wwPDB EM Validation Summary Report (i)

Oct 28, 2026 – 03:02 PM JST

PDB ID	:	21ZV / pdb_000021zv
EMDB ID	:	EMD-68127
Title	:	Cdc48-Ufd1-Npl4 complex processing Ub6 in the presence of ubx2
Authors	:	Pan, M.; Liu, L.; Zheng, Q.
Deposited on	:	2026-01-05
Resolution	:	3.20 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 (i) 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 (i)) were used in the production of this report:

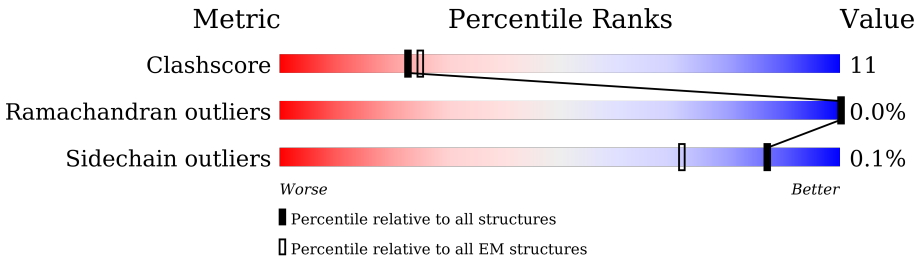
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.2
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using 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)	:	2.51

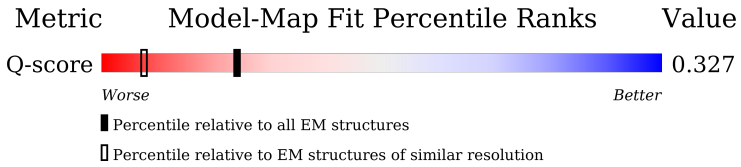
1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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	-
Q-score	-	25397	15020 (2.70 - 3.70)

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 <=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	B	361	5% 50% 16% 35%
2	C	76	41% 68% 25% 7%
2	L	76	14% 50% 13% 37%
2	N	76	7% 75% 18% • 5%

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Mol	Chain	Length	Quality of chain
2	O	76	
3	D	584	
4	A	835	
4	G	835	
4	H	835	
4	I	835	
4	J	835	
4	K	835	
4	P	835	
5	M	580	

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 22567 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 protein called Ubiquitin fusion degradation protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	236	Total	C	N	O	S	0	0
			1845	1187	298	349	11		

- Molecule 2 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	71	Total	C	N	O	S	0	0
			563	356	94	112	1		
2	L	48	Total	C	N	O		0	0
			382	242	69	71			
2	N	72	Total	C	N	O	S	0	0
			574	362	98	113	1		
2	O	71	Total	C	N	O	S	0	0
			563	356	94	112	1		

- Molecule 3 is a protein called UBX domain-containing protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	210	Total	C	N	O	S	0	0
			1703	1080	287	328	8		

- Molecule 4 is a protein called Cell division control protein 48.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	262	Total	C	N	O	S	0	0
			2016	1254	357	391	14		
4	G	250	Total	C	N	O	S	0	0
			1921	1197	345	365	14		
4	P	180	Total	C	N	O	S	0	0
			1443	907	252	278	6		
4	H	249	Total	C	N	O	S	0	0
			1913	1191	344	364	14		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	I	241	Total	C	N	O	S	0	0
			1857	1157	336	350	14		
4	J	251	Total	C	N	O	S	0	0
			1926	1200	346	366	14		
4	K	248	Total	C	N	O	S	0	0
			1905	1185	343	363	14		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	588	GLN	GLU	engineered mutation	UNP P25694
G	588	GLN	GLU	engineered mutation	UNP P25694
P	588	GLN	GLU	engineered mutation	UNP P25694
H	588	GLN	GLU	engineered mutation	UNP P25694
I	588	GLN	GLU	engineered mutation	UNP P25694
J	588	GLN	GLU	engineered mutation	UNP P25694
K	588	GLN	GLU	engineered mutation	UNP P25694

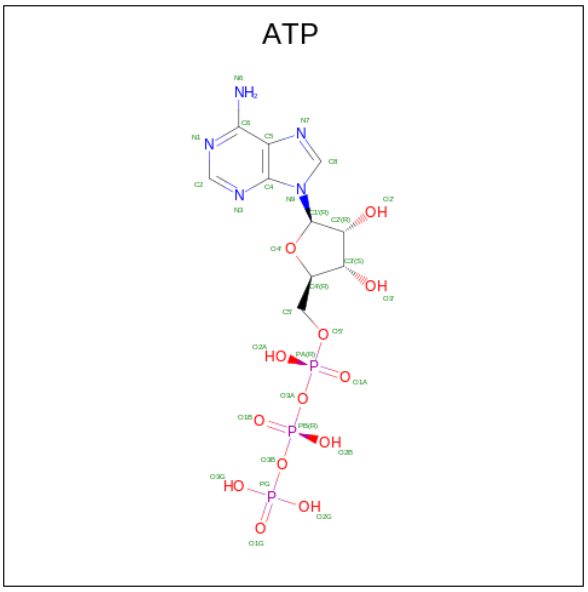
- Molecule 5 is a protein called Nuclear protein localization protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	M	468	Total	C	N	O	S	0	0
			3768	2387	628	732	21		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	494	PHE	ALA	engineered mutation	UNP P33755

- Molecule 6 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms					AltConf
6	A	1	Total	C	N	O	P	0
			31	10	5	13	3	
6	G	1	Total	C	N	O	P	0
			31	10	5	13	3	
6	H	1	Total	C	N	O	P	0
			31	10	5	13	3	
6	J	1	Total	C	N	O	P	0
			31	10	5	13	3	
6	J	1	Total	C	N	O	P	0
			31	10	5	13	3	
6	K	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 7 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
7	M	2	Total	Zn	0
			2	2	

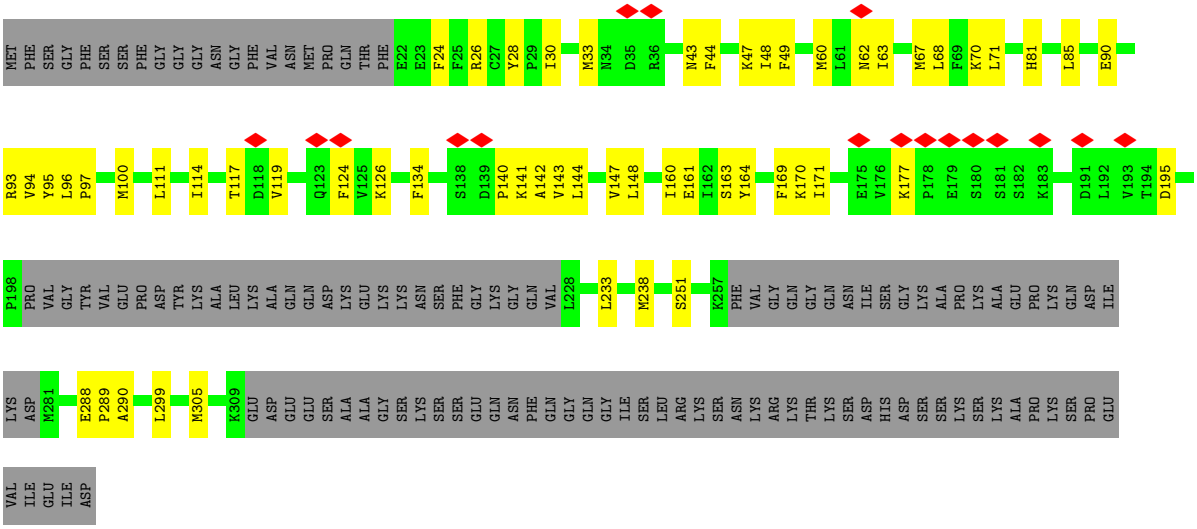
3 Residue-property plots (i)

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

• Molecule 1: Ubiquitin fusion degradation protein 1

Chain B:

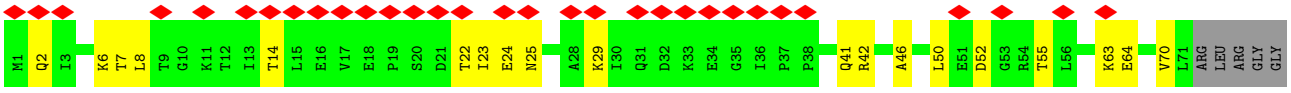




• Molecule 2: Ubiquitin

Chain C:

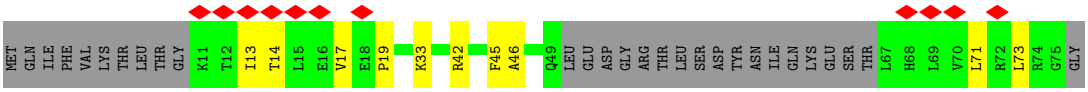




• Molecule 2: Ubiquitin

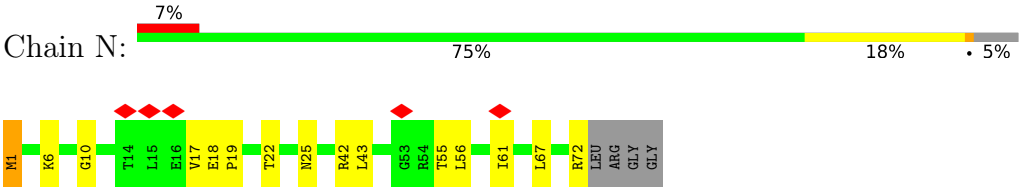
Chain L:





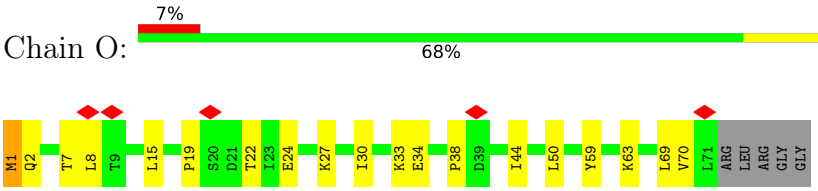
• Molecule 2: Ubiquitin

Chain N:



• Molecule 2: Ubiquitin

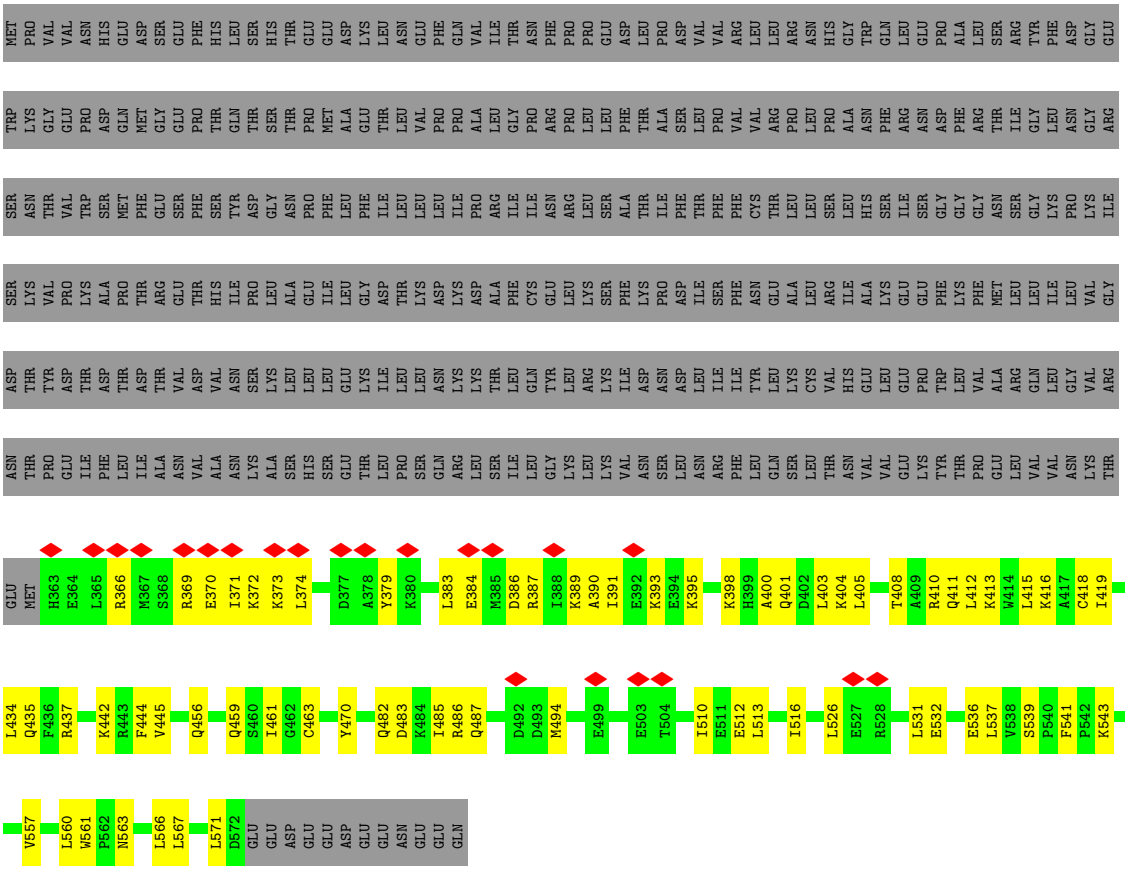
Chain O:



• Molecule 3: UBX domain-containing protein 2

Chain D:

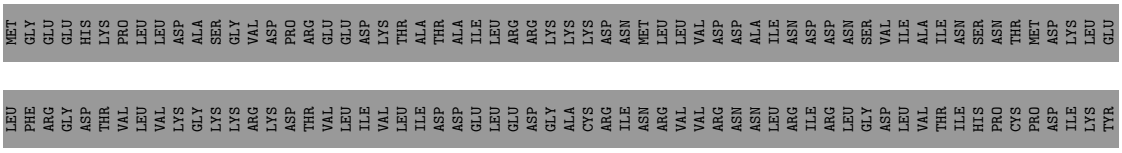


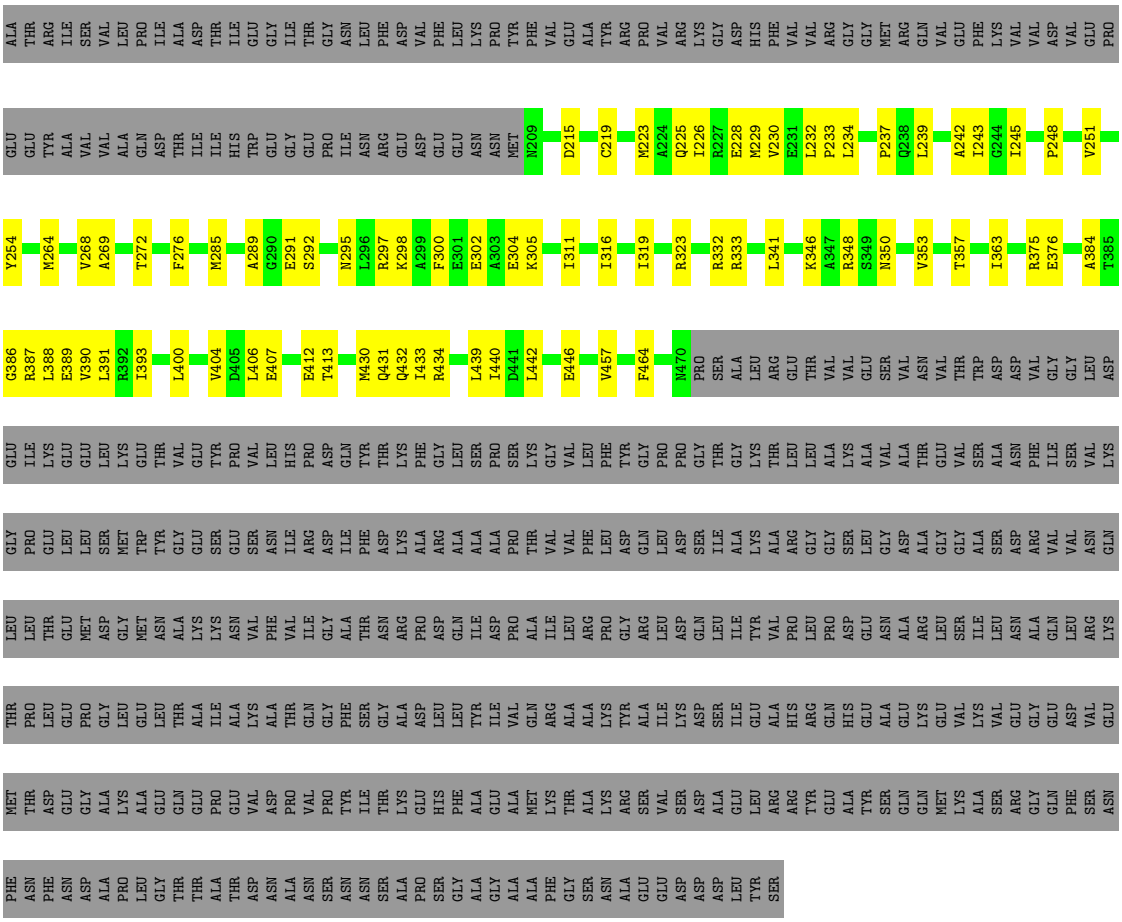


• Molecule 4: Cell division control protein 48

Chain A:

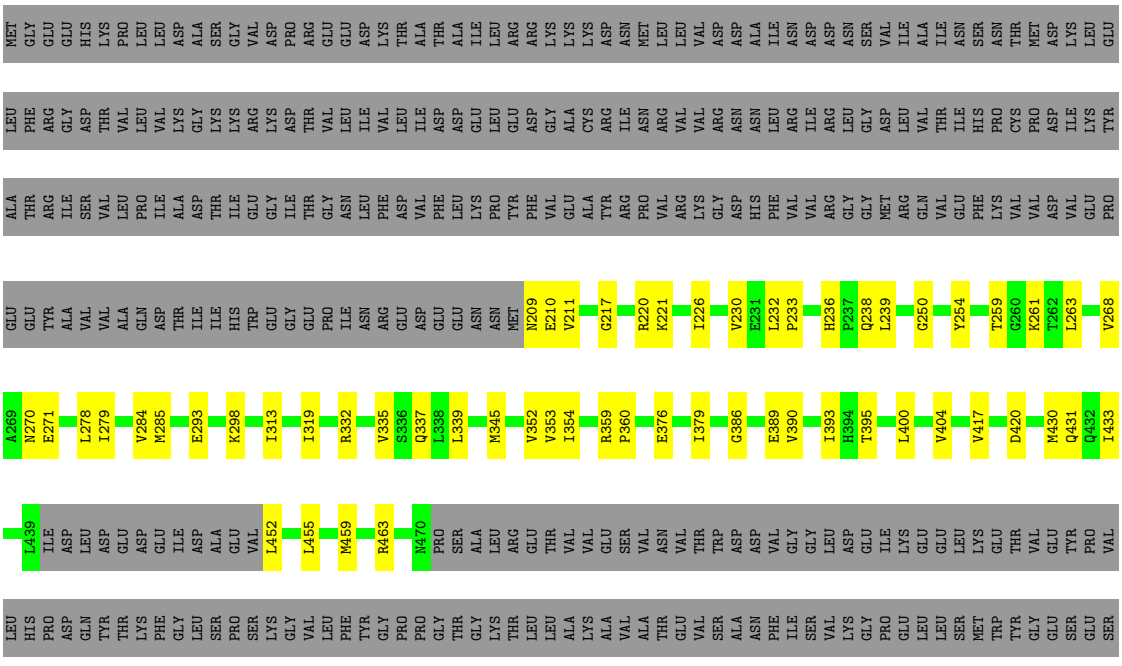


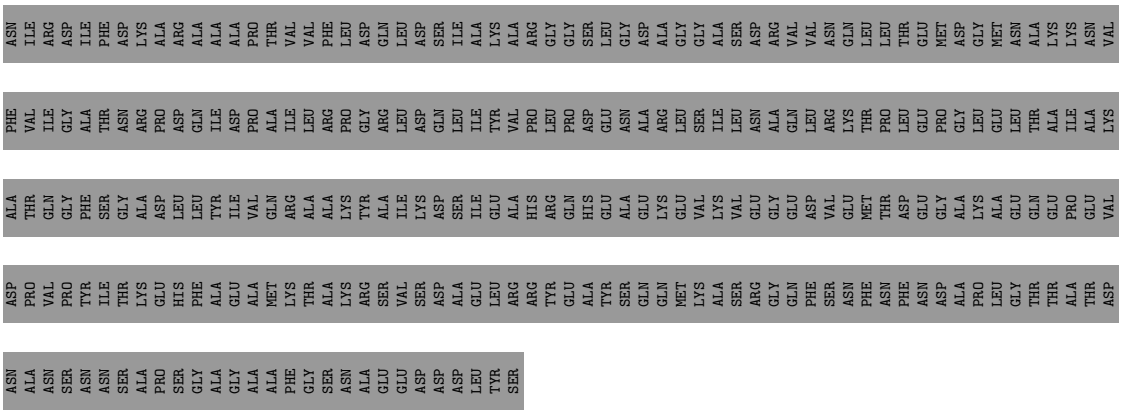




• Molecule 4: Cell division control protein 48

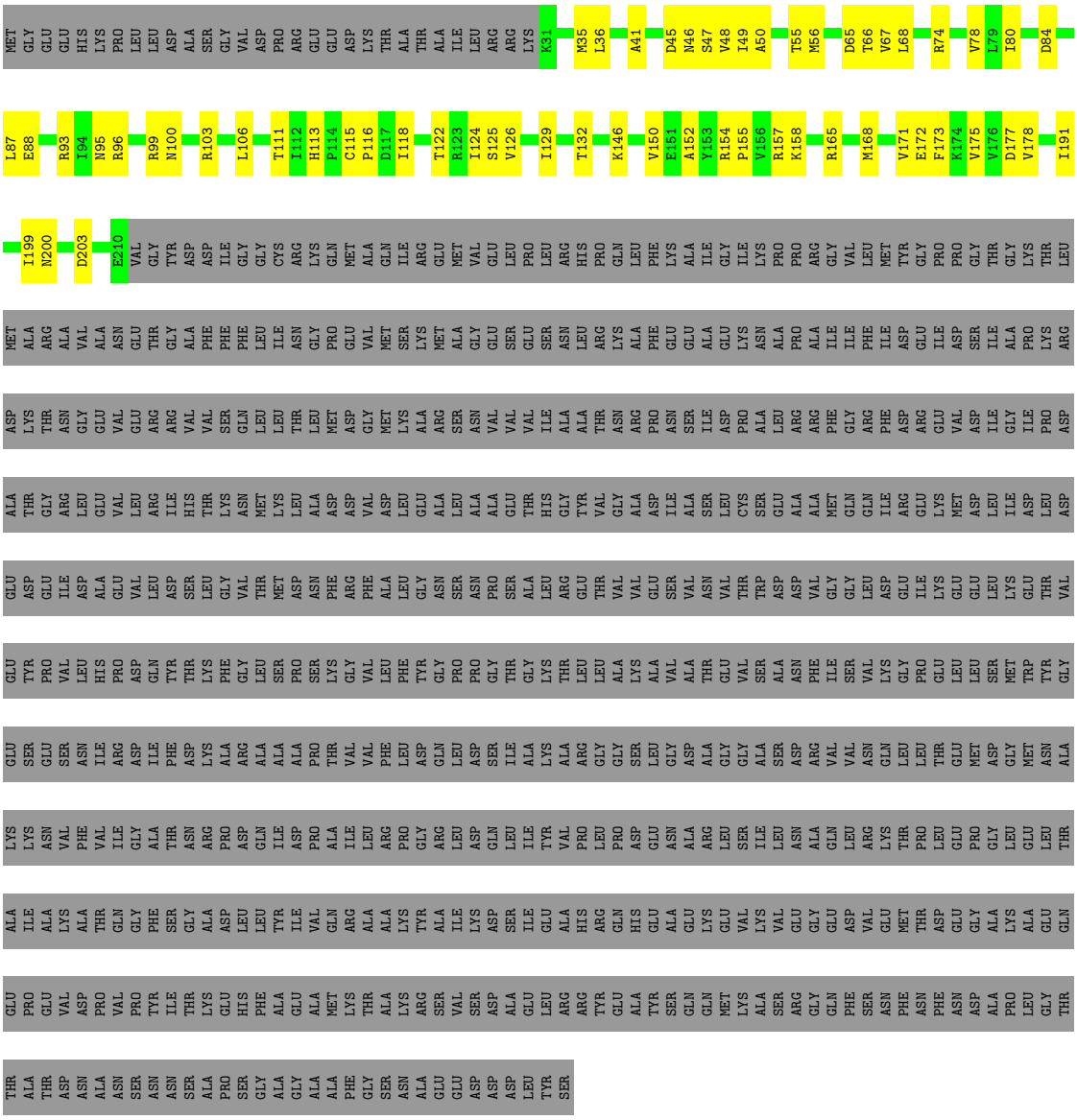
Chain G: 23% 7% 70%





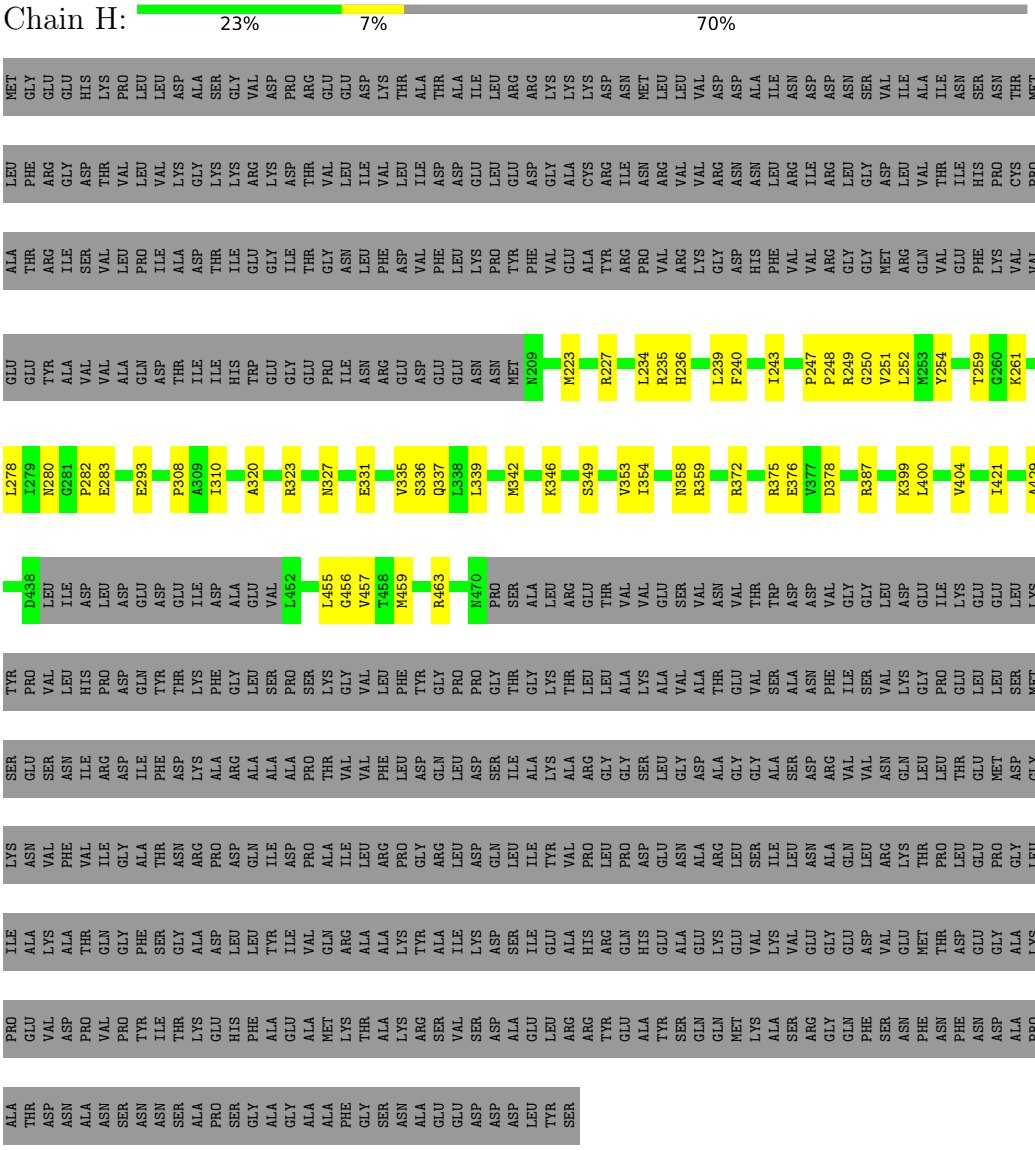
• Molecule 4: Cell division control protein 48

