



## wwPDB EM Validation Summary Report ⓘ

Oct 13, 2024 – 04:20 am BST

PDB ID : 5G05  
EMDB ID : EMD-3388  
Title : Cryo-EM structure of combined apo phosphorylated APC  
Authors : Zhang, S.; Chang, L.; Alfieri, C.; Zhang, Z.; Yang, J.; Maslen, S.; Skehel, M.; Barford, D.  
Deposited on : 2016-03-16  
Resolution : 3.40 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.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

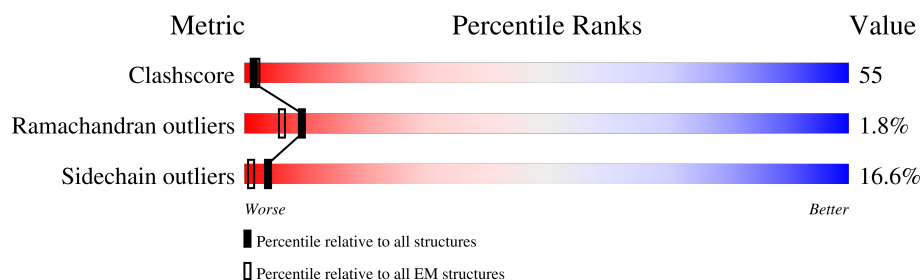
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.40 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.






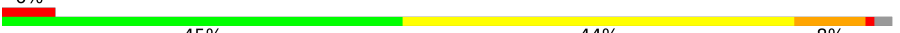
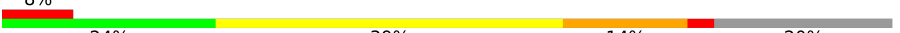

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1944	
2	B	84	
3	C	597	
3	P	597	
4	D	121	
5	E	110	
6	F	824	
6	H	824	

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Mol	Chain	Length	Quality of chain
7	G	85	
7	W	85	
8	I	808	
9	J	620	
9	K	620	
10	L	185	
11	M	74	
12	N	822	
13	O	755	
14	T	15	
15	X	599	
15	Y	599	

## 2 Entry composition [i](#)

There are 16 unique types of molecules in this entry. The entry contains 63181 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	1569	Total	C	N	O	S	0	0
			11890	7656	2014	2140	80		

- 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
			649	416	117	99	17		

- 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
			4306	2774	727	781	24		
3	P	492	Total	C	N	O	S	0	0
			4046	2613	679	730	24		

- 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
			436	277	73	86		

- 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 CELL DIVISION CYCLE PROTEIN 27 HOMOLOG.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	460	Total	C	N	O	S	0	0
			3618	2320	608	666	24		
6	H	488	Total	C	N	O	S	0	0
			3879	2489	655	709	26		

- 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
			220	137	41	41	1		
7	W	26	Total	C	N	O	S	0	0
			218	136	41	40	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	723	Total	C	N	O	S	0	0
			5634	3619	940	1041	34		

- Molecule 9 is a protein called CELL DIVISION CYCLE PROTEIN 16 HOMOLOG.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	504	Total	C	N	O	S	0	0
			4053	2604	687	737	25		
9	K	493	Total	C	N	O	S	0	0
			3988	2564	672	728	24		

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

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

- Molecule 11 is a protein called ANAPHASE-PROMOTING COMPLEX SUBUNIT 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	M	59	Total	C	N	O	S	0	0
			481	304	79	96	2		

- Molecule 12 is a protein called ANAPHASE-PROMOTING COMPLEX SUBUNIT 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	N	604	Total	C	N	O	S	0	0
			4767	3053	851	841	22		

- Molecule 13 is a protein called ANAPHASE-PROMOTING COMPLEX SUBUNIT 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	O	688	Total	C	N	O	S	0	0
			5400	3443	940	989	28		

- Molecule 14 is a protein called UNIDENTIFIED PEPTIDE.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	T	15	Total	C	N	O	0	0
			79	47	16	16		

- Molecule 15 is a protein called ANAPHASE-PROMOTING COMPLEX SUBUNIT 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	X	484	Total	C	N	O	S	0	0
			3767	2390	649	704	24		
15	Y	496	Total	C	N	O	S	0	0
			3862	2446	666	724	26		

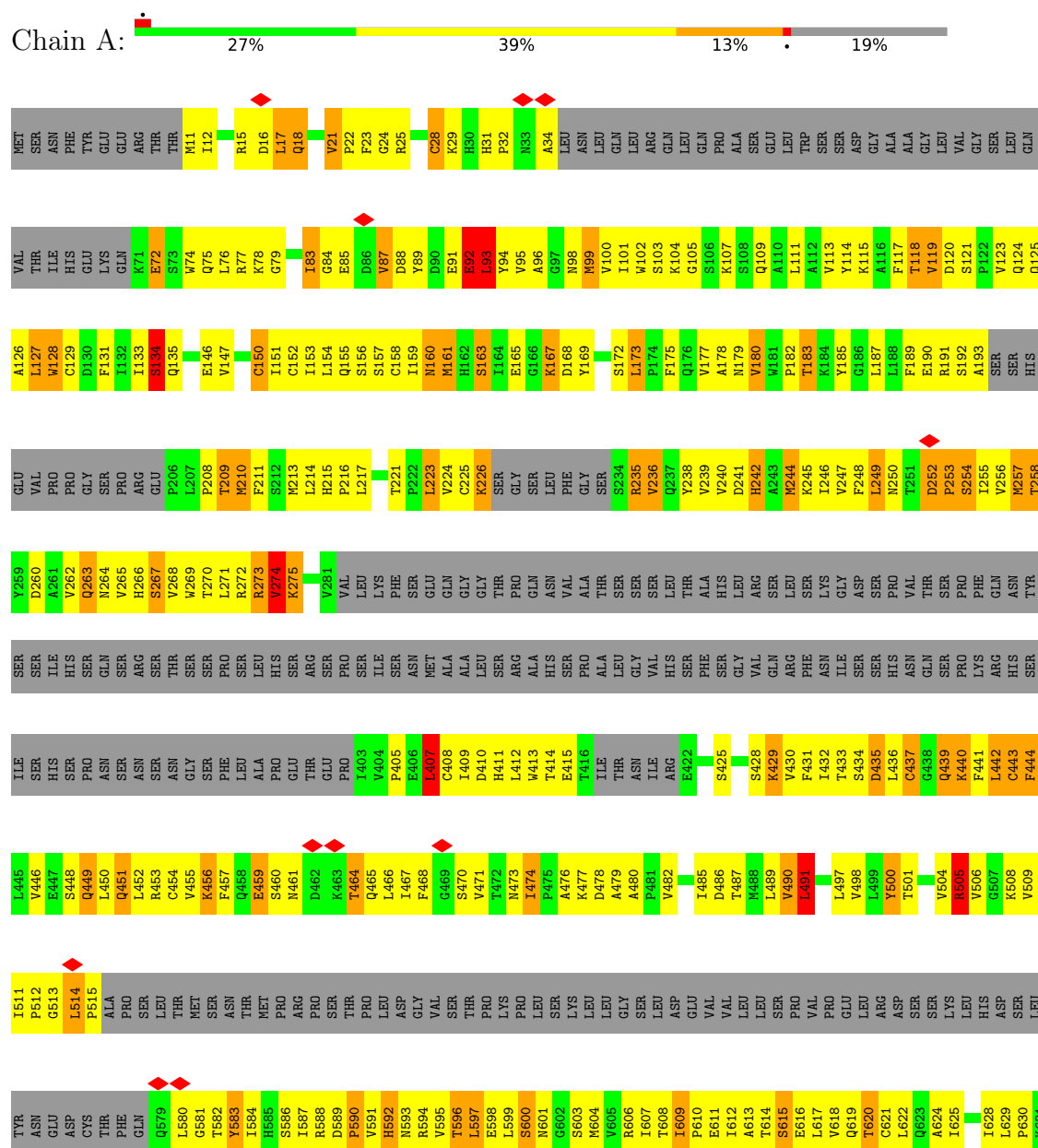
- Molecule 16 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

### 3 Residue-property plots

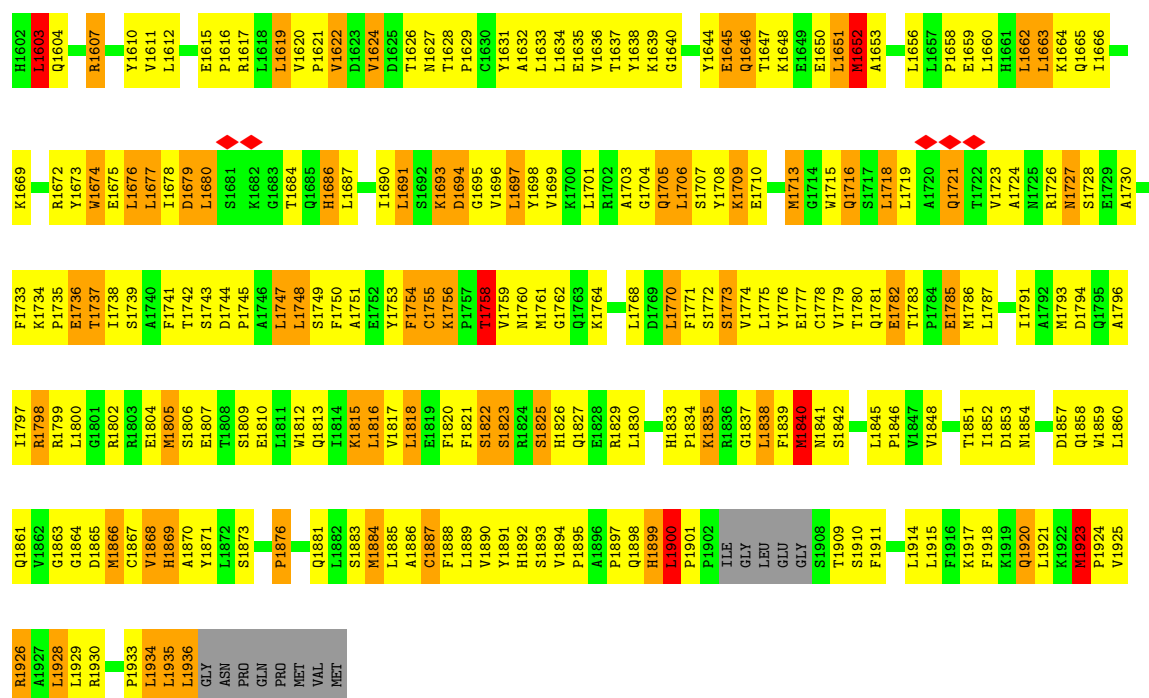
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

