



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 10:38 AM UTC

PDB ID : 6ZXE / pdb_00006zxe
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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

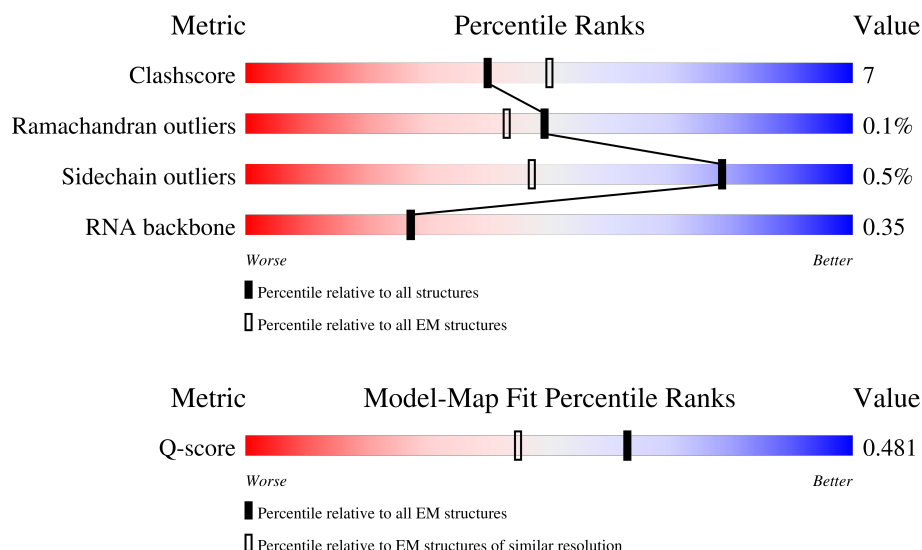
1 Overall quality at a glance i

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.



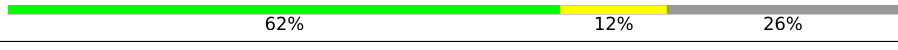
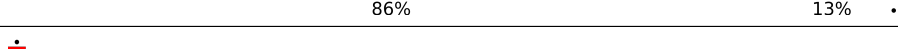
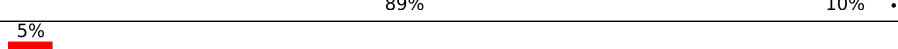
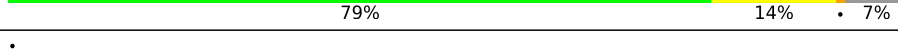
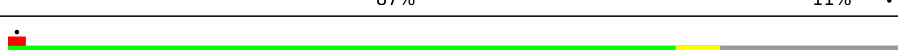
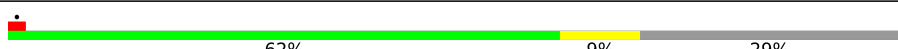
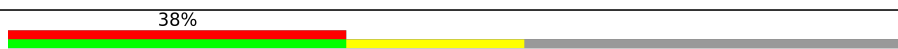
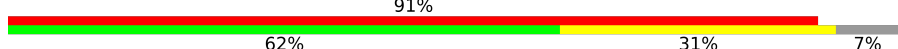
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	2	1873	
2	R	135	
3	A	295	

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Mol	Chain	Length	Quality of chain
4	B	264	
5	C	293	
6	E	263	
7	G	249	
8	H	194	
9	I	208	
10	J	194	
11	L	158	
12	N	151	
13	O	151	
14	V	83	
15	W	130	
16	X	143	
17	Y	133	
18	b	84	
19	e	59	
20	x	252	
21	y	412	
22	d	56	
23	D	243	
24	F	204	
25	K	165	
26	M	132	
27	P	145	
28	Q	146	

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Mol	Chain	Length	Quality of chain
29	S	152	
30	T	145	
31	U	119	
32	Z	125	
33	c	69	
34	f	156	
35	g	317	
36	k	583	
37	z	568	

2 Entry composition

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
1	2	1645	Total	C	N	O	P	0	0
			35125	15677	6304	11499	1645		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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
28	Q	139	Total	C	N	O	S	0	0
			1109	704	210	192	3		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

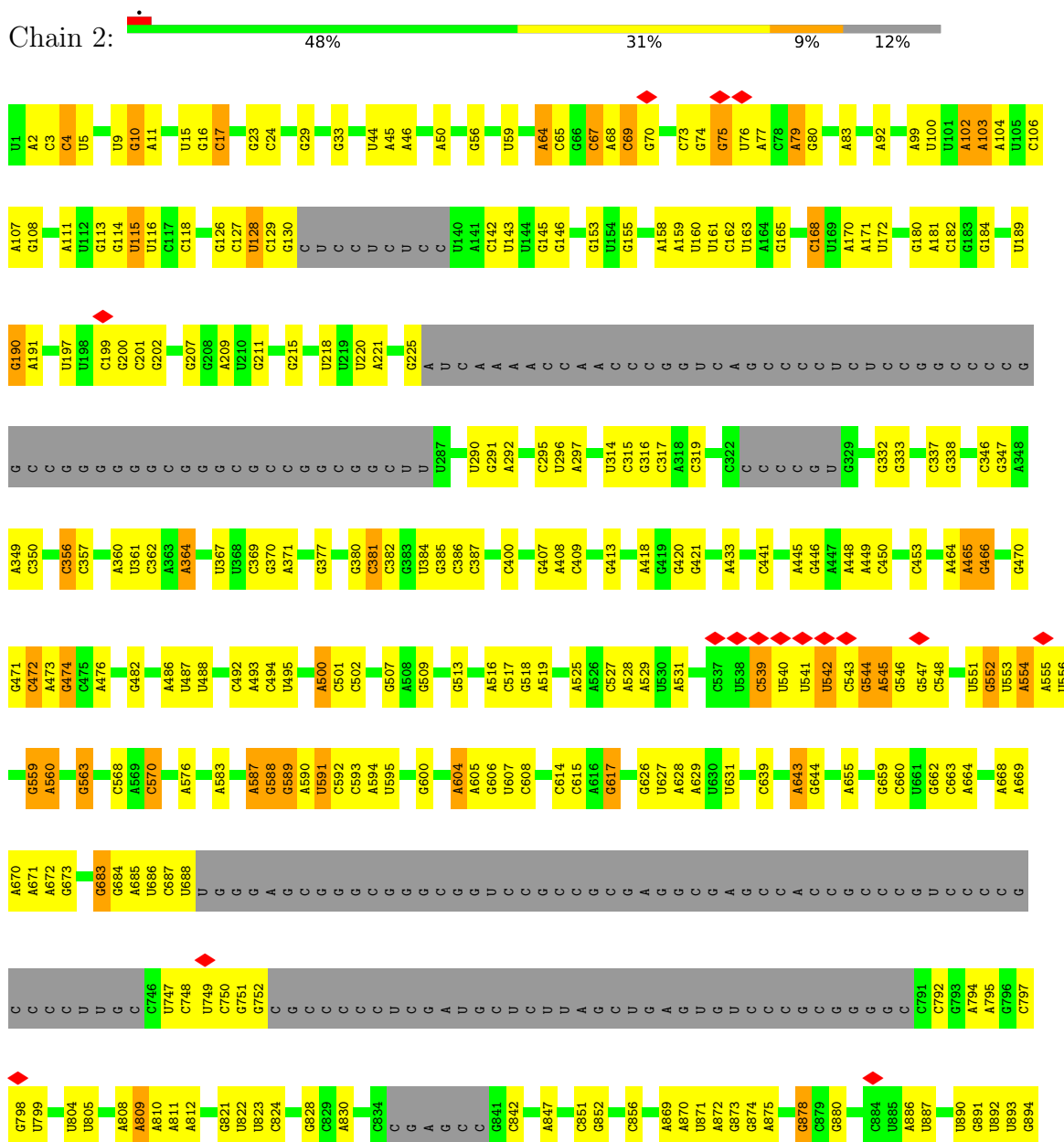
- Molecule 38 is ZINC ION (CCD ID: ZN) (formula: Zn).

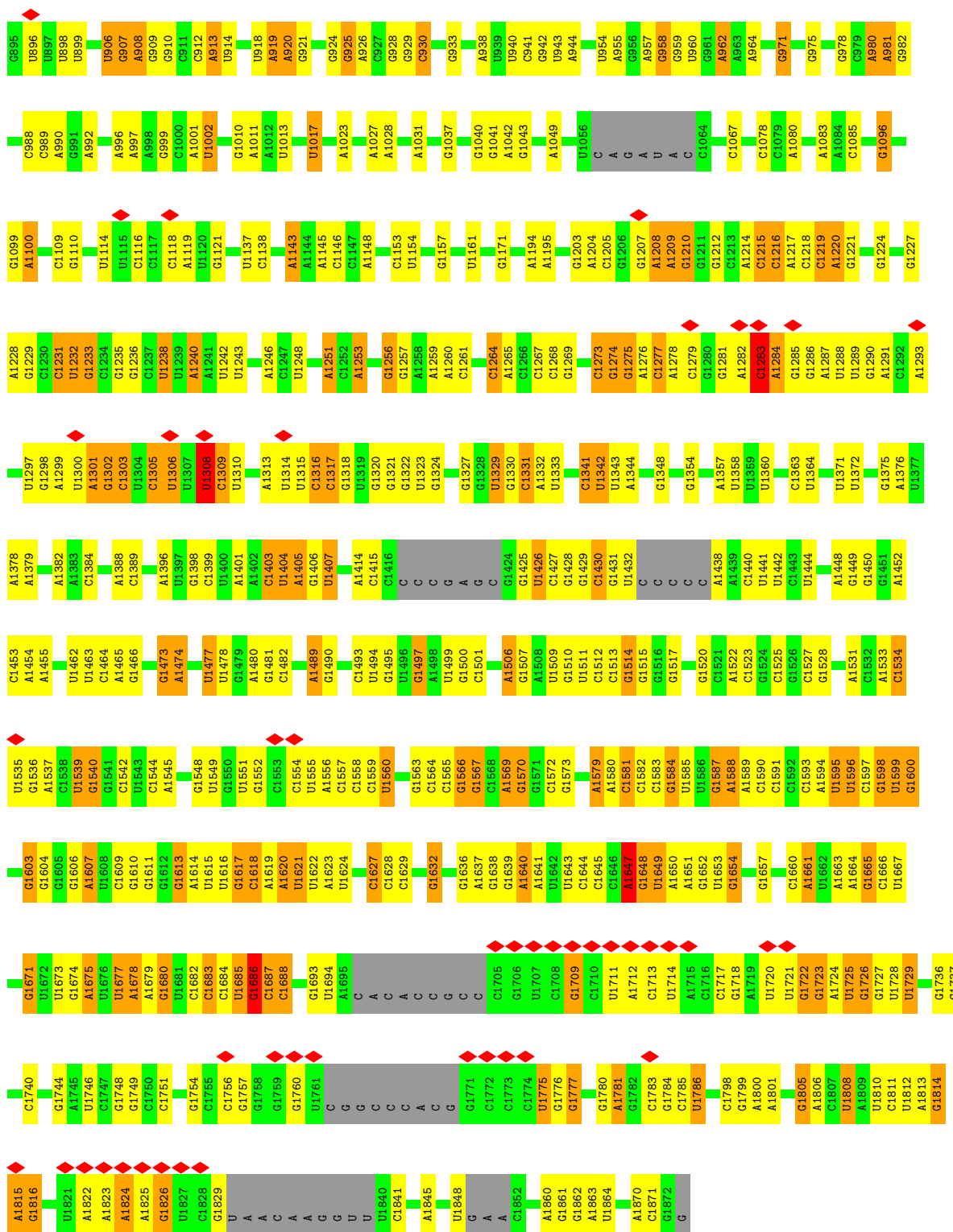
Mol	Chain	Residues	Atoms		AltConf
38	y	1	Total	Zn	0
			1	1	
38	f	1	Total	Zn	0
			1	1	

