



Full wwPDB EM Validation Report ⓘ

Nov 20, 2022 – 10:37 am GMT

PDB ID : 5L9T
EMDB ID : EMD-3433
Title : Model of human Anaphase-promoting complex/Cyclosome (APC/C-CDH1) with E2 UBE2S poised for polyubiquitination where UBE2S, APC2, and APC11 are modeled into low resolution density
Authors : Brown, N.G.; VanderLinden, R.; Dube, P.; Haselbach, D.; Peters, J.M.; Stark, H.; Schulman, B.A.
Deposited on : 2016-06-11
Resolution : 6.40 Å(reported)

This is a Full wwPDB EM Validation 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:

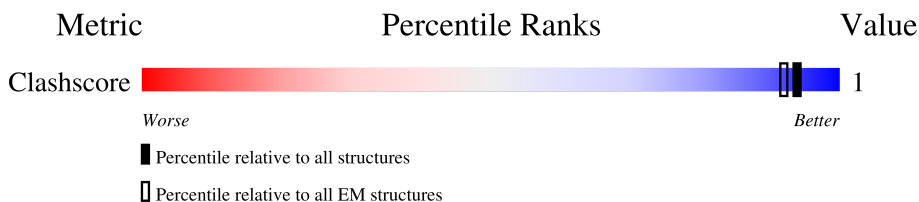
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

1 Overall quality at a glance i

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


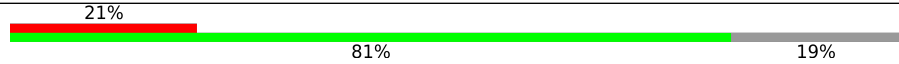
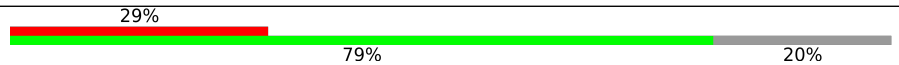

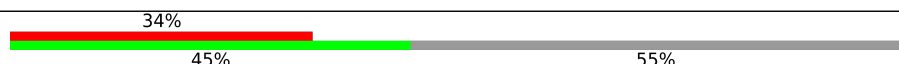
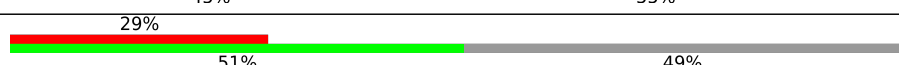

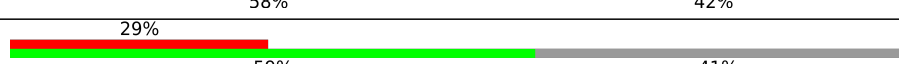


The reported resolution of this entry is 6.40 Å.

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	158937	4297

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	
4	D	121	
5	E	110	
6	F	824	
6	H	824	
7	G	85	
7	W	85	

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Mol	Chain	Length	Quality of chain
8	I	818	
9	J	620	
9	K	620	
10	L	185	
11	M	74	
12	N	822	
13	O	755	
14	R	493	
15	S	108	
16	T	185	
17	X	565	
17	Y	565	

2 Entry composition [i](#)

There are 17 unique types of molecules in this entry. The entry contains 8038 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	1380	Total C 1380 1380	0	1380

- Molecule 2 is a protein called Anaphase-promoting complex subunit 11.

Mol	Chain	Residues	Atoms	AltConf	Trace
2	B	68	Total C 68 68	0	68

- Molecule 3 is a protein called Cell division cycle protein 23 homolog.

Mol	Chain	Residues	Atoms	AltConf	Trace
3	C	475	Total C 475 475	0	475
3	P	443	Total C 443 443	0	443

- Molecule 4 is a protein called Anaphase-promoting complex subunit 15.

Mol	Chain	Residues	Atoms	AltConf	Trace
4	D	55	Total C 55 55	0	55

- Molecule 5 is a protein called Anaphase-promoting complex subunit 16.

Mol	Chain	Residues	Atoms	AltConf	Trace
5	E	56	Total C 56 56	0	56

- Molecule 6 is a protein called Cell division cycle protein 27 homolog.

Mol	Chain	Residues	Atoms	AltConf	Trace
6	F	482	Total C 482 482	0	482
6	H	483	Total C 483 483	0	483

- Molecule 7 is a protein called Anaphase-promoting complex subunit CDC26.

Mol	Chain	Residues	Atoms	AltConf	Trace
7	G	25	Total C 25 25	0	25
7	W	25	Total C 25 25	0	25

- Molecule 8 is a protein called Anaphase-promoting complex subunit 4.

Mol	Chain	Residues	Atoms	AltConf	Trace
8	I	727	Total C 727 727	0	727

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	809	GLY	-	expression tag	UNP Q9UJX5
I	810	GLY	-	expression tag	UNP Q9UJX5
I	811	SER	-	expression tag	UNP Q9UJX5
I	812	LEU	-	expression tag	UNP Q9UJX5
I	813	GLU	-	expression tag	UNP Q9UJX5
I	814	VAL	-	expression tag	UNP Q9UJX5
I	815	LEU	-	expression tag	UNP Q9UJX5
I	816	PHE	-	expression tag	UNP Q9UJX5
I	817	GLN	-	expression tag	UNP Q9UJX5
I	818	GLY	-	expression tag	UNP Q9UJX5

- Molecule 9 is a protein called Cell division cycle protein 16 homolog.

Mol	Chain	Residues	Atoms	AltConf	Trace
9	J	504	Total C 504 504	0	504
9	K	493	Total C 493 493	0	493

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

Mol	Chain	Residues	Atoms		AltConf	Trace
10	L	170	Total	C	0	170
			170	170		

- Molecule 11 is a protein called Anaphase-promoting complex subunit 13.

Mol	Chain	Residues	Atoms		AltConf	Trace
11	M	42	Total	C	0	42
			42	42		

- Molecule 12 is a protein called Anaphase-promoting complex subunit 2.

Mol	Chain	Residues	Atoms		AltConf	Trace
12	N	546	Total	C	0	546
			546	546		

- Molecule 13 is a protein called Anaphase-promoting complex subunit 5.

Mol	Chain	Residues	Atoms		AltConf	Trace
13	O	685	Total	C	0	685
			685	685		

- Molecule 14 is a protein called Fizzy-related protein homolog.

Mol	Chain	Residues	Atoms		AltConf	Trace
14	R	385	Total	C	0	385
			385	385		

- Molecule 15 is a protein called Ubiquitin_variant-Hsl1(substrate) fusion.

Mol	Chain	Residues	Atoms		AltConf	Trace
15	S	84	Total	C	0	84
			84	84		

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	-4	GLY	-	expression tag	UNP P0CG47
S	-3	SER	-	expression tag	UNP P0CG47
S	-2	GLY	-	expression tag	UNP P0CG47
S	-1	GLY	-	expression tag	UNP P0CG47
S	0	SER	-	expression tag	UNP P0CG47
S	4	LEU	PHE	engineered mutation	UNP P0CG47

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Chain	Residue	Modelled	Actual	Comment	Reference
S	8	PRO	LEU	engineered mutation	UNP P0CG47
S	9	ARG	THR	engineered mutation	UNP P0CG47
S	11	CYS	LYS	engineered mutation	UNP P0CG47
S	42	ILE	ARG	engineered mutation	UNP P0CG47
S	44	PHE	ILE	engineered mutation	UNP P0CG47
S	47	VAL	GLY	engineered mutation	UNP P0CG47
S	49	ARG	GLN	engineered mutation	UNP P0CG47
S	64	LYS	GLU	engineered mutation	UNP P0CG47
S	66	SER	THR	engineered mutation	UNP P0CG47
S	68	LEU	HIS	engineered mutation	UNP P0CG47
S	70	ALA	VAL	engineered mutation	UNP P0CG47
S	71	MET	LEU	engineered mutation	UNP P0CG47
S	73	VAL	LEU	engineered mutation	UNP P0CG47
S	74	PRO	ARG	engineered mutation	UNP P0CG47
S	815	LYS	GLY	engineered mutation	UNP P0CG47
S	817	LYS	-	linker	UNP P0CG47

- Molecule 16 is a protein called Ubiquitin-conjugating enzyme E2 S.

Mol	Chain	Residues	Atoms	AltConf	Trace
16	T	97	Total C 97 97	0	97

There are 46 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
T	-3	GLY	-	expression tag	UNP Q16763
T	-2	PRO	-	expression tag	UNP Q16763
T	-1	GLY	-	expression tag	UNP Q16763
T	0	SER	-	expression tag	UNP Q16763
T	118	PHE	CYS	conflict	UNP Q16763
T	?	-	GLY	deletion	UNP Q16763
T	?	-	PRO	deletion	UNP Q16763
T	?	-	SER	deletion	UNP Q16763
T	?	-	GLY	deletion	UNP Q16763
T	?	-	ARG	deletion	UNP Q16763
T	?	-	ALA	deletion	UNP Q16763
T	?	-	GLU	deletion	UNP Q16763
T	?	-	ALA	deletion	UNP Q16763
T	?	-	GLY	deletion	UNP Q16763
T	?	-	ARG	deletion	UNP Q16763
T	?	-	ALA	deletion	UNP Q16763

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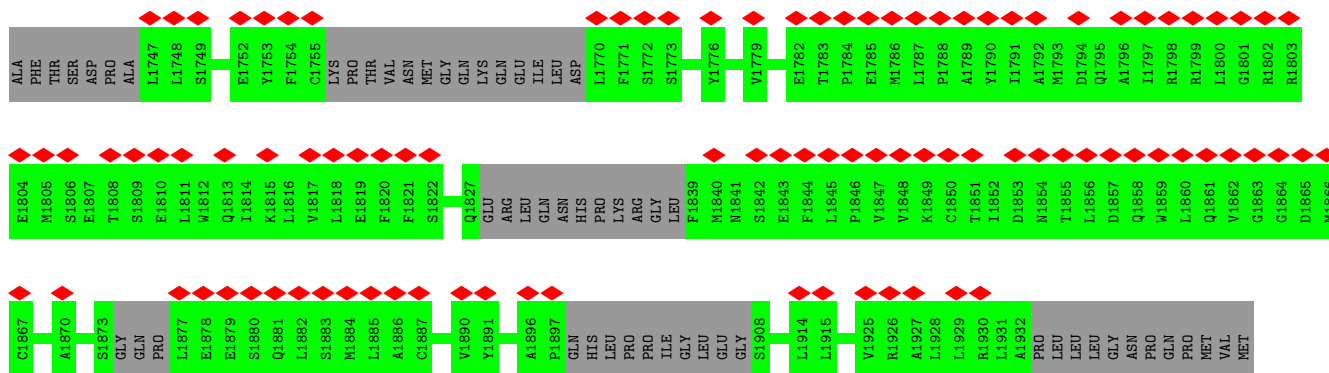
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Chain	Residue	Modelled	Actual	Comment	Reference
T	?	-	LEU	deletion	UNP Q16763
T	?	-	ALA	deletion	UNP Q16763
T	?	-	SER	deletion	UNP Q16763
T	?	-	GLY	deletion	UNP Q16763
T	?	-	THR	deletion	UNP Q16763
T	?	-	GLU	deletion	UNP Q16763
T	?	-	ALA	deletion	UNP Q16763
T	?	-	SER	deletion	UNP Q16763
T	?	-	SER	deletion	UNP Q16763
T	?	-	THR	deletion	UNP Q16763
T	?	-	ASP	deletion	UNP Q16763
T	?	-	PRO	deletion	UNP Q16763
T	?	-	GLY	deletion	UNP Q16763
T	?	-	ALA	deletion	UNP Q16763
T	?	-	PRO	deletion	UNP Q16763
T	?	-	GLY	deletion	UNP Q16763
T	?	-	GLY	deletion	UNP Q16763
T	?	-	PRO	deletion	UNP Q16763
T	?	-	GLY	deletion	UNP Q16763
T	?	-	GLY	deletion	UNP Q16763
T	?	-	ALA	deletion	UNP Q16763
T	?	-	GLU	deletion	UNP Q16763
T	?	-	GLY	deletion	UNP Q16763
T	?	-	PRO	deletion	UNP Q16763
T	?	-	MET	deletion	UNP Q16763
T	?	-	ALA	deletion	UNP Q16763
T	?	-	LYS	deletion	UNP Q16763
T	?	-	LYS	deletion	UNP Q16763
T	?	-	HIS	deletion	UNP Q16763
T	?	-	ALA	deletion	UNP Q16763

