



wwPDB EM Validation Summary Report ⓘ

Nov 3, 2024 – 04:33 am GMT

PDB ID : 8A5Y
EMDB ID : EMD-15199
Title : S. cerevisiae apo unphosphorylated APC/C.
Authors : Barford, D.; Fernandez-Vazquez, E.; Zhang, Z.; Yang, J.
Deposited on : 2022-06-16
Resolution : 4.90 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.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

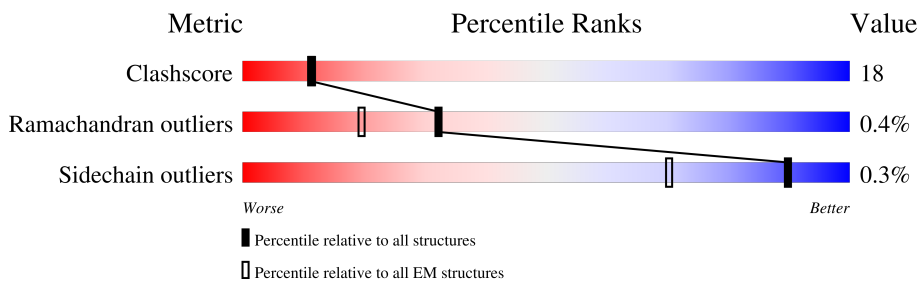
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.90 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	F	758	<div> <div>26%</div> <div>38%</div> <div>27%</div> <div>34%</div> </div>
1	H	758	<div> <div>54%</div> <div>43%</div> <div>23%</div> <div>33%</div> </div>
2	J	850	<div> <div>11%</div> <div>35%</div> <div>25%</div> <div>40%</div> </div>
2	K	850	<div> <div>45%</div> <div>36%</div> <div>24%</div> <div>41%</div> </div>
3	G	124	<div> <div>7%</div> <div>17%</div> <div>11%</div> <div>72%</div> </div>
3	W	124	<div> <div>28%</div> <div>19%</div> <div>10%</div> <div>72%</div> </div>
4	E	265	<div> <div>37%</div> <div>35%</div> <div>14%</div> <div>51%</div> </div>
5	T	853	<div> <div>40%</div> <div>54%</div> <div>22%</div> <div>24%</div> </div>

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Mol	Chain	Length	Quality of chain
6	U	165	
7	C	1748	
8	O	685	
9	D	626	
9	P	626	
10	I	170	
11	N	368	
12	Q	652	
13	A	250	

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 57866 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 Anaphase-promoting complex subunit CDC27.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	F	502	Total	C	N	O	S	0	0
			3991	2569	656	739	27		
1	H	505	Total	C	N	O	S	0	0
			4038	2599	664	748	27		

- Molecule 2 is a protein called Anaphase-promoting complex subunit CDC16.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	J	509	Total	C	N	O	S	0	0
			4124	2658	674	769	23		
2	K	505	Total	C	N	O	S	0	0
			4102	2642	673	764	23		

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	841	LYS	-	expression tag	UNP P09798
J	842	SER	-	expression tag	UNP P09798
J	843	SER	-	expression tag	UNP P09798
J	844	ILE	-	expression tag	UNP P09798
J	845	PRO	-	expression tag	UNP P09798
J	846	GLU	-	expression tag	UNP P09798
J	847	ASN	-	expression tag	UNP P09798
J	848	LEU	-	expression tag	UNP P09798
J	849	TYR	-	expression tag	UNP P09798
J	850	PHE	-	expression tag	UNP P09798
K	841	LYS	-	expression tag	UNP P09798
K	842	SER	-	expression tag	UNP P09798
K	843	SER	-	expression tag	UNP P09798
K	844	ILE	-	expression tag	UNP P09798
K	845	PRO	-	expression tag	UNP P09798
K	846	GLU	-	expression tag	UNP P09798
K	847	ASN	-	expression tag	UNP P09798

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Chain	Residue	Modelled	Actual	Comment	Reference
K	848	LEU	-	expression tag	UNP P09798
K	849	TYR	-	expression tag	UNP P09798
K	850	PHE	-	expression tag	UNP P09798

- Molecule 3 is a protein called Anaphase-promoting complex subunit CDC26.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	35	Total	C	N	O	S	0	0
			284	174	51	58	1		
3	W	35	Total	C	N	O	S	0	0
			284	174	51	58	1		

- Molecule 4 is a protein called Anaphase-promoting complex subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	130	Total	C	N	O	S	0	0
			1091	678	201	205	7		

- Molecule 5 is a protein called Anaphase-promoting complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	T	650	Total	C	N	O	S	0	0
			5362	3476	877	985	24		

- Molecule 6 is a protein called Anaphase-promoting complex subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	U	114	Total	C	N	O	S	0	0
			912	574	164	162	12		

- Molecule 7 is a protein called Anaphase-promoting complex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C	1406	Total	C	N	O	S	0	0
			10832	7003	1749	2034	46		

- Molecule 8 is a protein called Anaphase-promoting complex subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	O	658	Total	C	N	O	S	0	0
			5285	3399	869	990	27		

- Molecule 9 is a protein called Anaphase-promoting complex subunit CDC23.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	D	560	Total	C	N	O	S	0	0
			4524	2925	729	844	26		
9	P	556	Total	C	N	O	S	0	0
			4520	2923	738	832	27		

- Molecule 10 is a protein called Anaphase-promoting complex subunit SWM1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	111	Total	C	N	O	S	0	0
			906	568	158	176	4		

- Molecule 11 is a protein called Anaphase-promoting complex subunit MND2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	N	96	Total	C	N	O	S	0	0
			784	504	138	139	3		

- Molecule 12 is a protein called Anaphase-promoting complex subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Q	623	Total	C	N	O	S	0	0
			5086	3279	842	952	13		

- Molecule 13 is a protein called Anaphase-promoting complex subunit DOC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	A	218	Total	C	N	O	S	0	0
			1738	1113	303	312	10		

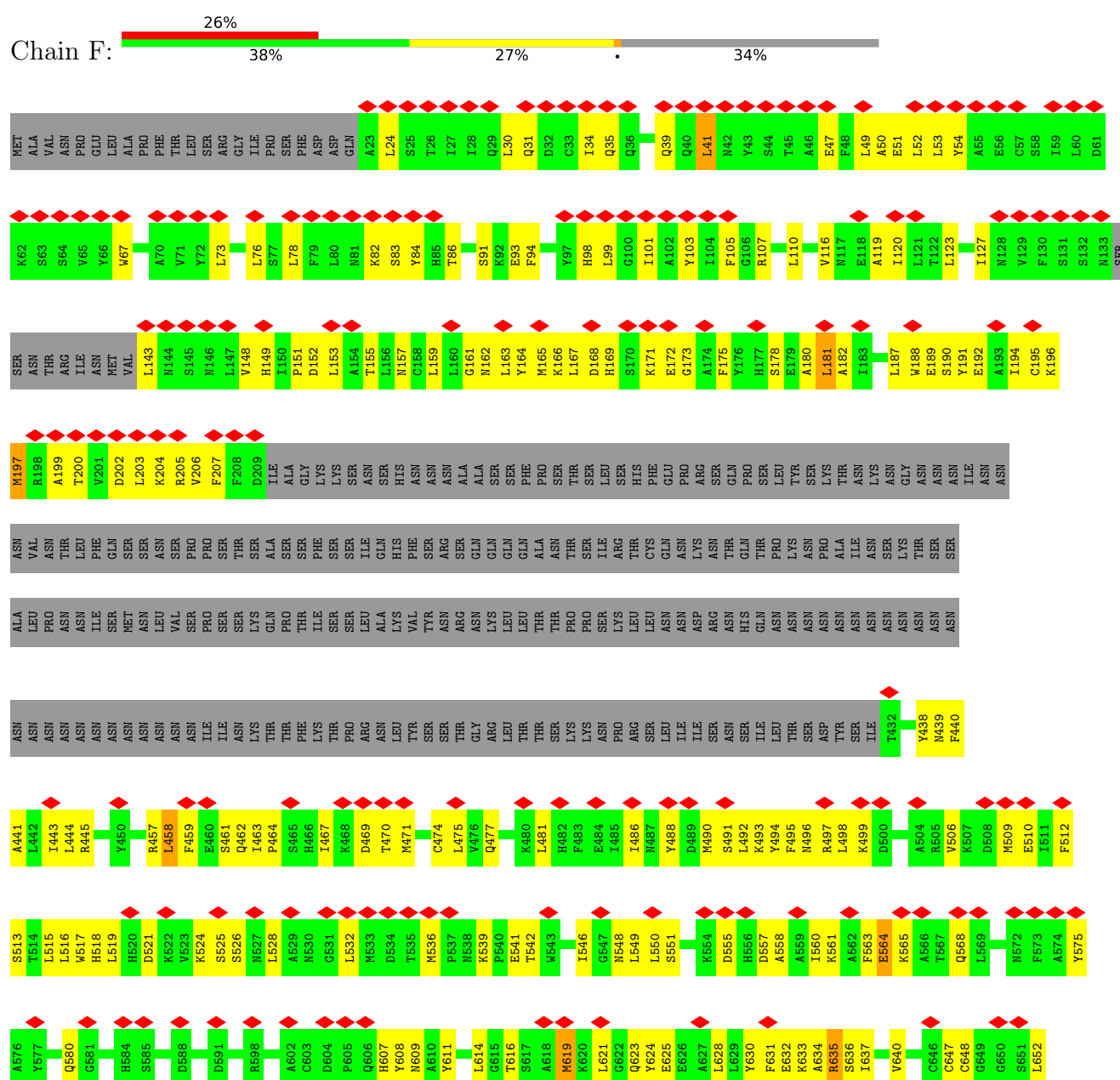
- Molecule 14 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

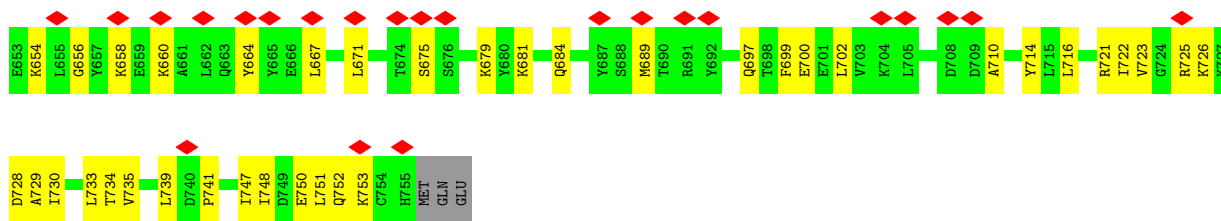
Mol	Chain	Residues	Atoms		AltConf
14	U	3	Total	Zn	0
			3	3	

3 Residue-property plots

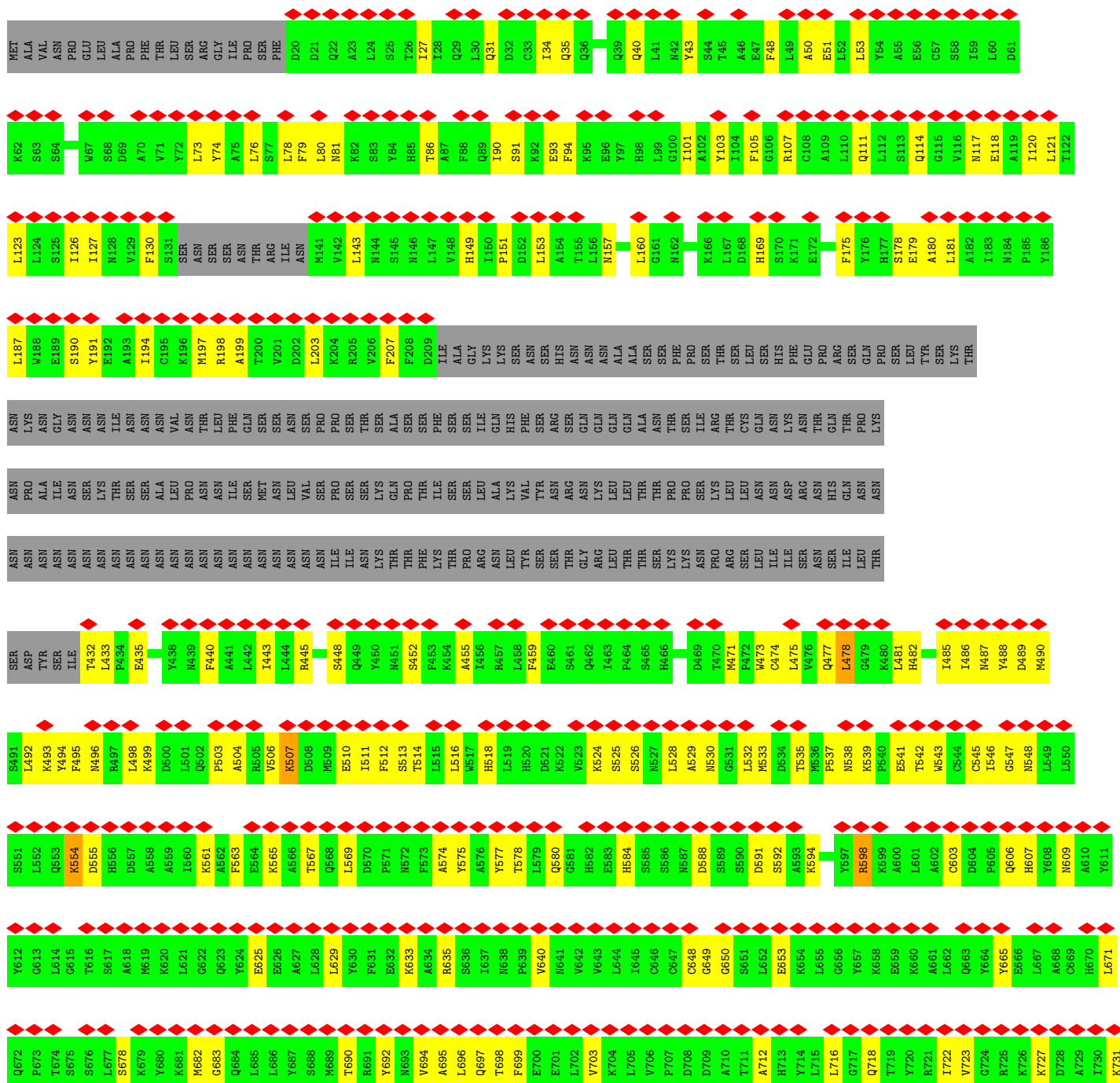
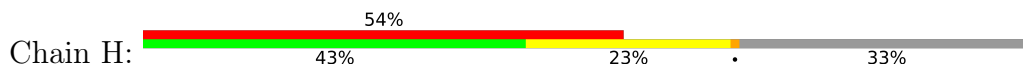
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Anaphase-promoting complex subunit CDC27