Chain P: 15% 7% 78%



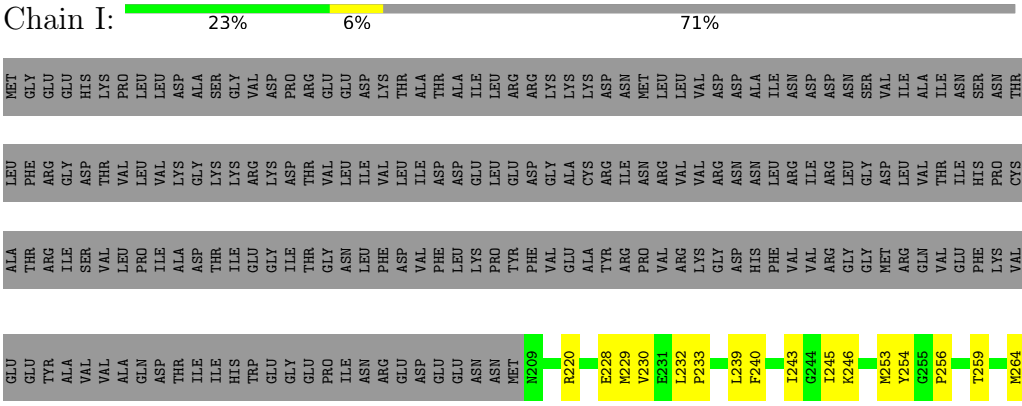
• Molecule 4: Cell division control protein 48

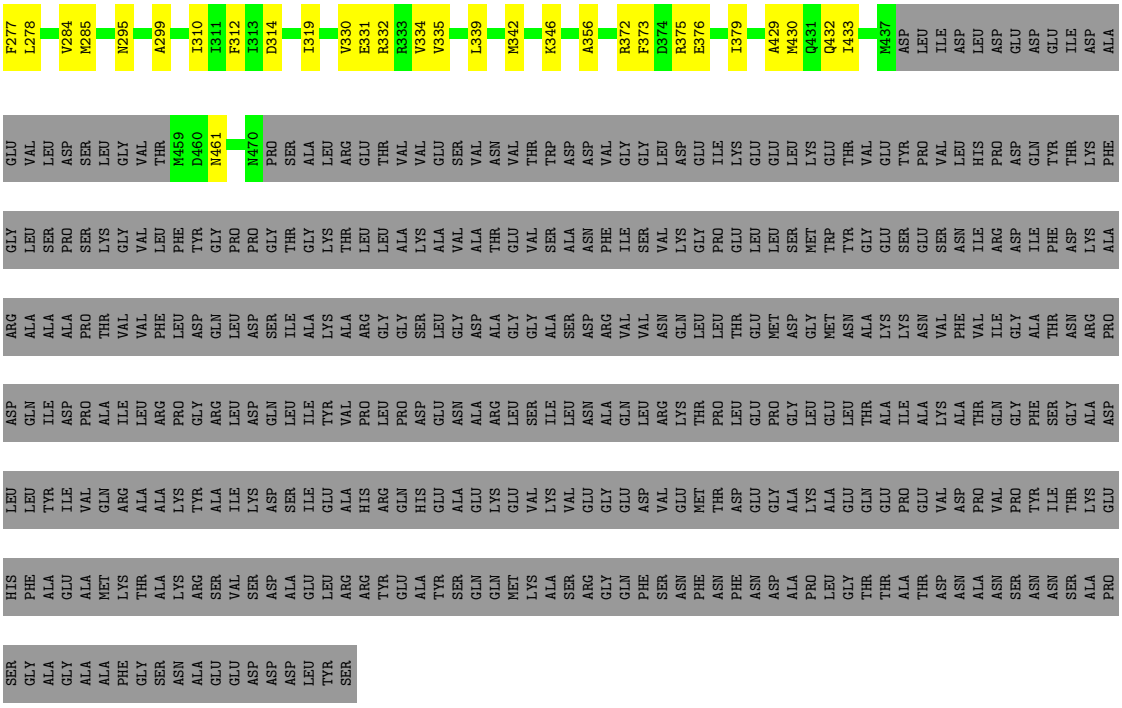
Chain H:



• Molecule 4: Cell division control protein 48

Chain I:

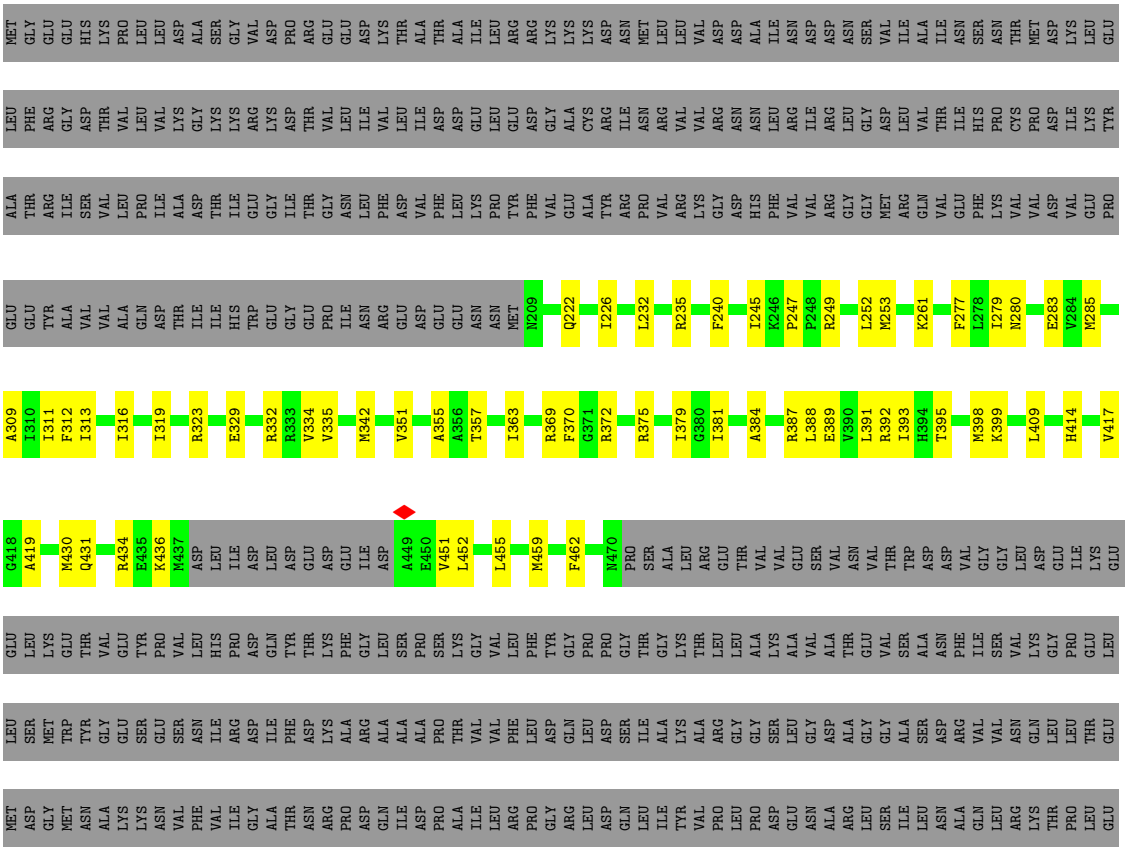


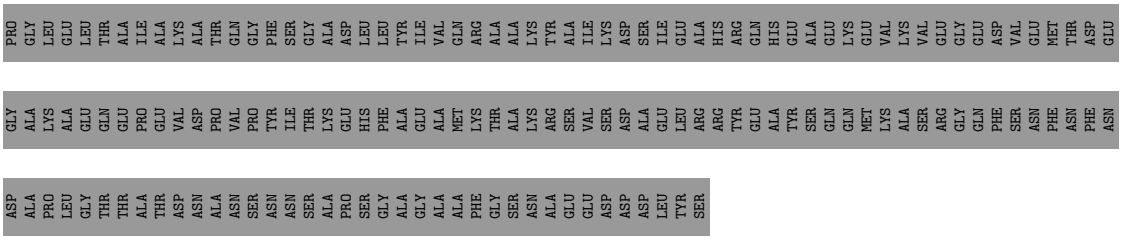


• Molecule 4: Cell division control protein 48

Chain J:



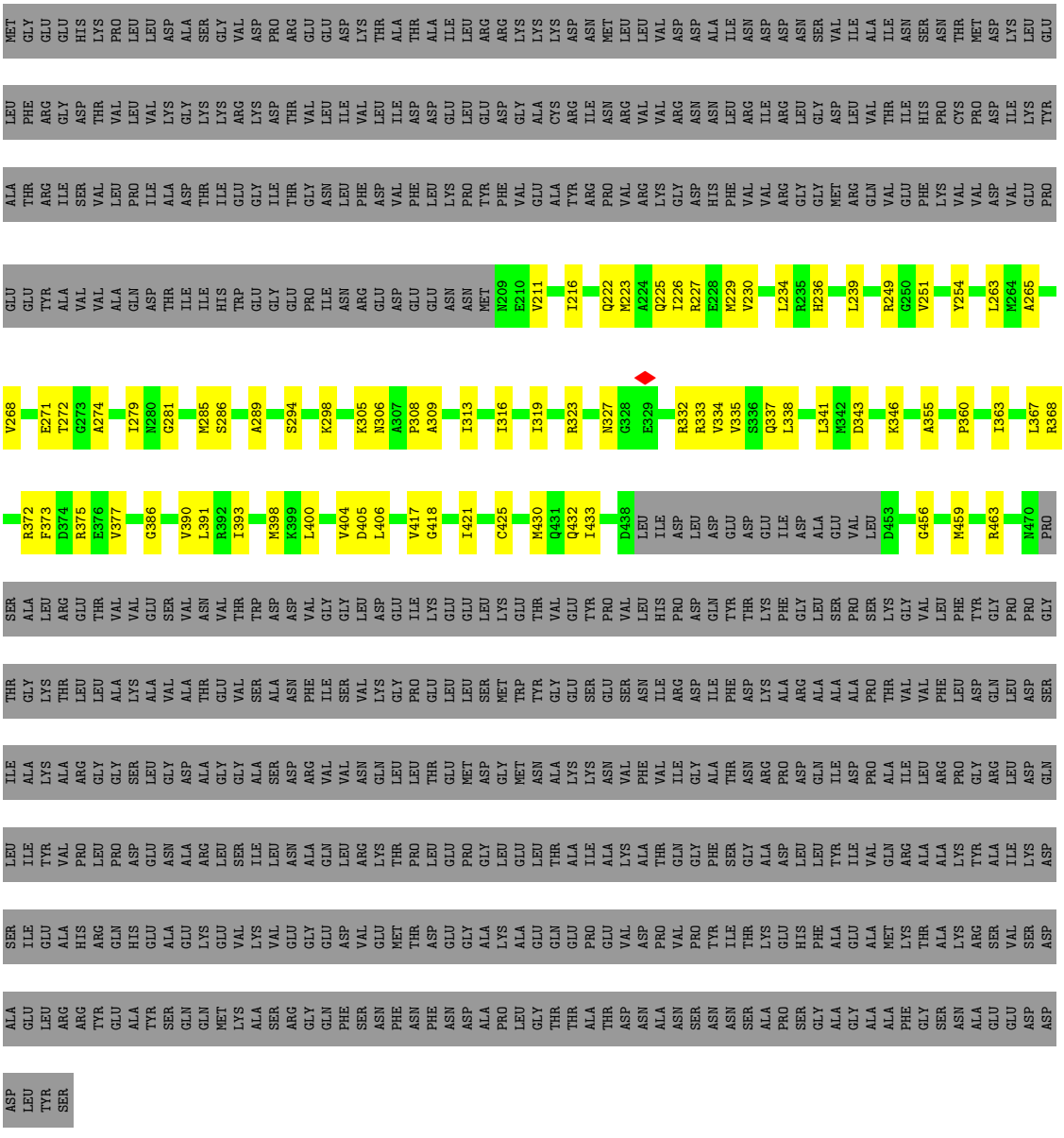




• Molecule 4: Cell division control protein 48

Chain K:

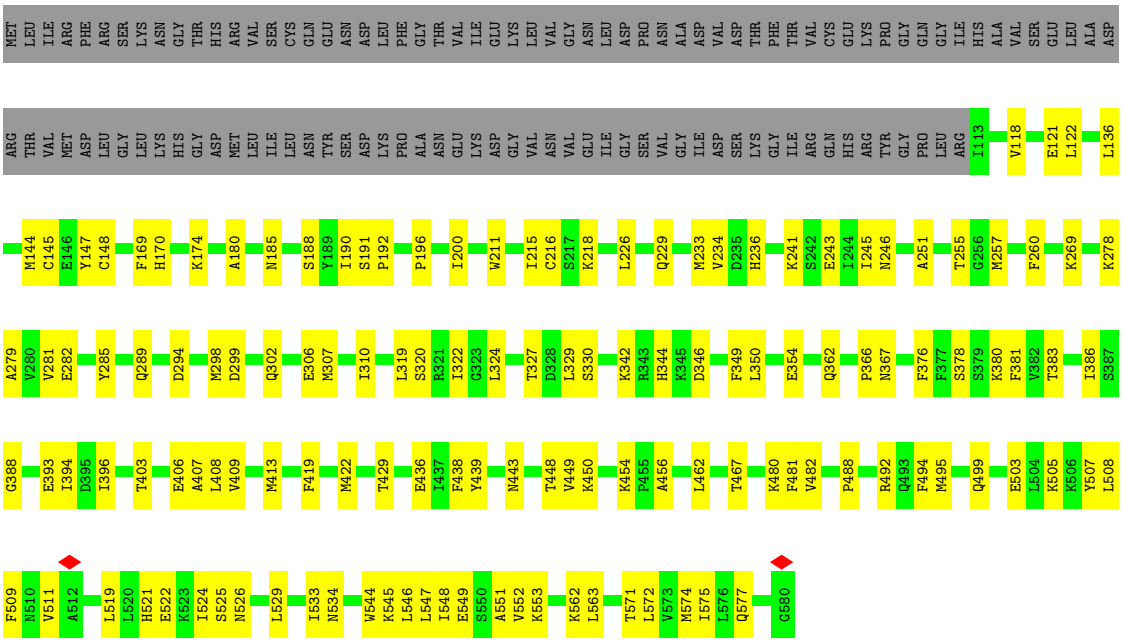




• Molecule 5: Nuclear protein localization protein 4

Chain M:




MET LEU ILE ARG PHE ARG SER LYS ASN GLY THR HIS ARG VAL SER CYS GLN GLU ASN ASP LEU PHE GLY THR VAL ILE GLU LYS LEU VAL GLY ASN LEU ASP PRO ASN ALA ASP VAL ASP PHE THR VAL CYS GLU LYS PRO GLY GLN GLY ILE HIS ALA VAL SER GLU LEU ALA ASP
ARG THR VAL MET ASP LEU GLY LEU LYS HIS GLY ASP MET LEU ILE LEU ASN TYR SER ASP LYS PRO ALA ASN GLU LYS ASP GLY VAL ASN VAL GLU ILE GLY SER VAL GLY ILE ASP SER LYS GLY ILE ARG GLN HIS ARG TYR GLY PRO LEU ARG I113 V118 E121 L122 L136
M144 C145 E146 Y147 C148 F169 H170 K174 A180 N185 S188 Y189 I190 S191 P192 P196 I200 W211 I215 C216 S217 K218 L226 Q229 M233 V234 D235 H236 K241 S242 E243 I244 I245 N246 A251 T255 G256 M257 F260 K269 K278
A279 V280 V281 E282 Y285 Q289 D294 M298 D299 Q302 E306 M307 I310 L319 S320 R321 I322 G323 L324 T327 D328 L329 S330 K342 R343 H344 K345 D346 F349 L350 E354 Q362 P366 N367 F376 F377 S378 S379 K380 F381 V382 T383 I386 S387
G388 E393 I394 D395 I396 T403 E406 A407 L408 V409 M413 F419 M422 T429 E436 I437 F438 Y439 N443 T448 V449 K450 K454 P455 A456 L462 T467 K480 F481 V482 P488 R492 Q493 F494 M495 Q499 E503 L504 K505 K506 Y507 L508
F509 N510 V511 A512 L519 L520 H521 E522 K523 I524 S525 N526 L529 I533 N534 W544 K545 L546 L547 I548 E549 S550 A551 V552 K553 K562 L563 T571 L572 V573 M574 I575 L576 Q577 G580

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	278701	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.698	Depositor
Minimum map value	-0.301	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	372.8, 372.8, 372.8	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.932, 0.932, 0.932	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ATP, 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	B	0.13	0/1881	0.34	0/2540
2	C	0.14	0/569	0.38	0/767
2	L	0.13	0/385	0.39	0/516
2	N	0.19	0/580	0.35	0/781
2	O	0.17	0/569	0.37	0/767
3	D	0.14	0/1737	0.42	0/2342
4	A	0.14	0/2043	0.40	0/2753
4	G	0.15	0/1947	0.38	0/2620
4	H	0.15	0/1939	0.43	2/2609 (0.1%)
4	I	0.13	0/1883	0.37	0/2532
4	J	0.12	0/1952	0.37	0/2627
4	K	0.15	0/1931	0.40	0/2598
4	P	0.15	0/1464	0.45	0/1982
5	M	0.14	0/3858	0.41	0/5210
All	All	0.14	0/22738	0.40	2/30644 (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
5	M	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	H	261	LYS	CB-CG-CD	6.74	126.80	111.30
4	H	261	LYS	CG-CD-CE	-5.56	98.52	111.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	M	454	LYS	Peptide

5.2 Too-close contacts (i)

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	B	1845	0	1872	41	0
2	C	563	0	586	15	0
2	L	382	0	406	7	0
2	N	574	0	599	11	0
2	O	563	0	586	10	0
3	D	1703	0	1695	56	0
4	A	2016	0	2021	51	0
4	G	1921	0	1939	44	0
4	H	1913	0	1925	46	0
4	I	1857	0	1874	36	0
4	J	1926	0	1943	44	0
4	K	1905	0	1916	53	0
4	P	1443	0	1447	44	0
5	M	3768	0	3636	100	0
6	A	31	0	12	0	0
6	G	31	0	12	1	0
6	H	31	0	10	0	0
6	J	62	0	20	1	0
6	K	31	0	12	2	0
7	M	2	0	0	0	0
All	All	22567	0	22511	503	0

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

The worst 5 of 503 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)
3:D:384:GLU:HA	3:D:387:ARG:HE	1.27	0.99
4:J:388:LEU:HG	4:J:392:ARG:HH12	1.26	0.95
4:P:99:ARG:HH22	4:P:106:LEU:HD22	1.36	0.90
1:B:305:MET:HE2	5:M:342:LYS:HG2	1.60	0.83
5:M:406:GLU:HA	5:M:409:VAL:HG22	1.60	0.82

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	
1	B	230/361 (64%)	225 (98%)	5 (2%)	0	100	100
2	C	69/76 (91%)	68 (99%)	1 (1%)	0	100	100
2	L	44/76 (58%)	34 (77%)	9 (20%)	1 (2%)	5	29
2	N	70/76 (92%)	68 (97%)	2 (3%)	0	100	100
2	O	69/76 (91%)	67 (97%)	2 (3%)	0	100	100
3	D	208/584 (36%)	206 (99%)	2 (1%)	0	100	100
4	A	260/835 (31%)	250 (96%)	10 (4%)	0	100	100
4	G	246/835 (30%)	236 (96%)	10 (4%)	0	100	100
4	H	245/835 (29%)	226 (92%)	19 (8%)	0	100	100
4	I	237/835 (28%)	219 (92%)	18 (8%)	0	100	100
4	J	247/835 (30%)	228 (92%)	19 (8%)	0	100	100
4	K	244/835 (29%)	228 (93%)	16 (7%)	0	100	100
4	P	178/835 (21%)	174 (98%)	4 (2%)	0	100	100
5	M	466/580 (80%)	406 (87%)	60 (13%)	0	100	100
All	All	2813/7674 (37%)	2635 (94%)	177 (6%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	L	45	PHE

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
1	B	210/314 (67%)	210 (100%)	0	100 100
2	C	65/68 (96%)	65 (100%)	0	100 100
2	L	43/68 (63%)	43 (100%)	0	100 100
2	N	66/68 (97%)	65 (98%)	1 (2%)	57 76
2	O	65/68 (96%)	63 (97%)	2 (3%)	35 66
3	D	190/533 (36%)	190 (100%)	0	100 100
4	A	215/695 (31%)	215 (100%)	0	100 100
4	G	204/695 (29%)	204 (100%)	0	100 100
4	H	203/695 (29%)	203 (100%)	0	100 100
4	I	196/695 (28%)	196 (100%)	0	100 100
4	J	204/695 (29%)	204 (100%)	0	100 100
4	K	202/695 (29%)	202 (100%)	0	100 100
4	P	162/695 (23%)	162 (100%)	0	100 100
5	M	421/517 (81%)	421 (100%)	0	100 100
All	All	2446/6501 (38%)	2443 (100%)	3 (0%)	87 91

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	N	1	MET
2	O	1	MET
2	O	2	GLN

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

Mol	Chain	Res	Type
4	K	470	ASN
5	M	367	ASN
2	O	2	GLN
5	M	315	GLN
4	I	358	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
6	ATP	H	901	-	29,33,33	0.36	0	44,52,52	0.57	1 (2%)
6	ATP	K	901	-	29,33,33	0.28	0	44,52,52	0.53	1 (2%)
6	ATP	J	902	-	29,33,33	0.28	0	44,52,52	0.52	1 (2%)
6	ATP	G	901	-	29,33,33	0.29	0	44,52,52	0.51	1 (2%)
6	ATP	A	901	-	29,33,33	0.29	0	44,52,52	0.50	1 (2%)
6	ATP	J	901	-	29,33,33	0.28	0	44,52,52	0.49	1 (2%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	ATP	H	901	-	-	8/22/38/38	0/3/3/3
6	ATP	K	901	-	-	3/22/38/38	0/3/3/3
6	ATP	J	902	-	-	5/22/38/38	0/3/3/3
6	ATP	G	901	-	-	5/22/38/38	0/3/3/3
6	ATP	A	901	-	-	4/22/38/38	0/3/3/3
6	ATP	J	901	-	-	6/22/38/38	0/3/3/3

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	H	901	ATP	PB-O3B-PG	2.15	140.22	132.83
6	J	901	ATP	PB-O3B-PG	2.07	139.92	132.83
6	G	901	ATP	PB-O3B-PG	2.06	139.91	132.83
6	J	902	ATP	PB-O3B-PG	2.06	139.90	132.83
6	K	901	ATP	PB-O3B-PG	2.05	139.87	132.83

There are no chirality outliers.

5 of 31 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	H	901	ATP	PB-O3B-PG-O2G
6	H	901	ATP	C5'-O5'-PA-O1A
6	H	901	ATP	C3'-C4'-C5'-O5'
6	J	901	ATP	C2'-C1'-N9-C8
6	J	902	ATP	PB-O3B-PG-O2G

There are no ring outliers.

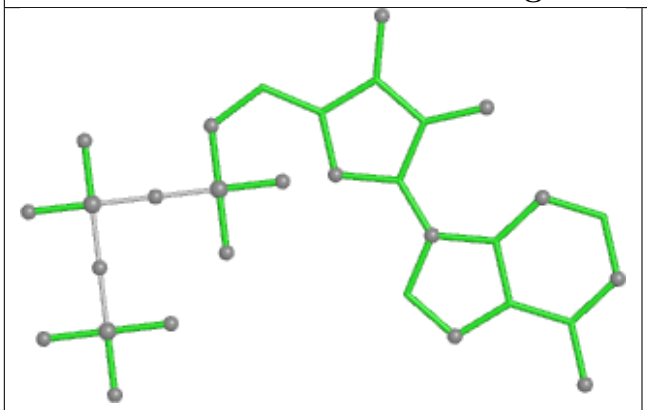
3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	K	901	ATP	2	0
6	J	902	ATP	1	0
6	G	901	ATP	1	0

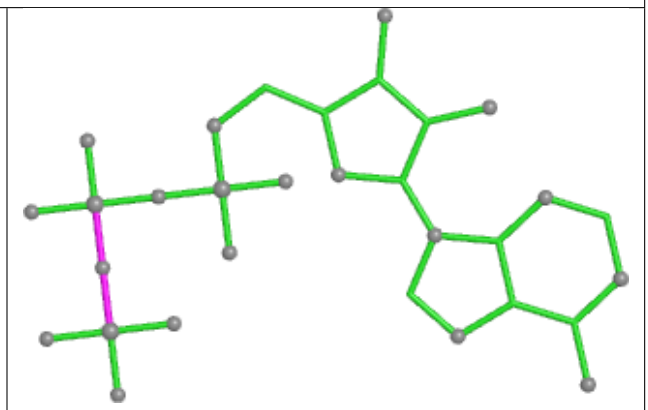
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