3 Residue-property plots

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

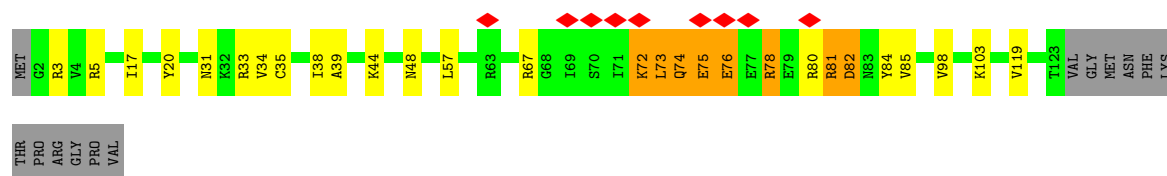
- Molecule 1: pre-18S ribosomal RNA





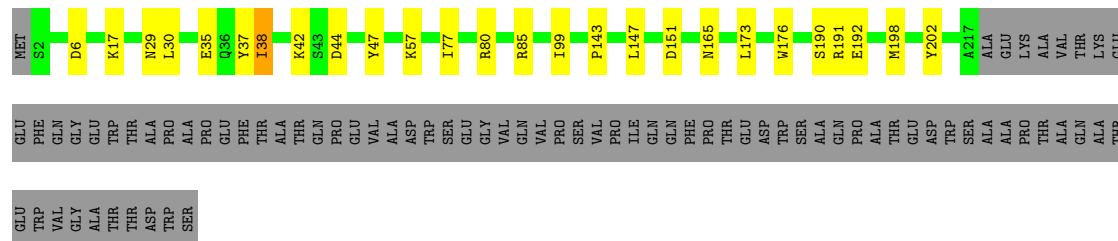
• Molecule 2: 40S ribosomal protein S17





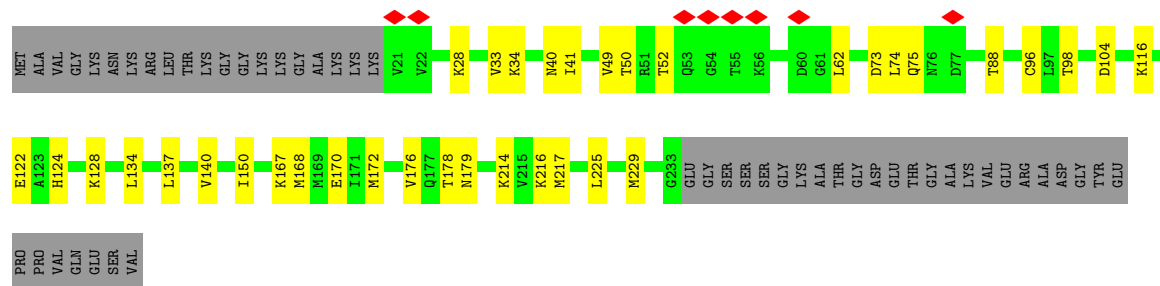
- Molecule 3: 40S ribosomal protein SA

Chain A: 64% 8% 27%



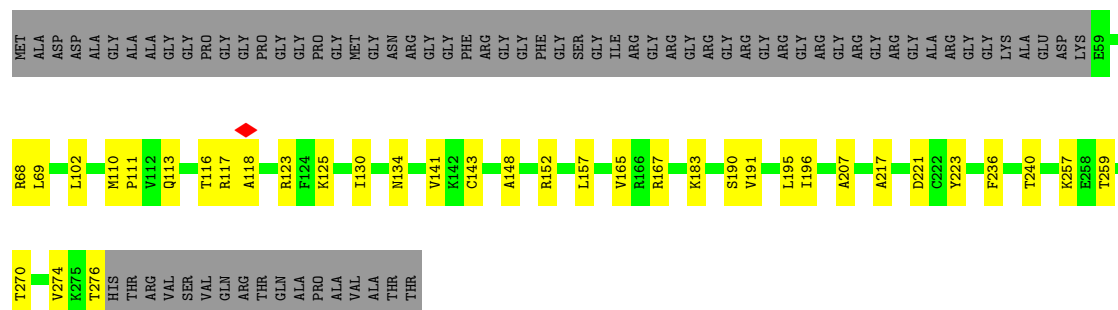
- Molecule 4: 40S ribosomal protein S3a

Chain B: 67% 14% 19%



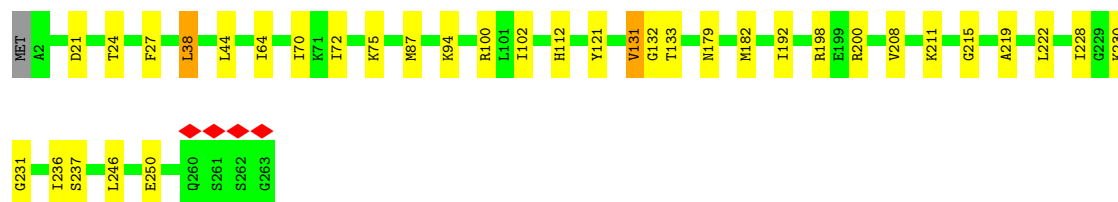
- Molecule 5: 40S ribosomal protein S2

Chain C: 62% 12% 26%

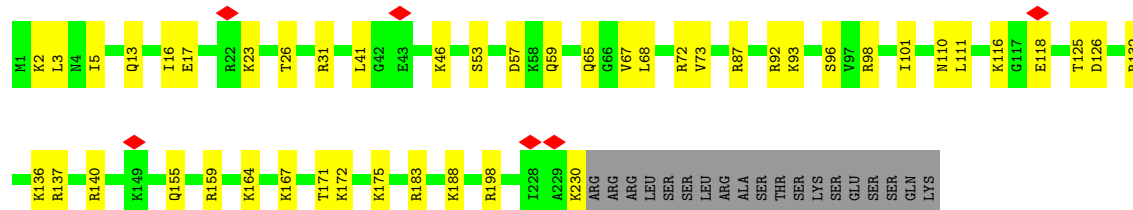


- Molecule 6: 40S ribosomal protein S4, X isoform

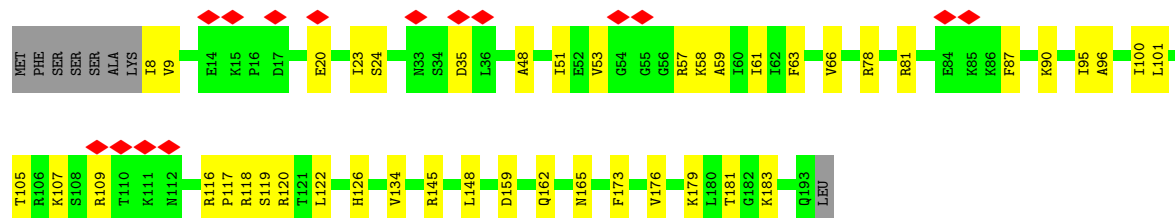
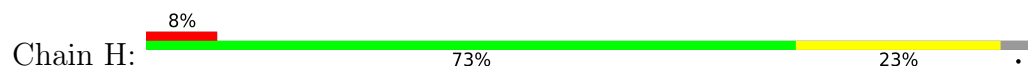
Chain E: 86% 13% 1%



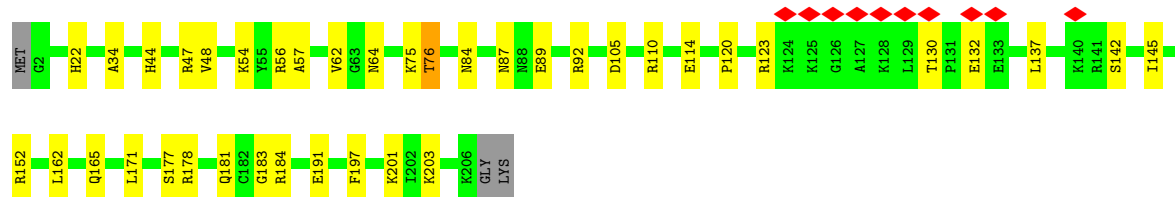
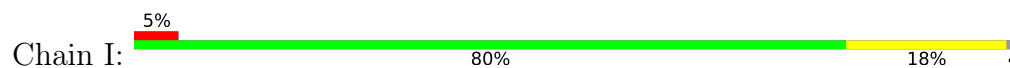
- Molecule 7: 40S ribosomal protein S6



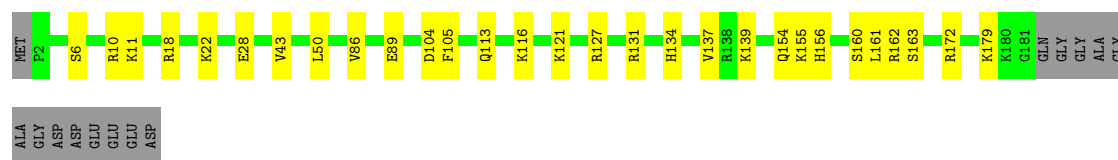
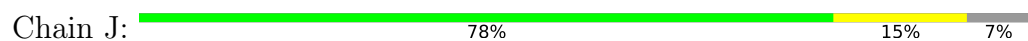
- Molecule 8: 40S ribosomal protein S7



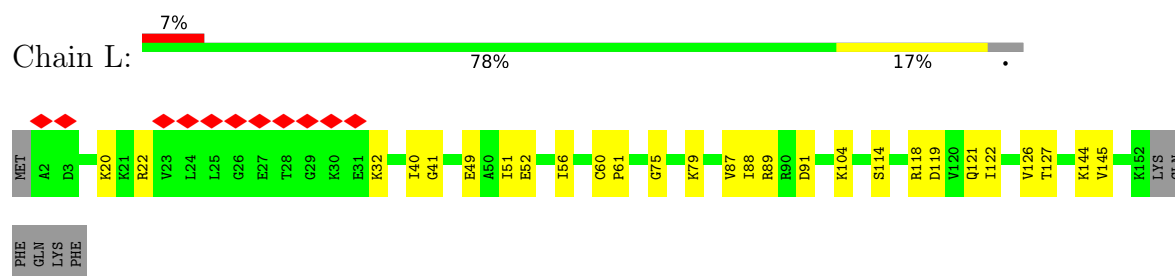
- Molecule 9: 40S ribosomal protein S8



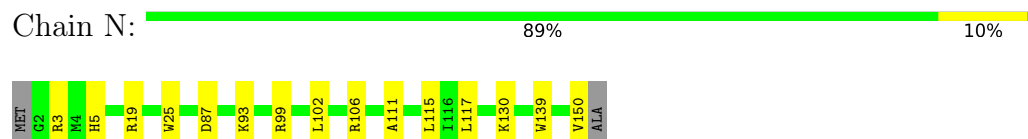
- Molecule 10: 40S ribosomal protein S9



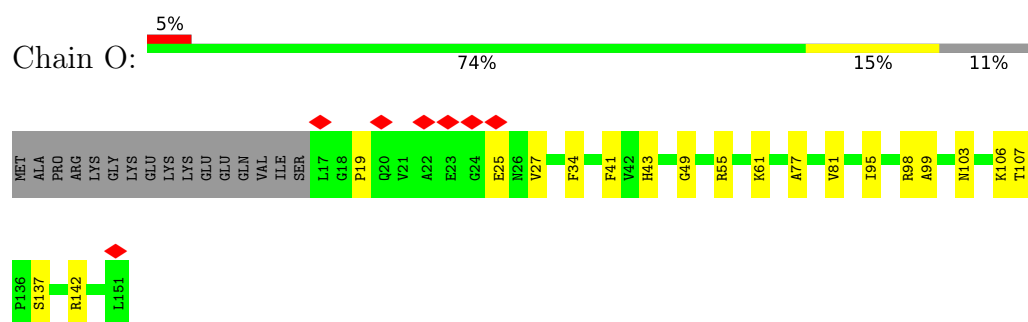
- Molecule 11: 40S ribosomal protein S11



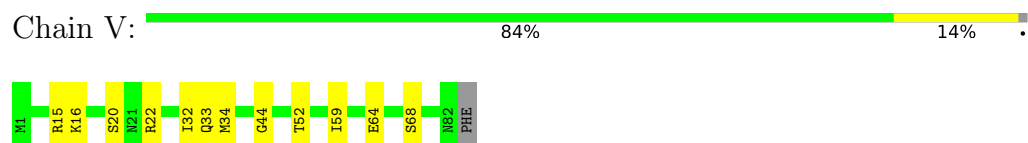
- Molecule 12: 40S ribosomal protein S13



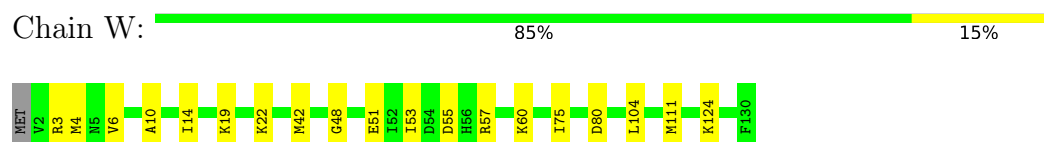
- Molecule 13: 40S ribosomal protein S14



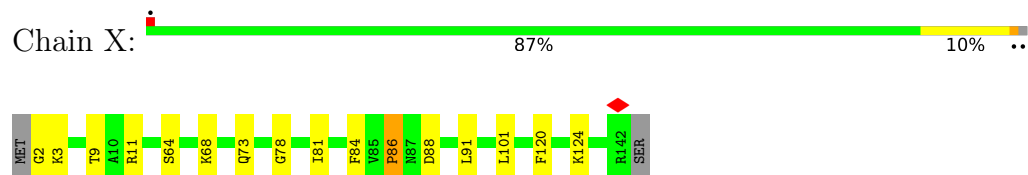
- Molecule 14: 40S ribosomal protein S21



