



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 11:58 AM UTC

PDB ID : 5G05 / pdb_00005g05
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

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

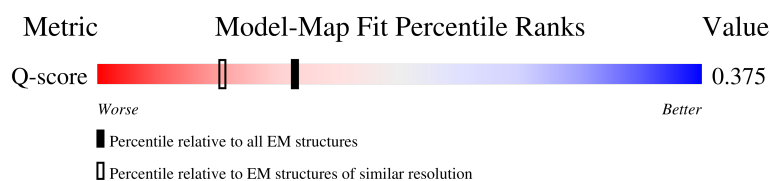
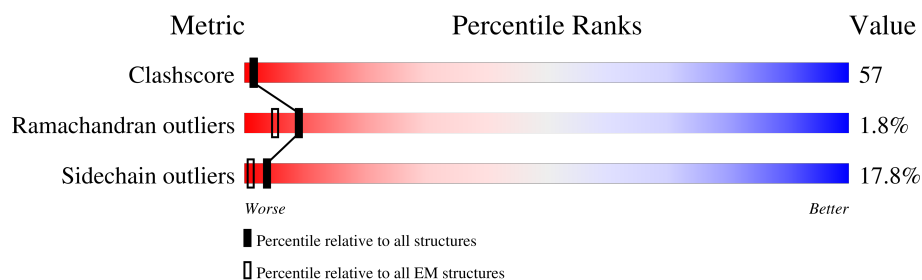
1 Overall quality at a glance

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.



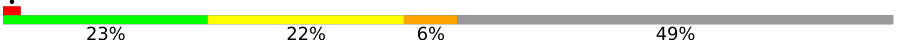
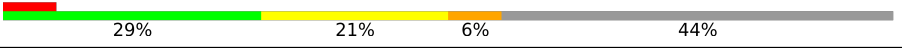
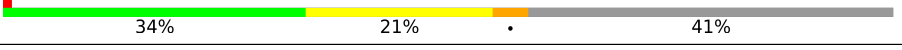
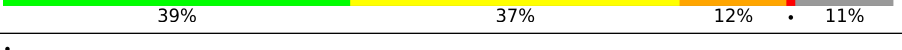
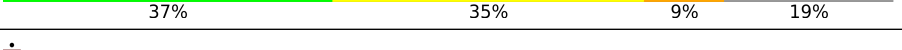
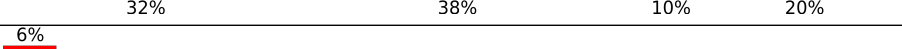
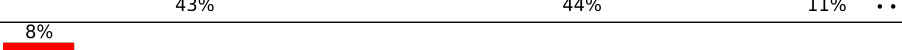
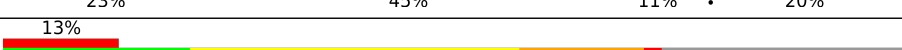
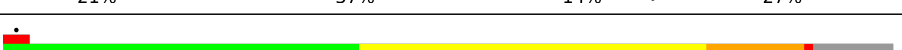
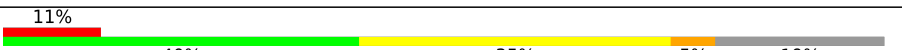
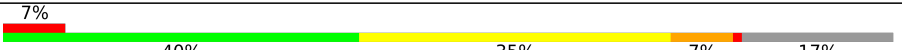
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	1944	
2	B	84	
3	C	597	
3	P	597	

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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	
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		

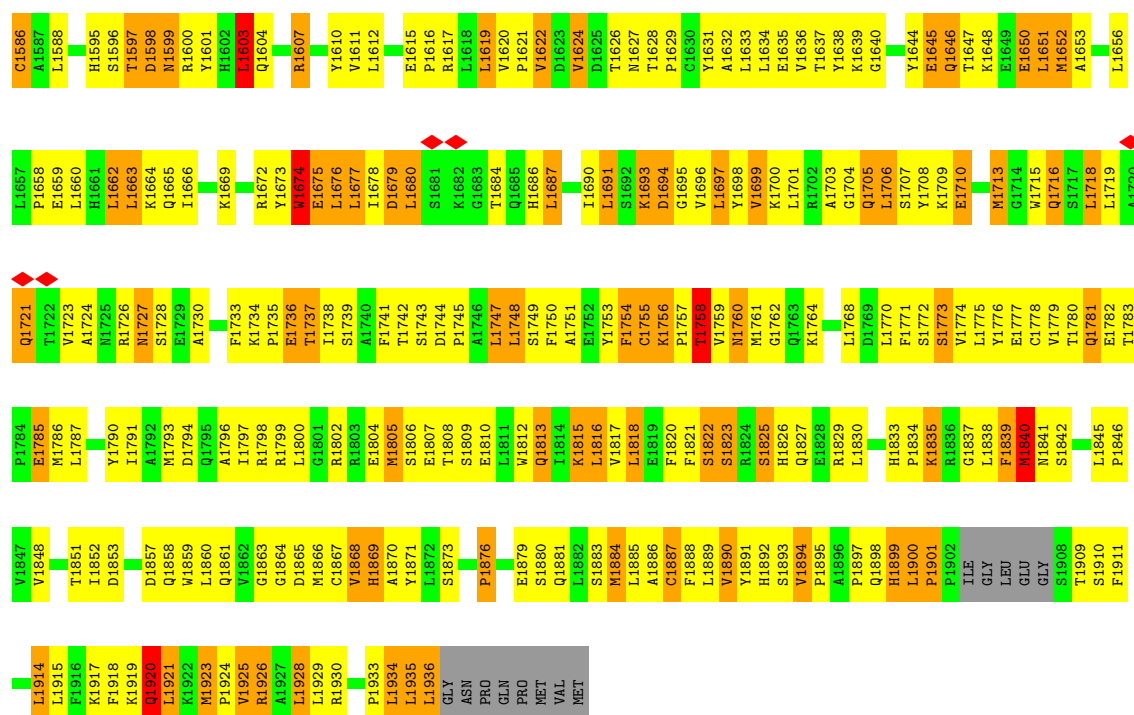
- Molecule 15 is a protein called ANAPHASE-PROMOTING COMPLEX SUBUNIT 7.

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		

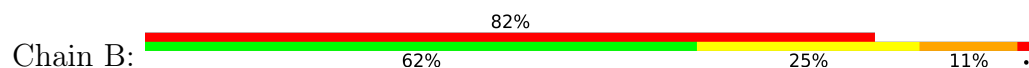
- Molecule 16 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

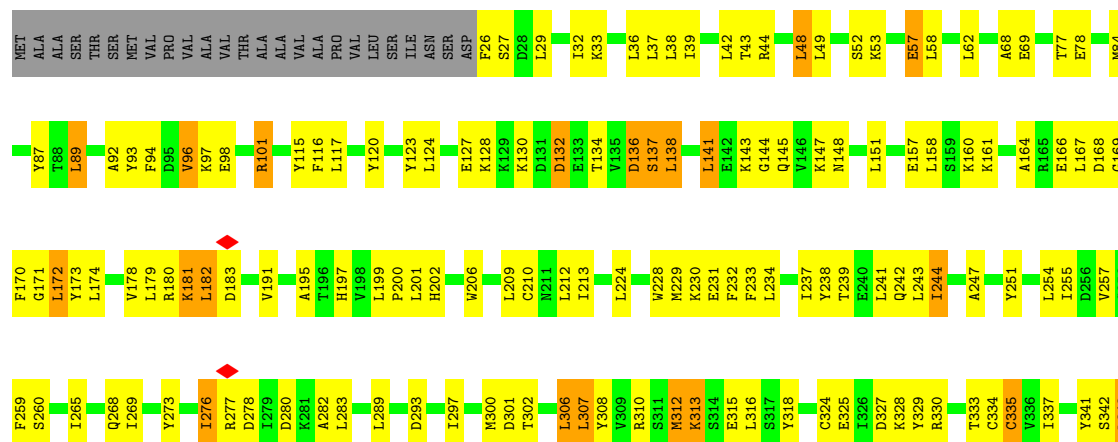
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SER	GLU	ILE	GLU	LEU	PRO	CYS	SER	GLU	ASP	L1462	L1463	L1464	E1465	T1466	S1467	S1468	Q1469	H1470	V1471	V1472	G1473	F1474	R1475	F1476	A1477	E1480	N1481	L1482	C1487	L1488	K1493	D1494	F1495	M1496	T1497	N1498	L1499	L1503	I1432	I1433	I1434	R1435	E1436	N1437	S1438	I1439	SER	LEU								
C1364	P1365	T1368	L1371	A1372	M1373	L1374	Y1375	L1376	K1377	T1378	N1379	N1380	L1381	L1382	L1383	W1386	P1390	D1391	T1392	L1395	L1396	D1397	F1398	L1404	L1405	T1408	L1409	C1412	W1416	L1420	P1421	N1422	W1425	S1428	N1429	V1430	P1431	Q1432	I1433	I1434	R1435	E1436	N1437	S1438	I1439	SER	LEU									
Y1294	G1299	A1301	L1302	G1303	M1304	V1305	C1306	L1307	G1308	H1309	G1310	S1311	N1312	L1313	L1314	G1315	M1316	L1319	N1320	V1321	P1322	E1323	Q1324	V1326	Q1327	Y1328	M1329	G1332	ARG	ARG	PHE	GLN	THR	MET	HIS	ARG	GLU	LYS	HIS	LYS	S1347	Q1351	I1352	K1353	E1354	G1355	D1356	T1357	I1358	N1359	V1360					
S1223	I1224	T1225	R1226	L1227	L1228	I1230	H1231	P1232	A1234	L1235	L1236	P1237	P1238	T1239	S1240	T1241	E1242	L1243	N1248	V1249	Q1250	V1251	V1254	V1255	L1259	V1260	Y1261	T1264	A1265	H1266	R1267	H1268	T1269	V1272	L1273	L1274	A1275	E1276	I1277	G1278	R1279	P1280	G1282	P1283	Y1287	D1290	R1291	E1292	S1293							
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L1026	S1029	E1030	D1031	L1032	R1033	V1034	Q1035	V1037	L1040	S1043	A1044	H1045	P1046	V1047	R1048	V1049	V1052	Q1053	Y1054	P1055	E1056	L1057	H1060	E1061	F1062	I1063	E1064	K1065	E1066	E1067	M1068	R1069	L1070	L1071	Q1072	L1073	C1074	Q1075	R1076	T1077	M1078	A1079	L1080	P1081	V1082	G1083	L1084	G1085	M1086	F1087	T1088	L1089	F1090			
Y959	Y960	H961	C962	R963	P966	A967	S968	D969	W970	P971	V974	L977	T978	G979	R980	Q981	D982	L983	S984	K985	C988	E989	P993	GLY	LYS	SER	VAL	PRO	GLY	THR	GLU	E1011	E1012	D1013	D1014	G1015	M1016	N1017	D1018	M1019	M1020	V1023	M1024	S1025												
F830	M831	H832	H833	P834	S835	F836	T837	T838	S839	E840	P841	G842	S843	I844	W845	Q846	W847	W848	C851	L852	K853	G854	E855	G856	M857	P858	P859	G860	L861	Y862	L863	P864	G865	I866	C867	R868	S870	R871	L872	V873	I877	A878	L879	E880	I881	L882	L887	VAL	SER	ASP	GLU	S892	Q893	Q894	Y895	
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PRQ	SER	THR	GLY	SER	D704	W707	E708	Y709	L710	L711	Y715	H716	H717	H718	G719	H722	L723	L724	L730	PRQ	SER	GLU	ALA	SER	GLN	MET	LYS	ASP	GLU	ASP	PHE	SER	GLN	ASN	L747	S748	D750	L751	L754	L755	F756	T757	H758	I759	SER	PRQ	VAL	F763	ILE	V765	L766	H767	L768	V769		
T633	A634	Q635	Q636	W637	L638	V639	K640	W641	N642	V643	H644	S645	A646	A647	P648	G649	G650	P651	Y652	H653	H654	S655	E656	W657	N658	L659	F660	V661	T662	C663	L664	M665	N666	M667	M668	G669	Y670	W677	T678	ARG	ASN	PHE	ASP	PHE	GLY	SER	LEU	SER	PRQ	VAL	ILE	V765	L766	H767	L768	V769