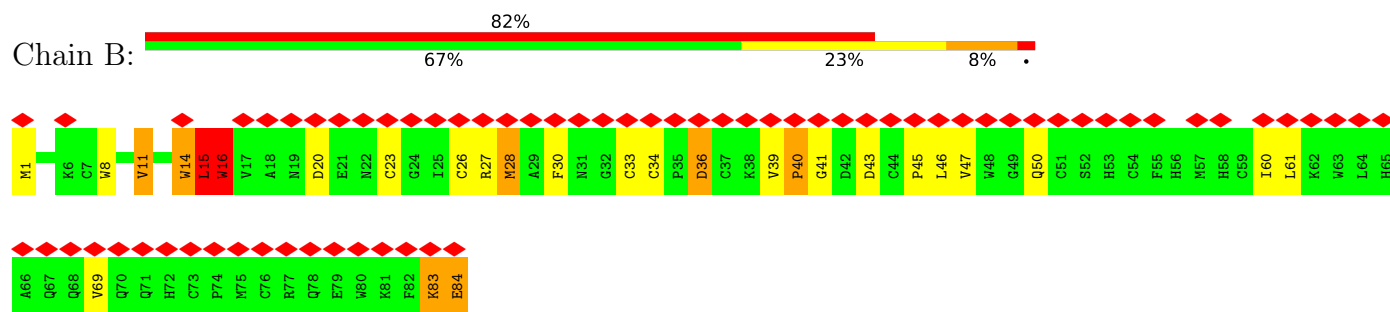




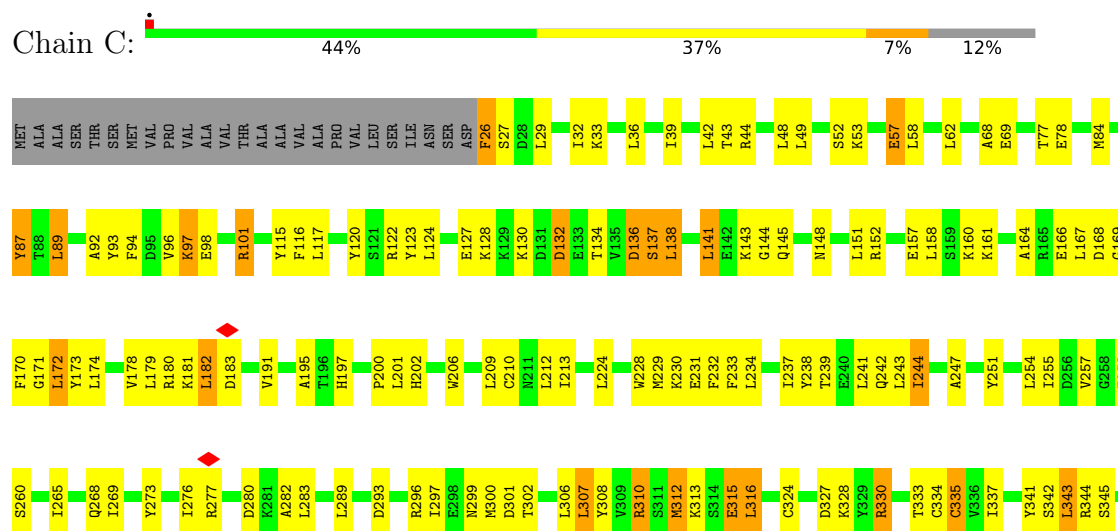




• Molecule 2: ANAPHASE-PROMOTING COMPLEX SUBUNIT 11

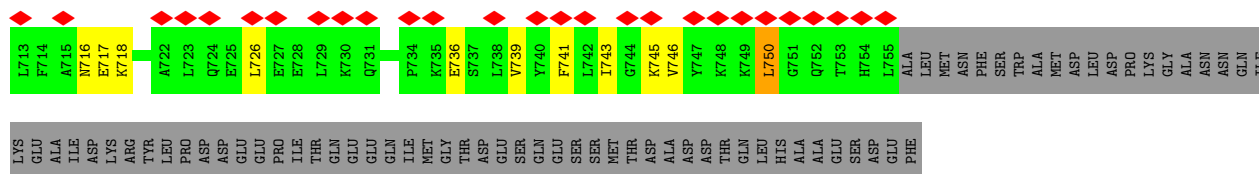


• Molecule 3: CELL DIVISION CYCLE PROTEIN 23 HOMOLOG

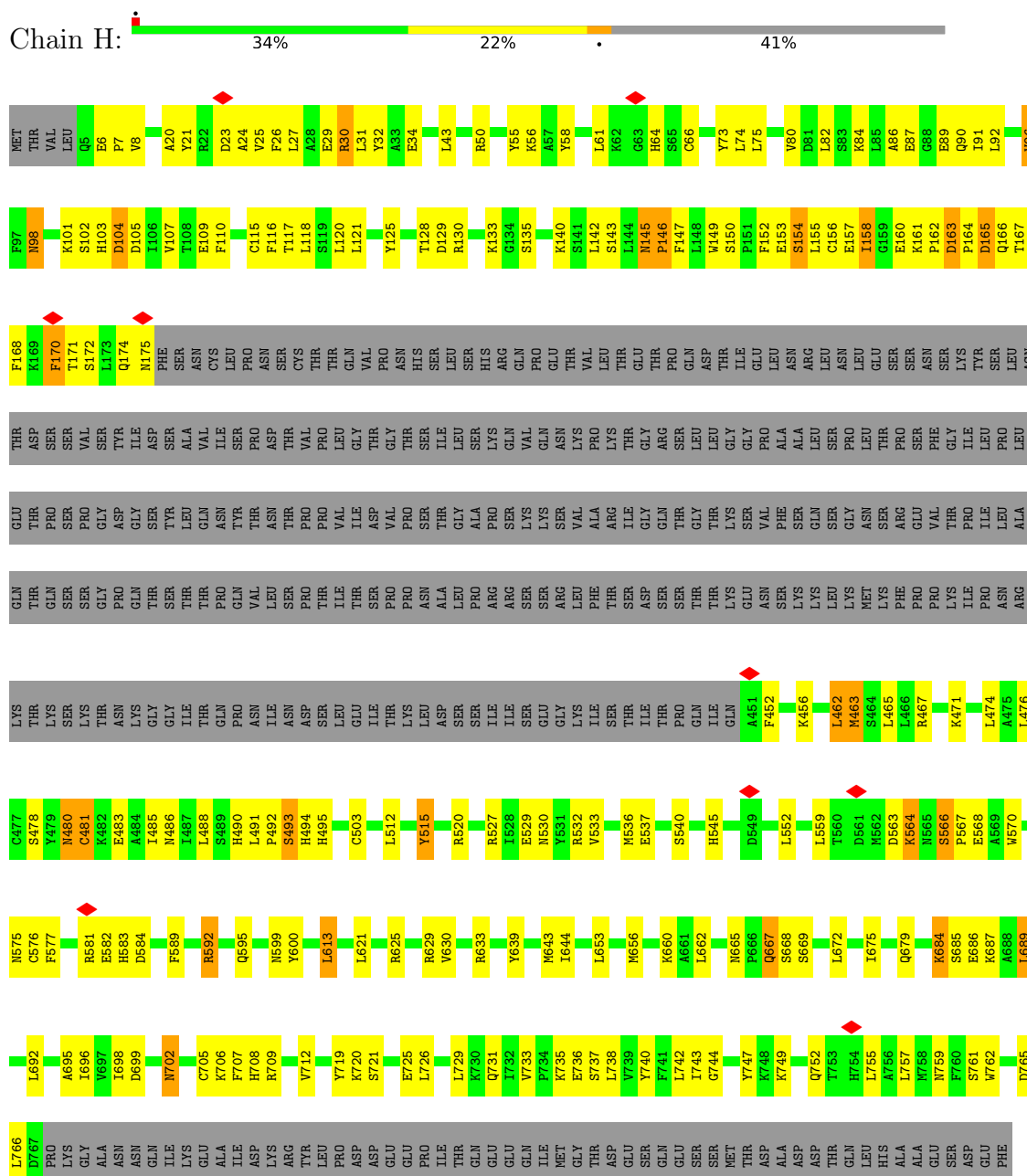




[illegible]