- Molecule 15: 40S ribosomal protein S15a



- Molecule 16: 40S ribosomal protein S23



- Molecule 17: 40S ribosomal protein S24

MET	ASN	D3	T4	V5	R10	K11	I25	D26	V27	L28	H29	T34	T50	P52	D53	V54	I55	K68	P69	G73	M74	I75	E86	R90	R104	G125	ALA	GLY	LYS	LYS	PRO	PRO	LYS	LYS	GLU
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- LYS VAL HTS GLY S5 K11 K26 R31 V45 VAL PRO THR PHE GLY LYS LYS LYS G54 S59

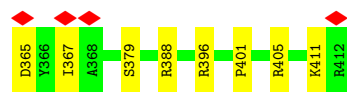
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|-----|
| MET | GLU | SER | GLU | MET | GLU | THR | GLN | SER | ALA | ARG | ALA | GLU | GLY | PHE | THR | GLN | VAL | THR | ARG | LYS | GLY | GLY | ARG | ARG | ALA | LYS | LYS | ARG | GLN | ALA | GLU | LEU | SER | ALA | ALA | GLY | GLY | GLU | GLY | GLY | ASP | THR | GLU | GLU | GLU | ARG | MET | ARG | GLY | ALA | ALA | PRO | ARG | LYS | VAL | PHE |
|-----|

PR0	PR0	LEU	CYS	GLY	ASP	GLY	LEU	LEU	SFR	GLY	LYS	E73	R76	K77	K89	I99	Q106	L111	E117	K122	L130	F136	L150	R154	S162	G187	I194	T198	A205	M217	M220	R242	A243	S246	R247	S248	A249	D250	L250
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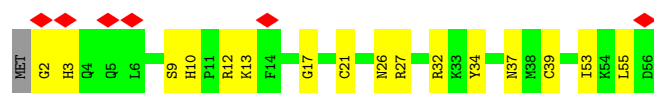
PHE

- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| MET | ALA | PRO | VAL | GLU | HIS | V7 | H17 | A18 | A19 | D22 | N26 | T29 | D39 | K40 | A41 | A47 | V48 | L49 | P50 | Y51 | E52 | D83 | V100 | S101 | H102 | E106 | H118 | P119 | E120 | L130 | P131 | TVR | LYS | PRO | LYS | PRO | PRO | GLN | GLU | THR | GLU | LYS | GLY | HIS | SER | ALA | CYS |
|-----|-----|-----|-----|-----|-----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

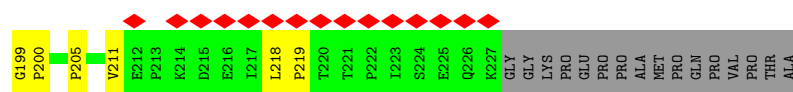
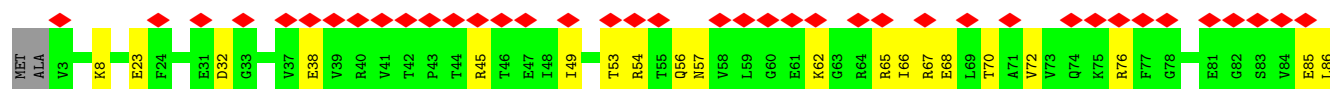
[illegible]



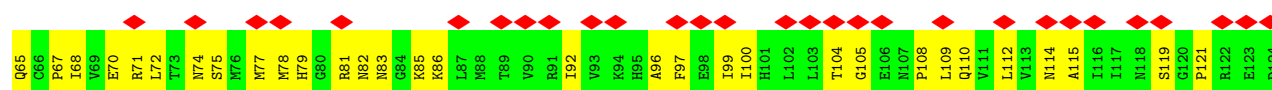
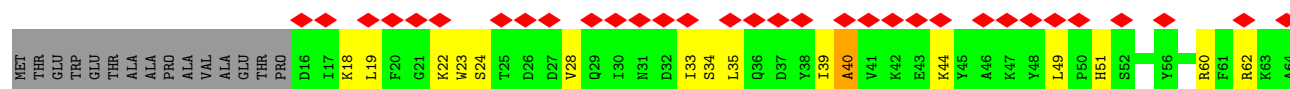
- Molecule 22: 40S ribosomal protein S29



- Molecule 23: 40S ribosomal protein S3

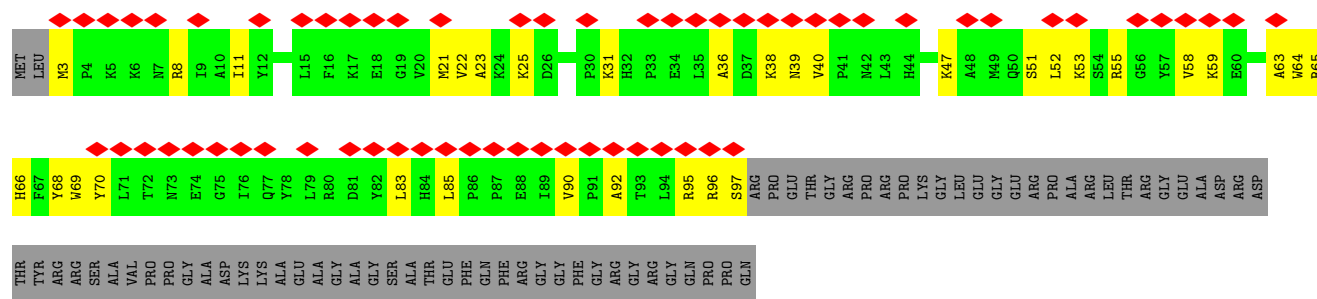


- Molecule 24: 40S ribosomal protein S5

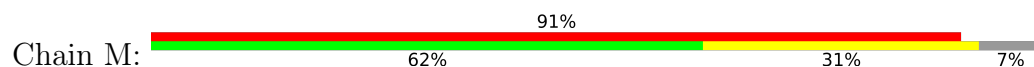


- Molecule 25: 40S ribosomal protein S10

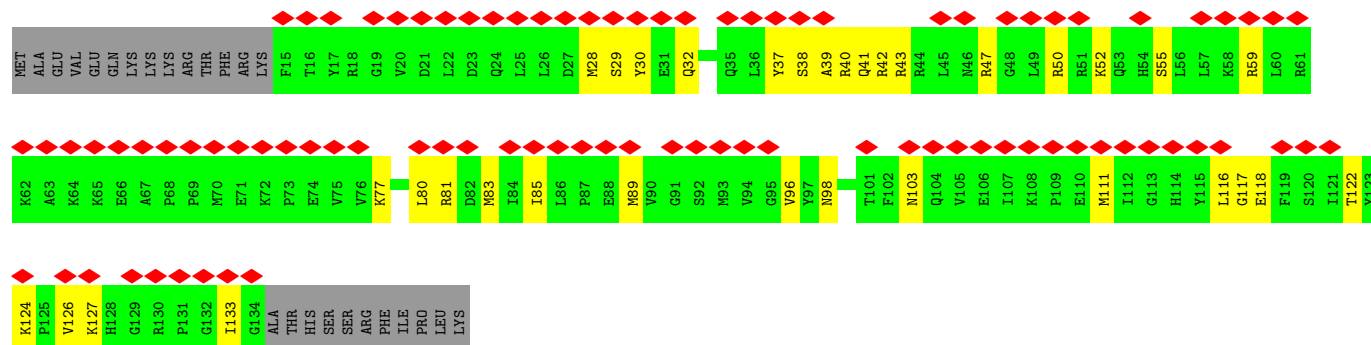




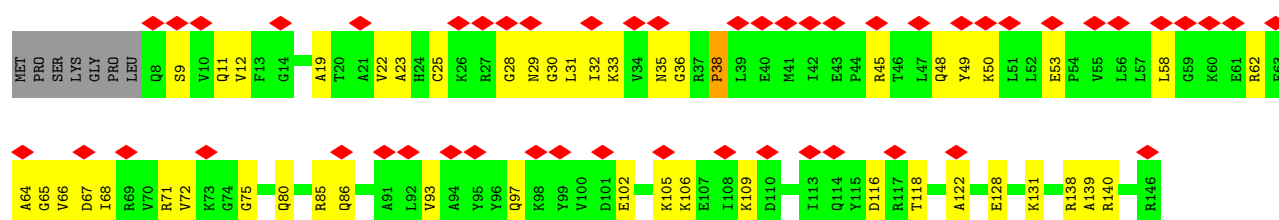
• Molecule 26: 40S ribosomal protein S12



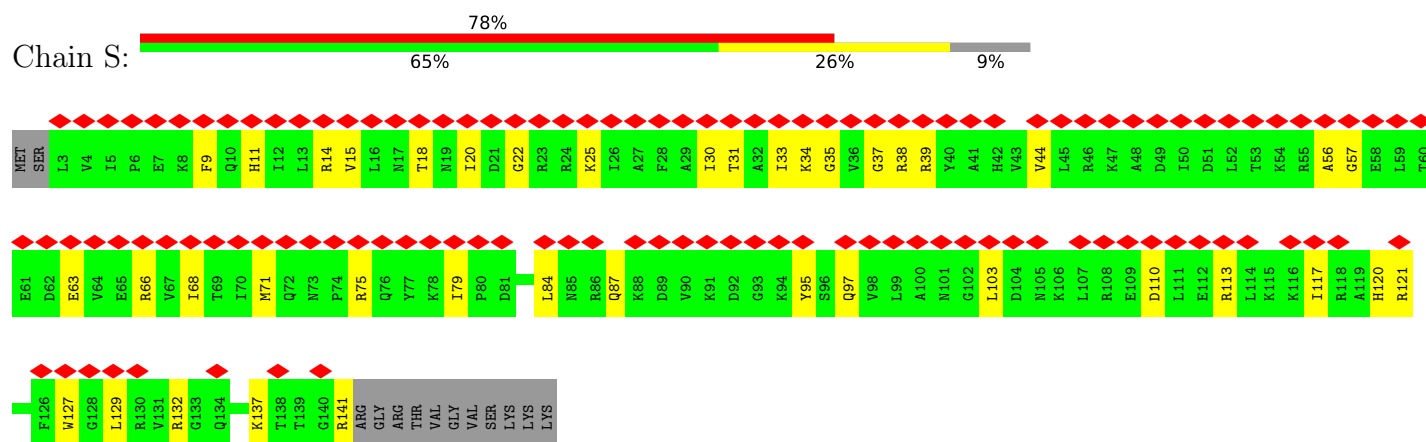
• Molecule 27: 40S ribosomal protein S15



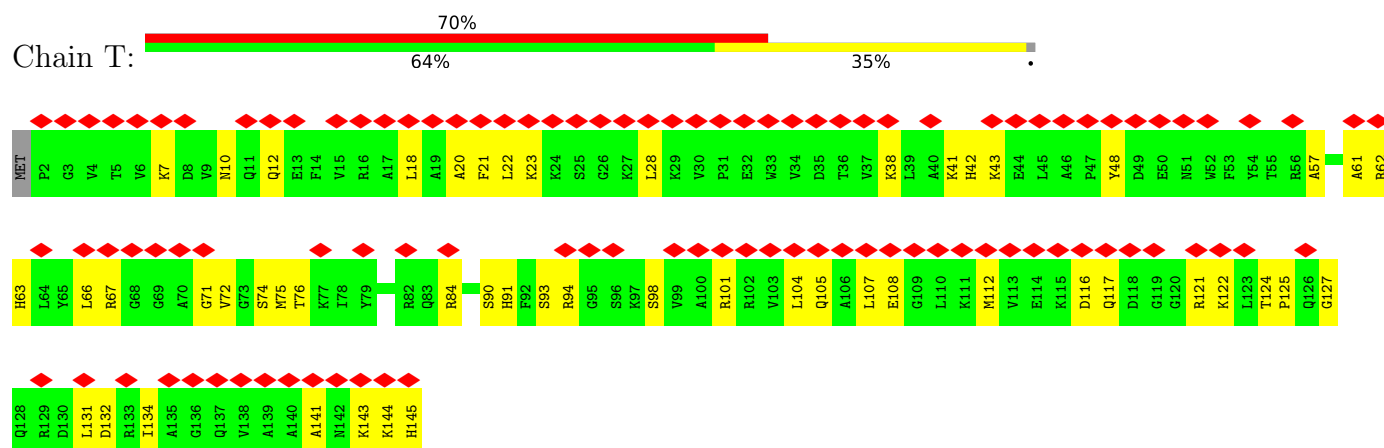
• Molecule 28: 40S ribosomal protein S16