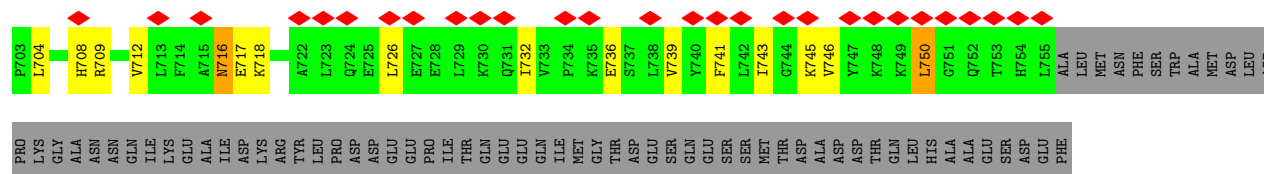
• Molecule 2: ANAPHASE-PROMOTING COMPLEX SUBUNIT 11



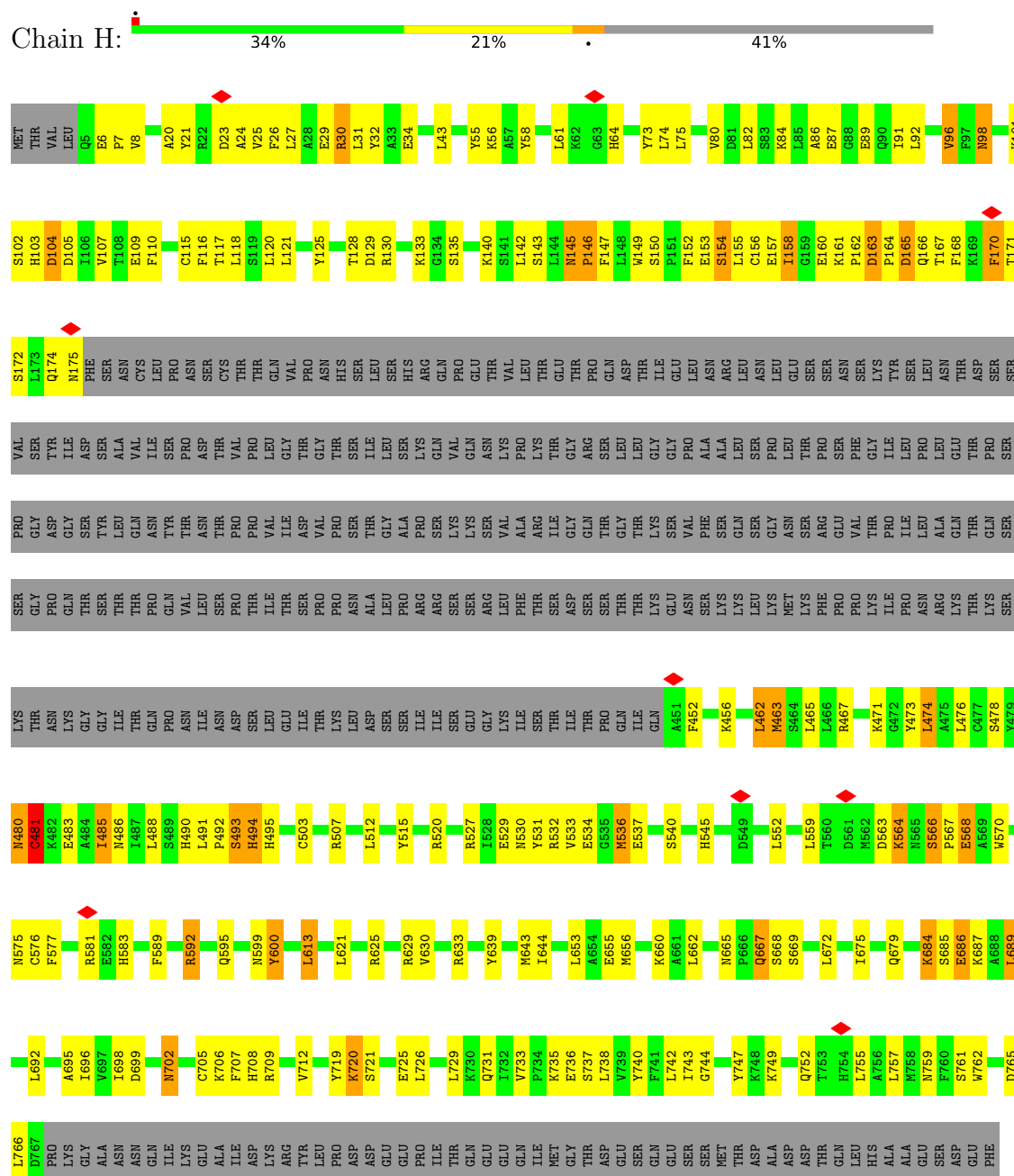
• Molecule 3: CELL DIVISION CYCLE PROTEIN 23 HOMOLOG