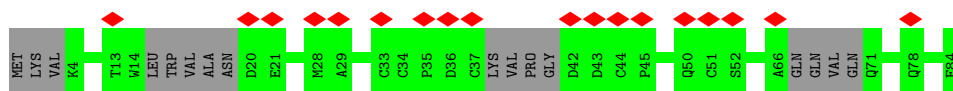
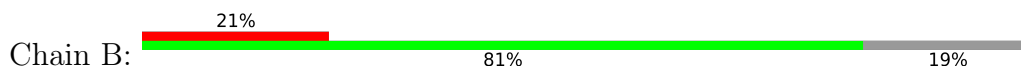
- Molecule 17 is a protein called Anaphase-promoting complex subunit 7.

Mol	Chain	Residues	Atoms	AltConf	Trace
17	X	397	Total C 397 397	0	397
17	Y	416	Total C 416 416	0	416

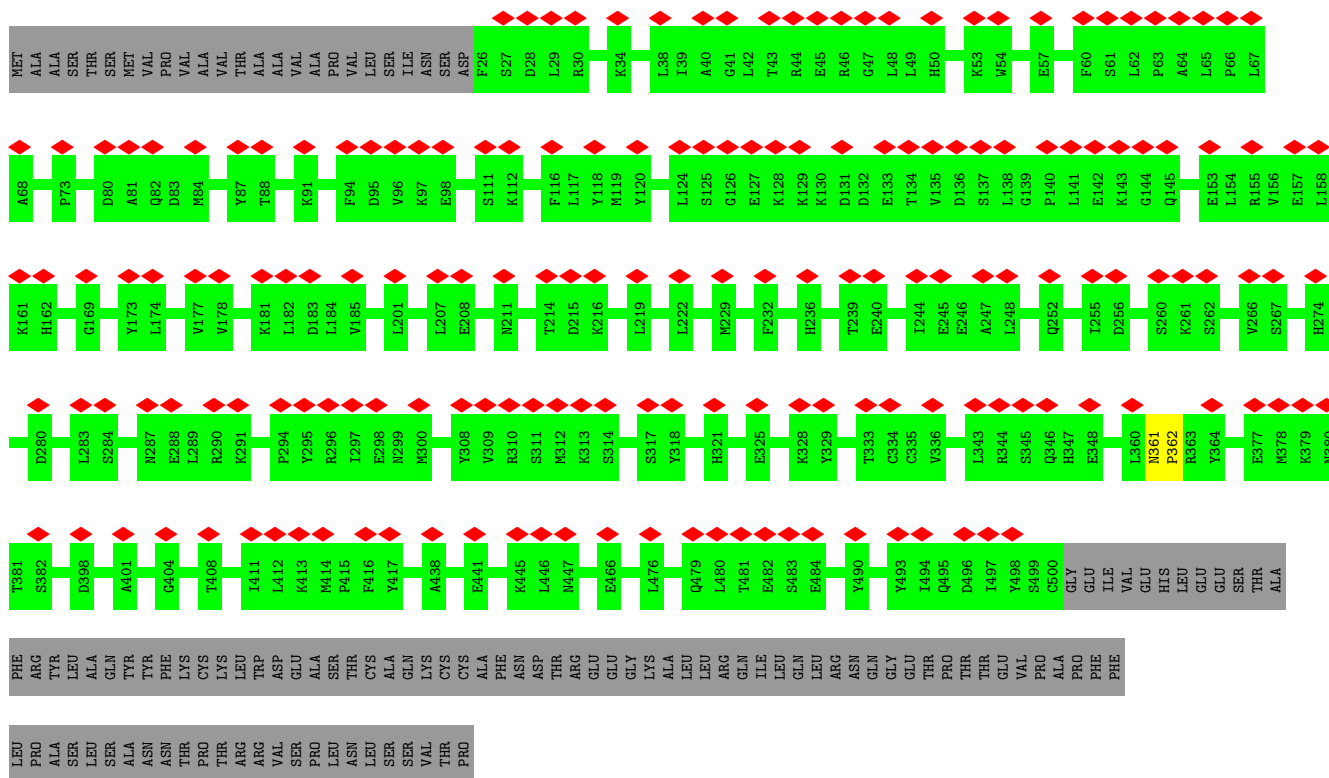
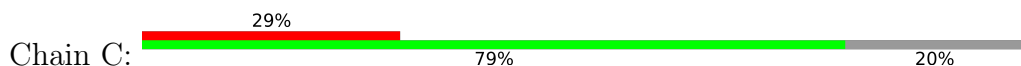
PRO	VAL	ILE	ALA	PRO	PRO	LYS	ALA	PRO	SER	GLU	THR	GLY	SER	D704	H767	L768	V769	M779	G780	E781	W847	V848	G854	P859	Y860	L863	P864	G865	I866	C867	R869	L872	V873	V874	L875	S876	I877	A878	L879	Y880	T812	L813	L882	GLY	ASP	GLU	THR	THR	GLY	GLN	ASP	VAL	SER	ASP	THR	LEU	LEU	PHE	T757	P760	A761	I762	F763	F764	V765	L766
H767	L768	V769	M779	G780	E781	W847	V848	G854	P859	Y860	L863	P864	G865	I866	C867	R869	L872	V873	V874	L875	S876	I877	A878	L879	Y880	T812	L813	L882	GLY	ASP	GLU	THR	THR	GLY	GLN	ASP	VAL	SER	ASP	THR	LEU	LEU	PHE	T757	P760	A761	I762	F763	F764	V765	L766															
P841	P842	S843	I844	Y845	Q846	W847	V848	G854	P859	Y860	L863	P864	G865	I866	C867	R869	L872	V873	V874	L875	S876	I877	A878	L879	Y880	T812	L813	L882	GLY	ASP	GLU	THR	THR	GLY	GLN	ASP	VAL	SER	ASP	THR	LEU	LEU	PHE	T757	P760	A761	I762	F763	F764	V765	L766															
GLN	GLU	GLU	ASN	PHE	ARG	SER	PHE	ARG	HIS	THR	THR	VAL	S824	R929	L930	V931	V932	T935	N936	V937	G938	F939	T940	L941	R942	D943	L944	E945	T946	L947	P948	F949	G950	I951	A952	L953	P954	I955	R956	D957	A958	I959	Y960	H961	C962	R963	E964	A967	S968	P971	E972	A973	V974	C975												
L976	L977	I978	G979	R980	Q981	S984	K985	Q986	ALA	CYS	GLU	GLY	ASN	LEU	PRO	PRO	GLY	LYS	SER	VAL	LEU	SER	ASP	VAL	PRO	SER	GLY	THR	GLU	THR	D1013	M1019	M1020	H1021	E1022	V1023	M1024	S1025	L1026	E1030	D1031	L1032	Q1035	D1036	R1039	L1040	L1041	V1047	R1048																	
V1049	M1050	V1051	Y1054	P1055	E1056	L1057	S1058	D1059	H1060	E1061	F1062	I1063	E1064	E1065	M1068	Y1092	H1093	P1094	T1097	E1098	L1100	P1101	K1104	L1105	M1106	L1107	T1108	G1109	R1110	A1111	P1112	P1113	R1114	M1115	T1116	T1117	V1118	D1119	L1120	M1121	S1122	G1123	M1124	I1125	D1126	V1127	P1128	M1130	L1146	K1146																
Q1152	I1153	N1161	H1165	A1166	E1167	L1168	A1169	N1170	M1177	A1178	L1181	M1182	G1183	H1184	L1188	A1189	T1190	I1193	L1197	T1198	K1199	G1200	H1201	E1202	M1203	I1206	G1207	L1210	G1211	A1214	L1217	G1218	I1224	T1226	L1228	I1232	P1233	L1234	L1236	P1237	P1238	T1239	S1240	T1241																						
E1242	L1243	D1244	V1246	H1247	M1248	V1251	A1252	H1253	V1254	V1255	G1256	L1259	Q1262	G1263	R1267	A1270	L1274	I1277	G1278	R1279	P1280	P1281	G1282	P1283	E1284	M1285	C1288	T1289	D1290	R1291	E1292	L1296	A1297	L1300	M1304	L1307	G1308	M1316	S1317	P1322	E1323	Y1326																								
M1329	V1330	G1331	G1332	H1333	ARG	PHE	GLN	THR	GLY	MET	HIS	ARG	GLU	LYS	HIS	S1347	P1348	S1349	Y1350	Q1351	I1352	K1353	E1354	G1355	D1356	T1357	I1358	M1359	V1360	D1361	C1364	P1365	G1366	L1369	A1370	L1371	A1372	M1373	R1381	D1385	R1388	A1389	T1392	M1393	Y1394	L1395	L1396	D1397	F1398	V1399	K1400															
P1401	E1402	C1412	N1422	S1423	K1424	D1427	S1428	N1429	V1430	R1435	E1436	N1437	ILE	SER	LEU	SER	SER	GLU	ILE	GLU	LEU	PRO	CYS	SER	GLU	ASP	L1452	M1453	N1454	L1454	E1455	S1458	V1462	I1465	A1466	C1469	L1472	G1473	F1476	E1480	N1481	L1482	K1493	D1494	T1497	S1500																				
A1501	P1502	M1503	A1504	S1505	V1506	P1509	L1512	E1513	L1516	S1517	V1518	V1519	L1520	L1523	A1524	M1525	V1526	M1527	G1531	F1541	M1544	K1546	N1546	G1547	G1548	E1549	M1550	M1551	H1559	L1562	G1563	L1564	L1565	F1566	G1569	G1570	R1571	L1574	S1575	T1576	S1577	S1580	L1581	L1584	L1585	C1586																				
A1587	L1588	Y1589	P1590	H1591	A1594	H1595	D1598	M1599	R1600	Y1601	Q1604	R1607	H1608	L1609	V1610	V1611	L1612	A1613	A1614	L1618	L1619	V1620	P1621	V1622	D1623	V1624	D1625	T1626	T1627	T1628	C1630	Y1631	A1632	L1633	Y1644	E1645	E1649	E1650	L1651	M1652	L1656	L1657	P1658	E1659	L1663	K1669	G1670	Y1671																		
R1672	L1676	I1677	L1678	D1679	SER	LYS	GLY	T1684	L1687	S1692	L1693	D1694	G1695	V1696	K1700	L1701	R1702	A1703	G1704	GLN	LEU	LEU	TYR	LYS	GLU	ASP	PRO	MET	GLY	TRP	GLN	LEU	LEU	ALA	GLN	THR	VAL	ALA	ASN	ARG	ASN	SER	ALA	ARG	ALA	PHE	LYS	PRO	GLU	THR	ILE	SER														



