



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 03:34 AM UTC

PDB ID : 6TM5 / pdb_00006tm5
EMDB ID : EMD-10518
Title : Cryo-EM structure of the Anaphase-promoting complex/Cyclosome, in complex with the Nek2A substrate at 3.9 angstrom resolution
Authors : Alfieri, C.; Barford, D.
Deposited on : 2019-12-03
Resolution : 3.90 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

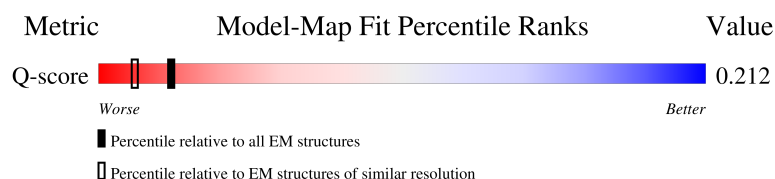
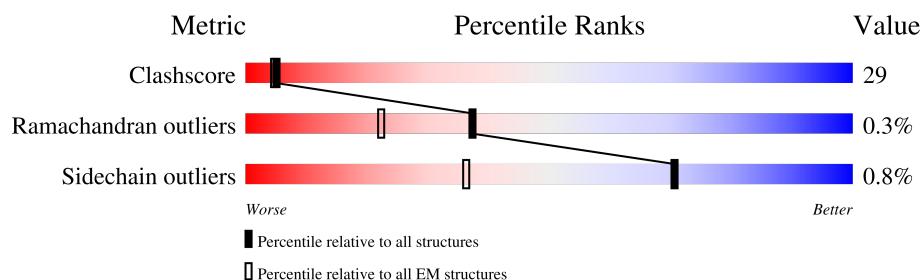
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	8855 (3.40 - 4.40)

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	

Continued on next page...

Continued from previous page...

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	
16	S	445	
17	Q	445	

2 Entry composition [i](#)

There are 18 unique types of molecules in this entry. The entry contains 63885 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		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	356	PHE	PRO	conflict	UNP Q9H1A4

- 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	736	Total	C	N	O	S	0	0
			5726	3676	957	1059	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	676	Total	C	N	O	S	0	0
			5337	3425	943	944	25		

- 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 Apc1 loop.

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 a protein called Serine/threonine-protein kinase Nek2.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	S	2	Total	C	N	O	S	0	0
			19	11	5	2	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	449	ALA	MET	conflict	UNP P51955

- Molecule 17 is a protein called Serine/threonine-protein kinase Nek2.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	3	Total	C	N	O	S	0	0
			23	13	6	3	1		

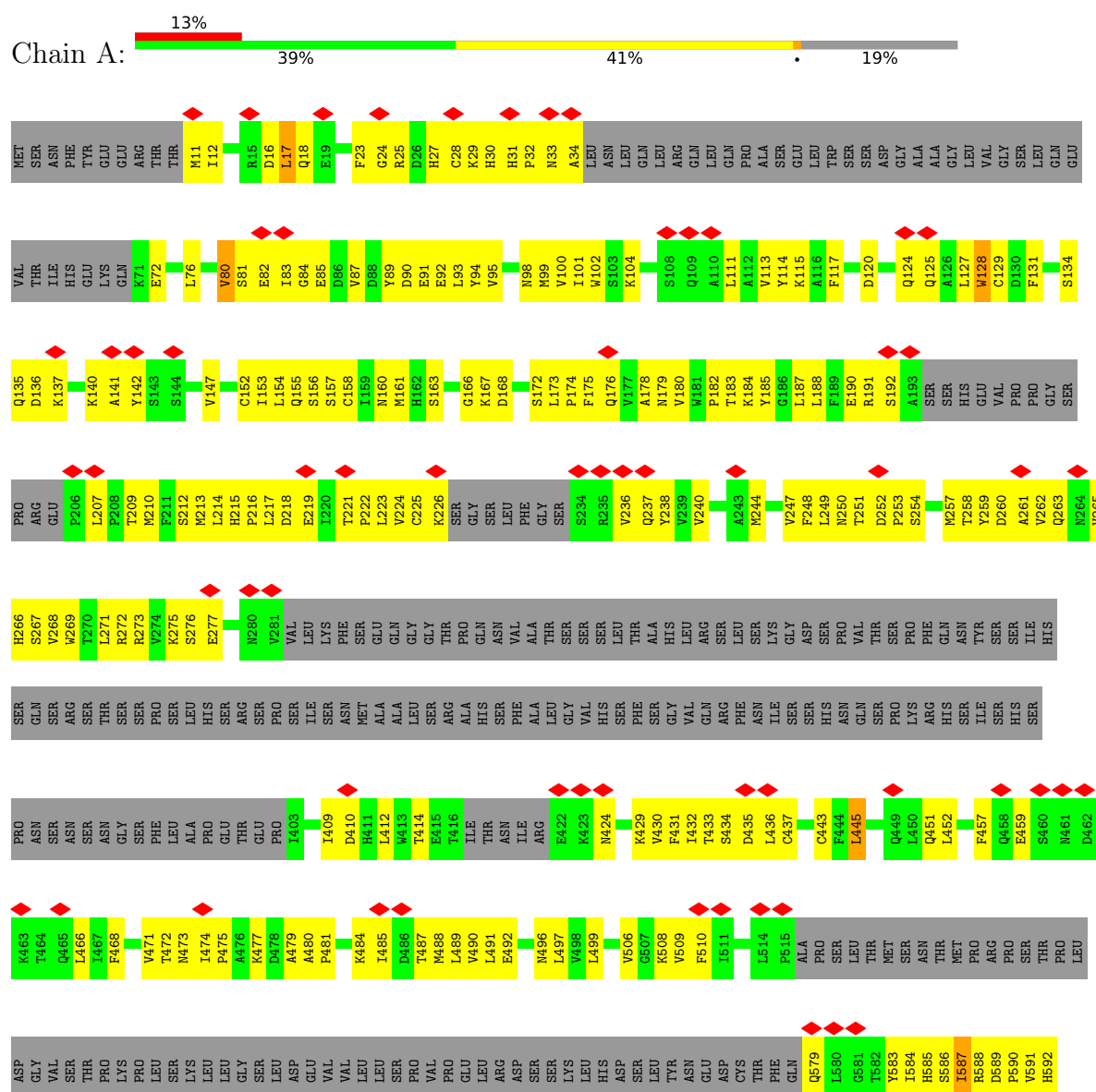
- Molecule 18 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

