



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 09:41 PM UTC

PDB ID : 5A31 / pdb_00005a31
EMDB ID : EMD-2925
Title : Structure of the human APC-Cdh1-Hsl1-UbcH10 complex.
Authors : Chang, L.; Zhang, Z.; Yang, J.; McLaughlin, S.H.; Barford, D.
Deposited on : 2015-05-26
Resolution : 4.30 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

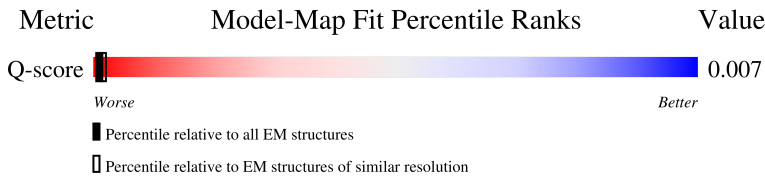
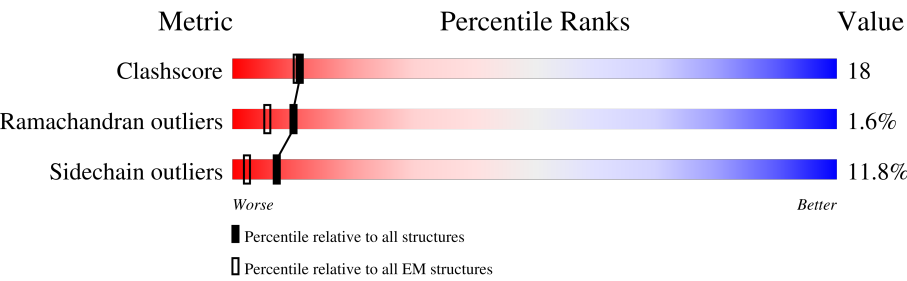
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.30 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	503 (5.20 - 6.20)

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	A	1441	 28% 58% 35% 6% .
2	B	84	 14% 48% 39% 8% 5%
3	C	597	 23% 58% 26% . 12%
3	P	597	 11% 55% 22% 5% 18%

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Mol	Chain	Length	Quality of chain
4	D	121	
5	E	110	
6	F	824	
6	H	824	
7	G	85	
7	W	85	
8	I	808	
9	J	620	
10	K	620	
11	L	185	
12	M	74	
13	N	703	
14	O	755	
15	Q	162	
16	R	386	
17	T	21	
18	U	24	
19	V	13	
20	X	599	
20	Y	599	

2 Entry composition [i](#)

There are 21 unique types of molecules in this entry. The entry contains 67685 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 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1441	Total	C	N	O	S	0	0
			10950	7046	1853	1977	74		

- Molecule 2 is a protein called ANAPHASE-PROMOTING COMPLEX SUBUNIT 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	84	Total	C	N	O	S	1	0
			650	418	117	98	17		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	13	LEU	THR	conflict	UNP Q9NYG5

- Molecule 3 is a protein called CELL DIVISION CYCLE PROTEIN 23 HOMOLOG.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	524	Total	C	N	O	S	0	0
			4305	2774	726	781	24		
3	P	491	Total	C	N	O	S	0	0
			4042	2611	678	729	24		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	161	LEU	LYS	conflict	UNP Q9UJX2
P	161	LEU	LYS	conflict	UNP Q9UJX2

- Molecule 4 is a protein called ANAPHASE-PROMOTING COMPLEX SUBUNIT 15.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	D	55	Total	C	N	O	0	0
			437	277	73	87		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	1	MET	-	expression tag	UNP P60006
D	2	SER	-	expression tag	UNP P60006
D	3	THR	-	expression tag	UNP P60006
D	4	LEU	-	expression tag	UNP P60006
D	5	TYR	-	expression tag	UNP P60006

- Molecule 5 is a protein called ANAPHASE-PROMOTING COMPLEX SUBUNIT 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	56	Total	C	N	O	S	0	0
			450	290	74	85	1		

- Molecule 6 is a protein called ANAPHASE-PROMOTING COMPLEX SUBUNIT 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	498	Total	C	N	O	S	0	0
			3923	2514	664	719	26		
6	H	483	Total	C	N	O	S	0	0
			3853	2473	650	704	26		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	475	SER	ALA	conflict	UNP P30260
F	484	SER	ALA	conflict	UNP P30260
H	475	SER	ALA	conflict	UNP P30260
H	484	SER	ALA	conflict	UNP P30260

- Molecule 7 is a protein called ANAPHASE-PROMOTING COMPLEX SUBUNIT CDC26.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	25	Total	C	N	O	S	0	0
			211	133	40	37	1		
7	W	25	Total	C	N	O	S	0	0
			213	133	40	39	1		

- Molecule 8 is a protein called ANAPHASE-PROMOTING COMPLEX SUBUNIT 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	730	Total	C	N	O	S	0	0
			5709	3660	950	1066	33		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	430	ASP	GLU	conflict	UNP Q9UJX5

- Molecule 9 is a protein called ANAPHASE-PROMOTING COMPLEX SUBUNIT 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	504	Total	C	N	O	S	0	0
			4047	2602	685	735	25		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	225	ASN	ASP	conflict	UNP Q13042
J	228	GLU	GLN	conflict	UNP Q13042
J	229	LYS	GLU	conflict	UNP Q13042
J	347	ALA	GLU	conflict	UNP Q13042
J	524	ALA	GLU	conflict	UNP Q13042

- Molecule 10 is a protein called ANAPHASE-PROMOTING COMPLEX SUBUNIT 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	493	Total	C	N	O	S	0	0
			3988	2565	673	726	24		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	228	GLU	GLN	conflict	UNP Q13042
K	229	LYS	GLU	conflict	UNP Q13042
K	265	LYS	ALA	conflict	UNP Q13042

- Molecule 11 is a protein called ANAPHASE-PROMOTING COMPLEX SUBUNIT 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	182	Total	C	N	O	S	0	0
			1435	898	263	268	6		

- Molecule 12 is a protein called ANAPHASE-PROMOTING COMPLEX SUBUNIT 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	59	Total	C	N	O	S	0	0
			493	310	79	102	2		

- Molecule 13 is a protein called ANAPHASE-PROMOTING COMPLEX SUBUNIT 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	703	Total	C	N	O	S	0	0
			5400	3438	968	969	25		

- Molecule 14 is a protein called ANAPHASE-PROMOTING COMPLEX SUBUNIT 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	685	Total	C	N	O	S	0	0
			5396	3439	939	991	27		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	42	SER	ASN	conflict	UNP Q9UJX4
O	55	VAL	MET	conflict	UNP Q9UJX4
O	63	GLN	LEU	conflict	UNP Q9UJX4
O	75	VAL	LEU	conflict	UNP Q9UJX4
O	79	LEU	TYR	conflict	UNP Q9UJX4
O	164	SER	ASN	conflict	UNP Q9UJX4
O	165	ASP	GLY	conflict	UNP Q9UJX4
O	167	ASN	LYS	conflict	UNP Q9UJX4

- Molecule 15 is a protein called FUSION PROTEIN - UBIQUITIN-CONJUGATING ENZYME E2 C, UBIQUITIN-CONJUGATING ENZYME E2 S.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Q	162	Total	C	N	O	S	1	0
			1227	789	204	229	5		

- Molecule 16 is a protein called THE ANAPHASE-PROMOTING COMPLEX CHAIN R.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	R	386	Total	C	N	O	S	0	0
			2990	1884	530	564	12		

- Molecule 17 is a protein called THE ANAPHASE-PROMOTING COMPLEX CHAIN T.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	T	21	Total	C	N	O	0	0
			109	65	22	22		

- Molecule 18 is a protein called THE ANAPHASE-PROMOTING COMPLEX CHAIN U.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	U	24	Total	C	N	O	0	0
			120	72	24	24		

- Molecule 19 is a protein called THE ANAPHASE-PROMOTING COMPLEX CHAIN V.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	V	13	Total	C	N	O	0	0
			99	64	19	16		

- Molecule 20 is a protein called ANAPHASE-PROMOTING COMPLEX SUBUNIT 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	X	484	Total	C	N	O	S	0	0
			3770	2394	650	705	21		
20	Y	496	Total	C	N	O	S	0	0
			3865	2450	667	725	23		

- Molecule 21 is ZINC ION (CCD ID: ZN) (formula: Zn).

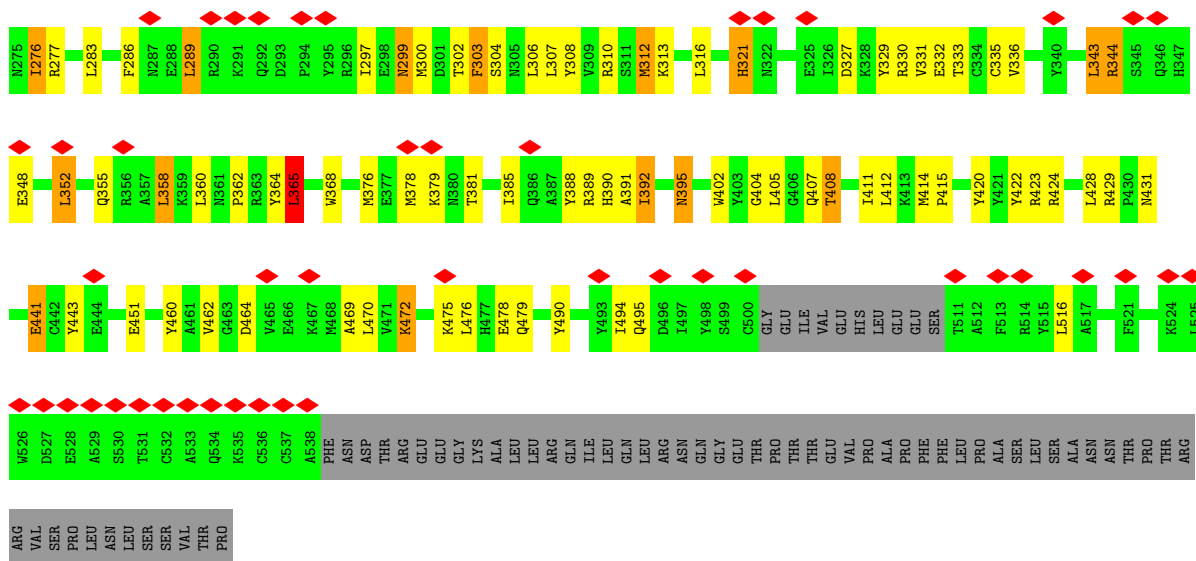
Mol	Chain	Residues	Atoms		AltConf
21	B	3	Total	Zn	0
			3	3	

