



wwPDB EM Validation Summary Report ⓘ

Aug 30, 2026 – 12:40 AM JST

PDB ID : 9VM8 / pdb_00009vm8
EMDB ID : EMD-65180
Title : Structure of DOCK6 octamer
Authors : Kukimoto-Niino, M.; Katsura, K.; Ishizuka-Katsura, Y.; Yonemochi, M.;
Hanada, K.; Shirouzu, M.
Deposited on : 2025-06-27
Resolution : 7.53 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:

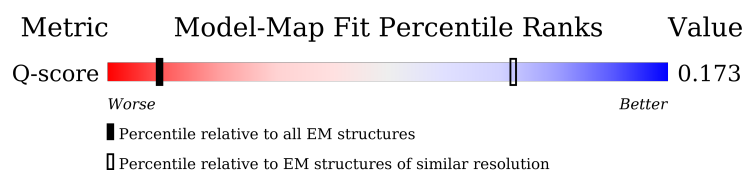
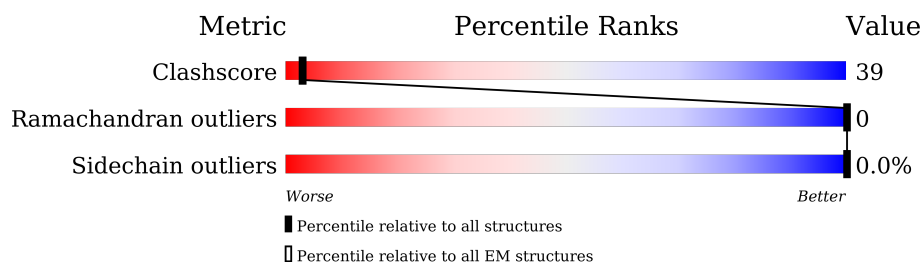
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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 7.53 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	374 (7.04 - 8.01)

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	2053	6% 29% 53% 18%
1	B	2053	6% 29% 53% 18%
1	C	2053	5% 28% 54% 18%
1	D	2053	5% 29% 53% 18%

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Mol	Chain	Length	Quality of chain
1	E	2053	15% 34% 49% 18%
1	F	2053	31% 37% 45% 18%
1	G	2053	30% 39% 43% 18%
1	H	2053	15% 33% 49% 18%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 107608 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 Dedicator of cytokinesis protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1683	Total	C	N	O	S	0	0
			13425	8576	2321	2469	59		
1	C	1689	Total	C	N	O	S	0	0
			13477	8609	2332	2477	59		
1	D	1689	Total	C	N	O	S	0	0
			13477	8609	2332	2477	59		
1	B	1683	Total	C	N	O	S	0	0
			13425	8576	2321	2469	59		
1	E	1689	Total	C	N	O	S	0	0
			13477	8609	2332	2477	59		
1	F	1683	Total	C	N	O	S	0	0
			13425	8576	2321	2469	59		
1	G	1683	Total	C	N	O	S	0	0
			13425	8576	2321	2469	59		
1	H	1689	Total	C	N	O	S	0	0
			13477	8609	2332	2477	59		

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	GLY	-	expression tag	UNP Q96HP0
A	-4	GLY	-	expression tag	UNP Q96HP0
A	-3	SER	-	expression tag	UNP Q96HP0
A	-2	GLY	-	expression tag	UNP Q96HP0
A	-1	GLY	-	expression tag	UNP Q96HP0
A	0	SER	-	expression tag	UNP Q96HP0
C	-5	GLY	-	expression tag	UNP Q96HP0
C	-4	GLY	-	expression tag	UNP Q96HP0
C	-3	SER	-	expression tag	UNP Q96HP0
C	-2	GLY	-	expression tag	UNP Q96HP0
C	-1	GLY	-	expression tag	UNP Q96HP0
C	0	SER	-	expression tag	UNP Q96HP0
D	-5	GLY	-	expression tag	UNP Q96HP0
D	-4	GLY	-	expression tag	UNP Q96HP0

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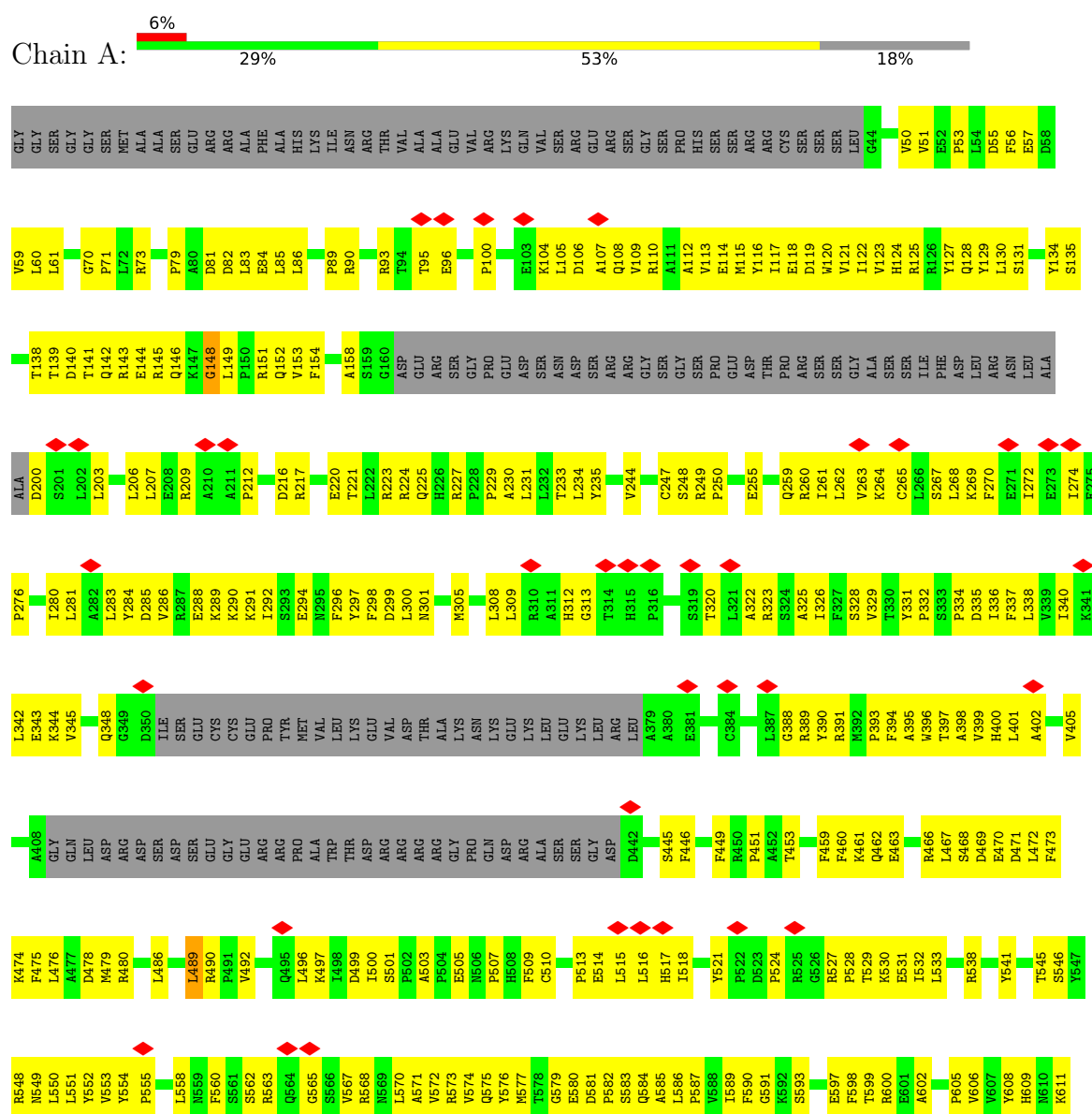
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Chain	Residue	Modelled	Actual	Comment	Reference
D	-3	SER	-	expression tag	UNP Q96HP0
D	-2	GLY	-	expression tag	UNP Q96HP0
D	-1	GLY	-	expression tag	UNP Q96HP0
D	0	SER	-	expression tag	UNP Q96HP0
B	-5	GLY	-	expression tag	UNP Q96HP0
B	-4	GLY	-	expression tag	UNP Q96HP0
B	-3	SER	-	expression tag	UNP Q96HP0
B	-2	GLY	-	expression tag	UNP Q96HP0
B	-1	GLY	-	expression tag	UNP Q96HP0
B	0	SER	-	expression tag	UNP Q96HP0
E	-5	GLY	-	expression tag	UNP Q96HP0
E	-4	GLY	-	expression tag	UNP Q96HP0
E	-3	SER	-	expression tag	UNP Q96HP0
E	-2	GLY	-	expression tag	UNP Q96HP0
E	-1	GLY	-	expression tag	UNP Q96HP0
E	0	SER	-	expression tag	UNP Q96HP0
F	-5	GLY	-	expression tag	UNP Q96HP0
F	-4	GLY	-	expression tag	UNP Q96HP0
F	-3	SER	-	expression tag	UNP Q96HP0
F	-2	GLY	-	expression tag	UNP Q96HP0
F	-1	GLY	-	expression tag	UNP Q96HP0
F	0	SER	-	expression tag	UNP Q96HP0
G	-5	GLY	-	expression tag	UNP Q96HP0
G	-4	GLY	-	expression tag	UNP Q96HP0
G	-3	SER	-	expression tag	UNP Q96HP0
G	-2	GLY	-	expression tag	UNP Q96HP0
G	-1	GLY	-	expression tag	UNP Q96HP0
G	0	SER	-	expression tag	UNP Q96HP0
H	-5	GLY	-	expression tag	UNP Q96HP0
H	-4	GLY	-	expression tag	UNP Q96HP0
H	-3	SER	-	expression tag	UNP Q96HP0
H	-2	GLY	-	expression tag	UNP Q96HP0
H	-1	GLY	-	expression tag	UNP Q96HP0
H	0	SER	-	expression tag	UNP Q96HP0

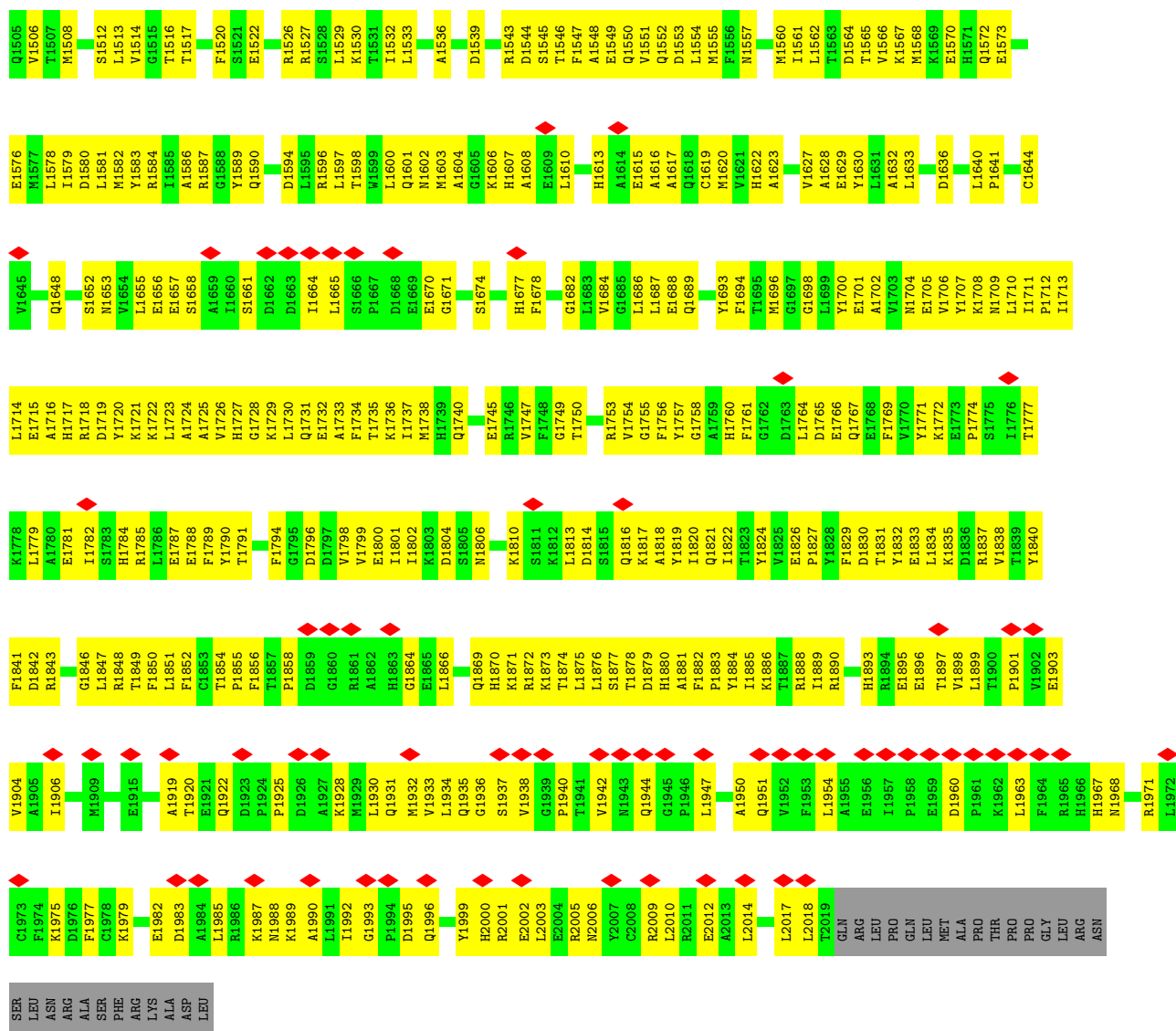
3 Residue-property plots

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.