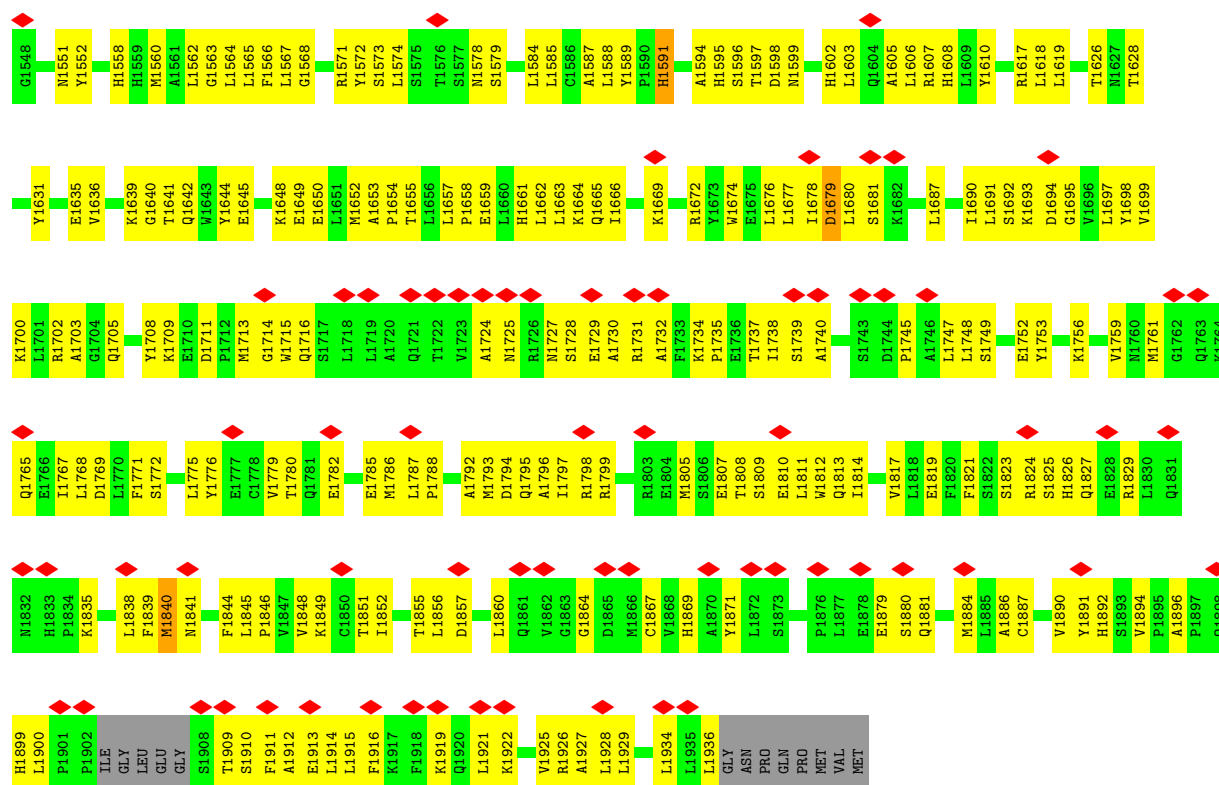
3 Residue-property plots

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



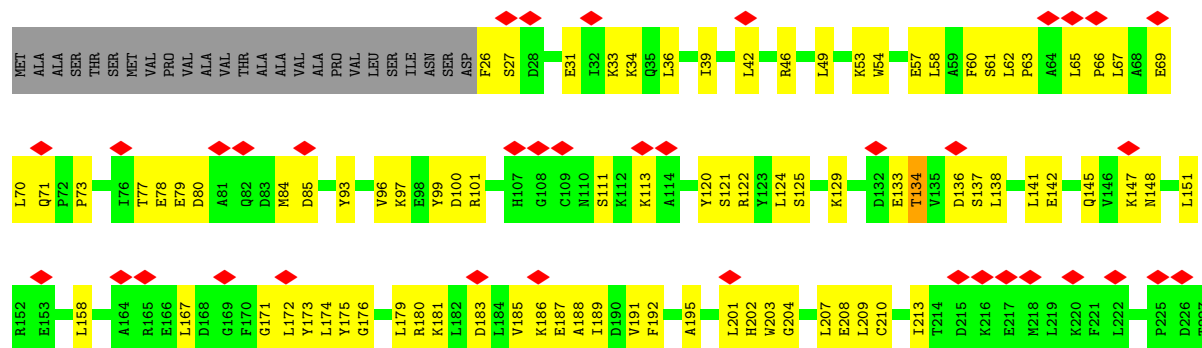
S1458	S1459	S1460	H1461	V1462	Y1463	H1464	H1465	G1473	E1480	N1481	L1482	S1483	L1488	H1489	L1493	D1494	F1495	N1503	A1504	S1505	V1506	T1507	G1508	P1509	H1510	N1511	L1512	C1515	V1519	L1520	L1521	S1522	L1523	A1524	M1525	V1526	M1527	A1528	L1533	K1534	V1535	L1536	Q1537	L1538	C1539	R1540	F1541	L1542	T1546	G1547				
M1379	N1380	S1382	D1386	V1386	L1387	R1388	D1391	L1395	F1398	E1402	F1403	L1404	L1405	L1406	L1409	A1410	R1411	C1412	L1413	L1414	L1419	L1420	P1421	W1425	S1428	Q1432	I1433	I1434	R1435	I1439	SER	LEU	SER	GLU	ILE	GLU	GLU	LEU	PRO	CYS	SER	GLU	ASP	L14452	E14455	L14456	L1457							
C1306	L1307	S1311	M1312	L1313	G1315	M1316	L1319	M1320	P1321	V1322	E1323	Q1324	L1325	Y1326	Q1327	Y1328	M1329	H1333	ARG	PHE	GLN	THR	GLY	MET	HIS	ARG	GLY	LYS	HIS	S1347	P1348	S1349	G1355	D1356	T1357	V1360	C1364	P1365	T1368	L1369	A1370	L1371	M1372	L1373	I1374	Y1375	K1376	K1377	L1378					
P1149	A1150	S1151	Q1152	I1153	D1154	S1155	A1156	V1159	Y1160	N1161	K1162	P1163	K1164	H1165	A1166	L1167	L1168	A1169	N1170	E1171	Y1172	L1176	L1181	N1182	G1183	H1184	L1185	T1186	K1187	L1191	N1192	I1193	H1194	D1195	Y1196	L1197	T1198	K1199	G1200	H1201	E1202	M1203	T1204	S1205	L1206	G1207	L1208	L1209	L1210	L1217	D1221	M1222		
S1223	R1226	L1227	L1228	S1229	I1230	P1233	P1238	T1239	S1240	T1241	E1242	L1243	D1244	M1248	V1251	G1256	L1259	W1260	Y1261	T1264	A1265	H1266	R1267	H1268	V1272	L1273	L1274	A1275	E1276	R1279	P1280	P1281	P1283	E1284	Y1287	C1288	T1289	D1290	L1291	E1292	L1300	A1301	L1302	G1303	M1304	V1305								
C1306	L1307	S1311	M1312	L1313	G1315	M1316	L1319	M1320	P1321	V1322	E1323	Q1324	L1325	Y1326	Q1327	Y1328	M1329	H1333	ARG	PHE	GLN	THR	GLY	MET	HIS	ARG	GLY	LYS	HIS	S1347	P1348	S1349	G1355	D1356	T1357	V1360	C1364	P1365	T1368	L1369	A1370	L1371	M1372	L1373	I1374	Y1375	K1376	K1377	L1378					
M1379	N1380	S1382	D1386	V1386	L1387	R1388	D1391	L1395	F1398	E1402	F1403	L1404	L1405	L1406	L1409	A1410	R1411	C1412	L1413	L1414	L1419	L1420	P1421	W1425	S1428	Q1432	I1433	I1434	R1435	I1439	SER	LEU	SER	GLU	ILE	GLU	GLU	LEU	PRO	CYS	SER	GLU	ASP	L14452	E14455	L14456	L1457							
P1149	A1150	S1151	Q1152	I1153	D1154	S1155	A1156	V1159	Y1160	N1161	K1162	P1163	K1164	H1165	A1166	L1167	L1168	A1169	N1170	E1171	Y1172	L1176	L1181	N1182	G1183	H1184	L1185	T1186	K1187	L1191	N1192	I1193	H1194	D1195	Y1196	L1197	T1198	K1199	G1200	H1201	E1202	M1203	T1204	S1205	L1206	G1207	L1208	L1209	L1210	L1217	D1221	M1222		
S1223	R1226	L1227	L1228	S1229	I1230	P1233	P1238	T1239	S1240	T1241	E1242	L1243	D1244	M1248	V1251	G1256	L1259	W1260	Y1261	T1264	A1265	H1266	R1267	H1268	V1272	L1273	L1274	A1275	E1276	R1279	P1280	P1281	P1283	E1284	Y1287	C1288	T1289	D1290	L1291	E1292	L1300	A1301	L1302	G1303	M1304	V1305								
C1306	L1307	S1311	M1312	L1313	G1315	M1316	L1319	M1320	P1321	V1322	E1323	Q1324	L1325	Y1326	Q1327	Y1328	M1329	H1333	ARG	PHE	GLN	THR	GLY	MET	HIS	ARG	GLY	LYS	HIS	S1347	P1348	S1349	G1355	D1356	T1357	V1360	C1364	P1365	T1368	L1369	A1370	L1371	M1372	L1373	I1374	Y1375	K1376	K1377	L1378					
M1379	N1380	S1382	D1386	V1386	L1387	R1388	D1391	L1395	F1398	E1402	F1403	L1404	L1405	L1406	L1409	A1410	R1411	C1412	L1413	L1414	L1419	L1420	P1421	W1425	S1428	Q1432	I1433	I1434	R1435	I1439	SER	LEU	SER	GLU	ILE	GLU	GLU	LEU	PRO	CYS	SER	GLU	ASP	L14452	E14455	L14456	L1457							
S1458	S1459	S1460	H1461	V1462	Y1463	H1464	H1465	G1473	E1480	N1481	L1482	S1483	L1488	H1489	L1493	D1494	F1495	N1503	A1504	S1505	V1506	T1507	G1508	P1509	H1510	N1511	L1512	C1515	V1519	L1520	L1521	S1522	L1523	A1524	M1525	V1526	M1527	A1528	L1533	K1534	V1535	L1536	Q1537	L1538	C1539	R1540	F1541	L1542	T1546	G1547				
MET	LYS	ASP	GLU	PHE	ASP	GLN	ASN	ASN	PHE	ASP	PHE	GLY	SER	LEU	SER	VAL	ILE	ALA	PRO	LYS	ALA	ARG	PRO	SER	GLU	THR	GLY	SER	D704	W707	L710	L711	N712	S713	D714	Y715	H716	V719	H722	L723	L724	N725	C729	L730	S731	PRO	SER	GLU	ALA	SER	GLN			
Y802	Y803	D804	H805	R808	D809	L813	V814	R815	T816	T817	G818	Q819	V820	C821	F822	C821	L822	Q823	A824	I825	K826	F827	I828	E832	I833	Q836	M837	L838	V839	K840	W841	V844	A847	P848	G849	G850	P851	S852	Y853	E856	M857	N858	L859	F860	V861	T862	C863							
E868	R869	S870	R871	L872	V873	L875	S876	L877	A878	L879	Y880	I881	L882	S886	L887	VAL	SER	ASP	GLU	S892	S893	Q894	Y895	L896	T897	T899	ILE	ALA	PRO	GLN	LYS	LEU	GLN	VAL	GLU	GLN	GLU	GLU	ASN	ARG	PHE	SER	THR	SER	V923	S924	S925	L926	A927	E928	R929			
L930	Y933	V937	G938	F939	T940	L941	R942	D943	L944	E945	P948	F949	G950	L951	A952	L953	P954	S955	R956	S957	A958	Y960	R963	Q965	P966	A967	S968	D969	Y970	P971	V974	C975	L976	L977	L978	G979	R980	Q981	D982	L983	S984	X985	Q986	A987	N991	L992	P993	LYS	GLY	LYS	SER			
VAL	LEU	SER	SER	ASP	VAL	PRO	SER	THR	GLU	THR	GLU	E1011	E1012	D1013	L1014	G1015	M1016	M1019	I1027	W1028	S1029	E1030	D1031	L1032	R1033	Q1034	Q1035	D1036	V1037	R1038	R1039	L1040	L1041	P1046	V1047	R1048	M1049	N1050	V1051	V1052	Q1053	Y1054	P1055	E1056	L1057	S1058	D1059	H1060	E1061	F1062	I1063	E1064	E1065	E1066
L1070	L1073	C1074	T1077	M1078	A1079	L1080	R1084	G1085	M1086	F1087	T1088	L1089	F1090	S1091	E1098	P1099	L1100	P1101	I1102	P1103	K1104	N1105	L1107	T1108	G1109	R1110	A1111	R1114	N1115	T1116	D1119	L1120	M1121	S1122	G1123	N1124	I1125	D1126	V1127	P1128	P1129	N1130	T1131	T1132	S1133	W1134	H1138	M1139	G1140	V1141				
P1149	A1150	S1151	Q1152	I1153	D1154	S1155	A1156	V1159	Y1160	N1161	K1162	P1163	K1164	H1165	A1166	L1167	L1168	A1169	N1170	E1171	Y1172	L1176	L1181	N1182	G1183	H1184	L1185	T1186	K1187	L1191	N1192	I1193	H1194	D1195	Y1196	L1197	T1198	K1199	G1200	H1201	E1202	M1203	T1204	S1205	L1206	G1207	L1208	L1209	L1210	L1217	D1221	M1222		
S1223	R1226	L1227	L1228	S1229	I1230	P1233	P1238	T1239	S1240	T1241	E1242	L1243	D1244	M1248	V1251	G1256	L1259	W1260	Y1261	T1264	A1265	H1266	R1267	H1268	V1272	L1273	L1274	A1275	E1276	R1279	P1280	P1281	P1283	E1284	Y1287	C1288	T1289	D1290	L1291	E1292	L1300	A1301	L1302	G1303	M1304	V1305								
C1306	L1307	S1311	M1312	L1313	G1315	M1316	L1319	M1320	P1321	V1322	E1323	Q1324	L1325	Y1326	Q1327	Y1328	M1329	H1333	ARG	PHE	GLN	THR	GLY	MET	HIS	ARG	GLY	LYS	HIS	S1347	P1348	S1349	G1355	D1356	T1357	V1360	C1364	P1365	T1368	L1369	A1370	L1371	M1372	L1373	I1374	Y1375	K1376	K1377	L1378					
M1379	N1380	S1382	D1386	V1386	L1387	R1388	D1391	L1395	F1398	E1402	F1403	L1404	L1405	L1406	L1409	A1410	R1411	C1412	L1413	L1414	L1419	L1420	P1421	W1425	S1428	Q1432	I1433	I1434	R1435	I1439	SER	LEU	SER	GLU	ILE	GLU	GLU	LEU	PRO	CYS	SER	GLU	ASP	L14452	E14455	L14456	L1457							
S1458	S1459	S1460	H1461	V1462	Y1463	H1464	H1465	G1473	E1480	N1481	L1482	S1483	L1488	H1489	L1493	D1494	F1495	N1503	A1504	S1505	V1506	T1507	G1508	P1509	H1510	N1511	L1512	C1515	V1519	L1520	L1521	S1522	L1523	A1524	M1525	V1526	M1527	A1528	L1533	K1534	V1535	L1536	Q1537	L1538	C1539	R1540	F1541	L1542	T1546	G1547				