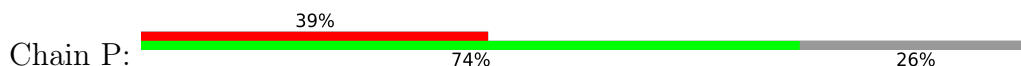
• Molecule 2: Anaphase-promoting complex subunit 11

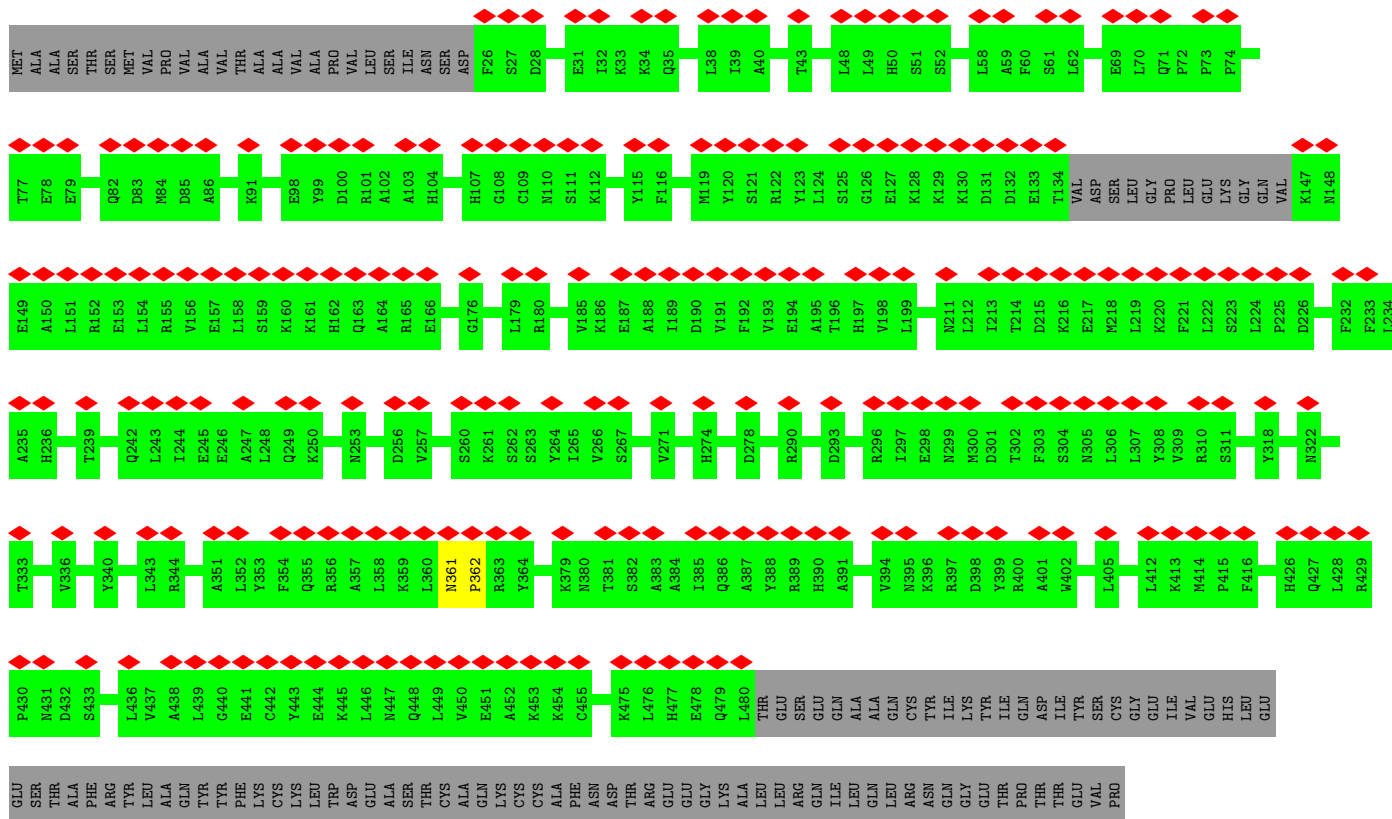


• Molecule 3: Cell division cycle protein 23 homolog

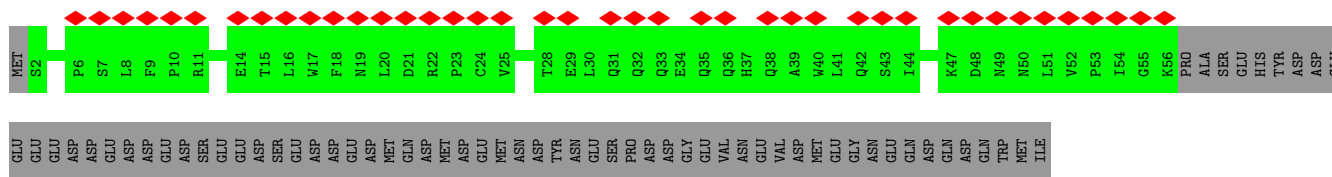


• Molecule 3: Cell division cycle protein 23 homolog

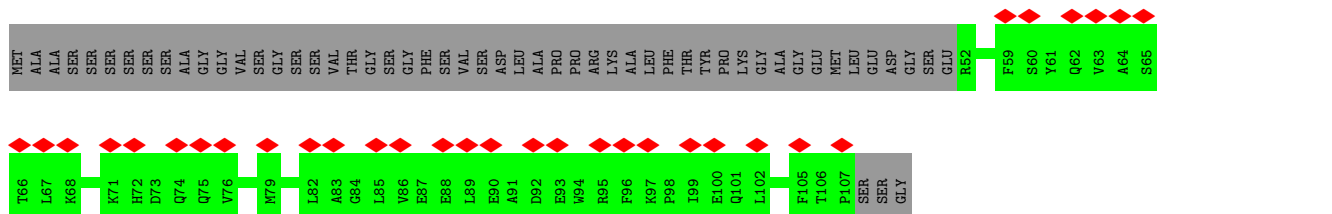




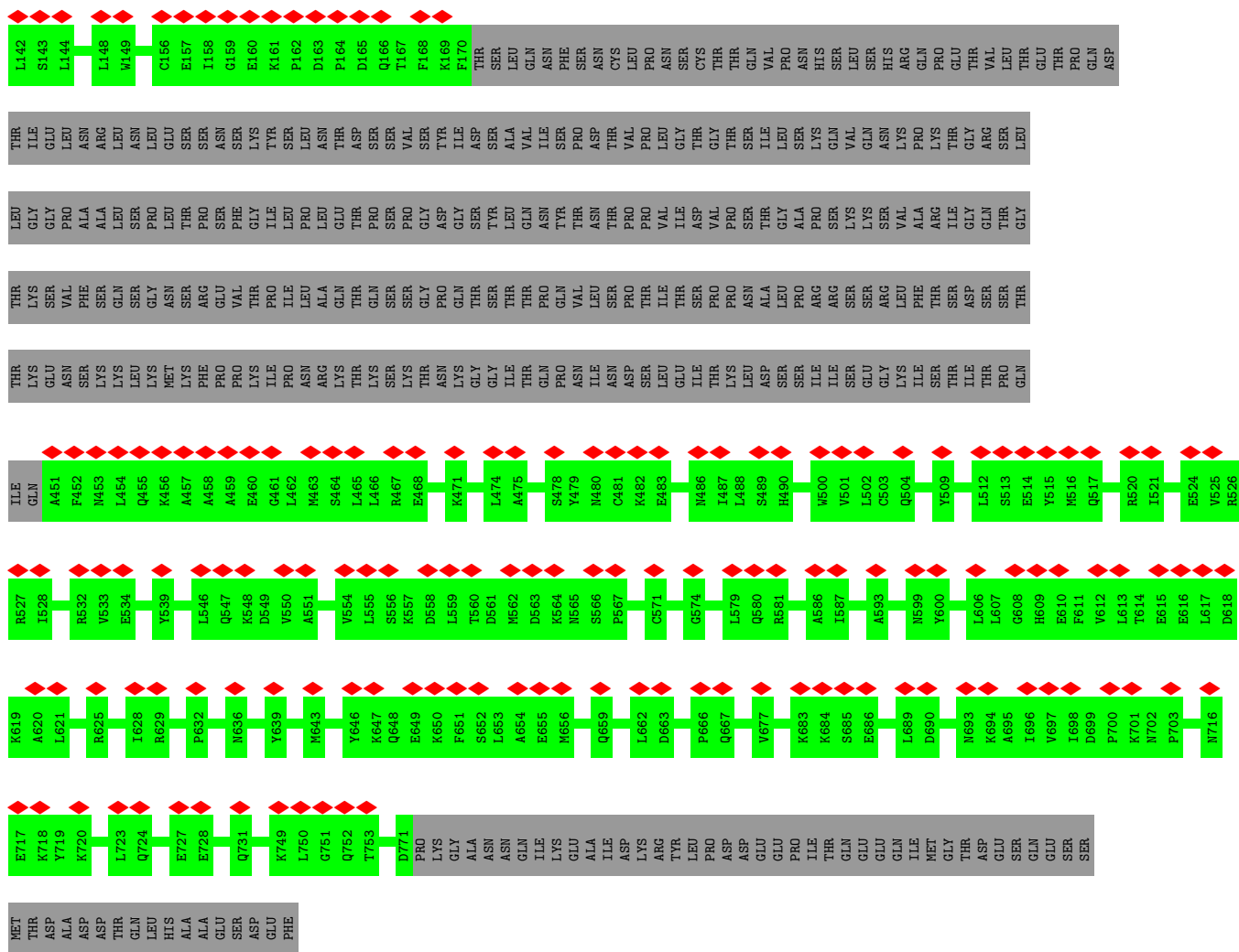
• Molecule 4: Anaphase-promoting complex subunit 15



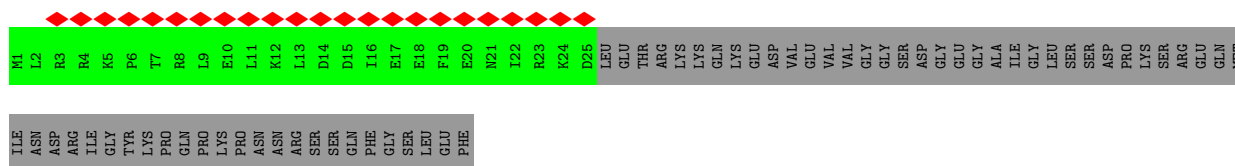
• Molecule 5: Anaphase-promoting complex subunit 16