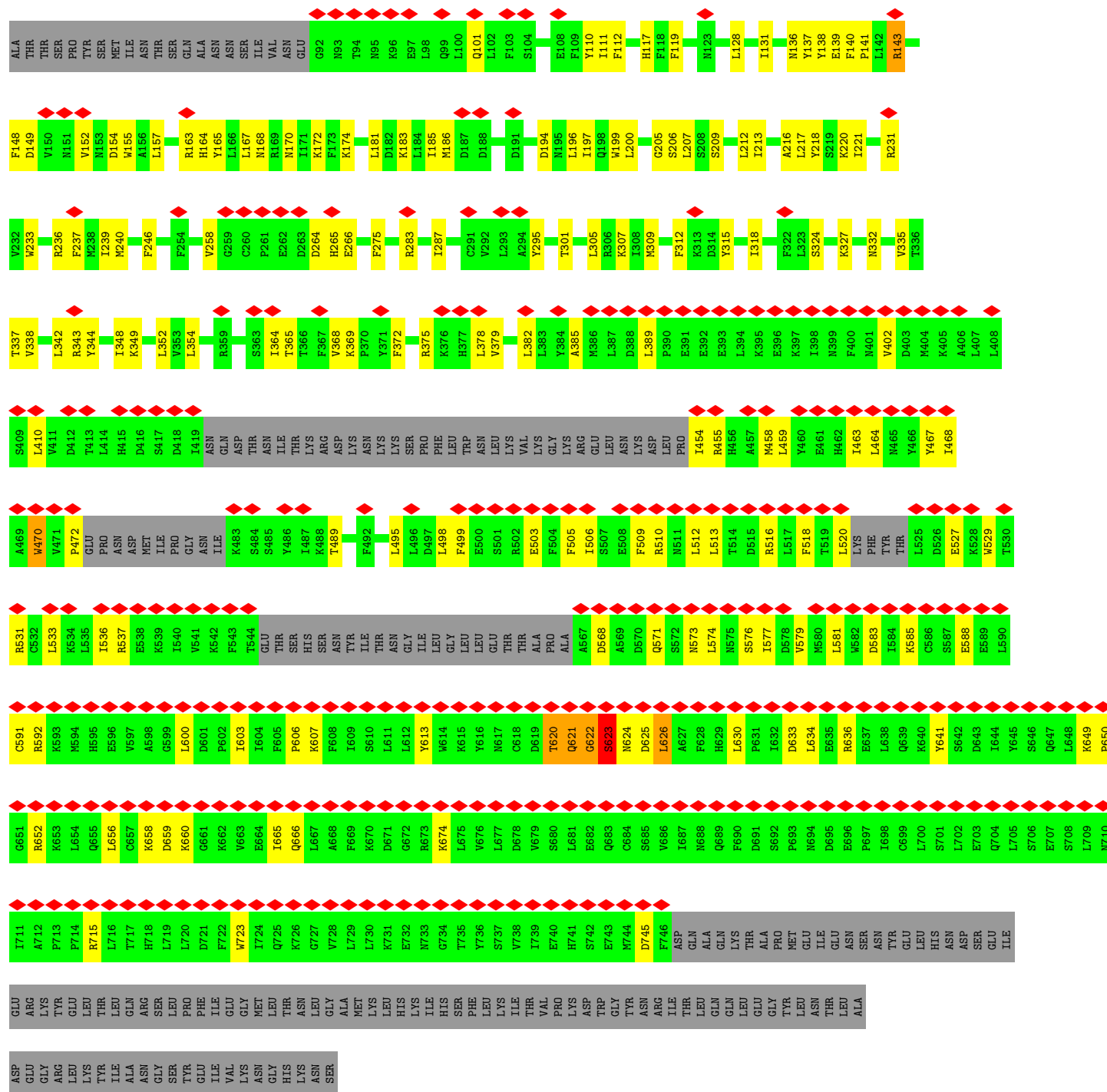


• Molecule 1: Anaphase-promoting complex subunit CDC27

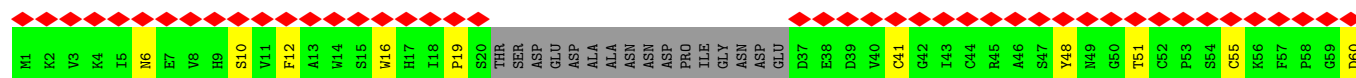


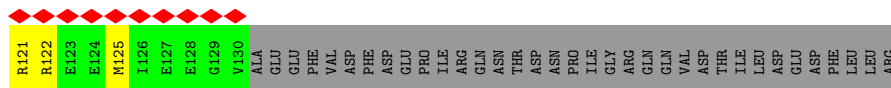


MET	PHE	VAL	ALA	ASP	GLU	ASP	L241	Q310	F370	N431	D493	K556	N616	L676	L737
LYS	VAL	ASN	ASN	LYS	VAL	HIS	M242	R311	A371	L432	E494	S557	L617	Q677	K738
CYS	ASN	ASN	ASN	ASN	VAL	ASN	Q243	F312	Q372	Y433	F495	S558	A618	L678	P739
LEU	VAL	ASN	ASN	ASN	HIS	ASN	H244	D313	N373	K434	N496	L559	E619	N679	N740
CYS	ALA	ASN	ASN	ASN	ASN	ASN	M245	D314	N374	I435	N498	L560	S620	N680	N741
THR	ALA	ASN	ASN	ASN	GLY	ASN	T246	A315	F375	N436	I499	D561	S621	S742	S743
CYS	ARG	ALA	ASN	ASN	ALA	ASN	T248	L316	N376	L437	P501	P562	F622	T683	S744
HIS	THR	THR	THR	THR	ALA	ALA	K255	D317	K377	S438	A502	S563	V623	R684	S745
THR	GLN	GLN	GLN	GLN	ALA	ALA	V256	V319	A378	Y440	Y503	F564	L624	R685	A746
ILE	GLN	GLN	GLN	GLN	VAL	VAL	Y257	I319	R379	I441	I504	A565	L625	K686	T745
VAL	LEU	LEU	LEU	LEU	VAL	VAL	N258	G320	D380	N442	G505	A566	Y626	L687	A746
ILE	PRO	PRO	PRO	PRO	VAL	VAL	I259	E321	F382	T443	C506	A567	D627	N688	L747
GLY	ASN	ASN	ASN	ASN	VAL	VAL	S260	Y322	F382	T443	L507	A568	L628	E689	N748
LYS	ASP	ASP	ASP	ASP	VAL	VAL	N261	N323	R383	E444	L508	L569	C629	N690	K749
ALA	ASN	ASN	ASN	ASN	ALA	ALA	D262	P324	R383	D445	F571	G570	P630	E691	N750
THR	GLN	GLN	GLN	GLN	ALA	ALA	P263	P325	I386	S449	E509	F571	N631	L692	A751
HIS	ASN	ASN	ASN	ASN	THR	THR	D264	S326	L387	N450	L510	A572	D632	A693	L752
THR	ASP	ASP	ASP	ASP	LEU	LEU	A266	GLU	V388	E451	S511	H573	P633	L754	E753
LYS	ARG	ARG	ARG	ARG	LEU	LEU	D265	ASP	D389	I452	N512	T574	L634	K695	L754
SER	GLN	GLN	GLN	GLN	SER	SER	A266	PRO	I390	L453	K513	Y575	V635	C696	N755
SER	PRO	PRO	PRO	PRO	LYS	LYS	Q271	THR	K391	K455	N514	A576	L636	F697	N756
ALA	TRP	TRP	TRP	TRP	GLY	GLY	V272	THR	N392	D456	K515	L577	L637	R698	L758
THR	ASN	ASN	ASN	ASN	LEU	LEU	N275	ALA	N392	K456	L516	E578	N637	C699	SER
ASN	THR	THR	THR	THR	LEU	LEU	N276	ALA	F393	D457	F517	S579	E638	E699	LEU
LEU	THR	THR	THR	THR	THR	THR	Q278	ASN	E394	K458	L518	Q581	N639	V700	ASP
LYS	THR	THR	THR	THR	THR	THR	Y279	MET	F396	L459	L518	E580	S640	L701	ALA
LEU	GLN	GLN	GLN	GLN	ALA	ALA	V280	SER	F396	L459	L518	E580	V641	E702	ASN
MET	SER	SER	SER	SER	ARG	ARG	I285	ASN	F396	L459	L518	E580	V641	E702	ASN
GLN	LEU	LEU	LEU	LEU	VAL	VAL	L286	ASN	F396	L459	L518	E580	V641	E702	ASN
ASN	LEU	LEU	LEU	LEU	VAL	VAL	T287	THR	F396	L459	L518	E580	V641	E702	ASN
PRO	ASN	ASN	ASN	ASN	VAL	VAL	R288	THR	F396	L459	L518	E580	V641	E702	ASN
SER	PRO	PRO	PRO	PRO	GLN	GLN	N289	THR	F396	L459	L518	E580	V641	E702	ASN
PRO	LEU	LEU	LEU	LEU	ARG	ARG	N290	THR	F396	L459	L518	E580	V641	E702	ASN
GLU	ILE	ILE	ILE	ILE	TYR	TYR	L291	THR	F396	L459	L518	E580	V641	E702	ASN
LYS	LYS	LYS	LYS	LYS	GLN	GLN	D292	THR	F396	L459	L518	E580	V641	E702	ASN
HIS	ASP	ASP	ASP	ASP	SER	SER	G293	THR	F396	L459	L518	E580	V641	E702	ASN
GLN	VAL	VAL	VAL	VAL	SER	SER	V294	THR	F396	L459	L518	E580	V641	E702	ASN
ASN	ASP	ASP	ASP	ASP	GLY	GLY	N295	THR	F396	L459	L518	E580	V641	E702	ASN
ASN	GLY	GLY	GLY	GLY	ILE	ILE	I296	THR	F396	L459	L518	E580	V641	E702	ASN
THR	THR	THR	THR	THR	VAL	VAL	L297	THR	F396	L459	L518	E580	V641	E702	ASN
LEU	PRO	PRO	PRO	PRO	ARG	ARG	C298	THR	F396	L459	L518	E580	V641	E702	ASN
ALA	HIS	HIS	HIS	HIS	ASP	ASP	R299	THR	F396	L459	L518	E580	V641	E702	ASN
SER	GLN	GLN	GLN	GLN	VAL	VAL	Y300	THR	F396	L459	L518	E580	V641	E702	ASN
ALA	ASP	ASP	ASP	ASP	VAL	VAL	L301	THR	F396	L459	L518	E580	V641	E702	ASN
SER	PRO	PRO	PRO	PRO	ARG	ARG	L302	THR	F396	L459	L518	E580	V641	E702	ASN
PRO	ASN	ASN	ASN	ASN	ASP	ASP	G303	THR	F396	L459	L518	E580	V641	E702	ASN
ASN	ASN	ASN	ASN	ASN	GLU	GLU	L304	THR	F396	L459	L518	E580	V641	E702	ASN
PRO	SER	SER	SER	SER	ASP	ASP	F306	THR	F396	L459	L518	E580	V641	E702	ASN
SER	THR	THR	THR	THR	VAL	VAL	V307	THR	F396	L459	L518	E580	V641	E702	ASN
THR	THR	THR	THR	THR	VAL	VAL	K308	THR	F396	L459	L518	E580	V641	E702	ASN
LEU	ALA	ALA	ALA	ALA	ASP	ASP	L309	THR	F396	L459	L518	E580	V641	E702	ASN
ALA	GLN	GLN	GLN	GLN	GLU	GLU		THR	F396	L459	L518	E580	V641	E702	ASN
ASP	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
GLU	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
ASP	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
GLU	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
ASP	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
GLU	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
ASP	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
GLU	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
ASP	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
GLU	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
ASP	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
GLU	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
ASP	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
GLU	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
ASP	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
GLU	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
ASP	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
GLU	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
ASP	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
GLU	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
ASP	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
GLU	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
ASP	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
GLU	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
ASP	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
GLU	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
ASP	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
GLU	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
ASP	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
GLU	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
ASP	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
GLU	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
ASP	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
GLU	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
ASP	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
GLU	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
ASP	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
GLU	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
ASP	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
GLU	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
ASP	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
GLU	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
ASP	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
GLU	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
ASP	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
GLU	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
ASP	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
GLU	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
ASP	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
GLU	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
ASP	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
GLU	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
ASP	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L518	E580	V641	E702	ASN
GLU	ASN	ASN	ASN	ASN	ASP	ASP		THR	F396	L459	L5				