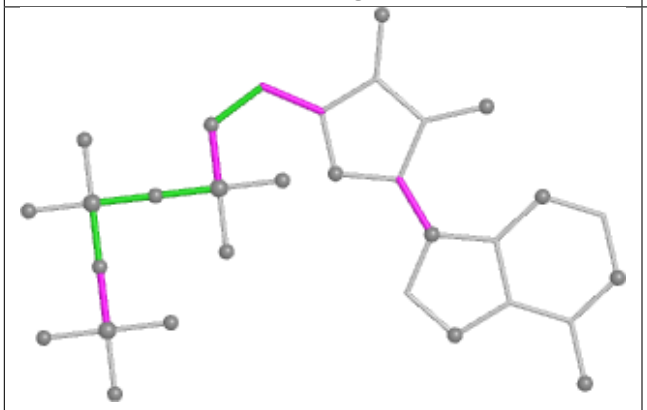
Ligand ATP H 901



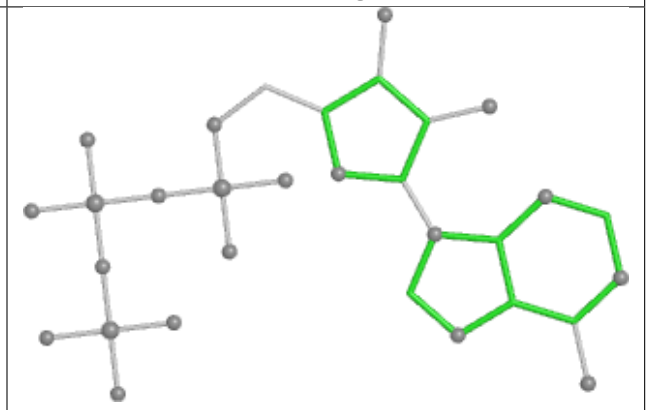
Bond lengths



Bond angles

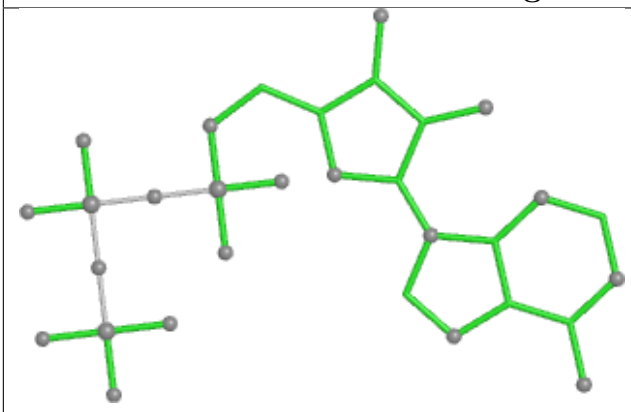


Torsions

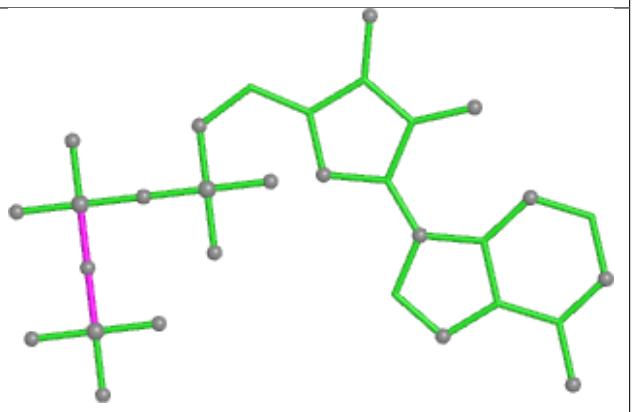


Rings

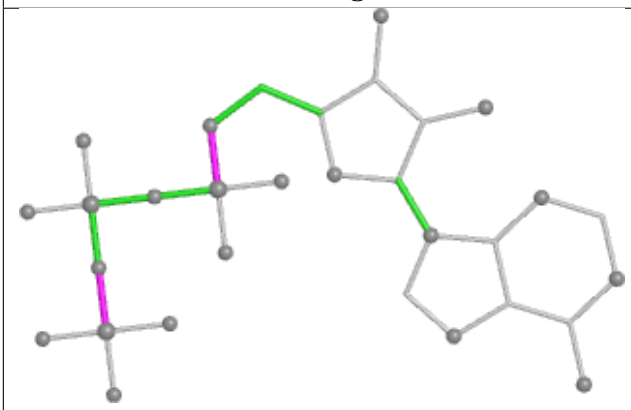
Ligand ATP K 901



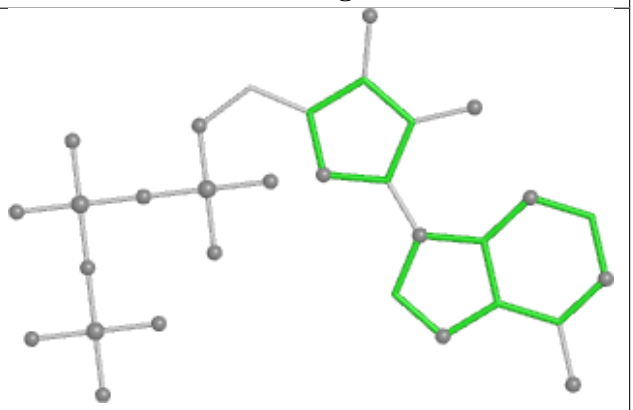
Bond lengths



Bond angles

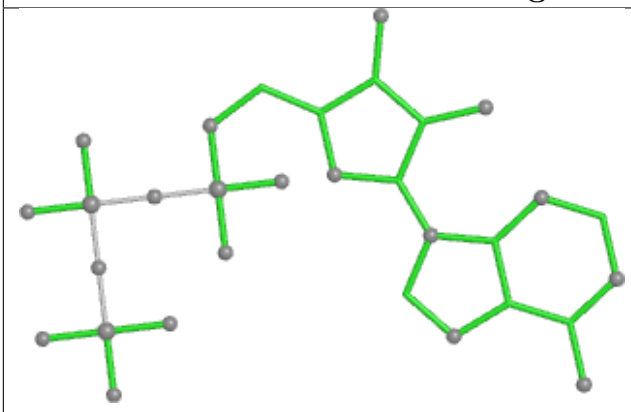


Torsions

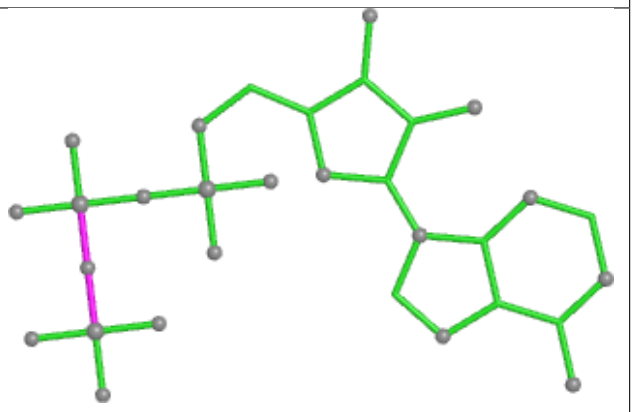


Rings

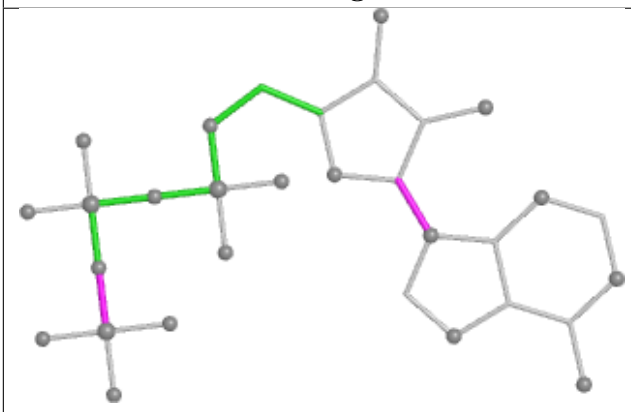
Ligand ATP J 902



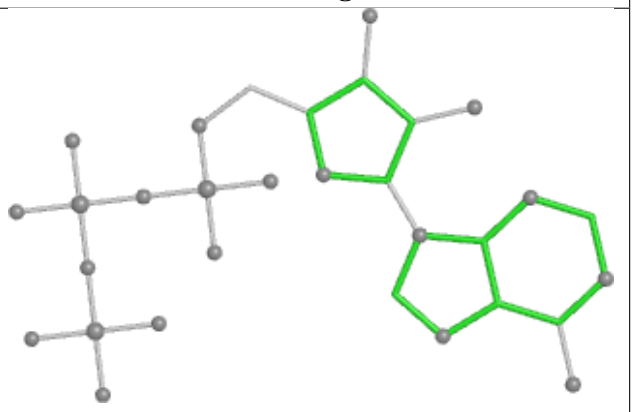
Bond lengths



Bond angles

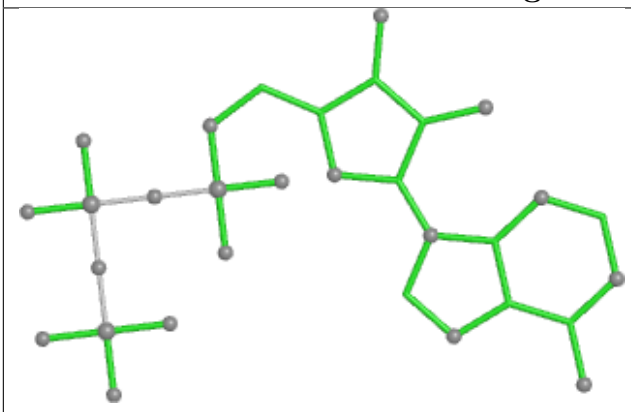


Torsions

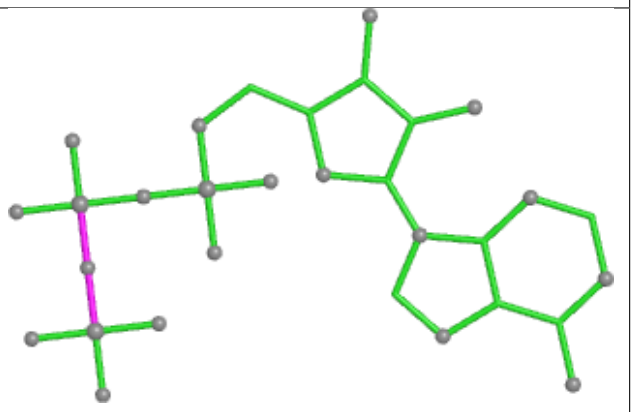


Rings

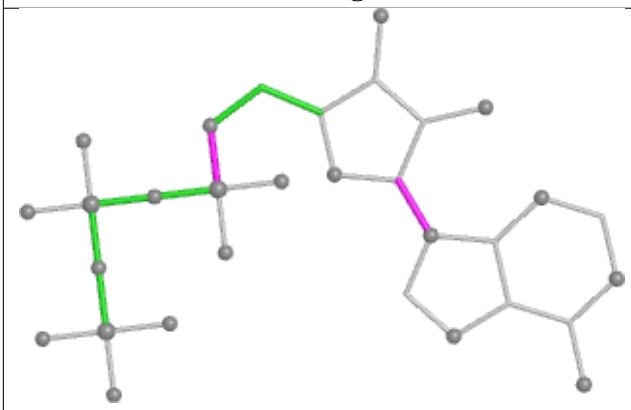
Ligand ATP G 901



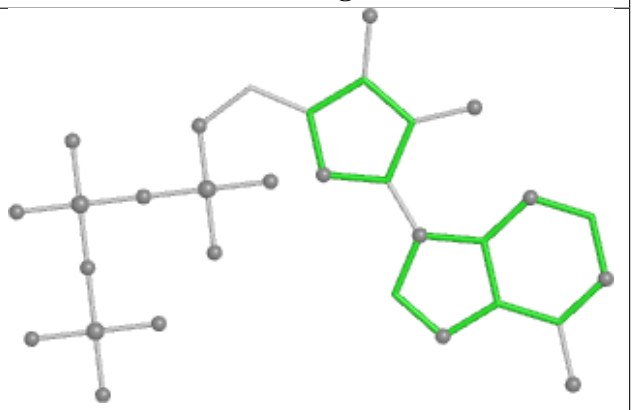
Bond lengths



Bond angles

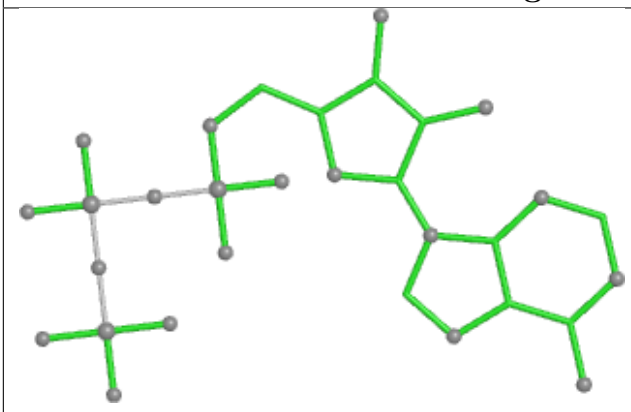


Torsions

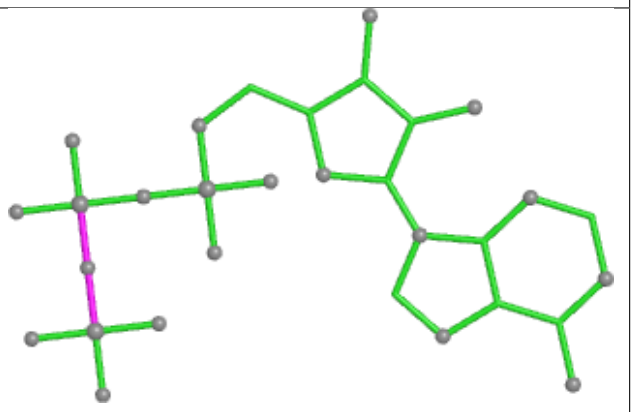


Rings

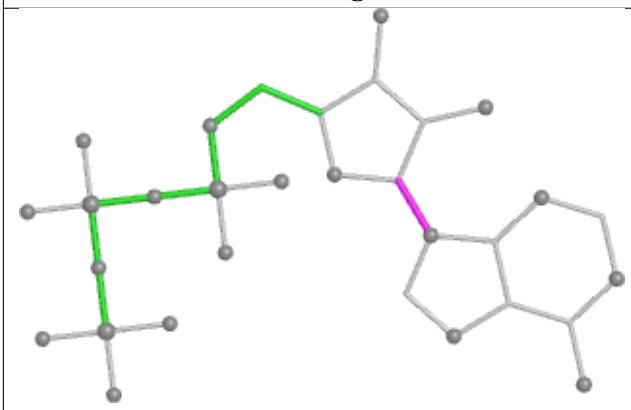
Ligand ATP A 901



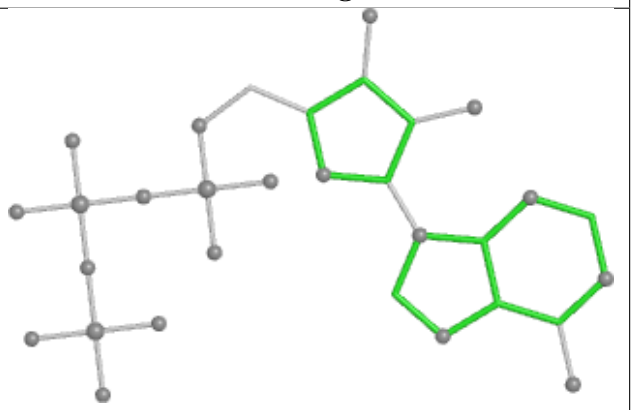
Bond lengths



Bond angles

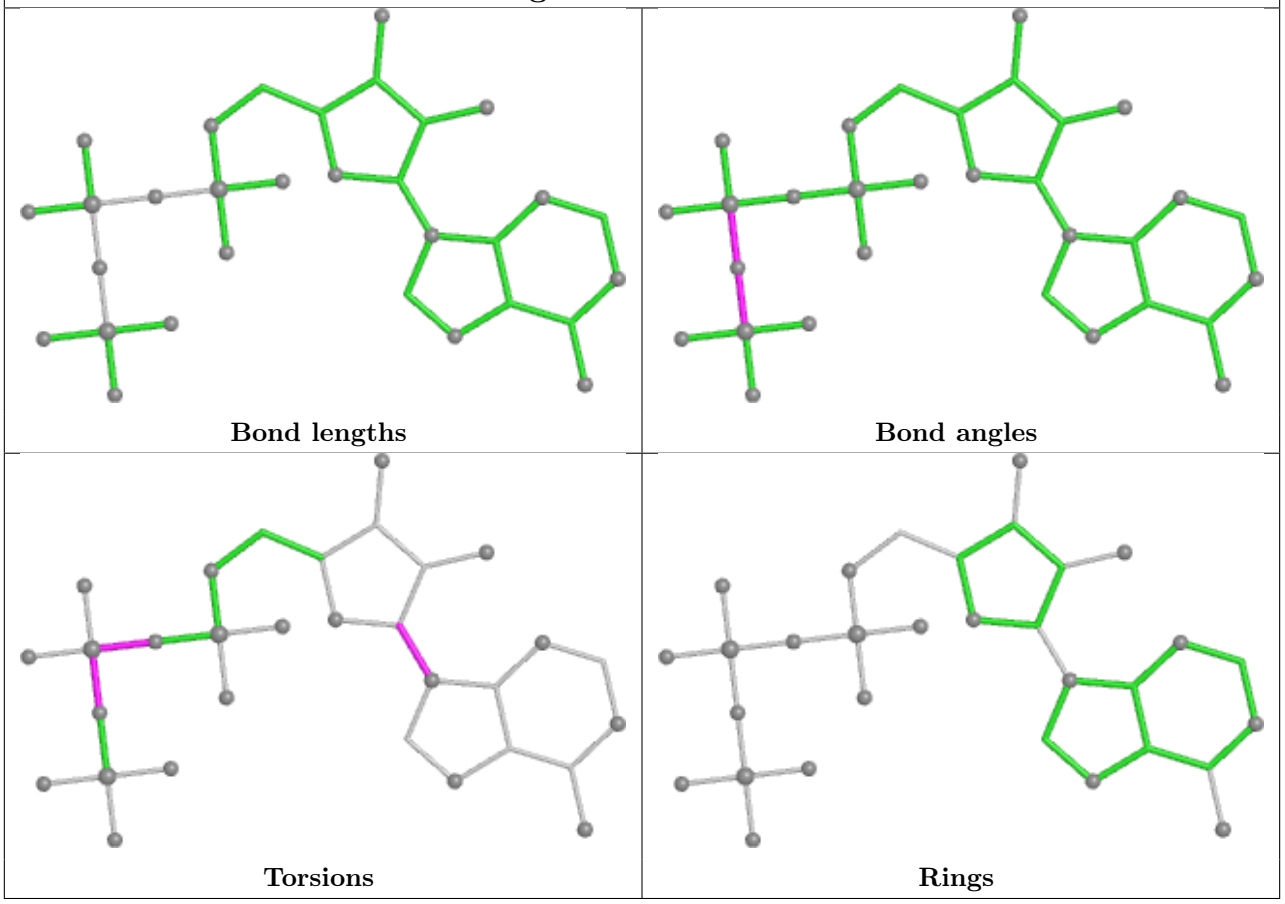


Torsions



Rings

Ligand ATP J 901



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.