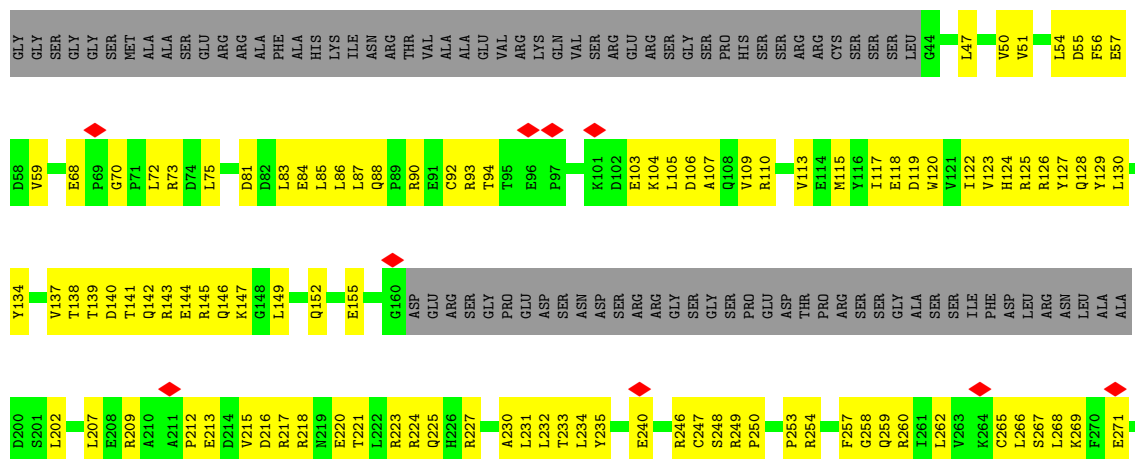
- Molecule 1: Dedicator of cytokinesis protein 6







• Molecule 1: Dedicator of cytokinesis protein 6



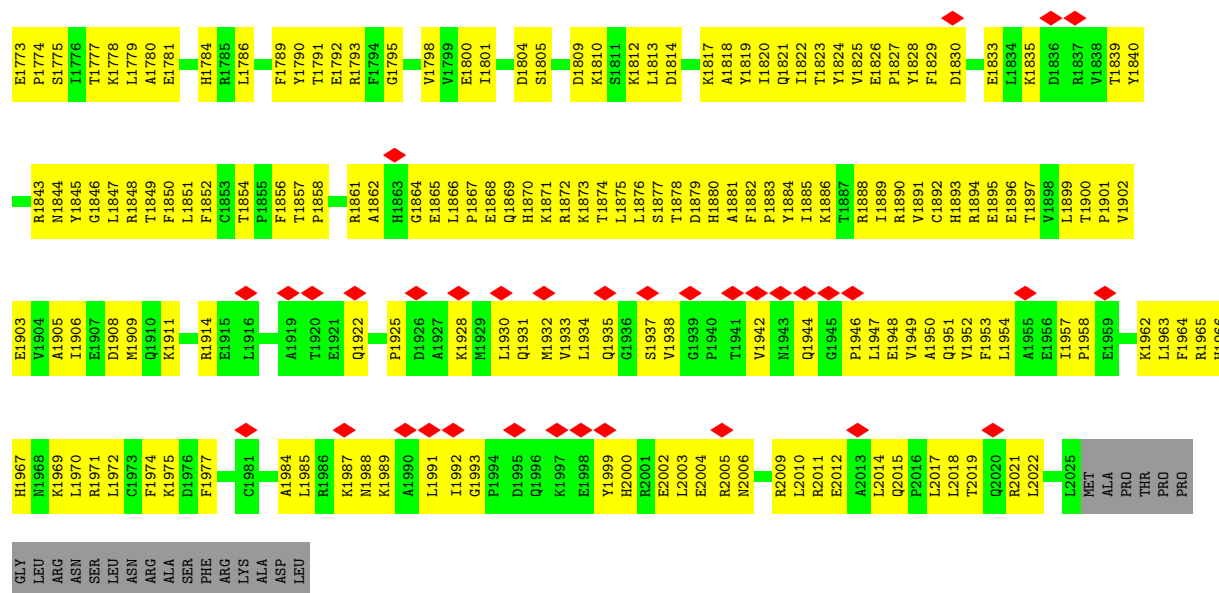
K1134	A1135	S1136	S1137	A1138	V1139	H1140	S1141	L1142	C1143	C1144	G1145	H1146	D1147	T1148	D1149	A1153	E1154	K1158	A1159	R1160	V1161	A1162	E1163	L1164	Y1165	L1166	P1167	L1168	L1169	S1170	R1171	A1172	R1173	D1174	T1175	L1176	P1177	R1178	L1179	F1182	A1183	E1184	GLY	PRO	GLY	GLN	ARG	SER	ARG	ARG	LEU	ALA	SER	MET	LEU	ASP	SER			
SER	PRO	SER	VAL	SER	SER	THR	THR	SER	GLN	SER	SER	THR	PHE	SER	SER	Q1087	A1088	P1089	D1090	P1091	K1092	V1093	T1094	F1097	E1098	L1099	S1100	G1101	P1102	F1103	R1104	Q1105	Q1106	H1107	F1108	L1109	A1110	G1111	L1112	L1113	L1114	T1115	E1116	L1117	A1118	L1119	A1120	L1121	E1122	P1123	E1124	A1128	F1129	L1130	L1131	H1132	K1133			
L947	L948	G949	Q950	R951	L952	D953	T954	P955	R956	K957	L958	R959	P960	P961	G962	R963	F964	L965	D966	D967	T968	T969	A970	L971	V972	G973	S974	G975	G976	L977	E978	V979	I980	T981	R982	V983	H984	K985	D986	V987	L988	L989	A990	E991	H992	L993	F994	F995	Q996	L997	A998	F999	F1000	L1001	S941	N942	A943	L944	H945	L946
SER	SER	SER	ASN	PRO	ASP	LEU	ALA	VAL	ALA	ALA	GLY	SER	SER	VAL	D896	D897	E898	R901	I902	L903	L907	L908	H909	E910	F911	L912	A913	Q914	Q915	W916	V917	I918	P919	S919	V923	R924	E925	E926	L927	L928	H928	A931	Q932	F933	F934	F935	Q936	L937	N938	V939	K940	S941	N942	A943	L944	H945	L946			
A822	Q823	D824	G827	H828	C829	P830	Q831	L832	A833	R834	Y835	V836	H837	A838	A839	F840	R841	L842	P843	T844	E846	P847	SER	PRO	ASP	GLY	ALA	ALA	PRO	PRO	VAL	THR	VAL	VAL	GLN	ALA	ALA	THR	LEU	ALA	ARG	GLY	SER	GLY	ARG	PRO	ALA	ALA	SER	LEU	THR	VAL	ALA	ARG	SER	LYS	ILE			
V753	E754	Q755	E756	L757	R758	A759	S760	L761	A767	S768	P769	E770	P771	L772	V773	A774	F775	S776	H777	F778	V779	L780	D781	K782	L783	V784	V785	S786	V787	L788	R789	Q790	P791	L792	I793	S794	G795	Q796	L797	V798	N799	L800	G801	R802	C803	E806	A807	N808	A809	H810	V811	V812	S813	L814	V815	S818				
E614	F615	Y616	E617	E618	F619	K620	L621	H622	L623	P624	V627	T628	E629	N630	H631	H632	L633	L634	F635	T636	F637	Y638	H639	V640	S641	G647	T648	A649	L650	E651	T652	P653	V654	G655	F656	T657	W658	G659	P660	L661	L662	Q663	H664	G665	R666	L667	R668	T669	F670	P671	L674	P675	S677	V678	D679					
R548	N549	L550	L551	L552	V553	Y554	P555	H556	S557	L558	N559	S562	A563	Q564	G565	S566	R568	N569	L570	A571	F509	C510	L511	S512	G513	P513	E514	L515	L516	G517	E518	K519	P520	Y521	V522	V523	L524	R525	G526	R527	P528	C529	K530	E531	L532	L533	E534	F535	P536	A537	V538	V539	Y540	E541	A542	H543	N544	P545	T546	Y547
F337	L338	V339	I340	K341	L342	E343	K344	V345	L346	G349	D350	ILE	SER	GLY	GLU	CYS	GLY	PRO	TRP	THR	TYR	MET	VAL	LEU	LYS	ASP	THR	ALA	ASN	LYS	GLY	GLY	ASP	D442	A443	C444	S445	F446	A449	R450	C394	L387	G388	R389	R390	R391	M392	M393	A394	F395	A396	W396	T397	Y398	P399	H400	L401	A402	D335	I336



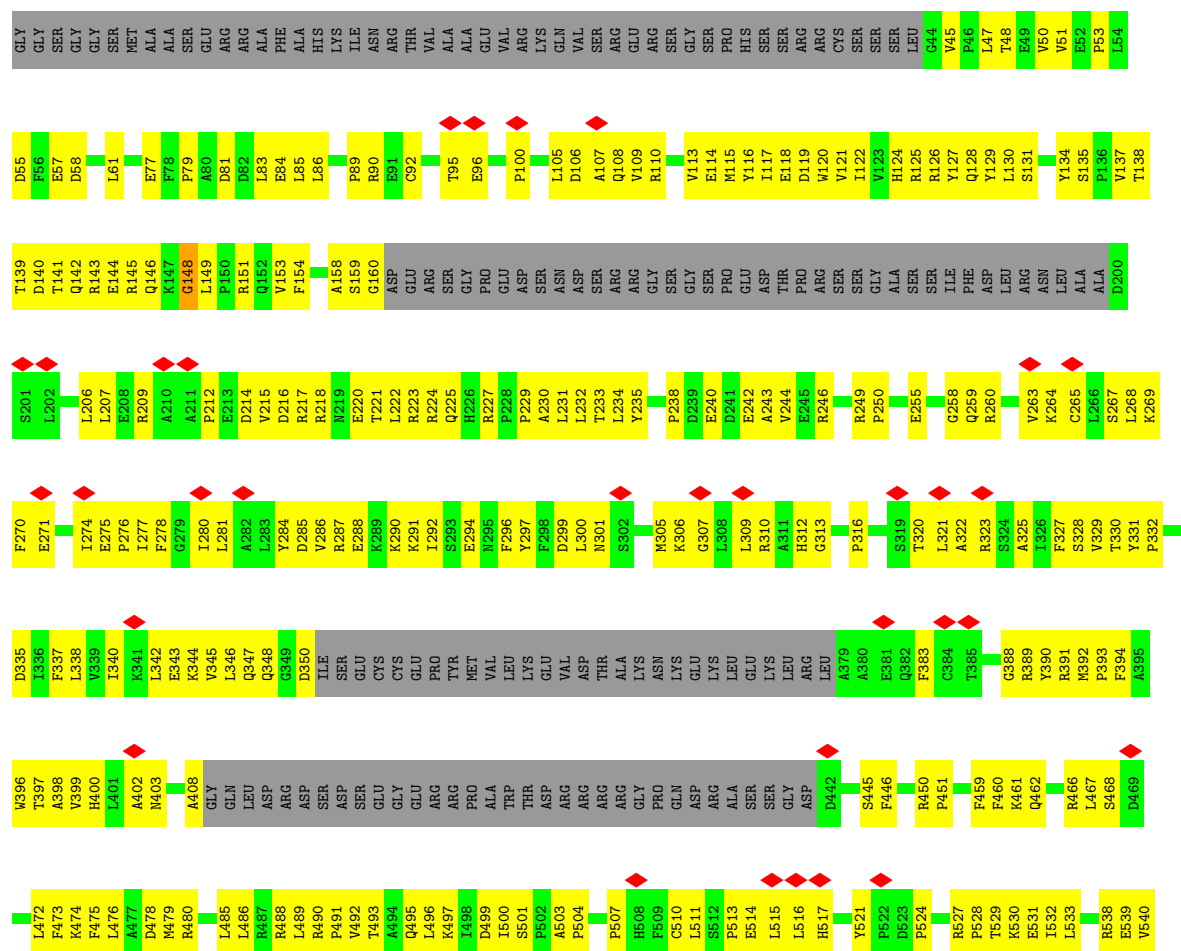
Chain D:



I1711	C1644	E1670	V1506	L1384	ARG	V1257	ASP	F1129	ALA	V1008	SER	L944
P1712	F1647	E1573	T1507	A1385	LEU	L1258	SER	L1130	SER	D1009	LYS	L947
L1714	L1510	L1578	M1508	E1387	GLU	V1259	ASP	H1131	PRO	R1010	ILE	L948
E1715	L1650	L1579	M1509	A1388	ALA	W1260	THR	H1132	SER	G1011	SER	
H1717	M1653	D1580	L1514	S1389	ILE	K1261	GLY	K1133	PRO	F1012	SER	
D1719	L1513	L1581	L1451	S1390	LEU	K1262	GLY	K1134	SER	V1013	SER	
M1582	G1515	L1582	F1452	V1391	GLY	N1263	GLY	A1135	VAL	F1014	ASN	
Y1583	T1516	Y1584	E1453	V1392	THR	T1264	ASP	I1136	SER	S1015	PRO	
R1584	T1517	R1585	E1454	L1393	ILE	P1266	ILE	A1138	THR	L1016	ASP	
I1585	Q1518	I1586	T1456	D1394	GLY	A1267	ALA	V1139	THR	R1017	LEU	
A1659	M1519	A1658	E1457	L1395	ALA	L1268	GLY	H1141	SER	A1019	ALA	
I1660	M1519	I1661	L1458	T1396	ARG	L1269	THR	S1141	GLN	H1020	VAL	
S1661	F1520	S1662	L1458	E1397	GLN	Q1270	ILE	L1142	SER	Y1021	ALA	
D1663	S1521	D1664	A1459	I1398	GLU	W1271	ASN	H1146	SER	G1022	PRO	
L1665	E1522	L1666	A1460	I1399	MET	W1272	PRO		THR	Q1023	GLY	
S1666	E1523	S1667	D1461	V1400	VAL		SER	D1149	PHE	V1024	SER	
P1667	H1524	P1668	L1462	Q1401	ARG	L1276	VAL	A1153	SER	A1025		
D1668	C1463	D1669	C1464	T1402	ARG	T1277	ALA	E1154	ALA	T1026		
G1671	R1465	G1672	R1466	V1403	SER	T1278	MET		ALA	R1027		
F1672	R1466	F1673	L1466	M1404	ARG	P1279	ALA	K1158	A1088	L1028		
S1673	L1467	S1674	L1467	L1405	GLU	Q1280	ILE	A1162	P1089	Q1029		
G1675	R1468	G1676	R1468	S1406	ARG	L1281	ALA	L1164	D1090	S1030		
K1676	H1469	K1677	H1469	E1407	SER	G1282	GLY	R1159	P1091	P1031		
F1678	C1470	F1679	C1470	A1408	PRO	L1283	GLY	A1159	K1092	L970		
E1680	I1532	E1681	I1532	R1409	PHE	L1284	PRO	V1161	V1093	V972		
L1683	L1533	L1684	L1533	E1410	GLY	D1285	LEU	A1162	T1094	S973		
V1684	S1472	V1685	S1472	S1411	GLY	D1286	ALA	E1163	S1095	S974		
L1687	R1473	L1688	R1473	V1412	PRO	L1287	PRO	L1164	M1096	V975		
E1688	T1476	E1689	T1476	L1413	GLU	Y1288	GLY	V1165	F1097	V976		
F1689	I1477	F1690	I1477	G1414	ASN	Y1289	SER	L1166	E1098	L977		
A1690	R1478	A1691	R1478	A1415	VAL	L1290	ARG	P1167	L1099	E978		
G1692	H1480	G1693	H1480	L1416	ARG	C1291	ALA	D1175	S1100	L1040		
Y1693	D1544	Y1694	D1544	L1417	TRP	E1291	SER	T1175	G1101	R1041		
F1694	S1481	F1695	S1481	V1419	ARG	A1293	ILE	P1177	P1102	M1042		
T1695	A1482	T1696	A1482	L1420	LYS	F1295	SER	R1178	F1103	R982		
M1696	A1483	M1697	A1483	L1421	SER	E1296	GLN	L1179	A1104	F1044		
G1697	S1484	G1698	S1484	Y1422	VAL	Y1297	GLY	F1182	Q1105	T1045		
L1699	L1485	L1700	L1485	S1423	THR	K1300	PRO	E1183	L1112	R985		
A1701	Y1486	A1702	Y1486	L1424	HIS	A1301	THR	E1184	L1113	K986		
E1702	G1487	E1703	G1487	G1425	TRP	A1302	ALA	GLY	L1114	L1007		
D1703	L1488	D1704	L1488	S1426	LYS	F1303	SER	PRO	T1115	F999		
L1704	M1489	L1705	M1489	A1427	GLN	K1301	ALA	GLY	E1116	P1000		
V1706	Q1490	V1707	Q1490	Q1428	THR	A1302	ARG	GLY	A1117	L1057		
Y1707	L1491	Y1708	L1491	L1431	SER	F1303	ALA	GLY	A1118	N1058		
K1708	N1492	K1709	N1492	F1432	ASP	K1301	GLY	GLY	A1119	L1059		
L1710	F1493	L1711	F1493	L1433	ARG	A1302	ILE	GLN	L1120	P1060		
	E1494		E1494	Q1434	VAL	F1303	A1244	GLY	L1121	C1061		
	L1495		L1495	H1435	ASP	K1301	L1245	PRO	E1117	S1062		
	G1496		G1496	H1436	LYS	A1302	S1246	GLY	A1118	D1003		
	H1497		H1497	L1437	THR	F1303	A1247	GLY	A1119	L1004		
	N1498		N1498	G1437	PHE	K1301	E1248	GLN	L1120	L1006		
	F1499		F1499	L1437	LYS	A1302	S1249	GLY	L1121	S1005		
	A1500		A1500	M1374	THR	F1303	E1250	GLY	E1117	L1007		
	R1501		R1501	E1375	LEU	K1301	T1251	GLY	A1118	L1007		
	V1502		V1502	A1378	LEU	A1302	T1252	GLY	A1119	L1007		
	K1503		K1503	A1378	ASP	F1303	L1253	GLY	L1120	L1007		
	M1504		M1504	G1382	MET	K1301	L1254	GLY	E1117	L1007		
	Q1505		Q1505	L1504	LYS	A1302	A1255	GLY	A1118	L1007		
				V1444	ALA	F1303	C1256	GLY	A1119	L1007		
						K1301		GLY	A1120	L1007		
						A1302		GLY	L1121	L1007		
						F1303		GLY	E1117	L1007		
						K1301		GLY	A1118	L1007		
						A1302		GLY	L1119	L1007		
						F1303		GLY	A1120	L1007		
						K1301		GLY	L1121	L1007		
						A1302		GLY	E1122	L1007		
						F1303		GLY	L1123	L1007		
						K1301		GLY	E1124	L1007		
						A1302		GLY	A1125	L1007		
						F1303		GLY	A1126	L1007		
						K1301		GLY	A1127	L1007		
						A1302		GLY	A1128	L1007		
						F1303		GLY	A1129	L1007		
						K1301		GLY	A1130	L1007		
						A1302		GLY	A1131	L1007		
						F1303		GLY	A1132	L1007		
						K1301		GLY	A1133	L1007		
						A1302		GLY	A1134	L1007		
						F1303		GLY	A1135	L1007		
						K1301		GLY	A1136	L1007		
						A1302		GLY	A1137	L1007		
						F1303		GLY	A1138	L1007		
						K1301		GLY	A1139	L1007		
						A1302		GLY	A1140	L1007		
						F1303		GLY	A1141	L1007		
						K1301		GLY	A1142	L1007		
						A1302		GLY	A1143	L1007		
						F1303		GLY	A1144	L1007		
						K1301		GLY	A1145	L1007		
						A1302		GLY	A1146	L1007		
						F1303		GLY	A1147	L1007		
						K1301		GLY	A1148	L1007		
						A1302		GLY	A1149	L1007		
						F1303		GLY	A1150	L1007		
						K1301		GLY	A1151	L1007		
						A1302		GLY	A1152	L1007		
						F1303		GLY	A1153	L1007		
						K1301		GLY	A1154	L1007		
						A1302		GLY	A1155	L1007		
						F1303		GLY	A1156	L1007		
						K1301		GLY	A1157	L1007		
						A1302		GLY	A1158	L1007		
						F1303		GLY	A1159	L1007		
						K1301		GLY	A1160	L1007		
						A1302		GLY	A1161	L1007		
						F1303		GLY	A1162	L1007		
						K1301		GLY	A1163	L1007		
						A1302		GLY	A1164	L1007		
						F1303		GLY	A1165	L1007		
						K1301		GLY	A1166	L1007		
						A1302		GLY	A1167	L1007		
						F1303		GLY	A1168	L1007		
						K1301		GLY	A1169	L1007		
						A1302		GLY	A1170	L1007		
						F1303		GLY	A1171	L1007		
						K1301		GLY	A1172	L1007		
						A1302		GLY	A1173	L1007		
						F1303		GLY	A1174	L1007		
						K1301		GLY	A1175	L1007		
						A1302		GLY	A1176	L1007		
						F1303		GLY	A1177	L1007		
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						F1303		GLY	A1180	L1007		
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						F1303		GLY	A1186	L1007		
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						F1303		GLY	A1195	L1007		
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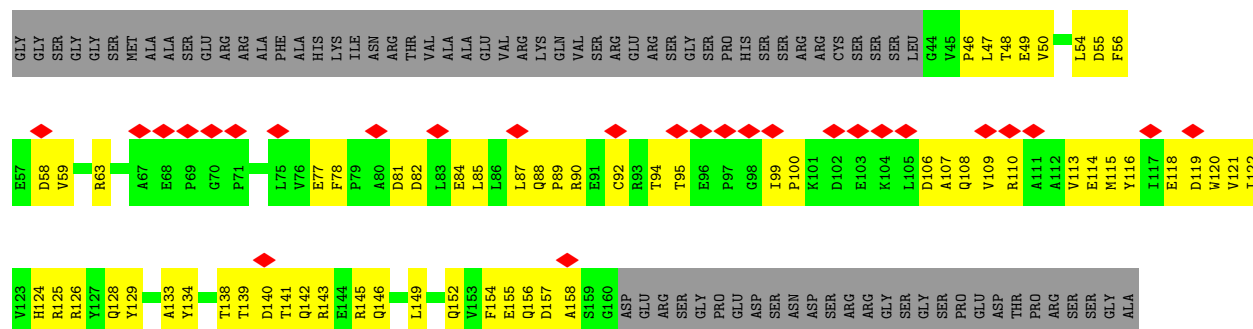