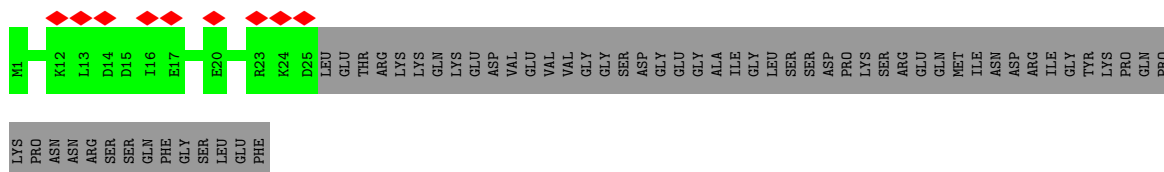
• Molecule 6: Cell division cycle protein 27 homolog



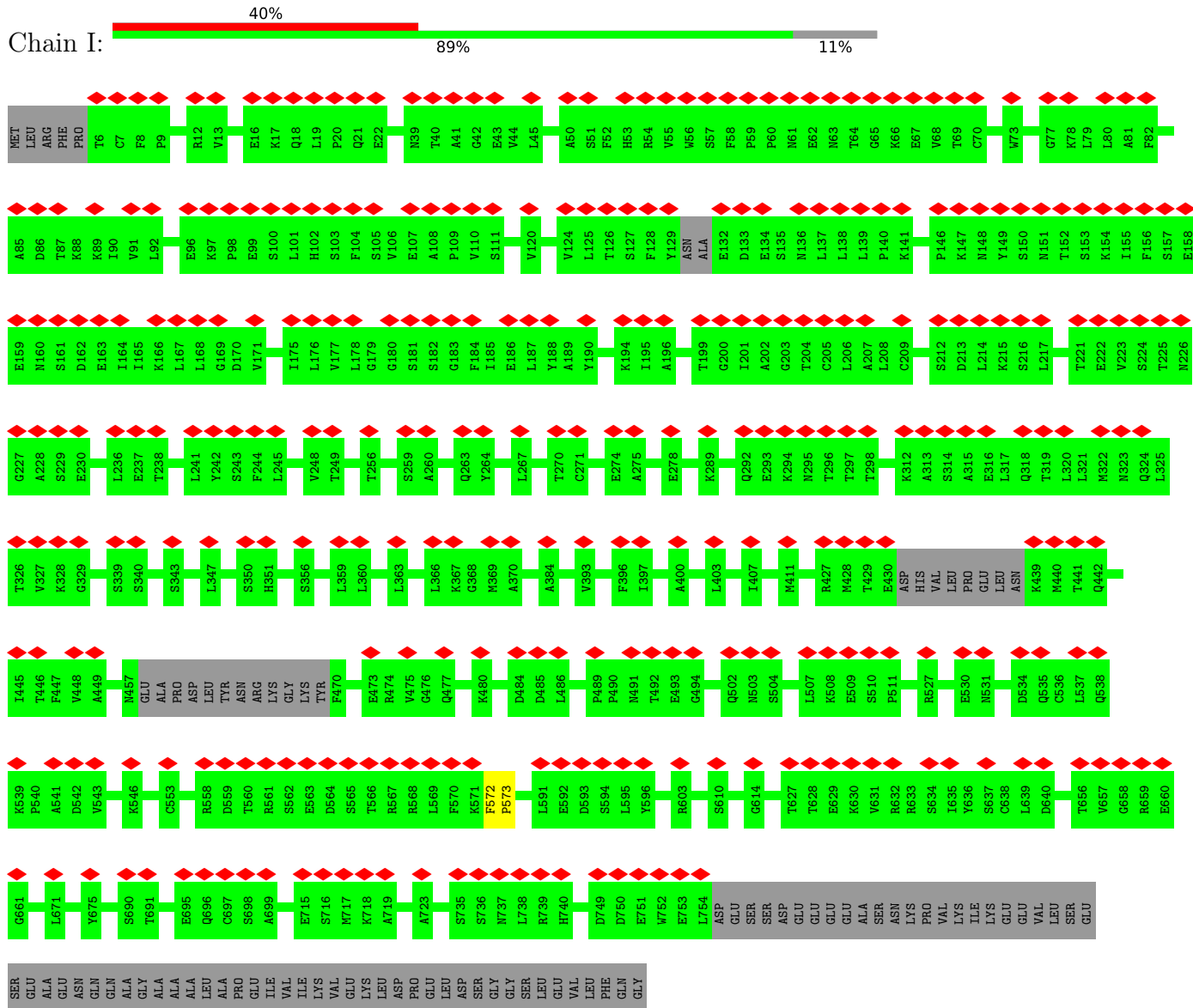
• Molecule 7: Anaphase-promoting complex subunit CDC26



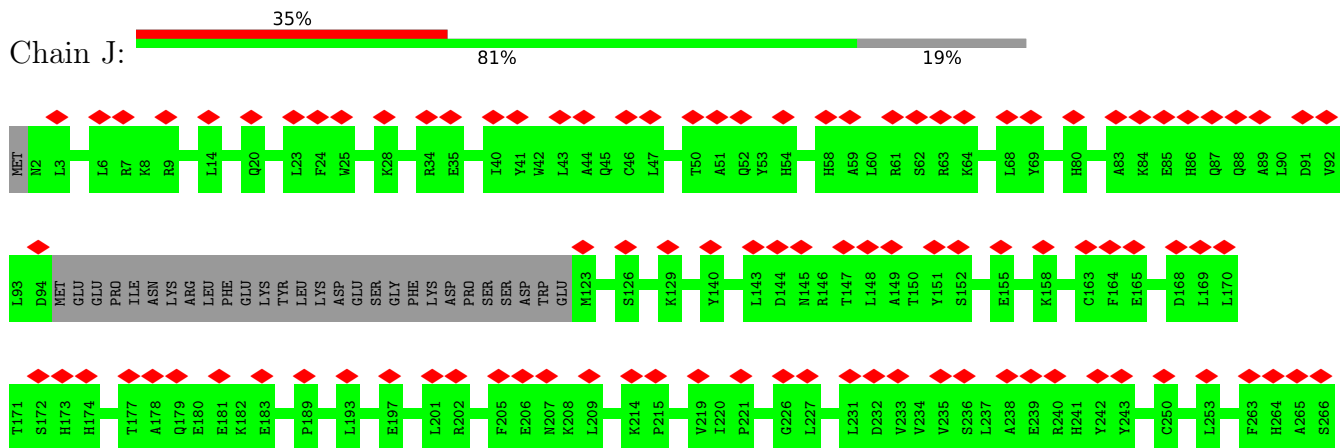
• Molecule 7: Anaphase-promoting complex subunit CDC26

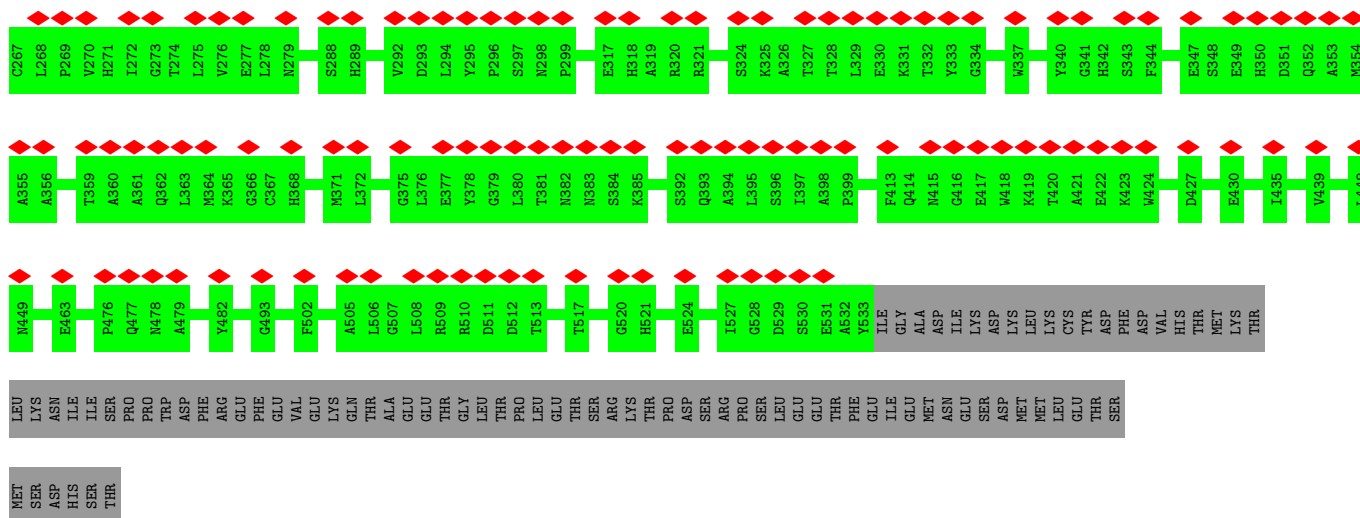


• Molecule 8: Anaphase-promoting complex subunit 4

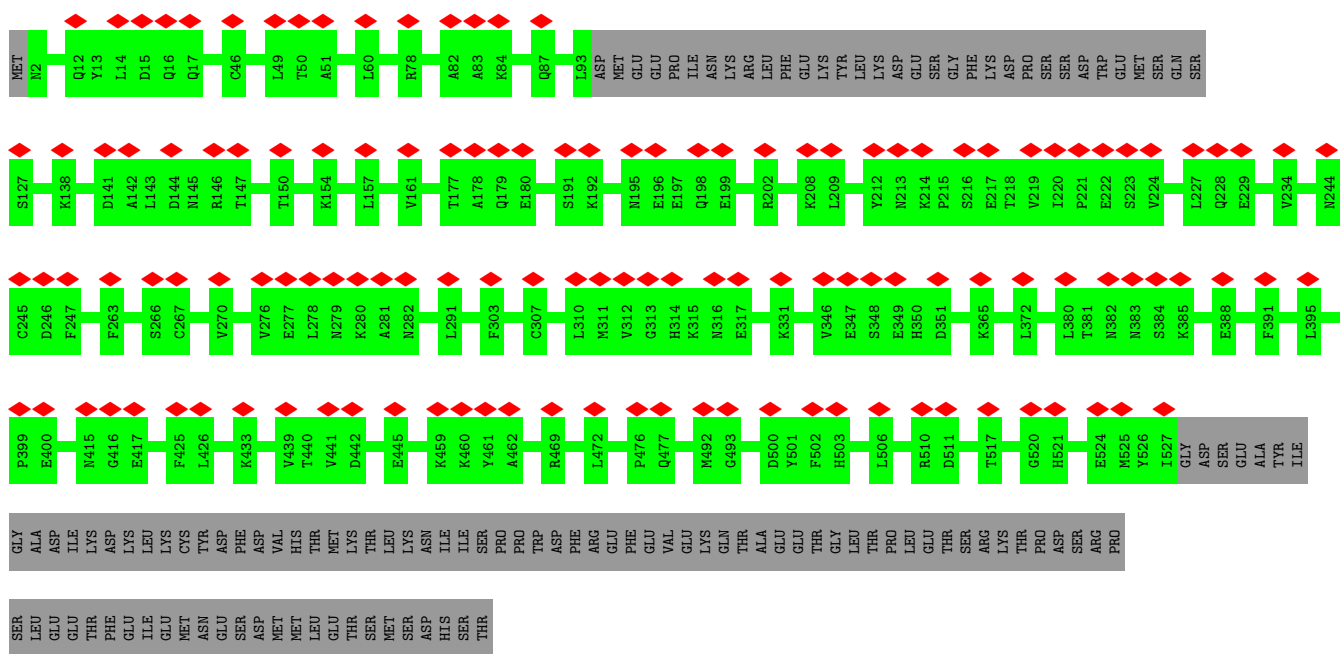
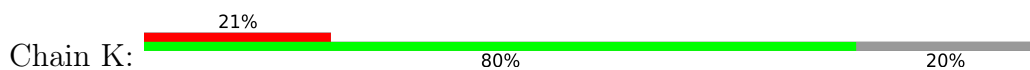