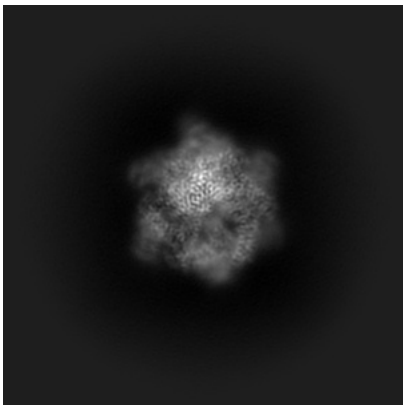
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-68127. These allow visual inspection of the internal detail of the map and identification of artifacts.

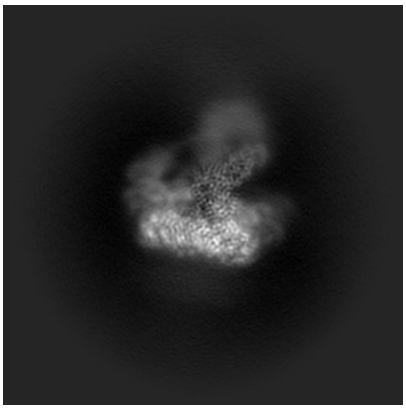
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

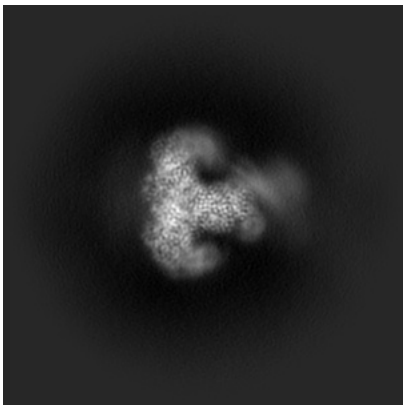
6.1.1 Primary map



X

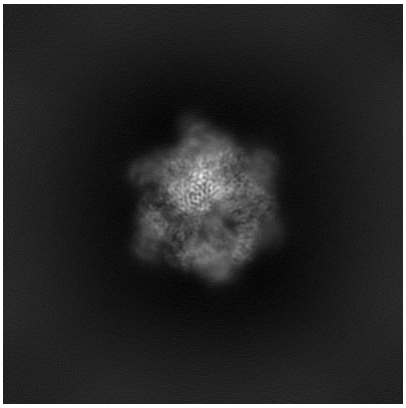


Y

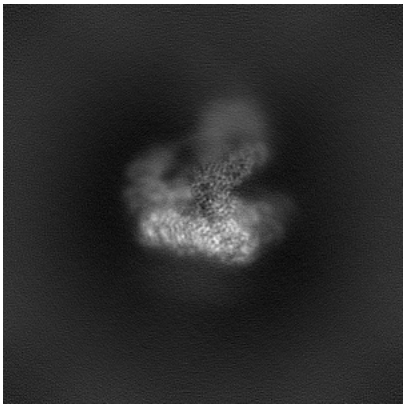


Z

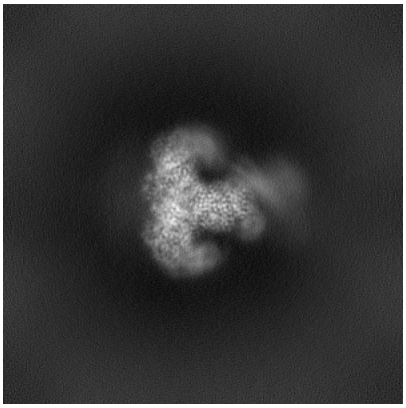
6.1.2 Raw map



X



Y

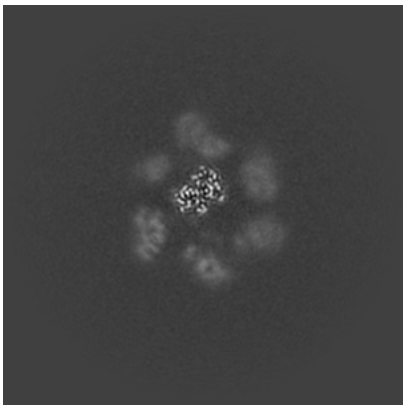


Z

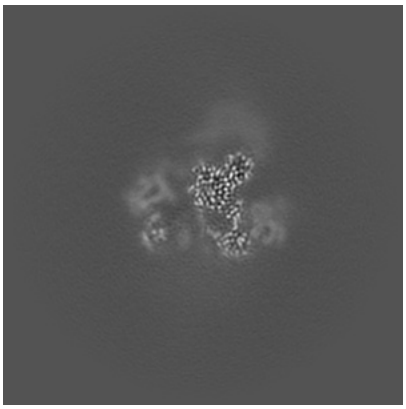
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

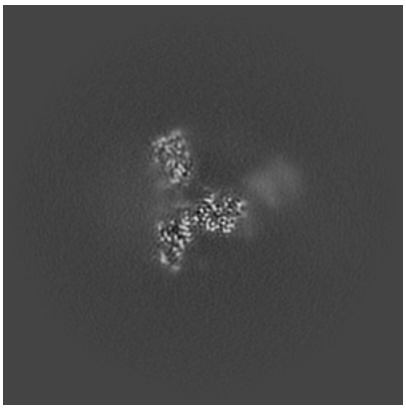
6.2.1 Primary map



X Index: 200

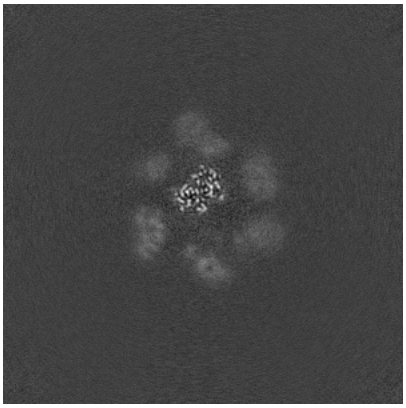


Y Index: 200

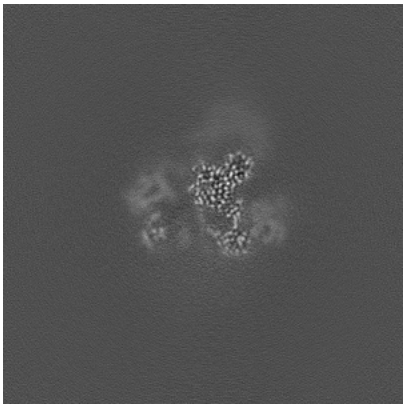


Z Index: 200

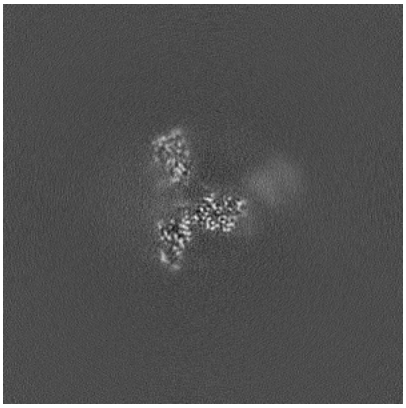
6.2.2 Raw map



X Index: 200



Y Index: 200

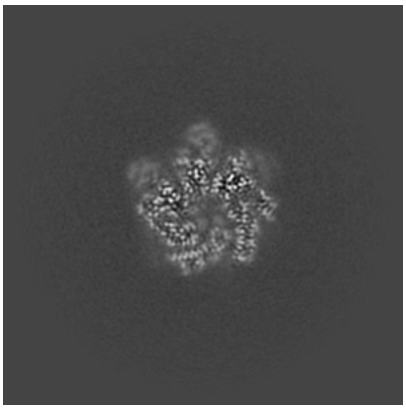


Z Index: 200

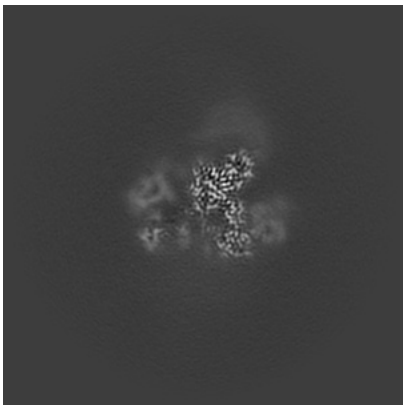
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

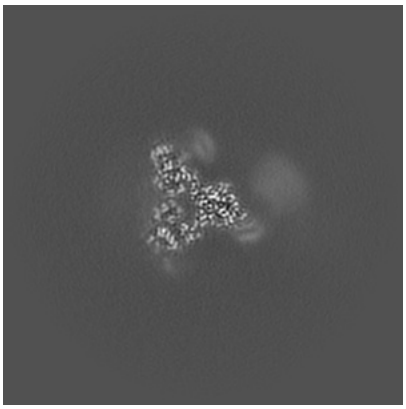
6.3.1 Primary map



X Index: 169

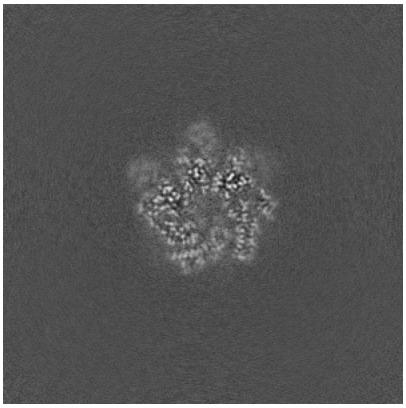


Y Index: 198

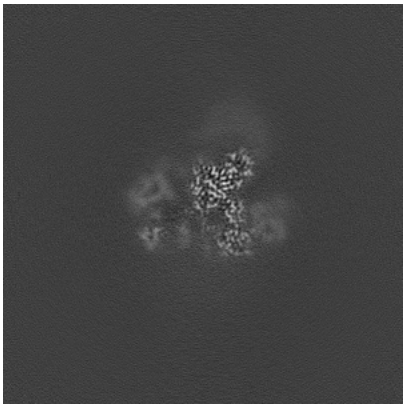


Z Index: 215

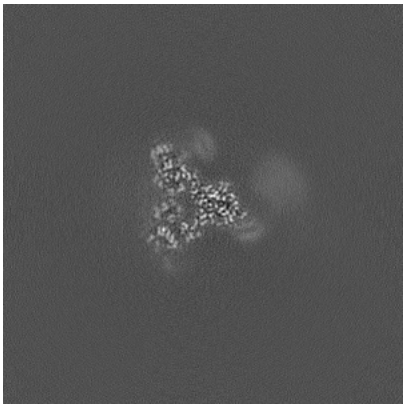
6.3.2 Raw map



X Index: 169



Y Index: 198

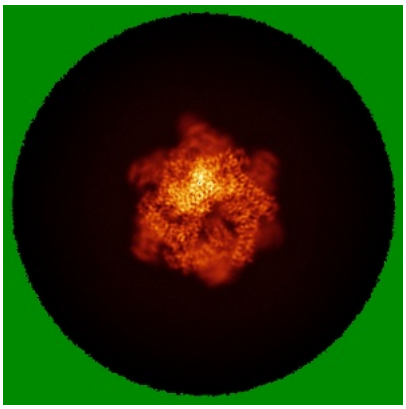


Z Index: 215

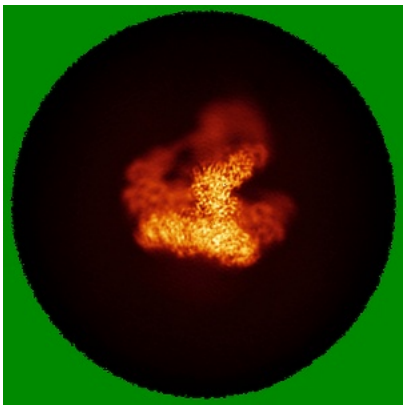
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

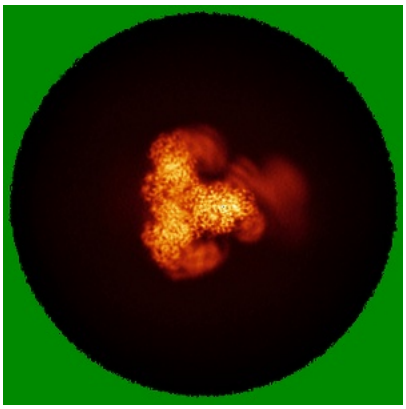
6.4.1 Primary map



X

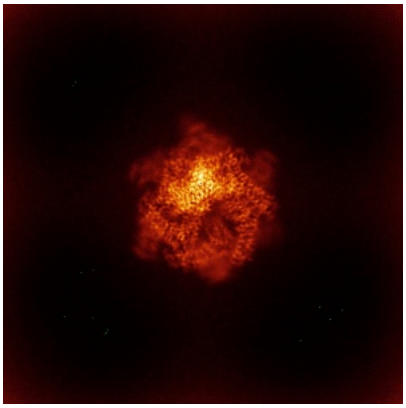


Y

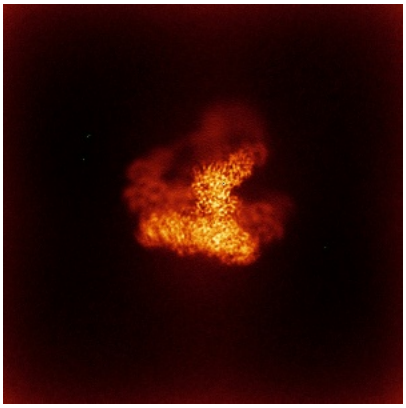


Z

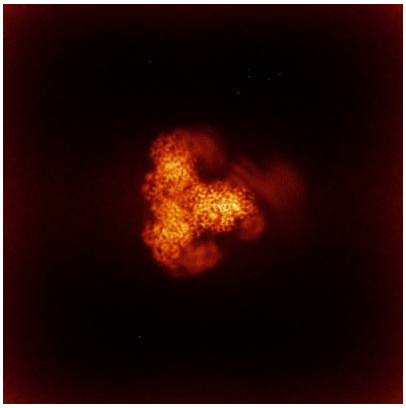
6.4.2 Raw map



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)

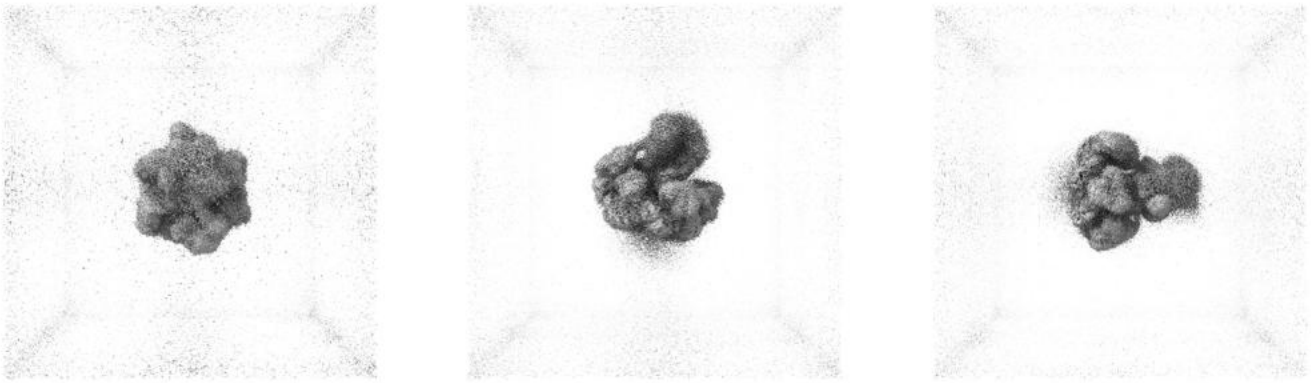
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.05. 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.