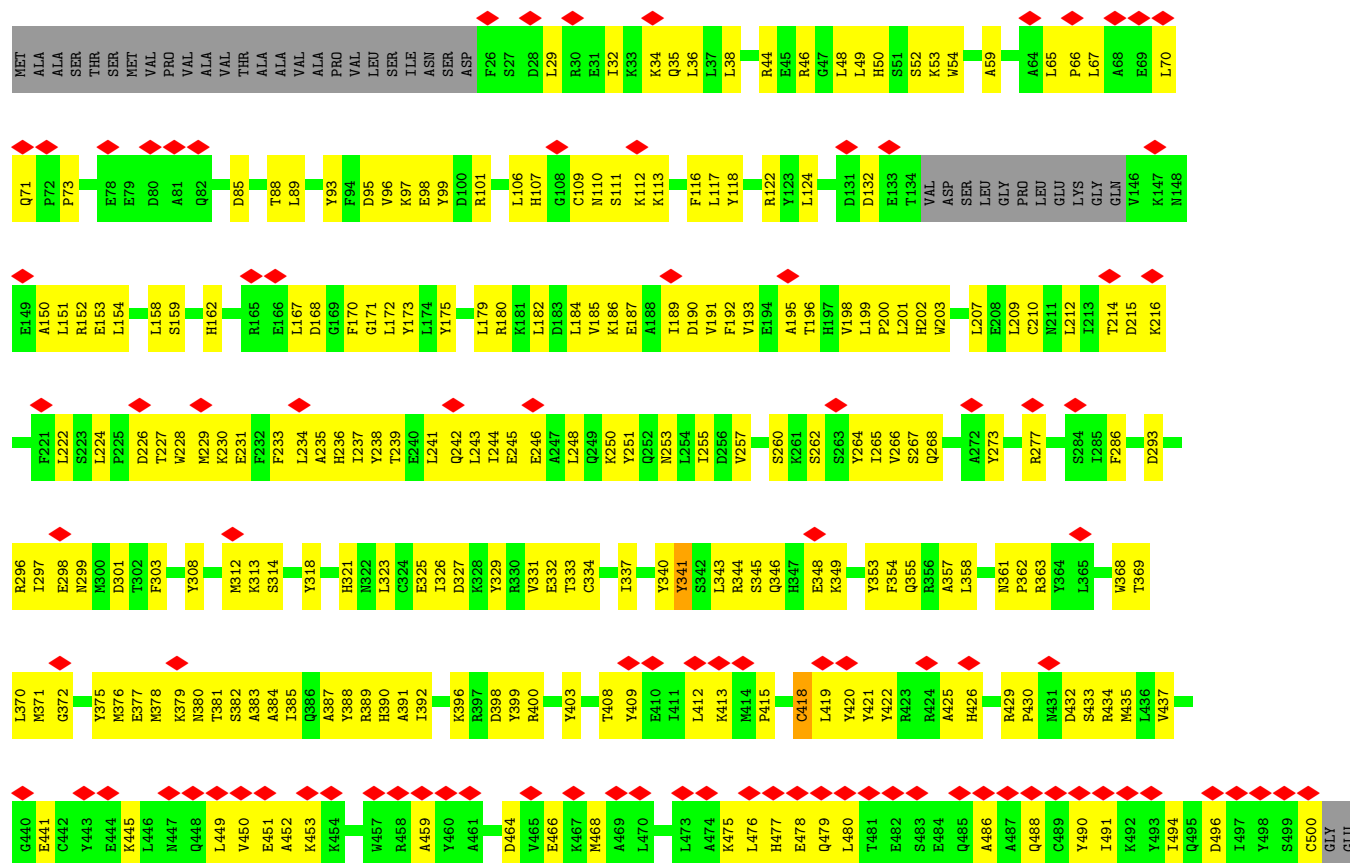
• Molecule 2: Anaphase-promoting complex subunit 11



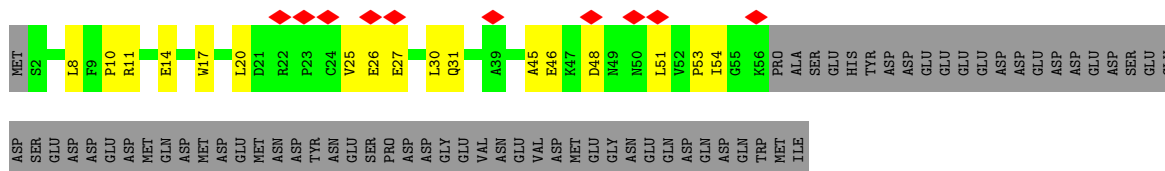
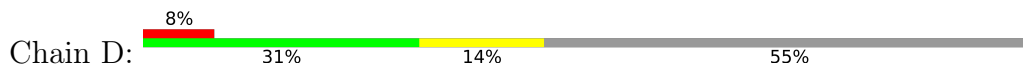
• Molecule 3: Cell division cycle protein 23 homolog



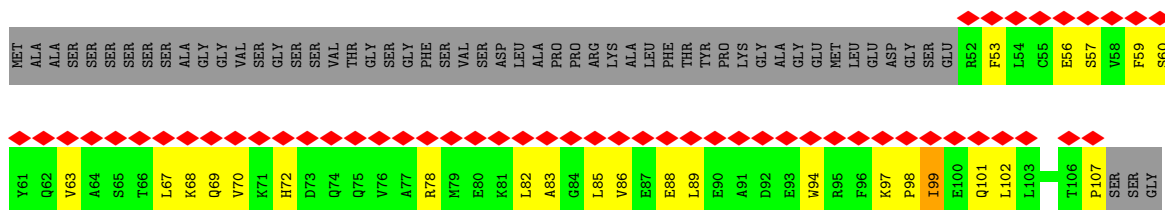
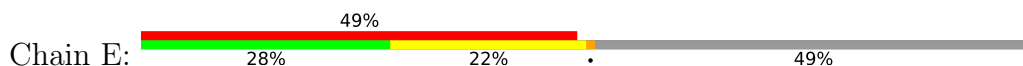
- Molecule 3: Cell division cycle protein 23 homolog



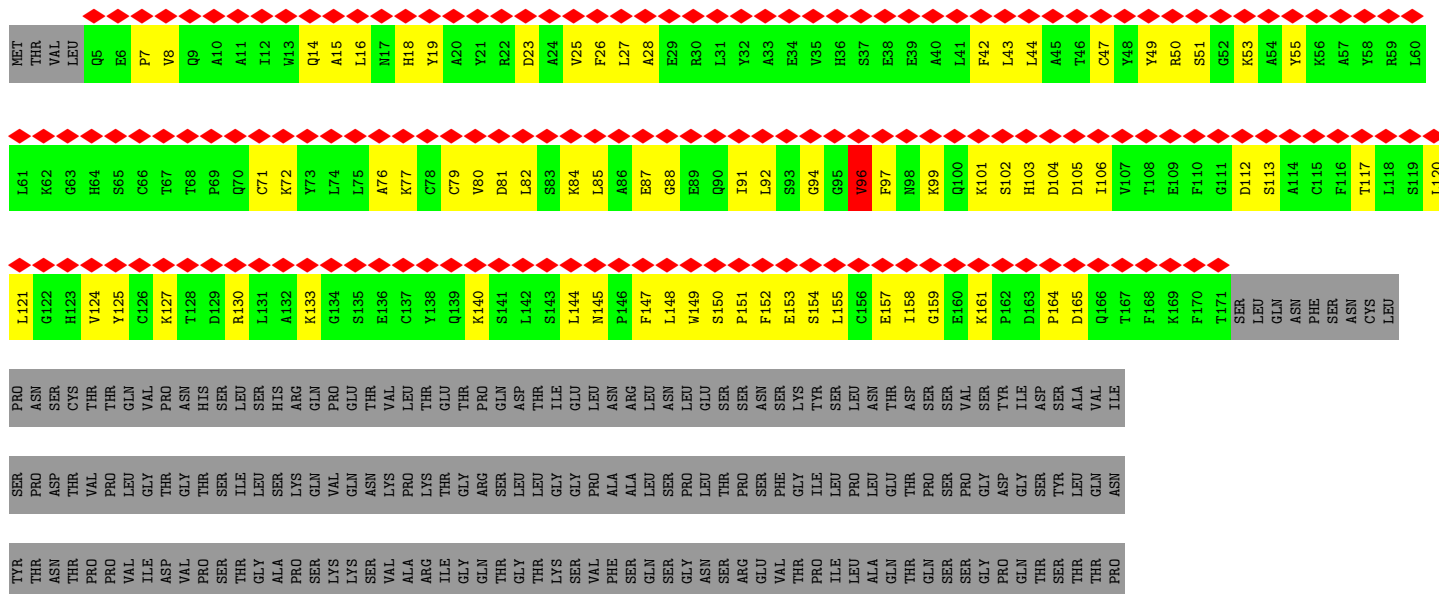
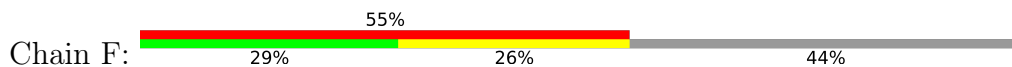
- Molecule 4: Anaphase-promoting complex subunit 15