• Molecule 1: Dedicator of cytokinesis protein 6



S1389	ALA	M1263	GLU	S1441	SER	L1007	L944	A807	K744	V676	V607	Y641
L1390	ILE	T1264	GLY	L1142	VAL	V1008	H945	M808	D745	S677	Y608	T545
V1391	LEU	E1265	ASP	L1143	SER	R1009	L946	A909	L746	V678	H609	
V1392	GLY	P1266	ILE	C1144	SER	R1010	L947	H810	V747	D679	N610	
L1393	THR	A1267	ALA	G1145	THR	G1011		V811	L748	Q680	K611	R548
D1394	ILE	H1146	GLY	H1146	THR	F1012	Q950	S813	S749	P681	S612	N549
T1395	THR	D1147	THR	D1147	SER	V1013	R951	L814	E750	P682	P613	L550
L1396	ALA	T1148	ILE	T1148	GLN	F1014	L952	D953	G751	Y685	E614	L551
E1397	ARG	D1149	ASN	D1149	SER	L1015	D953	V815	V753	S686	F615	Y552
I1398	GLN	R1150	PRO	R1150	PRO	T954	T954	H816	E754	V687	E616	V553
V1399	GLU	P1151	THR	P1151	THR	V1017	P955	R817	ASP	L688	E618	
V1400	VAL	A1152	VAL	A1152	PHE	R1018	R956	S818	ASP	T689	F619	L558
Q1401	VAL	A1153	ALA	A1153	SER	H1020	K957	L819	T755	P690	K820	N559
T1402	ARG	E1154	MET	E1154	SER	H1020	L958		L757	D691	L621	F560
T1403	ARG	V1157	ALA	V1157	Q1087	Y1021	R959	G826	R758	V692	L622	S561
V1403	SER	A1088	ILE	A1088	A1088	K1022	F960	G827	L761	S692	L623	R563
M1404	GLU	P1089	ALA	P1089	GLY	V1024	P961	H828		M697	T628	Q564
S1405	ARG	D1090	GLY	D1090	VAL	A1025	F964	P830	L764	R698	E629	G565
E1407	ARG	P1091	GLY	P1091	VAL	T1026	L965	Q831	R765	V699	N630	S566
A1408	SER	K1092	PRO	K1092	VAL	R1027	D966	L832	A767	V700	H631	V567
R1409	LEU	V1093	LEU	V1093	D897	L1028	D967	A833		D701	H632	R568
E1410	ALA	T1094	ALA	T1094	E898	Q1029	D968	A834	E770	G702	L633	N569
S1411	GLY	S1095	GLY	S1095	V899		T969	Y835		H703	L634	L570
V1412	PRO	M1096	SER	V1166		N1033	A970	R836		K704		A571
L1413	GLU	P1167	ARG	P1167		P1034	L971	H837	L772	F707	Y638	V572
G1414	ASN	L1168	ALA	L1168		A1035	V972	R837	V773	S708	H639	R573
A1415	VAL	L1169	SER	L1169		A1036	G973	Y838	A774	V709	V640	V574
L1416	ILE	S1170	ILE	S1170		L1037	S974	A839	F775	S715	Q575	Q575
L1417	TRP	T1171	SER	T1171		L1038	V975		S776	S716	Y576	M577
K1418	ARG	A1172	GLN	A1172		T1039	G976		H777	E710	C642	T578
V1419	LYS	R1173	GLY	R1173		L1040	L977		T778	T712	R645	G579
SER	PRO	D1174	PRO	D1174		R1041	S978		V779	A713	P646	E580
T1421	VAL	T1175	PRO	T1175		M1042	V979		D781	S715	G647	D581
V1422	THR	L1176	THR	L1176		E1043	T981	ASP	K782	S715	T648	P582
S1423	HIS	P1177	ALA	P1177		F1044	R982	GLY	L783	S716	Q583	S583
K1299	SER	R1178	SER	R1178		T1045	R983	ALA	V784	S717	A649	Q584
K1300	TRP	L1179	ARG	L1179		R1046	V984	PRO	R785	V717		
K1301	LYS	L1179	ARG	L1179		L1047	H984	PRO	L786	H718	T652	A585
S1426	GLN	F1182	ALA	F1182		L1048	K985	VAL	V787	Q720	P653	L586
F1303	THR	E1183	GLY	E1183		C1049	D986	THR	I788	P719	V654	P587
Q1428	GLU	A1184	C1243	A1184		S1050	V987	VAL	R789	D721	G655	V588
S1429	ASP	E1184	A1244	E1184		E1051	L989	GLN	P791	P722	G655	I589
A1430	ARG	GLY	L1245	GLY		E1052	A990	ALA	I792	F656	F656	F590
L1431	VAL	PRO	S1246	GLN		H1053	E991	ALA	T793	T657	W658	G591
F1432	ASP	GLY	A1247	GLY		V1054	H992	THR	I793	G659	S593	K592
L1433	LEU	ARG	E1248	ARG		T1055	L993	ALA	S794	F727	P660	S594
Q1434	THR	SER	S1250	SER		L1056	N994	ARG	G795	F728	L661	C595
H1435	PHE	R1251	R1251	ARG		L1057	A995	GLY	Q796	T729	Q663	C596
G1436	LYS	L1252	T1252	LEU		N1058	S996	GLY	I797	L730	H664	F597
L1437	LYS	L1253	L1253	ALA			L997	SER	N799	V731	G665	T599
A1438	SER	L1254	L1254	ALA		L1064	A931	GLY	F798	H732	R666	R600
T1439	LEU	L1255	A1255	SER		S1065	A998	GLY	N799	V733	L667	E601
Q1440	ASP	C1256	C1256	MET		PRO	F999	ARG	R800	L734	R668	A602
R1441	MET	C1257	C1257	LEU		PRO	F934	ARG	G801	E735	T669	F603
L1442	LYS	V1257	V1257	ASP		ALA	F1000	ALA	R802	E736		T604
L1443	ALA	L1258	L1258	ASP		ALA	L1001	SER	G803			F605
L1444	ARG	W1259	W1259	SER		SER	S1002	LEU	A804	F741	C673	V606
V1444	ARG	V1260	V1260	ASP		PRO	D1003	THR	F805	R742	L674	
S1445	LEU	L1261	L1261	THR		SER	L1004	TYR	A805	L743		
K1446	GLU	T1262	K1262	GLY		PRO		ALA				
F1447	GLY											

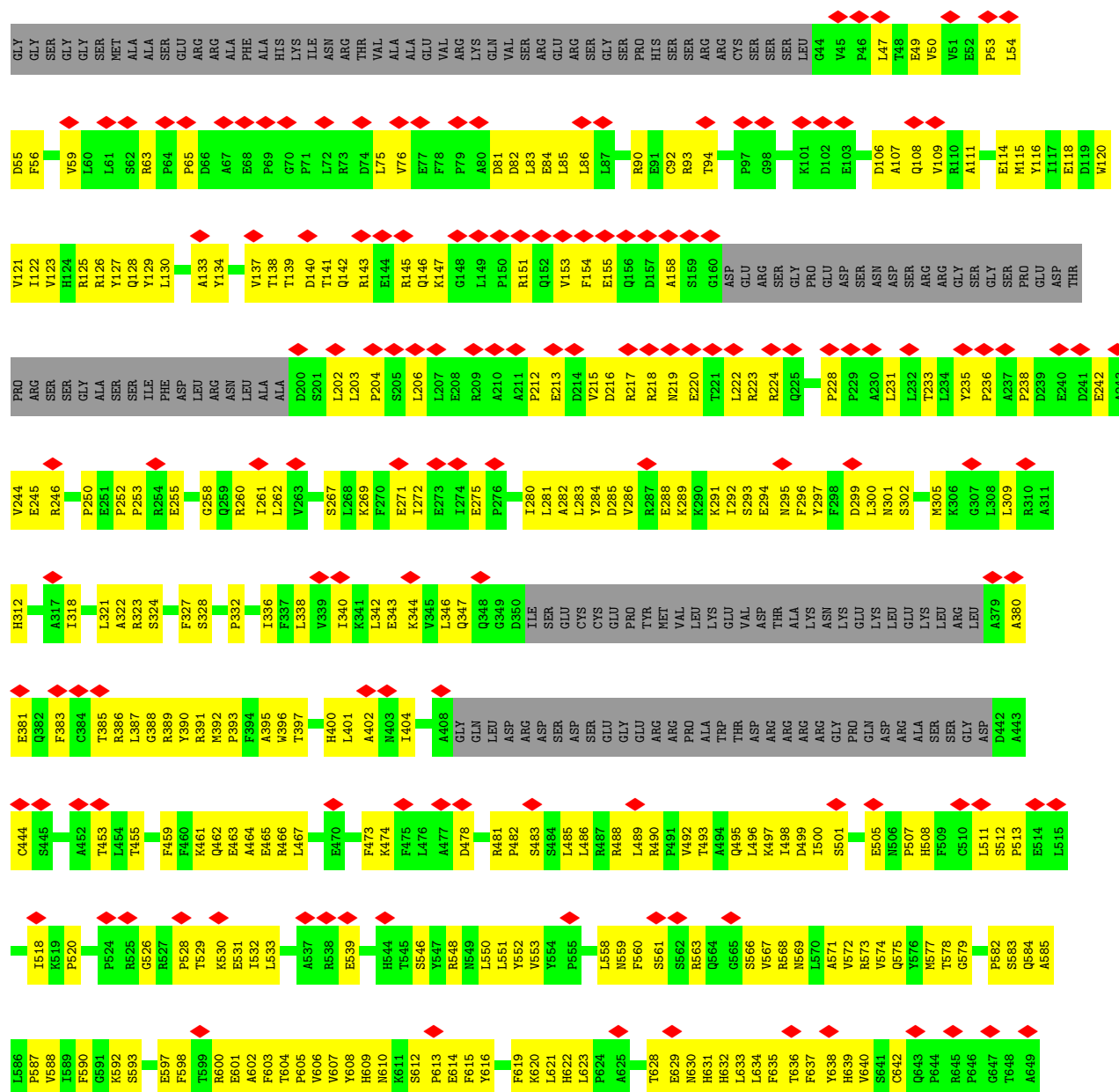
- Molecule 1: Dedicator of cytokinesis protein 6