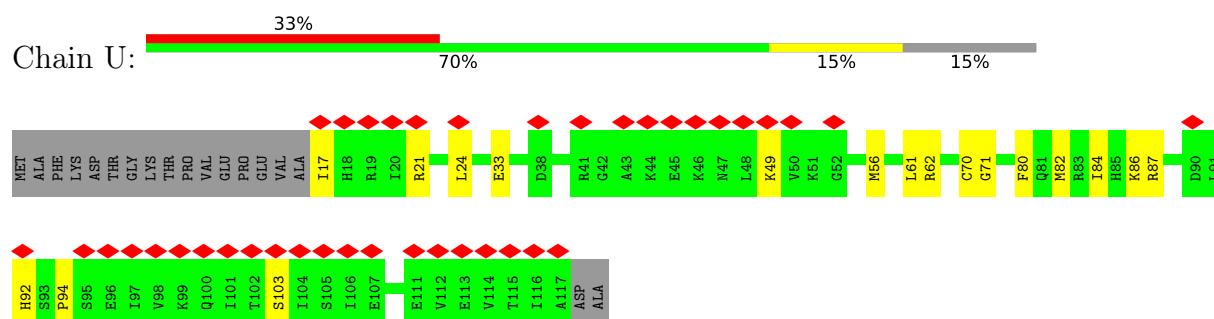
- Molecule 29: 40S ribosomal protein S18



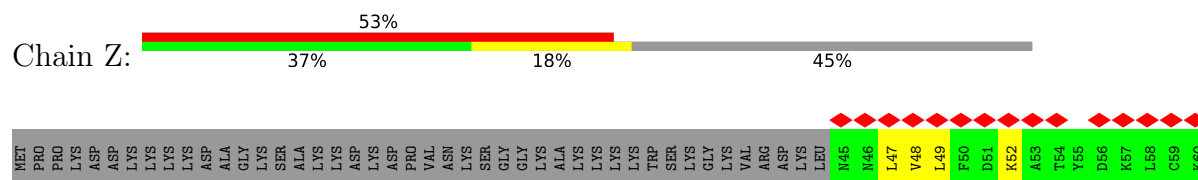
- Molecule 30: 40S ribosomal protein S19

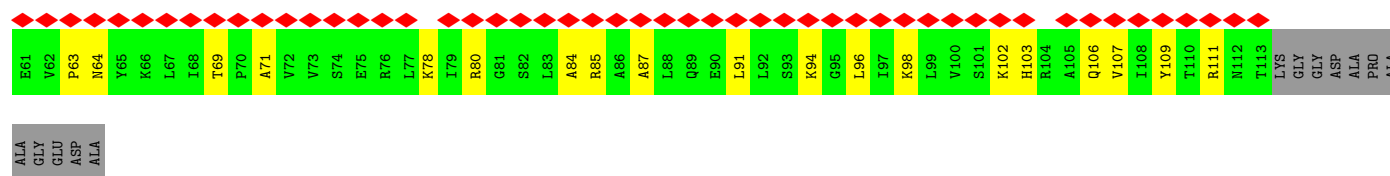


- Molecule 31: 40S ribosomal protein S20

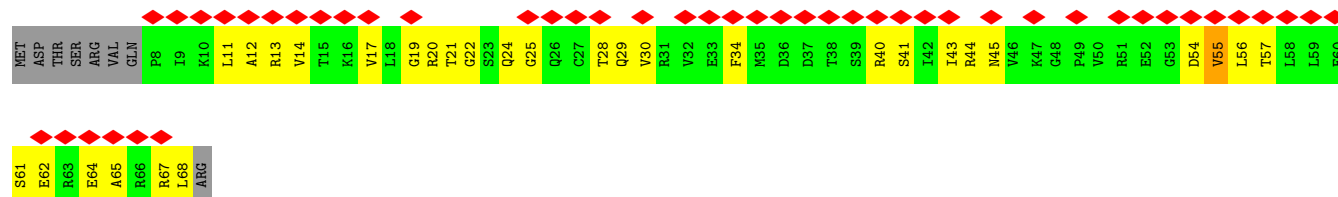


- Molecule 32: 40S ribosomal protein S25

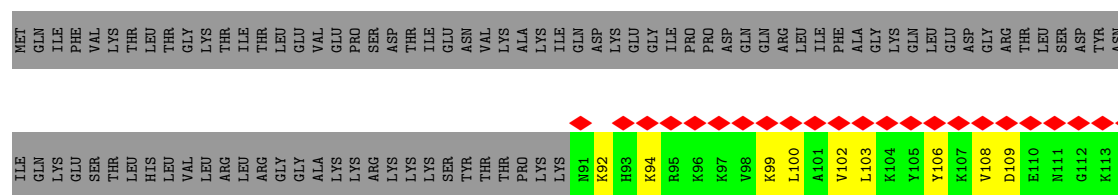




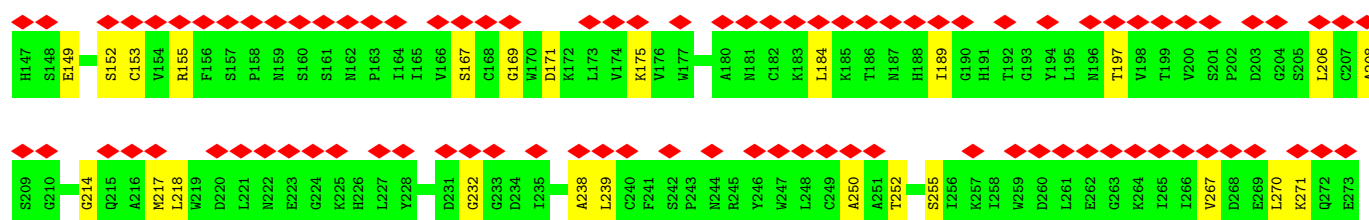
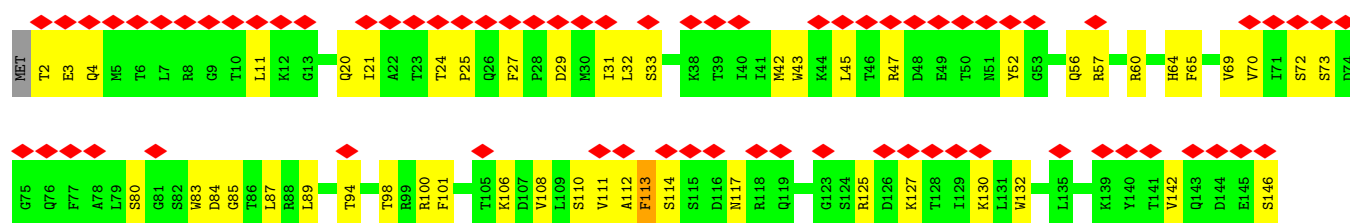
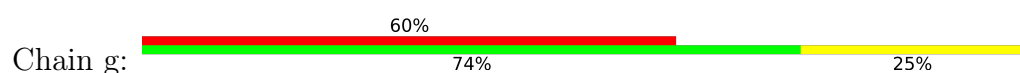
• Molecule 33: 40S ribosomal protein S28