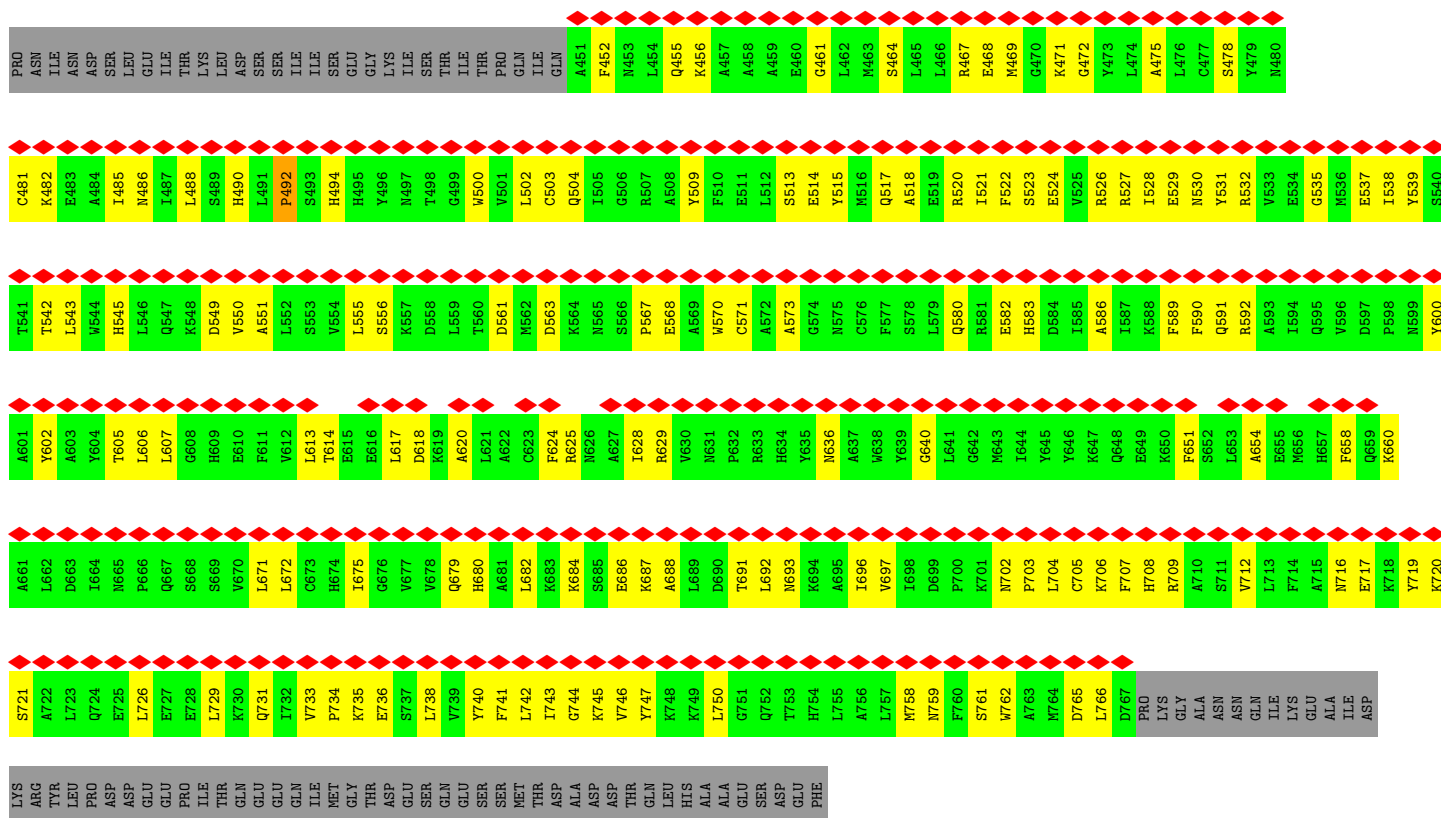


- Molecule 5: Anaphase-promoting complex subunit 16

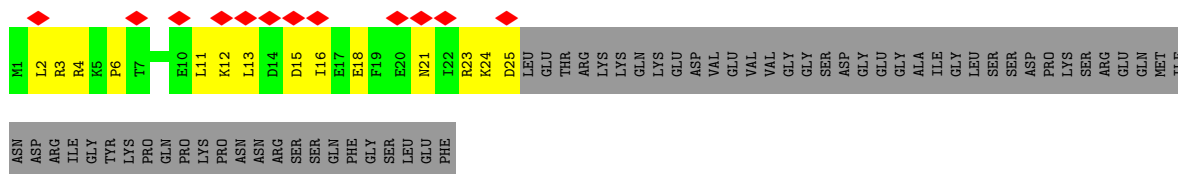


- Molecule 6: Cell division cycle protein 27 homolog





• Molecule 7: Anaphase-promoting complex subunit CDC26



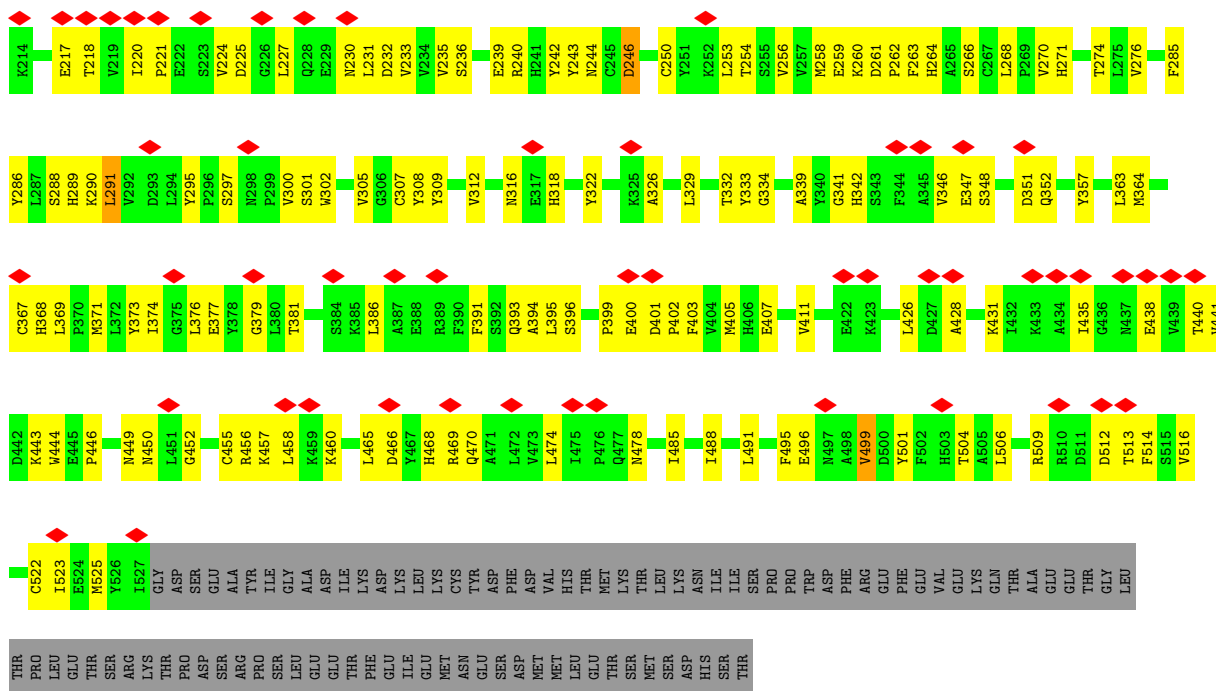
• Molecule 7: Anaphase-promoting complex subunit CDC26



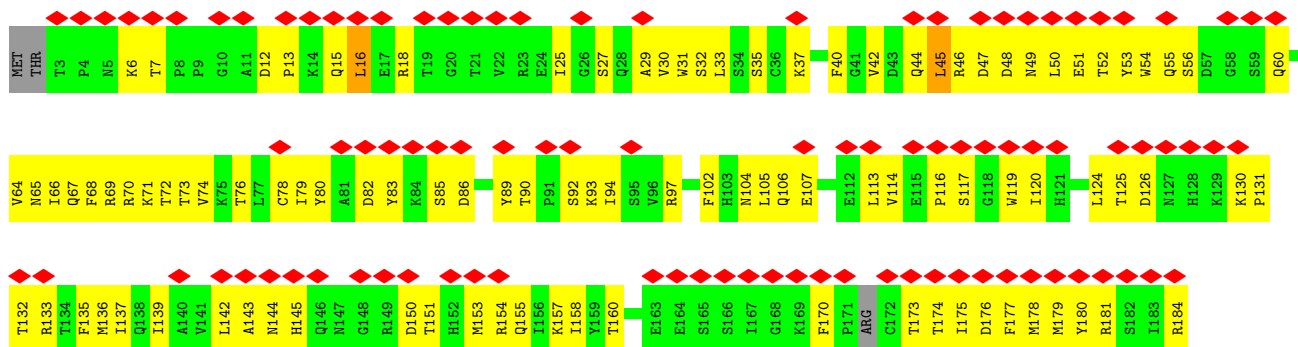
• Molecule 8: Anaphase-promoting complex subunit 4



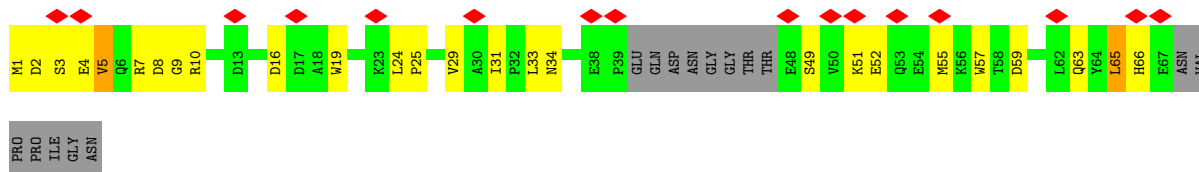




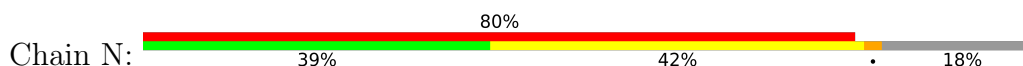
• Molecule 10: Anaphase-promoting complex subunit 10