3 Residue-property plots

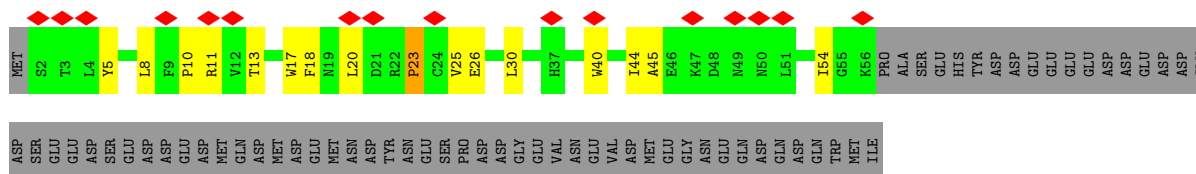
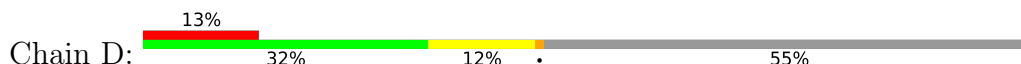
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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 1

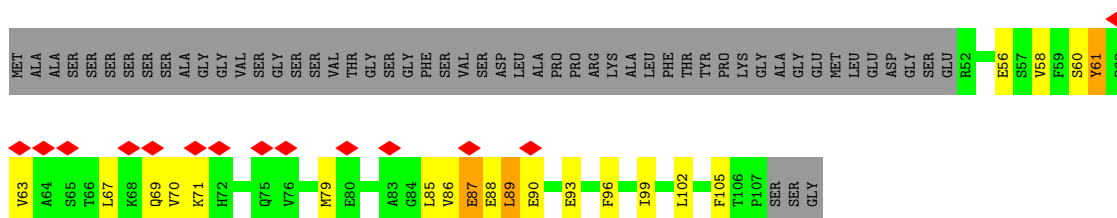
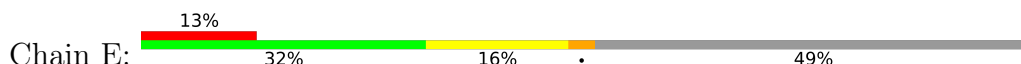




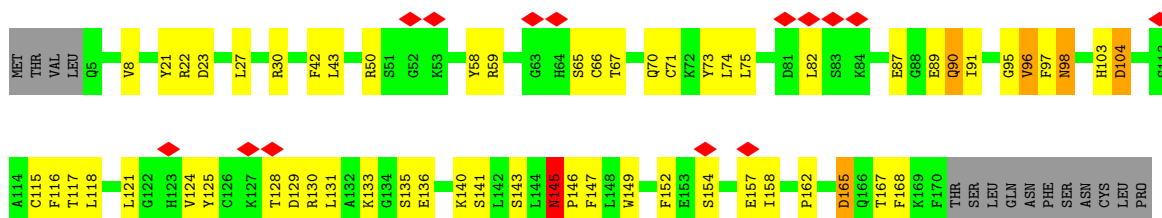
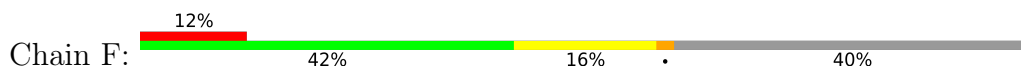
• Molecule 4: ANAPHASE-PROMOTING COMPLEX SUBUNIT 15