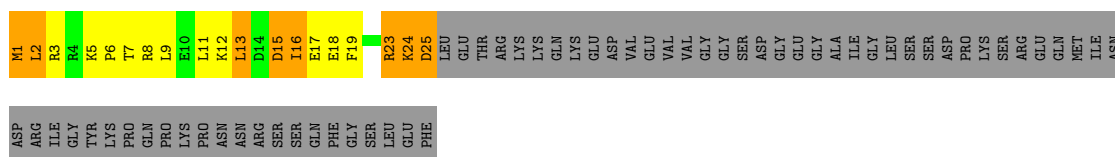


• Molecule 6: CELL DIVISION CYCLE PROTEIN 27 HOMOLOG

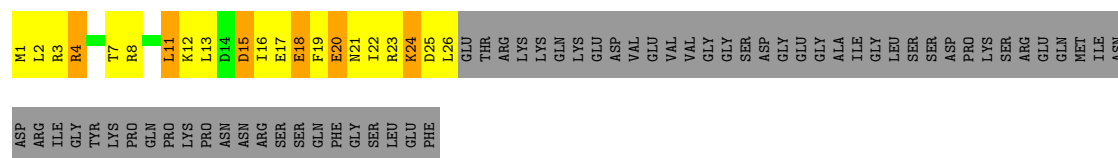


• Molecule 7: ANAPHASE-PROMOTING COMPLEX SUBUNIT CDC26

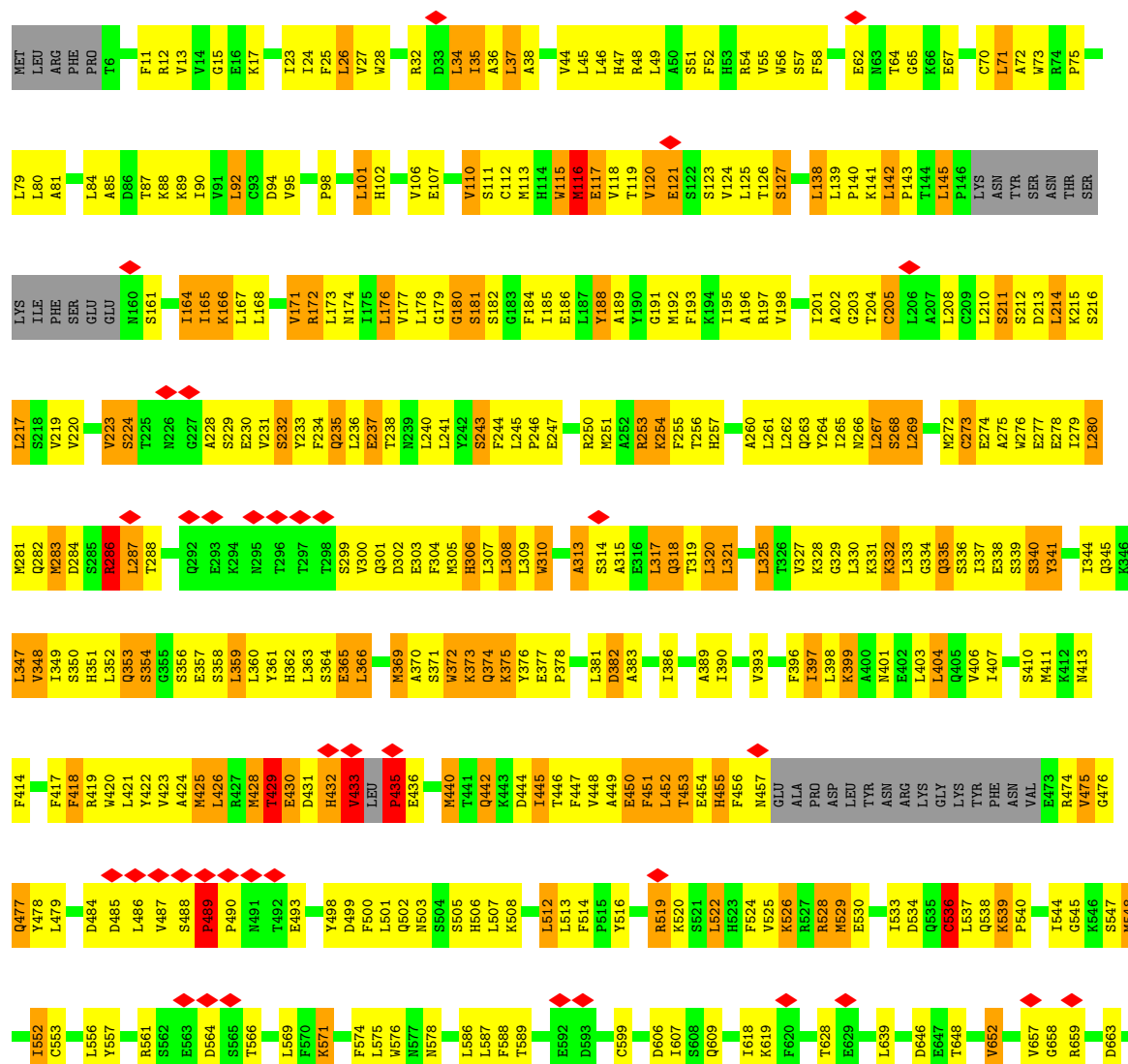


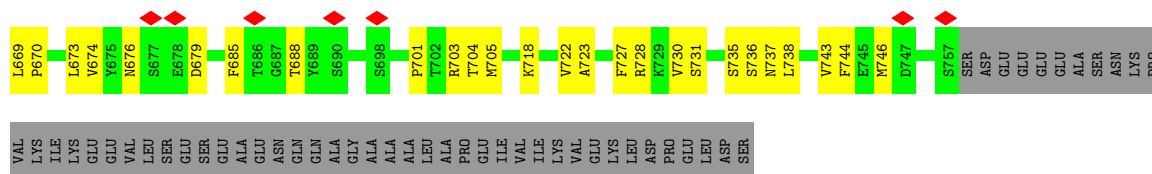


• Molecule 7: ANAPHASE-PROMOTING COMPLEX SUBUNIT CDC26

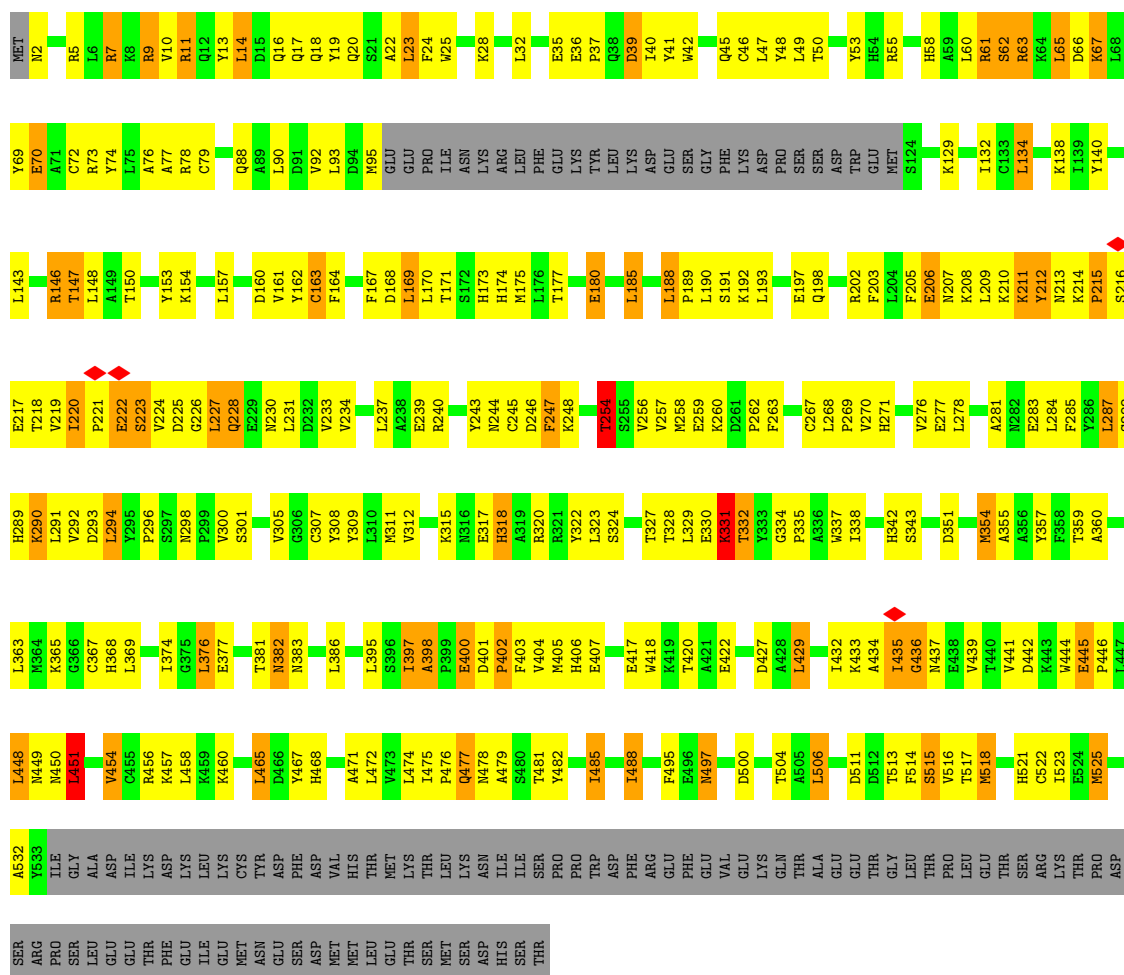


• Molecule 8: ANAPHASE-PROMOTING COMPLEX SUBUNIT 4

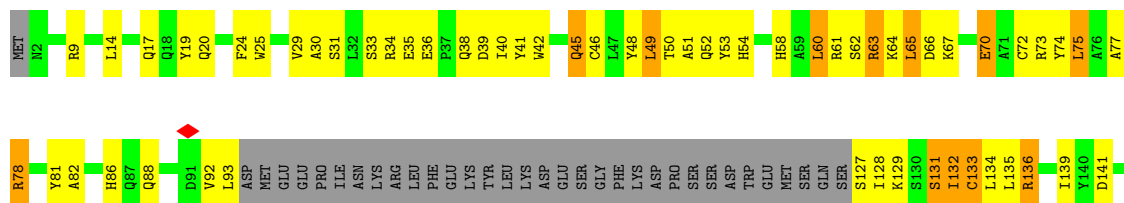


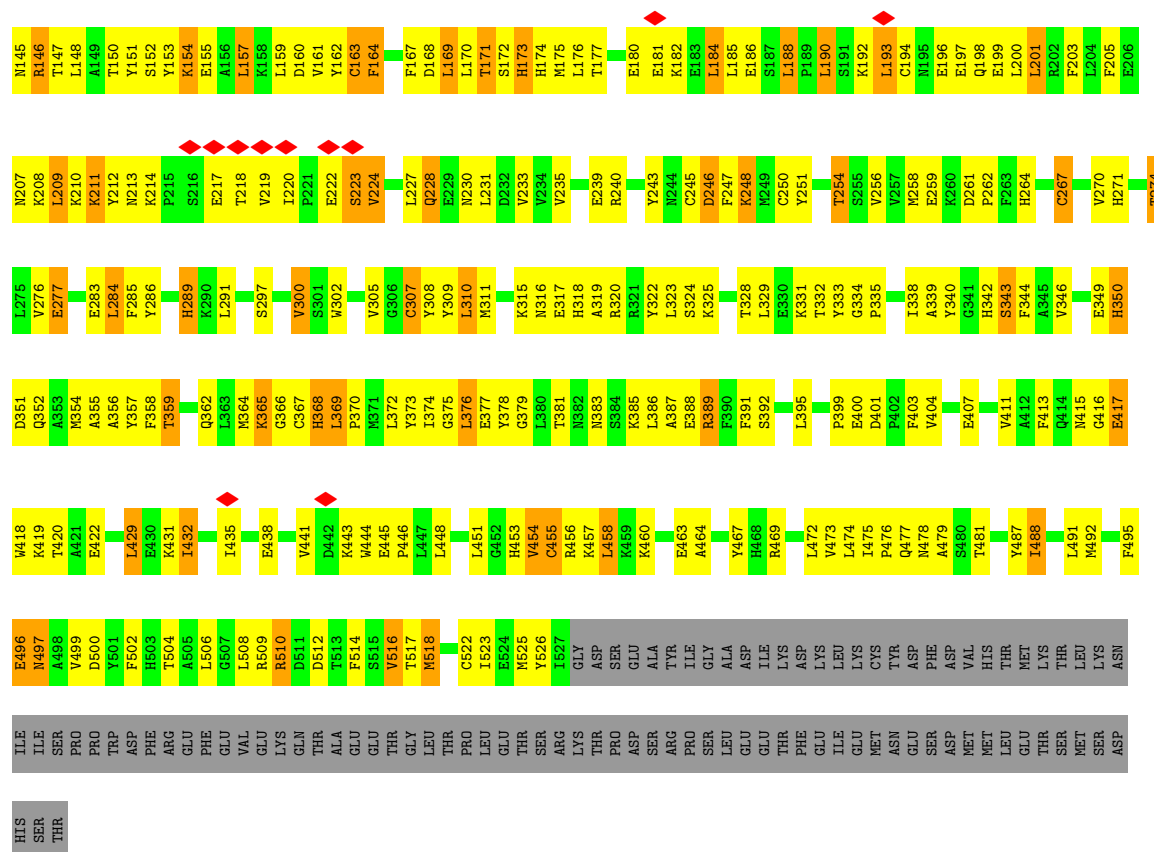


• Molecule 9: CELL DIVISION CYCLE PROTEIN 16 HOMOLOG