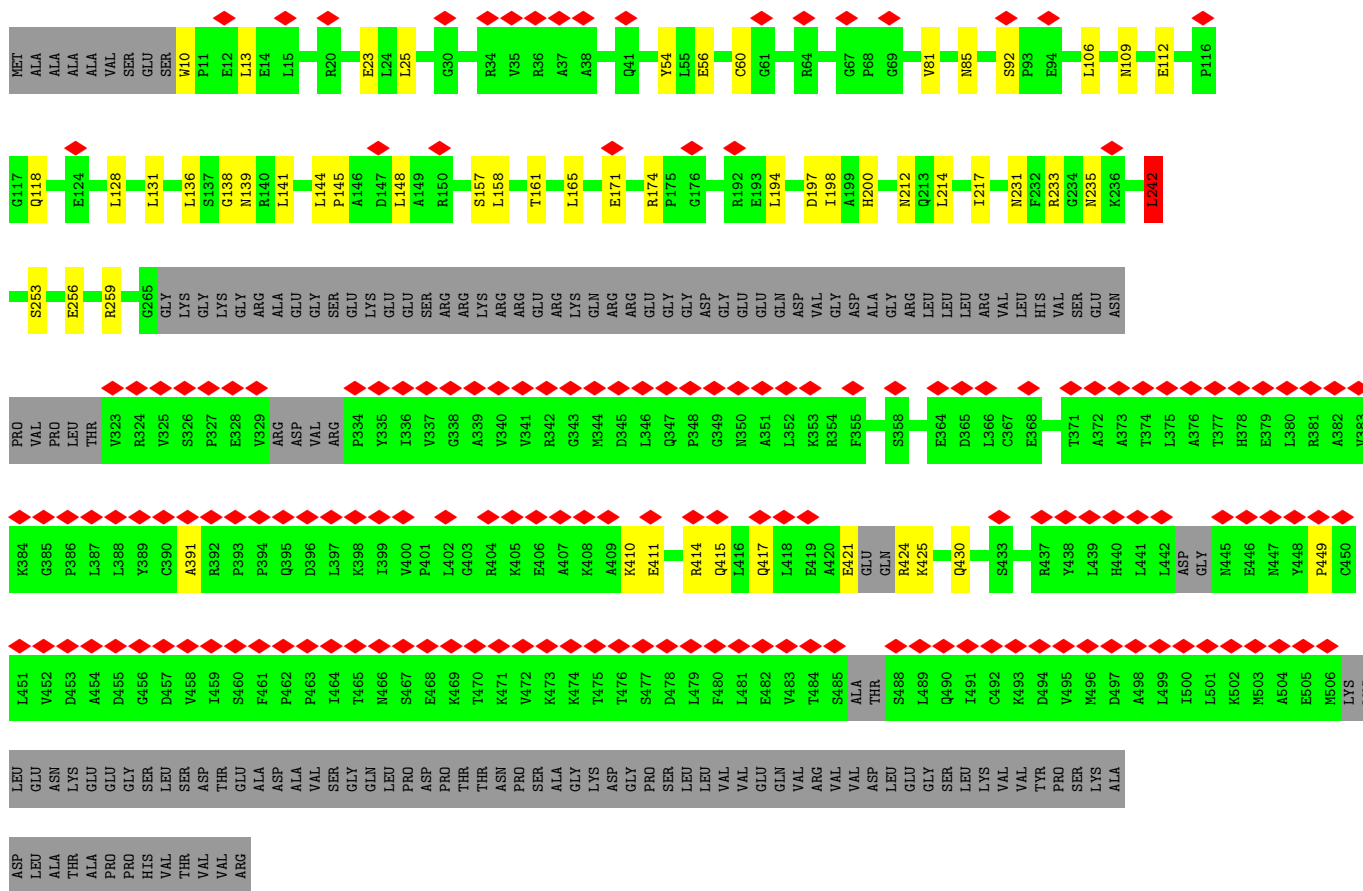


• Molecule 34: Ubiquitin-40S ribosomal protein S27a

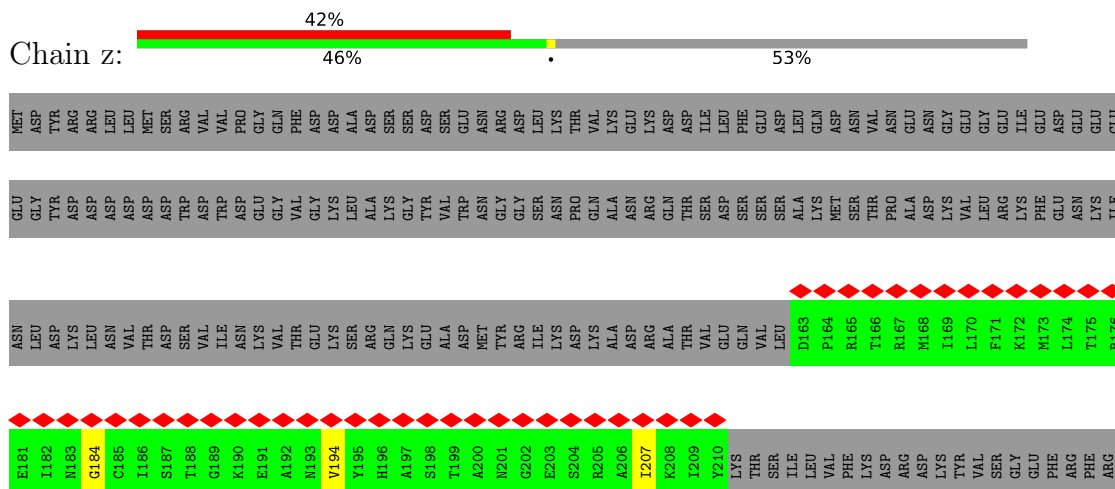


• Molecule 35: Receptor of activated protein C kinase 1





- Molecule 37: Serine/threonine-protein kinase RIO1



GLY LYS	LYS	D421	C361	R301	K241
	VAL	E422	A362	E302	M242
LYS	PRO	E423	N363	L303	V243
	ALA	V424	V364	Y304	K244
LYS	LEU	F425	N365	L305	T245
	GLU	K426	D366	Q306	W246
LYS	ASN	ARG	V307	V307	A247
	GLN		ALA	E248	
LYS	VAL	TYR	F368	I308	K249
	GLU	ILE	M369	Q309	E250
LYS	GLU	PRO	R370	Y310	M251
	ARG	THR	ARG	H371	R252
LYS	CYS	THR	S372	R312	N253
	SER	LEU	LEU	R313	L254
LYS	SER	ASN	V373	M314	I255
	ASP	GLU	A374	Y315	R256
LYS	SER	VAL	V375	Q316	L257
	GLU	LYS	M376	AS18	N258
LYS	ASP	ASN	T377	D317	T259
	ILE	TYR	V378	A318	A260
LYS	GLY	GLU	V379	R319	E261
	SER	ARG	ASP	L320	I262
LYS	SER	GLU	R379	A323	P263
	GLU	MET	E380	D324	C264
LYS	CYS	ASP	L381	L325	P265
	SER	ILE	F382	S326	E266
LYS	THR	ILE	E383	E327	P267
	ASP	MET	F384	F328	I268
LYS	SER	LYS	V385	N329	M269
	GLU	LEU	T386	M330	L270
LYS	GLU	GLU	D387	L331	R271
	GLN	GLY	P388	Y332	S272
LYS	GLY	ASP	S389	H333	H273
	HIS	MET	I390	G334	V274
LYS	ALA	ASN	T391	G335	L275
	ARG	ASN	H392	G336	V276
LYS	PRO	ALA	ASP	V337	M277
	LYS	GLN	N394	Y338	S278
LYS	HIS	ASP	M395	I339	F279
	THR	ILE	D396	I340	I280
LYS	THR	LEU	A397	D341	G281
	ASP	TYR	Y398	V342	K282
LYS	ASP	GLN	L399	S343	D283
	ILE	THR	S400	Q344	D284
LYS	K531	VAL	K401	S345	M285
	E559	THR	A402	V346	P286
LYS	LYS	GLY	A406	E347	A287
	THR	LEU	S407	H348	P288
LYS	ALA	GLN	Q408	L289	L289
	LYS	LYS	R409	H350	L290
LYS	LYS	LYS	T410	P351	K291
	THR	ASP	E412	H352	N292
LYS	THR	ASP	E413	A353	V293
	LYS	LEU	R414	L354	Q294
LYS	LYS	SER	S415	E355	L295
	LYS	GLY	S416	F356	S296
LYS	LYS	VAL	Q417	L357	E297
	LYS	GLN	D418	R358	S298
LYS	LYS	GLN	H419	K359	K299
	LYS	GLN	V420	D360	A300

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 ⓘ

5.1 Standard geometry ⓘ

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	0.51	0/39273	0.54	7/61196 (0.0%)
2	R	0.48	0/1002	0.74	0/1345
3	A	0.53	0/1742	0.59	0/2367
4	B	0.45	0/1756	0.57	0/2350
5	C	0.53	0/1726	0.66	0/2332
6	E	0.53	0/2118	0.57	0/2849
7	G	0.42	0/1885	0.55	0/2510
8	H	0.40	0/1524	0.57	0/2042
9	I	0.49	0/1711	0.58	0/2282
10	J	0.53	0/1524	0.62	2/2035 (0.1%)
11	L	0.53	0/1250	0.57	1/1673 (0.1%)
12	N	0.46	0/1226	0.52	0/1649
13	O	0.44	0/1022	0.60	0/1372
14	V	0.51	0/631	0.52	0/844
15	W	0.58	0/1051	0.61	0/1406
16	X	0.52	0/1116	0.58	0/1490
17	Y	0.51	0/1031	0.56	0/1370
18	b	0.45	0/653	0.56	0/876
19	e	0.44	0/377	0.51	0/493
20	x	0.46	0/1413	0.60	0/1906
21	y	0.41	0/2283	0.57	0/3106
22	d	0.31	0/470	0.50	0/623
23	D	0.30	0/1780	0.58	0/2397
24	F	0.30	0/1516	0.63	0/2037
25	K	0.28	0/824	0.59	0/1112
26	M	0.26	0/963	0.55	0/1291
27	P	0.28	0/1003	0.59	0/1341
28	Q	0.32	0/1126	0.63	0/1506
29	S	0.26	0/1169	0.58	0/1567
30	T	0.26	0/1142	0.53	0/1530
31	U	0.32	0/813	0.54	0/1092
32	Z	0.27	0/555	0.64	0/747

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	c	0.31	0/481	0.69	0/643
34	f	0.23	0/487	0.57	0/646
35	g	0.26	0/2496	0.54	0/3398
36	k	0.31	0/2920	0.55	1/3977 (0.0%)
37	z	0.24	0/1314	0.57	0/1830
All	All	0.46	0/85373	0.56	11/123230 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
23	D	0	1
24	F	0	2
28	Q	0	1
All	All	0	4

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1256	G	C2'-C3'-O3'	10.84	125.76	109.50
10	J	137	VAL	CA-C-N	6.70	134.34	121.54
10	J	137	VAL	C-N-CA	6.70	134.34	121.54
11	L	41	GLY	N-CA-C	6.12	119.90	112.49
1	2	1686	G	C2'-C3'-O3'	5.84	122.47	113.70

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 ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	35125	0	17734	360	0
2	R	990	0	1037	32	0
3	A	1705	0	1706	17	0
4	B	1729	0	1803	22	0
5	C	1690	0	1777	27	0
6	E	2076	0	2177	24	0
7	G	1862	0	2018	40	0
8	H	1501	0	1593	31	0
9	I	1682	0	1769	29	0
10	J	1499	0	1618	20	0
11	L	1229	0	1302	15	0
12	N	1202	0	1289	12	0
13	O	1009	0	1034	16	0
14	V	625	0	628	9	0
15	W	1034	0	1080	16	0
16	X	1098	0	1167	12	0
17	Y	1014	0	1082	11	0
18	b	640	0	665	7	0
19	e	375	0	409	3	0
20	x	1391	0	1467	17	0
21	y	2246	0	1980	26	0
22	d	459	0	452	13	0
23	D	1752	0	1848	41	0
24	F	1495	0	1549	63	0
25	K	800	0	818	26	0
26	M	953	0	990	26	0
27	P	984	0	1028	30	0
28	Q	1109	0	1174	34	0
29	S	1151	0	1208	27	0
30	T	1122	0	1153	39	0
31	U	803	0	873	13	0
32	Z	549	0	599	20	0
33	c	479	0	507	29	0
34	f	478	0	484	16	0
35	g	2439	0	2393	53	0
36	k	2886	0	2563	33	0
37	z	1317	0	577	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	f	1	0	0	0	0
38	y	1	0	0	0	0
All	All	80500	0	63551	1003	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 1003 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1622:U:H3	27:P:122:THR:HG1	1.12	0.97
1:2:1748:G:H1	1:2:1786:U:H3	1.13	0.95
2:R:74:GLN:O	2:R:74:GLN:HG2	1.66	0.93
1:2:1657:G:H1	1:2:1667:U:H3	0.94	0.91
2:R:78:ARG:HG2	2:R:78:ARG:HH11	1.43	0.84

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	R	120/135 (89%)	109 (91%)	10 (8%)	1 (1%)	16	50
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	J	178/194 (92%)	162 (91%)	15 (8%)	1 (1%)	21	56
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%)	18	53
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%)	21	56
21	y	319/412 (77%)	293 (92%)	25 (8%)	1 (0%)	36	70
22	d	53/56 (95%)	48 (91%)	5 (9%)	0	100	100
23	D	223/243 (92%)	210 (94%)	13 (6%)	0	100	100
24	F	187/204 (92%)	162 (87%)	24 (13%)	1 (0%)	24	60
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%)	18	53
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%)	49	80

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 ⓘ

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%)	102 (93%)	8 (7%)	13	42
3	A	180/243 (74%)	179 (99%)	1 (1%)	78	88
4	B	194/231 (84%)	193 (100%)	1 (0%)	81	89
5	C	184/225 (82%)	184 (100%)	0	100	100
6	E	224/225 (100%)	222 (99%)	2 (1%)	70	85
7	G	200/218 (92%)	200 (100%)	0	100	100
8	H	167/174 (96%)	167 (100%)	0	100	100
9	I	178/180 (99%)	177 (99%)	1 (1%)	78	88
10	J	160/168 (95%)	159 (99%)	1 (1%)	78	88
11	L	135/142 (95%)	133 (98%)	2 (2%)	57	80
12	N	130/131 (99%)	130 (100%)	0	100	100
13	O	105/119 (88%)	104 (99%)	1 (1%)	68	84
14	V	66/67 (98%)	66 (100%)	0	100	100
15	W	112/113 (99%)	111 (99%)	1 (1%)	70	85
16	X	113/115 (98%)	112 (99%)	1 (1%)	70	85
17	Y	108/115 (94%)	107 (99%)	1 (1%)	70	85
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%)	68	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	d	48/49 (98%)	48 (100%)	0	100	100
23	D	189/202 (94%)	189 (100%)	0	100	100
24	F	159/170 (94%)	159 (100%)	0	100	100
25	K	86/136 (63%)	86 (100%)	0	100	100
26	M	104/108 (96%)	104 (100%)	0	100	100
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%)	114 (100%)	0	100	100
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%)	50	76
34	f	52/140 (37%)	52 (100%)	0	100	100
35	g	271/275 (98%)	270 (100%)	1 (0%)	84	90
36	k	231/487 (47%)	230 (100%)	1 (0%)	84	90
All	All	4627/5624 (82%)	4602 (100%)	25 (0%)	78	89

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	L	56	ILE
15	W	104	LEU
36	k	242	LEU
13	O	25	GLU
16	X	9	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 83 such sidechains are listed below:

Mol	Chain	Res	Type
27	P	79	HIS
35	g	119	GLN
28	Q	80	GLN
32	Z	64	ASN
36	k	78	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1631/1873 (87%)	493 (30%)	42 (2%)

5 of 493 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 ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 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.

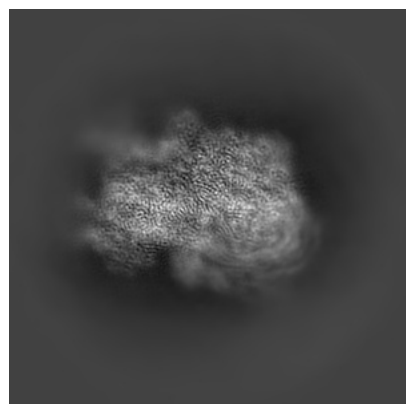
6 Map visualisation [i](#)

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.

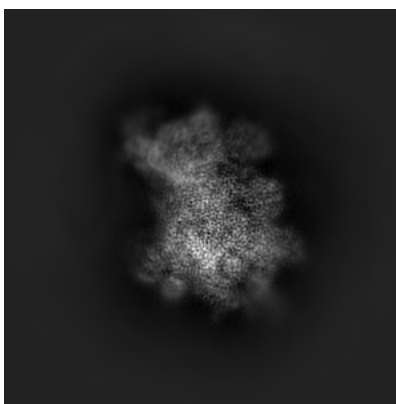
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