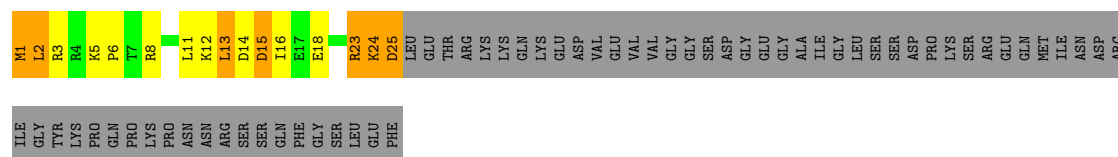


• Molecule 6: CELL DIVISION CYCLE PROTEIN 27 HOMOLOG



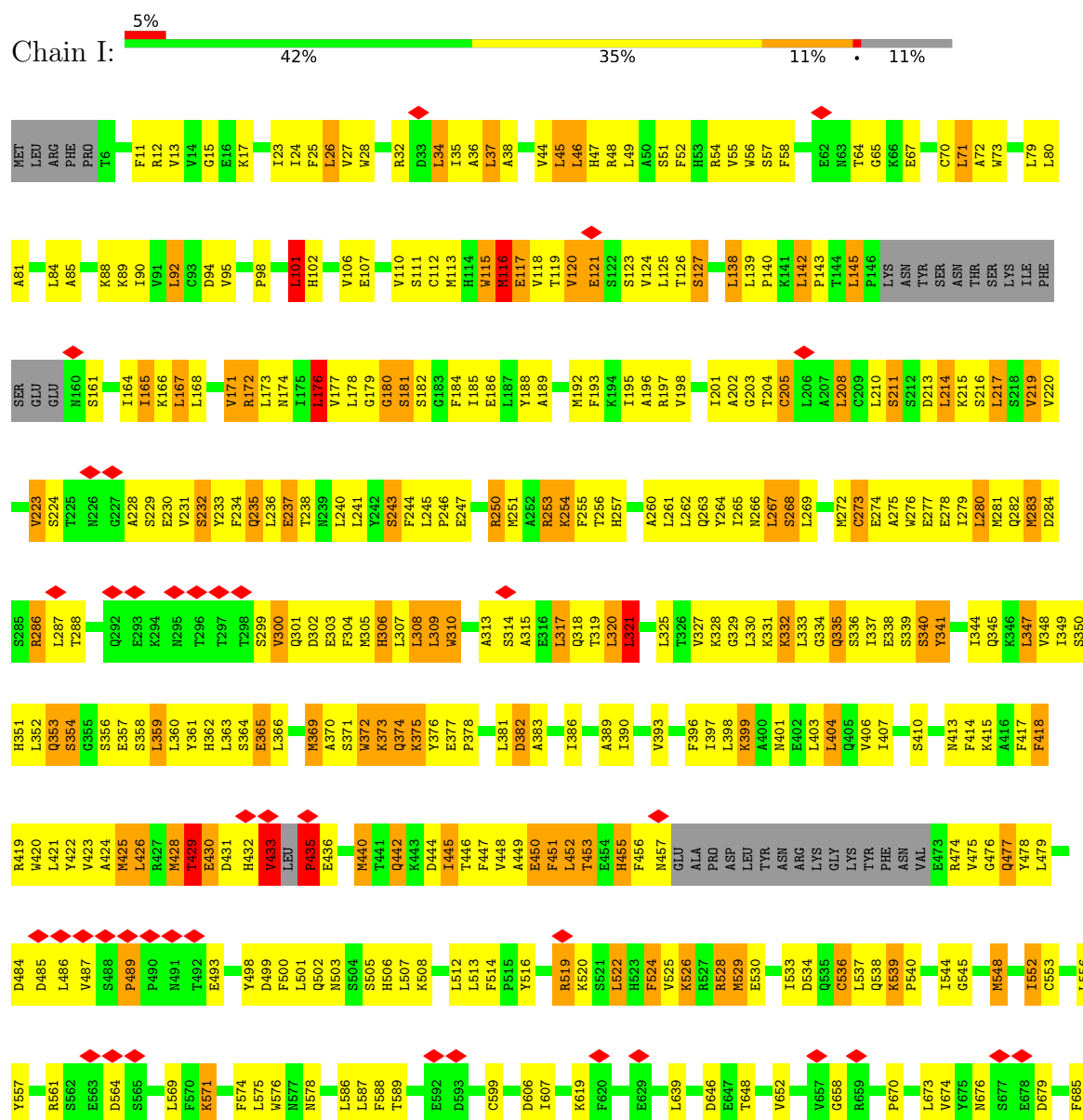
• Molecule 7: ANAPHASE-PROMOTING COMPLEX SUBUNIT CDC26



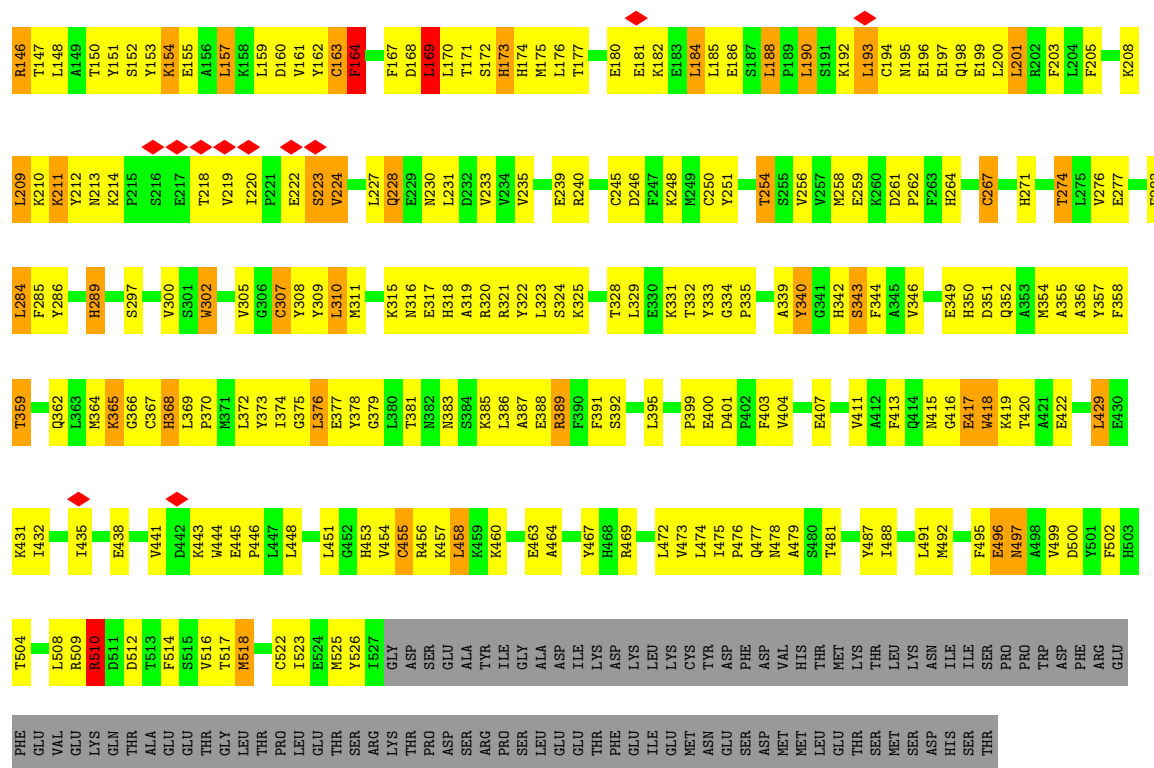


# Molecule 7: ANAPHASE-PROMOTING COMPLEX SUBUNIT CDC26

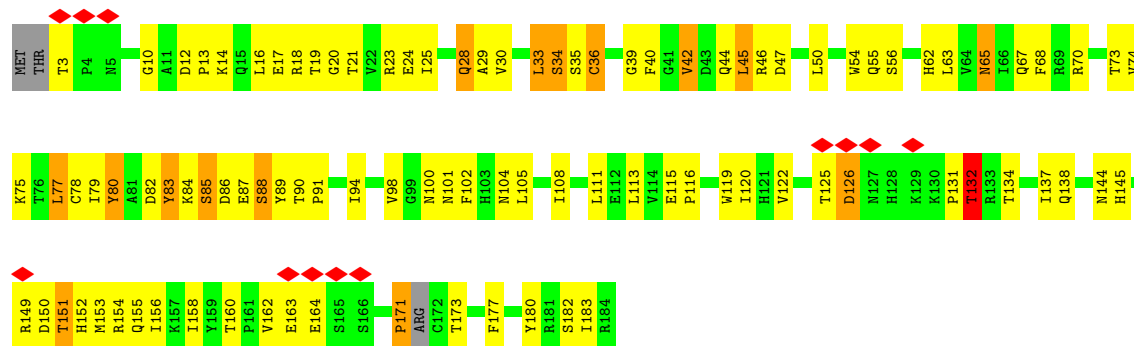
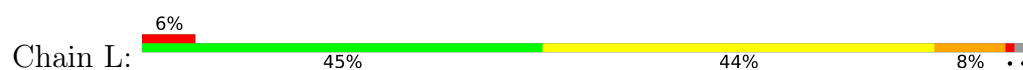
# Molecule 8: ANAPHASE-PROMOTING COMPLEX SUBUNIT 4