• Molecule 11: Anaphase-promoting complex subunit 13

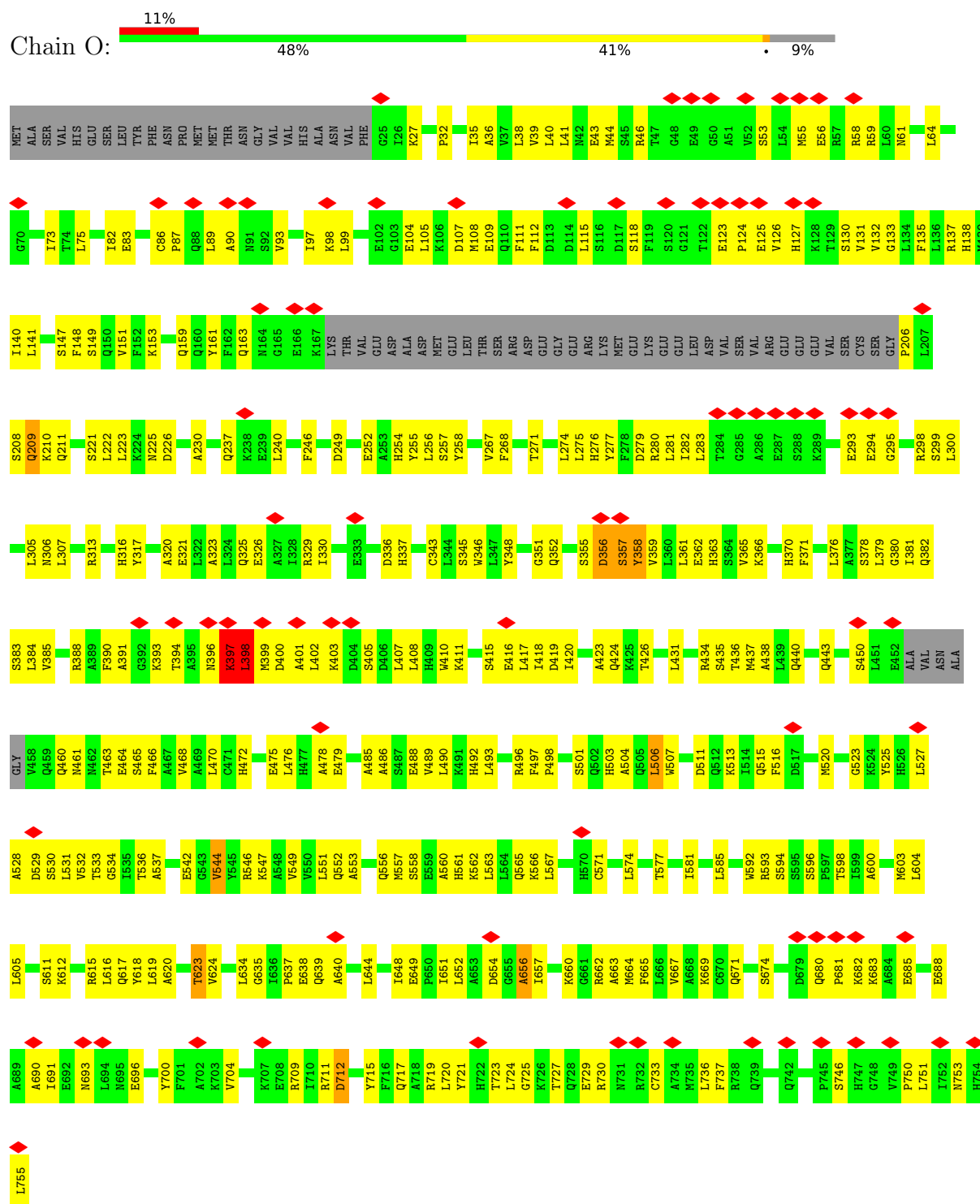


• Molecule 12: Anaphase-promoting complex subunit 2

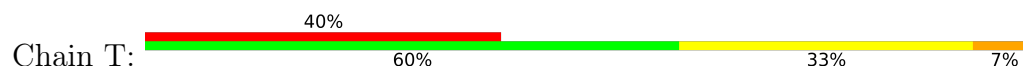


A786	L787	A788	E789	I790	D791	L792	Q793	E794	L795	Q796	G797	Y798	L799	Q800	K801	K802	V803	R804	D805	Q806	Q807	L808	V809	Y810	S811	A812	G813	V814	Y815	R816	L817	P818	LYS	ASN	CYS	SER																															
N726	M727	V728	L729	I730	ASP	SER	ASP	ASP	GLU	GLU	ASP	SER	GLY	MET	GLY	ALA	SER	GLN	E748	E749	E750	L751	L752	L753	F754	W755	T756	Y757	V758	Q759	A760	M761	L762	T763	N764	L765	E766	S767	L768	S769	L770	D771	R772	I773	Y774	N775	M776	L777	R778	M779	F780	V781	W782	T783	G784	P785											
I666	L667	L668	Y669	F670	G671	D672	Q673	A674	S675	W676	T677	L678	E679	E680	L681	S682	K683	A684	V685	K686	M687	P688	V689	A690	L691	L692	R693	R694	R695	M696	S697	V698	W699	L700	Q701	Q702	G703	V704	L705	R706	E707	E708	P709	F710	G711	T712	F713	S714	V715	I716	E717	E718	E719	R720	P721	V722	Q723	R724	D725								
D606	E607	K608	L609	E610	V611	P612	E613	D614	I615	R616	A617	A618	L619	E620	A621	Y622	K624	K625	E626	Y627	Q628	L629	K630	A631	M632	R633	T634	L635	S636	W637	K638	H639	T640	L641	G642	L643	V644	T645	M646	H647	V648	E649	L650	A651	D652	R653	T654	L655	S656	V657	A658	E659	T660	P661	V662	Q663	A664	V665									
K546	L547	R548	F549	G550	E551	A552	P553	M554	H555	F556	C557	E558	V559	M560	L561	K562	D563	M564	A565	D566	S567	R568	R569	I570	N571	A572	N573	I574	R575	E576	E577	D578	E579	K580	R581	P582	A583	E584	E585	Q586	P587	P588	F589	G590	V591	Y592	A593	V594	I595	L596	S597	S598	E599	F600	W601	P602	P603	F604	K605								
D486	ALA	ASP	PRO	GLY	LYS	SER	SER	LYS	ARG	ARG	SER	S499	D500	I501	I502	S503	L504	L505	V506	S507	I508	Y509	G510	S511	K512	D513	L514	F515	I516	N517	E518	Y519	R520	S521	L522	L523	A524	D525	R526	L527	L528	H529	Q530	F531	S532	F533	S534	P535	E536	R537	E538	I539	R540	N541	E542	V543	L544	L545									
E422	P423	I424	R425	E426	Y427	L428	R429	T430	R431	E432	D433	T434	V435	R436	Q437	L438	A440	G441	L442	L443	GLY	ASP	SER	ASP	GLY	THR	GLY	ASP	LEU	ALA	VAL	GLY	LEU	SER	LYS	THR	PRO	ALA	SER	LEU	GLY	THR	GLY	GLN	ASP	SER	ASP	S474	W480	V481	P482	D483	P484	V485													
K362	Y363	C364	L365	E366	T367	T368	D369	Q370	R371	Q372	Q373	L374	L375	V376	S377	L378	K379	A380	A381	L382	E383	T384	R385	L386	L387	H388	P389	G390	V391	I335	A337	S338	L339	R340	I341	E342	L343	L344	F345	S346	I347	V348	R349	D350	F351	E288	H289	K290	S354	R355	P356	A357	M414	V415	I416	L417	E418	V419	A420	C421							
K302	V303	F304	LEU	GLN	ASP	GLY	PRO	ALA	ARG	PRO	ALA	ALA	SER	PRO	GLU	ALA	GLY	N319	T320	L321	R322	R323	W324	A325	L382	E383	T384	R385	L386	L387	H388	P389	F332	Y333	R334	V391	I335	Y336	T393	D395	L396	I397	T398	L399	Y400	I401	L402	S402	A403	I404	K405	A406	L407	R408	V409	L410	D411	P412	S413	M414	V415	I416	L417	E418	V419	A420	C421
Q242	L243	S244	Q245	V246	L247	H248	R249	L250	S251	L252	E253	E254	R255	V256	S257	A258	E259	A260	V261	T262	T263	T264	H266	Q267	V268	T269	R270	E271	M273	V273	E274	D275	R276	C277	R278	Q279	E280	Y281	E282	R283	S284	F285	L286	R287	E288	F289	H290	K291	S294	R355	P356	A357	T294	R295	V296	V297	Q298	W299	L300	G301							
L122	D123	P124	Y125	L126	R127	S128	L129	E130	L131	L132	E133	K134	R135	T136	R137	L138	G139	L140	L141	M142	G143	T144	G145	A146	Q147	G148	L149	R150	E151	E152	V153	H154	T155	L156	L157	R158	G159	V160	L161	F162	F163	S164	T165	P166	C107	T168	F169	Q170	E171	M172	L173	Q174	R175	L176	Y177	C179	F180	L181									
V61	L62	R63	G64	H65	G66	L67	H68	S69	V70	L71	E72	E73	W74	F75	V76	L79	Q80	N81	D82	L83	Q84	A85	N86	I87	S88	P89	E90	F91	W92	N93	A94	I95	S96	Q97	C98	E99	N100	S101	A102	D103	E104	P105	Q106	C107	L108	L109	L110	L111	L112	D113	A114	F115	G116	L118	E119	S120	R121										
ALA	ALA	ALA	VAL	VAL	VAL	ALA	GLY	ASP	ASP	ASP	SER	R15	P16	G17	Q18	E19	L20	L21	V22	A23	V24	N25	T26	V27	S28	T29	G30	L31	V32	P33	PRO	ALA	ALA	LEU	LEU	VAL	SER	SER	ARG	THR	SER	SER	GLY	ALA	VAL	PRO	P50	A51	E52	E53	E54	L55	R56	A57	V59	E60											

• Molecule 13: Anaphase-promoting complex subunit 5



• Molecule 14: Apc1 loop



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	233840	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 ($e^-/\text{\AA}^2$)	29	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.201	Depositor
Minimum map value	-0.165	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.023	Depositor
Map size (Å)	388.69998, 388.69998, 388.69998	wwPDB
Map dimensions	338, 338, 338	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.15, 1.15, 1.15	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.54	0/12168	0.73	4/16587 (0.0%)
2	B	0.28	0/674	0.65	0/913
3	C	0.54	0/4404	0.67	0/5945
3	P	0.43	0/4141	0.60	0/5593
4	D	0.48	0/446	0.69	0/610
5	E	0.44	0/459	0.55	0/619
6	F	0.40	0/3704	0.60	2/5019 (0.0%)
6	H	0.49	0/3969	0.63	0/5366
7	G	0.29	0/221	0.59	0/292
7	W	0.48	0/219	0.80	0/291
8	I	0.48	1/5849 (0.0%)	0.69	7/7937 (0.1%)
9	J	0.41	0/4152	0.60	0/5623
9	K	0.44	0/4086	0.61	0/5533
10	L	0.43	0/1468	0.68	2/1993 (0.1%)
11	M	0.43	0/490	0.71	1/665 (0.2%)
12	N	0.37	0/5442	0.67	5/7376 (0.1%)
13	O	0.58	0/5499	0.71	0/7432
14	T	0.44	0/78	1.16	2/107 (1.9%)
15	X	0.30	0/3827	0.57	2/5180 (0.0%)
15	Y	0.29	0/3922	0.57	0/5304
16	S	0.15	0/18	0.42	0/21
17	Q	0.75	0/22	1.02	0/26
All	All	0.46	1/65258 (0.0%)	0.66	25/88432 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	8

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	2
6	F	0	1
6	H	0	1
8	I	0	4
9	K	0	1
12	N	0	7
13	O	0	7
14	T	0	1
All	All	0	32

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	I	145	LEU	C-N	-5.12	1.29	1.33

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1506	VAL	N-CA-C	-9.15	104.44	112.12
12	N	121	ARG	CA-C-N	9.06	138.00	121.70
12	N	121	ARG	C-N-CA	9.06	138.00	121.70
12	N	704	VAL	N-CA-C	7.92	125.81	109.34
11	M	65	LEU	N-CA-C	-7.24	104.97	114.31

There are no chirality outliers.

5 of 32 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	128	TRP	Peptide
1	A	140	LYS	Peptide
1	A	424	ASN	Peptide
1	A	824	ASP	Peptide
1	A	855	GLU	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	11565	726	0
2	B	649	0	597	65	0
3	C	4306	0	4275	230	0
3	P	4046	0	3998	253	0
4	D	436	0	396	25	0
5	E	450	0	435	22	0
6	F	3618	0	3452	207	0
6	H	3879	0	3805	215	0
7	G	220	0	233	19	0
7	W	218	0	222	32	0
8	I	5726	0	5594	391	0
9	J	4053	0	3960	242	0
9	K	3988	0	3913	181	0
10	L	1435	0	1382	90	0
11	M	481	0	457	37	0
12	N	5337	0	5257	376	0
13	O	5400	0	5418	297	0
14	T	79	0	77	4	0
15	X	3767	0	3820	244	0
15	Y	3862	0	3915	303	0
16	S	19	0	21	7	0
17	Q	23	0	24	30	0
18	B	3	0	0	0	0
All	All	63885	0	62816	3676	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 29.