• Molecule 9: Cell division cycle protein 16 homolog

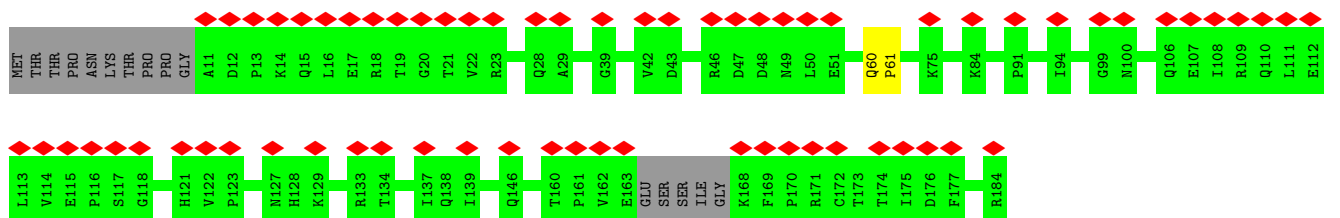
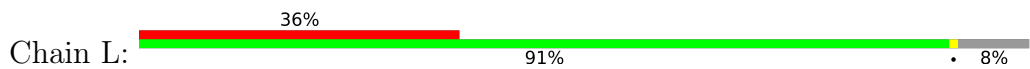




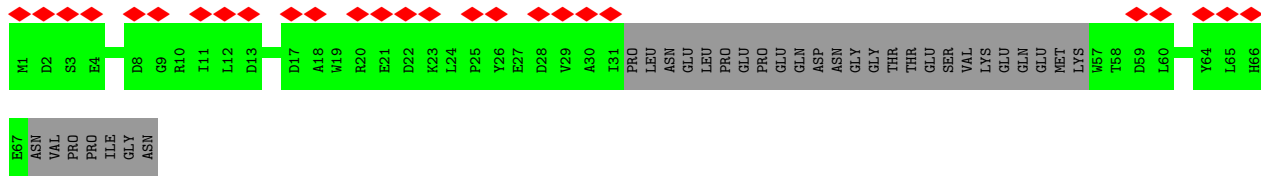
• Molecule 9: Cell division cycle protein 16 homolog



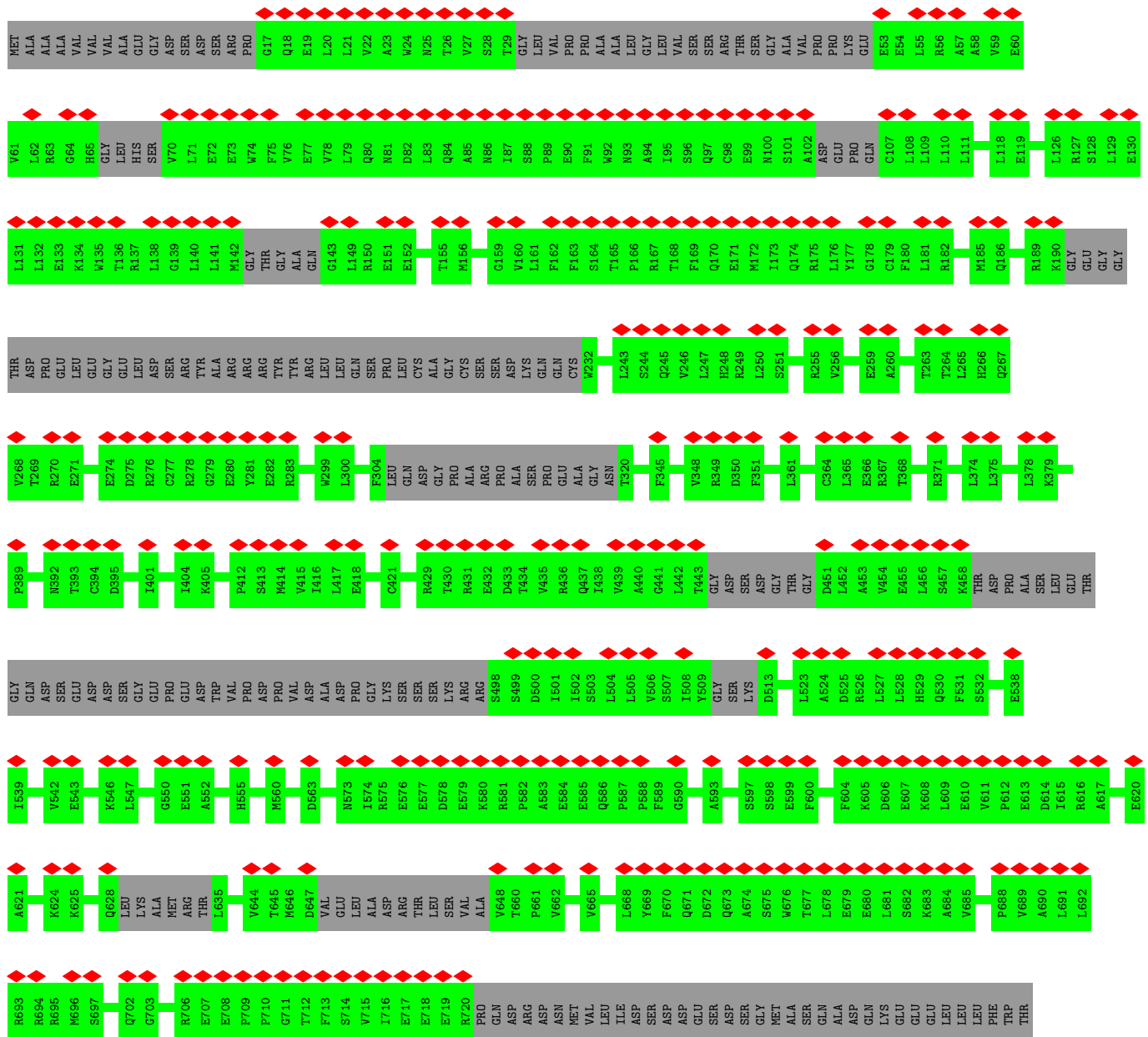
• Molecule 10: Anaphase-promoting complex subunit 10

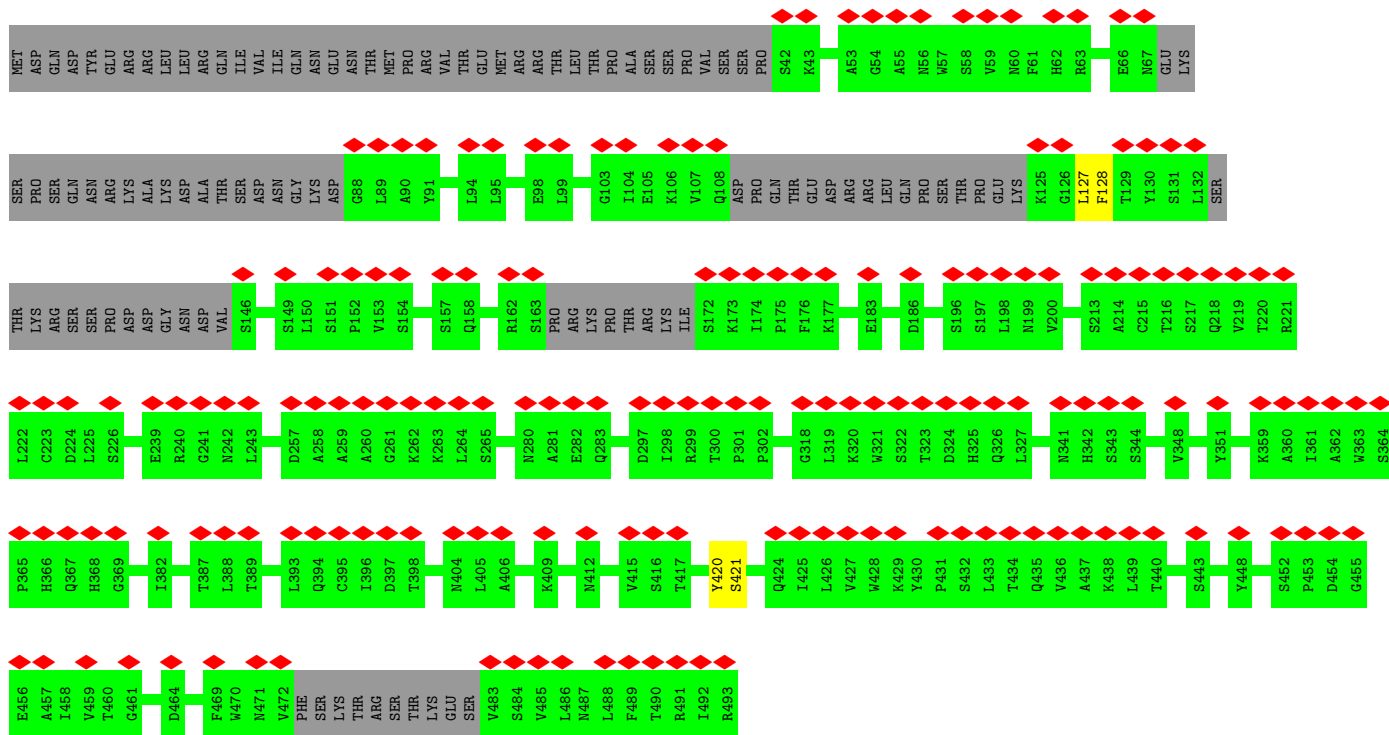


- Molecule 11: Anaphase-promoting complex subunit 13

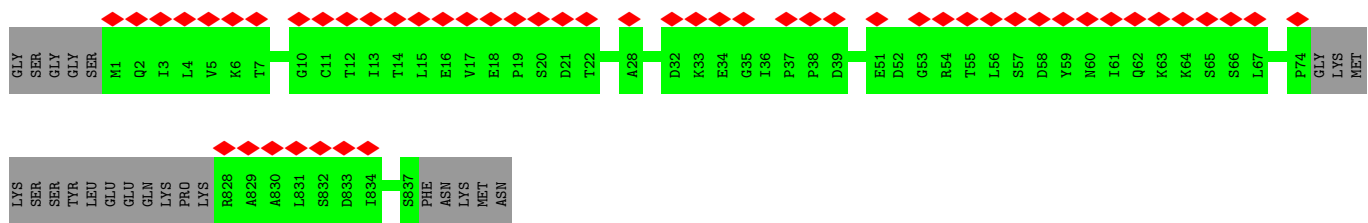
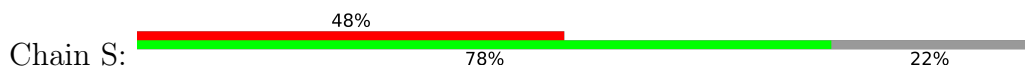