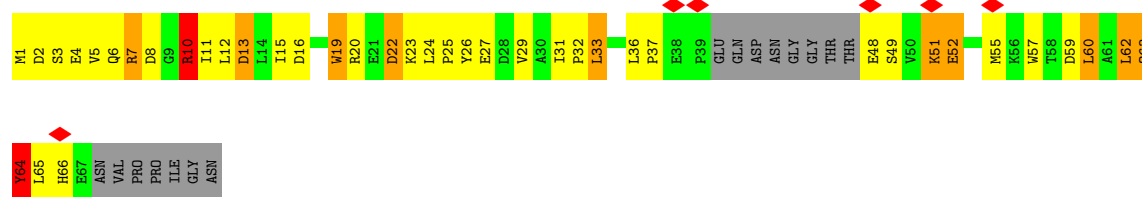
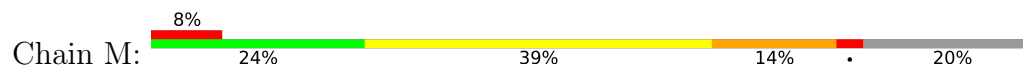




• Molecule 10: ANAPHASE-PROMOTING COMPLEX SUBUNIT 10



• Molecule 11: ANAPHASE-PROMOTING COMPLEX SUBUNIT 13

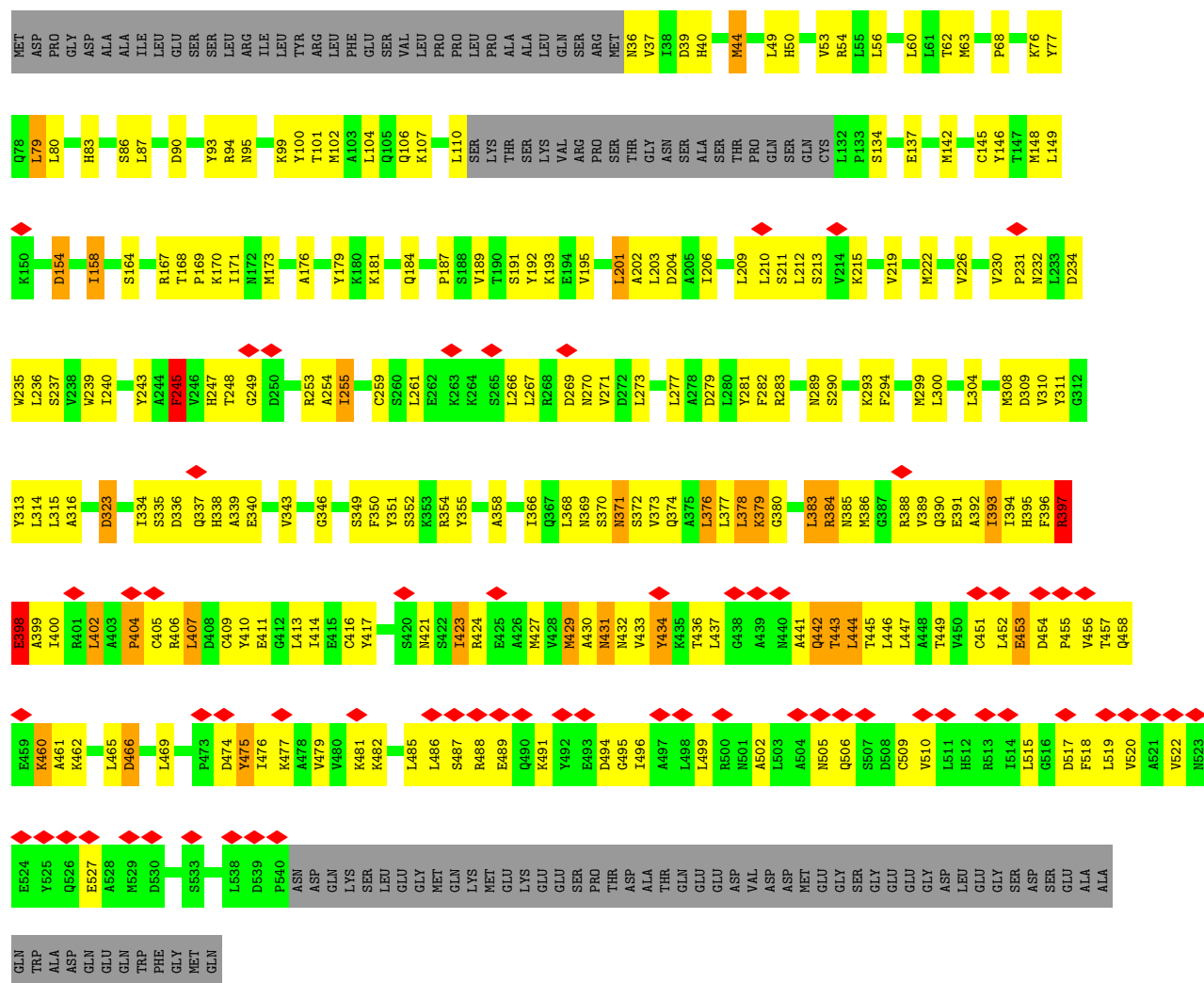


• Molecule 12: ANAPHASE-PROMOTING COMPLEX SUBUNIT 2

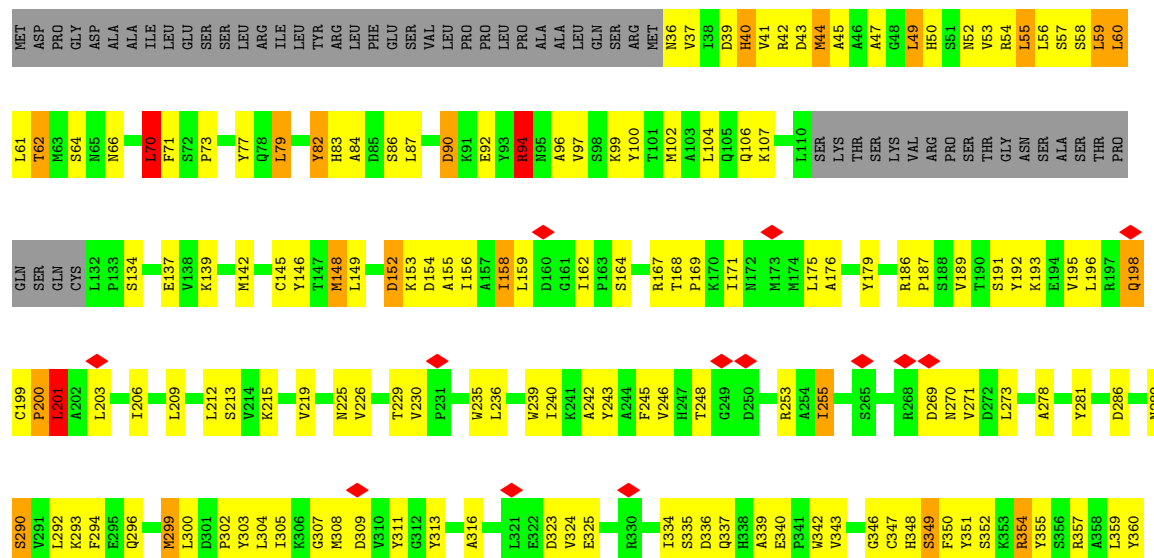


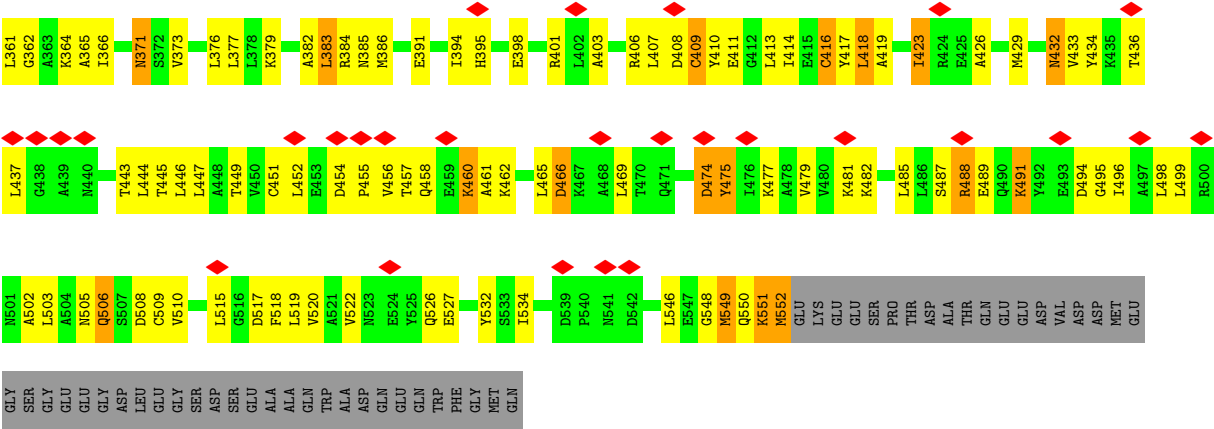






• Molecule 15: ANAPHASE-PROMOTING COMPLEX SUBUNIT 7





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	921993	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	27	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	0.440	Depositor
Minimum map value	-0.185	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.015	Depositor
Recommended contour level	0.08	Depositor
Map size ( $\text{\AA}$ )	386.24, 386.24, 386.24	wwPDB
Map dimensions	284, 284, 284	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.36, 1.36, 1.36	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	0.73	11/12168 (0.1%)	0.93	35/16587 (0.2%)
2	B	0.63	0/674	0.95	2/913 (0.2%)
3	C	0.73	1/4403 (0.0%)	0.93	10/5942 (0.2%)
3	P	0.66	1/4141 (0.0%)	0.89	6/5593 (0.1%)
4	D	0.62	0/446	0.83	1/610 (0.2%)
5	E	0.56	0/459	0.68	0/619
6	F	0.68	1/3704 (0.0%)	0.82	4/5019 (0.1%)
6	H	0.71	1/3969 (0.0%)	0.85	2/5366 (0.0%)
7	G	0.56	0/221	0.93	1/292 (0.3%)
7	W	0.57	0/219	0.93	1/291 (0.3%)
8	I	0.72	3/5754 (0.1%)	0.96	20/7806 (0.3%)
9	J	0.72	3/4152 (0.1%)	0.97	10/5623 (0.2%)
9	K	0.71	2/4085 (0.0%)	0.90	6/5530 (0.1%)
10	L	0.74	1/1468 (0.1%)	0.93	3/1993 (0.2%)
11	M	0.65	1/490 (0.2%)	0.98	5/665 (0.8%)
12	N	0.75	7/4861 (0.1%)	0.98	16/6585 (0.2%)
13	O	0.87	3/5499 (0.1%)	0.95	12/7432 (0.2%)
14	T	0.70	0/78	1.02	0/107
15	X	0.64	2/3827 (0.1%)	0.87	6/5180 (0.1%)
15	Y	0.56	0/3922	0.83	9/5304 (0.2%)
All	All	0.71	37/64540 (0.1%)	0.91	149/87457 (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	1
8	I	0	5
12	N	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
14	T	0	1
All	All	0	8