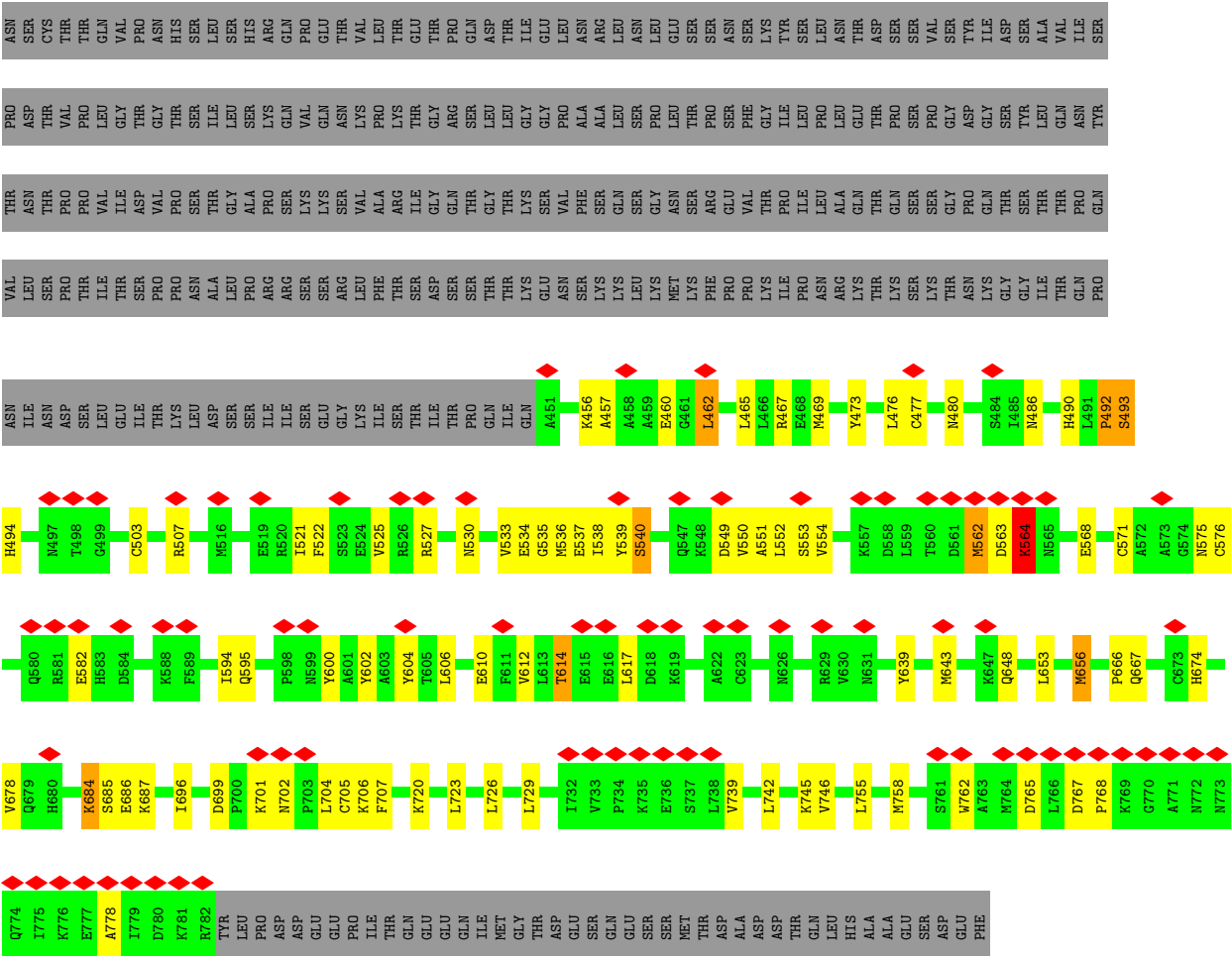


• Molecule 5: ANAPHASE-PROMOTING COMPLEX SUBUNIT 16

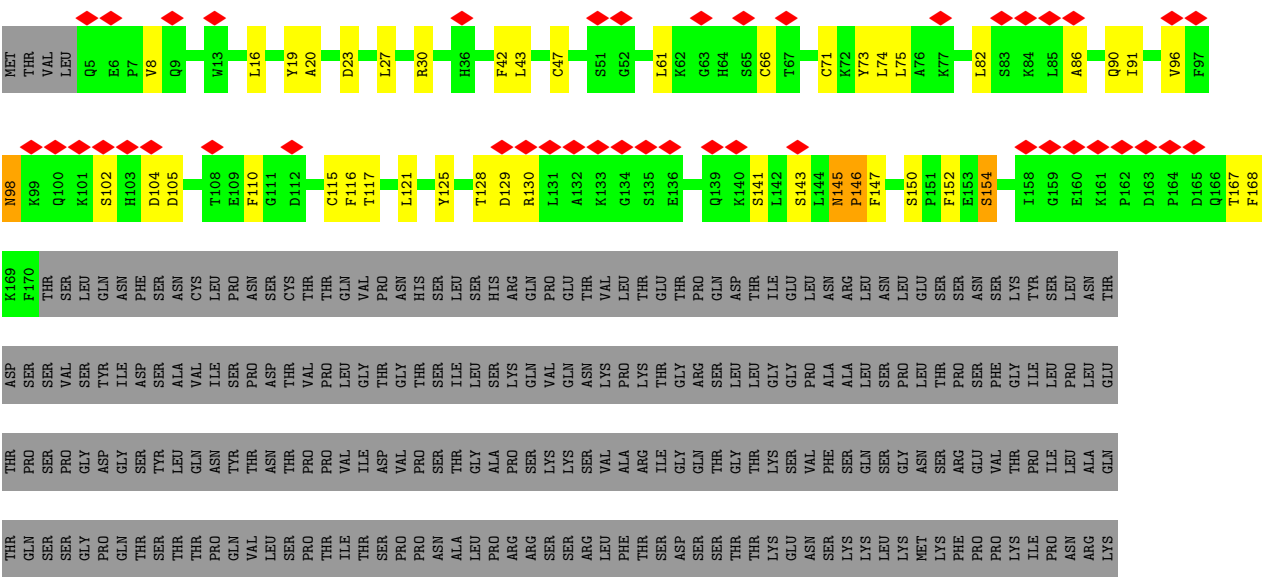


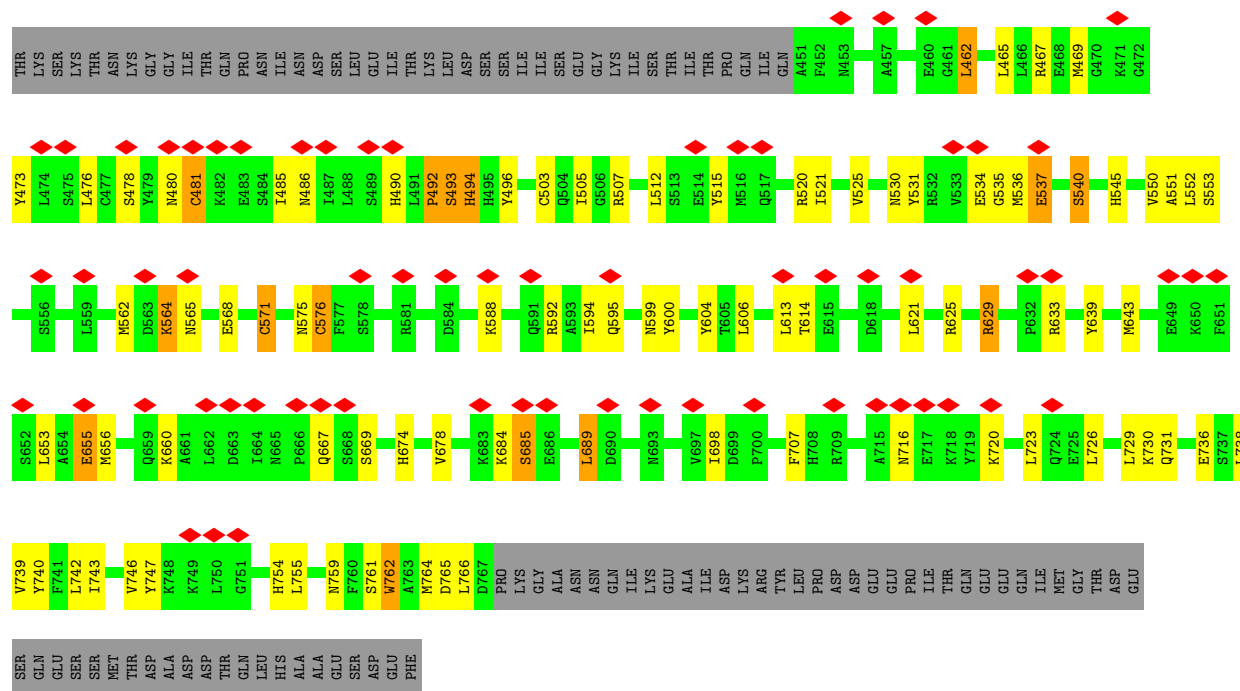
• Molecule 6: ANAPHASE-PROMOTING COMPLEX SUBUNIT 3



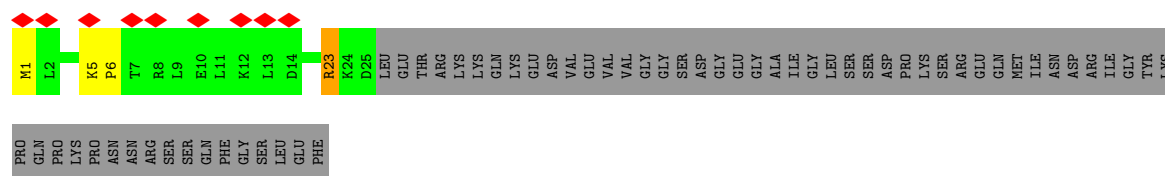


• Molecule 6: ANAPHASE-PROMOTING COMPLEX SUBUNIT 3

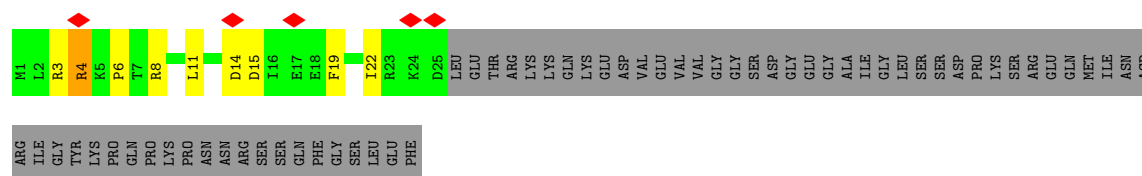




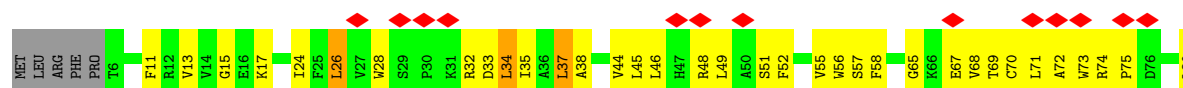
• Molecule 7: ANAPHASE-PROMOTING COMPLEX SUBUNIT CDC26