- Molecule 12: Anaphase-promoting complex subunit 2

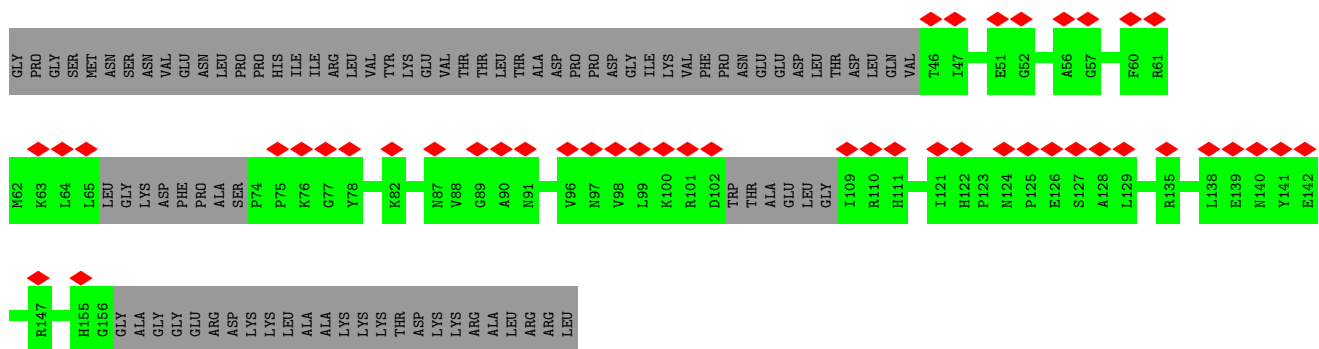




• Molecule 15: Ubiquitin_variant-Hsl1(substrate) fusion



• Molecule 16: Ubiquitin-conjugating enzyme E2 S



• Molecule 17: Anaphase-promoting complex subunit 7

LEU
LEU
ARG
ASN
ALA
THR
LEU
ALA
ASN
GLN
SER
ASP
CYS
VAL
LEU
HIS
SER
ARG
ILE
LEU
GLY
GLY
ASP
PHE
LEU
VAL
VAL
ALA
VAL
ASN
GLU
TYR
GLN
GLN
ALA
GLU
ALA
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ASP
GLN
TYR
SER
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GLU
ALA
ALA
GLN
TRP
ALA
ASP
GLN
TYR
GLU
GLN
TRP
PHE
GLY
MET
GLN

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	135578	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.206	Depositor
Minimum map value	-0.089	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.065	Depositor
Map size (Å)	401.92, 401.92, 401.92	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.57, 1.57, 1.57	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	1380	0	0	3	0
2	B	68	0	0	0	0
3	C	475	0	0	1	0
3	P	443	0	0	1	0
4	D	55	0	0	0	0
5	E	56	0	0	0	0
6	F	482	0	0	0	0
6	H	483	0	0	0	0
7	G	25	0	0	0	0
7	W	25	0	0	0	0
8	I	727	0	0	1	0
9	J	504	0	0	0	0
9	K	493	0	0	0	0
10	L	170	0	0	1	0
11	M	42	0	0	0	0
12	N	546	0	0	0	0
13	O	685	0	0	1	0
14	R	385	0	0	2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	S	84	0	0	0	0
16	T	97	0	0	0	0
17	X	397	0	0	0	0
17	Y	416	0	0	0	0
All	All	8038	0	0	10	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 1.

All (10) 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)
14:R:420:TYR:CA	14:R:421:SER:CA	2.81	0.59
1:A:1670:GLY:CA	1:A:1671:PRO:CA	2.84	0.54
14:R:127:LEU:CA	14:R:128:PHE:CA	2.92	0.48
3:P:361:ASN:CA	3:P:362:PRO:CA	2.92	0.47
1:A:1100:LEU:CA	1:A:1101:PRO:CA	2.93	0.46
10:L:60:GLN:CA	10:L:61:PRO:CA	2.93	0.46
3:C:361:ASN:CA	3:C:362:PRO:CA	2.97	0.43
8:I:572:PHE:CA	8:I:573:PRO:CA	2.96	0.42
13:O:123:GLU:CA	13:O:124:PRO:CA	2.99	0.41
1:A:1112:PRO:CA	1:A:1113:PRO:CA	2.99	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

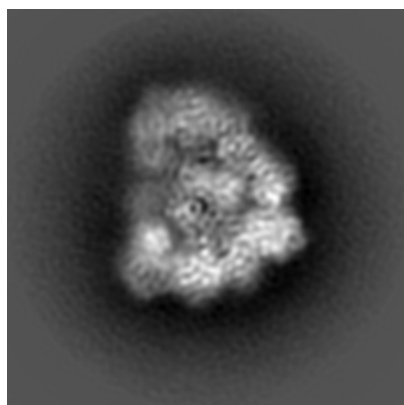
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3433. These allow visual inspection of the internal detail of the map and identification of artifacts.

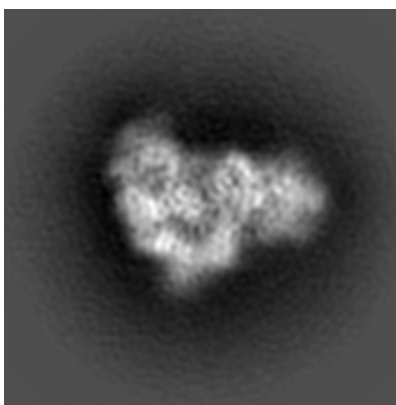
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

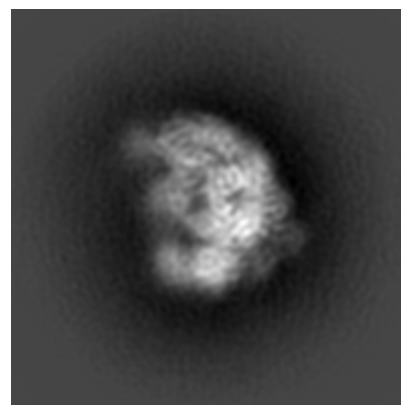
6.1.1 Primary map



X



Y

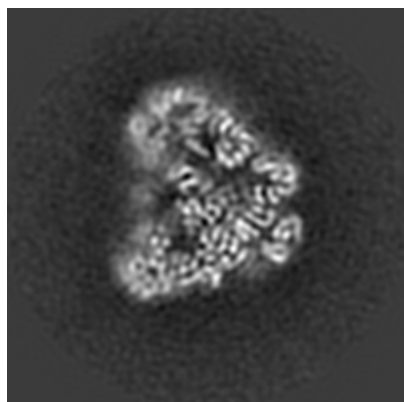


Z

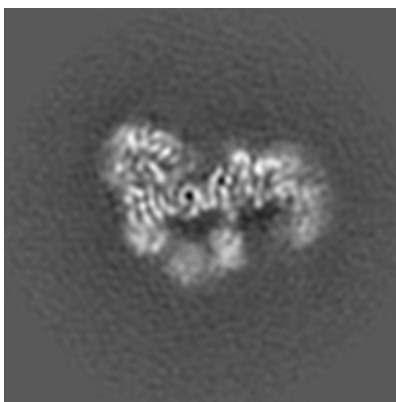
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

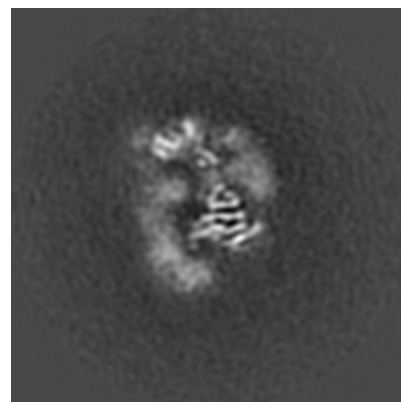
6.2.1 Primary map



X Index: 128



Y Index: 128

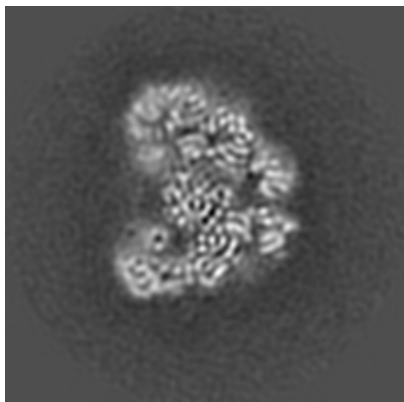


Z Index: 128

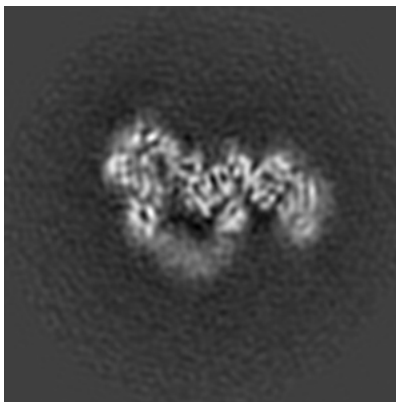
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

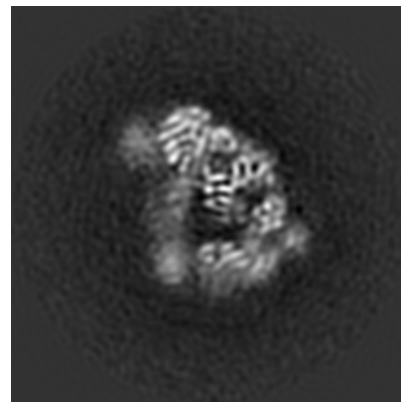
6.3.1 Primary map



X Index: 134



Y Index: 121

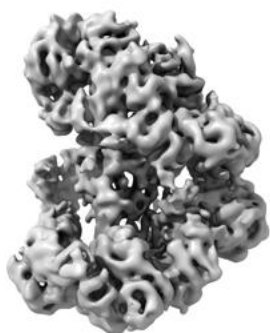


Z Index: 104

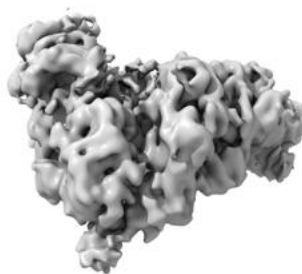
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