The worst 5 of 37 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	O	116	SER	C-N	24.88	1.91	1.34
13	O	135	PHE	C-N	13.64	1.65	1.34
12	N	427	TYR	CG-CD2	-9.69	1.26	1.39
12	N	600	PHE	CG-CD1	-9.42	1.24	1.38
1	A	236	VAL	N-CA	8.96	1.64	1.46

The worst 5 of 149 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	I	433	VAL	O-C-N	-16.78	89.22	121.10
1	A	505	ARG	NE-CZ-NH1	11.43	126.01	120.30
9	J	61	ARG	NE-CZ-NH2	-11.40	114.60	120.30
13	O	388	ARG	NE-CZ-NH2	-10.83	114.89	120.30
9	J	61	ARG	NE-CZ-NH1	10.42	125.51	120.30

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1652	MET	Peptide
8	I	429	THR	Mainchain
8	I	433	VAL	Mainchain,Peptide
8	I	658	GLY	Peptide
8	I	727	PHE	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	11890	0	11555	1834	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	649	0	595	33	0
3	C	4306	0	4273	274	0
3	P	4046	0	3998	248	0
4	D	436	0	396	25	0
5	E	450	0	435	31	0
6	F	3618	0	3452	380	0
6	H	3879	0	3805	267	0
7	G	220	0	233	30	0
7	W	218	0	222	26	0
8	I	5634	0	5522	590	0
9	J	4053	0	3960	371	0
9	K	3988	0	3911	440	0
10	L	1435	0	1381	165	0
11	M	481	0	457	72	0
12	N	4767	0	4686	1268	0
13	O	5400	0	5416	464	0
14	T	79	0	77	8	0
15	X	3767	0	3820	438	0
15	Y	3862	0	3914	412	0
16	B	3	0	0	0	0
All	All	63181	0	62108	6914	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 55.

The worst 5 of 6914 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:P:89:LEU:HD11	3:P:105:PHE:CE2	1.34	1.62
12:N:184:TYR:CZ	12:N:302:LYS:HE2	1.22	1.62
15:Y:104:LEU:HD11	15:Y:142:MET:CE	1.20	1.59
3:P:89:LEU:HD11	3:P:105:PHE:CD2	1.37	1.58
1:A:948:PRO:CB	1:A:1813:GLN:HE22	1.12	1.57

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	1539/1944 (79%)	1372 (89%)	112 (7%)	55 (4%)	3	16
2	B	83/84 (99%)	72 (87%)	7 (8%)	4 (5%)	2	12
3	C	518/597 (87%)	490 (95%)	23 (4%)	5 (1%)	13	39
3	P	486/597 (81%)	466 (96%)	16 (3%)	4 (1%)	16	44
4	D	53/121 (44%)	47 (89%)	5 (9%)	1 (2%)	6	26
5	E	54/110 (49%)	54 (100%)	0	0	100	100
6	F	454/824 (55%)	433 (95%)	19 (4%)	2 (0%)	30	60
6	H	484/824 (59%)	469 (97%)	10 (2%)	5 (1%)	13	39
7	G	23/85 (27%)	23 (100%)	0	0	100	100
7	W	24/85 (28%)	23 (96%)	0	1 (4%)	2	14
8	I	717/808 (89%)	682 (95%)	20 (3%)	15 (2%)	5	24
9	J	500/620 (81%)	468 (94%)	25 (5%)	7 (1%)	9	31
9	K	487/620 (78%)	456 (94%)	27 (6%)	4 (1%)	16	44
10	L	180/185 (97%)	169 (94%)	9 (5%)	2 (1%)	12	37
11	M	55/74 (74%)	49 (89%)	5 (9%)	1 (2%)	7	27
12	N	590/822 (72%)	547 (93%)	26 (4%)	17 (3%)	3	19
13	O	682/755 (90%)	643 (94%)	27 (4%)	12 (2%)	7	27
14	T	13/15 (87%)	11 (85%)	1 (8%)	1 (8%)	1	5
15	X	480/599 (80%)	463 (96%)	12 (2%)	5 (1%)	13	39
15	Y	492/599 (82%)	473 (96%)	15 (3%)	4 (1%)	16	44
All	All	7914/10368 (76%)	7410 (94%)	359 (4%)	145 (2%)	9	27

5 of 145 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	274	VAL

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Mol	Chain	Res	Type
1	A	514	LEU
1	A	723	LEU
1	A	813	LEU
1	A	823	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	1243/1720 (72%)	967 (78%)	276 (22%)	1	2
2	B	65/75 (87%)	54 (83%)	11 (17%)	1	6
3	C	452/520 (87%)	384 (85%)	68 (15%)	2	9
3	P	422/520 (81%)	368 (87%)	54 (13%)	3	13
4	D	46/115 (40%)	41 (89%)	5 (11%)	5	19
5	E	47/89 (53%)	35 (74%)	12 (26%)	0	1
6	F	371/727 (51%)	310 (84%)	61 (16%)	2	7
6	H	408/727 (56%)	368 (90%)	40 (10%)	6	23
7	G	25/77 (32%)	16 (64%)	9 (36%)	0	0
7	W	23/77 (30%)	15 (65%)	8 (35%)	0	0
8	I	607/730 (83%)	508 (84%)	99 (16%)	2	7
9	J	425/548 (78%)	363 (85%)	62 (15%)	2	10
9	K	423/548 (77%)	356 (84%)	67 (16%)	2	8
10	L	155/170 (91%)	139 (90%)	16 (10%)	6	22
11	M	52/67 (78%)	38 (73%)	14 (27%)	0	1
12	N	490/724 (68%)	372 (76%)	118 (24%)	0	1
13	O	573/650 (88%)	469 (82%)	104 (18%)	1	5
14	T	1/2 (50%)	1 (100%)	0	100	100
15	X	406/513 (79%)	370 (91%)	36 (9%)	8	27
15	Y	417/513 (81%)	373 (89%)	44 (11%)	5	20

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	6651/9112 (73%)	5547 (83%)	1104 (17%)	<b>4</b> <b>7</b>

5 of 1104 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	O	585	LEU
13	O	693	ASN
13	O	581	ILE
15	X	383	LEU
6	F	129	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 190 such sidechains are listed below:

Mol	Chain	Res	Type
11	M	53	GLN
13	O	503	HIS
12	N	267	GLN
13	O	219	GLN
13	O	741	HIS

### 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 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
13	O	2
12	N	1
3	C	1
9	K	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	N	563:ASP	C	564:MET	N	2.51
1	C	344:ARG	C	345:SER	N	2.01
1	K	219:VAL	C	220:ILE	N	2.00
1	O	116:SER	C	117:ASP	N	1.91
1	O	135:PHE	C	136:LEU	N	1.65

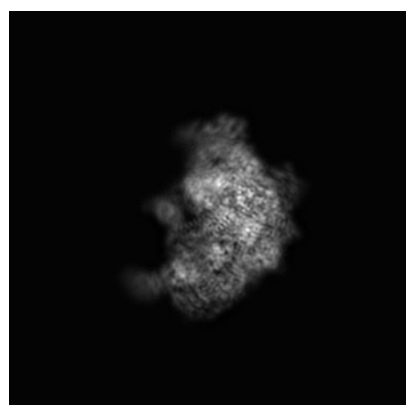
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3388. These allow visual inspection of the internal detail of the map and identification of artifacts.