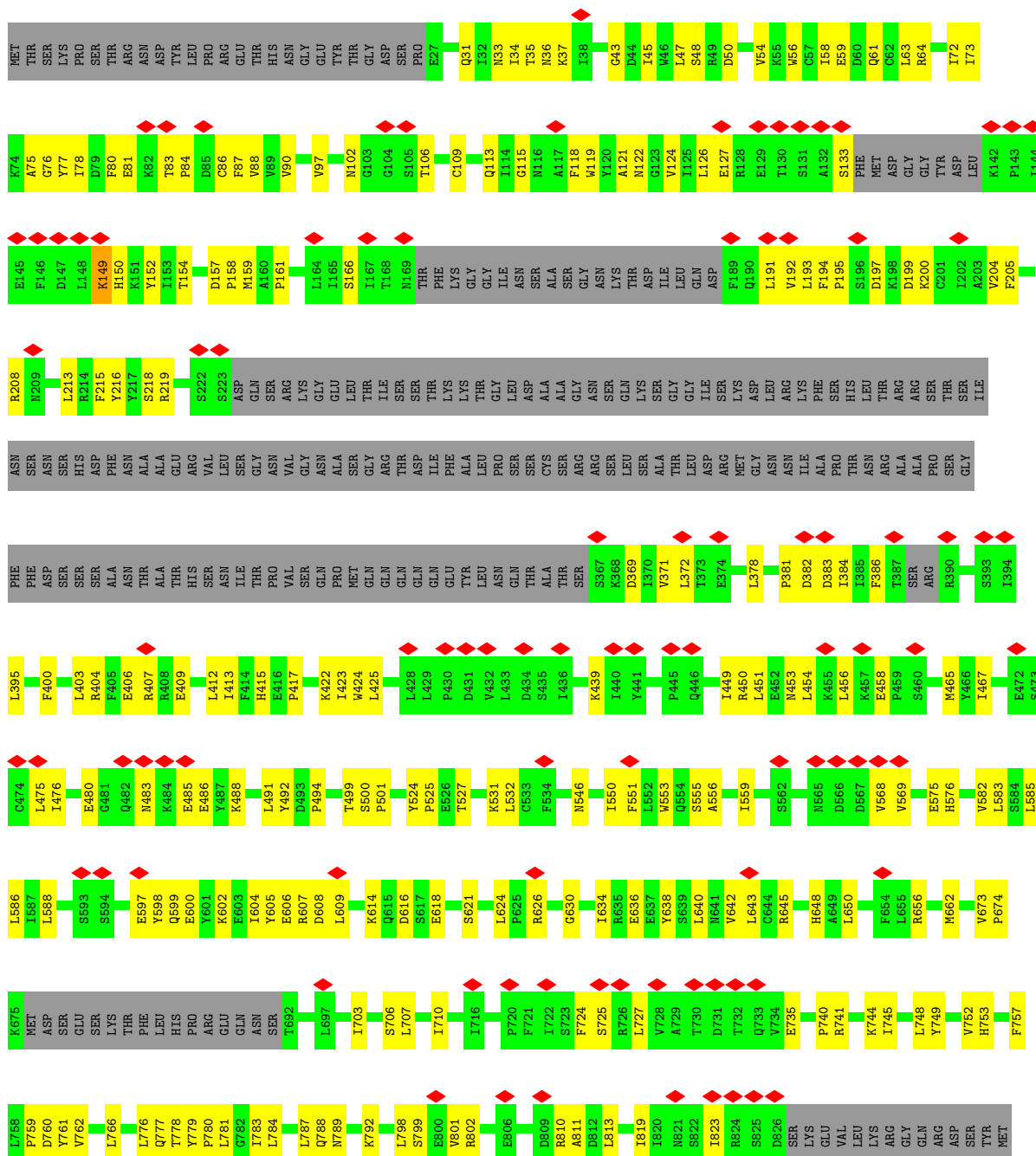


• Molecule 6: Anaphase-promoting complex subunit 11





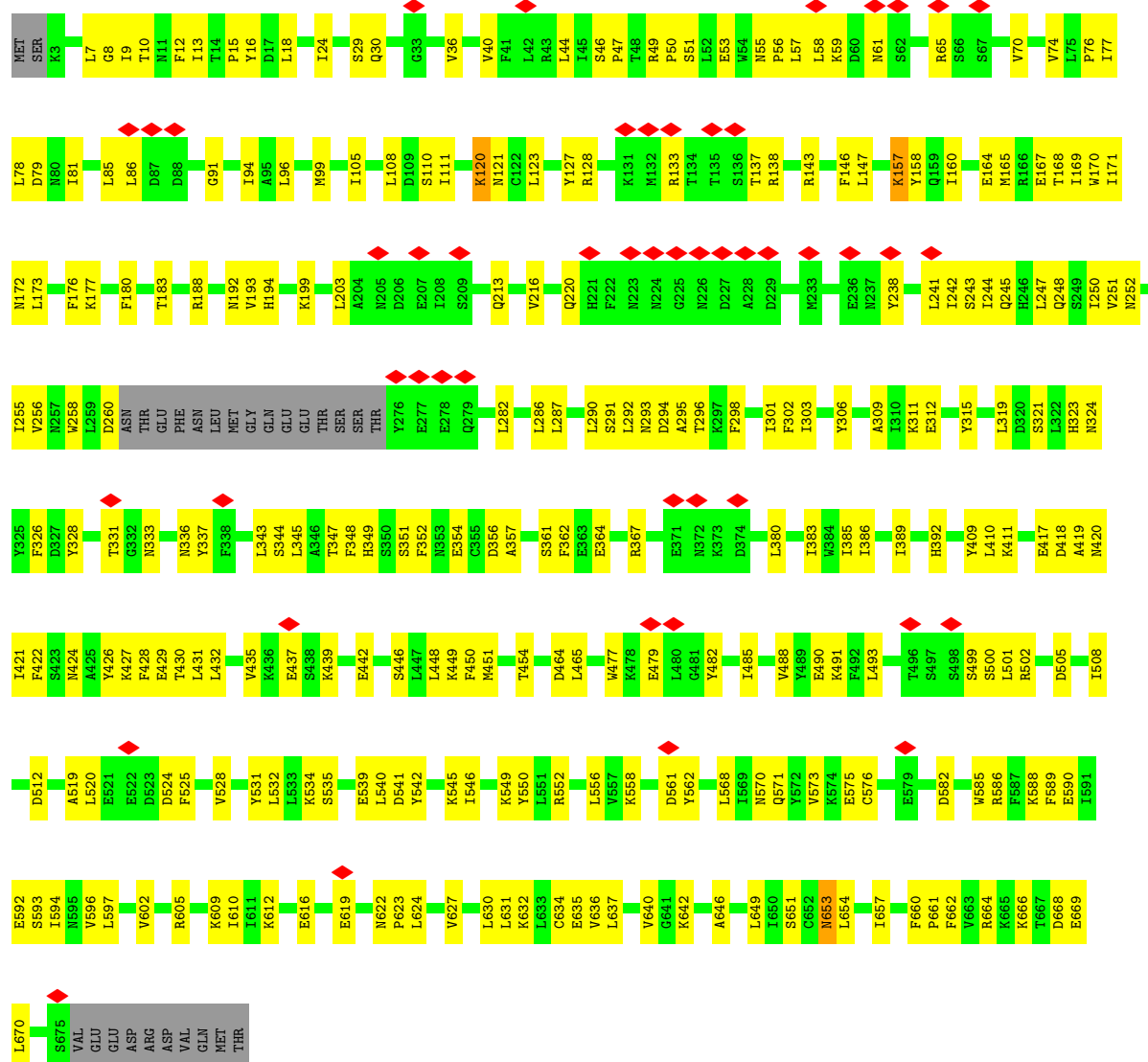
Chain C: 30% 50% 30% 20%



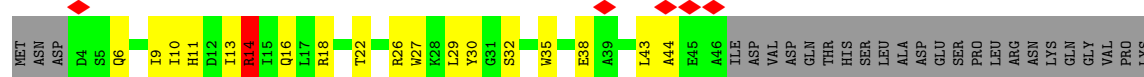
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Y1532	T1533	T1534	P1535	H1536	P1537	L1538	Q1539	E1540	L1541	K1542	H1543	F1544	W1545	S1623	V1549	E1550	P1551	R1552	I1556	K1557	D1558	I1559	D1563	N1566	N1567	V1568	P1569	L1572	V1573	V1574	E1575	E1576	D1577	V1578	E1579	K1580	E1581	E1582	V1583	I1584	R1585	E1586	I1587	S1588	T1589	P1590	C1591	D1595	F1596	S1601	I1602	L1605							
SER	SER	ASN	GLY	SER	ASP	ILE	S1475	D1476	P1477	T1478	A1479	Y1480	L1481	E1482	D1483	K1484	K1485	D1486	I1487	D1488	D1489	H1490	Y1491	G1492	K1493	F1494	I1495	N1496	T1497	N1498	L1499	A1500	L1501	F1505	S1508	G1509	Q1510	Y1511	A1512	L1513	N1514	T1515	S1516	L1517	E1518	E1519	S1520	I1521	A1522	F1523	M1526	S1527	V1528	L1529	P1530	T1531			
R1408	R1409	Y1410	K1411	Y1412	L1413	H1414	E1415	Y1416	A1417	S1418	G1419	P1420	Y1421	S1422	D1423	L1424	PHE	GLN	ILE	PRO	SER	SER	LYS	SER	ASP	VAL	SER	GLY	VAL	THR	THR	THR	GLY	ASN	ASN	PRO	GLY	ASN	SER	ASP	ARG	GLU	VAL	THR	GLU	ALA	ALA	SER	LEU	ASP	ASP	GLU	ARG						
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R1342	F1343	A1344	S1345	N1348	L1349	K1350	I1351	R1352	L1355	L1356	D1360	K1361	F1362	L1363	P1364	L1365	Y1366	Y1368	P1369	F1370	K1371	Q1372	N1373	K1374	D1375	F1376	T1379	I1380	I1383	N1384	V1385	L1386	T1387	N1388	V1389	L1390	V1391	S1392	S1393	L1394	S1395	M1396	V1397	M1398	C1399	A1400	S1401	G1402	D1403	L1404	E1405	V1406	L1407						
R1408	R1409	Y1410	K1411	Y1412	L1413	H1414	E1415	Y1416	A1417	S1418	G1419	P1420	Y1421	S1422	D1423	L1424	PHE	GLN	ILE	PRO	SER	SER	LYS	SER	ASP	VAL	SER	GLY	VAL	THR	THR	THR	GLY	ASN	ASN	PRO	GLY	ASN	SER	ASP	ARG	GLU	VAL	THR	GLU	ALA	ALA	SER	LEU	ASP	ASP	GLU	ARG						
SER	SER	ASN	GLY	SER	ASP	ILE	S1475	D1476	P1477	T1478	A1479	Y1480	L1481	E1482	D1483	K1484	K1485	D1486	I1487	D1488	D1489	H1490	Y1491	G1492	K1493	F1494	I1495	N1496	T1497	N1498	L1499	A1500	L1501	F1505	S1508	G1509	Q1510	Y1511	A1512	L1513	N1514	T1515	S1516	L1517	E1518	E1519	S1520	I1521	A1522	F1523	M1526	S1527	V1528	L1529	P1530	T1531			
Y1532	T1533	T1534	P1535	H1536	P1537	L1538	Q1539	E1540	L1541	K1542	H1543	F1544	W1545	S1623	V1549	E1550	P1551	R1552	I1556	K1557	D1558	I1559	D1563	N1566	N1567	V1568	P1569	L1572	V1573	V1574	E1575	E1576	D1577	V1578	E1579	K1580	E1581	E1582	V1583	I1584	R1585	E1586	I1587	S1588	T1589	P1590	C1591	D1595	F1596	S1601	I1602	L1605							
M1606	H1607	G1608	Y1609	F1610	P1611	N1615	F1616	T1617	K1618	D1619	Y1620	S1621	A1622	S1623	D1624	F1625	P1626	S1627	G1628	G1629	T1630	I1631	Q1635	R1636	K1637	S1638	N1639	S1640	V1641	K1645	N1650	V1651	E1652	H1655	L1658	S1665	K1666	Y1667	Y1668	S1669	L1670	LEU	ASN	LEU	LYS	ASN	GLU	GLN	G1676	N1679	Q1684								
A902	G903	L904	I905	F906	S907	E908	D909	K910	R911	V915	V916	L919	Y922	R923	P924	T925	K926	T927	Q928	F929	F930	T931	T932	K933	T934	E935	Y936	A937	Q938	I939	L940	A941	Q942	K943	K944	Y945	F946	A947	K948	I949	M950	A951	L952	R953	T954	C955	T956	N957	G958	V959	G960	W961	G962	A963	V964	A965			
LEU	C942	K943	V944	L946	A947	K948	N949	R950	S951	S952	LEU	SER	K955	K956	P957	S958	D959	I960	Y961	S962	I963	L964	I967	V968	K969	S970	A971	S972	GLN	VAL	PRO	LEU	ASP	GLY	SER	ALA	MET	ARG	MET	SER	ASN	ILE	GLN	ASP	ASP	GLU	G995	R996	S997	L998	K999	L900	N901						
Y966	A967	T968	E969	K970	P971	T972	S973	T974	Q975	R976	Y977	Y978	Y979	L984	S985	S986	V987	F988	D989	D991	T992	K993	T994	T995	V996	K997	A998	P999	E1000	D1001	I1002	A1003	H1004	D1005	I1006	V1007	E1008	W1009	G1010	Q1011	F1012	H1013	G1019	L1020	R1021	I1022	S1023	K1024	G1025	A1026	T1027	G1028	T1029	T1030					
I1034	A1035	F1036	K1037	P1038	F1039	K1040	E1041	D1043	H1046	F1049	L1050	L1051	G1052	L1055	G1057	H1058	K1060	N1061	L1062	E1063	E1064	W1065	H1066	I1067	Y1068	N1069	Y1070	L1071	S1072	P1073	R1074	N1075	T1076	H1077	I1078	I1080	G1081	L1082	L1083	G1085	M1086	S1087	S1088	I1089	K1091	G1092	S1093	M1094	D1095	S1096									