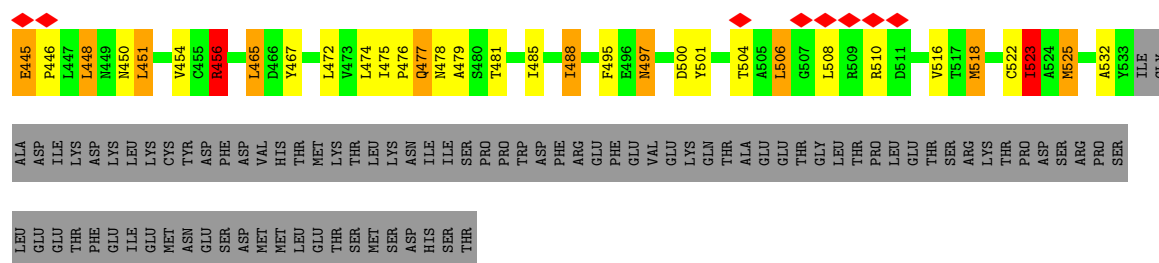


• Molecule 7: ANAPHASE-PROMOTING COMPLEX SUBUNIT CDC26

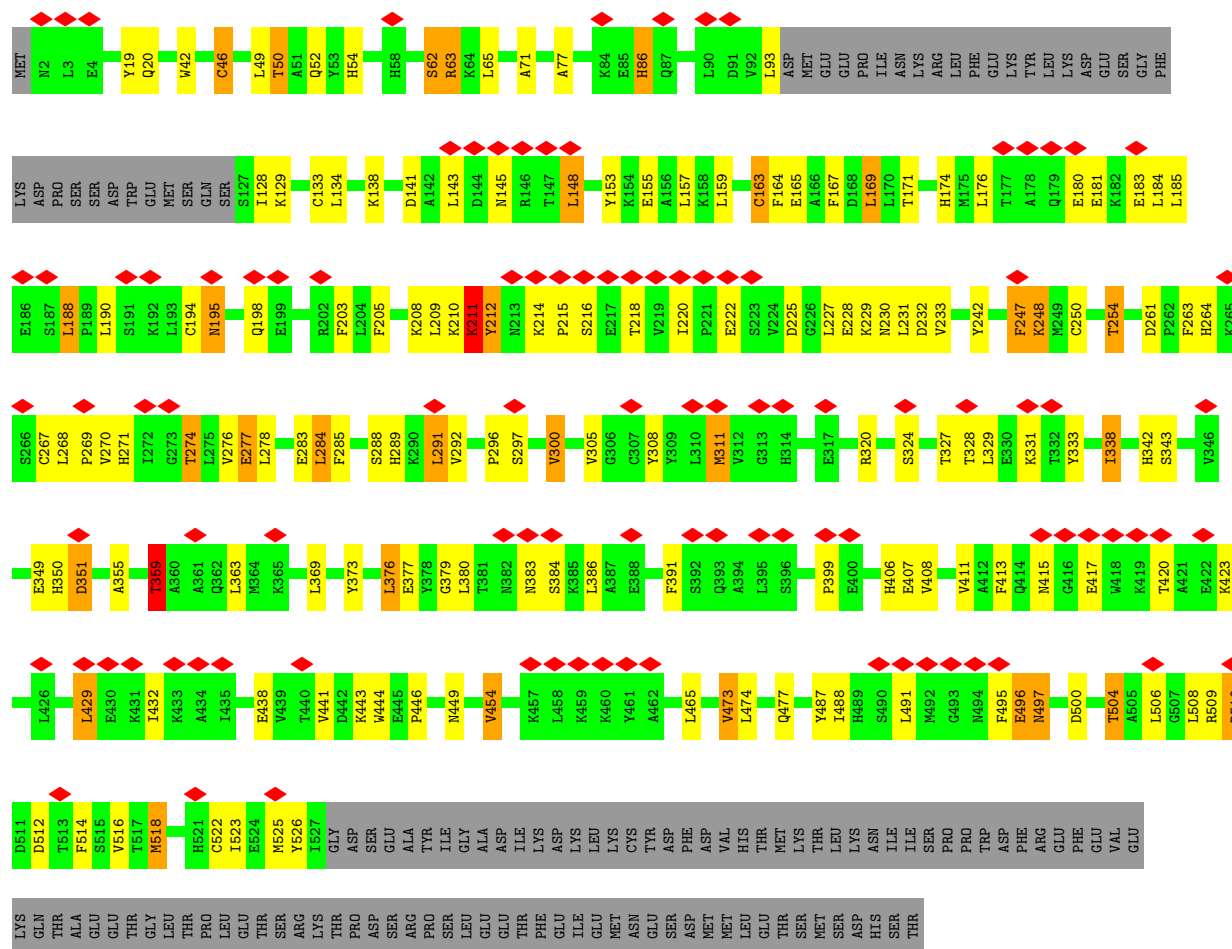


• Molecule 8: ANAPHASE-PROMOTING COMPLEX SUBUNIT 4

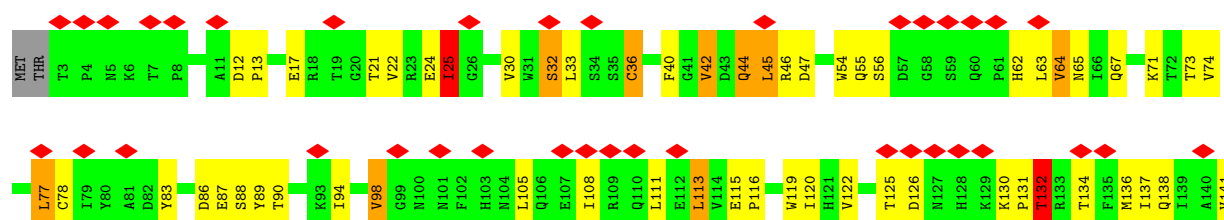


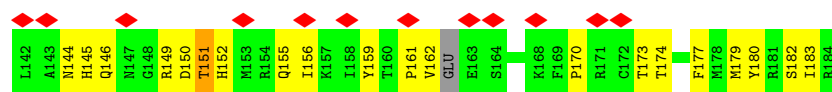


• Molecule 10: ANAPHASE-PROMOTING COMPLEX SUBUNIT 6

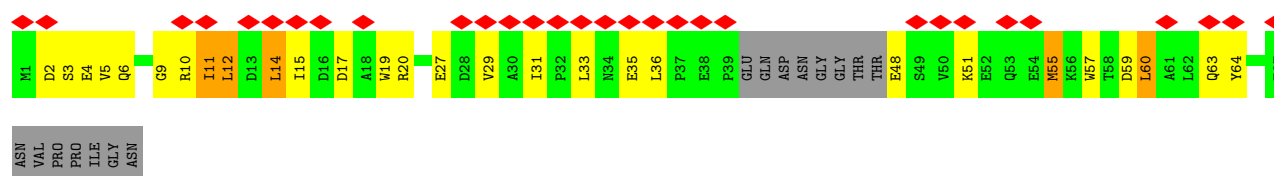
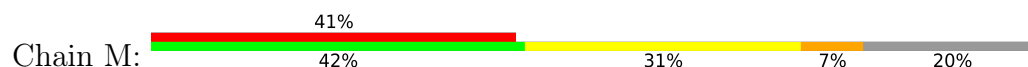


• Molecule 11: ANAPHASE-PROMOTING COMPLEX SUBUNIT 10





• Molecule 12: ANAPHASE-PROMOTING COMPLEX SUBUNIT 13



• Molecule 13: ANAPHASE-PROMOTING COMPLEX SUBUNIT 2

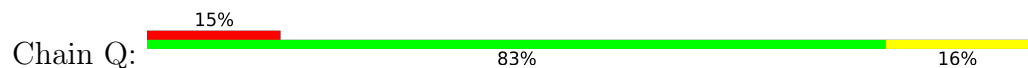


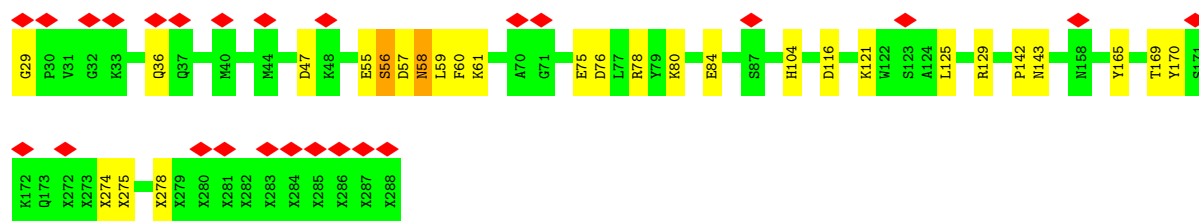


• Molecule 14: ANAPHASE-PROMOTING COMPLEX SUBUNIT 5

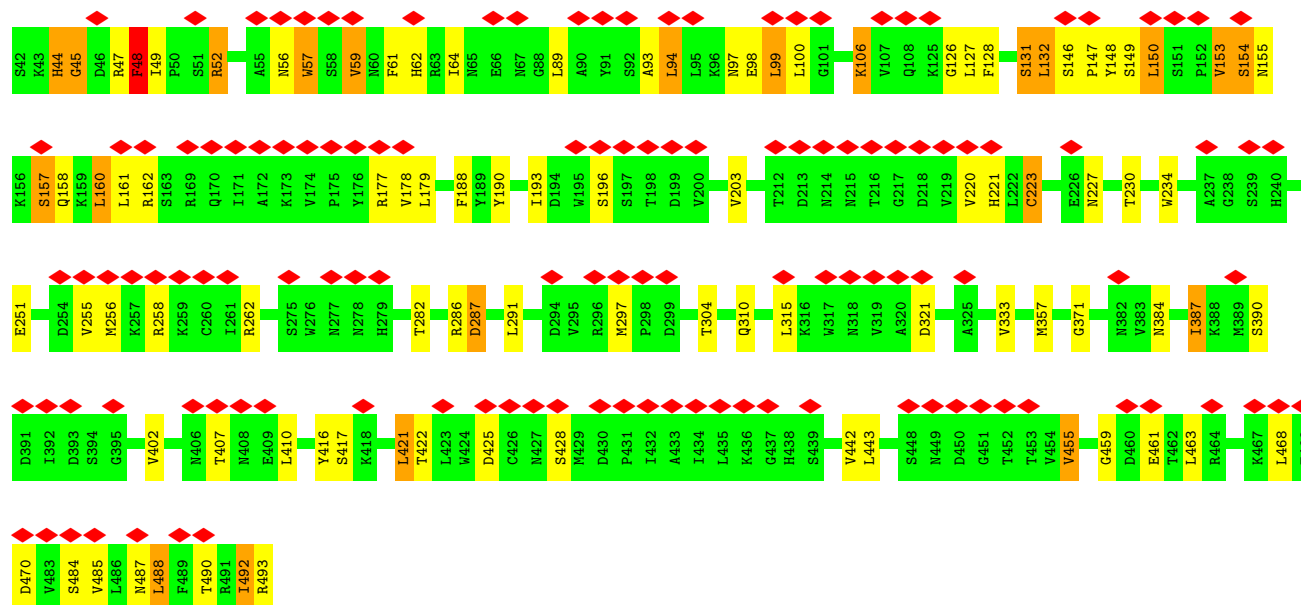
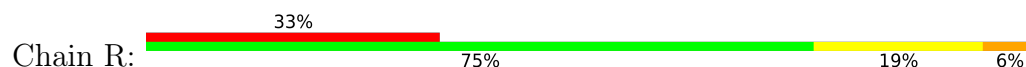


• Molecule 15: FUSION PROTEIN - UBIQUITIN-CONJUGATING ENZYME E2 C, UBIQUITIN-CONJUGATING ENZYME E2 S

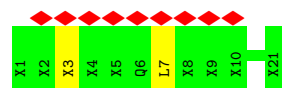
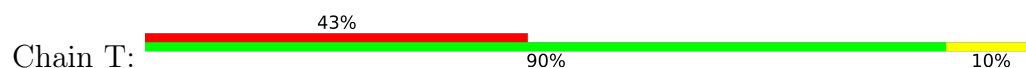




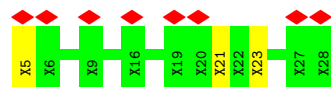
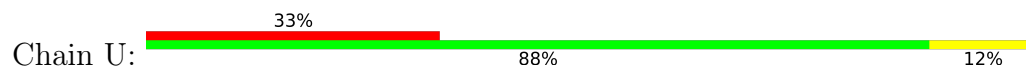
• Molecule 16: THE ANAPHASE-PROMOTING COMPLEX CHAIN R



