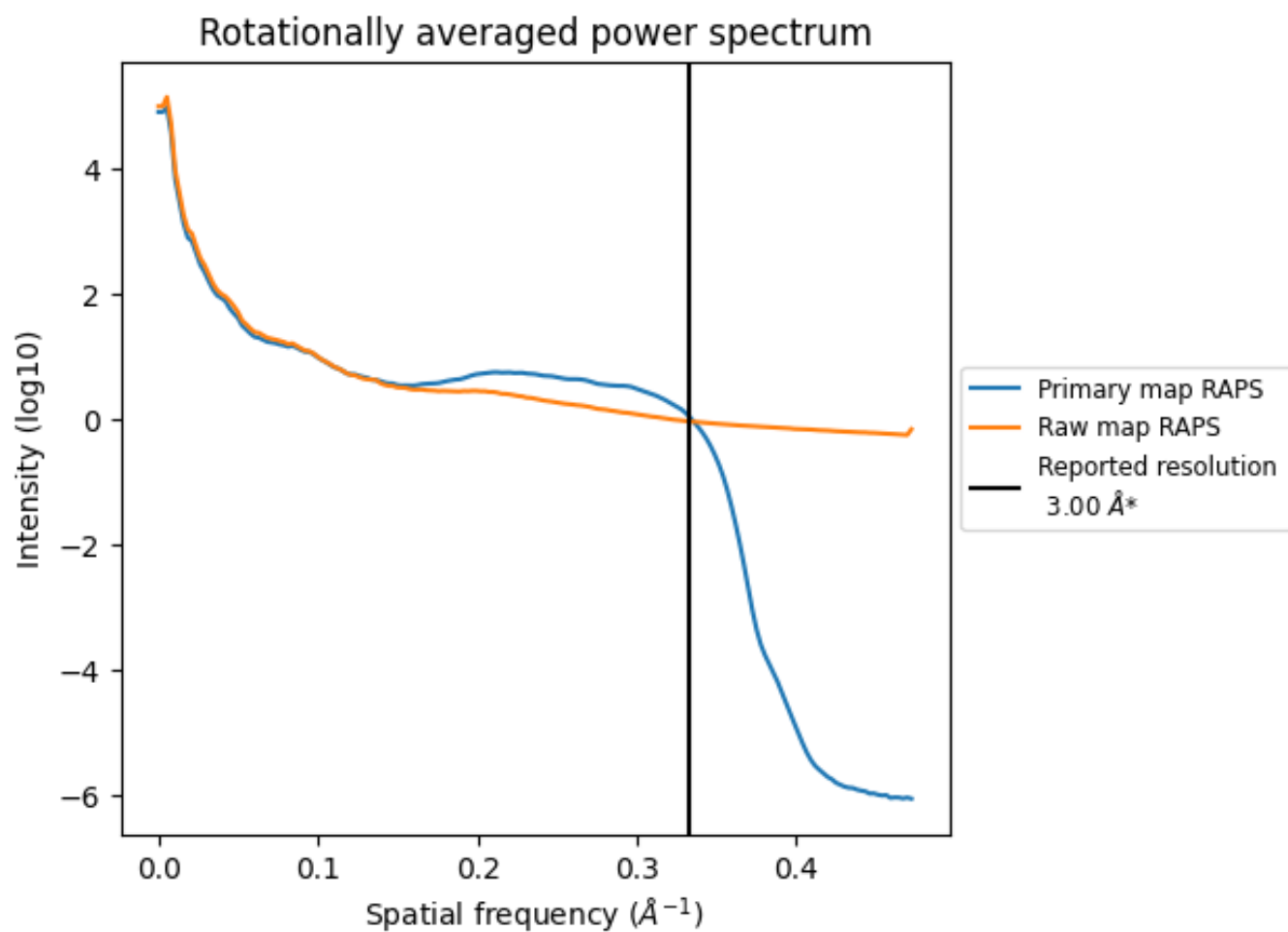
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 568 nm<sup>3</sup>; this corresponds to an approximate mass of 513 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](#)