K1097	L1098	I1099	K1100	V1101	I1102	S1103	V1104	H1105	L1106	V1107	A1108	F1109	L1110	P1111	S1112	G1113	S1114	S1115	D1116	L1117	M1118	I1119	L1120	L1121	K1122	L1123	G1124	T1125	A1126	G1127	I1128	I1129	G1130	M1131	M1133	G1132	L1134	Y1135	L1136	M1137	S1138	R1139	H1140	K1141	R1142	M1143	G1145	D1146	S1147	F1148	Q1150	L1151	V1152	S1153	L1154	M1156			
V1157	M1158	L1159	E1160	M1161	V1162	A1163	E1164	E1165	E1166	Y1167	R1168	L1169	A1170	A1171	G1172	I1173	S1174	L1175	G1176	L1177	L1180	G1181	A1182	G1183	Q1184	T1185	K1186	LEU	ARG	LYS	TRP	ASP	SER	SER	LEU	GLY	GLY	ASP	ASP	LEU	PRO	GLU	VAL	TYR	ASP	SER	SER	VAL	GLU	Q1213	M1214	V1215	M1216	Y1217					
E1218	D1219	L1220	T1221	T1222	K1223	L1224	L1225	E1226	I1227	V1228	T1229	S1230	Y1231	Y1232	D1233	V1234	E1235	N1236	D1237	W1238	I1239	P1240	E1241	G1242	Q1244	I1245	G1246	A1247	V1248	L1249	A1250	M1252	L1253	L1254	F1255	L1256	K1257	S1258	N1259	N1260	F1261	G1262	I1263	S1264	N1265	M1266	L1267	K1268	V1269	D1270	L1271	K1272	E1273	I1274	L1275	K1276	A1277		
M1278	I1279	N1280	T1281	R1282	P1283	E1284	L1285	L1286	E1290	W1291	A1292	I1296	L1297	W1298	E1299	F1300	I1301	G1302	D1303	D1304	L1305	S1306	F1307	I1308	M1309	K1310	D1311	V1312	D1313	I1314	G1315	V1316	K1317	F1318	S1319	E1320	L1321	N1322	T1323	D1324	L1325	L1326	P1327	I1328	L1329	Y1330	T1331	M1332	G1333	I1335	L1336	L1337	M1338	G1340	I1341				
R1342	F1343	A1344	S1345	N1348	L1349	K1350	I1351	R1352	L1355	L1356	D1360	K1361	F1362	L1363	P1364	L1365	Y1366	Y1368	P1369	F1370	K1371	Q1372	N1373	K1374	D1375	F1376	T1379	I1380	I1383	N1384	V1385	L1386	T1387	N1388	V1389	L1390	V1391	S1392	S1393	L1394	S1395	M1396	V1397	M1398	C1399	A1400	S1401	G1402	D1403	L1404	E1405	V1406	L1407						
R1408	R1409	Y1410	K1411	Y1412	L1413	H1414	E1415	Y1416	A1417	S1418	G1419	P1420	Y1421	S1422	D1423	L1424	PHE	GLN	ILE	PRO	SER	SER	LYS	SER	ASP	VAL	SER	GLY	VAL	THR	THR	THR	GLY	ASN	ASN	PRO	GLY	ASN	SER	ASP	ARG	GLU	VAL	THR	GLU	ALA	ALA	SER	LEU	ASP	ASP	GLU	ARG						
M1278	I1279	N1280	T1281	R1282	P1283	E1284	L1285	L1286	E1290	W1291	A1292	I1296	L1297	W1298	E1299	F1300	I1301	G1302	D1303	D1304	L1305	S1306	F1307	I1308	M1309	K1310	D1311	V1312	D1313	I1314	G1315	V1316	K1317	F1318	S1319	E1320	L1321	N1322	T1323	D1324	L1325	L1326	P1327	I1328	L1329	Y1330	T1331	M1332	G1333	I1335	L1336	L1337	M1338	G1340	I1341				
R1342	F1343	A1344	S1345	N1348	L1349	K1350	I1351	R1352	L1355	L1356	D1360	K1361	F1362	L1363	P1364	L1365	Y1366	Y1368	P1369	F1370	K1371	Q1372	N1373	K1374	D1375	F1376	T1379	I1380	I1383	N1384	V1385	L1386	T1387	N1388	V1389	L1390	V1391	S1392	S1393	L1394	S1395	M1396	V1397	M1398	C1399	A1400	S1401	G1402	D1403	L1404	E1405	V1406	L1407						
R1408	R1409	Y1410	K1411	Y1412	L1413	H1414	E1415	Y1416	A1417	S1418	G1419	P1420	Y1421	S1422	D1423	L1424	PHE	GLN	ILE	PRO	SER	SER	LYS	SER	ASP	VAL	SER	GLY	VAL	THR	THR	THR	GLY	ASN	ASN	PRO	GLY	ASN	SER	ASP	ARG	GLU	VAL	THR	GLU	ALA	ALA	SER	LEU	ASP	ASP	GLU	ARG						
M1278	I1279	N1280	T1281	R1282	P1283	E1284	L1285	L1286	E1290	W1291	A1292	I1296	L1297	W1298	E1299	F1300	I1301	G1302	D1303	D1304	L1305	S1306	F1307	I1308	M1309	K1310	D1311	V1312	D1313	I1314	G1315	V1316	K1317	F1318	S1319	E1320	L1321	N1322	T1323	D1324	L1325	L1326	P1327	I1328	L1329	Y1330	T1331	M1332	G1333	I1335	L1336	L1337	M1338	G1340	I1341				
R1342	F1343	A1344	S1345	N1348	L1349	K1350	I1351	R1352	L1355	L1356	D1360	K1361	F1362	L1363	P1364	L1365	Y1366	Y1368	P1369	F1370	K1371	Q1372	N1373	K1374	D1375	F1376	T1379	I1380	I1383	N1384	V1385	L1386	T1387	N1388	V1389	L1390	V1391	S1392	S1393	L1394	S1395	M1396	V1397</																

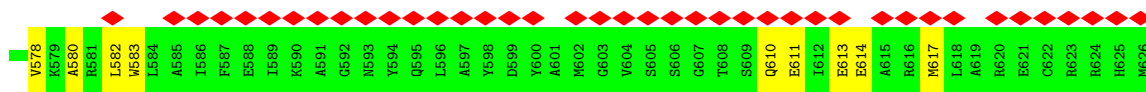


• Molecule 8: Anaphase-promoting complex subunit 5

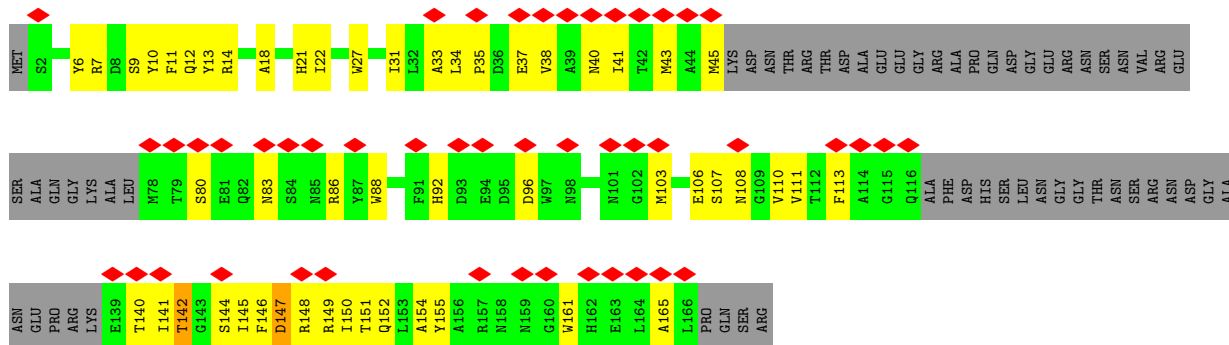


• Molecule 9: Anaphase-promoting complex subunit CDC23

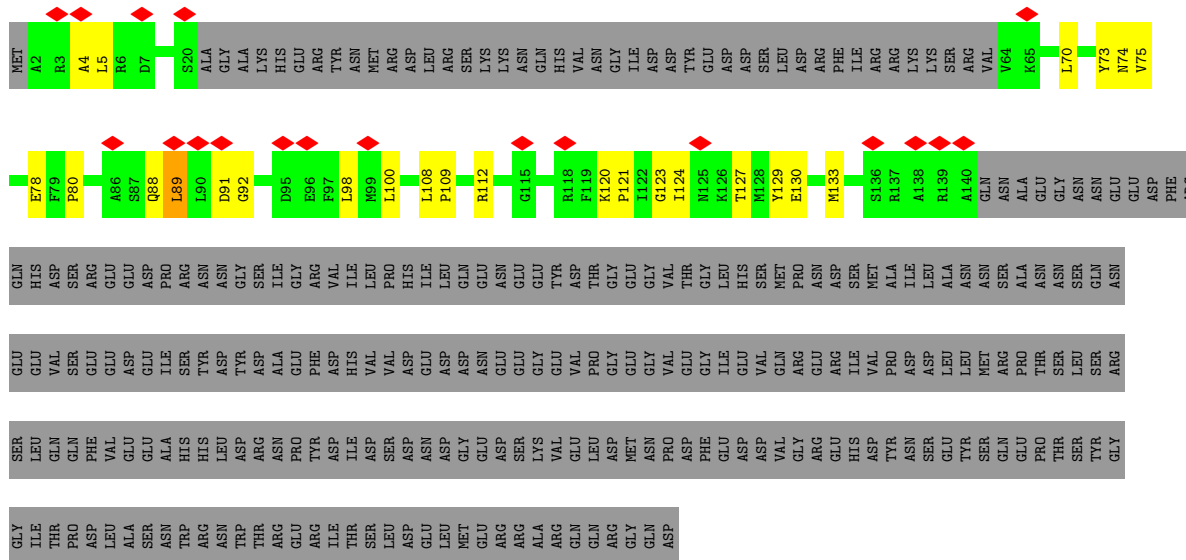




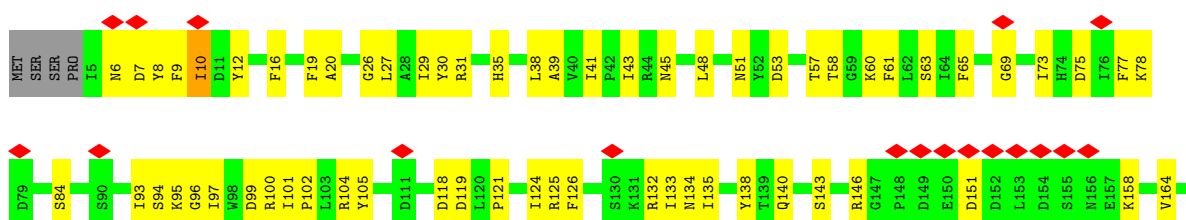
• Molecule 10: Anaphase-promoting complex subunit SWM1