• Molecule 17: THE ANAPHASE-PROMOTING COMPLEX CHAIN T



• Molecule 18: THE ANAPHASE-PROMOTING COMPLEX CHAIN U

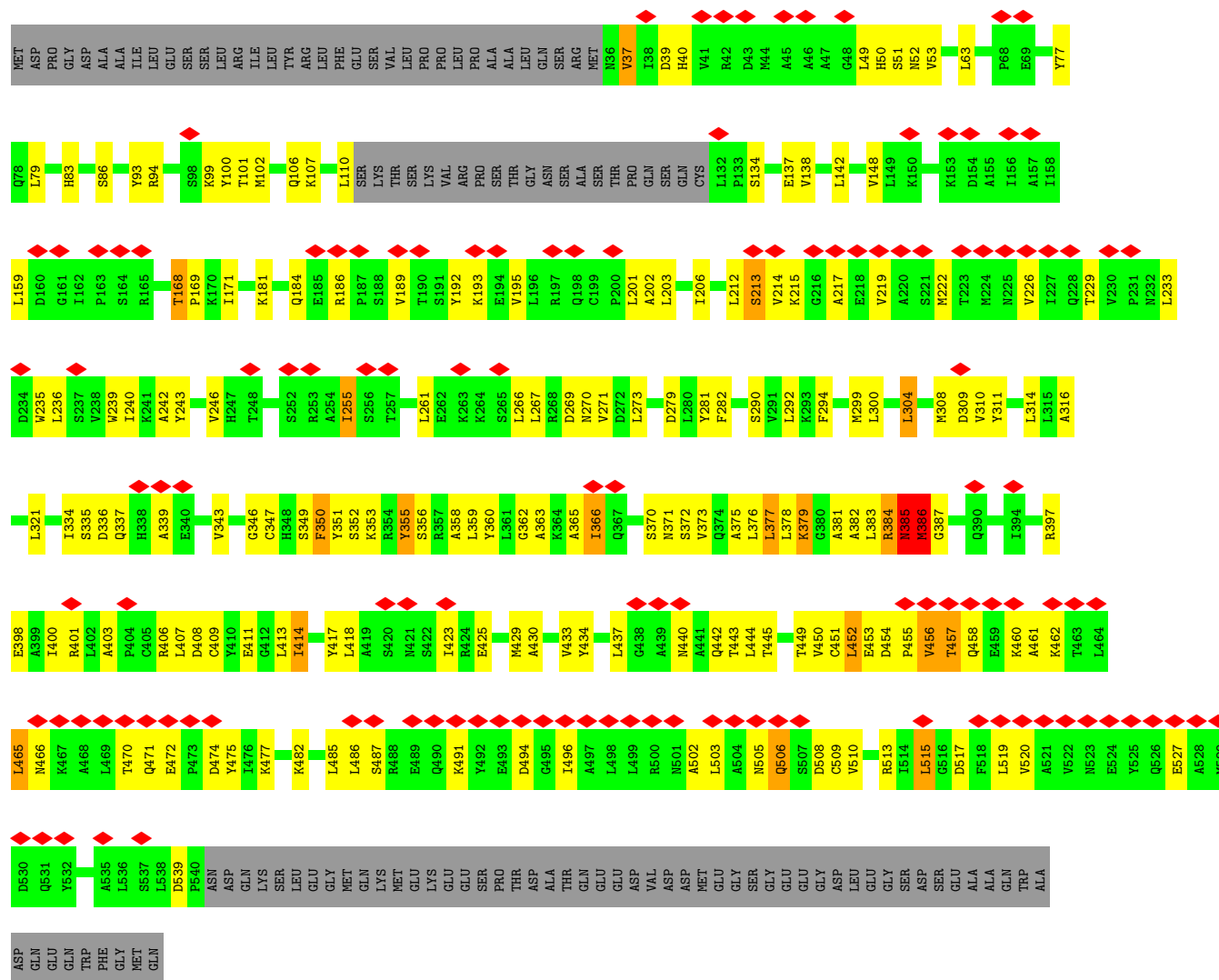


• Molecule 19: THE ANAPHASE-PROMOTING COMPLEX CHAIN V

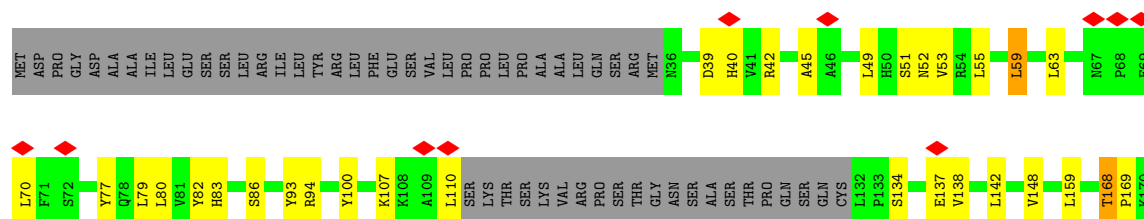




• Molecule 20: ANAPHASE-PROMOTING COMPLEX SUBUNIT 7



• Molecule 20: ANAPHASE-PROMOTING COMPLEX SUBUNIT 7





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	19939	Depositor
Resolution determination method	Not provided	
CTF correction method	Not provided	
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	16	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	78000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.397	Depositor
Minimum map value	-0.133	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.07	Depositor
Map size ($\text{\AA}$)	354.0, 354.0, 354.0	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.77, 1.77, 1.77	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	A	1.05	12/10949 (0.1%)	1.26	46/14903 (0.3%)
2	B	0.72	0/675	1.14	2/914 (0.2%)
3	C	1.01	3/4403 (0.1%)	1.20	7/5945 (0.1%)
3	P	0.91	0/4137	1.16	6/5587 (0.1%)
4	D	0.93	0/447	1.27	3/612 (0.5%)
5	E	0.93	0/459	1.10	0/619
6	F	0.92	1/4013 (0.0%)	1.18	12/5428 (0.2%)
6	H	0.91	0/3943	1.17	10/5329 (0.2%)
7	G	0.81	0/212	1.25	0/281
7	W	0.92	0/214	1.22	0/284
8	I	0.83	2/5827 (0.0%)	1.16	18/7899 (0.2%)
9	J	0.97	5/4146 (0.1%)	1.23	16/5615 (0.3%)
10	K	1.07	2/4086 (0.0%)	1.25	18/5532 (0.3%)
11	L	0.96	1/1468 (0.1%)	1.24	9/1993 (0.5%)
12	M	1.00	0/502	1.25	3/680 (0.4%)
13	N	0.83	3/4885 (0.1%)	1.19	21/6596 (0.3%)
14	O	1.03	4/5494 (0.1%)	1.25	21/7425 (0.3%)
15	Q	0.73	0/1174	0.98	4/1601 (0.2%)
16	R	0.85	0/3052	1.08	14/4139 (0.3%)
17	T	0.92	0/13	1.01	0/16
19	V	0.95	0/99	1.07	0/130
20	X	0.87	6/3830 (0.2%)	1.12	8/5187 (0.2%)
20	Y	0.78	0/3925	1.12	5/5311 (0.1%)
All	All	0.94	39/67953 (0.1%)	1.19	223/92026 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	9
8	I	0	2
9	J	0	1
13	N	0	28
16	R	0	2
17	T	0	1
20	X	0	1
All	All	0	44

The worst 5 of 39 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	K	229	LYS	CB-CG	29.76	2.41	1.52
20	X	385	ASN	N-CA	15.23	1.65	1.46
20	X	386	MET	N-CA	10.12	1.58	1.46
20	X	385	ASN	CA-C	8.12	1.63	1.52
1	A	589	ASP	N-CA	7.82	1.52	1.46

The worst 5 of 223 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	K	229	LYS	CA-CB-CG	-14.97	84.15	114.10
20	X	366	ILE	CB-CA-C	-10.43	98.06	112.14
20	Y	366	ILE	CB-CA-C	-10.42	98.08	112.14
3	P	96	VAL	N-CA-C	10.34	121.16	110.72
11	L	132	THR	CB-CA-C	-10.32	91.99	109.65

There are no chirality outliers.

5 of 44 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	11	MET	Peptide
1	A	124	GLN	Peptide
1	A	14	ALA	Peptide
1	A	83	ILE	Peptide
1	A	86	ASP	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	A	10950	0	10677	433	0
2	B	650	0	598	123	0
3	C	4305	0	4273	126	0
3	P	4042	0	3998	147	0
4	D	437	0	396	14	0
5	E	450	0	435	12	0
6	F	3923	0	3813	96	0
6	H	3853	0	3788	104	0
7	G	211	0	220	4	0
7	W	213	0	220	9	0
8	I	5709	0	5597	133	0
9	J	4047	0	3962	132	0
10	K	3988	0	3917	126	0
11	L	1435	0	1382	66	0
12	M	493	0	469	28	0
13	N	5400	0	4967	445	0
14	O	5396	0	5425	175	0
15	Q	1227	0	1128	28	0
16	R	2990	0	2913	64	0
17	T	109	0	32	3	0
18	U	120	0	27	2	0
19	V	99	0	111	1	0
20	X	3770	0	3829	258	0
20	Y	3865	0	3925	165	0
21	B	3	0	0	0	0
All	All	67685	0	66102	2433	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 2433 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)
13:N:435:VAL:CG1	13:N:515:PHE:CE2	1.81	1.63
1:A:1116:THR:CG2	13:N:779:MET:HE1	1.29	1.59
1:A:1114:ARG:HE	13:N:779:MET:CG	1.13	1.57
2:B:14:TRP:CH2	2:B:41:GLY:N	1.73	1.54
13:N:502:ILE:CG1	13:N:548:ARG:HH12	1.21	1.50

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	A	1354/1441 (94%)	1217 (90%)	106 (8%)	31 (2%)	5	28
2	B	83/84 (99%)	69 (83%)	8 (10%)	6 (7%)	1	11
3	C	520/597 (87%)	495 (95%)	23 (4%)	2 (0%)	30	66
3	P	485/597 (81%)	459 (95%)	25 (5%)	1 (0%)	43	77
4	D	53/121 (44%)	46 (87%)	6 (11%)	1 (2%)	6	32
5	E	54/110 (49%)	54 (100%)	0	0	100	100
6	F	494/824 (60%)	477 (97%)	11 (2%)	6 (1%)	10	42
6	H	479/824 (58%)	462 (96%)	12 (2%)	5 (1%)	12	47
7	G	23/85 (27%)	23 (100%)	0	0	100	100
7	W	23/85 (27%)	23 (100%)	0	0	100	100
8	I	722/808 (89%)	690 (96%)	28 (4%)	4 (1%)	21	58
9	J	500/620 (81%)	467 (93%)	28 (6%)	5 (1%)	12	47
10	K	489/620 (79%)	458 (94%)	26 (5%)	5 (1%)	12	47
11	L	180/185 (97%)	169 (94%)	9 (5%)	2 (1%)	11	45
12	M	55/74 (74%)	46 (84%)	9 (16%)	0	100	100
13	N	572/703 (81%)	501 (88%)	33 (6%)	38 (7%)	1	12
14	O	677/755 (90%)	645 (95%)	24 (4%)	8 (1%)	10	42
15	Q	144/162 (89%)	139 (96%)	5 (4%)	0	100	100
16	R	374/386 (97%)	334 (89%)	35 (9%)	5 (1%)	9	41
17	T	2/21 (10%)	2 (100%)	0	0	100	100
19	V	11/13 (85%)	8 (73%)	1 (9%)	2 (18%)	0	2
20	X	480/599 (80%)	462 (96%)	15 (3%)	3 (1%)	21	58
20	Y	492/599 (82%)	471 (96%)	16 (3%)	5 (1%)	12	47
All	All	8266/10313 (80%)	7717 (93%)	420 (5%)	129 (2%)	10	37

5 of 129 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	274	VAL
1	A	630	PRO
1	A	857	ALA
1	A	860	TYR
1	A	1125	ILE