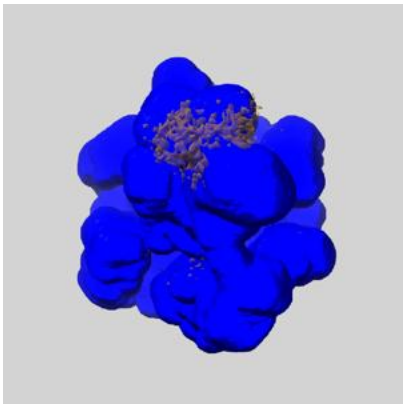
6.6 Mask visualisation (i)

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

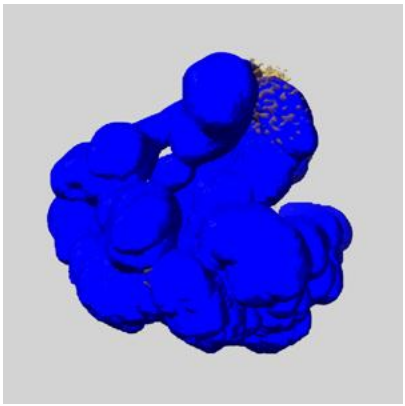
A mask typically either:

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

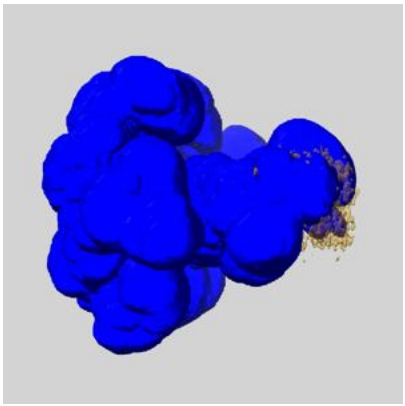
6.6.1 emd_68127_msk_1.map (i)



X

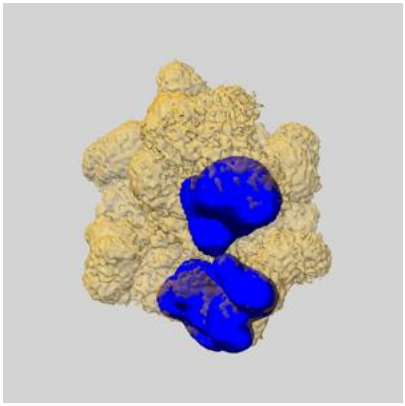


Y

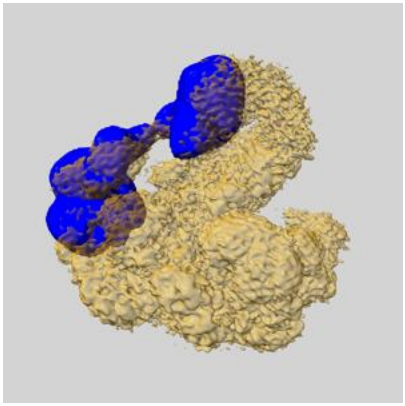


Z

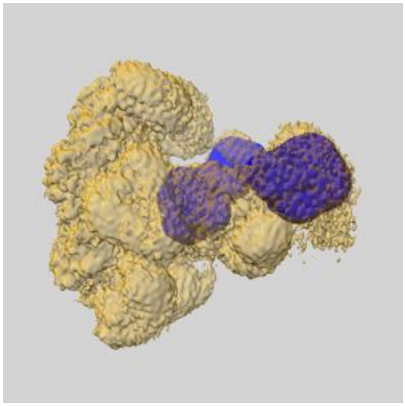
6.6.2 emd_68127_msk_2.map (i)



X



Y

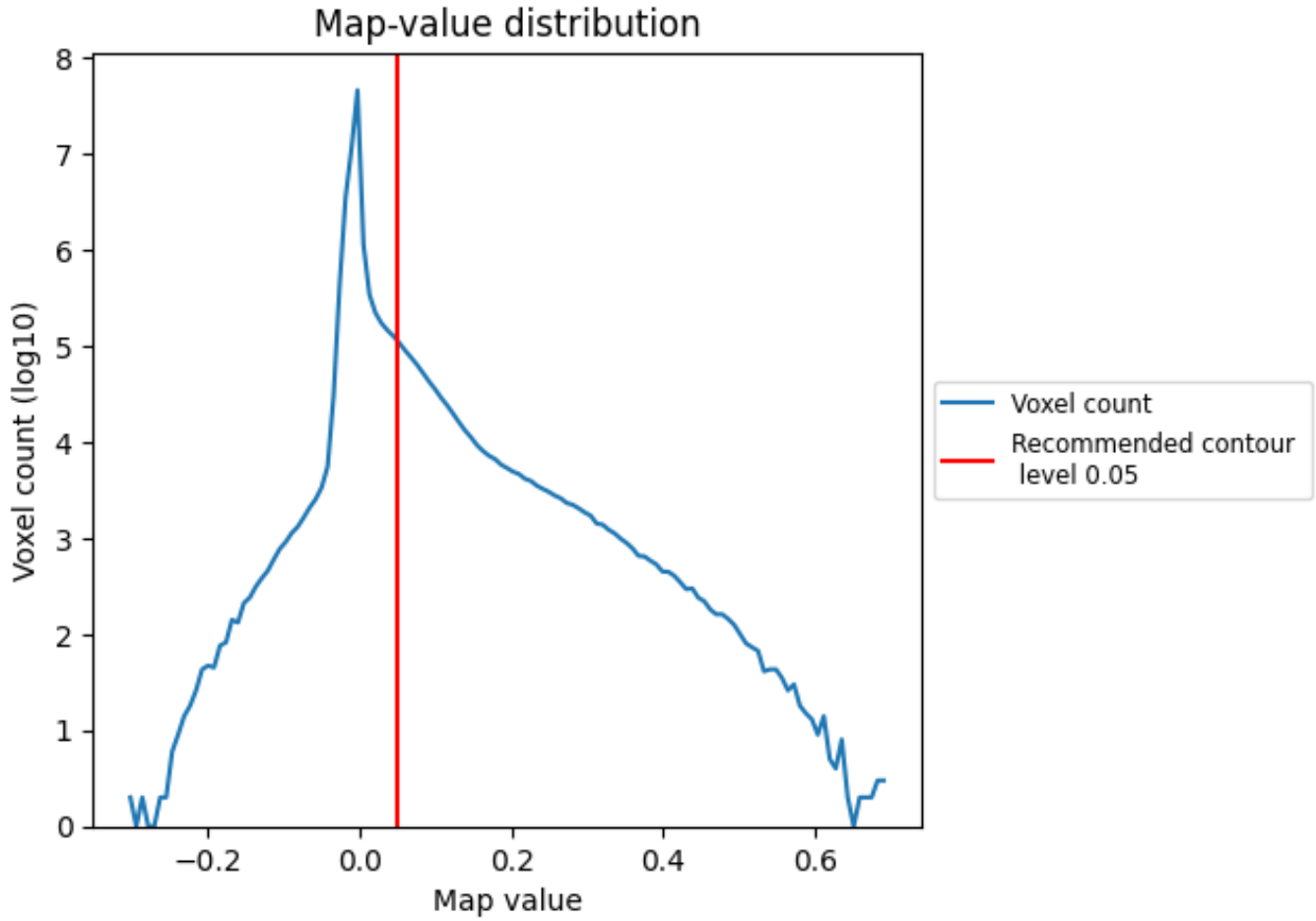


Z

7 Map analysis

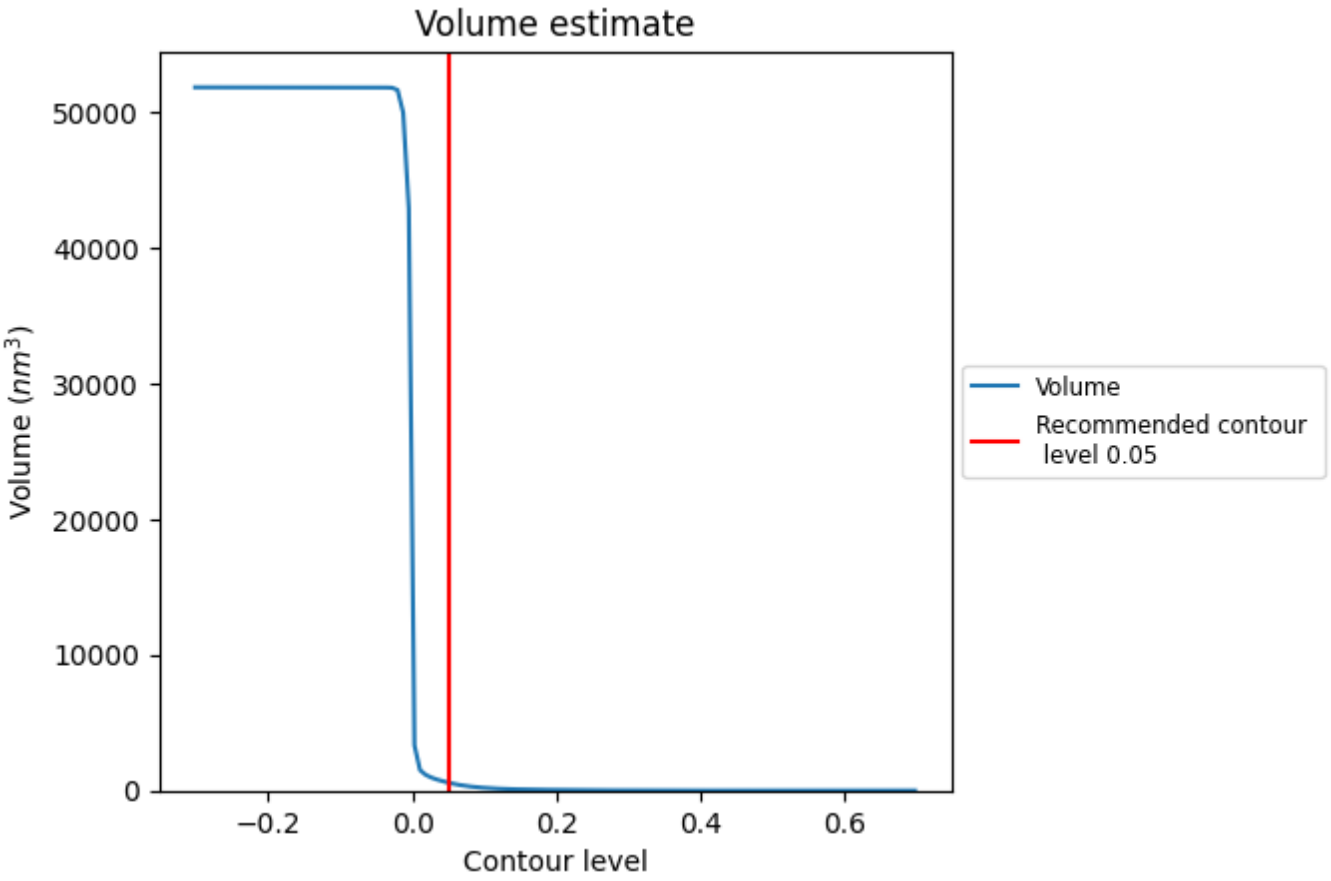
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

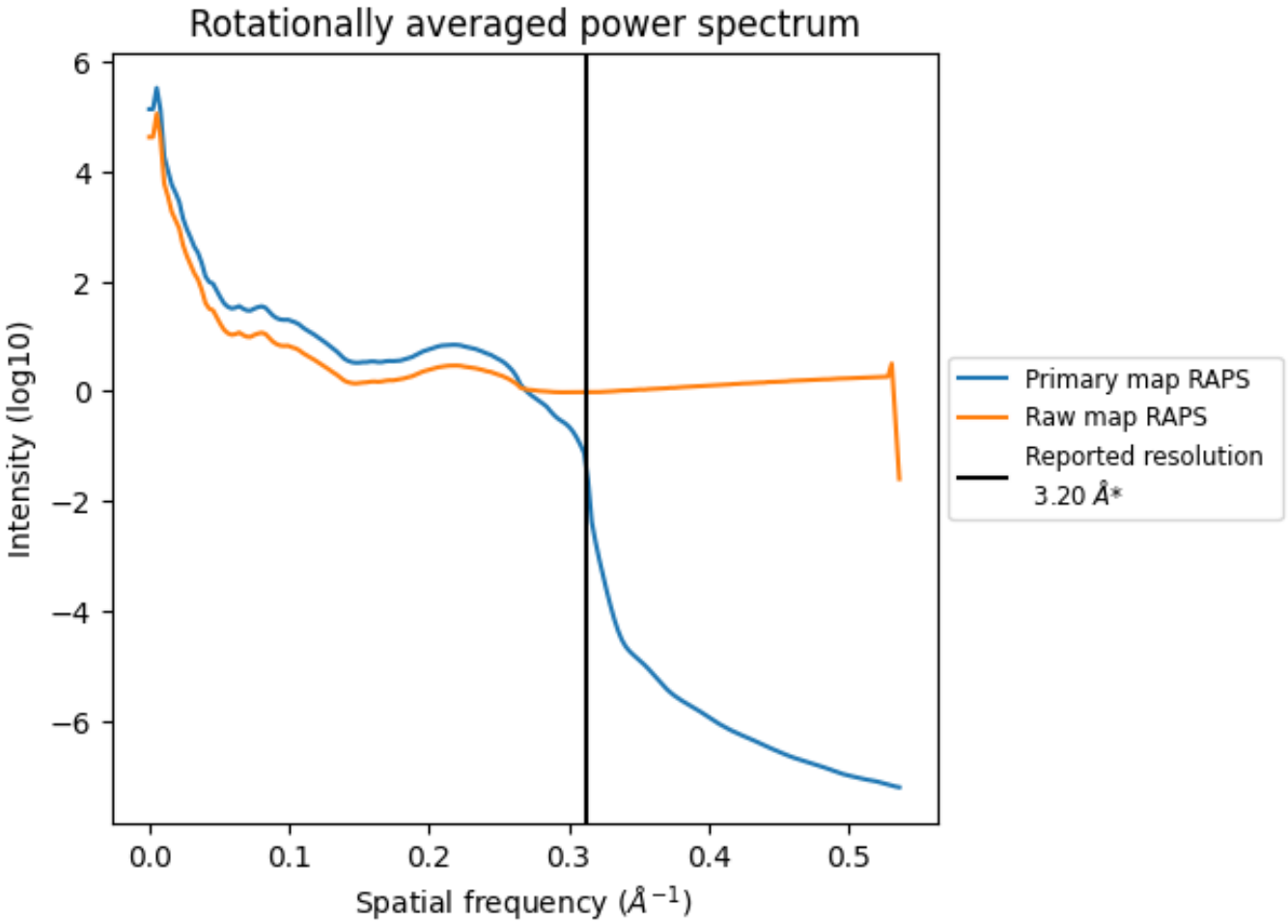
7.2 Volume estimate (i)