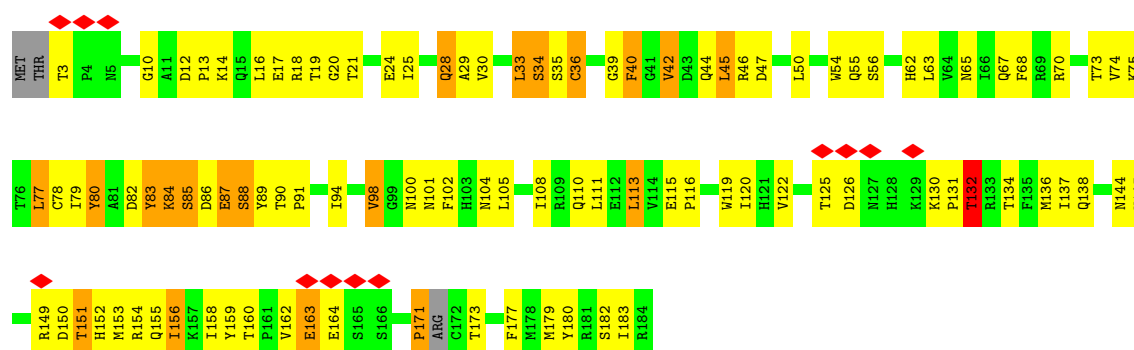
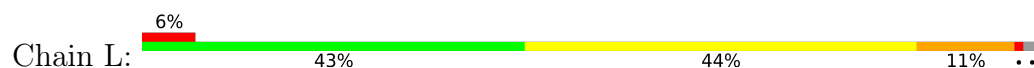


• Molecule 9: CELL DIVISION CYCLE PROTEIN 16 HOMOLOG

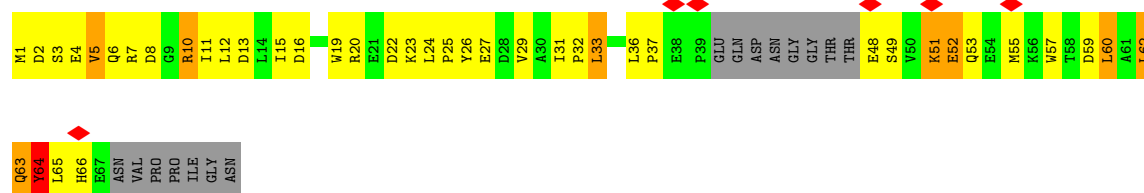
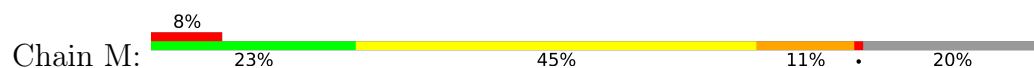




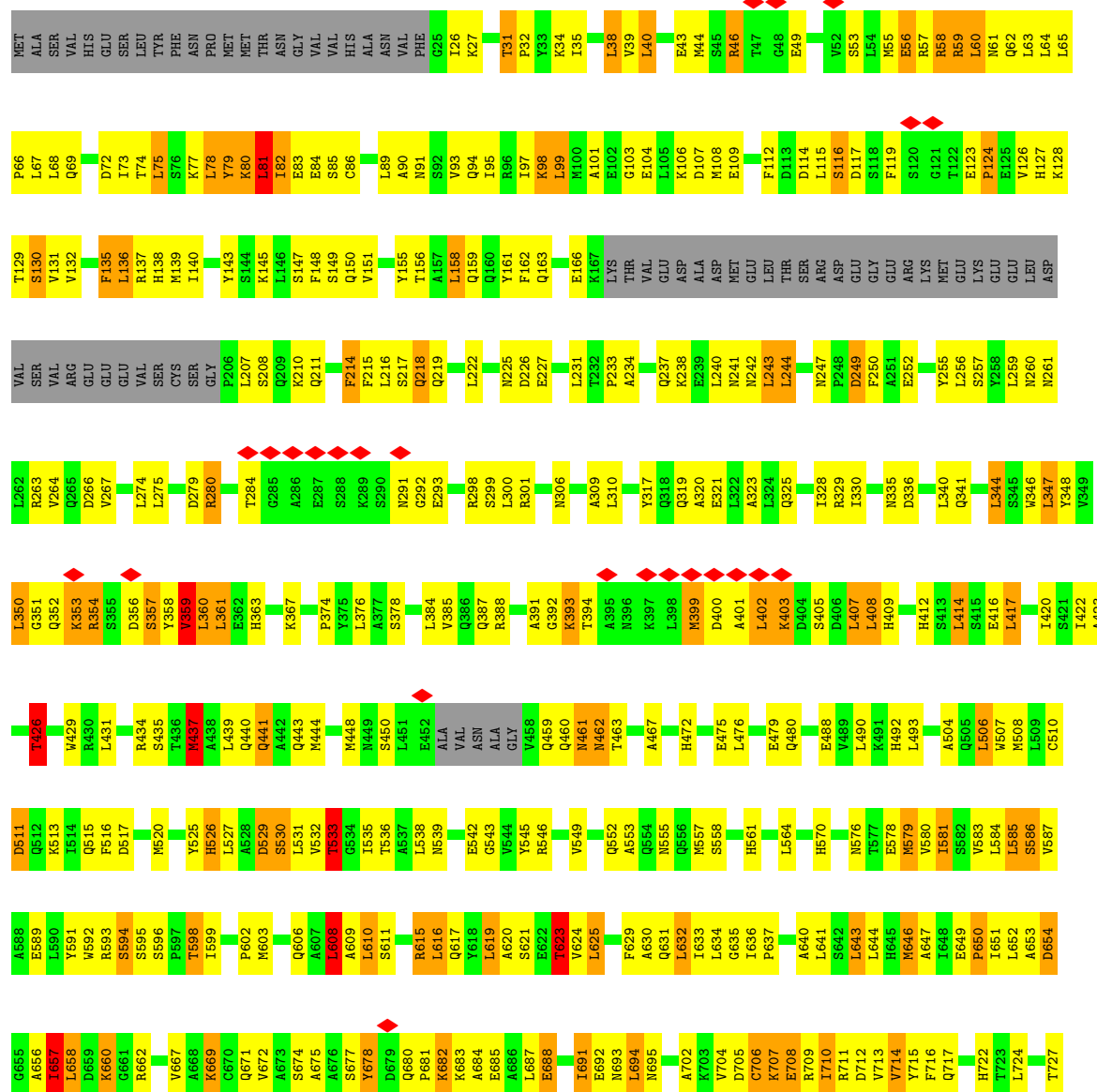
• Molecule 10: ANAPHASE-PROMOTING COMPLEX SUBUNIT 10



• Molecule 11: ANAPHASE-PROMOTING COMPLEX SUBUNIT 13

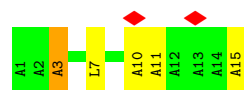


Chain O: 



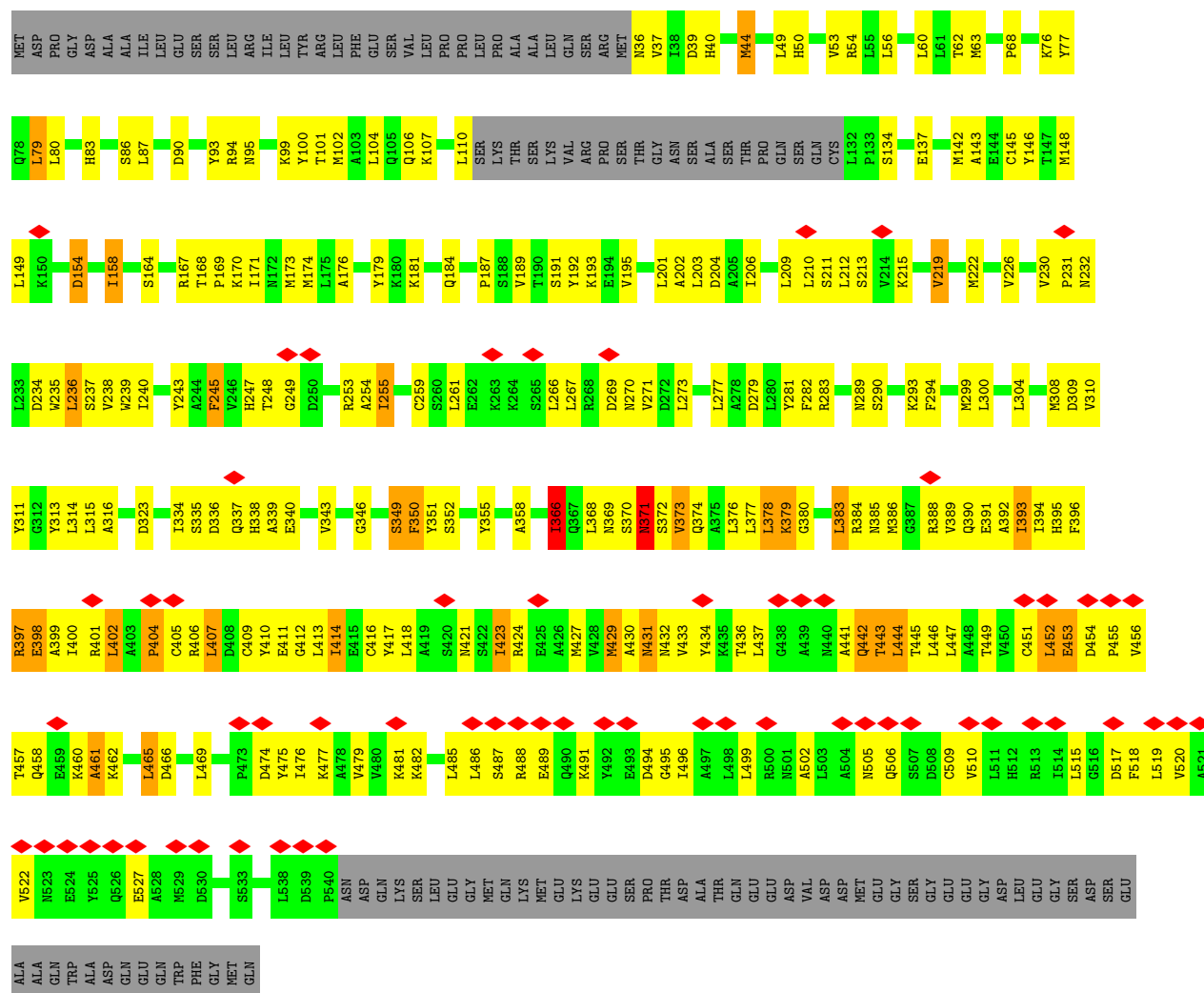
• Molecule 14: UNIDENTIFIED PEPTIDE

Chain T: 