The worst 5 of 3676 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:277:ARG:CZ	17:Q:498:MET:HE1	1.28	1.55
3:P:400:ARG:NH1	17:Q:499:ARG:HB2	1.18	1.42
3:P:400:ARG:NH1	17:Q:499:ARG:CB	1.91	1.33
3:P:400:ARG:NH1	17:Q:498:MET:O	1.62	1.33
3:P:277:ARG:NH2	17:Q:498:MET:CE	1.92	1.32

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%)	1253 (81%)	283 (18%)	3 (0%)	43	74
2	B	83/84 (99%)	73 (88%)	10 (12%)	0	100	100
3	C	520/597 (87%)	462 (89%)	58 (11%)	0	100	100
3	P	486/597 (81%)	437 (90%)	49 (10%)	0	100	100
4	D	53/121 (44%)	45 (85%)	8 (15%)	0	100	100
5	E	54/110 (49%)	52 (96%)	2 (4%)	0	100	100
6	F	454/824 (55%)	423 (93%)	30 (7%)	1 (0%)	43	74
6	H	484/824 (59%)	424 (88%)	57 (12%)	3 (1%)	21	55
7	G	23/85 (27%)	23 (100%)	0	0	100	100
7	W	24/85 (28%)	22 (92%)	1 (4%)	1 (4%)	2	20
8	I	732/808 (91%)	620 (85%)	108 (15%)	4 (0%)	24	59
9	J	500/620 (81%)	457 (91%)	42 (8%)	1 (0%)	43	74
9	K	489/620 (79%)	448 (92%)	41 (8%)	0	100	100
10	L	180/185 (97%)	154 (86%)	26 (14%)	0	100	100
11	M	55/74 (74%)	48 (87%)	7 (13%)	0	100	100
12	N	662/822 (80%)	592 (89%)	66 (10%)	4 (1%)	21	55
13	O	682/755 (90%)	588 (86%)	89 (13%)	5 (1%)	18	53
14	T	13/15 (87%)	9 (69%)	3 (23%)	1 (8%)	1	12
15	X	480/599 (80%)	447 (93%)	33 (7%)	0	100	100
15	Y	492/599 (82%)	453 (92%)	37 (8%)	2 (0%)	30	64
17	Q	1/445 (0%)	1 (100%)	0	0	100	100
All	All	8006/10813 (74%)	7031 (88%)	950 (12%)	25 (0%)	37	69

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	I	452	LEU
12	N	434	THR
12	N	531	PHE
15	Y	215	LYS
1	A	1840	MET

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%)	1231 (99%)	12 (1%)	68	75
2	B	65/75 (87%)	65 (100%)	0	100	100
3	C	452/520 (87%)	448 (99%)	4 (1%)	70	75
3	P	422/520 (81%)	420 (100%)	2 (0%)	81	82
4	D	46/115 (40%)	46 (100%)	0	100	100
5	E	47/89 (53%)	46 (98%)	1 (2%)	47	65
6	F	371/727 (51%)	371 (100%)	0	100	100
6	H	408/727 (56%)	405 (99%)	3 (1%)	76	78
7	G	25/77 (32%)	25 (100%)	0	100	100
7	W	23/77 (30%)	23 (100%)	0	100	100
8	I	614/730 (84%)	609 (99%)	5 (1%)	73	77
9	J	425/548 (78%)	424 (100%)	1 (0%)	87	87
9	K	423/548 (77%)	420 (99%)	3 (1%)	76	78
10	L	155/170 (91%)	153 (99%)	2 (1%)	61	71
11	M	52/67 (78%)	51 (98%)	1 (2%)	50	66
12	N	549/724 (76%)	544 (99%)	5 (1%)	70	75
13	O	573/650 (88%)	565 (99%)	8 (1%)	59	71
14	T	1/2 (50%)	1 (100%)	0	100	100
15	X	406/513 (79%)	404 (100%)	2 (0%)	81	82
15	Y	417/513 (81%)	415 (100%)	2 (0%)	81	82

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	S	2/401 (0%)	2 (100%)	0	100	100
17	Q	2/402 (0%)	2 (100%)	0	100	100
All	All	6721/9915 (68%)	6670 (99%)	51 (1%)	70	77

5 of 51 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	K	499	VAL
12	N	392	ASN
15	Y	301	ASP
10	L	16	LEU
12	N	108	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 166 such sidechains are listed below:

Mol	Chain	Res	Type
13	O	449	ASN
15	X	289	ASN
13	O	552	GLN
3	P	322	ASN
15	X	506	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](#)

There are no chain breaks in this entry.

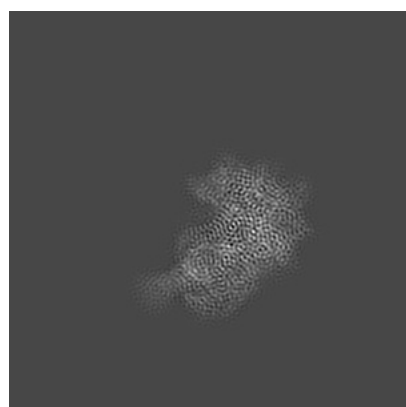
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10518. These allow visual inspection of the internal detail of the map and identification of artifacts.

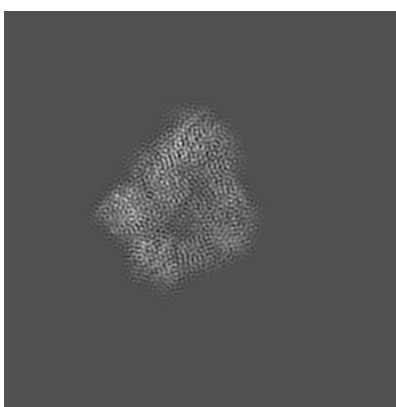
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

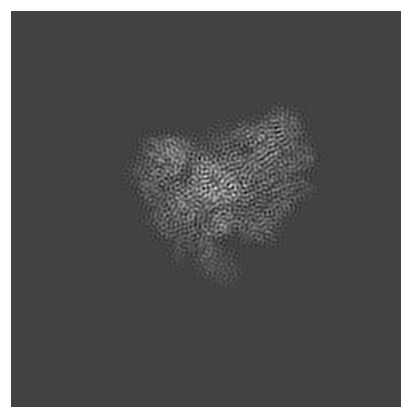
6.1.1 Primary map



X



Y

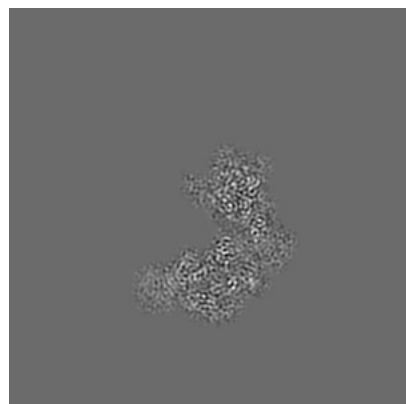


Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 169



Y Index: 169

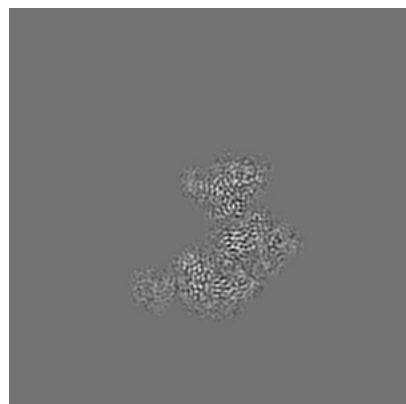


Z Index: 169

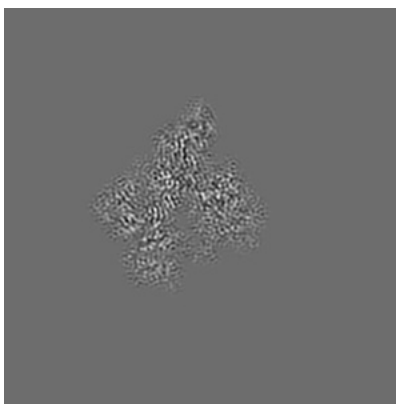
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

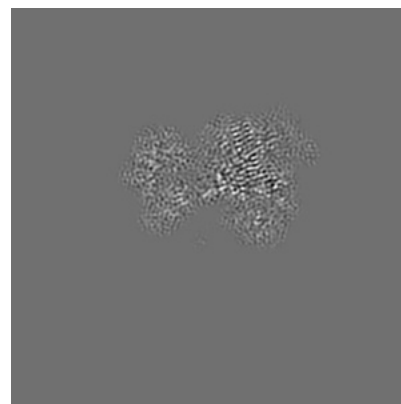
6.3.1 Primary map



X Index: 177



Y Index: 185

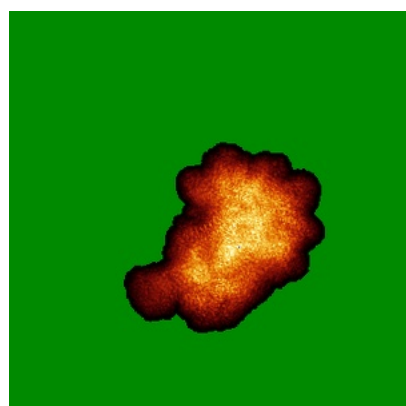


Z Index: 139

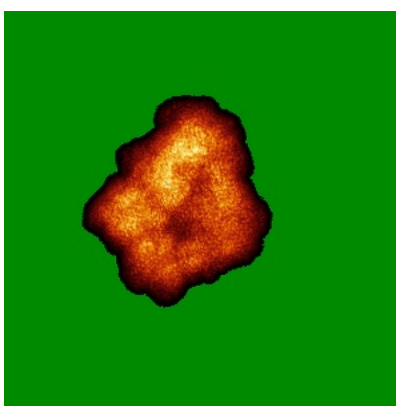
The images above show the largest variance slices of the map in three orthogonal directions.