V975	K906	E846	K782	A713	P582	I518	A452	G388	I326	K364	SER
G976	L907	P847	L783	V714	S583	K519	T453	R389	F327	C265	SER
L977	H909	SER	W784	S715	Q584	P520	T456	Y390	S328	L268	ILE
E978	E910	LEU	R785	W716	A585	Y521	V456	R391	S329	S267	PHE
V979	E911	PRO	R786	W717	L586	P522	T457	F394	L268	L268	ASP
T980	L912	ASP	L787	Q720	P587	D523	N457	F394	K269	K269	LEU
T981	A913	ALA	I788	W723	V588	P524	N458	A395	F270	F270	ARG
L982	L914	PRO	R789	W724	L589	P525	F459	A395	E271	E271	ASN
V983	Q915	PRO	W790	L724	L589	R525	F460	W396	L272	L272	LEU
H984	W916	VAL	W791	D725	F590	G526	K461	T397	E273	E273	ALA
K985	V917	THR	L792	K726	G591	R527	K462	A398	I277	I277	D200
D986	W918	THR	L793	L659	S593	P528	K463	V399	G279	G279	S205
V987	S919	VAL	W794	P659	S594	P529	R466	H400	I280	I280	S205
E988	S920	GLN	L795	L661	C595	L532	L467	L401	L281	L281	L202
L989	G795	ALA	L796	L662	S596	L533	S468	A402	L282	L282	L203
A990	G796	ALA	W797	L663	T599	L533	D469	N403	L283	L283	L204
E991	L797	THR	H731	Q663	E601	E531	E470	I404	L284	L284	S205
E992	L798	LEU	H732	H664	A602	L533	F473	A408	G279	G279	L207
H993	W798	ALA	L733	G665	E601	E534	K474	GLY	L285	L285	L207
L994	N799	ARG	L734	R666	A602	E535	F475	ASP	L286	L286	R209
N994	L800	GLY	E735	L667	P605	P536	L476	ASP	V285	V285	P212
A998	G803	GLY	E736	T669	G605	A537	K477	ASP	G348	G348	E213
F999	A804	ARG	G670	G670	H609	R538	L477	SER	I344	I344	D216
F1000	F805	PRO	P671	P671	H609	E539	A477	SER	V345	V345	N219
L1001	E806	ALA	F672	C673	N610	H544	D478	ASP	G347	G347	E220
S1002	A807	LEU	L743	K611	K611	Y547	M479	GLY	Q289	Q289	T221
D1003	M808	TYR	K744	D745	S612	R548	R480	GLY	K290	K290	T221
L1004	A809	LEU	D745	D745	P613	N549	R481	GLY	K291	K291	L222
L1005	H810	ALA	L748	L748	P613	R549	P482	GLY	L292	L292	R223
S1006	W811	ARG	G677	G677	P613	L550	P483	GLY	S293	S293	R224
L1007	H815	SER	D678	D678	E614	L551	S484	ARG	E294	E294	R227
V1008	R816	LYS	G679	G679	F615	L551	S484	ARG	N295	N295	L231
D1009	S941	ILE	Q680	Q680	E617	Y552	L485	PRO	F296	F296	L232
R1010	L819	SER	G751	G751	S617	V553	L486	TRP	Y297	Y297	L232
G1011	E820	SER	P681	P681	K620	V553	L486	TRP	F298	F298	L233
F1012	E821	SER	P682	P682	L621	Y554	L486	TRP	F298	F298	L233
F1014	A822	SER	Q683	Q683	H622	P555	L486	TRP	F298	F298	L234
S1015	Q823	ASN	S684	S684	H622	P555	L486	TRP	F298	F298	L234
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V1017	D824	ASP	S684	S684	H622	P555	L486	TRP	F298	F298	Y235
R1018	A825	LEU	S685	S685	L623	H556	L486	TRP	F298	F298	Y235
A1019	R826	ALA	S686	S686	A625	S557	L486	TRP	F298	F298	Y235
H1020	G827	VAL	V687	V687	A625	L558	L486	TRP	F298	F298	Y235
R956	H828	VAL	L688	L688	C626	N559	L486	TRP	F298	F298	Y235
K957	C829	ALA	L688	L688	C626	N559	L486	TRP	F298	F298	Y235
L958	C829	PRO	L688	L688	C626	N559	L486	TRP	F298	F298	Y235
R959	P830	GLY	L688	L688	C626	N559	L486	TRP	F298	F298	Y235
F960	Q831	SER	L688	L688	C626	N559	L486	TRP	F298	F298	Y235
G961	L832	VAL	L688	L688	C626	N559	L486	TRP	F298	F298	Y235
G962	Y835	D896	L694	L694	H631	Q564	L486	TRP	F298	F298	Y235
R963	W836	D897	P695	P695	H631	Q564	L486	TRP	F298	F298	Y235
F964	H837	E898	P697	P697	H631	Q564	L486	TRP	F298	F298	Y235
D967	Y838	E899	P697	P697	H631	Q564	L486	TRP	F298	F298	Y235
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A1035	F840	R901	R841	R841	H631	Q564	L486	TRP	F298	F298	Y235
A1036	R841	T902	R841	R841	H631	Q564	L486	TRP	F298	F298	Y235
P1034	L842	L903	R841	R841	H631	Q564	L486	TRP	F298	F298	Y235
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P1034	T845	S905	R841	R841	H631	Q564	L486	TRP	F298	F298	Y235
A1036	T845	S905	R841	R841	H631	Q564	L486	TRP	F298	F298	Y235
P1034	T845	S905	R841	R841	H631	Q564	L486	TRP	F298	F298	Y235
A1036	T845	S905	R841	R841							



- Molecule 1: Deducator of cytokinesis protein 6

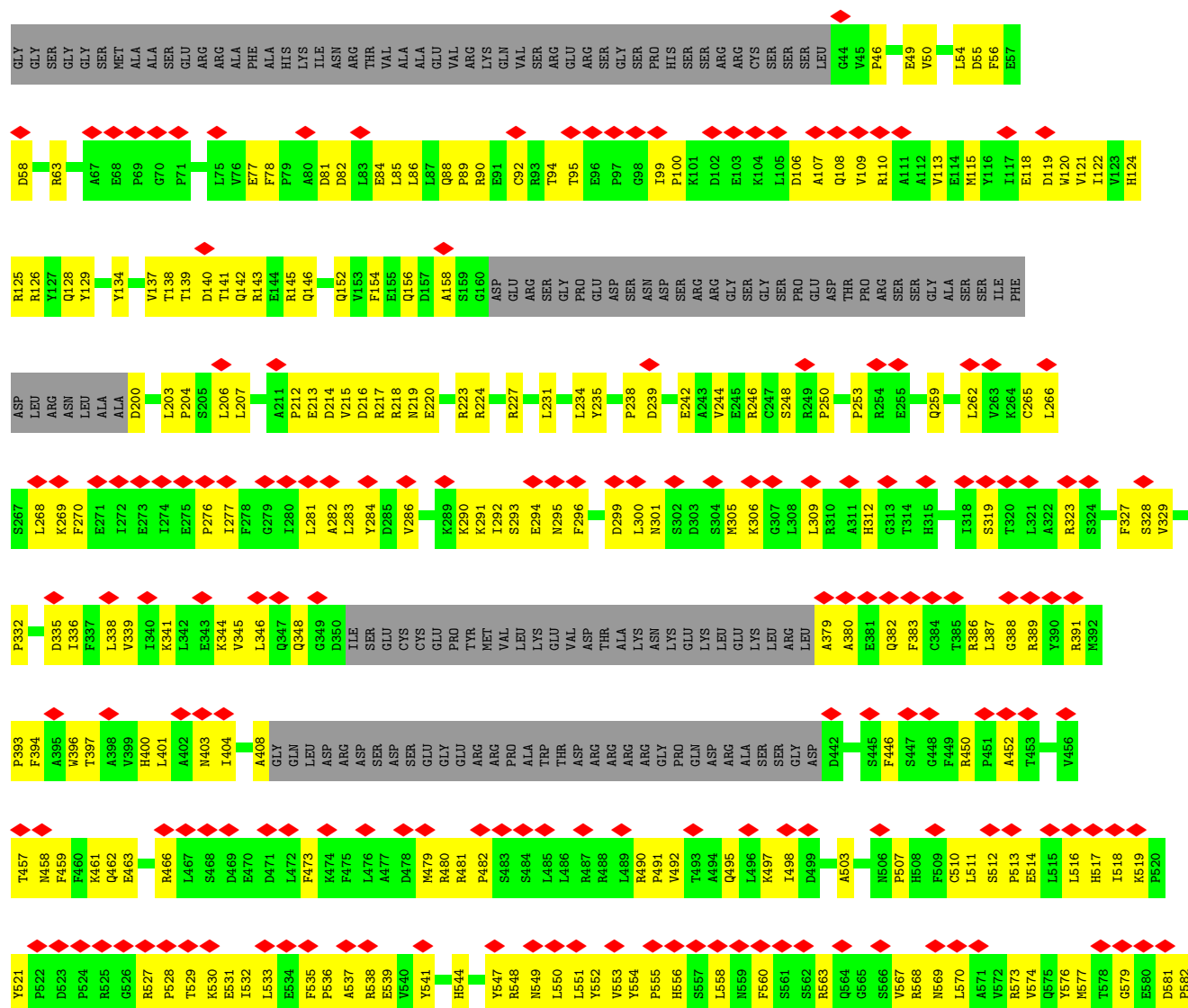


A1430	L1431	F1432	L1433	Q1434	H1435	G1436	L1437	A1438	T1439	Q1440	R1441	A1442	L1443	V1444	S1445	K1446	F1447	P1448	E1449	L1450	L1451	F1452	D1455	L1458	C1459	A1460	D1461	L1462	C1463	L1464	R1465	L1466	L1467	R1468	H1469	G1470	G1471	S1472	R1473	L1474	S1475	T1476	L1477	R1478	T1479	H1480	A1481	S1482	A1483	S1484	L1485	Y1486	L1487	Q1428	S1429	R1490	L1491
THR	PHE	LYS	LYS	SER	LEU	ASP	MET	LYS	ALA	ARG	GLU	GLU	ALA	ILE	LEU	GLY	THR	ILE	GLY	ALA	ARG	GLN	GLU	MET	VAL	ARG	ARG	PRO	PHE	GLY	ASN	PRO	GLU	ASN	VAL	ARG	TRP	ARG	LYS	SER	VAL	THR	HIS	TRP	LYS	GLN	THR	SER	ASP	ARG	VAL	ASP	LYS				
C1243	A1244	S1246	S1249	S1250	R1251	T1252	L1253	L1254	A1255	C1256	V1257	L1258	W1259	V1260	L1261	K1262	N1263	L1264	E1265	P1266	A1267	L1268	L1269	Q1270	R1271	W1272	L1276	T1277	L1278	P1279	Q1280	L1281	G1282	R1283	L1287	L1288	Y1289	L1290	C1291	A1294	F1295	E1296	Y1297	K1300	K1301	A1302	F1303	GLU	ARG	ILE	ASN	SER	LEU				
L1113	L1114	T1115	E1116	L1117	L1121	E1122	P1123	E1124	A1125	A1128	F1129	L1130	L1131	H1132	K1133	L1134	A1135	I1136	V1139	H1140	L1143	C1144	D1147	T1148	R1151	Y1152	A1153	E1154	A1155	T1156	V1157	R1160	V1161	A1162	E1163	L1164	P1167	L1168	L1169	S1170	I1171	A1172	R1173	L1176	F1177	R1178	L1179	H1180	D1181	F1182							
E1052	H1053	Y1054	V1055	T1056	L1057	M1058	L1059	P1060	C1061	L1064	S1065	PRO	PRO	ALA	SER	PRO	PRO	SER	VAL	SER	THR	THR	GLN	SER	SER	THR	PHE	SER	Q1087	A1088	P1089	D1090	P1091	K1092	V1093	T1094	S1095	M1096	F1097	E1098	L1099	S1100	G1101	P1102	F1103	R1104	Q1105	Q1106	H1107	F1108	L1109	A1110	G1111	L1112			
K985	D986	E988	E991	H992	L993	N994	F1000	L1001	S1002	D1003	L1004	L1005	L1006	L1007	V1008	D1009	R1010	G1011	F1012	V1013	F1014	S1015	L1016	V1017	R1018	A1019	H1020	Y1021	K1022	Q1023	V1024	A1025	L1026	R1027	L1028	Q1029	S1030	S1031	P1034	L1037	L1038	T1039	L1040	R1041	M1042	E1043	F1044	L1045	R1046	I1047	L1048	C1049	S1050	H1051			
L914	Q915	W916	V917	V918	R924	I927	L928	Q929	H930	A931	W932	F933	F934	F935	Q936	L937	H938	V939	K940	S941	L944	L947	L952	D953	T954	P955	R956	R959	F960	P961	R963	F964	L965	D966	D967	I968	T969	A970	L971	V972	G973	S974	V975	G976	L977	E978	V979	L980	T981	R982	L983	H984					
I788	R789	P790	V791	I792	Q796	I797	V798	N799	L800	G801	R802	G803	A804	F805	G806	A807	M808	A809	H810	V811	V812	S813	L814	V815	H816	R817	S818	L819	Y820	A821	A822	Q823	D824	A825	R826	G827	H828	C829	L832	Y835	V836	H837	Y838	A839	F840	R841	L842	P843	T845	E846	P847	SER	LEU	PRO	ASP		
L650	E651	T652	P653	V654	G655	T656	W658	I659	P660	L661	G662	Q663	H664	G665	R666	L667	R668	T669	F672	G673	L674	S677	V678	S684	Y685	S686	V687	P690	D691	V692	A693	G696	W697	R698	W699	V700	D701	G702	H703	F706	S708	L711	T712	A713	T714	S715	S716	V717	H718	P719							
Y723	L724	P725	K726	V727	F728	T729	L730	V731	H732	V733	L734	E735	E736	G737	F741	M742	L743	H744	D745	T746	L747	L748	S749	E750	G751	N752	Y753	E754	Q755	E756	L757	R758	A759	S760	L761	A762	A763	L764	A767	E770	P771	L772	V773	S776	V779	L780	D781	K782	L783	V784	S785	L786	V787				