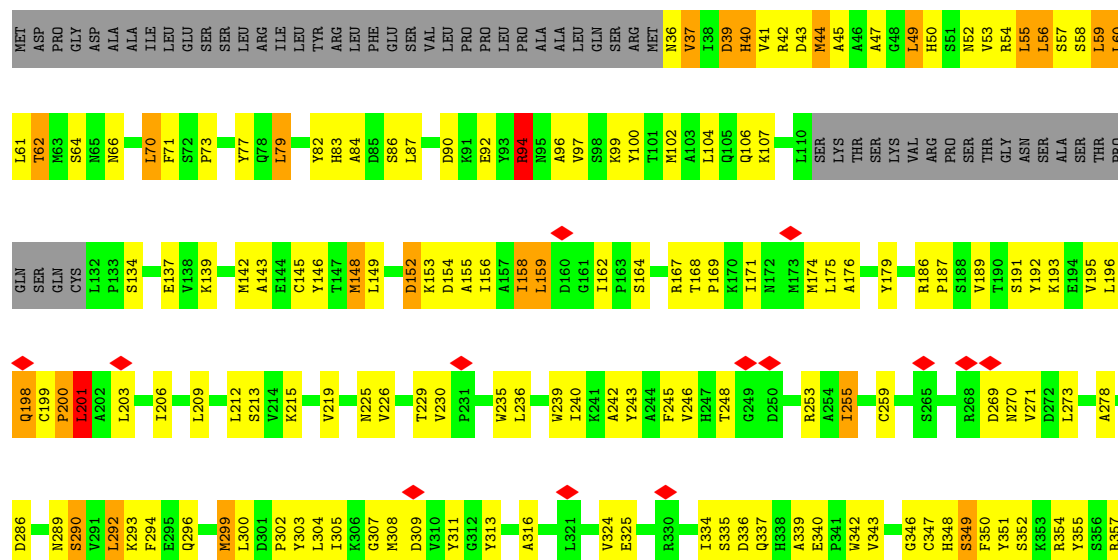
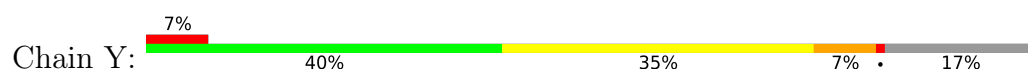


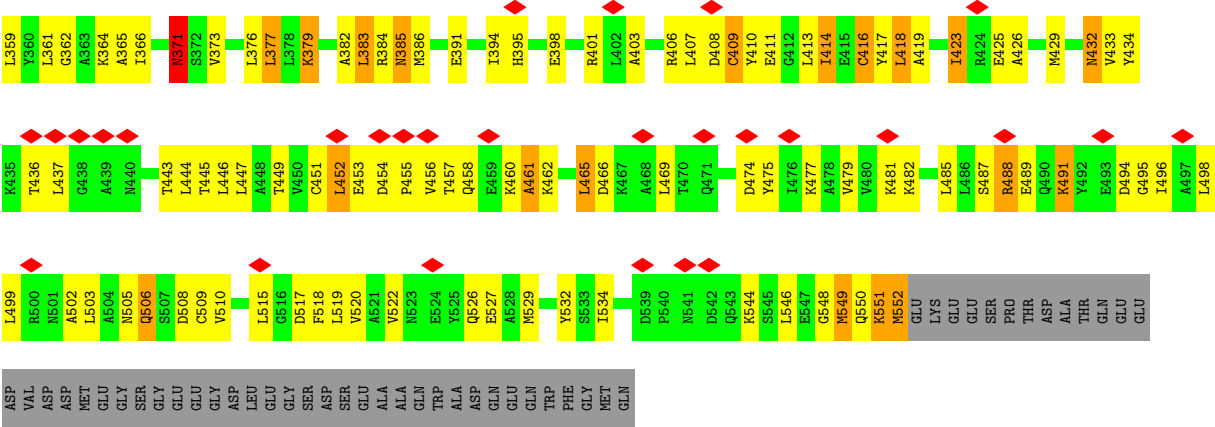
• Molecule 15: ANAPHASE-PROMOTING COMPLEX SUBUNIT 7

Chain X: 



• 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	1.00	25/12168 (0.2%)	1.20	45/16587 (0.3%)
2	B	0.87	0/674	1.18	2/913 (0.2%)
3	C	0.99	6/4403 (0.1%)	1.17	7/5942 (0.1%)
3	P	0.89	0/4141	1.11	3/5593 (0.1%)
4	D	0.91	0/446	1.18	2/610 (0.3%)
5	E	0.80	1/459 (0.2%)	0.98	0/619
6	F	0.88	0/3704	1.10	8/5019 (0.2%)
6	H	0.92	2/3969 (0.1%)	1.10	6/5366 (0.1%)
7	G	0.78	0/221	1.10	0/292
7	W	0.82	0/219	1.17	0/291
8	I	1.00	12/5754 (0.2%)	1.28	35/7806 (0.4%)
9	J	0.98	3/4152 (0.1%)	1.21	24/5623 (0.4%)
9	K	0.99	3/4085 (0.1%)	1.18	14/5530 (0.3%)
10	L	1.01	1/1468 (0.1%)	1.17	7/1993 (0.4%)
11	M	0.85	0/490	1.05	0/665
12	N	0.91	11/4861 (0.2%)	1.24	27/6585 (0.4%)
13	O	1.31	13/5499 (0.2%)	1.22	14/7432 (0.2%)
14	T	1.06	0/78	1.56	0/107
15	X	0.90	0/3827	1.14	7/5180 (0.1%)
15	Y	0.79	0/3922	1.10	7/5304 (0.1%)
All	All	0.98	77/64540 (0.1%)	1.18	208/87457 (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 77 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	O	116	SER	C-N	42.46	1.91	1.33
13	O	135	PHE	C-N	22.80	1.65	1.34
1	A	236	VAL	N-CA	14.46	1.64	1.46
8	I	433	VAL	N-CA	13.17	1.62	1.46
9	K	224	VAL	N-CA	-11.70	1.31	1.46

The worst 5 of 208 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	I	433	VAL	O-C-N	-27.96	89.22	121.10
8	I	433	VAL	CA-C-N	-18.57	96.63	119.84
8	I	433	VAL	C-N-CA	-18.57	96.63	119.84
12	N	611	VAL	N-CA-C	-12.42	93.55	108.45
12	N	121	ARG	N-CA-C	12.41	124.35	111.07

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	Peptide,Mainchain
8	I	658	GLY	Peptide
8	I	727	PHE	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	A	11890	0	11555	1904	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	649	0	595	40	0
3	C	4306	0	4273	287	0
3	P	4046	0	3998	254	0
4	D	436	0	396	28	0
5	E	450	0	435	31	0
6	F	3618	0	3452	385	0
6	H	3879	0	3805	274	0
7	G	220	0	233	32	0
7	W	218	0	222	30	0
8	I	5634	0	5522	603	0
9	J	4053	0	3960	381	0
9	K	3988	0	3911	451	0
10	L	1435	0	1381	173	0
11	M	481	0	457	75	0
12	N	4767	0	4686	1297	0
13	O	5400	0	5416	477	0
14	T	79	0	77	8	0
15	X	3767	0	3820	448	0
15	Y	3862	0	3914	415	0
16	B	3	0	0	0	0
All	All	63181	0	62108	7118	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 57.

The worst 5 of 7118 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)
15:Y:104:LEU:CD1	15:Y:142:MET:HE1	1.23	1.68
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

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%)	2	16
2	B	83/84 (99%)	72 (87%)	7 (8%)	4 (5%)	2	11
3	C	518/597 (87%)	490 (95%)	23 (4%)	5 (1%)	12	40
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	59
6	H	484/824 (59%)	469 (97%)	10 (2%)	5 (1%)	12	40
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%)	11	38
11	M	55/74 (74%)	49 (89%)	5 (9%)	1 (2%)	6	26
12	N	590/822 (72%)	547 (93%)	26 (4%)	17 (3%)	3	19
13	O	682/755 (90%)	643 (94%)	27 (4%)	12 (2%)	6	26
14	T	13/15 (87%)	11 (85%)	1 (8%)	1 (8%)	1	5
15	X	480/599 (80%)	463 (96%)	12 (2%)	5 (1%)	12	40
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	26

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%)	941 (76%)	302 (24%)	1	2
2	B	65/75 (87%)	52 (80%)	13 (20%)	1	4
3	C	452/520 (87%)	381 (84%)	71 (16%)	2	10
3	P	422/520 (81%)	369 (87%)	53 (13%)	4	18
4	D	46/115 (40%)	42 (91%)	4 (9%)	9	32
5	E	47/89 (53%)	33 (70%)	14 (30%)	0	1
6	F	371/727 (51%)	304 (82%)	67 (18%)	2	7
6	H	408/727 (56%)	368 (90%)	40 (10%)	7	27
7	G	25/77 (32%)	12 (48%)	13 (52%)	0	0
7	W	23/77 (30%)	16 (70%)	7 (30%)	0	0
8	I	607/730 (83%)	495 (82%)	112 (18%)	1	7
9	J	425/548 (78%)	362 (85%)	63 (15%)	3	12
9	K	423/548 (77%)	351 (83%)	72 (17%)	2	9
10	L	155/170 (91%)	136 (88%)	19 (12%)	4	18
11	M	52/67 (78%)	37 (71%)	15 (29%)	0	1
12	N	490/724 (68%)	370 (76%)	120 (24%)	1	2
13	O	573/650 (88%)	468 (82%)	105 (18%)	2	7
14	T	1/2 (50%)	1 (100%)	0	100	100
15	X	406/513 (79%)	365 (90%)	41 (10%)	7	25
15	Y	417/513 (81%)	367 (88%)	50 (12%)	5	19