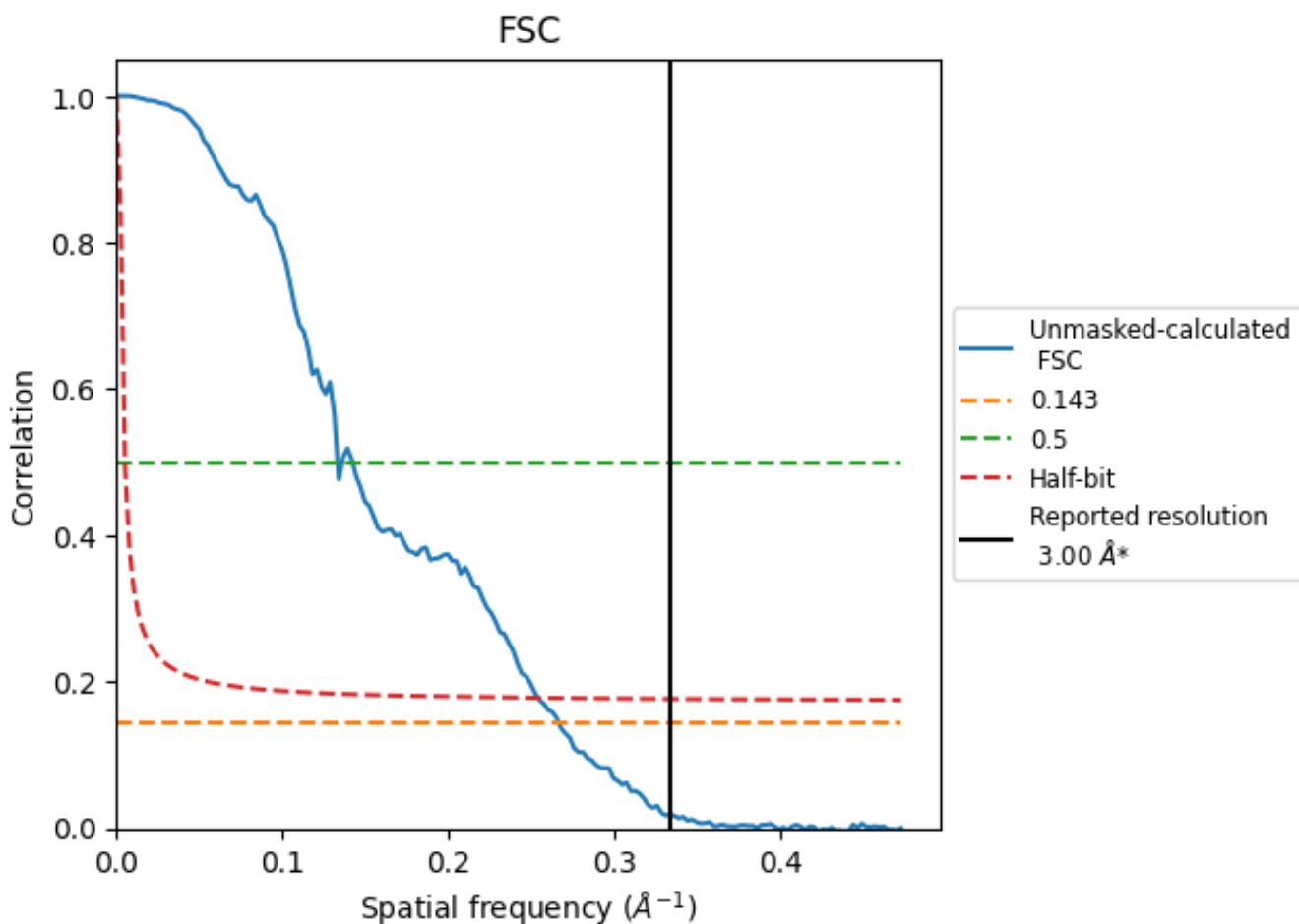


\*Reported resolution corresponds to spatial frequency of  $0.333 \text{ \AA}^{-1}$

## 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 0.333 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

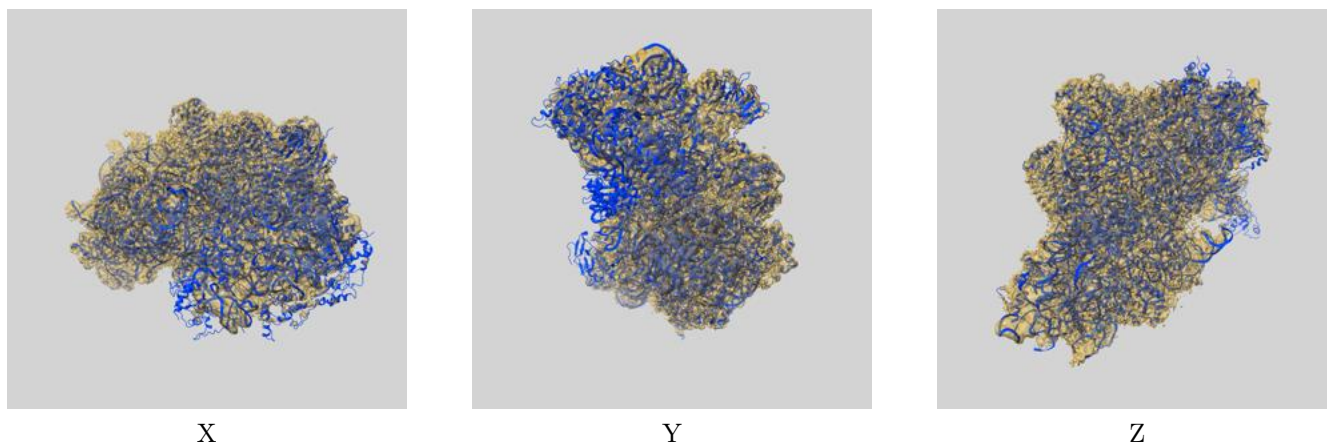
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.76	7.51	3.94

\*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 3.76 differs from the reported value 3.0 by more than 10 %

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

This section contains information regarding the fit between EMDB map EMD-11518 and PDB model 6ZXE. Per-residue inclusion information can be found in section 3 on page 11.