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	A	1150/1206 (95%)	984 (86%)	166 (14%)	3	15
2	B	65/75 (87%)	53 (82%)	12 (18%)	1	10
3	C	452/520 (87%)	393 (87%)	59 (13%)	4	17
3	P	422/520 (81%)	372 (88%)	50 (12%)	5	19
4	D	46/115 (40%)	42 (91%)	4 (9%)	9	30
5	E	47/89 (53%)	33 (70%)	14 (30%)	0	2
6	F	407/729 (56%)	366 (90%)	41 (10%)	7	24
6	H	408/729 (56%)	373 (91%)	35 (9%)	10	30
7	G	22/77 (29%)	20 (91%)	2 (9%)	9	28
7	W	23/77 (30%)	21 (91%)	2 (9%)	9	30
8	I	620/730 (85%)	568 (92%)	52 (8%)	10	30
9	J	424/546 (78%)	363 (86%)	61 (14%)	3	15
10	K	423/549 (77%)	374 (88%)	49 (12%)	5	20
11	L	155/170 (91%)	142 (92%)	13 (8%)	10	30
12	M	55/67 (82%)	44 (80%)	11 (20%)	1	8
13	N	516/526 (98%)	452 (88%)	64 (12%)	4	18
14	O	578/651 (89%)	483 (84%)	95 (16%)	2	12
15	Q	122/127 (96%)	121 (99%)	1 (1%)	73	77
16	R	326/334 (98%)	291 (89%)	35 (11%)	6	22

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	T	1/2 (50%)	1 (100%)	0	100	100
19	V	10/10 (100%)	7 (70%)	3 (30%)	0	2
20	X	407/513 (79%)	376 (92%)	31 (8%)	12	33
20	Y	418/513 (82%)	381 (91%)	37 (9%)	9	29
All	All	7097/8875 (80%)	6260 (88%)	837 (12%)	7	19

5 of 837 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	K	195	ASN
13	N	592	TYR
20	X	539	ASP
10	K	331	LYS
10	K	194	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 188 such sidechains are listed below:

Mol	Chain	Res	Type
13	N	800	GLN
3	P	35	GLN
14	O	211	GLN
14	O	472	HIS
3	P	305	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	20
13	N	10
16	R	5
15	Q	1

The worst 5 of 36 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Q	173:GLN	C	272:UNK	N	71.87
1	A	986:ALA	C	1013:ASP	N	34.04
1	N	730:ILE	C	747:LYS	N	25.53
1	N	458:UNK	C	476:UNK	N	22.96
1	R	132:LEU	C	146:SER	N	22.90

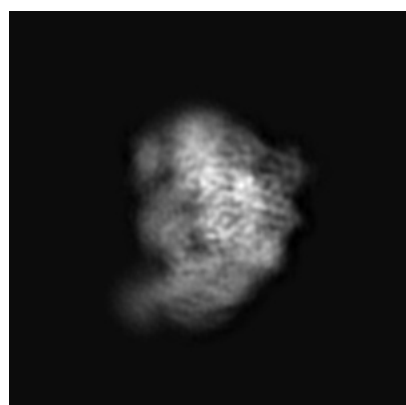
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2925. These allow visual inspection of the internal detail of the map and identification of artifacts.

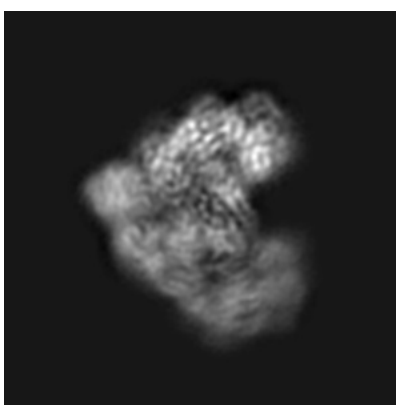
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

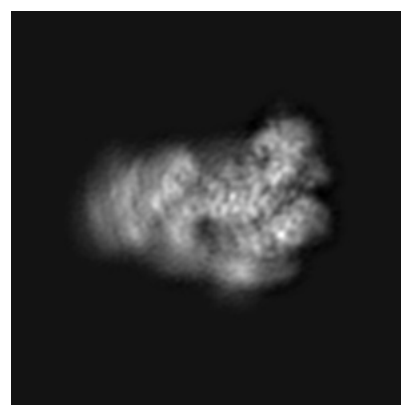
6.1.1 Primary map



X



Y



Z

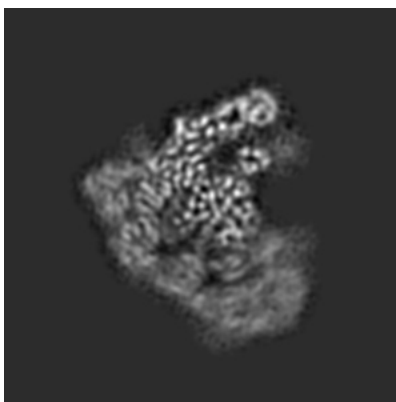
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

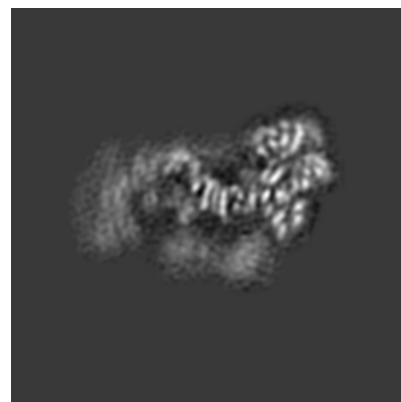
6.2.1 Primary map



X Index: 100



Y Index: 100



Z Index: 100

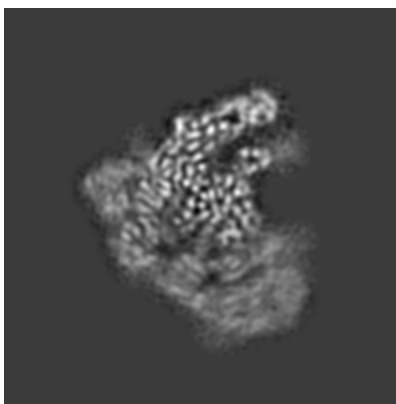
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

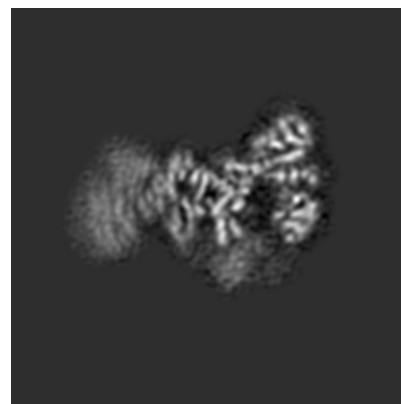
6.3.1 Primary map



X Index: 136



Y Index: 101

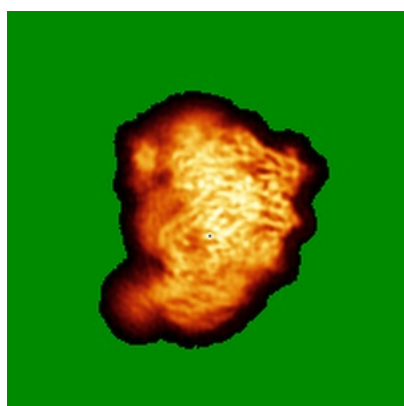


Z Index: 112

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

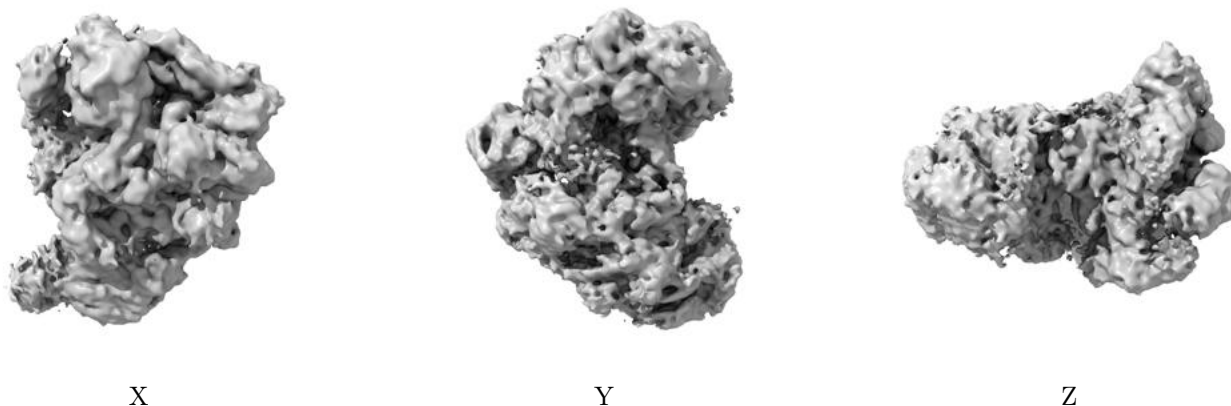


Z

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 0.07. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