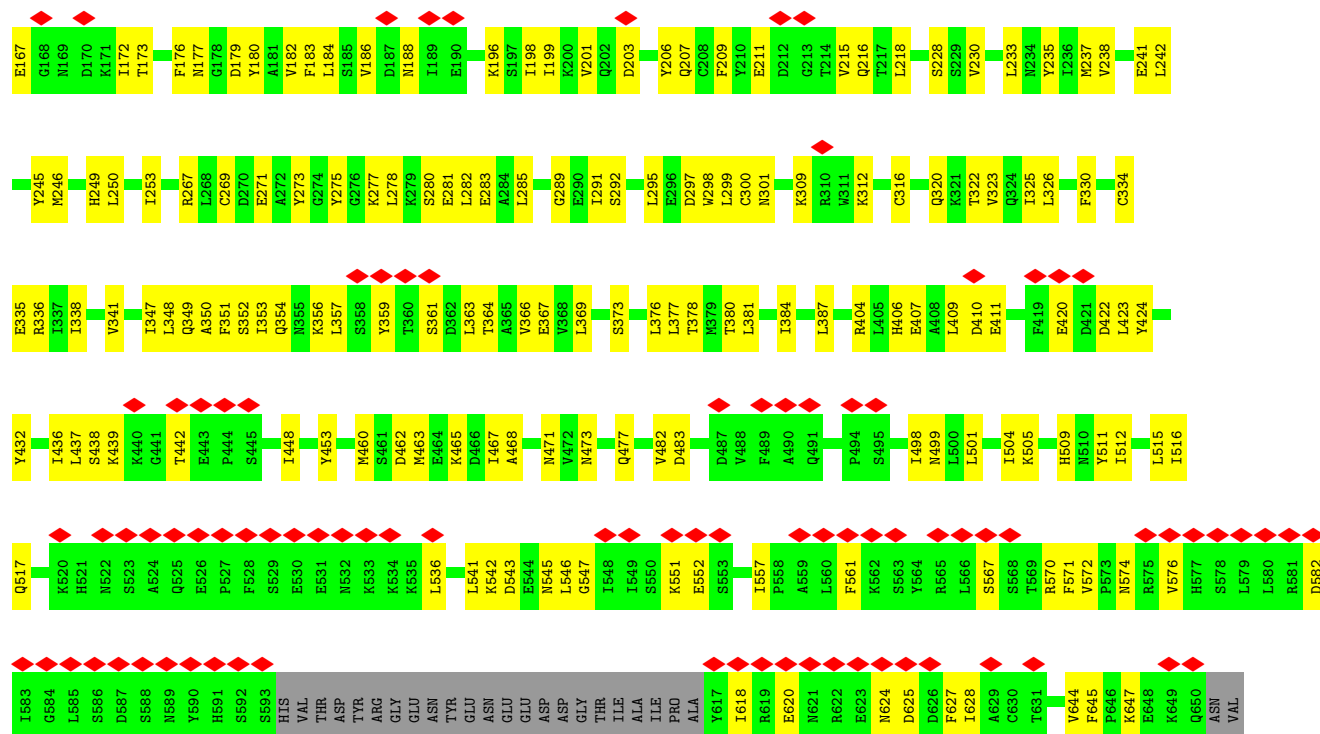


• Molecule 11: Anaphase-promoting complex subunit MND2

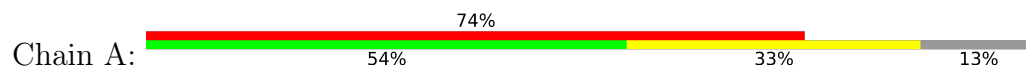


• Molecule 12: Anaphase-promoting complex subunit 4





● Molecule 13: Anaphase-promoting complex subunit DOC1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	372535	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	59	Depositor
Minimum defocus (nm)	2600	Depositor
Maximum defocus (nm)	9000	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.214	Depositor
Minimum map value	-0.106	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.05	Depositor
Map size (\AA)	353.28, 353.28, 353.28	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.38, 1.38, 1.38	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	F	0.31	0/4079	0.60	7/5525 (0.1%)
1	H	0.28	0/4126	0.53	1/5585 (0.0%)
2	J	0.30	0/4210	0.61	5/5688 (0.1%)
2	K	0.30	0/4188	0.57	0/5657
3	G	0.28	0/285	0.76	0/384
3	W	0.27	0/285	0.58	0/384
4	E	0.29	0/1108	0.60	1/1481 (0.1%)
5	T	0.26	0/5479	0.53	1/7420 (0.0%)
6	U	0.26	0/936	0.57	0/1265
7	C	0.28	0/11057	0.58	4/15038 (0.0%)
8	O	0.29	0/5384	0.58	0/7287
9	D	0.28	0/4621	0.56	2/6243 (0.0%)
9	P	0.27	0/4618	0.55	0/6231
10	I	0.32	0/930	0.66	0/1263
11	N	0.27	0/800	0.64	1/1076 (0.1%)
12	Q	0.27	0/5193	0.53	0/7024
13	A	0.25	0/1780	0.56	0/2411
All	All	0.28	0/59079	0.57	22/79962 (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	T	0	4
7	C	0	1
All	All	0	5

There are no bond length outliers.

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	752	LEU	CB-CG-CD2	-7.79	97.76	111.00
7	C	1363	LEU	CA-CB-CG	6.89	131.16	115.30
2	J	482	CYS	CA-CB-SG	6.65	125.98	114.00
1	F	458	LEU	CA-CB-CG	6.61	130.51	115.30
1	F	181	LEU	CA-CB-CG	-6.18	101.08	115.30

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	C	1551	PRO	Peptide
5	T	620	THR	Peptide
5	T	621	GLN	Peptide
5	T	622	GLY	Peptide
5	T	623	SER	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	F	3991	0	3947	183	0
1	H	4038	0	4010	141	0
2	J	4124	0	4085	186	0
2	K	4102	0	4065	184	0
3	G	284	0	293	19	0
3	W	284	0	293	21	0
4	E	1091	0	1058	38	0
5	T	5362	0	5336	157	0
6	U	912	0	873	31	0
7	C	10832	0	10637	435	0
8	O	5285	0	5290	235	0
9	D	4524	0	4391	139	0
9	P	4520	0	4415	143	0
10	I	906	0	813	60	0
11	N	784	0	784	24	0
12	Q	5086	0	5095	180	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	A	1738	0	1705	59	0
14	U	3	0	0	0	0
All	All	57866	0	57090	2031	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 18.

The worst 5 of 2031 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:T:463:ILE:HG12	7:C:1412:TYR:HE1	1.24	1.02
7:C:78:ILE:HD13	7:C:119:TRP:HD1	1.30	0.95
7:C:902:ALA:HA	7:C:905:ILE:HG12	1.49	0.92
9:P:95:LEU:HD11	9:P:104:CYS:HB2	1.53	0.91
2:K:453:LEU:HD12	2:K:459:LEU:HD23	1.52	0.90

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	F	496/758 (65%)	479 (97%)	17 (3%)	0	100	100
1	H	499/758 (66%)	483 (97%)	13 (3%)	3 (1%)	22	59
2	J	505/850 (59%)	488 (97%)	17 (3%)	0	100	100
2	K	501/850 (59%)	487 (97%)	14 (3%)	0	100	100
3	G	33/124 (27%)	33 (100%)	0	0	100	100
3	W	33/124 (27%)	33 (100%)	0	0	100	100
4	E	120/265 (45%)	118 (98%)	2 (2%)	0	100	100
5	T	638/853 (75%)	613 (96%)	19 (3%)	6 (1%)	14	50

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	U	110/165 (67%)	108 (98%)	1 (1%)	1 (1%)	14	50
7	C	1380/1748 (79%)	1287 (93%)	87 (6%)	6 (0%)	30	68
8	O	654/685 (96%)	625 (96%)	26 (4%)	3 (0%)	25	64
9	D	554/626 (88%)	536 (97%)	15 (3%)	3 (0%)	25	64
9	P	550/626 (88%)	527 (96%)	23 (4%)	0	100	100
10	I	105/170 (62%)	94 (90%)	10 (10%)	1 (1%)	13	48
11	N	92/368 (25%)	89 (97%)	3 (3%)	0	100	100
12	Q	619/652 (95%)	597 (96%)	21 (3%)	1 (0%)	44	78
13	A	212/250 (85%)	203 (96%)	8 (4%)	1 (0%)	25	64
All	All	7101/9872 (72%)	6800 (96%)	276 (4%)	25 (0%)	32	68

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	588	ASP
5	T	621	GLN
5	T	624	ASN
5	T	745	ASP
7	C	844	VAL

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	
1	F	433/684 (63%)	432 (100%)	1 (0%)	92	94
1	H	440/684 (64%)	439 (100%)	1 (0%)	92	94
2	J	450/760 (59%)	449 (100%)	1 (0%)	92	94
2	K	448/760 (59%)	445 (99%)	3 (1%)	81	87
3	G	34/115 (30%)	34 (100%)	0	100	100
3	W	34/115 (30%)	34 (100%)	0	100	100
4	E	123/246 (50%)	123 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	T	608/804 (76%)	606 (100%)	2 (0%)	91	92
6	U	103/149 (69%)	103 (100%)	0	100	100
7	C	1177/1568 (75%)	1174 (100%)	3 (0%)	91	92
8	O	597/643 (93%)	594 (100%)	3 (0%)	86	89
9	D	477/560 (85%)	475 (100%)	2 (0%)	89	91
9	P	477/560 (85%)	475 (100%)	2 (0%)	89	91
10	I	95/144 (66%)	93 (98%)	2 (2%)	48	67
11	N	83/332 (25%)	83 (100%)	0	100	100
12	Q	572/598 (96%)	572 (100%)	0	100	100
13	A	190/226 (84%)	188 (99%)	2 (1%)	70	80
All	All	6341/8948 (71%)	6319 (100%)	22 (0%)	90	92

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	D	14	ARG
9	P	371	ASN
9	P	138	ASN
10	I	147	ASP
5	T	143	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
8	O	61	ASN
12	Q	320	GLN
8	O	333	ASN
9	P	535	ASN
8	O	220	GLN

5.3.3 RNA ⓘ

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 3 ligands modelled in this entry, 3 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.

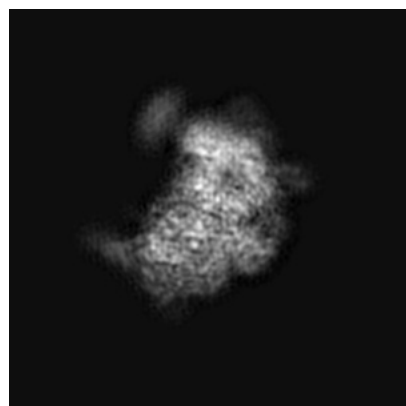
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15199. These allow visual inspection of the internal detail of the map and identification of artifacts.