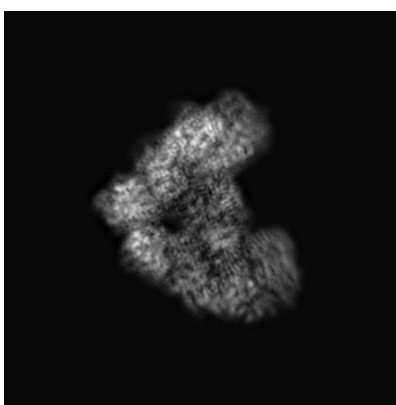
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

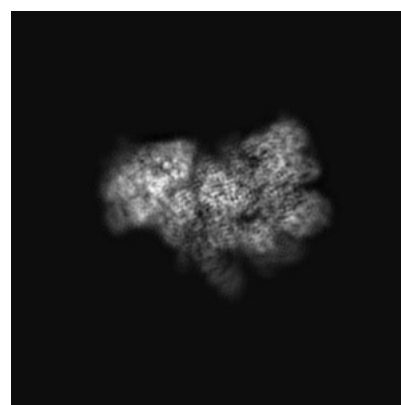
#### 6.1.1 Primary map



X



Y

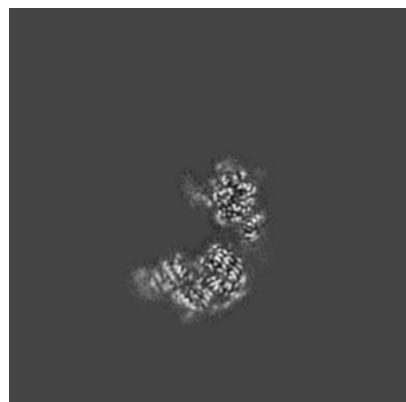


Z

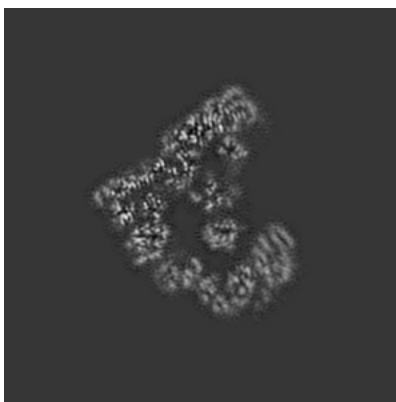
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

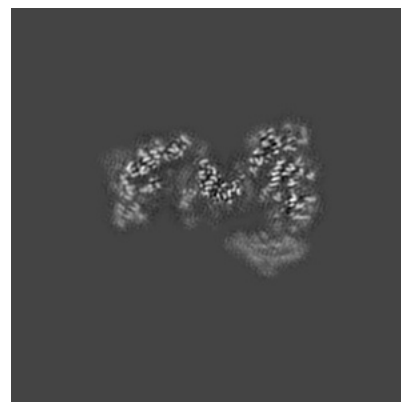
#### 6.2.1 Primary map



X Index: 142



Y Index: 142

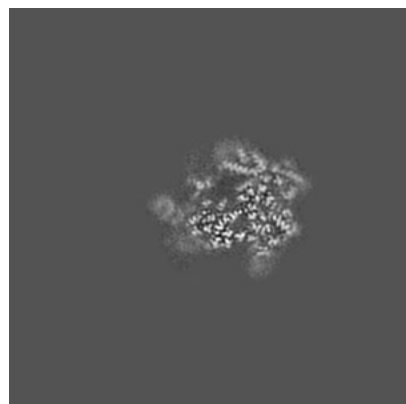


Z Index: 142

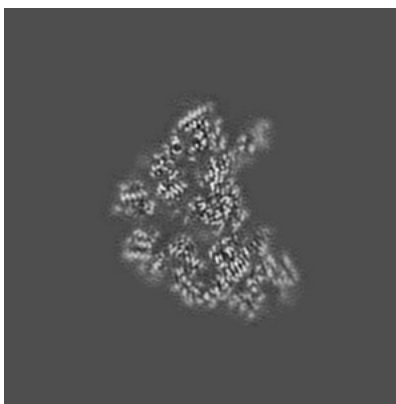
The images above show central slices of the map in three orthogonal directions.

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

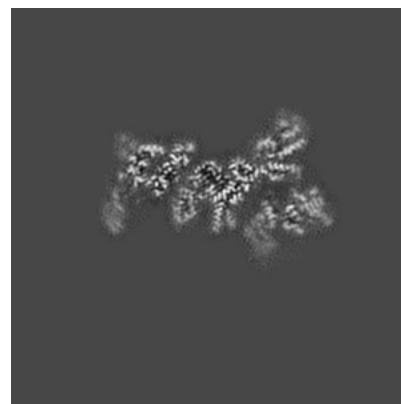
### 6.3.1 Primary map



X Index: 191



Y Index: 163

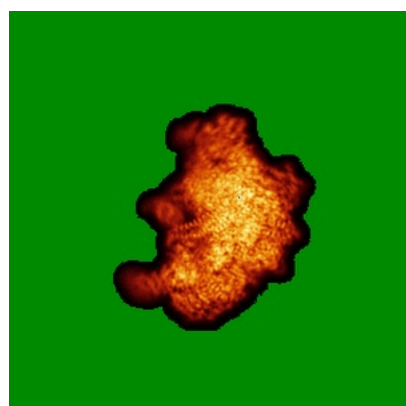


Z Index: 154

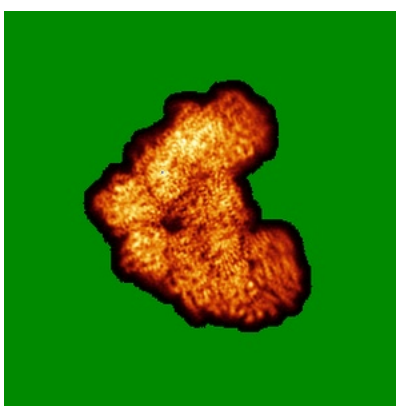
The images above show the largest variance slices of the map in three orthogonal directions.

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

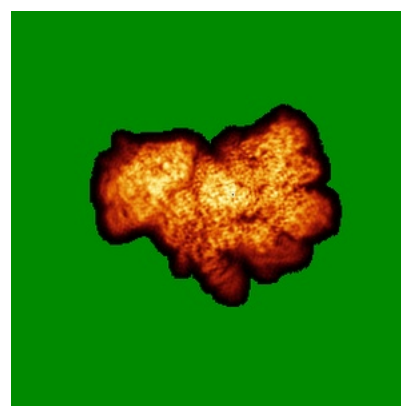
### 6.4.1 Primary map



X



Y

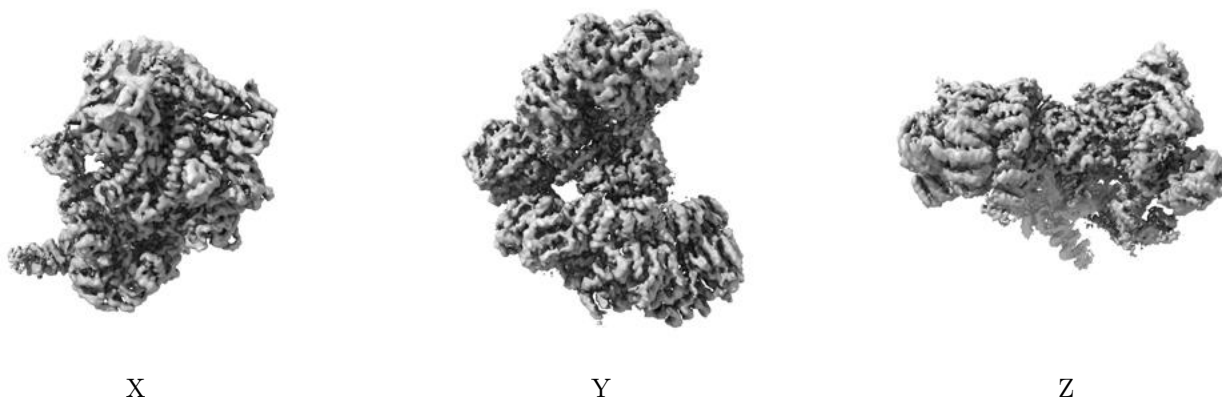


Z

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

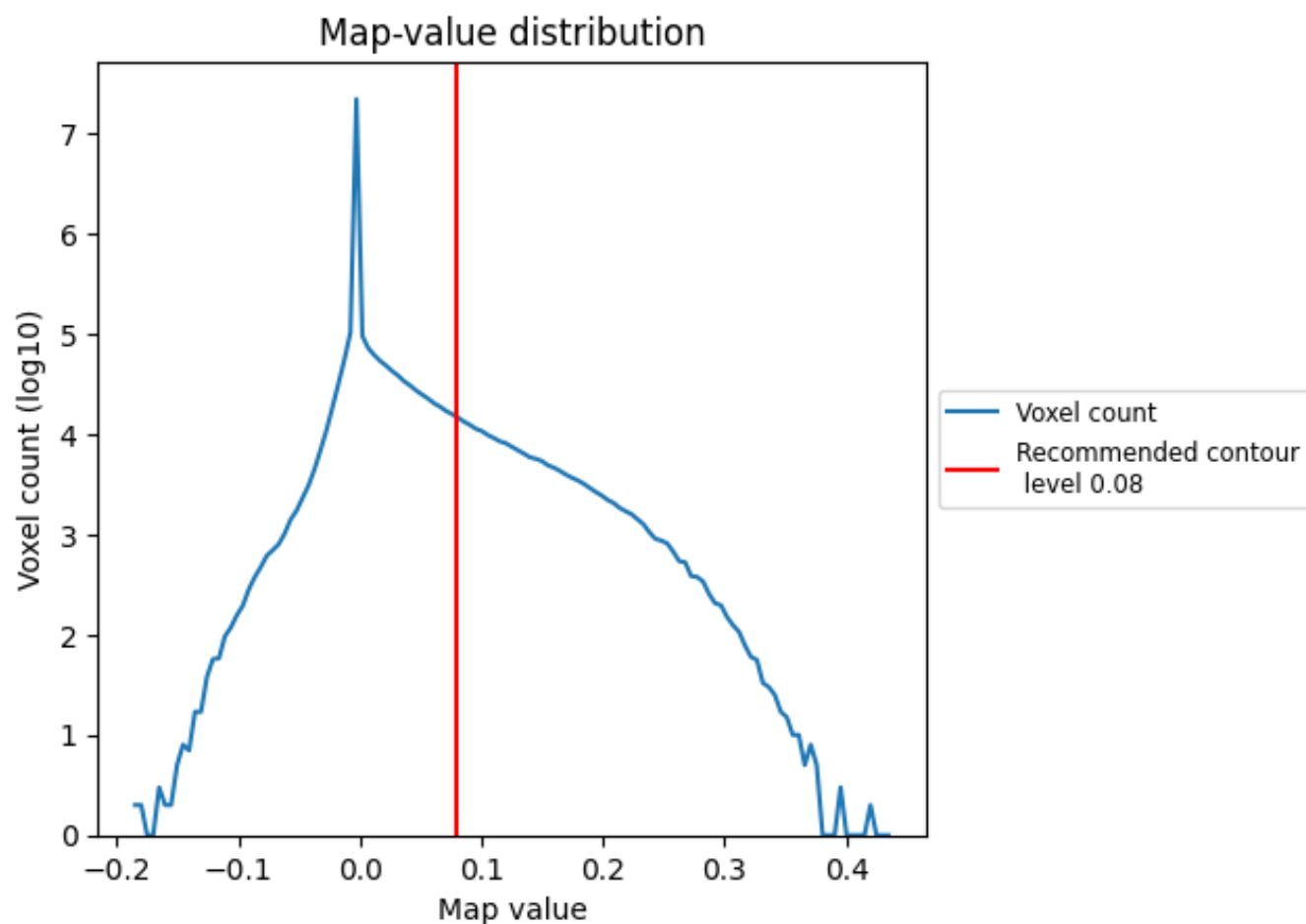
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