V123	H124	R125	Y127	Q128	Y129	L130	S131	A132	Y134	V137	T138	T139	D140	Q141	Q142	R143	E144	R145	Q146	K147	G148	L149	P150	R151	Q152	V153	F154	E155	Q156	D157	A158	S159	G160	ASP	GLU	ARG	SER	GLY	PRO	GLU	ASP	SER	ASN	ASP	SER	ARG	ARG	GLY	SER	GLY	SER	PRO	GLU	ASP	THR	PRO
ARG	SER	GLY	ALA	SER	SER	ILE	PHE	ASP	LEU	ARG	ASN	LEU	ALA	D200	S201	L202	L203	P204	S205	L206	L207	E208	R209	A210	A211	E213	D214	V215	D216	R217	R218	N219	E220	T221	L222	R223	R224	Q225	P228	P229	A230	L231	L232	T233	L234	Y235	P236	A237	P238	D239	E240	D241	E242	V243		
E245	R246	P250	E255	Q259	R260	I261	L262	V263	K264	C265	K269	F270	E271	I272	E273	I274	E275	P276	I277	E278	G279	I280	L281	A282	L283	Y284	D285	V286	R287	E288	K289	K290	K291	I292	S293	E294	N295	F296	Y297	F298	D299	L300	N301	S302	M305	K306	G307	H312	H315	P316	A317	I318				
L321	A325	I326	F327	S328	V329	T330	Y331	I336	F337	L338	V339	I340	K341	L342	E343	K344	V345	Q347	Q348	G349	D350	ILE	SER	GLU	CYS	CYS	GLU	PRO	TYR	MET	VAL	LEU	LYS	GLU	VAL	ASP	THR	ALA	LYS	ASN	LYS	GLU	LEU	LEU	LEU	A379	A380	F383	C384	T385						
R386	L387	G388	R389	Y390	R391	M392	P393	F394	A395	V396	H400	L401	A402	N403	A408	GLY	GLN	LEU	ASP	ARG	ASP	SER	SER	GLU	GLY	GLY	ALA	THR	THR	THR	ARG	ARG	ARG	ARG	GLY	PRO	GLN	ASP	ARG	ALA	SER	GLY	ASP	D442	A443	C444	S445	A452	T453	V456						
Q462	E463	A464	E465	R466	L472	F473	K474	F475	L476	A477	D478	R481	S483	S484	L485	R488	A494	Q495	L496	K497	L498	D499	I500	S501	P502	A503	P504	E505	N506	P507	H508	Q575	Y576	M577	T578	C510	L511	S512	P513	E514	L515	L516	H517	L518	R519	P520	P524	R525	T529	K530	E531	I532	L533	E534		
F535	P536	A537	R538	E539	H544	Y547	R548	N549	L550	L551	Y552	V553	Y554	P555	H556	S557	L558	N559	F560	S561	S562	R563	Q564	S565	S566	L567	A571	V572	R573	V574	Q575	Y576	M577	T578	C510	L511	S512	P513	E514	L515	L516	H517	L518	R519	P520	P524	R525	T529	K530	E531	I532	L533	E534			
T604	P605	V606	V607	Y608	H609	N610	K611	S612	P613	E614	F615	Y616	E617	S618	F619	K620	L621	H622	S623	F624	A625	T628	E629	H630	H631	H632	L633	L634	T636	F637	V638	H639	V640	C542	Q643	G647	T648	A649	L650	E651	G655	F656	T657	W658	T659	P660	L661	L662	Q663	R666	L667	R668				
L674	S677	F683	S684	Y685	S686	Y687	L688	T689	P690	A693	L694	F695	G696	H697	A763	L764	R765	V773	S776	H777	L780	D781	L783	V784	R785	L786	V787	I788	R789	P790	F791	I792	Q720	D721	F722	Y723	L724	D725	K726	F727	T728	L730	W731	H732	W733	W734	E735	E736	G737	A738	F739	F740	F741			
R742	L743	T746	Y747	S749	E750	V753	E754	Q755	E756	L757	R758	L761	R763	A764	T845	L764	R765	V773	S776	H777	L780	D781	L783	V784	R785	L786	V787	I788	R789	P790	F791	I792	Q796	F722	Y723	L724	D725	K726	F727	T728	L730	W731	H732	W733	W734	E735	E736	G737	A738	F739	F740	F741				
D824	A825	H828	L832	Y835	R836	H837	Y838	A839	L842	R843	G844	T845	L764	R765	V773	S776	H777	L780	D781	L783	V784	R785	L786	V787	I788	R789	P790	F791	I792	Q796	F722	Y723	L724	D725	K726	F727	T728	L730	W731	H732	W733	W734	E735	E736	G737	A738	F739	F740	F741							
LEU	ALA	VAL	ALA	PRO	GLY	SER	VAL	D896	D897	E898	V899	S900	R901	L902	L903	A904	S905	K906	L907	L908	H909	E910	E911	A913	L914	Q915	W916	V917	R924	E925	A926	I927	L928	Q929	H930	A931	W932	F933	M938	M942	A943	L944	L947	R951	K1022	L952	D953	T954	A1025	P955	R956	R959	F960	P961		
G962	R963	F964	L965	D966	D967	I968	T969	A970	L971	V972	G973	S974	Y975	G976	L977	E978	V979	I980	T981	R982	Y983	H984	K985	D986	N984	A998	D1003	L1004	L1005	S1006	L1007	V1008	D1009	R1010	G1011	F1012	V1013	F1014	S1015	L1016	V1017	R1018	A1019	H1020	Y1021	K1022	L1023	S1030	I1031							



- Molecule 1: Dedicator of cytokinesis protein 6







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	102384	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50.1	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	64000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.075	Depositor
Minimum map value	-0.038	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.008	Depositor
Map size (Å)	452.2, 452.2, 452.2	wwPDB
Map dimensions	340, 340, 340	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.33, 1.33, 1.33	Depositor

5 Model quality

5.1 Standard geometry

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	0.29	0/13741	0.61	5/18646 (0.0%)
1	B	0.29	0/13741	0.58	2/18646 (0.0%)
1	C	0.30	0/13794	0.61	3/18718 (0.0%)
1	D	0.29	0/13794	0.59	0/18718
1	E	0.23	0/13794	0.55	0/18718
1	F	0.21	0/13741	0.56	4/18646 (0.0%)
1	G	0.21	0/13741	0.53	0/18646
1	H	0.23	0/13794	0.55	2/18718 (0.0%)
All	All	0.26	0/110140	0.57	16/149456 (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	C	0	1
1	D	0	1
1	H	0	1
All	All	0	3

There are no bond length outliers.

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	489	LEU	CA-C-N	16.87	144.44	120.49
1	F	489	LEU	C-N-CA	16.87	144.44	120.49
1	A	489	LEU	CA-C-N	13.31	142.59	121.83
1	A	489	LEU	C-N-CA	13.31	142.59	121.83
1	C	1914	ARG	CB-CG-CD	7.93	129.53	111.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	1277	THR	Peptide
1	D	1277	THR	Peptide
1	H	1516	THR	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	13425	0	13390	1202	0
1	B	13425	0	13390	1220	0
1	C	13477	0	13448	1206	0
1	D	13477	0	13448	1173	0
1	E	13477	0	13448	996	0
1	F	13425	0	13390	845	0
1	G	13425	0	13390	835	0
1	H	13477	0	13448	983	0
All	All	107608	0	107352	8321	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 39.

The worst 5 of 8321 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)
1:G:674:LEU:O	1:G:707:PHE:HB3	1.37	1.20
1:F:674:LEU:O	1:F:707:PHE:HB3	1.47	1.15
1:B:674:LEU:O	1:B:707:PHE:HB3	1.48	1.12
1:A:674:LEU:O	1:A:707:PHE:HB3	1.51	1.10
1:A:772:LEU:O	1:A:776:SER:HB3	1.50	1.10

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	1667/2053 (81%)	1506 (90%)	161 (10%)	0	100	100
1	B	1667/2053 (81%)	1501 (90%)	166 (10%)	0	100	100
1	C	1673/2053 (82%)	1490 (89%)	183 (11%)	0	100	100
1	D	1673/2053 (82%)	1506 (90%)	167 (10%)	0	100	100
1	E	1673/2053 (82%)	1552 (93%)	121 (7%)	0	100	100
1	F	1667/2053 (81%)	1566 (94%)	101 (6%)	0	100	100
1	G	1667/2053 (81%)	1570 (94%)	97 (6%)	0	100	100
1	H	1673/2053 (82%)	1546 (92%)	127 (8%)	0	100	100
All	All	13360/16424 (81%)	12237 (92%)	1123 (8%)	0	100	100

There are no Ramachandran outliers to report.

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	1470/1773 (83%)	1470 (100%)	0	100	100
1	B	1470/1773 (83%)	1470 (100%)	0	100	100
1	C	1476/1773 (83%)	1476 (100%)	0	100	100
1	D	1476/1773 (83%)	1476 (100%)	0	100	100
1	E	1476/1773 (83%)	1476 (100%)	0	100	100
1	F	1470/1773 (83%)	1469 (100%)	1 (0%)	88	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	1470/1773 (83%)	1470 (100%)	0	100	100
1	H	1476/1773 (83%)	1476 (100%)	0	100	100
All	All	11784/14184 (83%)	11783 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	1910	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 156 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	1689	GLN
1	H	994	ASN
1	G	301	ASN
1	G	1767	GLN
1	H	1731	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](#)

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

There are no chain breaks in this entry.

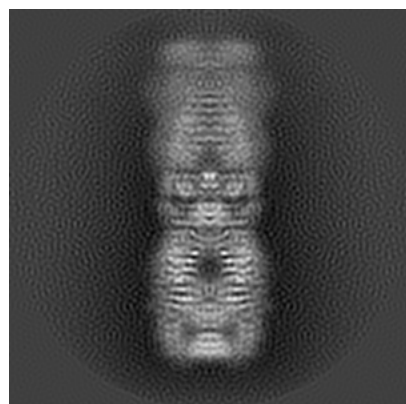
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-65180. These allow visual inspection of the internal detail of the map and identification of artifacts.

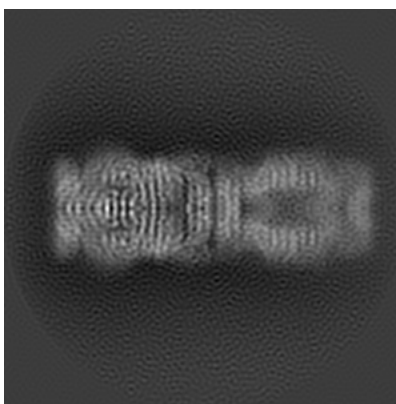
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

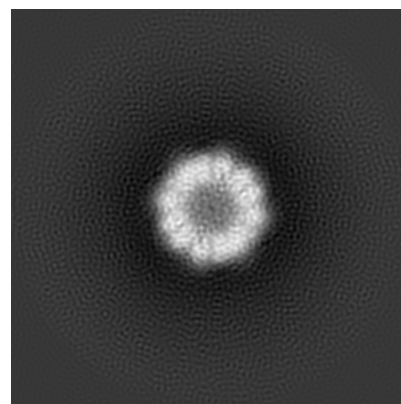
6.1.1 Primary map



X

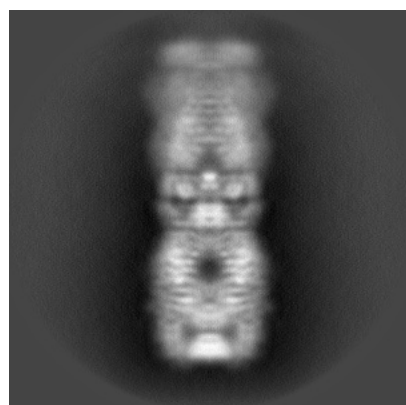


Y

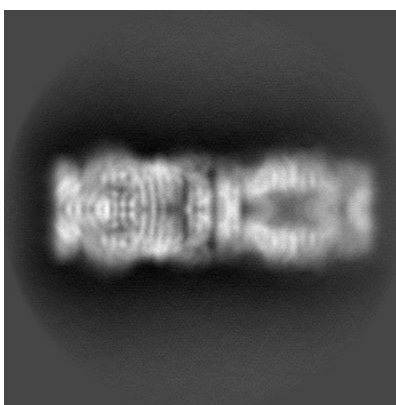


Z

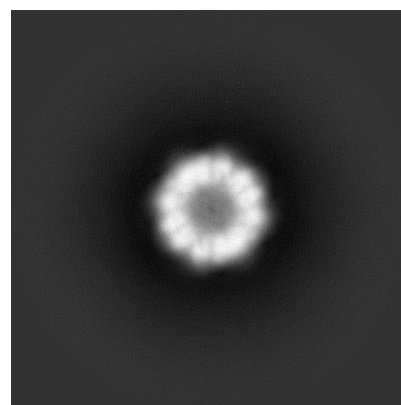
6.1.2 Raw map



X



Y

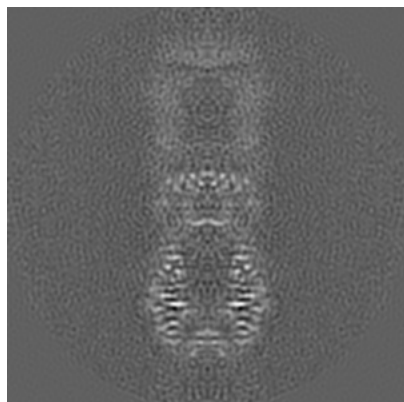


Z

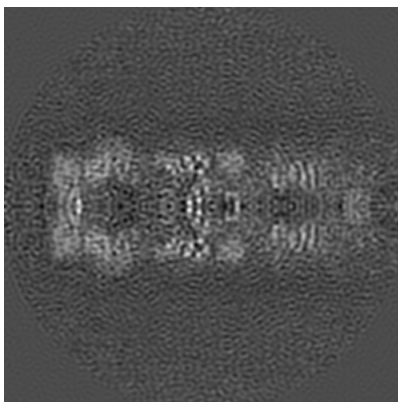
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