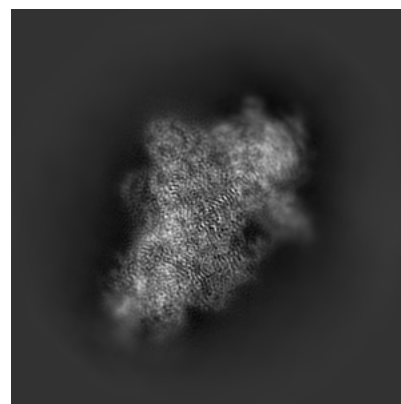
6.1.1 Primary map



X

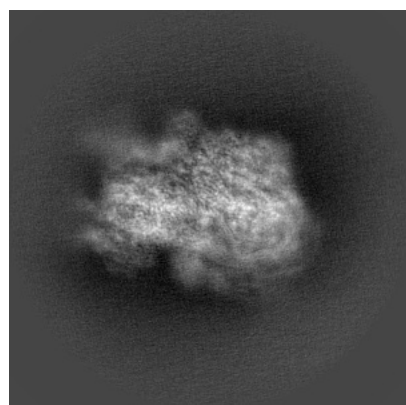


Y

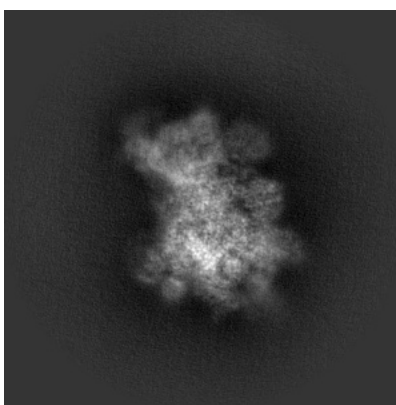


Z

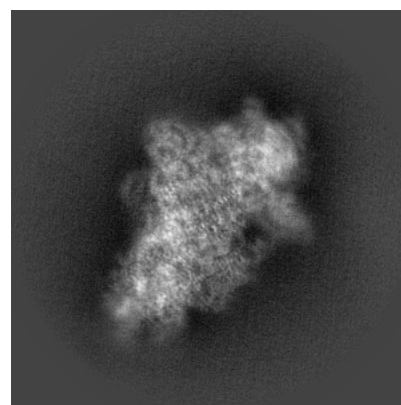
6.1.2 Raw map



X



Y

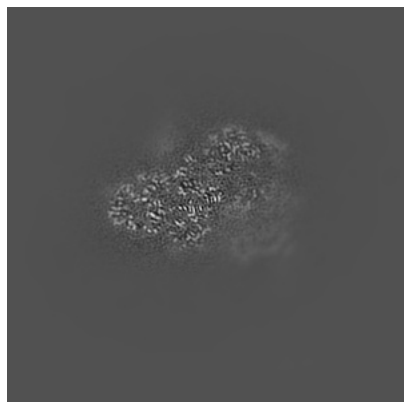


Z

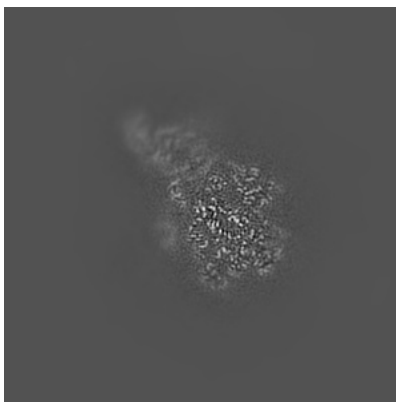
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

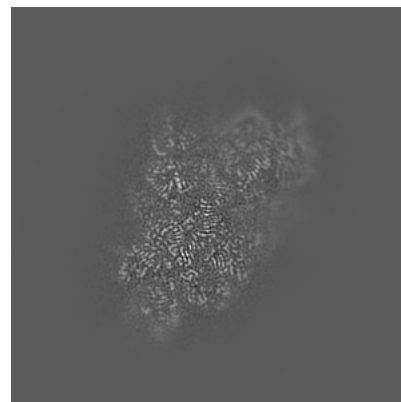
6.2.1 Primary map



X Index: 180

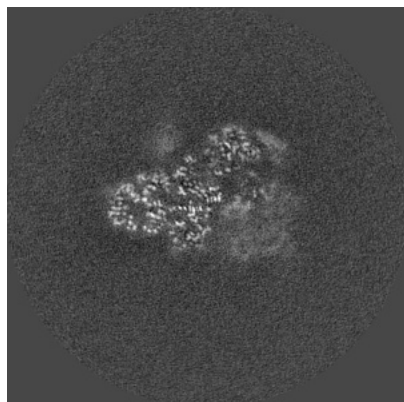


Y Index: 180

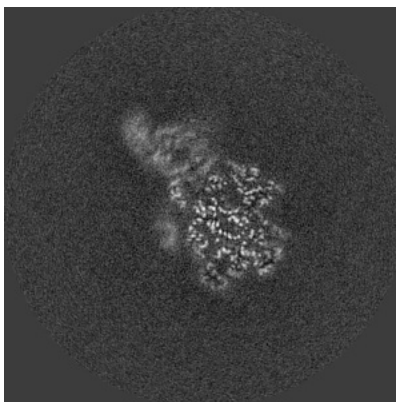


Z Index: 180

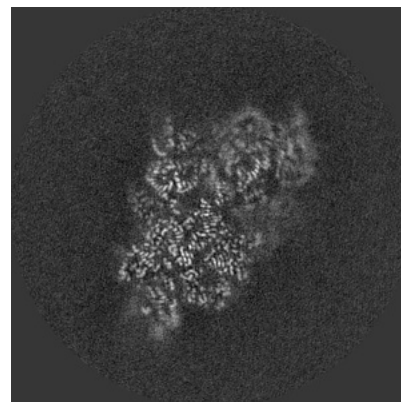
6.2.2 Raw map



X Index: 180



Y Index: 180

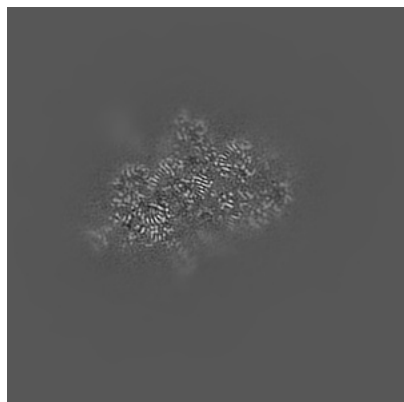


Z Index: 180

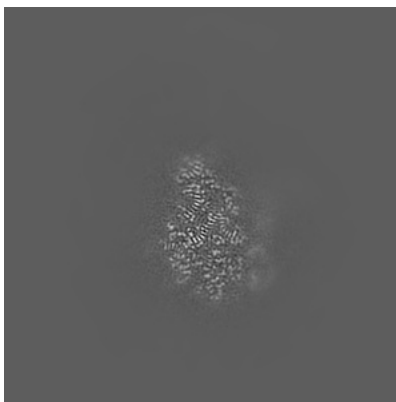
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

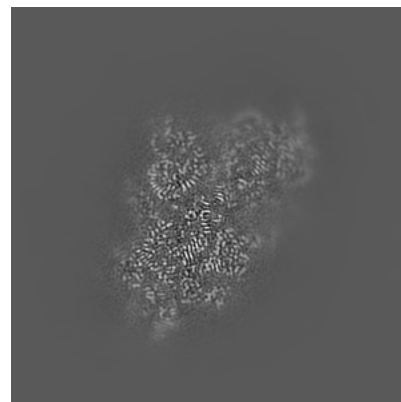
6.3.1 Primary map



X Index: 155

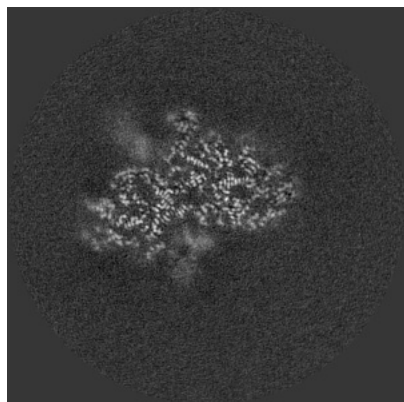


Y Index: 134

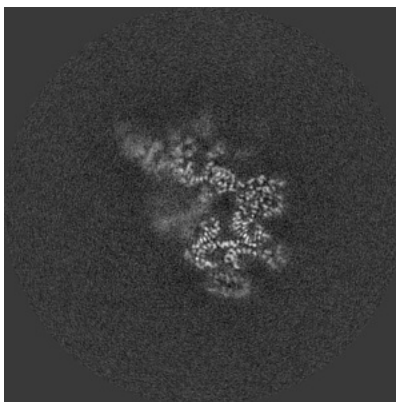


Z Index: 182

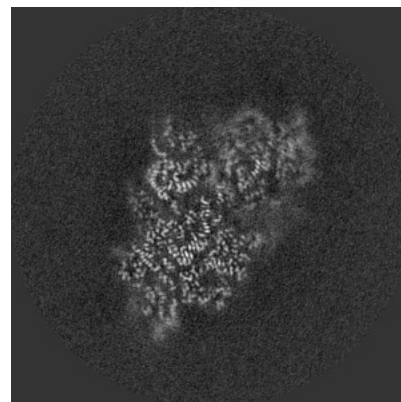
6.3.2 Raw map



X Index: 147



Y Index: 199

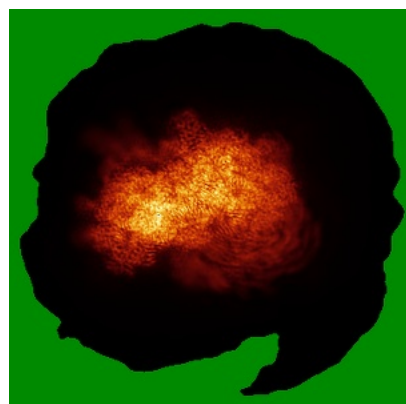


Z Index: 181

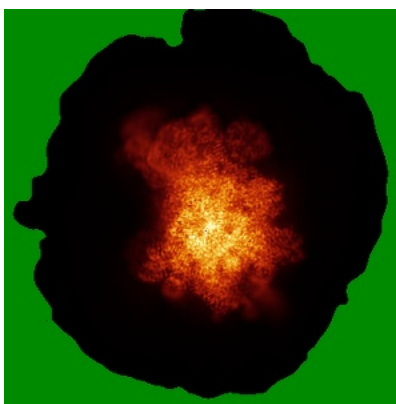
The images above show the largest variance slices of the map in three orthogonal directions.

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

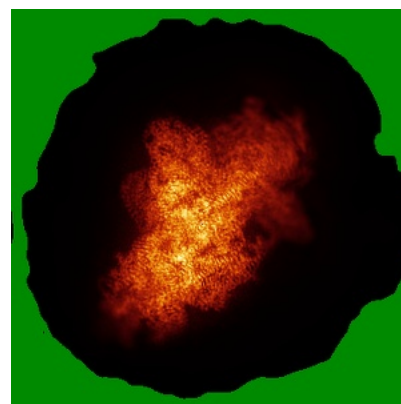
6.4.1 Primary map



X

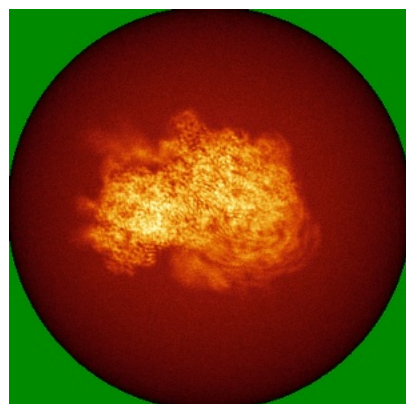


Y

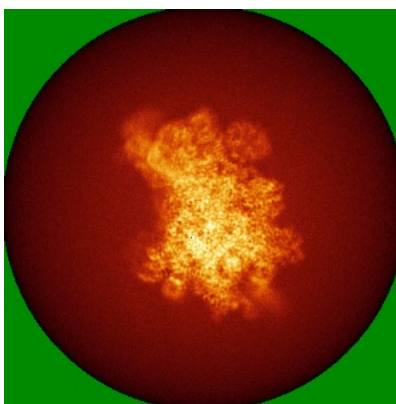


Z

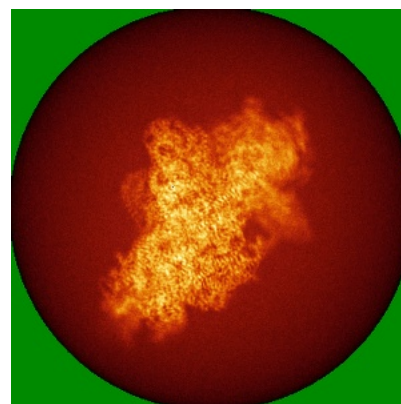
6.4.2 Raw map



X



Y



Z

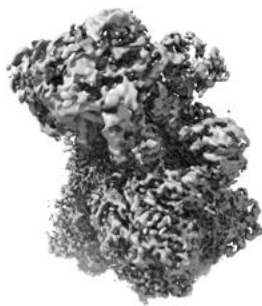
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

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.

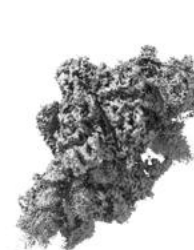
6.5.2 Raw map



X



Y



Z

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.