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	6651/9112 (73%)	5470 (82%)	1181 (18%)	4 7

5 of 1181 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	O	38	LEU
15	Y	148	MET
13	O	243	LEU
13	O	31	THR
3	P	97	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 222 such sidechains are listed below:

Mol	Chain	Res	Type
9	J	271	HIS
15	Y	541	ASN
12	N	242	GLN
15	Y	458	GLN
15	X	106	GLN

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

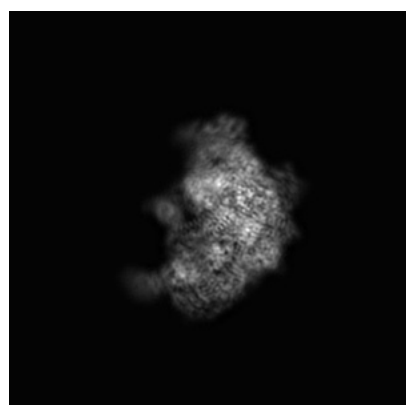
6 Map visualisation [i](#)

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.

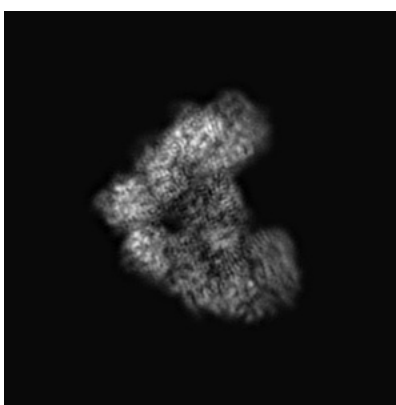
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

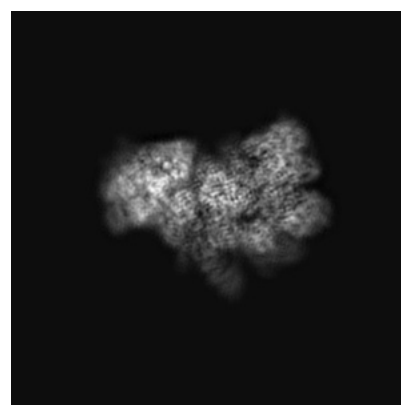
6.1.1 Primary map



X



Y

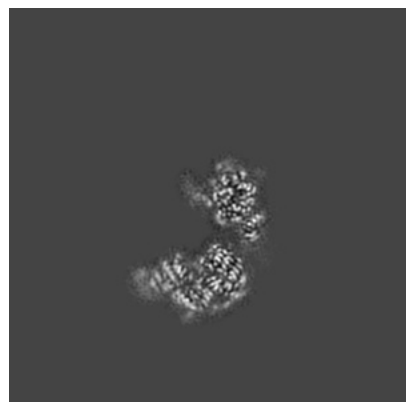


Z

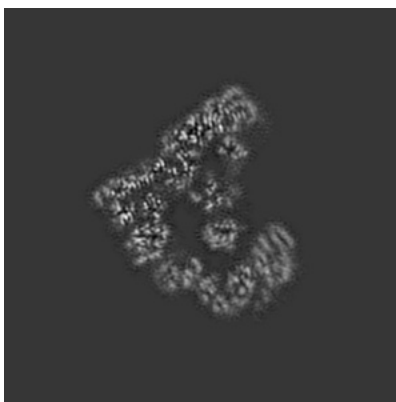
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

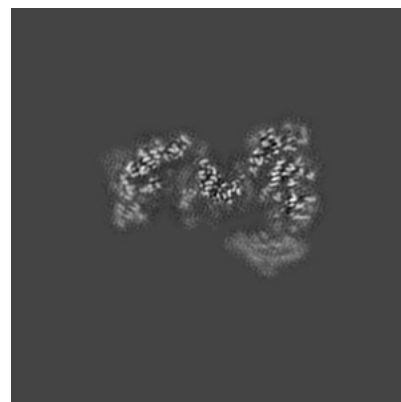
6.2.1 Primary map



X Index: 142



Y Index: 142

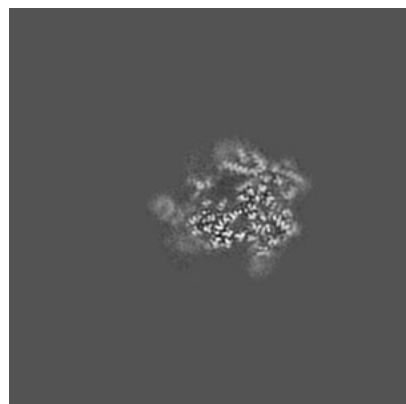


Z Index: 142

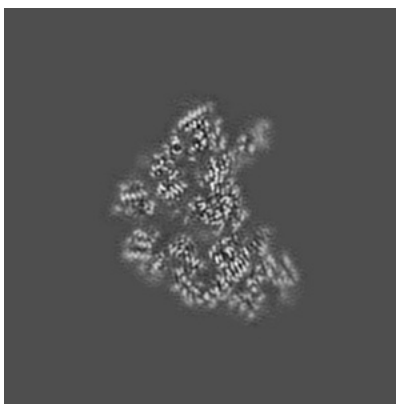
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

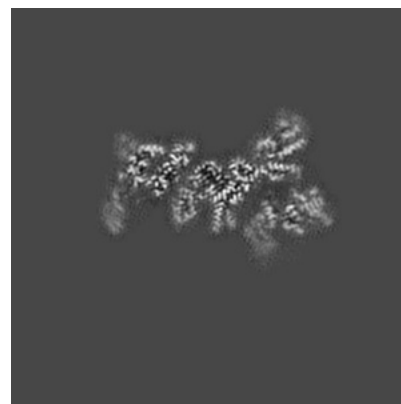
6.3.1 Primary map



X Index: 191



Y Index: 163

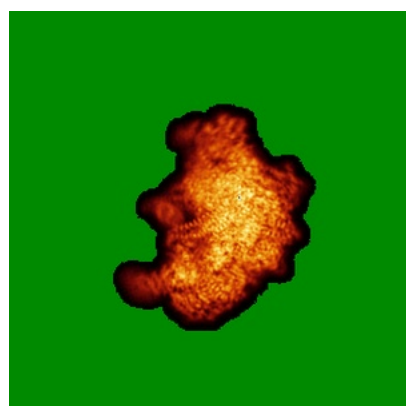


Z Index: 154

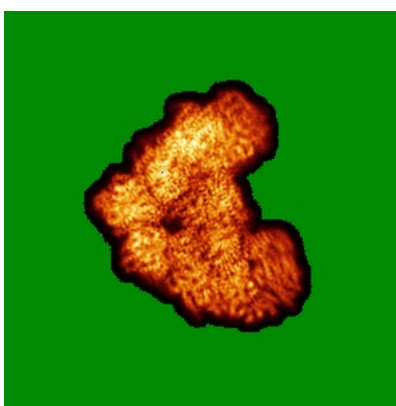
The images above show the largest variance slices of the map in three orthogonal directions.

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

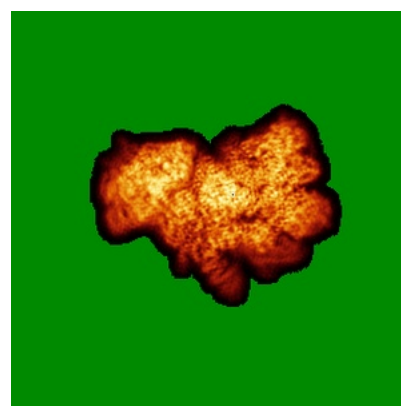
6.4.1 Primary map



X



Y

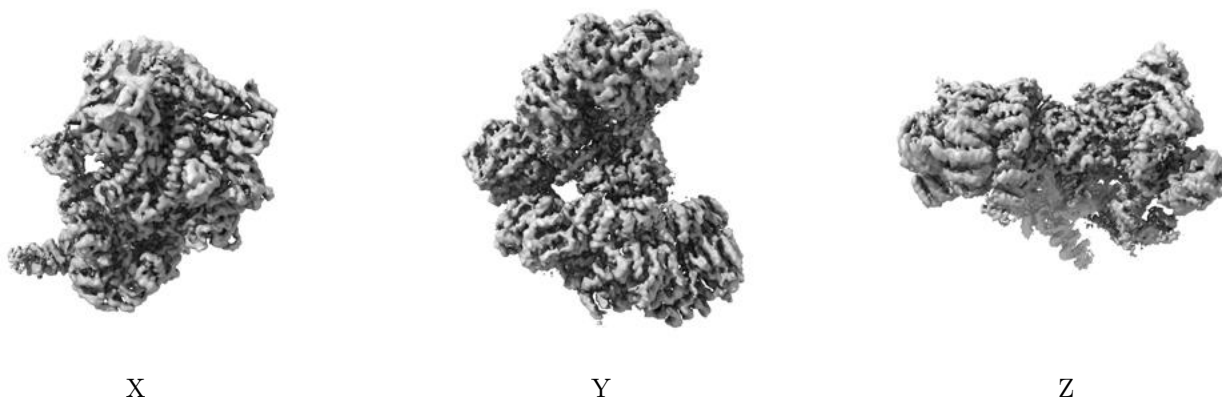


Z

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.