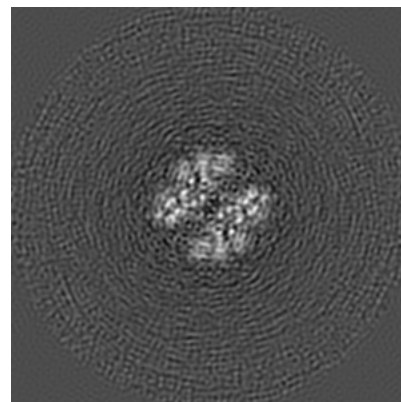
6.2.1 Primary map



X Index: 170

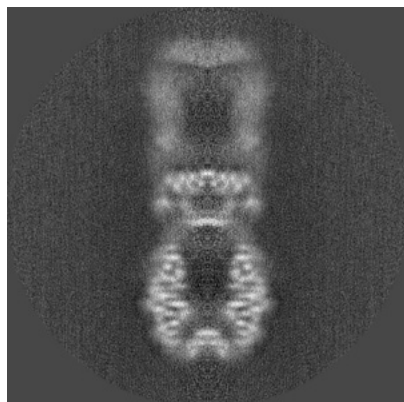


Y Index: 170

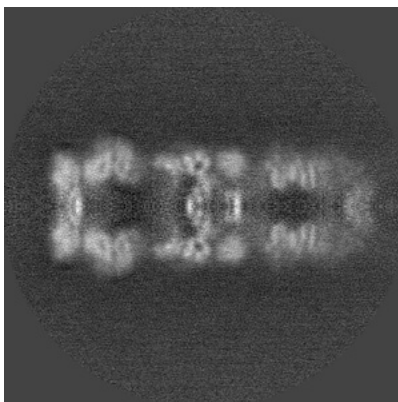


Z Index: 170

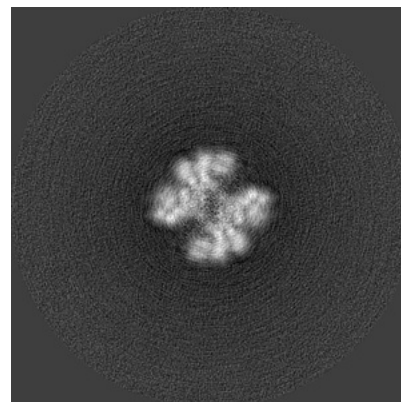
6.2.2 Raw map



X Index: 170



Y Index: 170



Z Index: 170

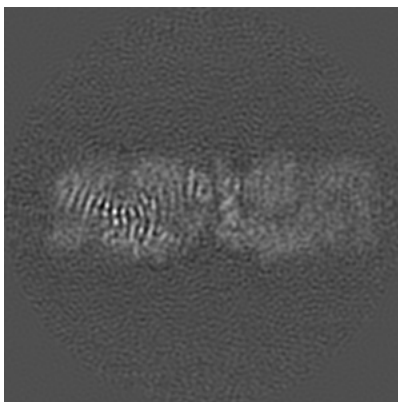
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

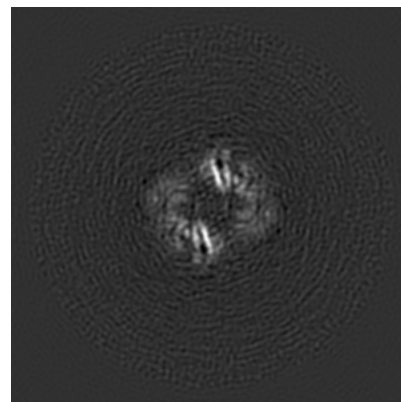
6.3.1 Primary map



X Index: 166

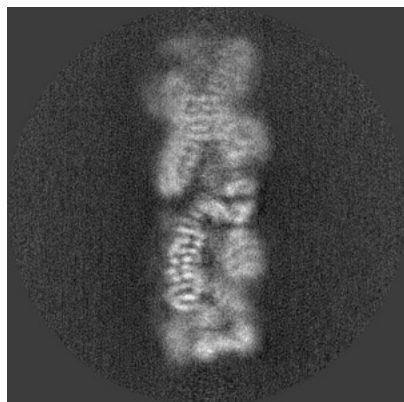


Y Index: 143

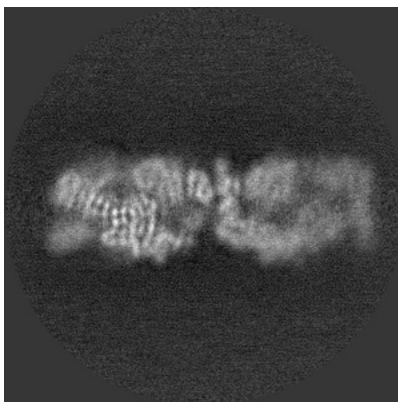


Z Index: 94

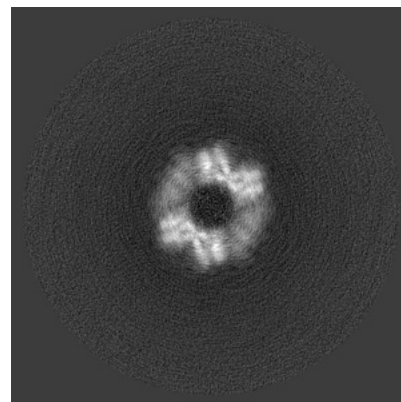
6.3.2 Raw map



X Index: 146



Y Index: 144

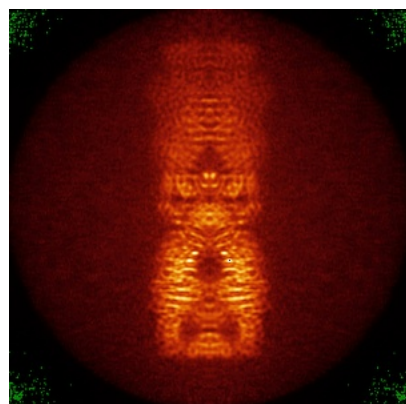


Z Index: 110

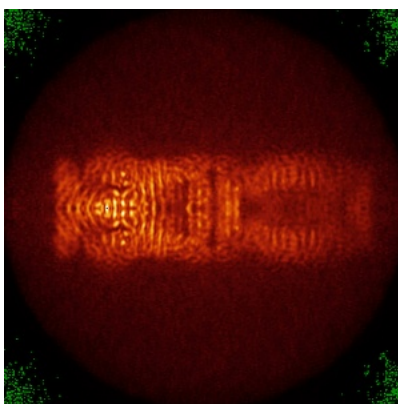
The images above show the largest variance slices of the map in three orthogonal directions.

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

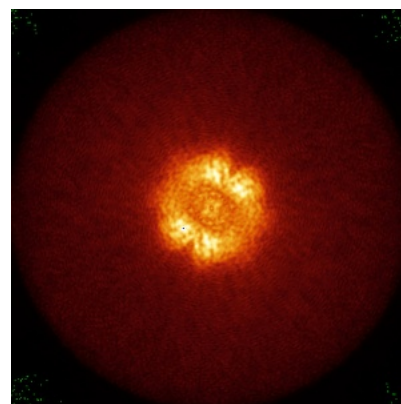
6.4.1 Primary map



X

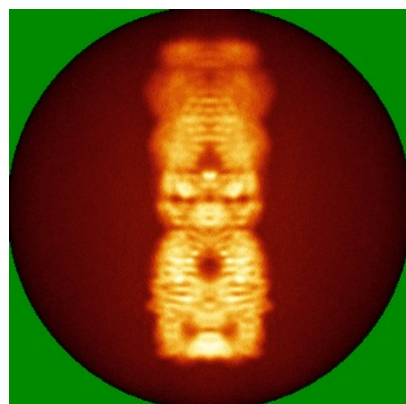


Y

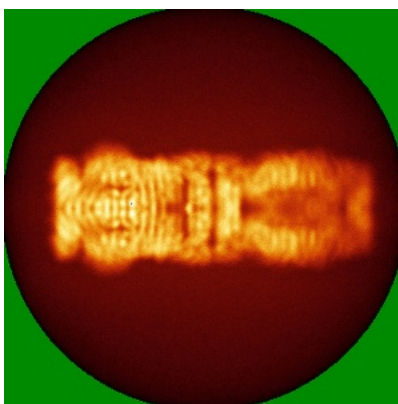


Z

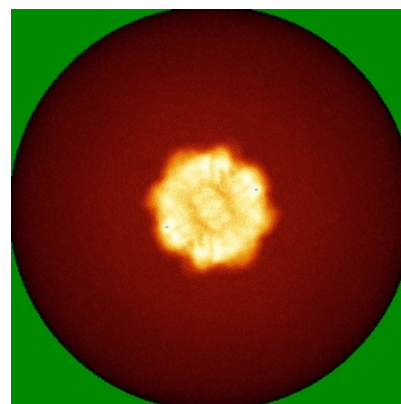
6.4.2 Raw map



X



Y

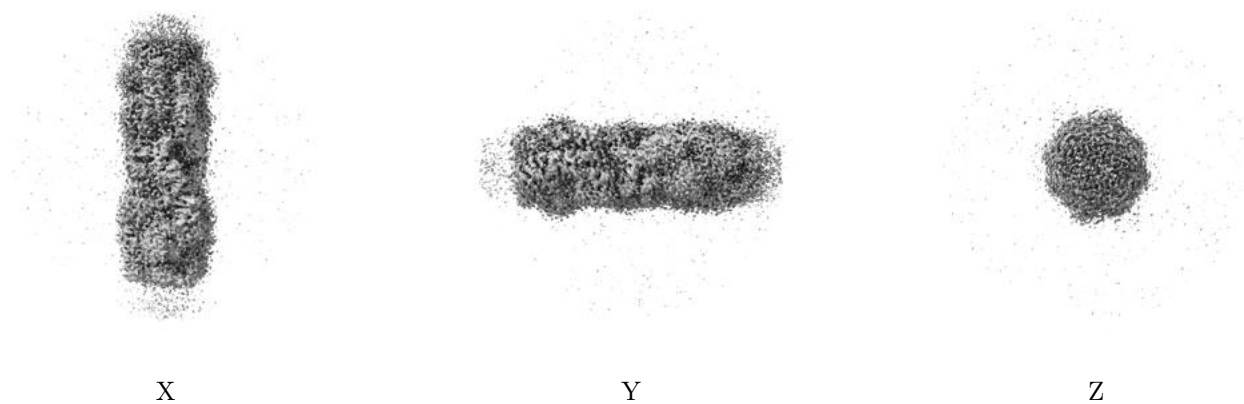


Z

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.