The volume at the recommended contour level is 580 nm^3; this corresponds to an approximate mass of 523 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)

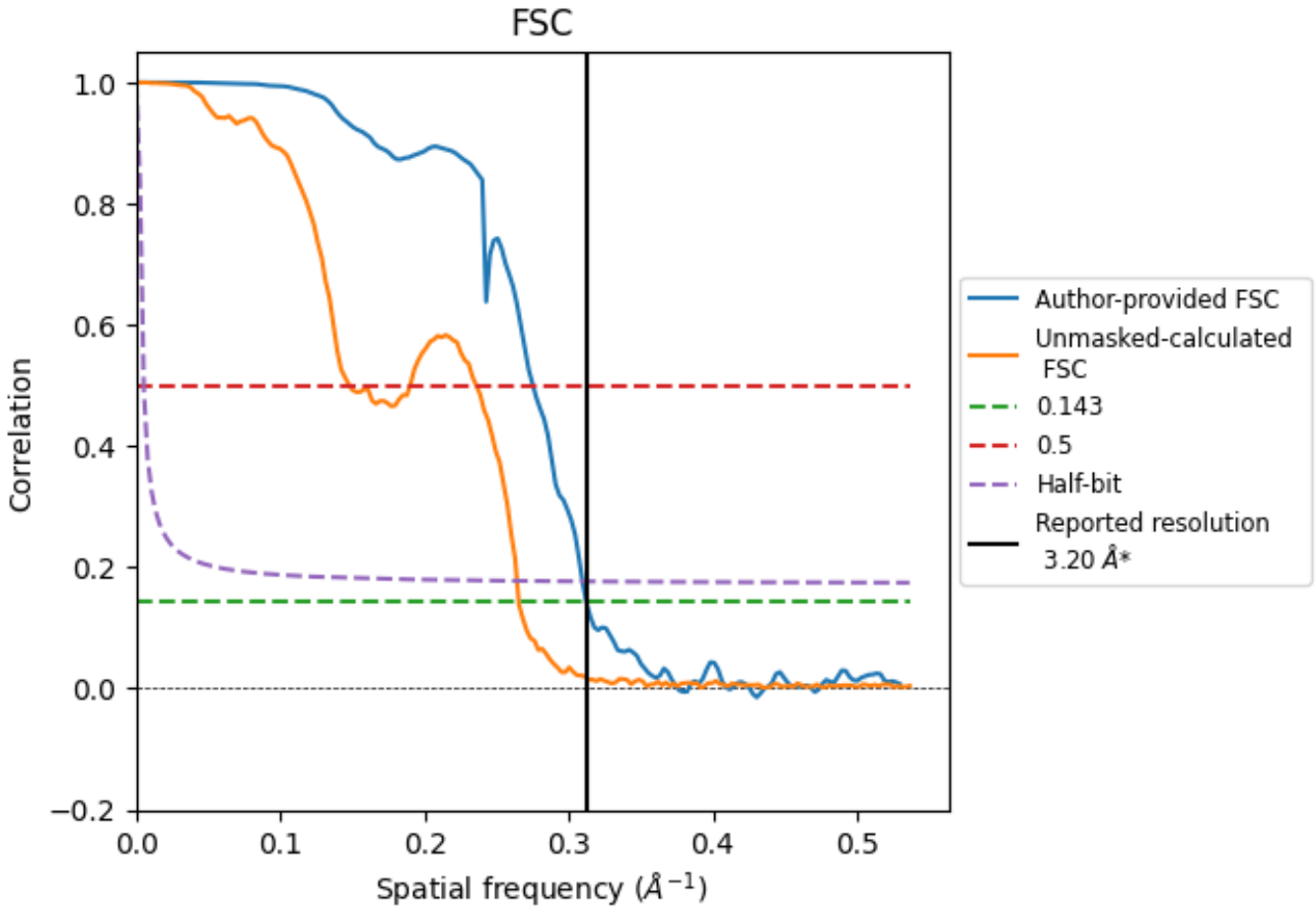


*Reported resolution corresponds to spatial frequency of 0.312 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.312 Å^{-1}

8.2 Resolution estimates (i)

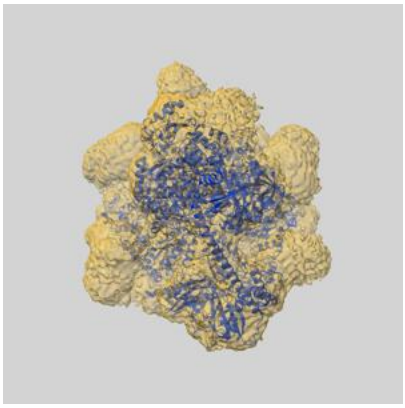
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.20	3.63	3.23
Unmasked-calculated*	3.77	6.76	3.79

*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 3.77 differs from the reported value 3.2 by more than 10 %

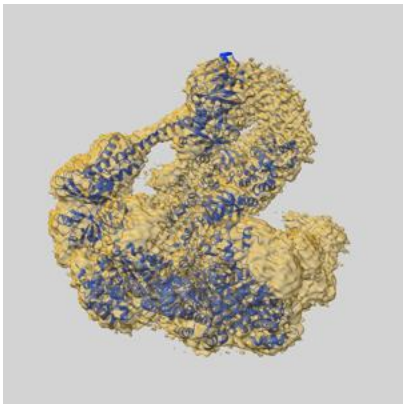
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-68127 and PDB model 21ZV. Per-residue inclusion information can be found in section 3 on page 7.

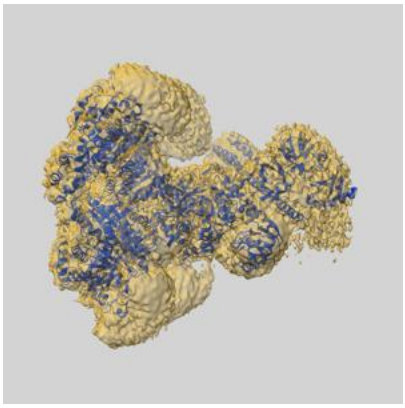
9.1 Map-model overlay



X



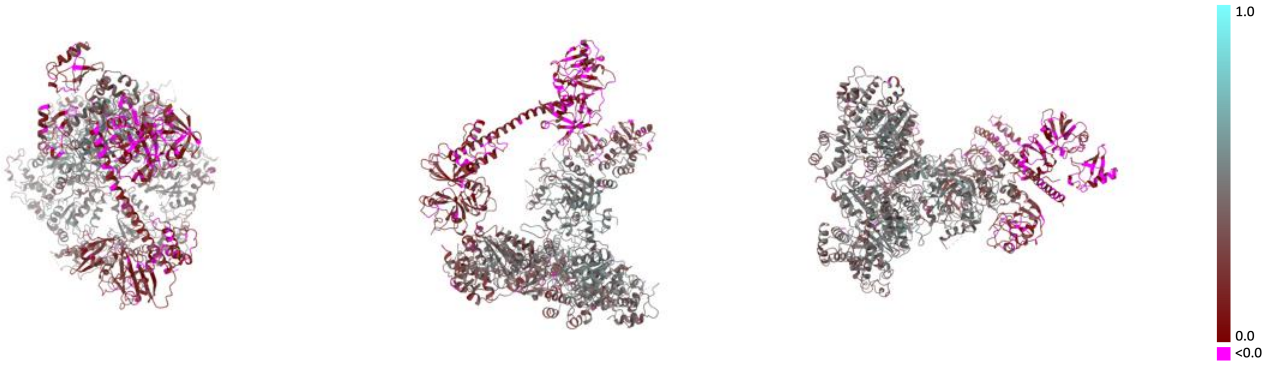
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05 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.

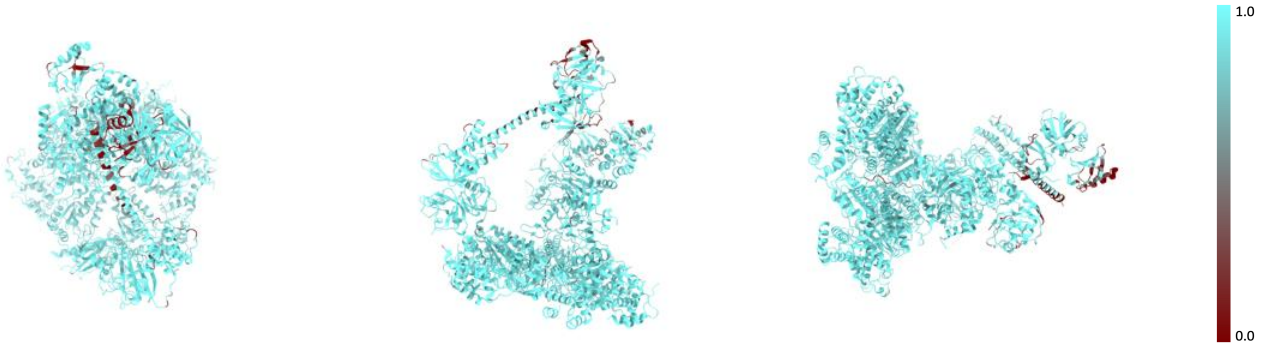
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

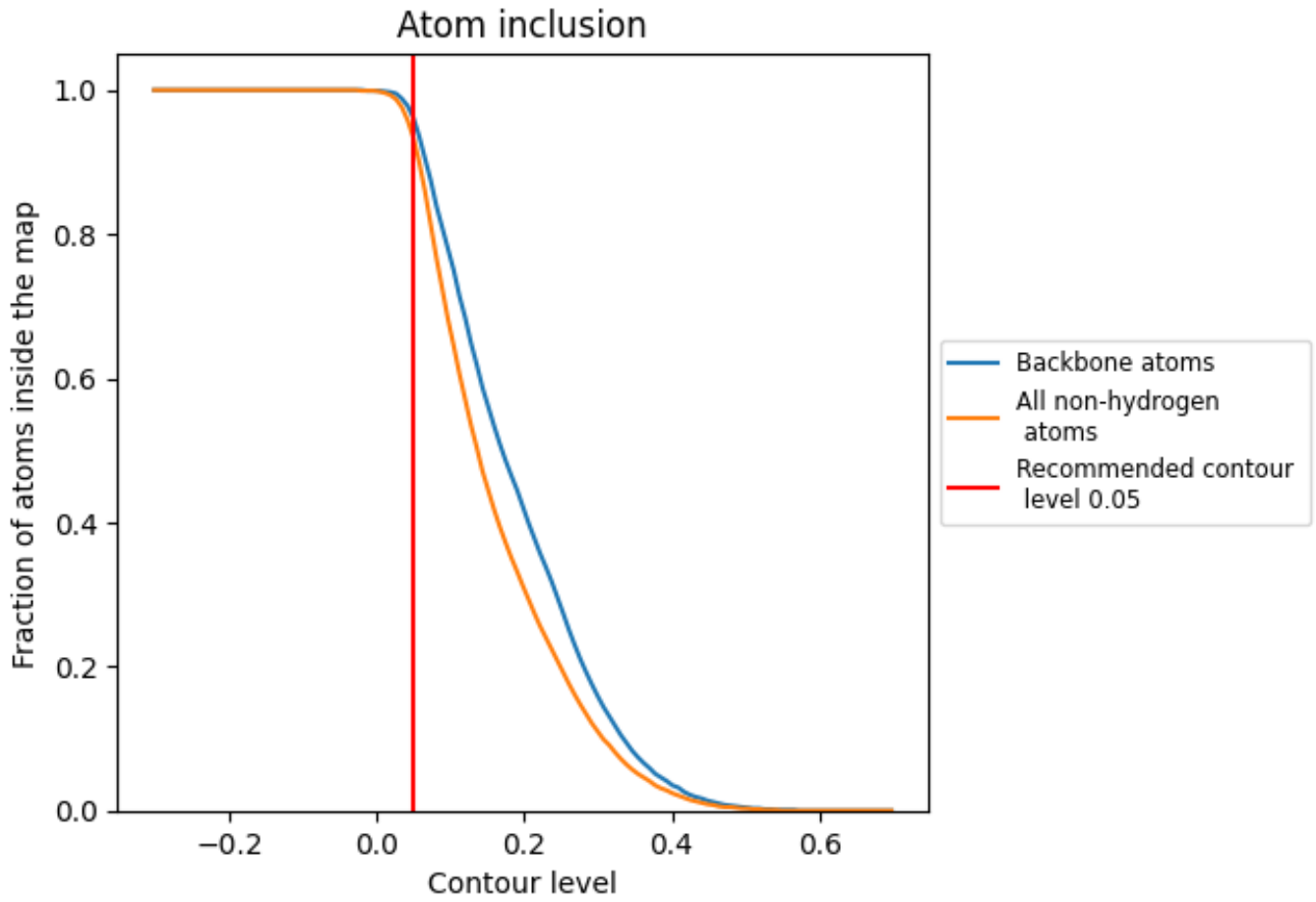
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.05).

9.4 Atom inclusion (i)



At the recommended contour level, 96% of all backbone atoms, 93% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9330	0.3270
A	0.9730	0.4210
B	0.8870	0.1480
C	0.5110	0.0290
D	0.8490	0.1040
G	0.9770	0.4370
H	0.9820	0.4170
I	0.9750	0.4250
J	0.9580	0.3650
K	0.9770	0.3360
L	0.7450	0.2850
M	0.9590	0.4500
N	0.8590	0.1600
O	0.8640	0.1320
P	0.9650	0.1780