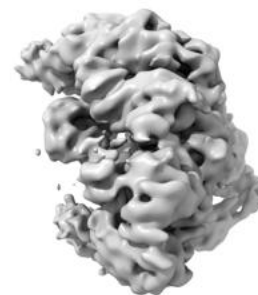
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.065. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

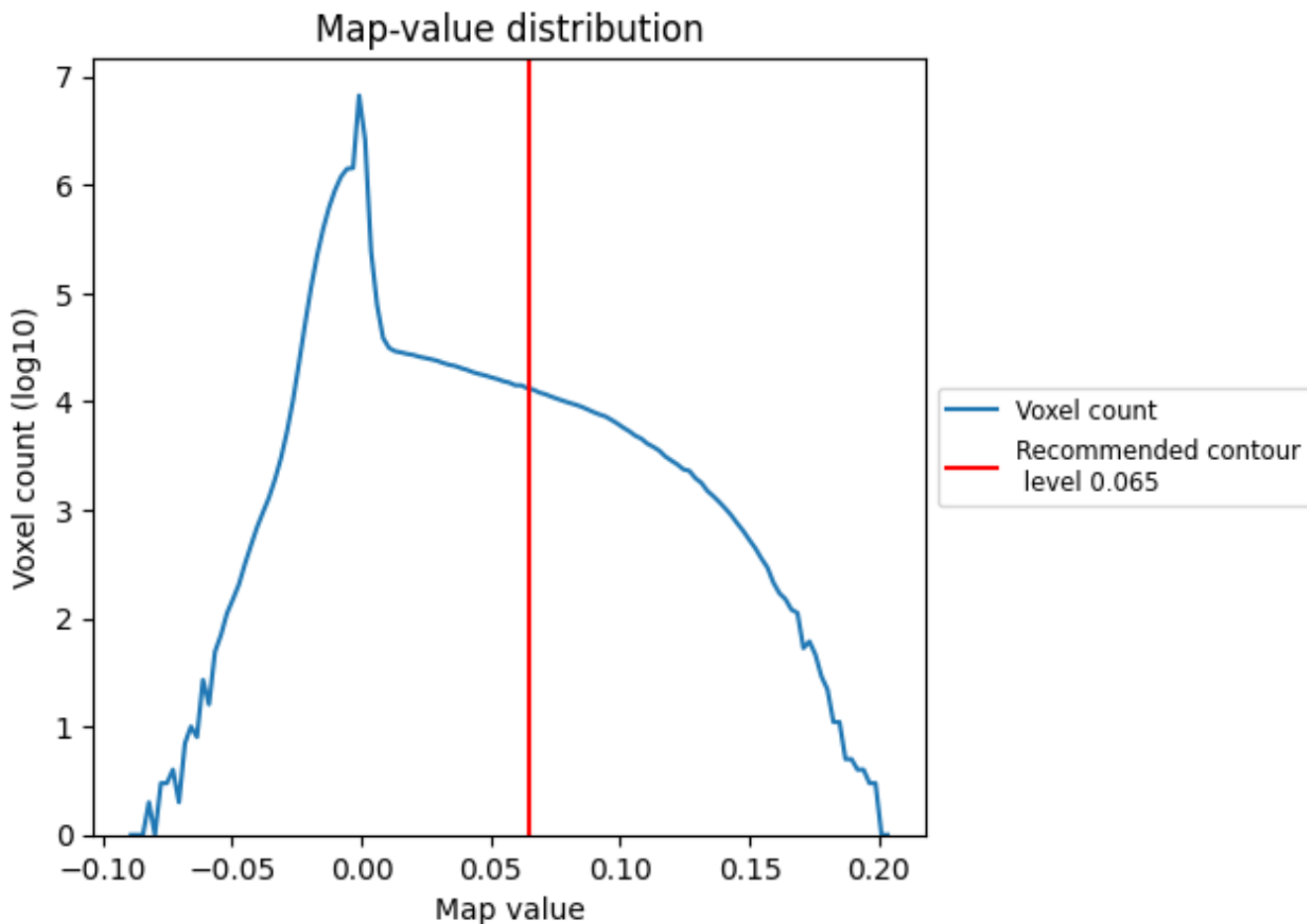
6.5 Mask visualisation

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

7 Map analysis [i](#)

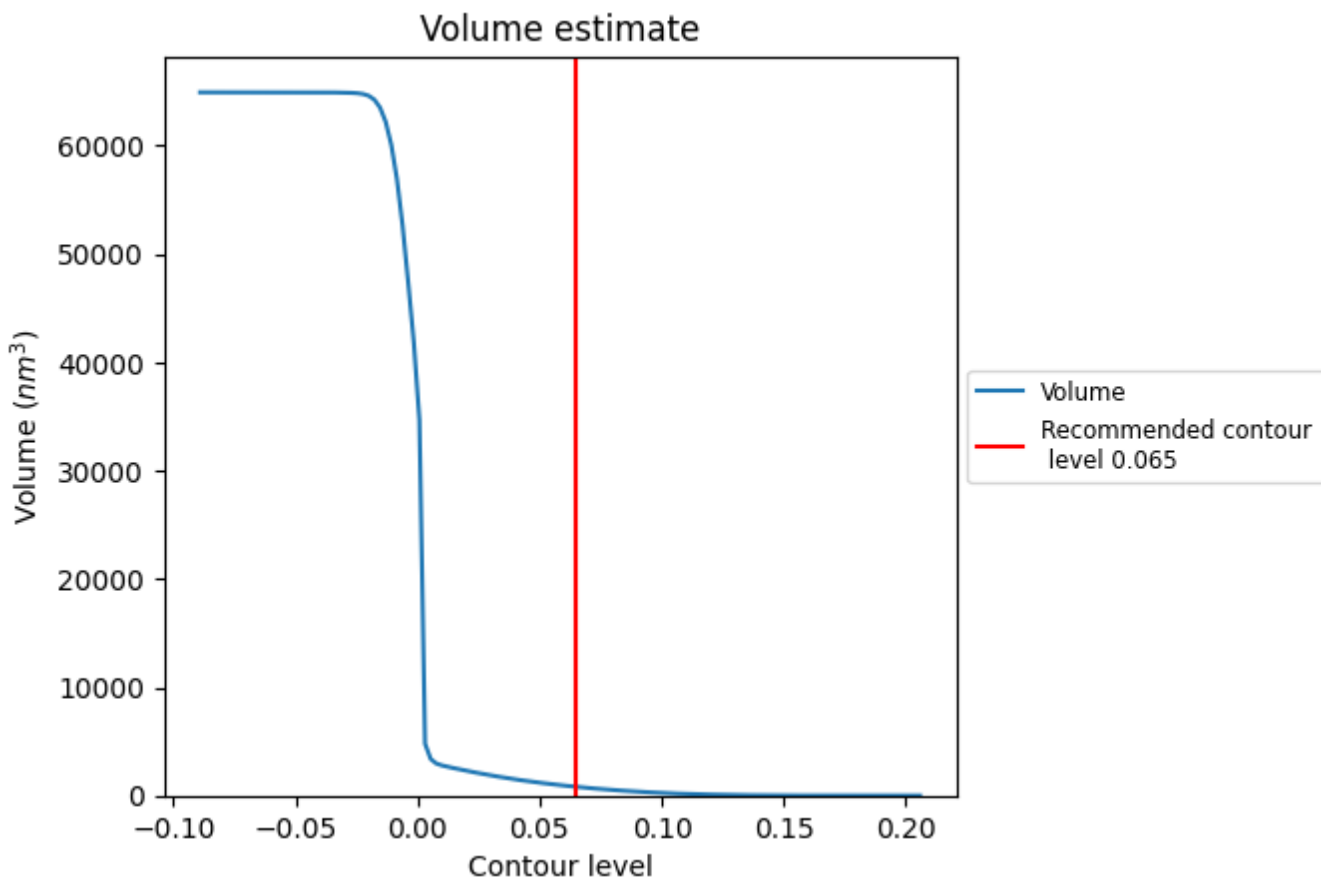
This section contains the results of statistical analysis of the map.

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.

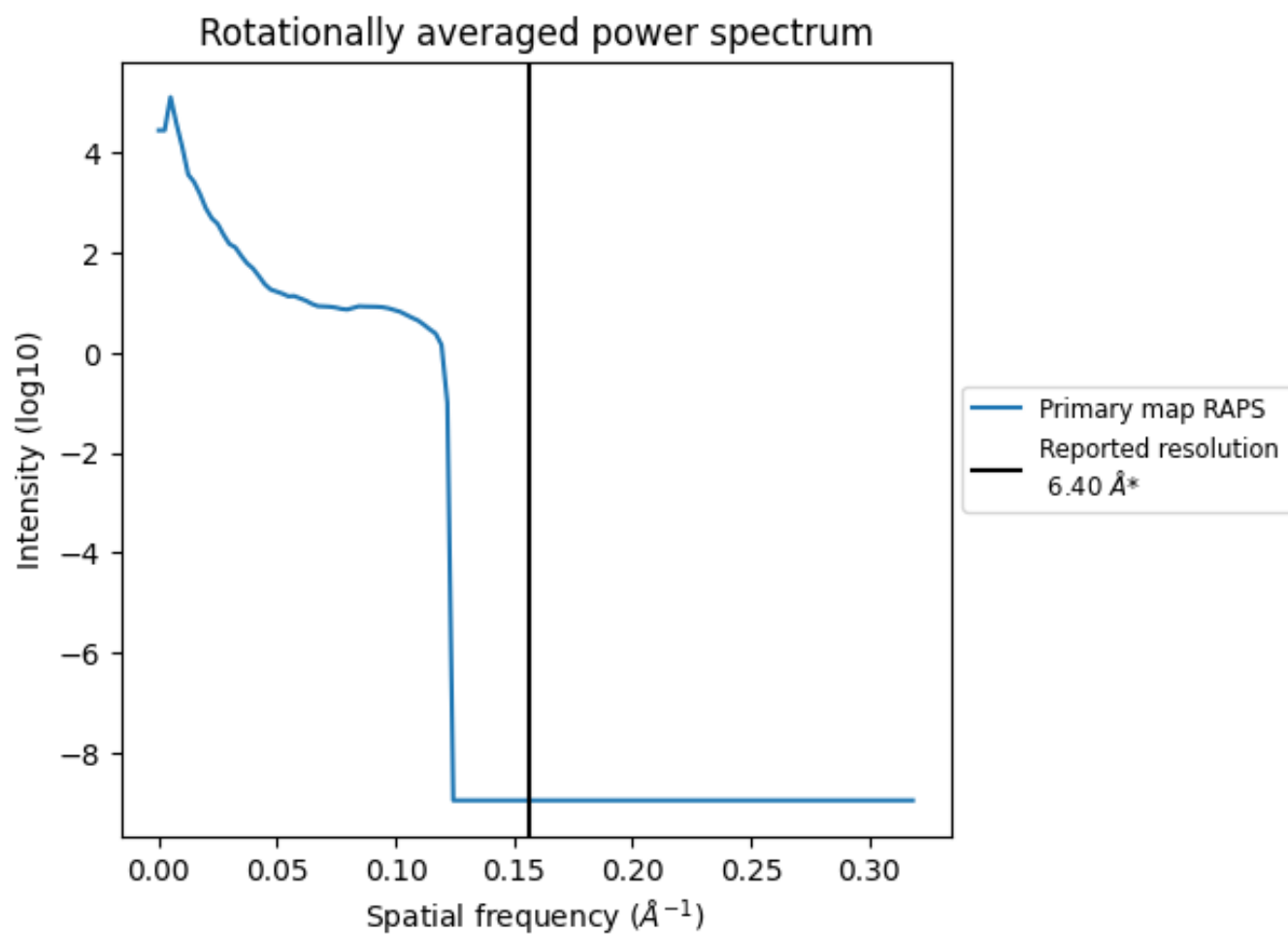
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 807 nm³; this corresponds to an approximate mass of 729 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.156\AA^{-1}