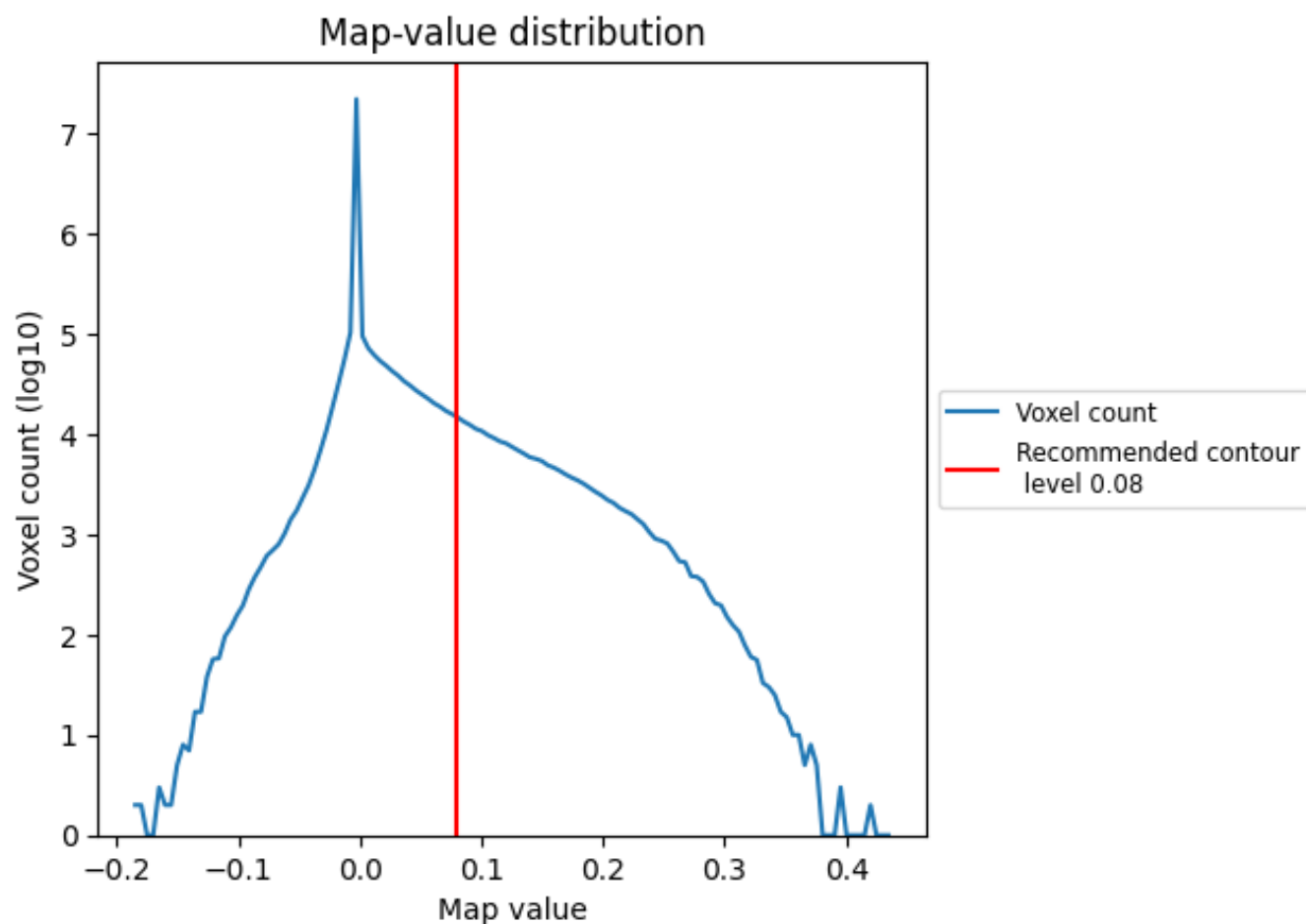
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

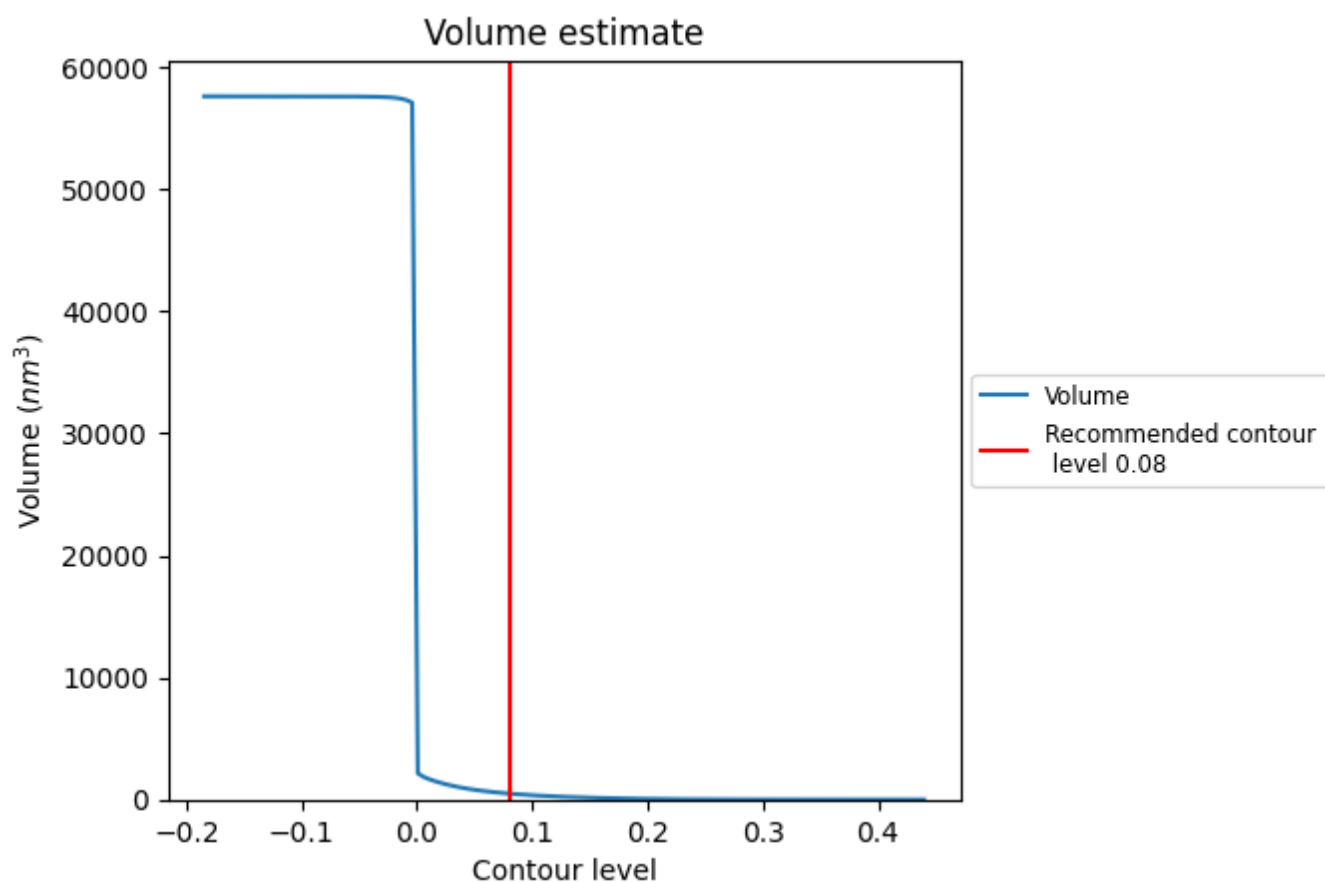
This section contains the results of statistical analysis of the map.

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.

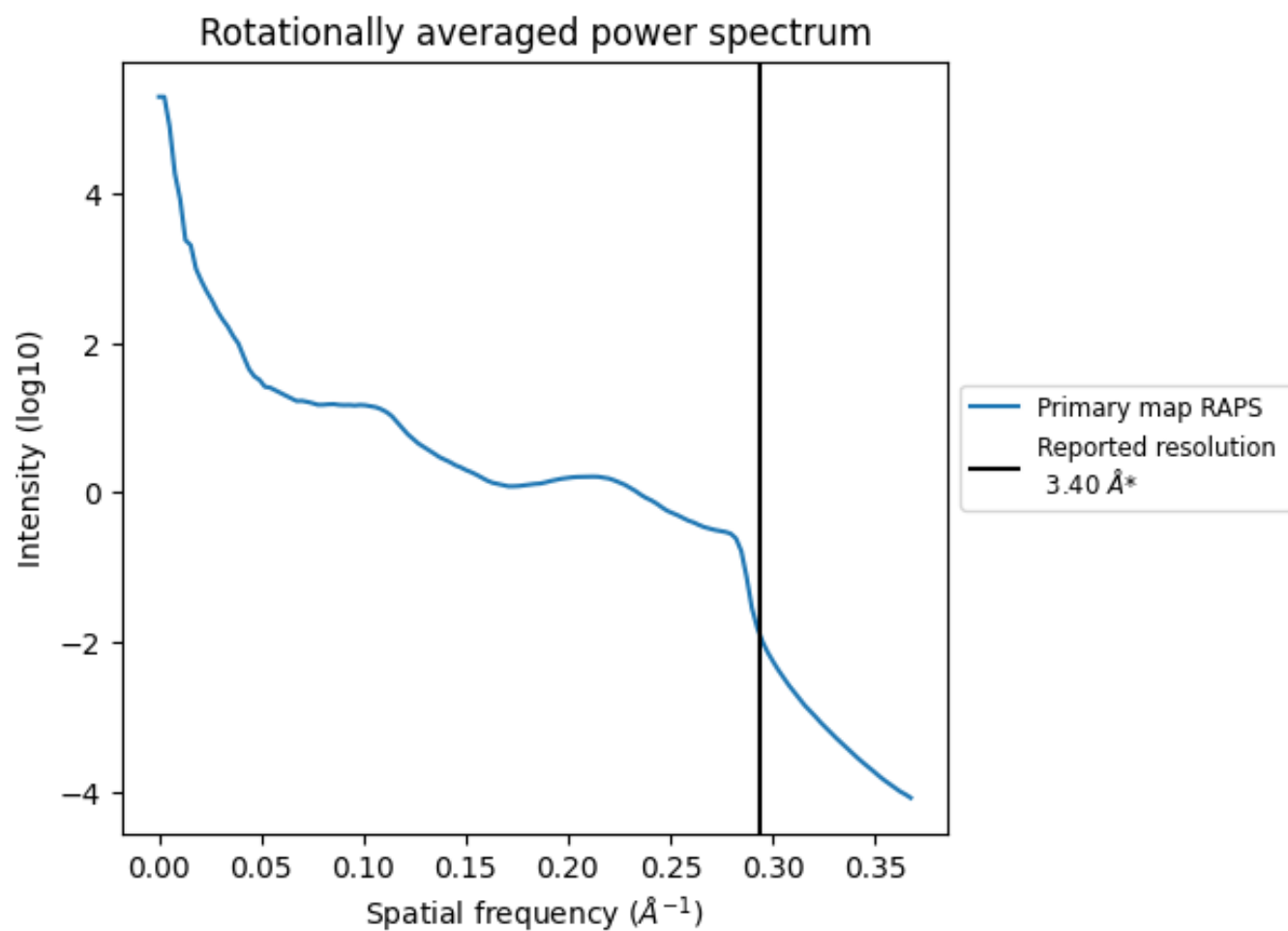
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 488 nm³; 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⁻¹