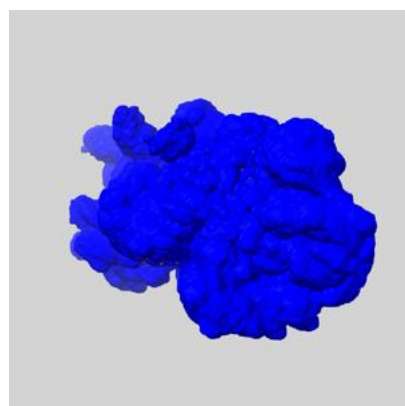
6.6 Mask visualisation [i](#)

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

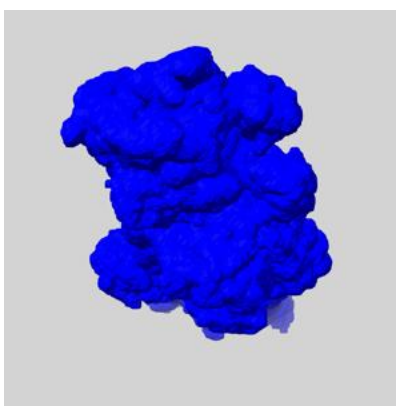
A mask typically either:

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

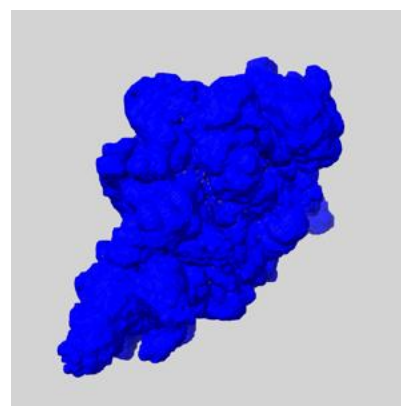
6.6.1 emd_11518_msk_1.map [i](#)



X



Y

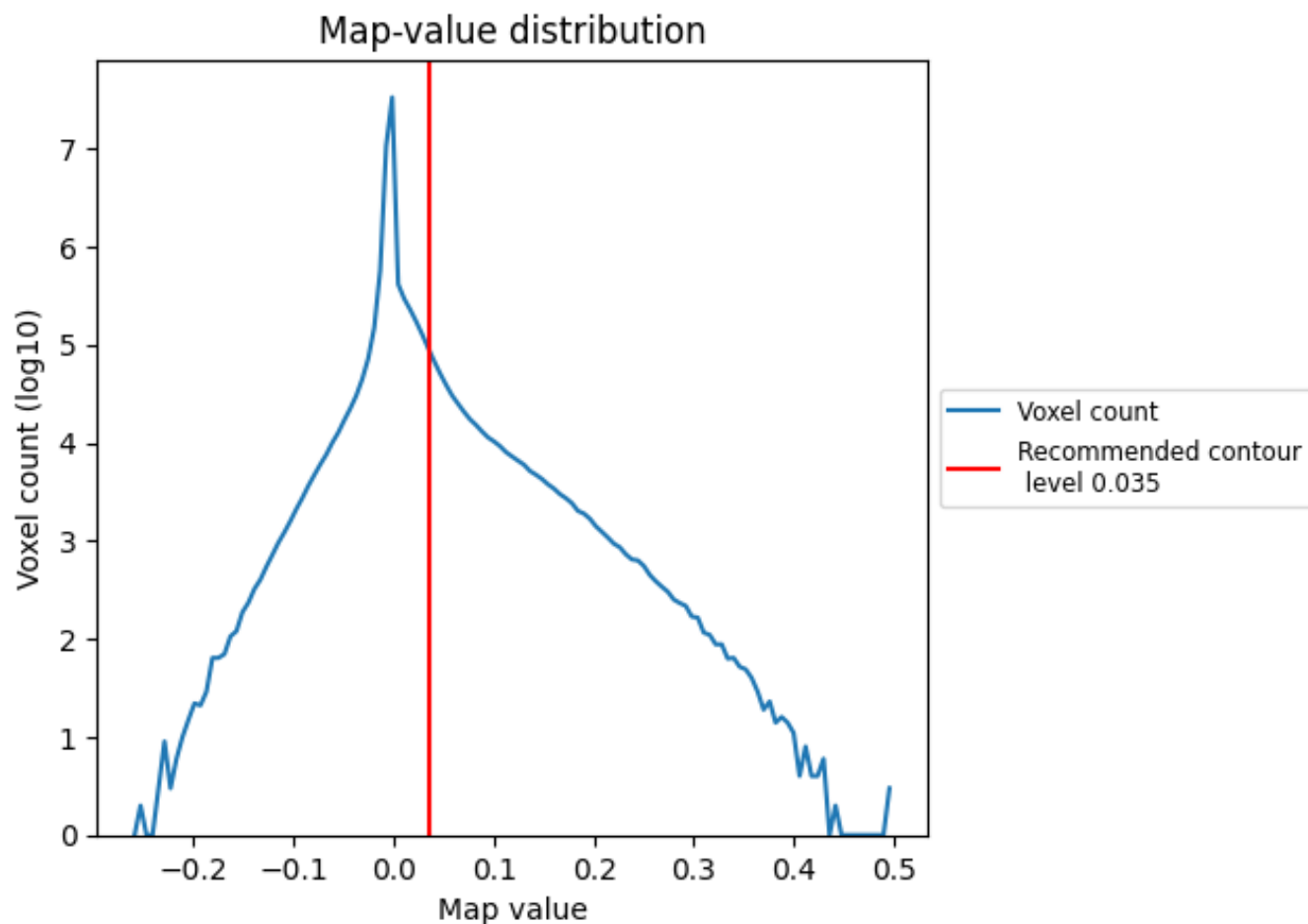


Z

7 Map analysis [i](#)

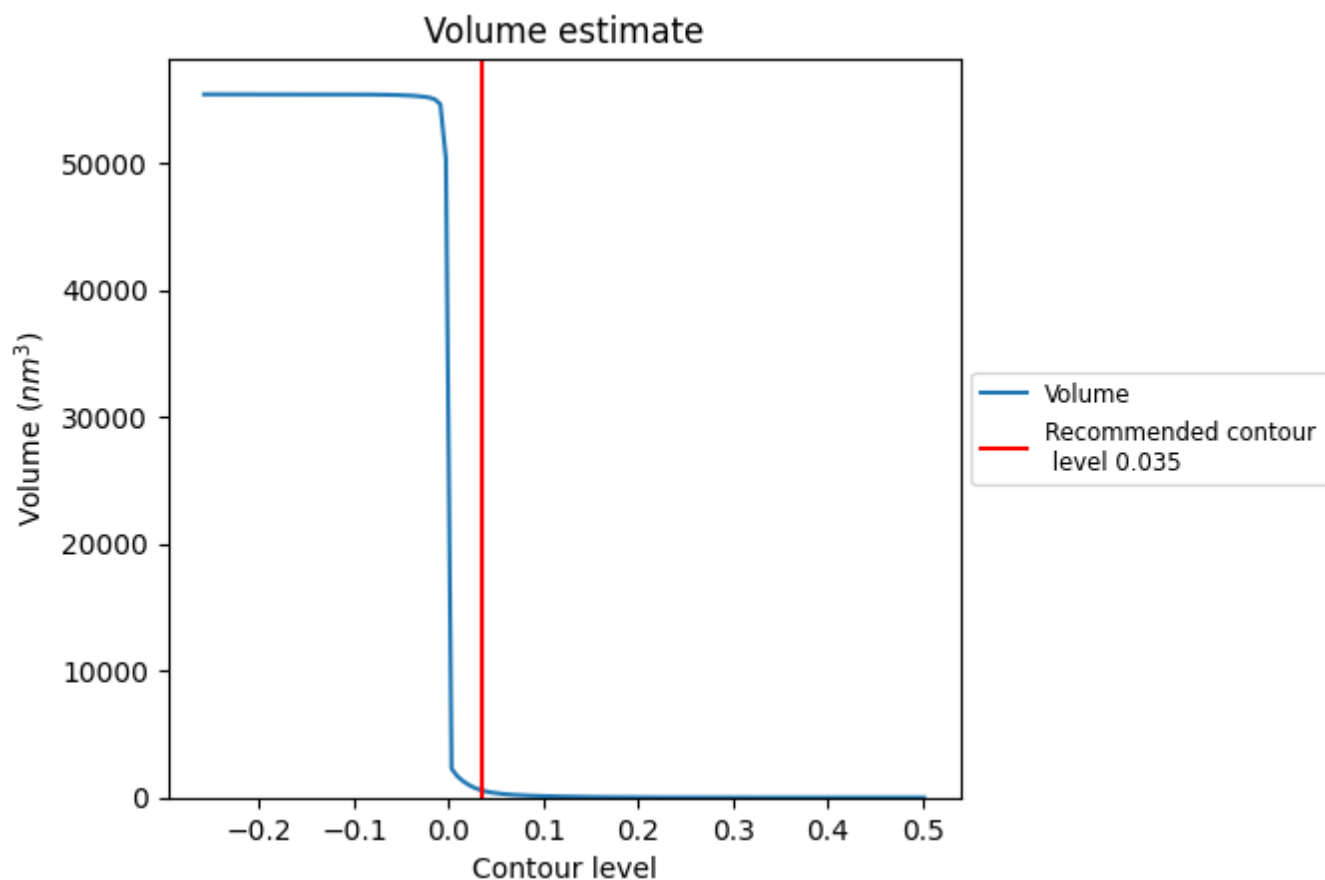
This section contains the results of statistical analysis of the map.

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.

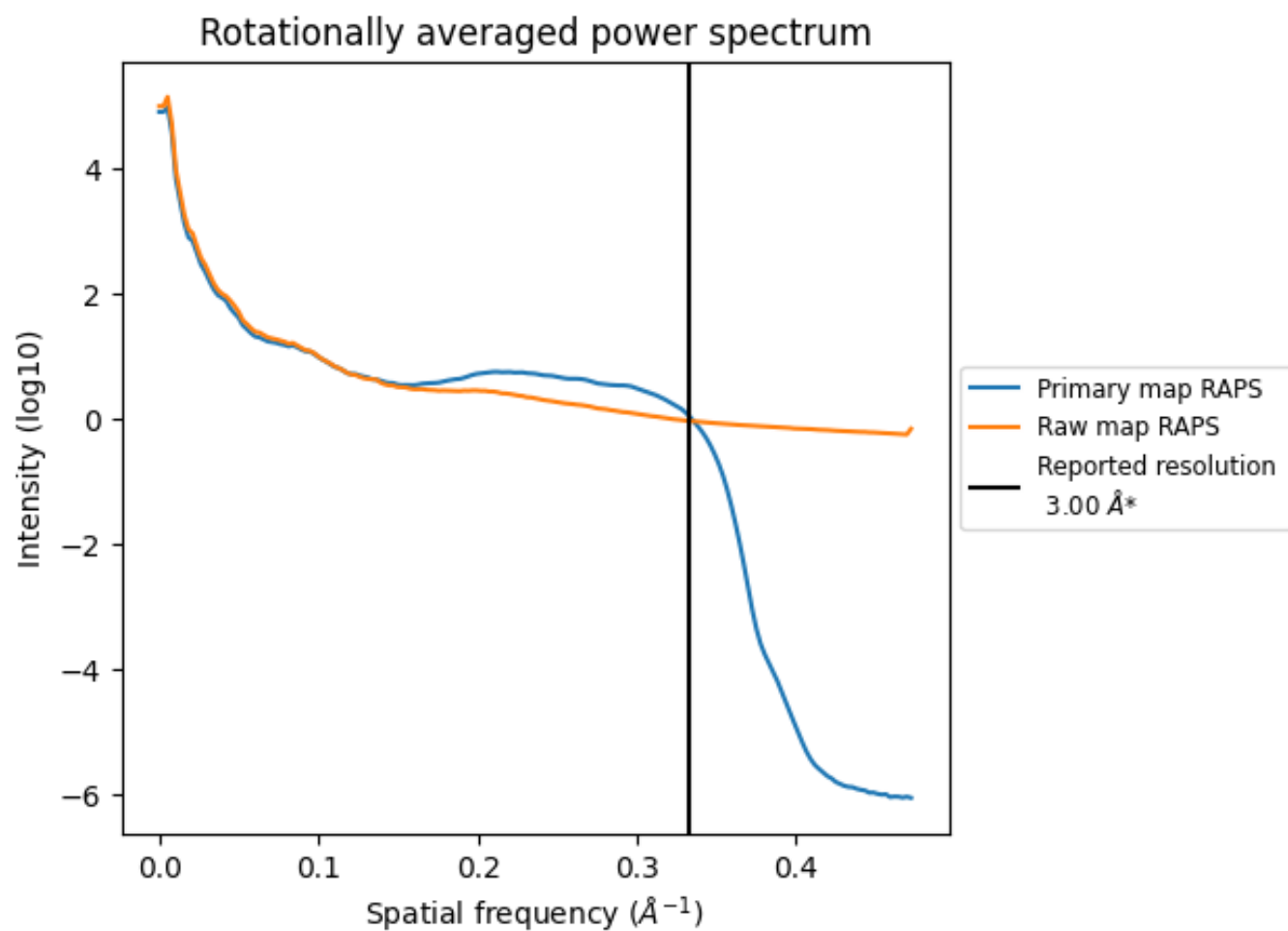
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 568 nm^3 ; 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 ⓘ