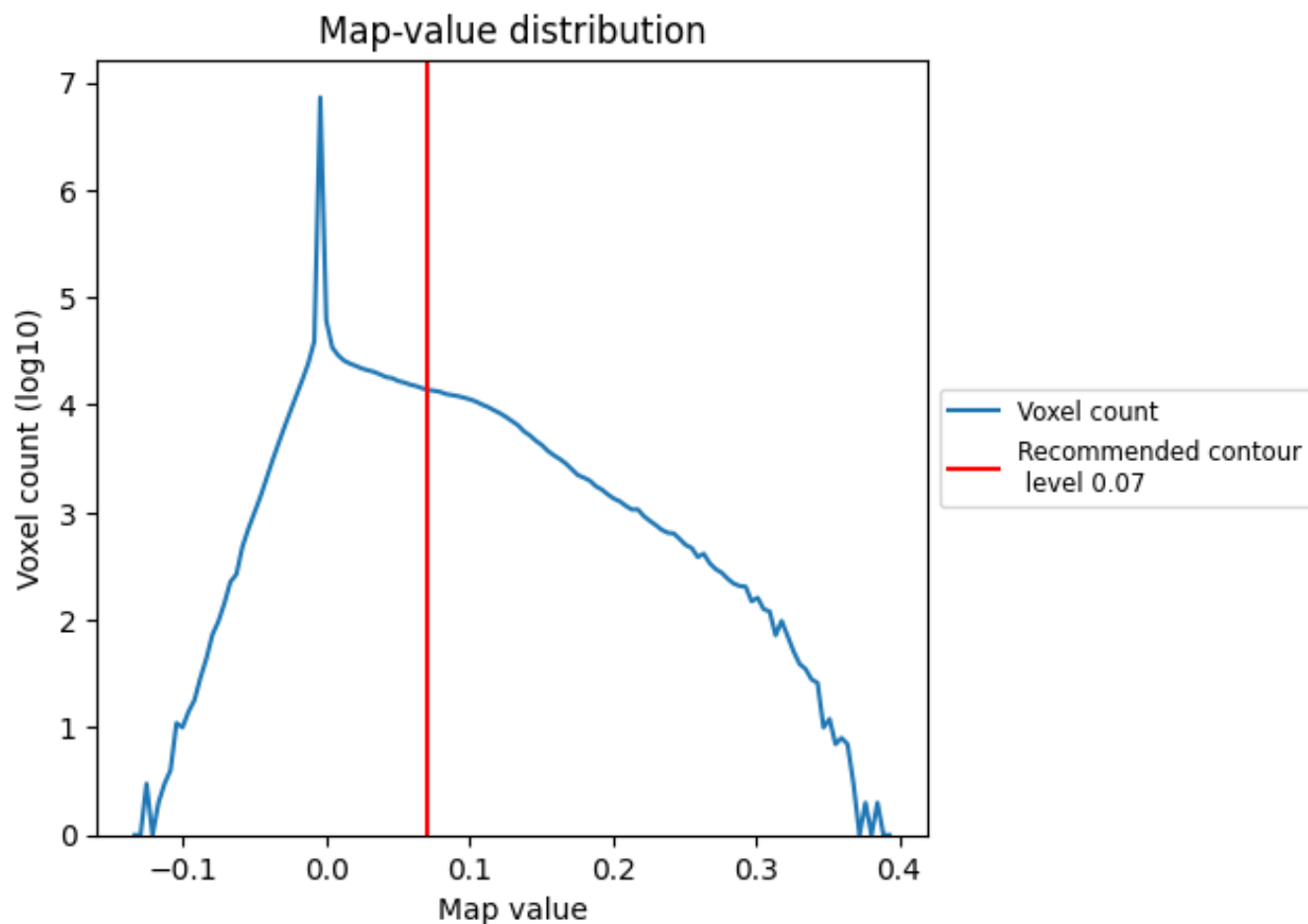
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

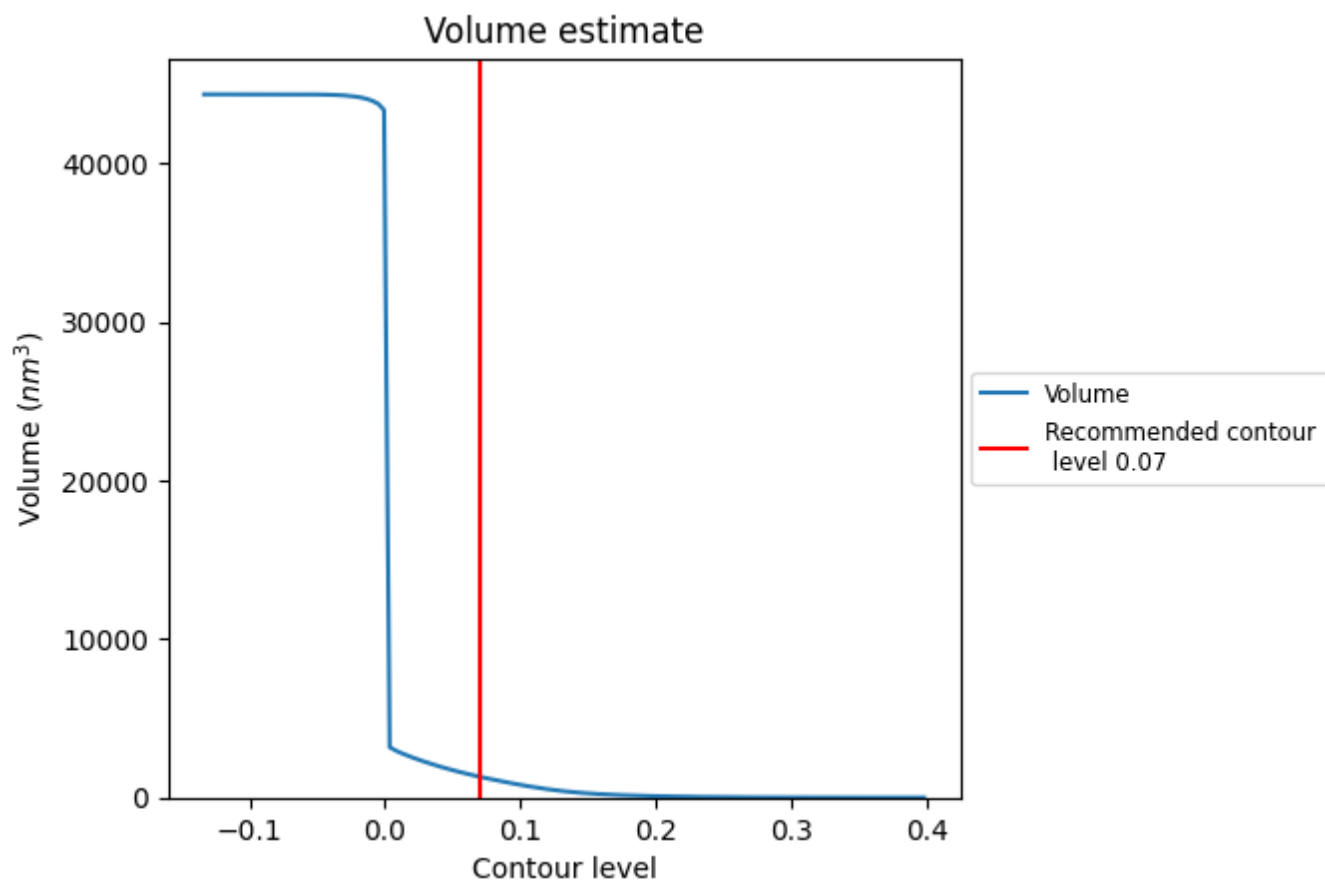
This section contains the results of statistical analysis of the map.

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.

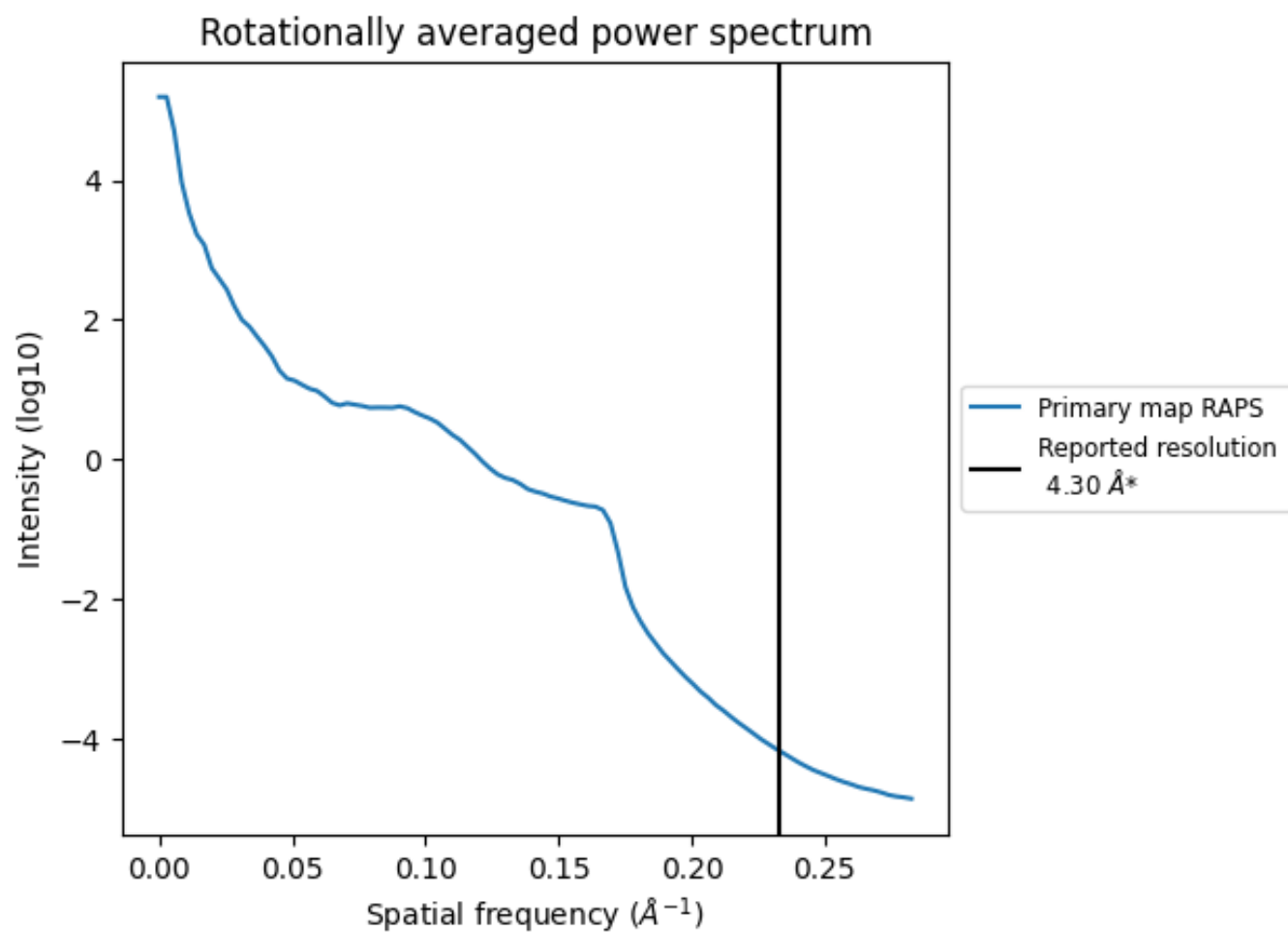
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1309 nm³; this corresponds to an approximate mass of 1182 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 0.233 Å⁻¹

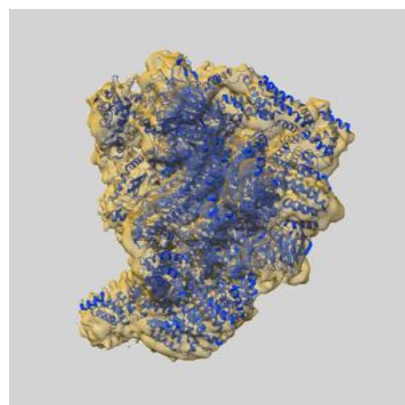
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

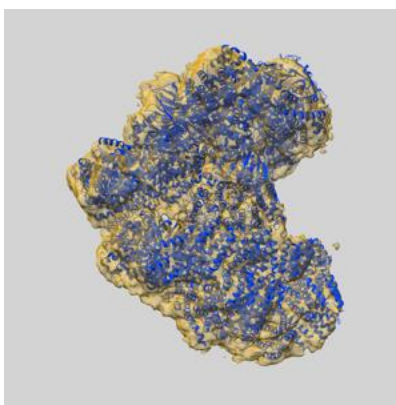
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-2925 and PDB model 5A31. Per-residue inclusion information can be found in [section 3](#) on [page 9](#).