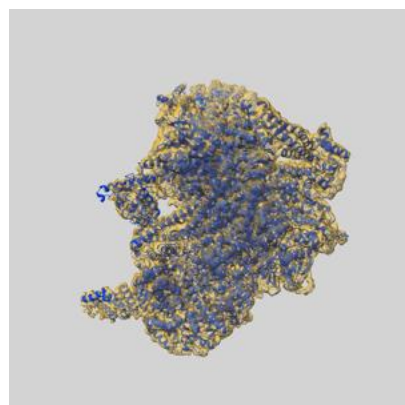
8 Fourier-Shell correlation

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

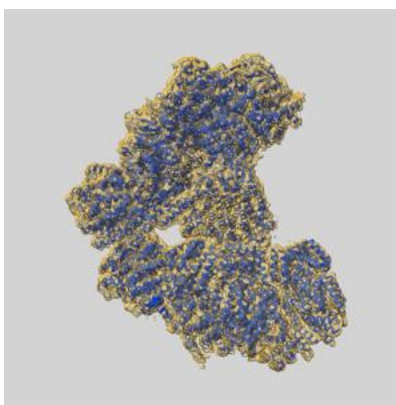
9 Map-model fit [i](#)

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

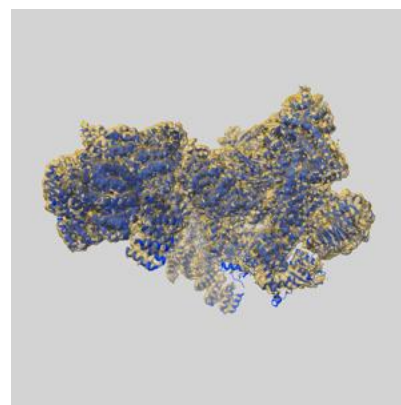
9.1 Map-model overlay [i](#)



X



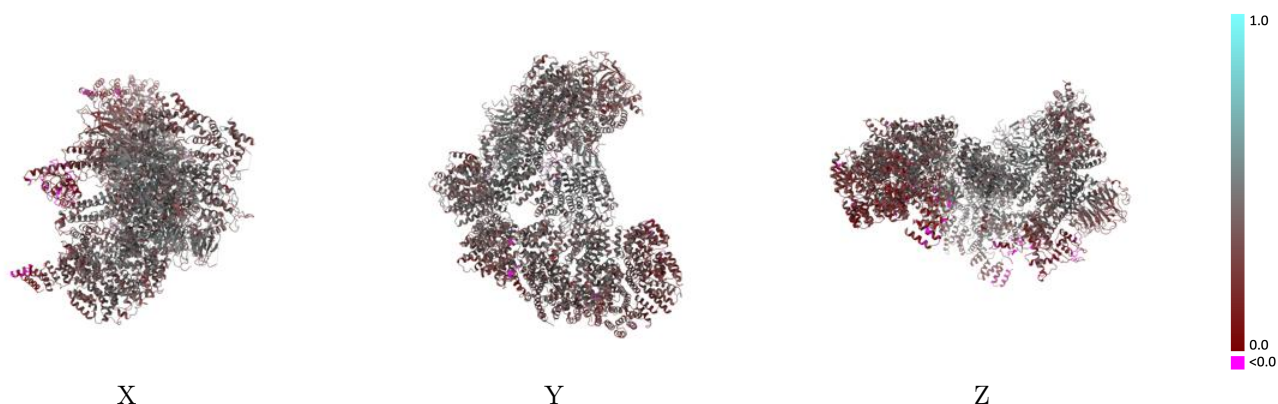
Y



Z

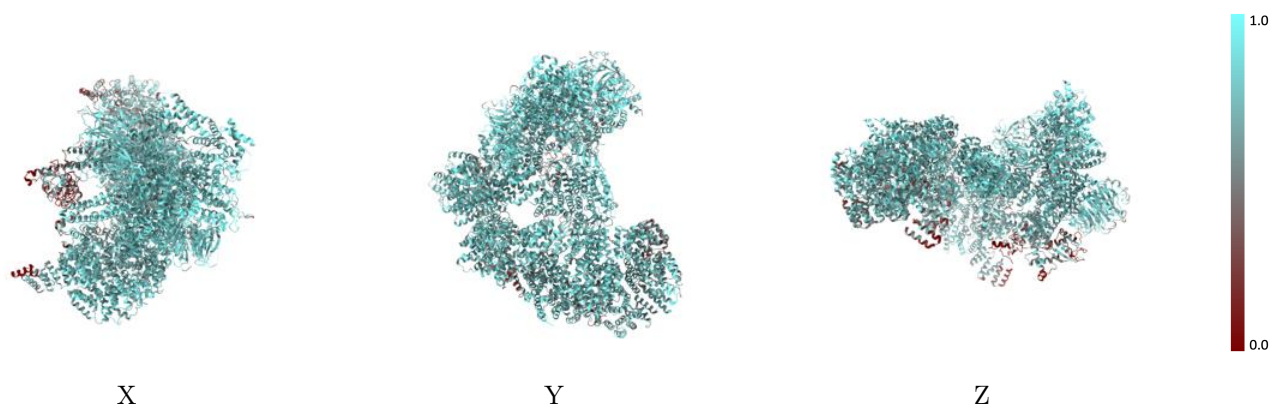
The images above show the 3D surface view of the map at the recommended contour level 0.08 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



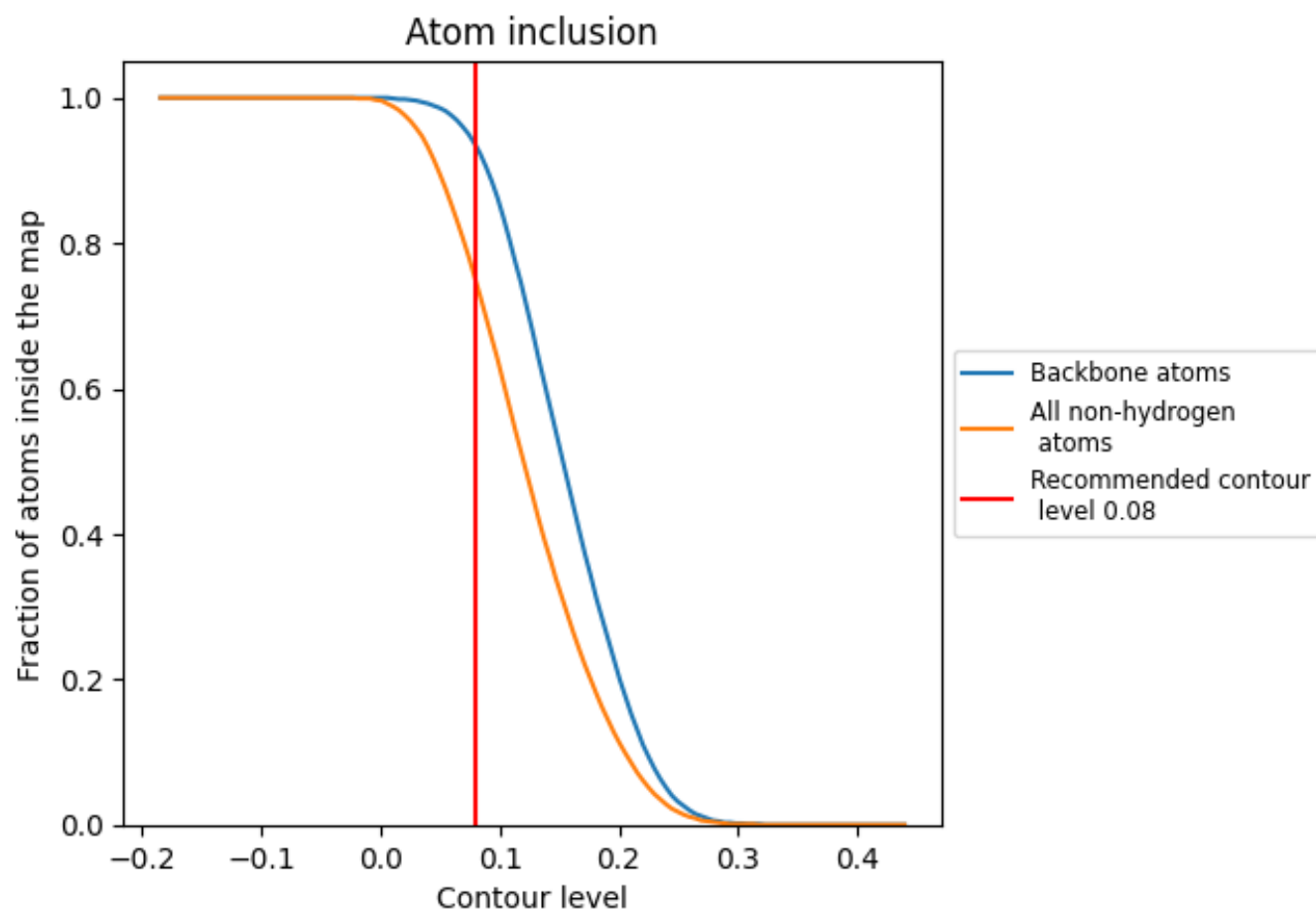
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