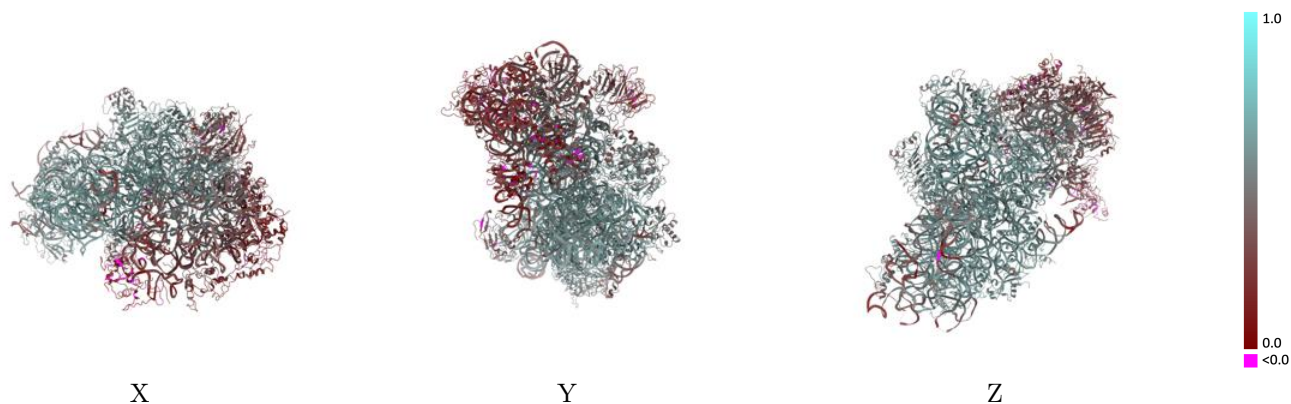
### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.035 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.