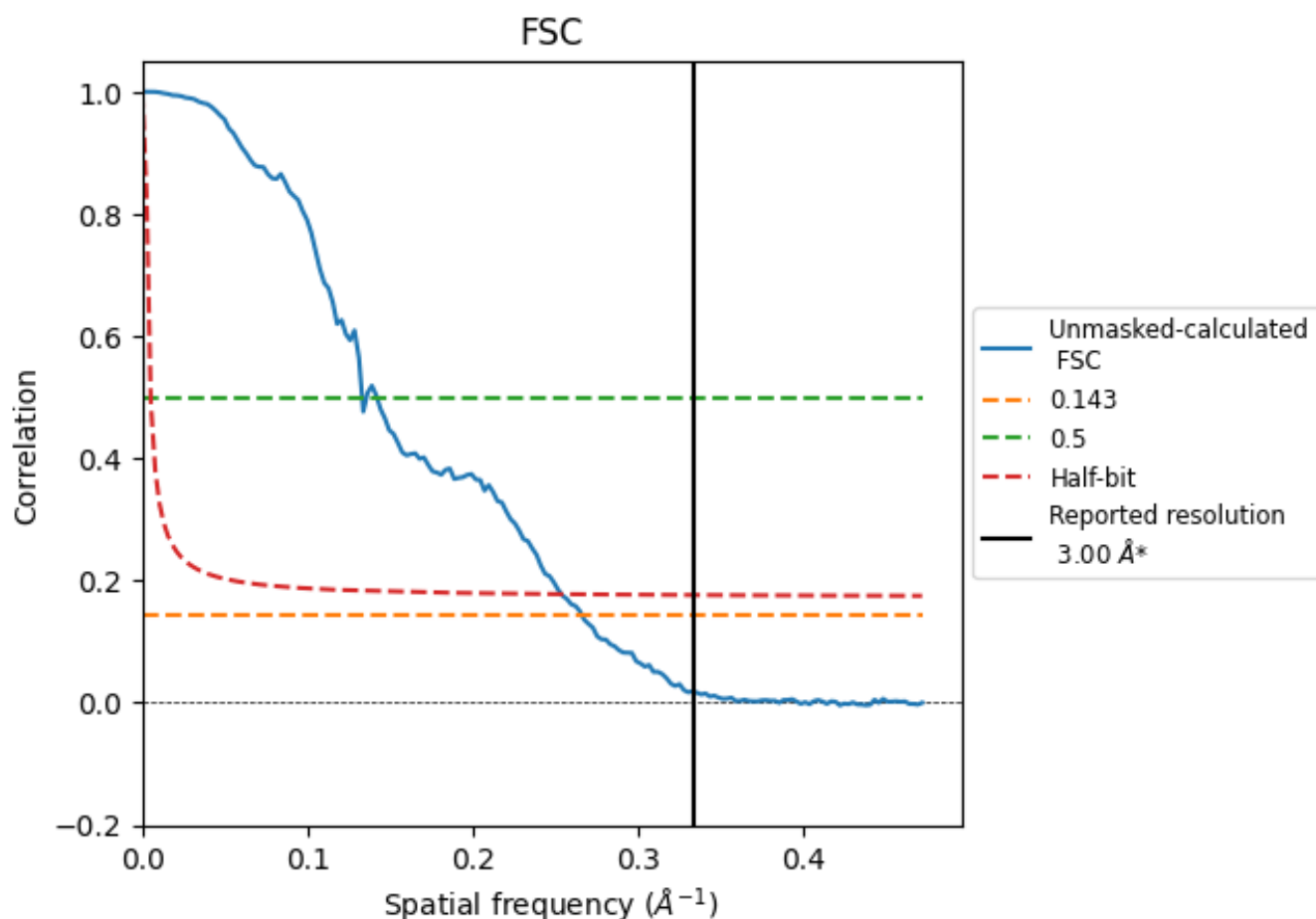


*Reported resolution corresponds to spatial frequency of $0.333 \text{ \AA}^{-1}$

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⁻¹

8.2 Resolution estimates [i](#)

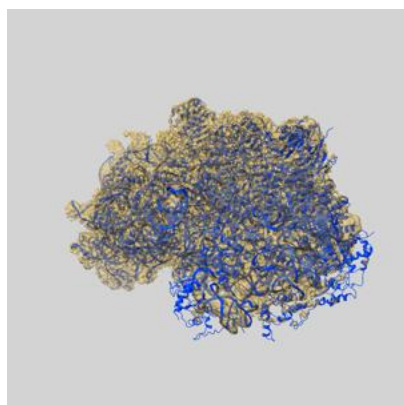
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.76	7.51	3.94

*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 %

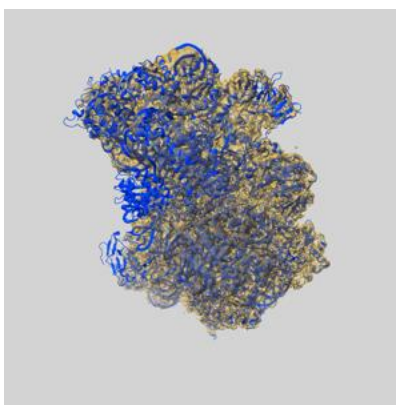
9 Map-model fit [i](#)

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.

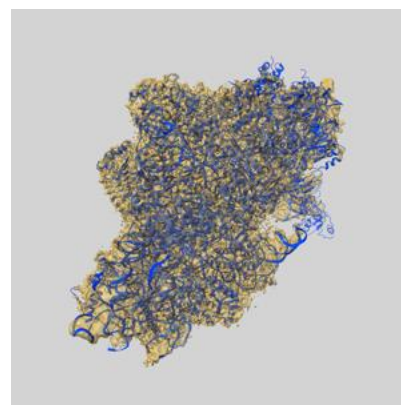
9.1 Map-model overlay [i](#)



X



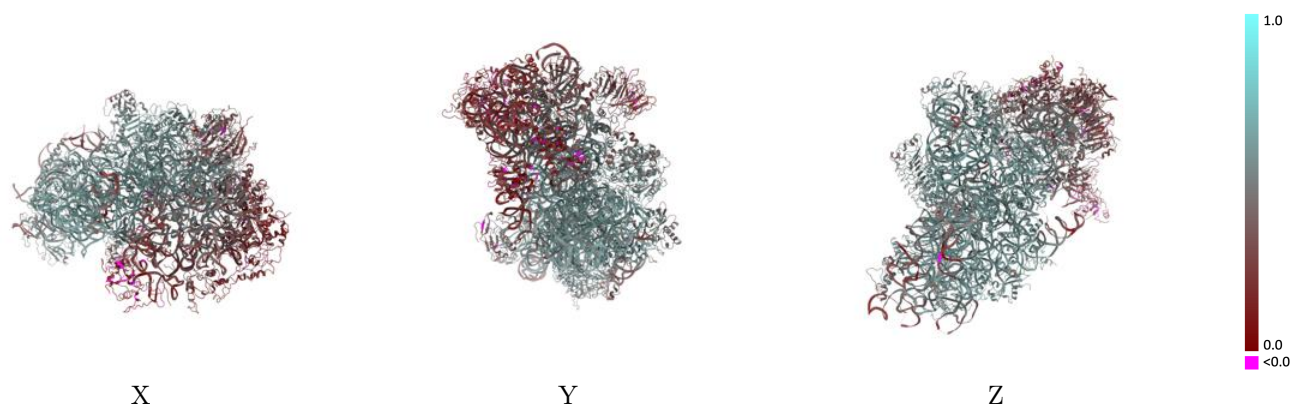
Y



Z

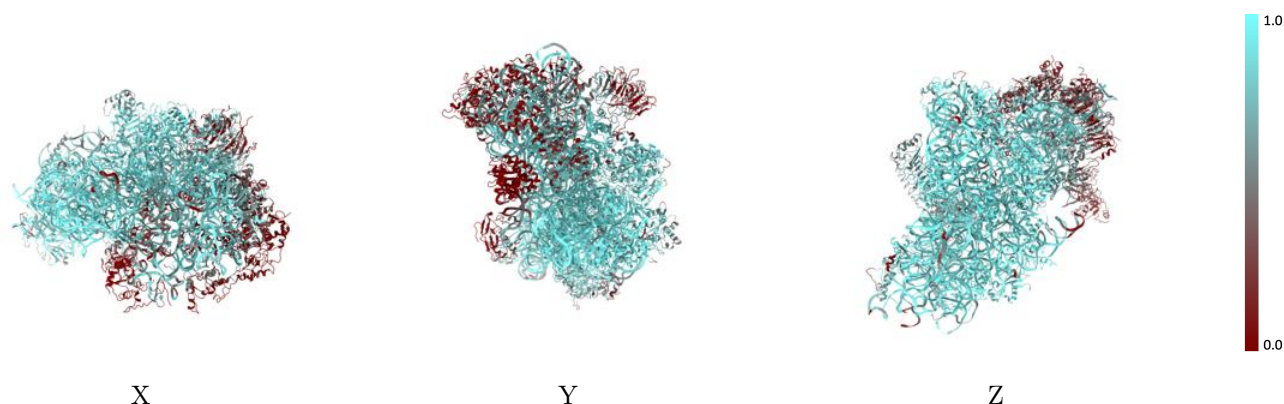
The images above show the 3D surface view of the map at the recommended contour level 0.035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



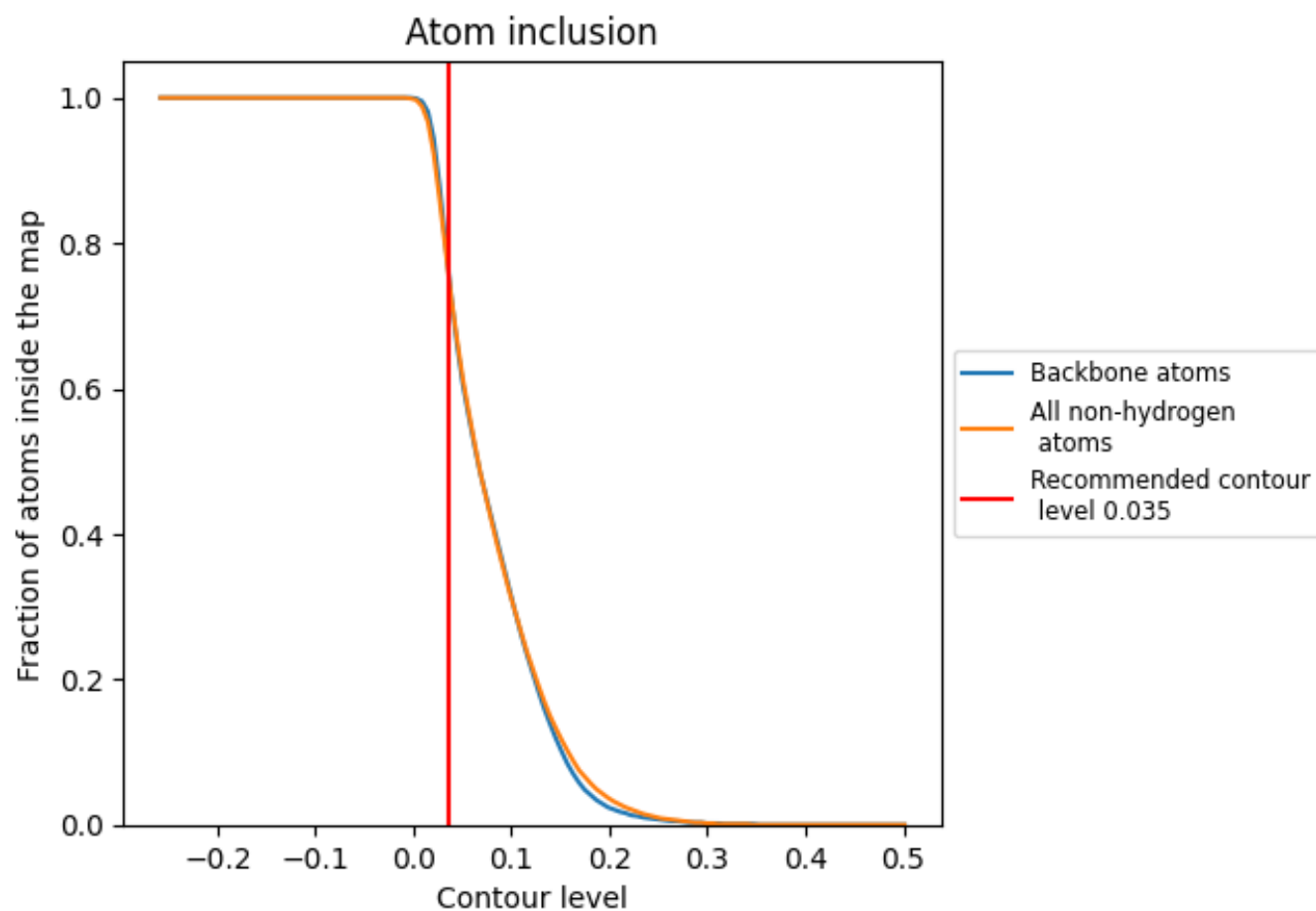
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



Continued on next page...

Continued from previous page...

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