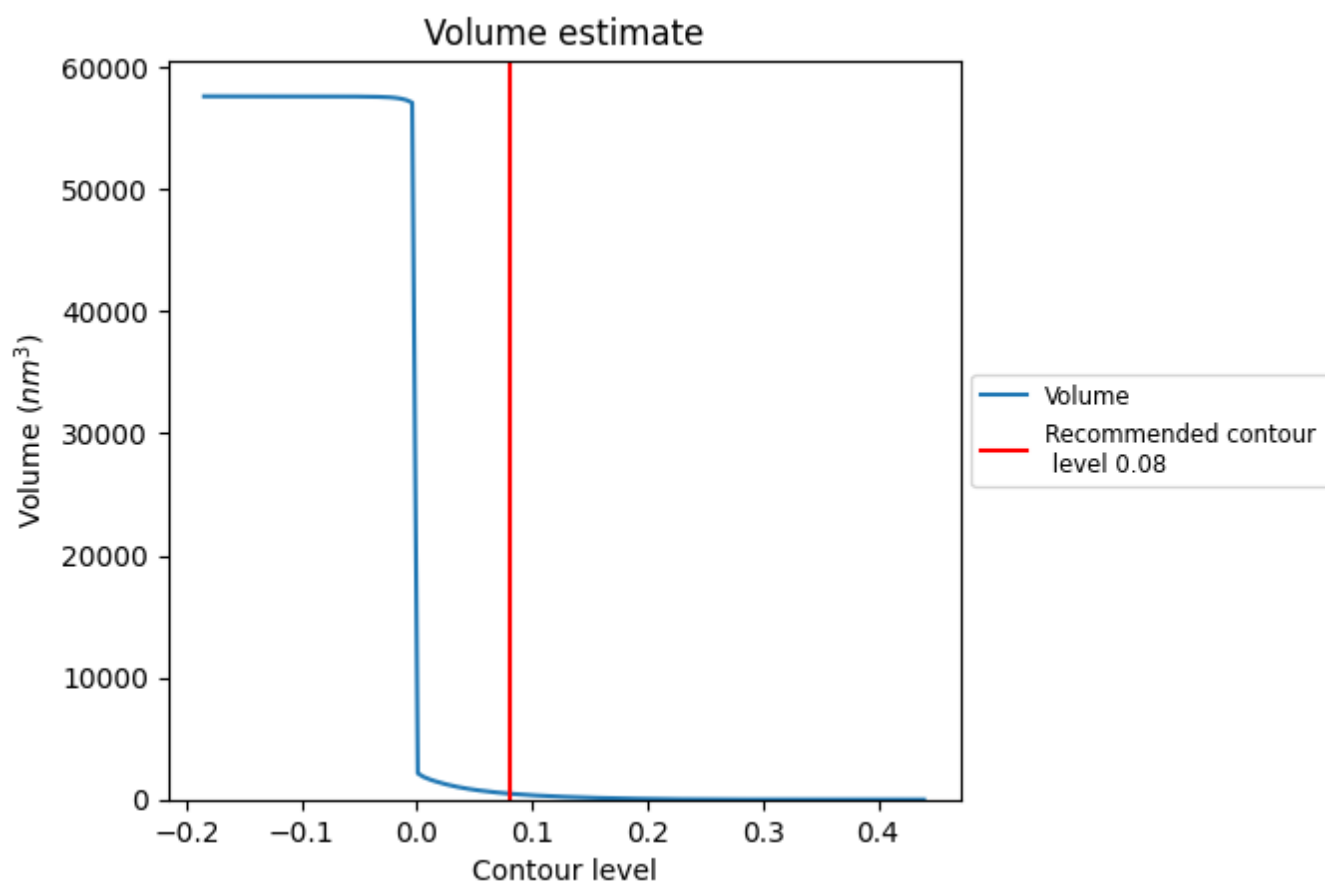
This section contains the results of statistical analysis of the map.

### 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](#)

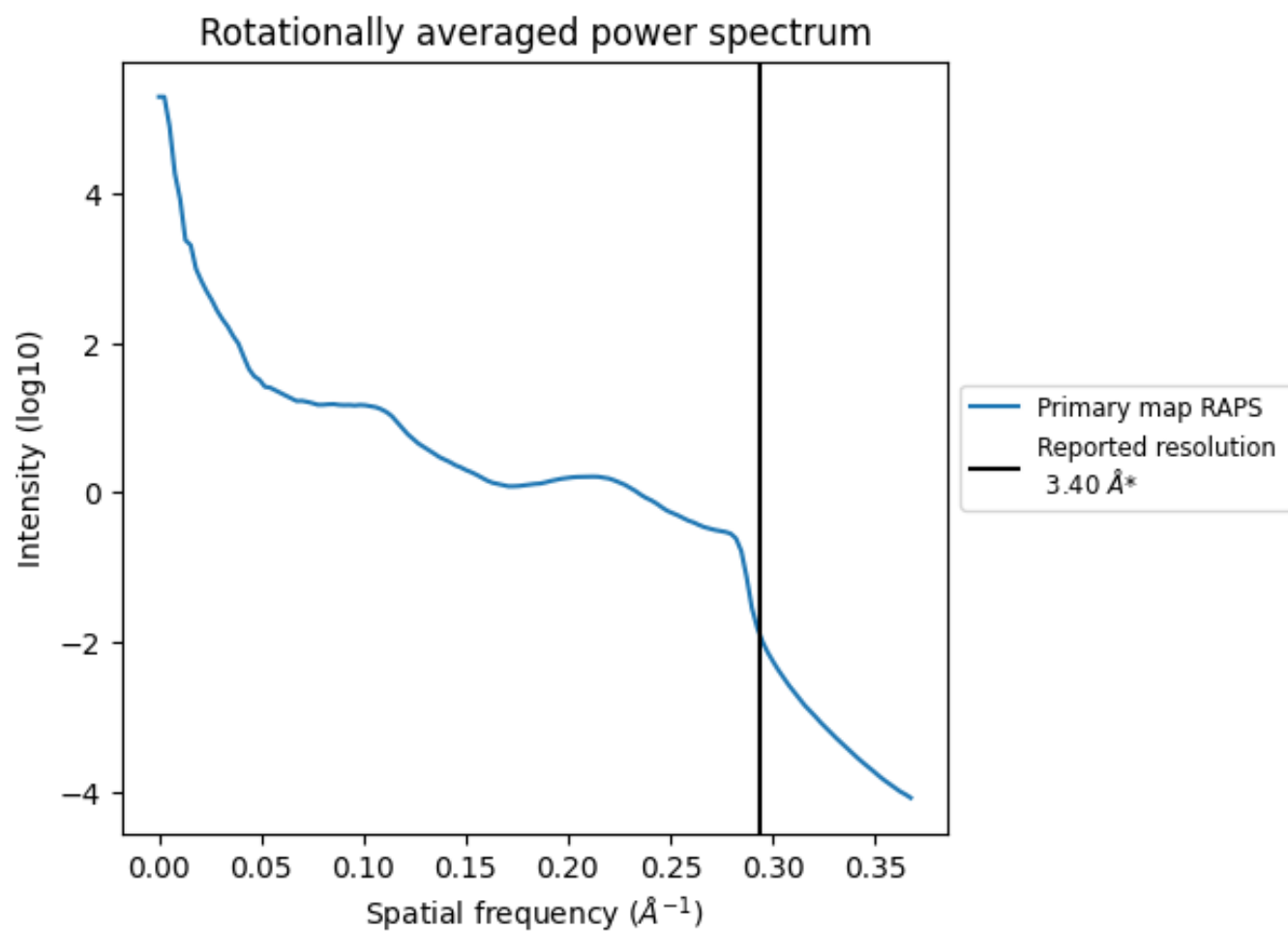


The volume at the recommended contour level is 488 nm<sup>3</sup>; this corresponds to an approximate mass of 441 kDa.