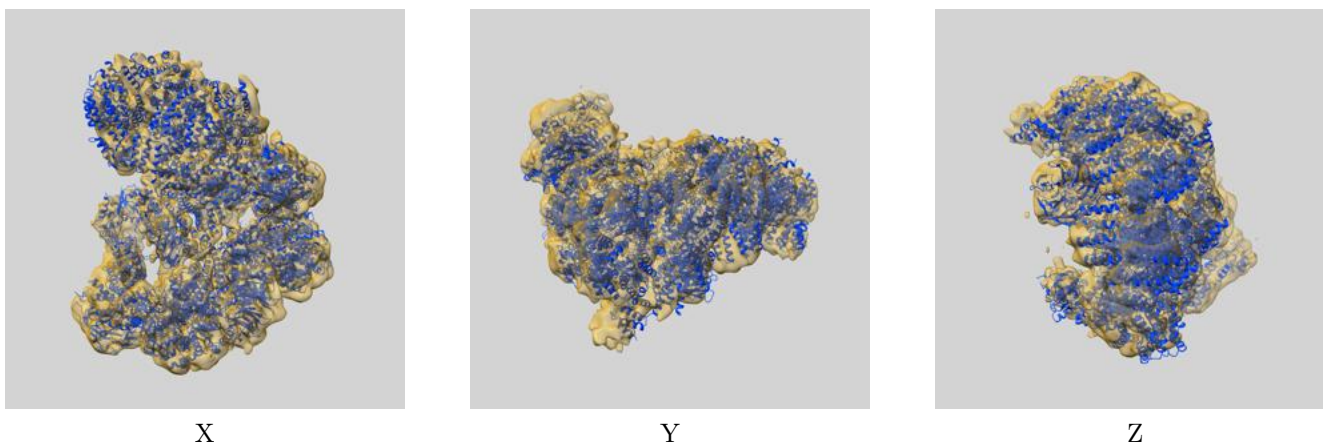
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

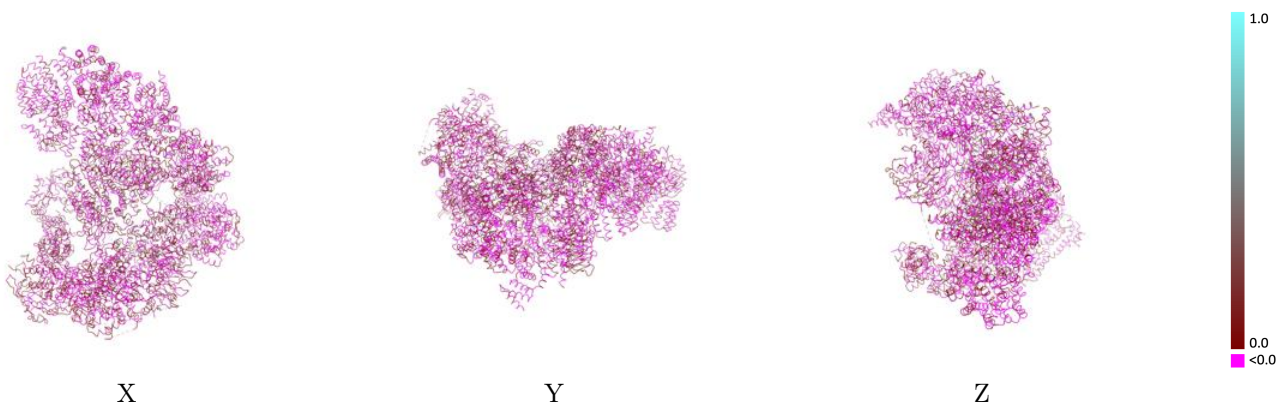
This section contains information regarding the fit between EMDB map EMD-3433 and PDB model 5L9T. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlay [i](#)



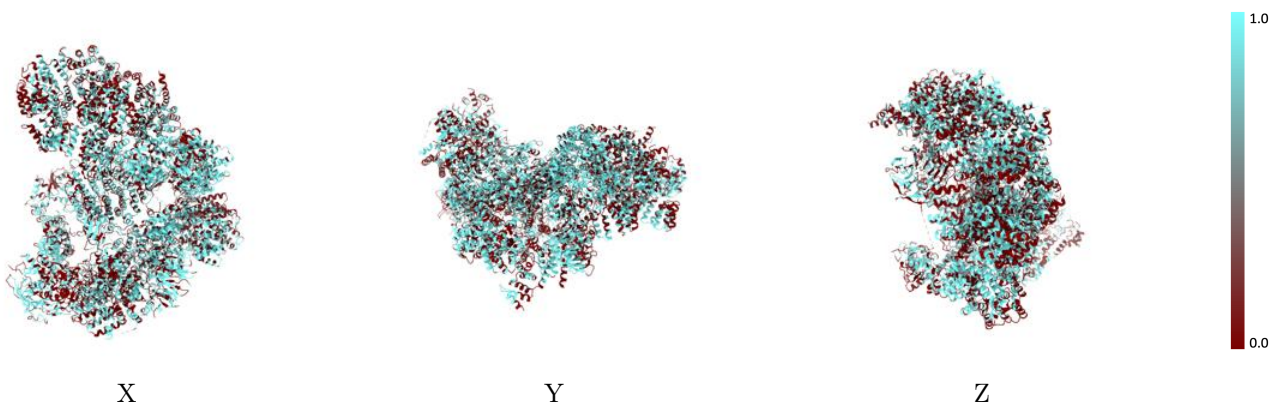
The images above show the 3D surface view of the map at the recommended contour level 0.065 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



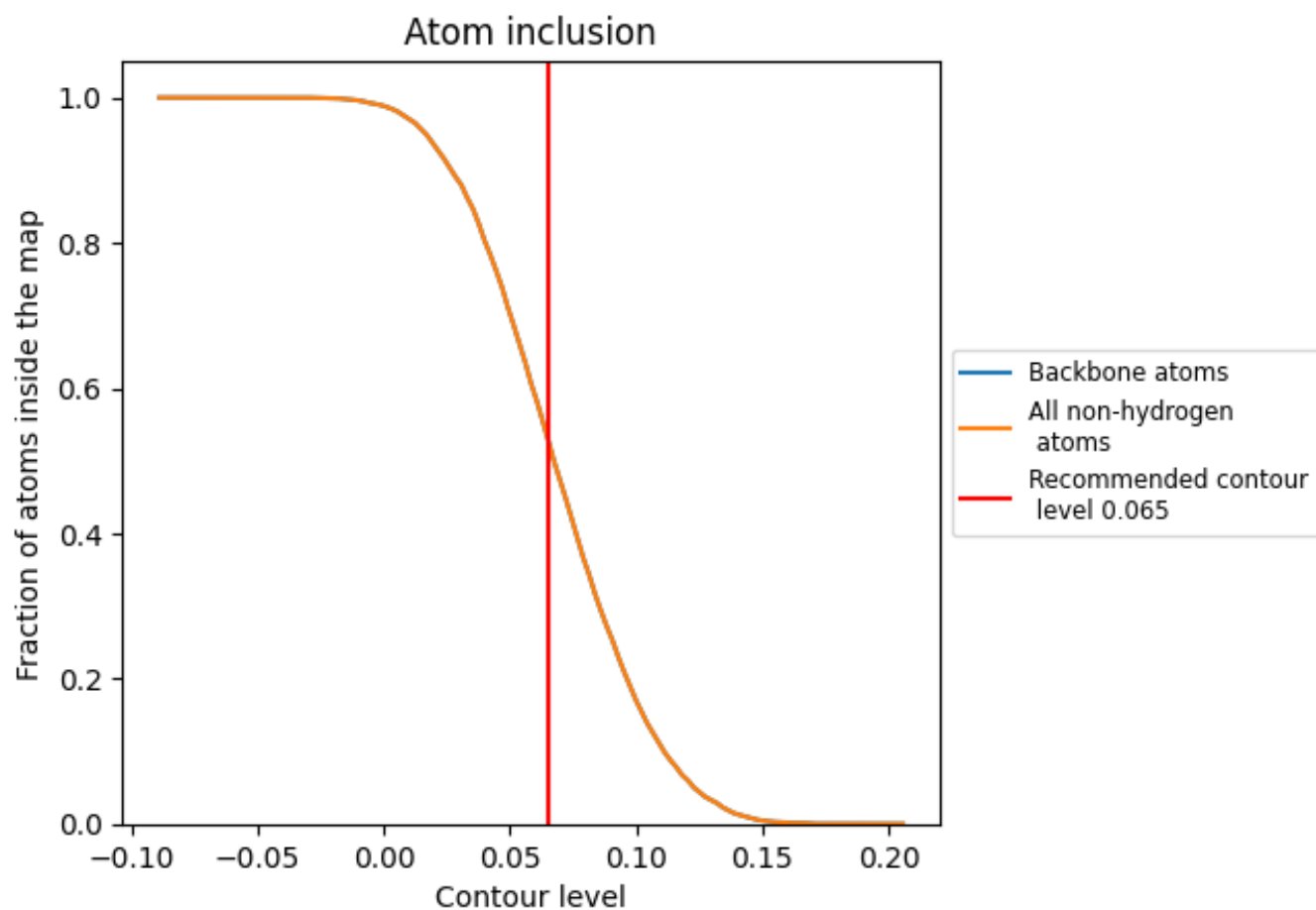
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.065).















































9.4 Atom inclusion [i](#)



At the recommended contour level, 53% of all backbone atoms, 53% 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 (0.065) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5300	 0.0200
A	 0.5029	 0.0460
B	 0.7353	 0.0960
C	 0.6295	 0.0360
D	 0.2545	 0.0010
E	 0.4286	 -0.0170
F	 0.5207	 -0.0290
G	 0.0800	 -0.1230
H	 0.5052	 -0.0140
I	 0.5516	 0.0420
J	 0.5694	 -0.0200
K	 0.7383	 0.0700
L	 0.6059	 0.0710
M	 0.3810	 0.0660
N	 0.4377	 0.0370
O	 0.5036	 0.0180
P	 0.4808	 -0.0420
R	 0.5403	 0.0320
S	 0.3810	 0.0450
T	 0.5258	 0.0410
W	 0.6400	 0.1460
X	 0.4559	 -0.0220
Y	 0.5433	 -0.0000