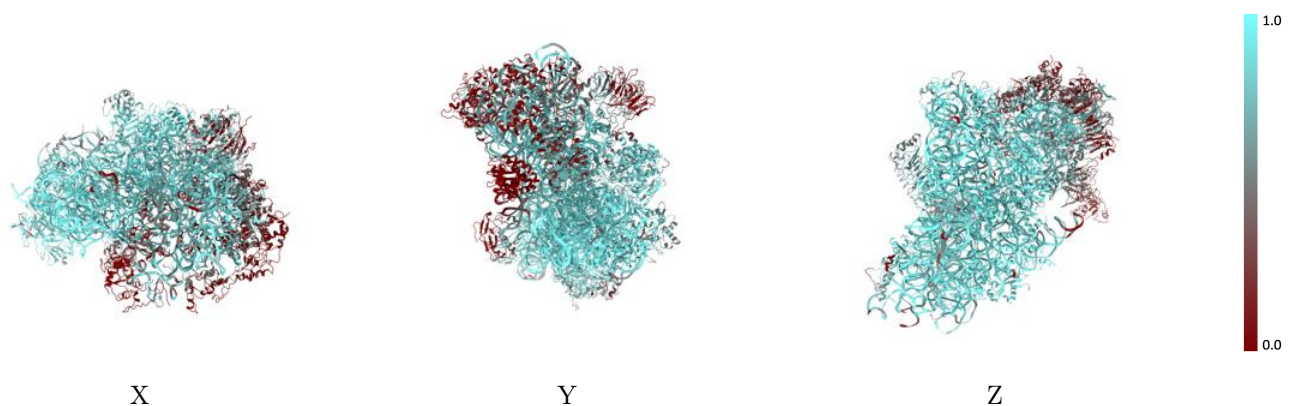


## 9.2 Q-score mapped to coordinate model [i](#)



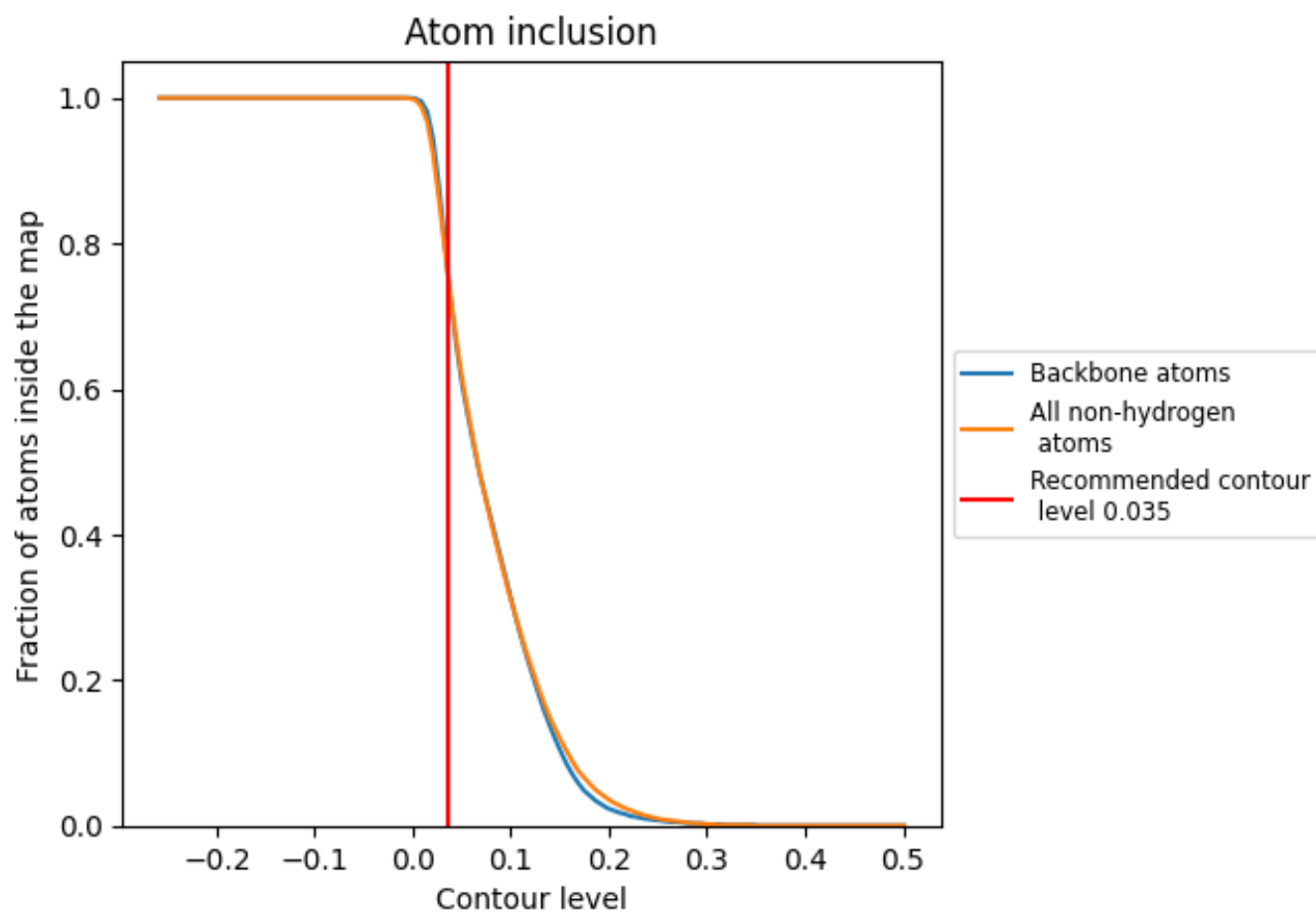
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.035).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 76% 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 (0.035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7650	 0.4810
2	 0.8970	 0.5070
A	 0.9330	 0.5910
B	 0.8630	 0.5590
C	 0.9180	 0.5900
D	 0.5420	 0.3930
E	 0.9290	 0.6010
F	 0.3520	 0.2650
G	 0.8340	 0.5320
H	 0.7750	 0.5010
I	 0.8730	 0.5580
J	 0.9350	 0.5880
K	 0.3410	 0.2780
L	 0.8860	 0.5840
M	 0.0360	 0.1300
N	 0.9250	 0.5840
O	 0.8370	 0.5500
P	 0.2160	 0.2370
Q	 0.5390	 0.3800
R	 0.7460	 0.4810
S	 0.1500	 0.1960
T	 0.2660	 0.2510
U	 0.5000	 0.4310
V	 0.9200	 0.5860
W	 0.9550	 0.6080
X	 0.9350	 0.6010
Y	 0.9200	 0.5840
Z	 0.0600	 0.1540
b	 0.8840	 0.5620
c	 0.2840	 0.2100
d	 0.7690	 0.4700
e	 0.8890	 0.5700
f	 0.1460	 0.1220
g	 0.3500	 0.3100
k	 0.5420	 0.4860



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Chain	Atom inclusion	Q-score
x	 0.8810	 0.5710
y	 0.7950	 0.5100
z	 0.1160	 0.2540