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

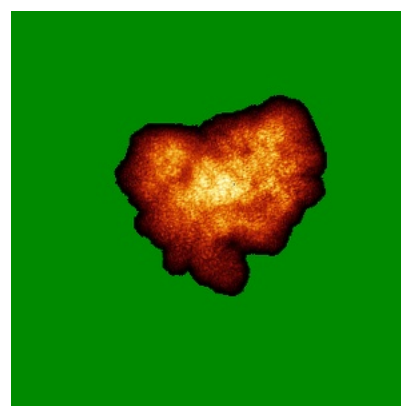
6.4.1 Primary map



X



Y

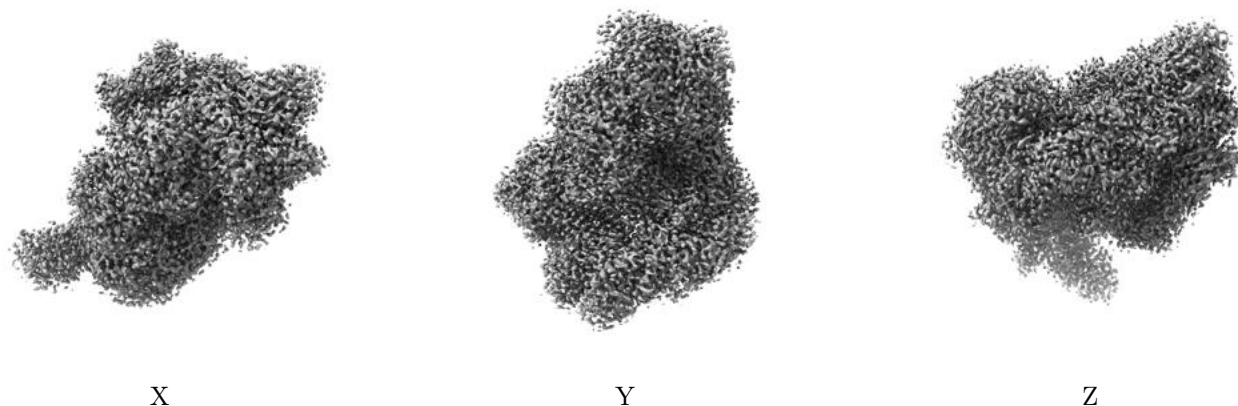


Z

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

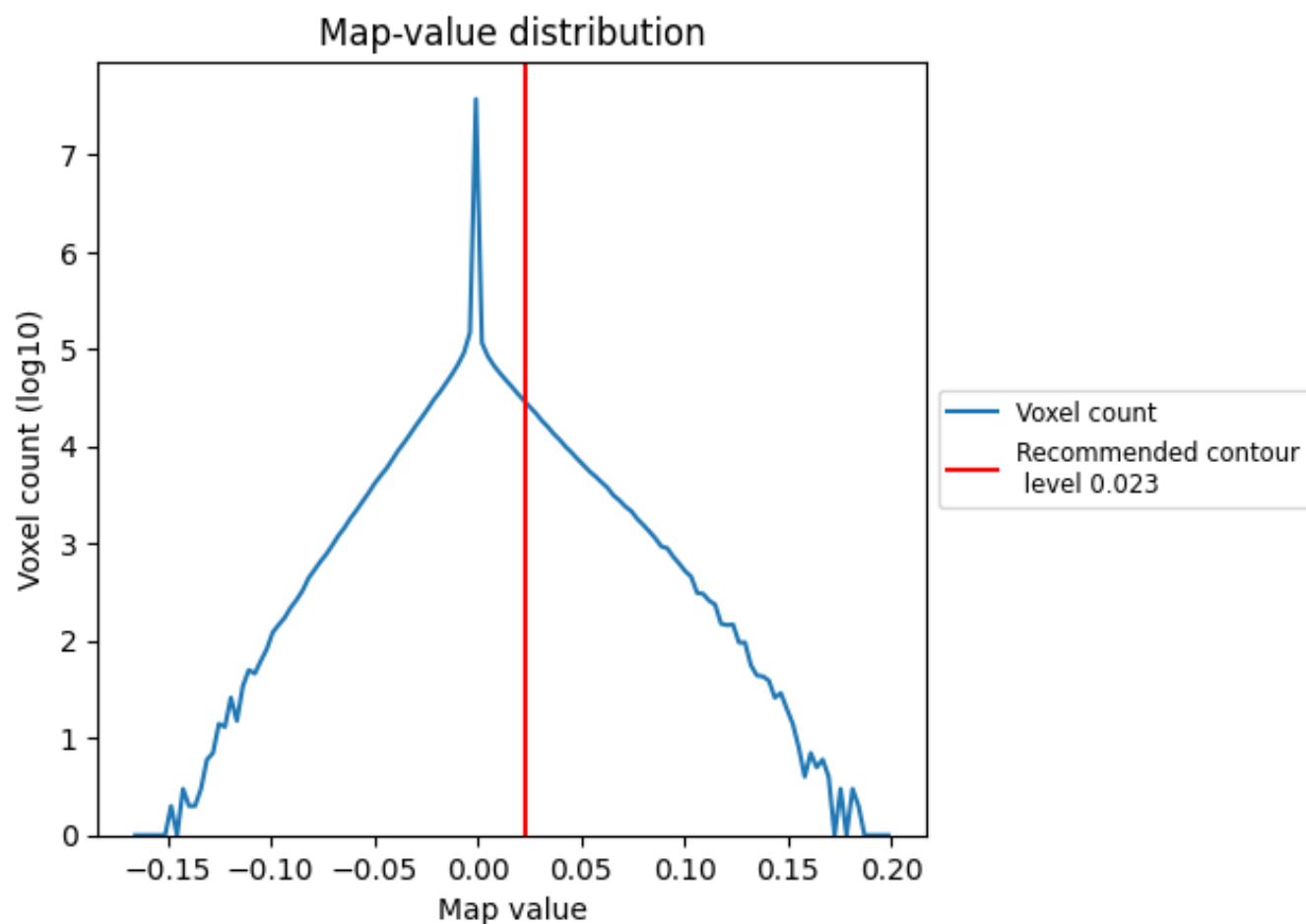
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

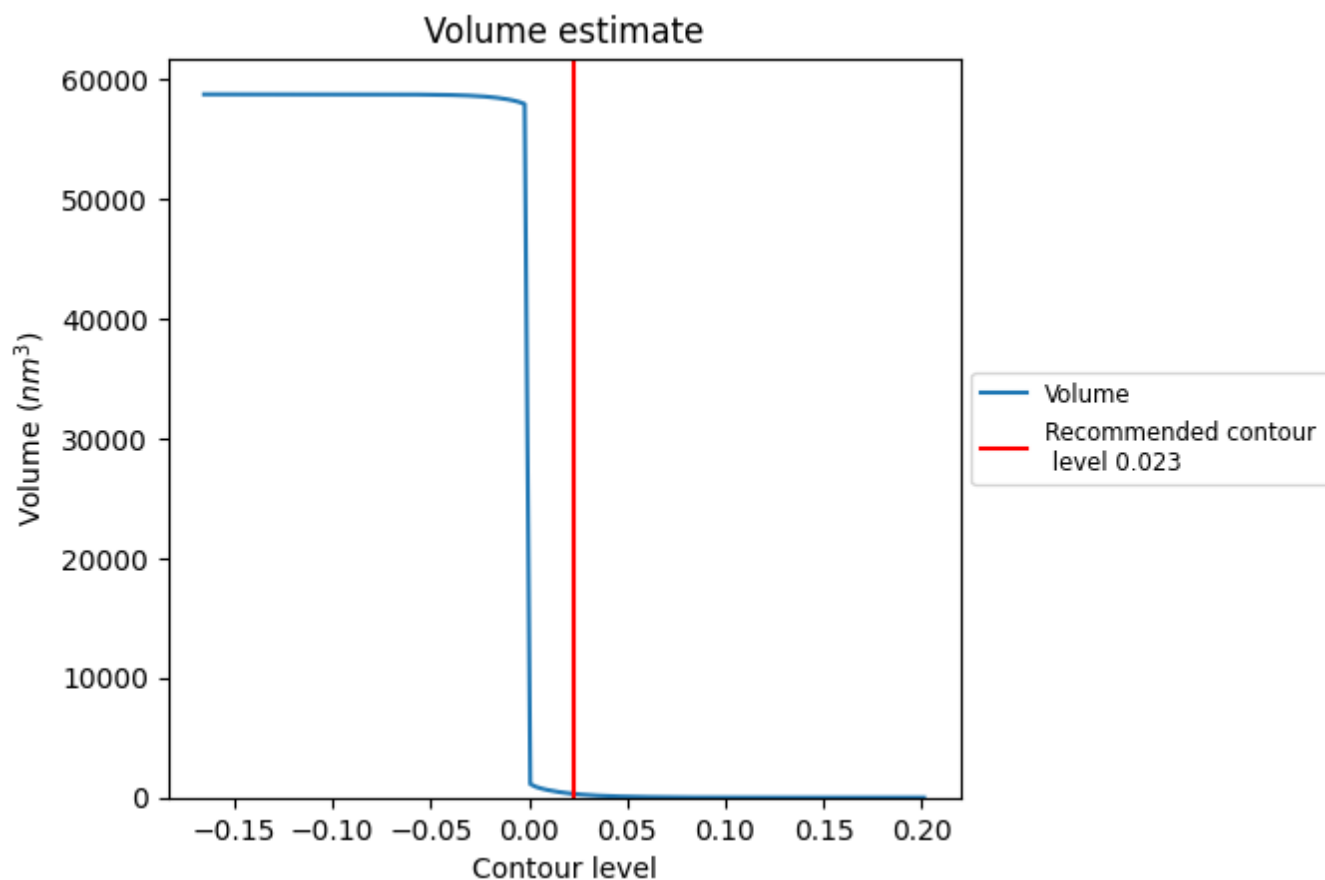
This section contains the results of statistical analysis of the map.

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.

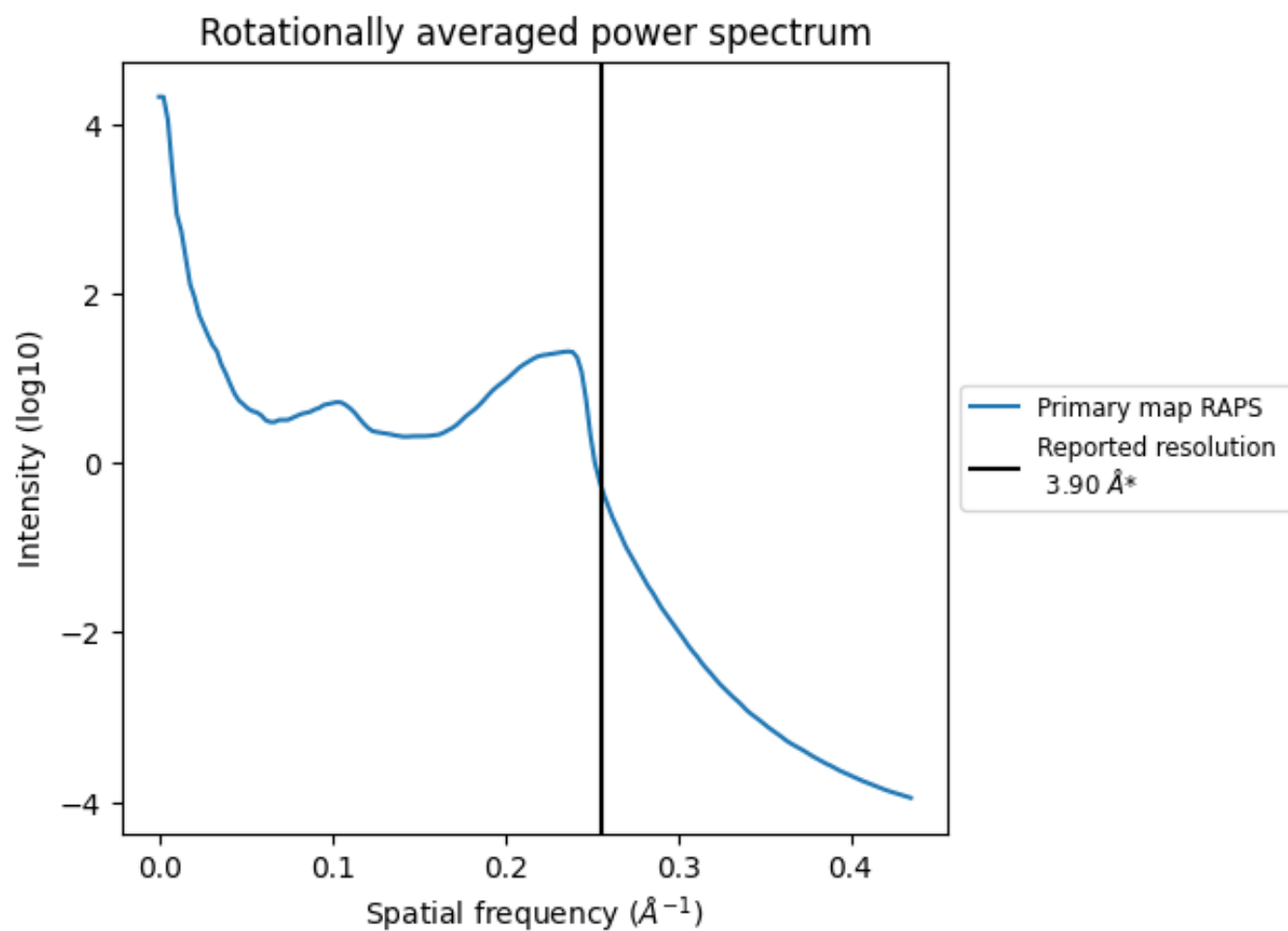
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 308 nm³; this corresponds to an approximate mass of 278 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 0.256 Å⁻¹