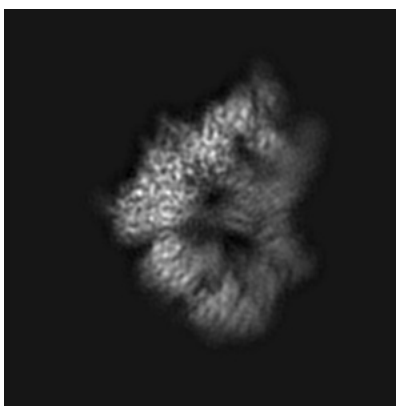
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

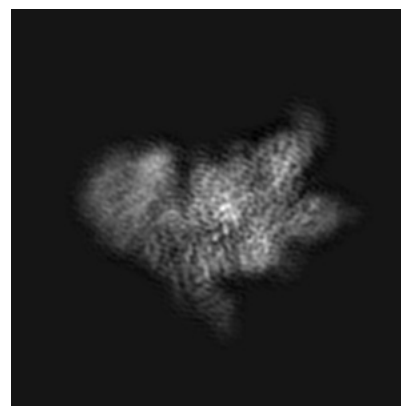
6.1.1 Primary map



X

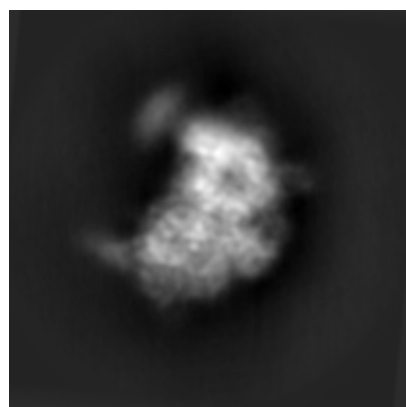


Y

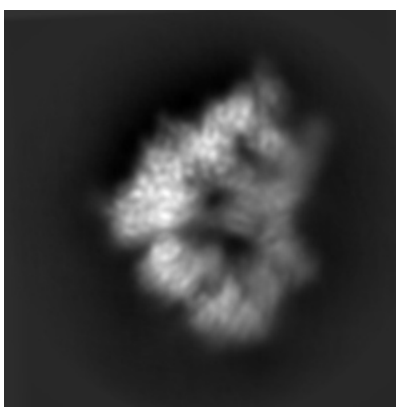


Z

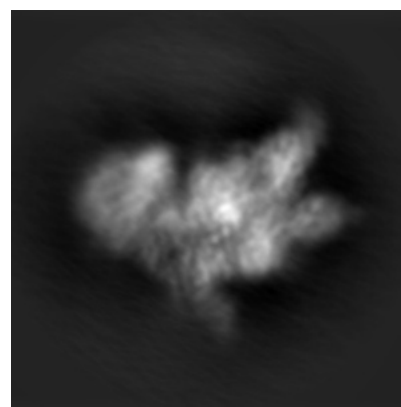
6.1.2 Raw map



X



Y

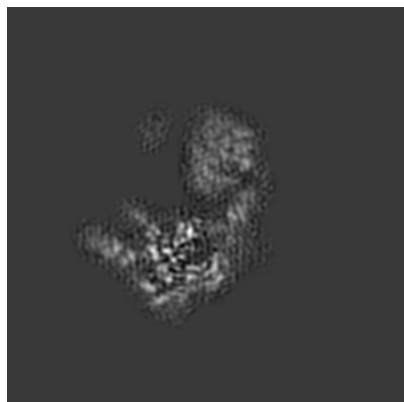


Z

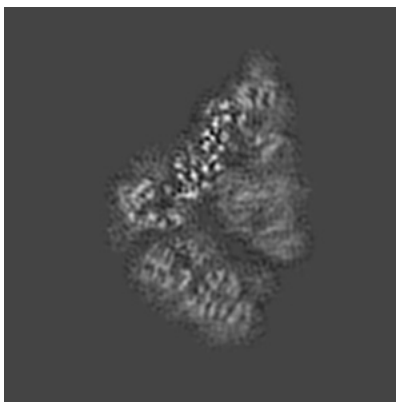
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

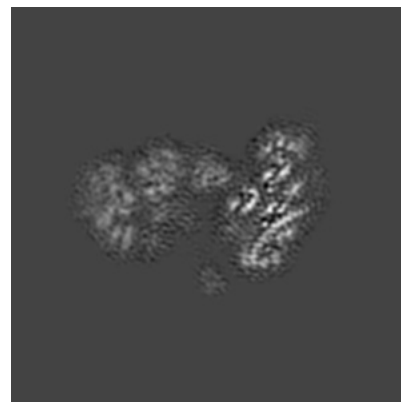
6.2.1 Primary map



X Index: 128

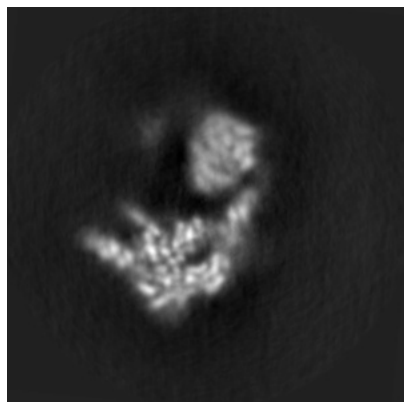


Y Index: 128

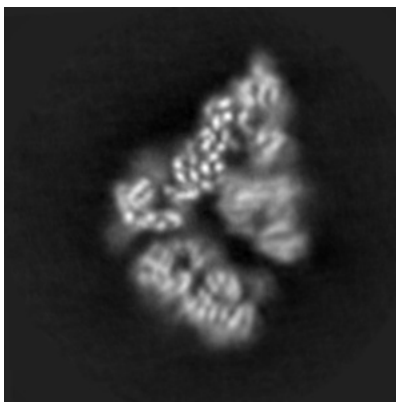


Z Index: 128

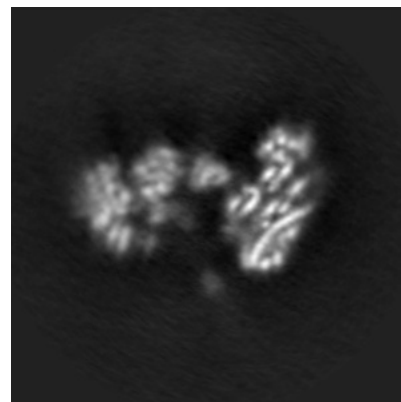
6.2.2 Raw map



X Index: 128



Y Index: 128



Z Index: 128

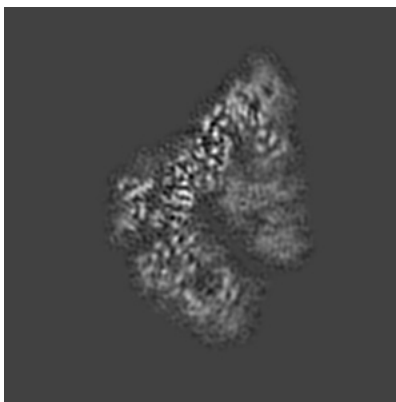
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

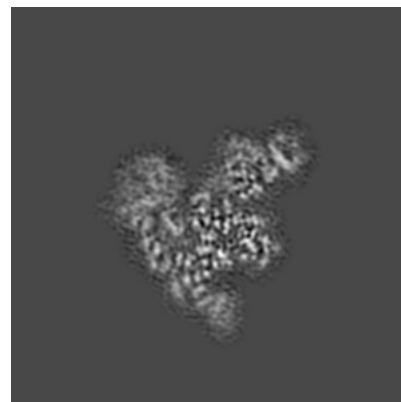
6.3.1 Primary map



X Index: 137

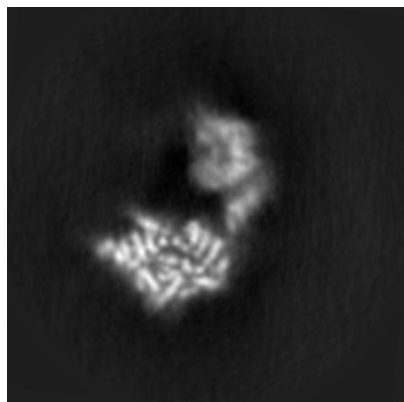


Y Index: 122

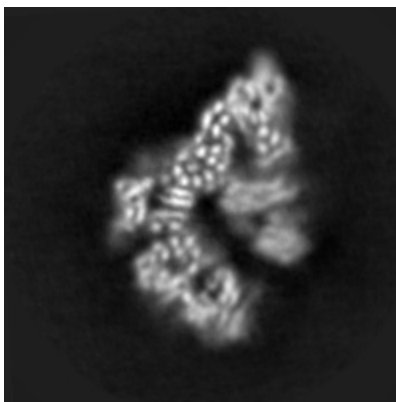


Z Index: 105

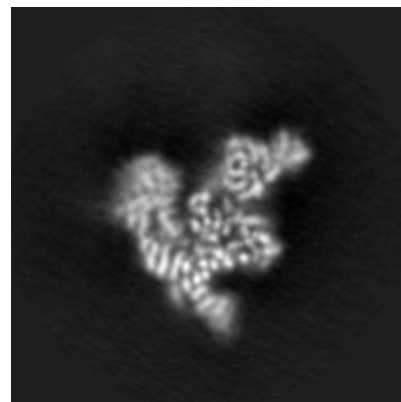
6.3.2 Raw map



X Index: 123



Y Index: 123

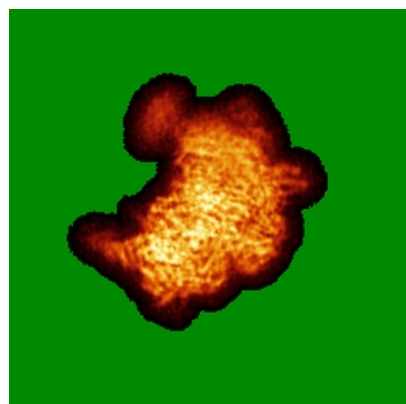


Z Index: 103

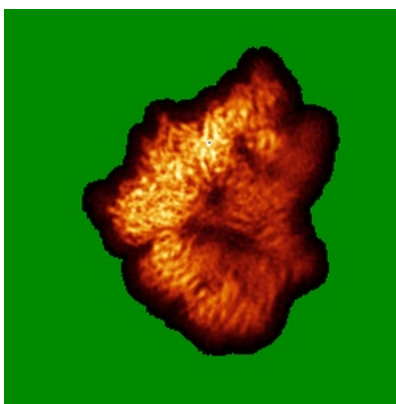
The images above show the largest variance slices of the map in three orthogonal directions.

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

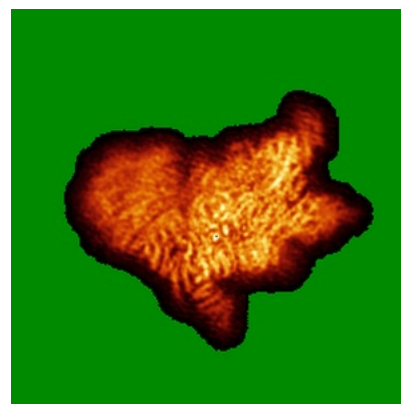
6.4.1 Primary map



X

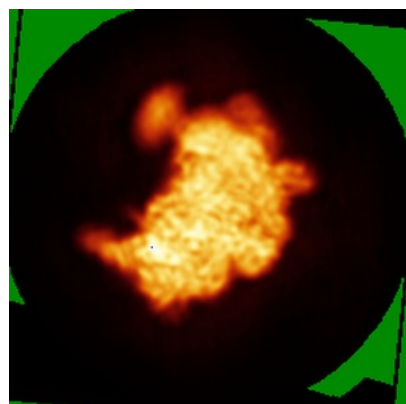


Y

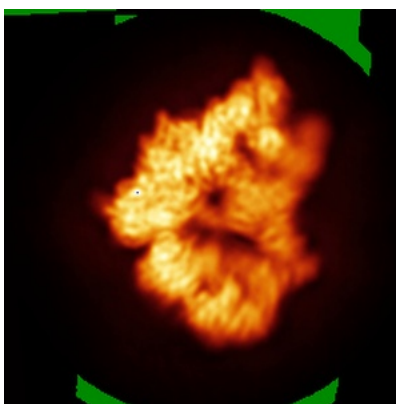


Z

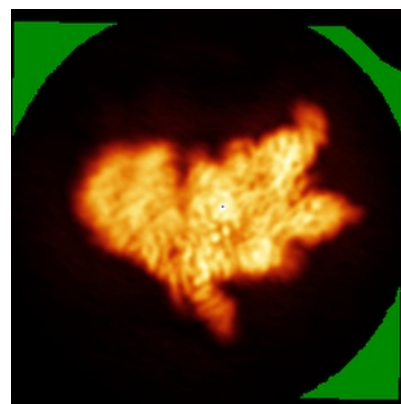
6.4.2 Raw map



X



Y



Z

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

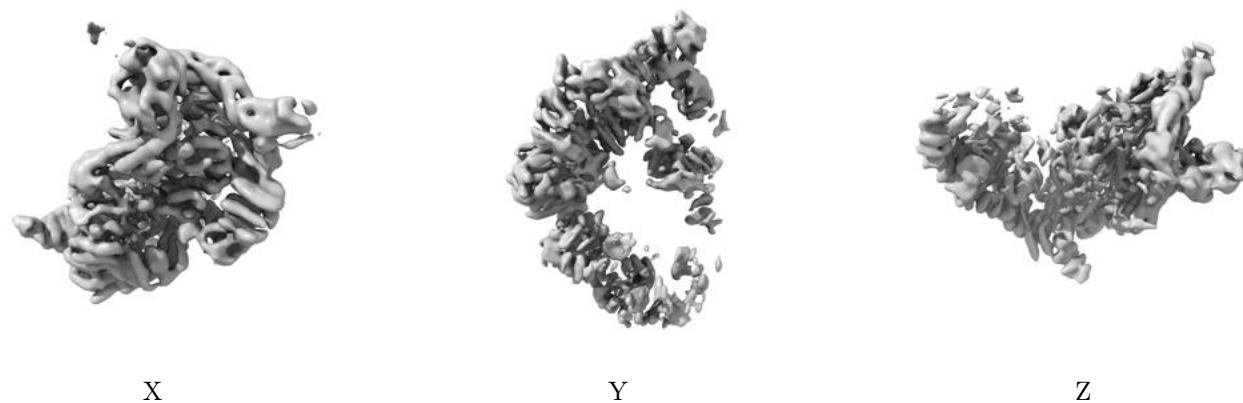
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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