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 0.294 Å<sup>-1</sup>

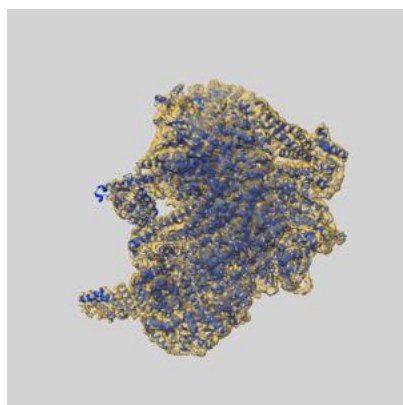
## 8 Fourier-Shell correlation

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

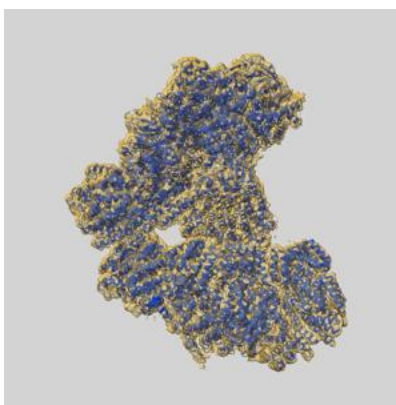
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3388 and PDB model 5G05. Per-residue inclusion information can be found in section [3](#) on page [7](#).

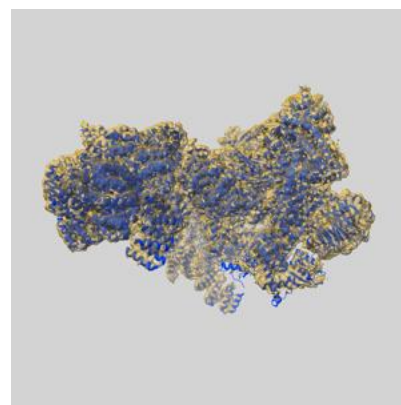
### 9.1 Map-model overlay [i](#)



X



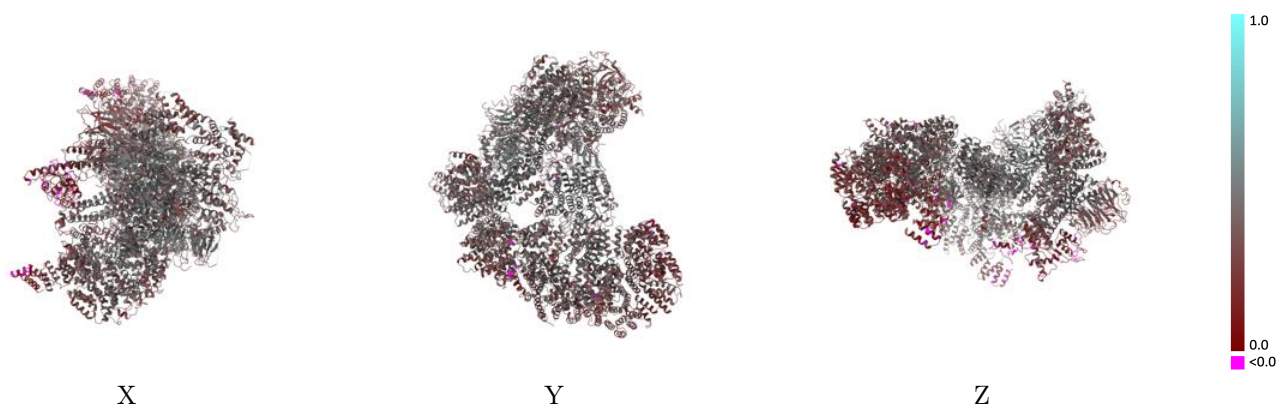
Y



Z

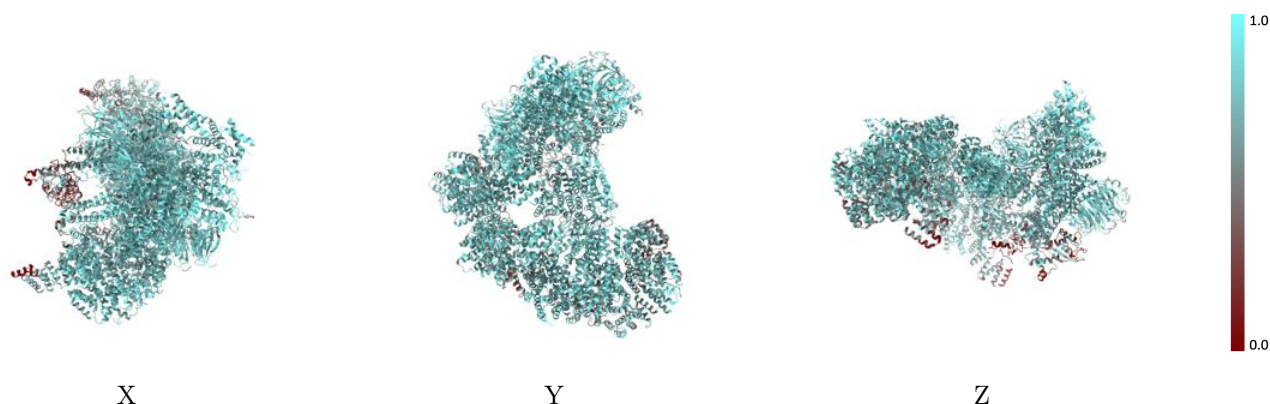
The images above show the 3D surface view of the map at the recommended contour level 0.08 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



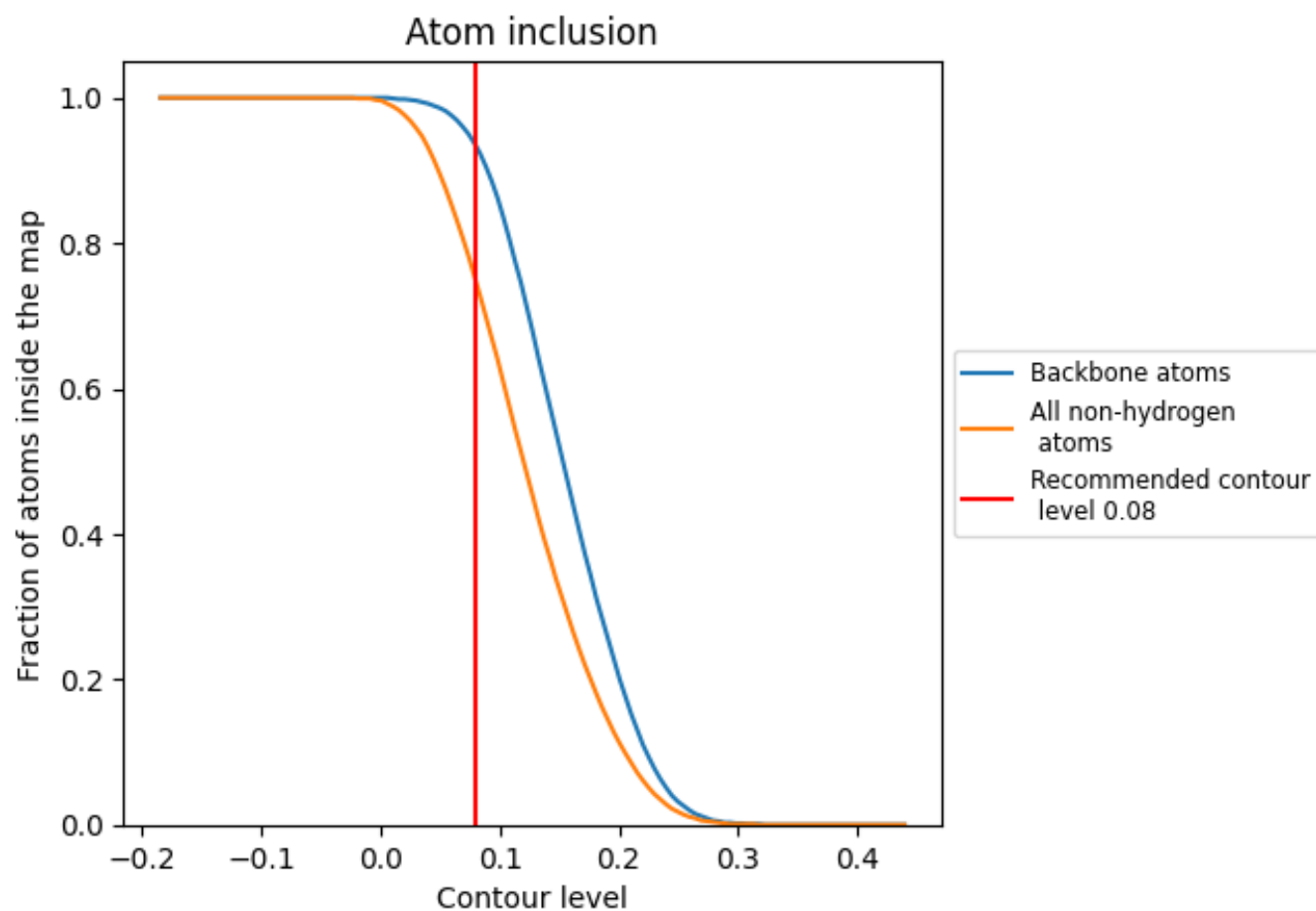
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.08).











































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 75% 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 (0.08) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7480	 0.3750
A	 0.8150	 0.4400
B	 0.1770	 0.0870
C	 0.7970	 0.4190
D	 0.7520	 0.4040
E	 0.7410	 0.4040
F	 0.7080	 0.3510
G	 0.7450	 0.3740
H	 0.7830	 0.4030
I	 0.7660	 0.3820
J	 0.7850	 0.3650
K	 0.7790	 0.3950
L	 0.7400	 0.3790
M	 0.6600	 0.4070
N	 0.6330	 0.2980
O	 0.8010	 0.4350
P	 0.7480	 0.3480
T	 0.7720	 0.4360
W	 0.7480	 0.4360
X	 0.6440	 0.2640
Y	 0.6600	 0.2730