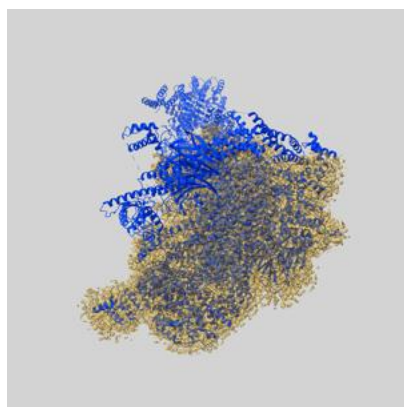
8 Fourier-Shell correlation

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

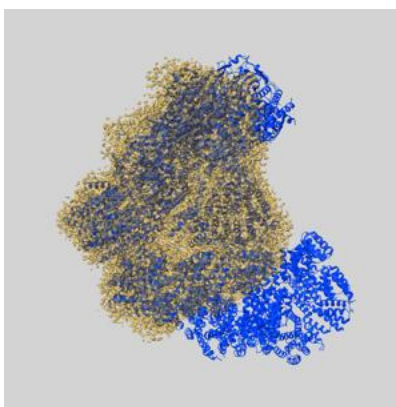
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10518 and PDB model 6TM5. Per-residue inclusion information can be found in section [3](#) on page [8](#).

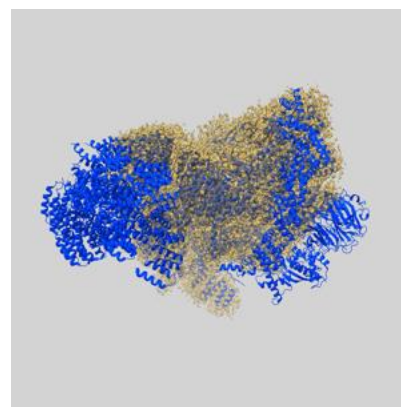
9.1 Map-model overlay [i](#)



X



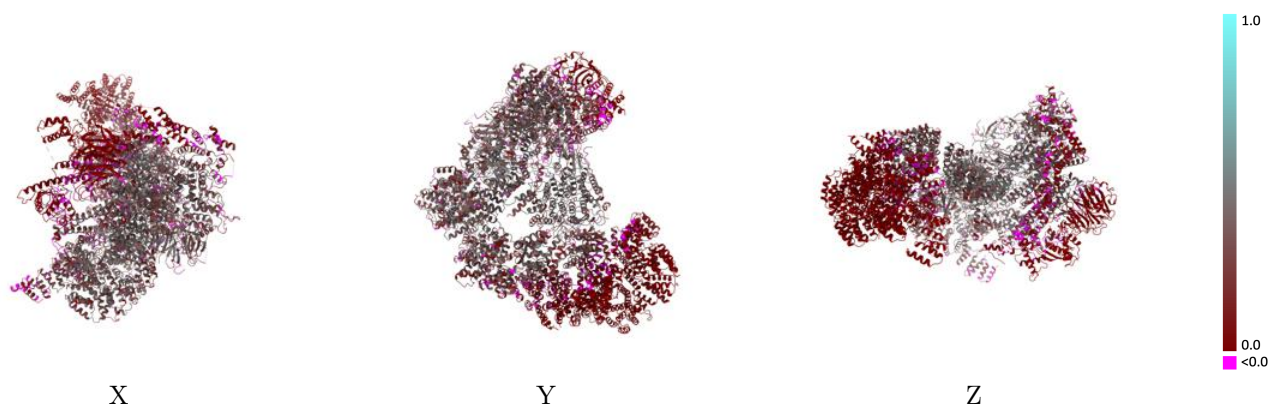
Y



Z

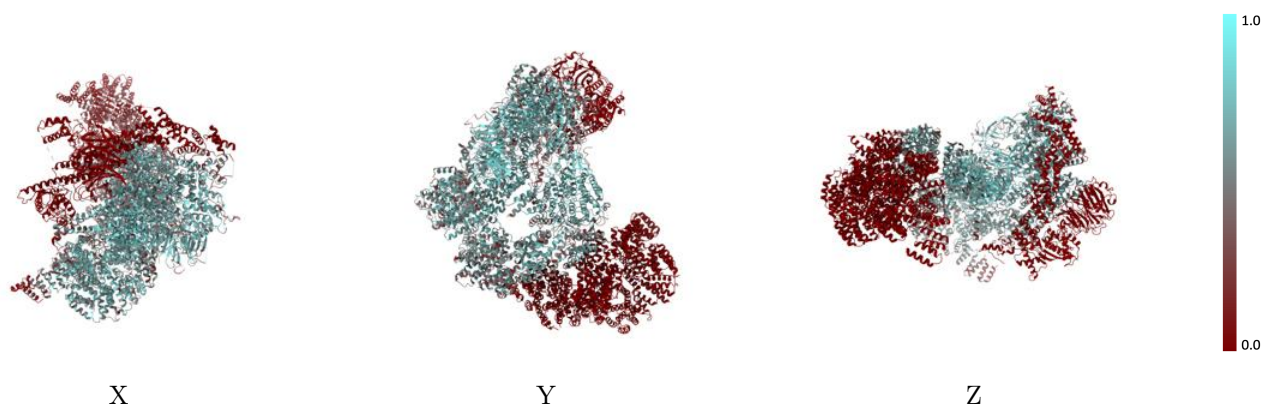
The images above show the 3D surface view of the map at the recommended contour level 0.023 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



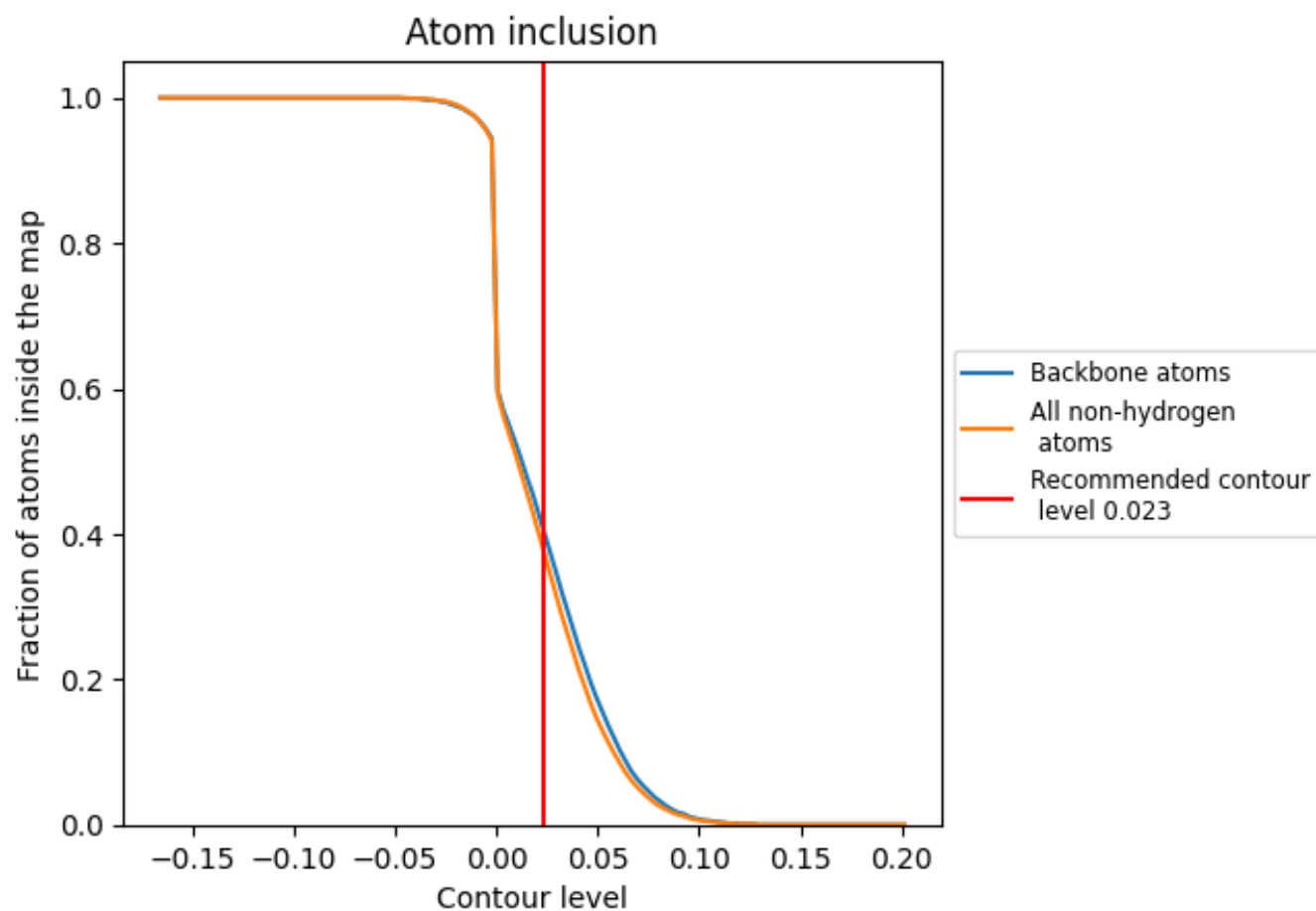
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.023).

9.4 Atom inclusion [i](#)



At the recommended contour level, 41% of all backbone atoms, 38% 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 (0.023) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3810	 0.2120
A	 0.6490	 0.3470
B	 0.0020	 0.0290
C	 0.6470	 0.3530
D	 0.6390	 0.3260
E	 0.0380	 0.0930
F	 0.0100	 0.0280
G	 0.4100	 0.2260
H	 0.0280	 0.0560
I	 0.2790	 0.1660
J	 0.5620	 0.2910
K	 0.5760	 0.3100
L	 0.3980	 0.2180
M	 0.5460	 0.3010
N	 0.0270	 0.0550
O	 0.6720	 0.3600
P	 0.5690	 0.2900
Q	 0.5710	 0.4260
S	 0.0000	 0.0000
T	 0.5440	 0.2430
W	 0.5480	 0.3010
X	 0.0000	 0.0010
Y	 0.0000	 0.0000