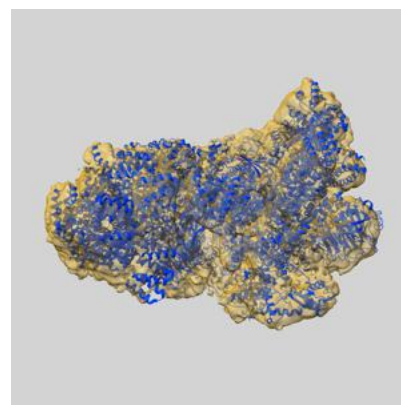
9.1 Map-model overlay [i](#)



X



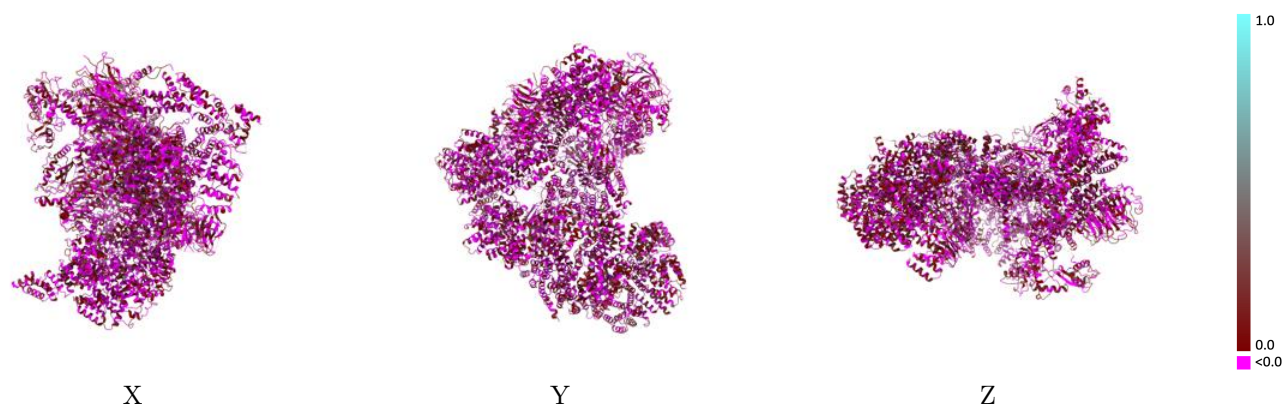
Y



Z

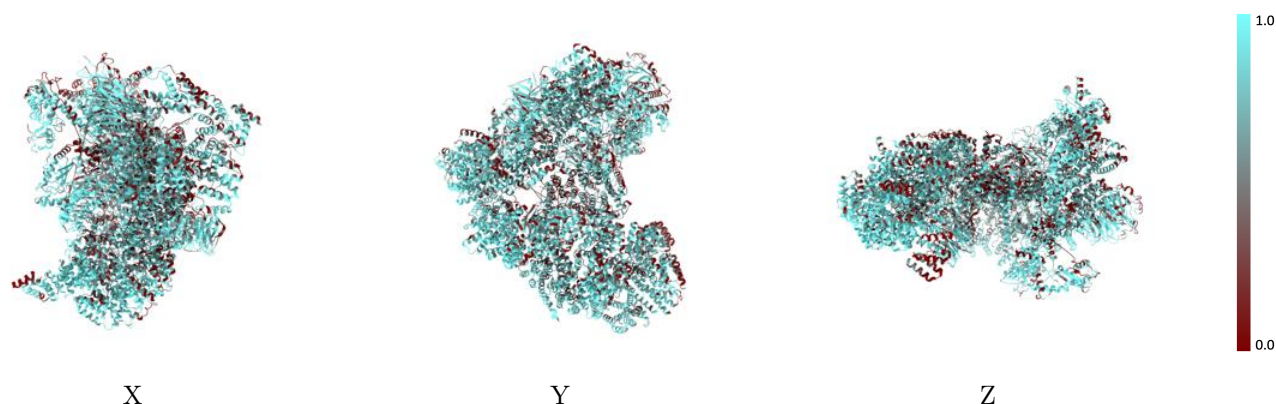
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



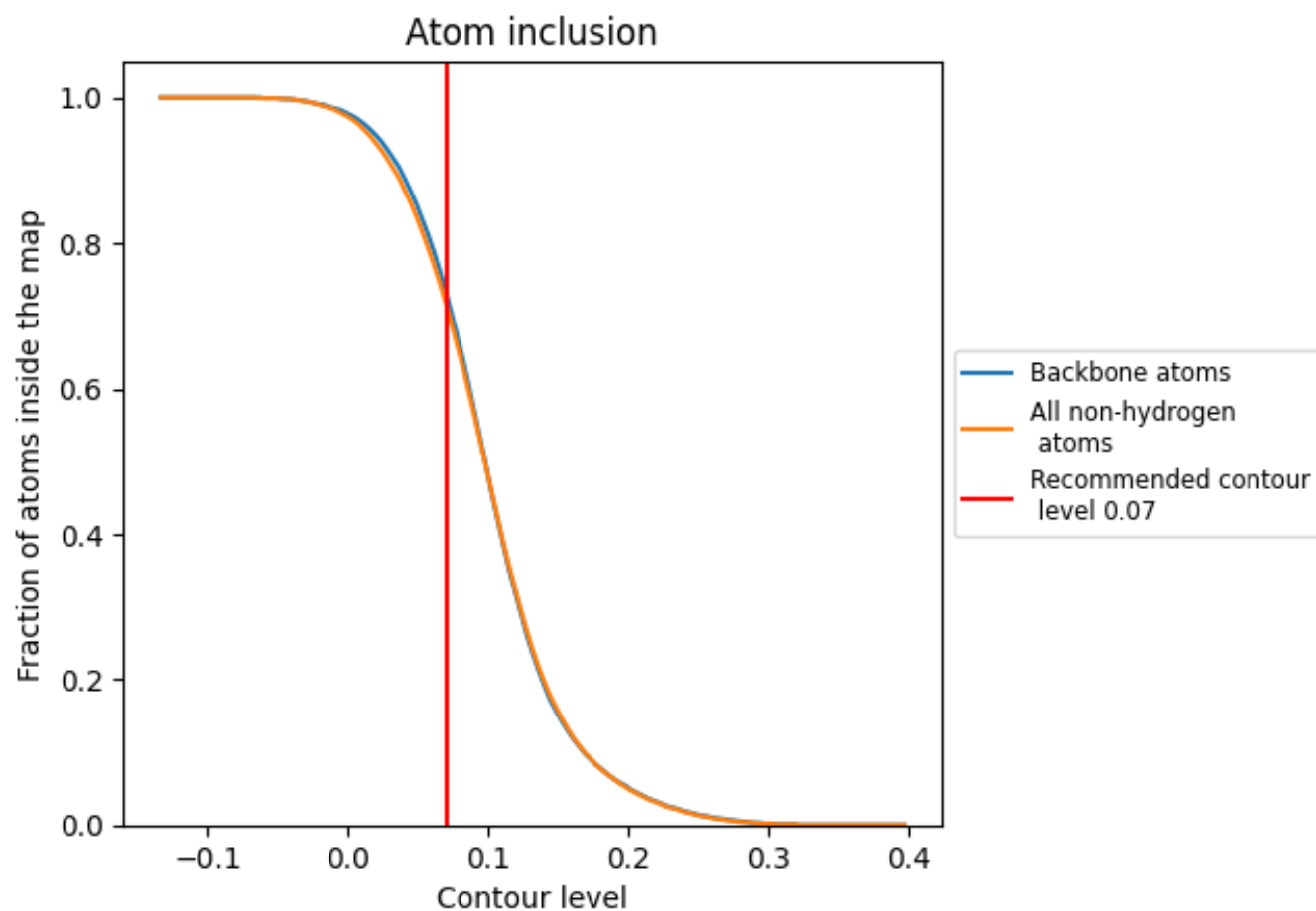
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.07).

9.4 Atom inclusion ⓘ



At the recommended contour level, 73% of all backbone atoms, 72% 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 (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7180	 0.0070
A	 0.6670	 -0.0150
B	 0.8150	 0.0470
C	 0.6680	 -0.0110
D	 0.6020	 0.0420
E	 0.6100	 0.0040
F	 0.7770	 -0.0020
G	 0.5670	 -0.0150
H	 0.7160	 0.0300
I	 0.7470	 0.0370
J	 0.8000	 -0.0120
K	 0.7540	 0.0240
L	 0.6690	 0.0160
M	 0.4560	 -0.0260
N	 0.6780	 -0.0050
O	 0.7120	 0.0230
P	 0.8140	 -0.0260
Q	 0.8290	 0.0480
R	 0.6390	 -0.0080
T	 0.5320	 -0.0430
U	 0.6500	 -0.0220
V	 0.5050	 0.0200
W	 0.7710	 0.0460
X	 0.6950	 0.0350
Y	 0.7890	 0.0250