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

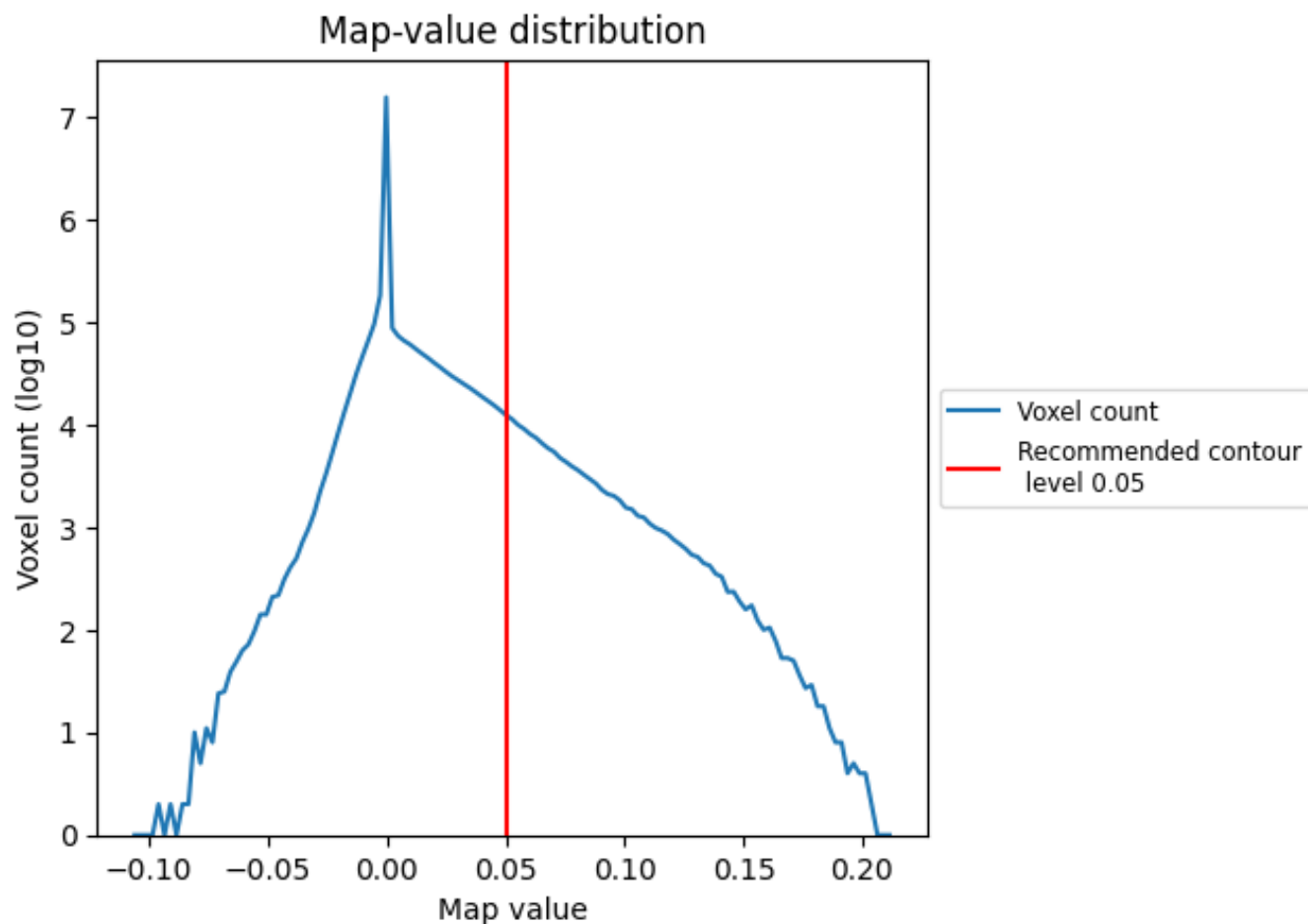
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

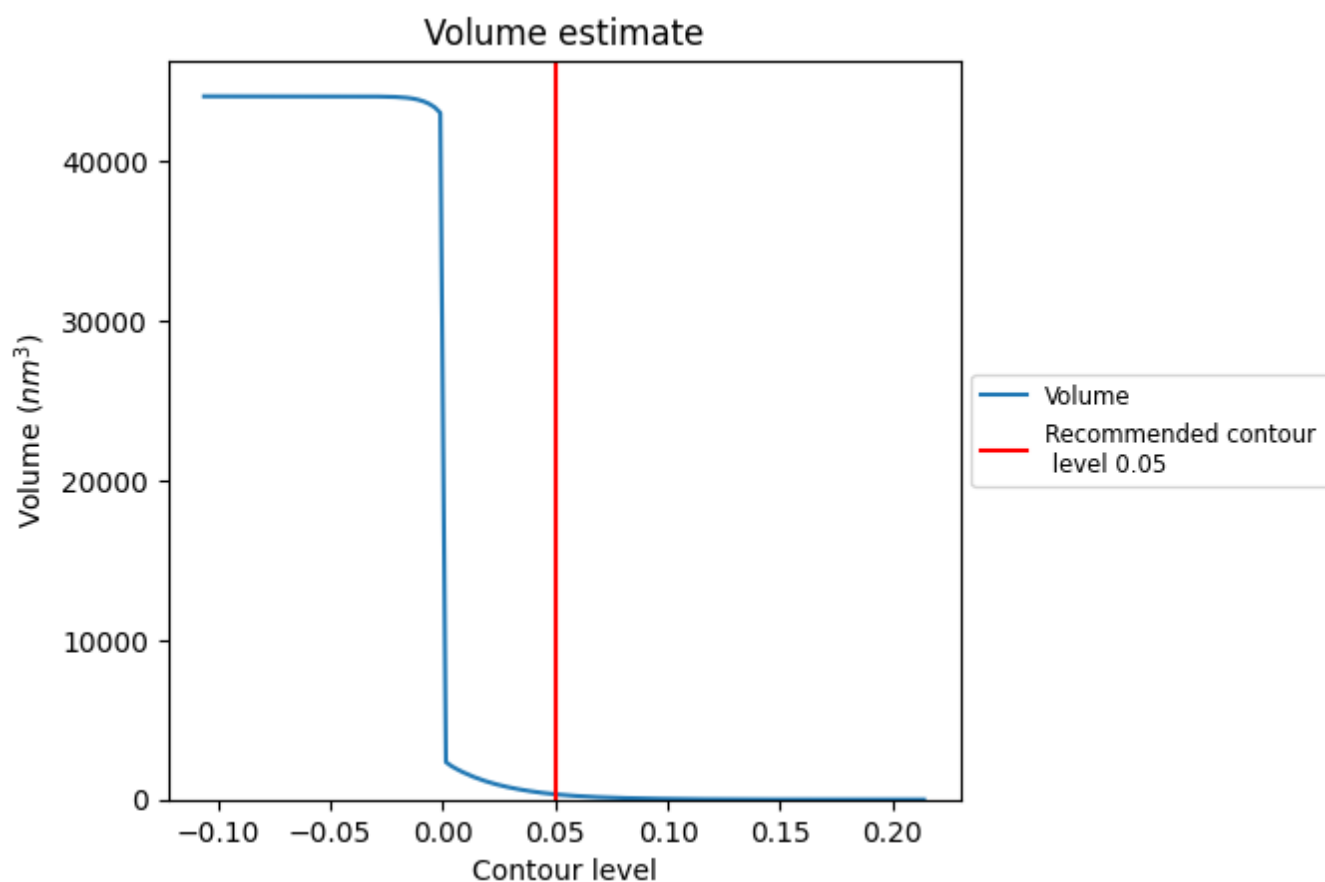
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

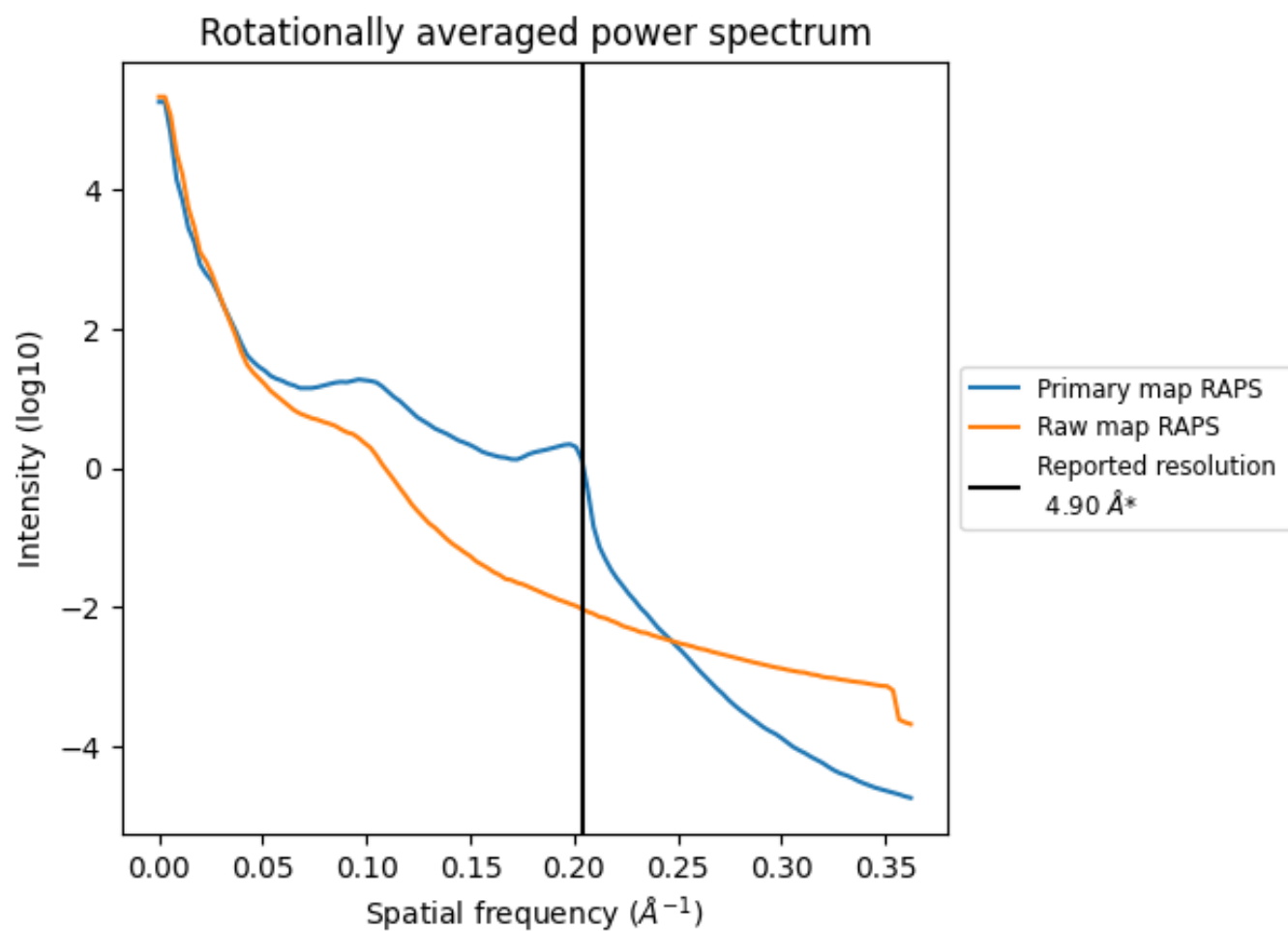
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 332 nm³; this corresponds to an approximate mass of 300 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 ⓘ

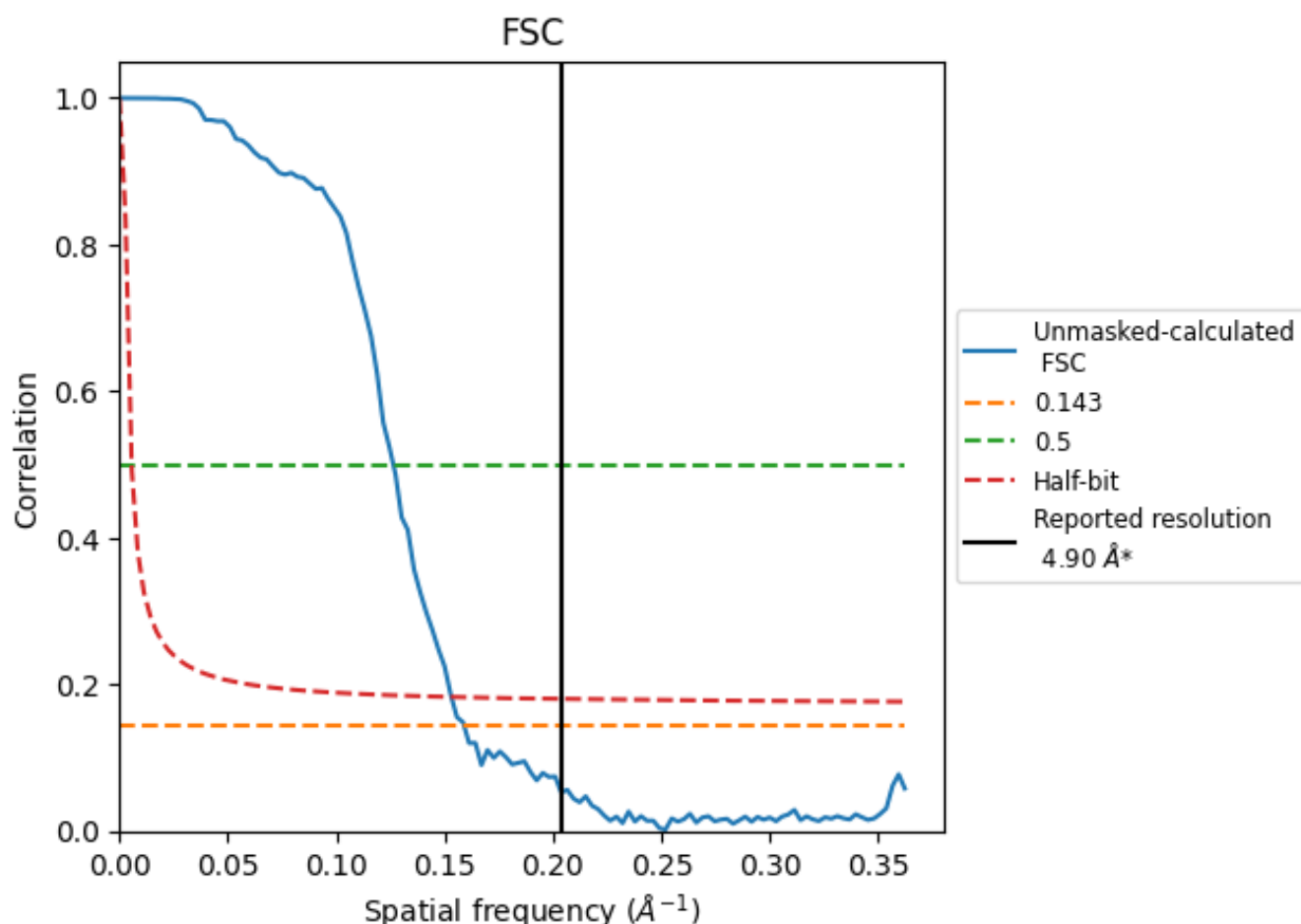


*Reported resolution corresponds to spatial frequency of 0.204 Å⁻¹

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 0.204 Å⁻¹

8.2 Resolution estimates [i](#)

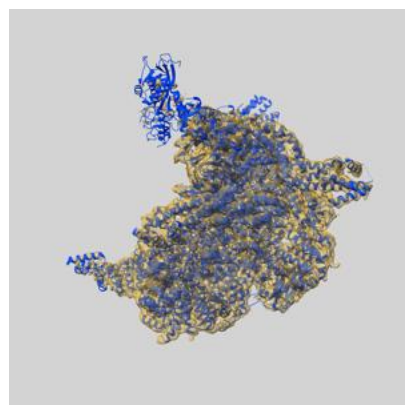
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.29	7.92	6.53

*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 6.29 differs from the reported value 4.9 by more than 10 %

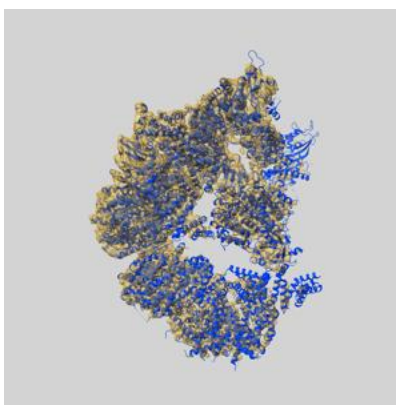
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-15199 and PDB model 8A5Y. Per-residue inclusion information can be found in section [3](#) on page [7](#).

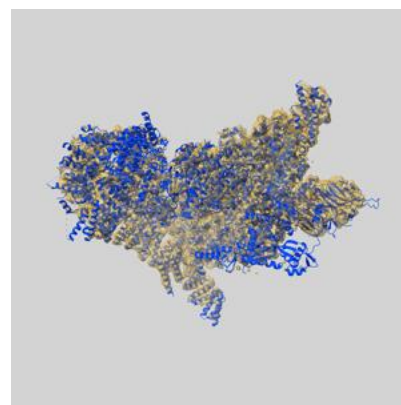
9.1 Map-model overlay [i](#)



X



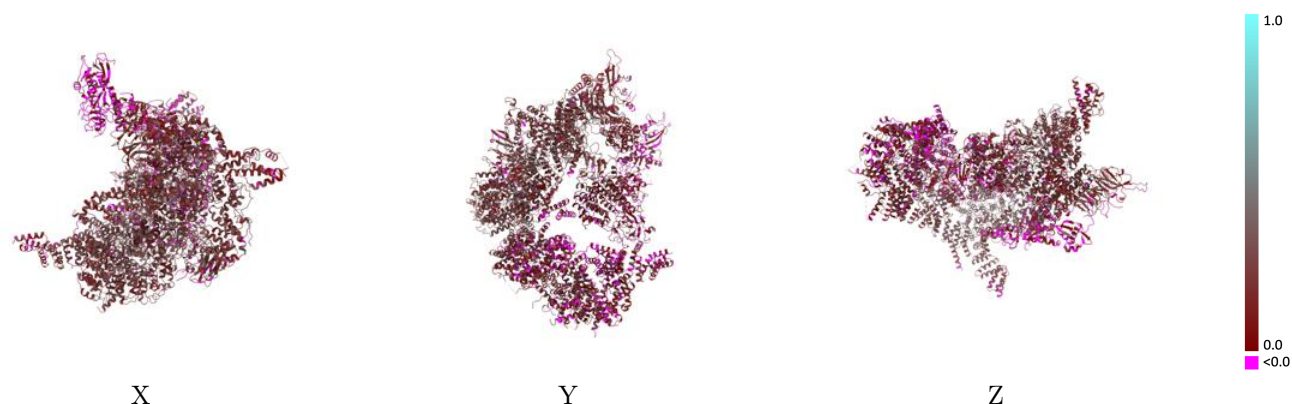
Y



Z

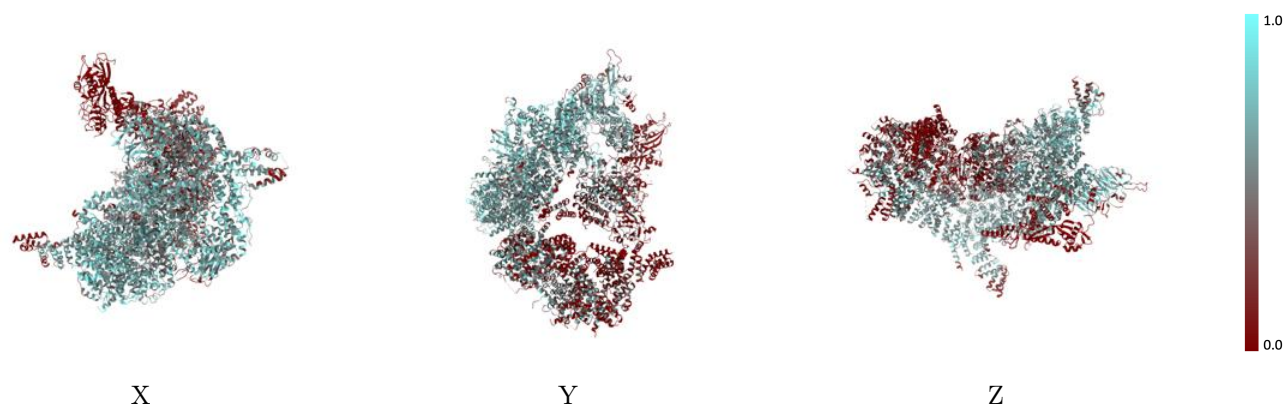
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



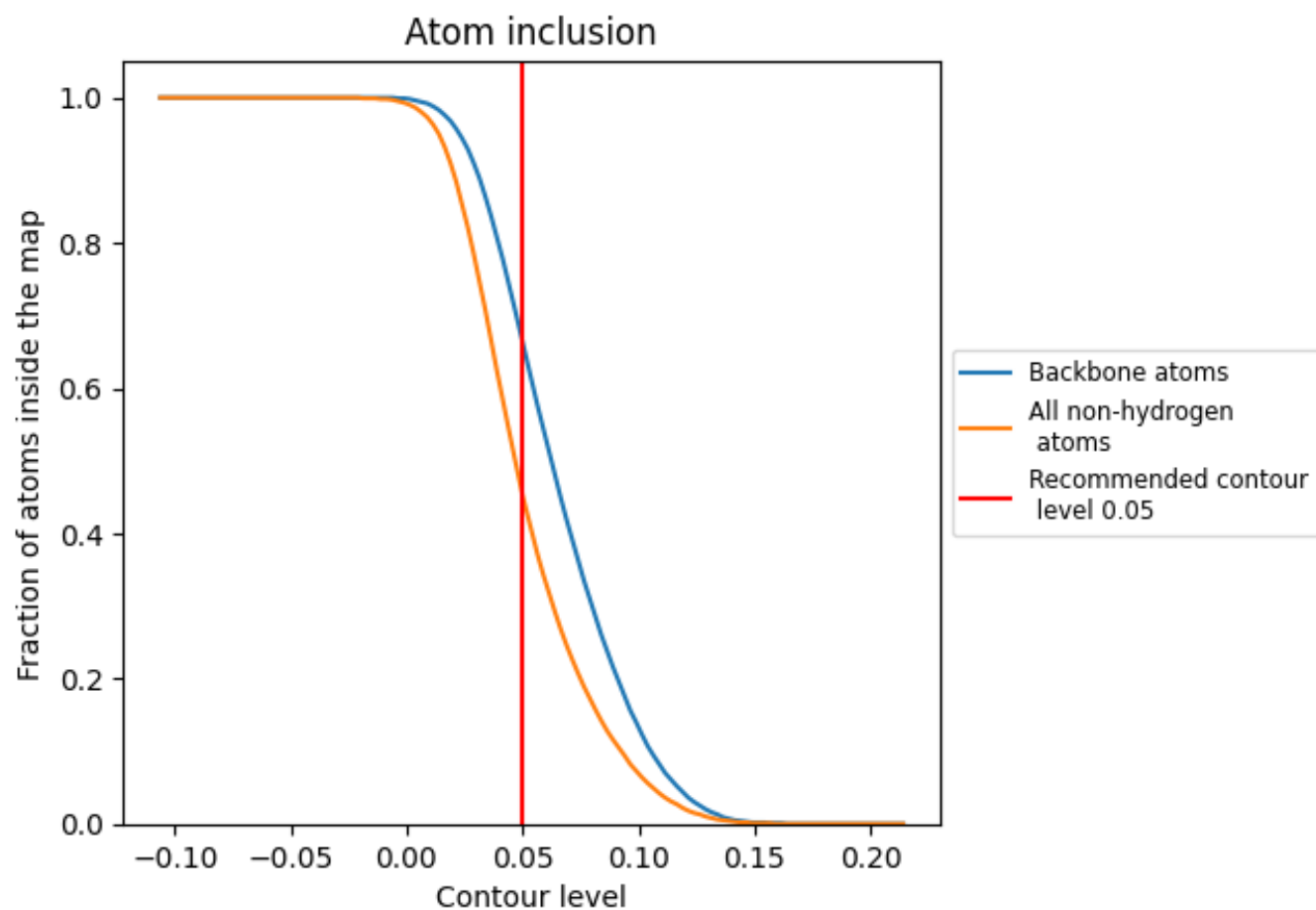
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 66% of all backbone atoms, 45% 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	<div></div> 0.4520	<div></div> 0.1920
A	<div></div> 0.1560	<div></div> 0.1200
C	<div></div> 0.4760	<div></div> 0.2100
D	<div></div> 0.5670	<div></div> 0.2290
E	<div></div> 0.2190	<div></div> 0.1580
F	<div></div> 0.4520	<div></div> 0.1750
G	<div></div> 0.5320	<div></div> 0.2140
H	<div></div> 0.1840	<div></div> 0.1270
I	<div></div> 0.4670	<div></div> 0.2180
J	<div></div> 0.5690	<div></div> 0.2010
K	<div></div> 0.2380	<div></div> 0.1160
N	<div></div> 0.6130	<div></div> 0.2960
O	<div></div> 0.6550	<div></div> 0.2750
P	<div></div> 0.6030	<div></div> 0.2300
Q	<div></div> 0.5890	<div></div> 0.2310
T	<div></div> 0.3430	<div></div> 0.1390
U	<div></div> 0.0110	<div></div> 0.0180
W	<div></div> 0.0070	<div></div> 0.0220

1.0

0.0

<0.0