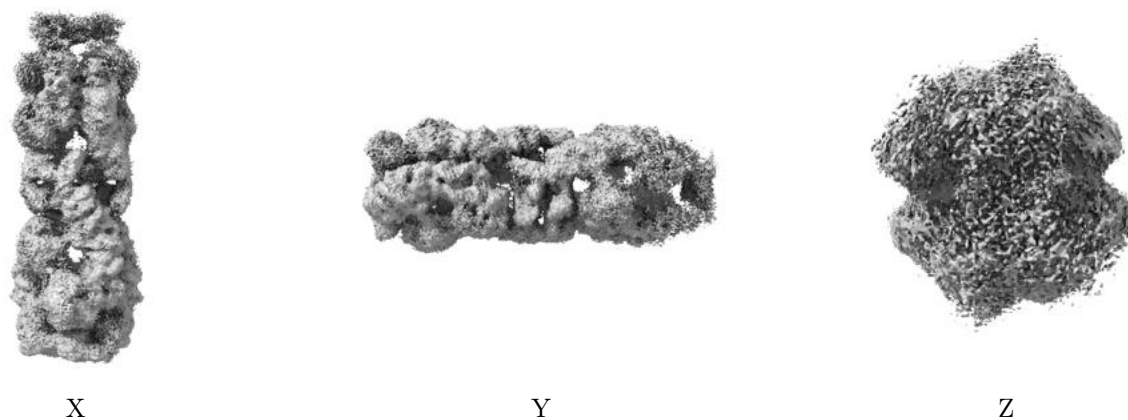
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.008. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

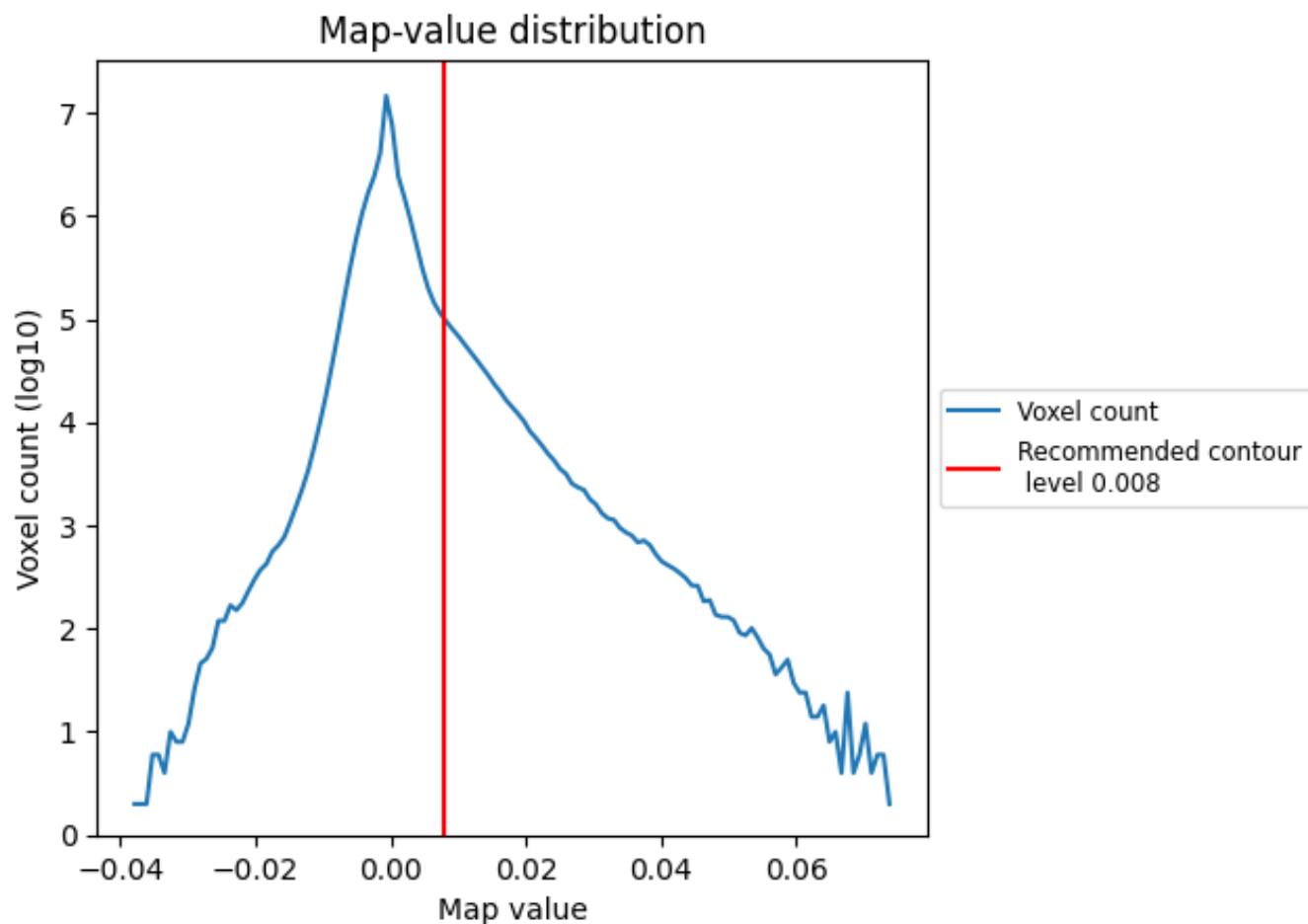
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

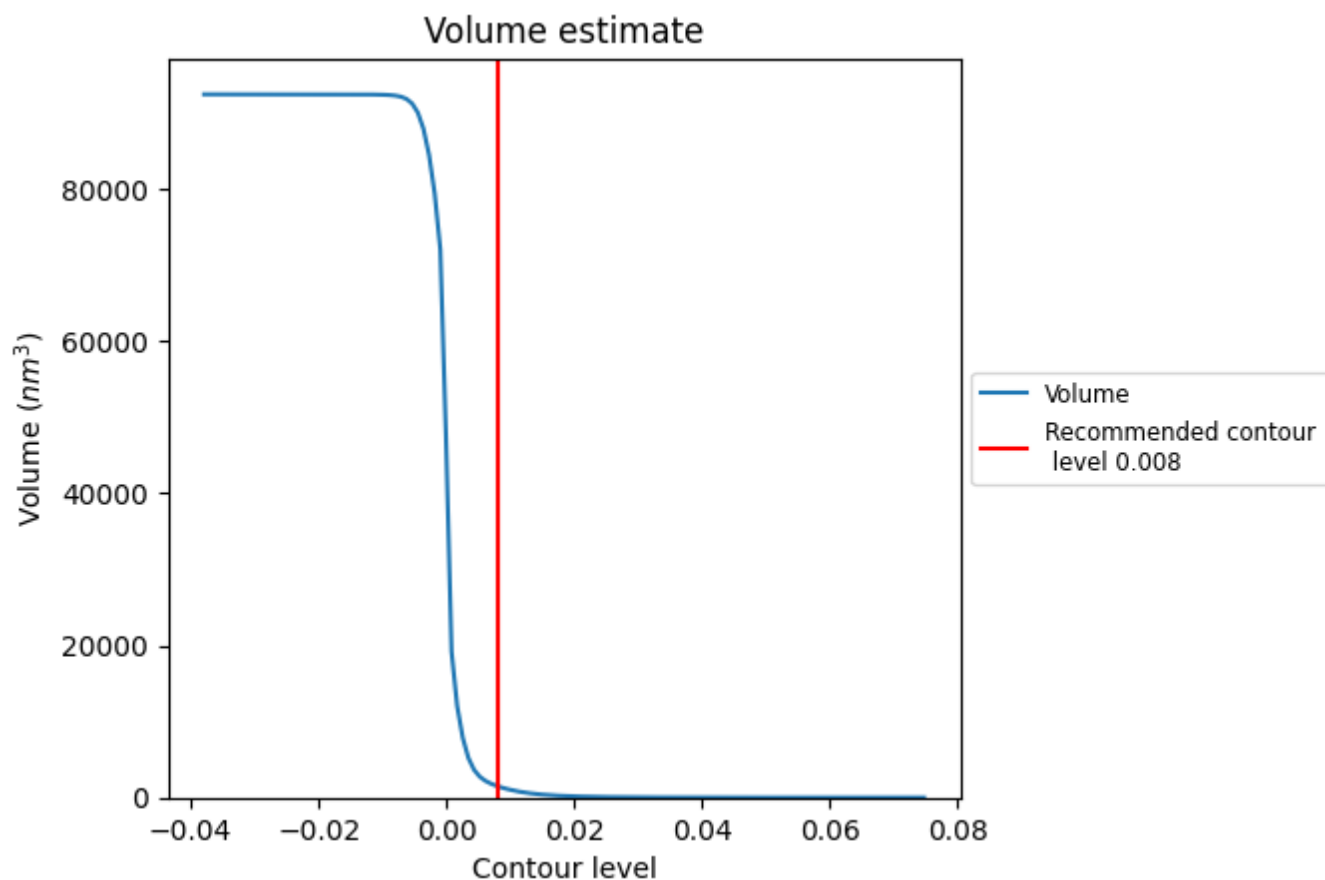
This section contains the results of statistical analysis of the map.

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.

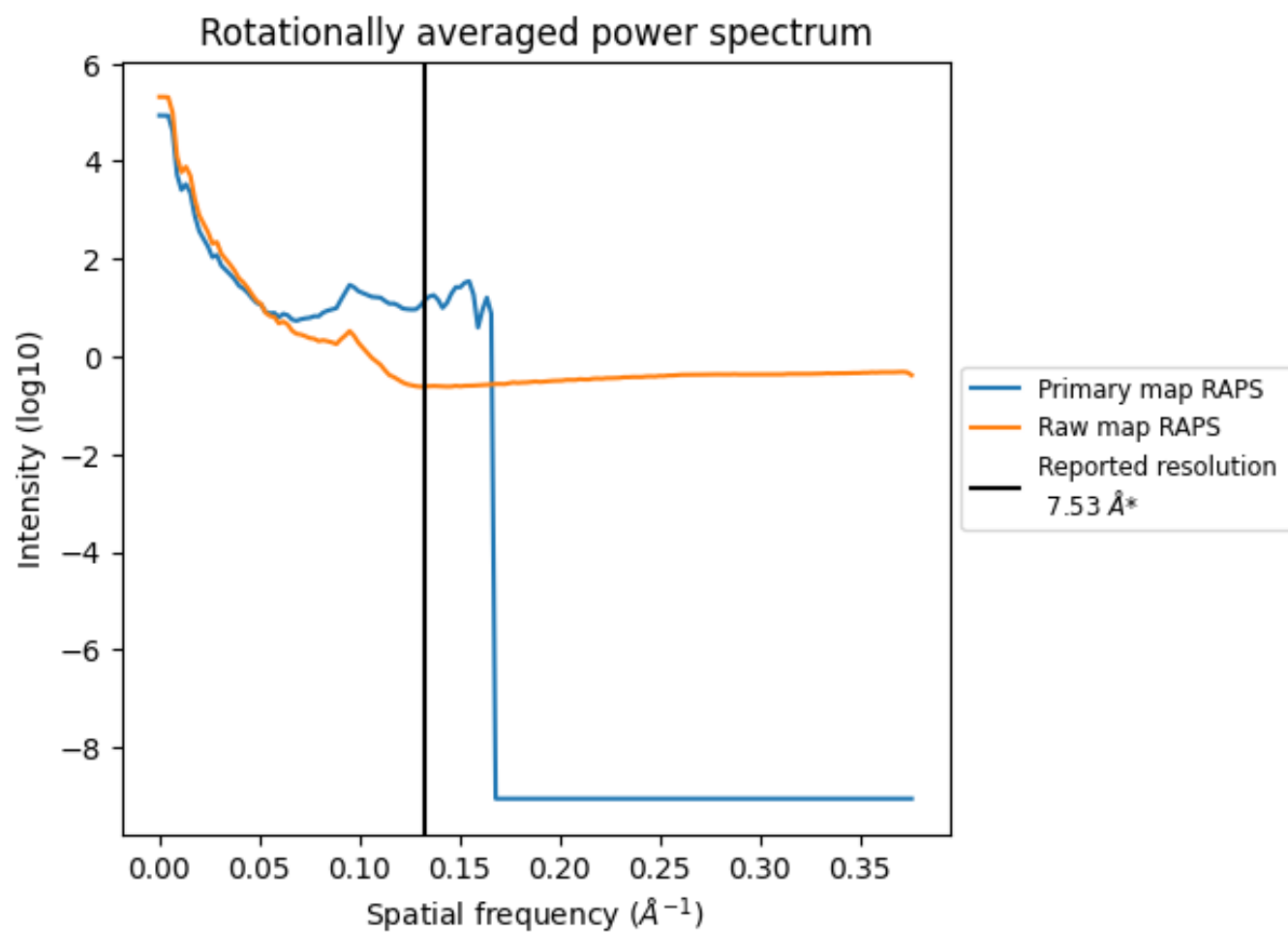
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1498 nm³; this corresponds to an approximate mass of 1353 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 ⓘ

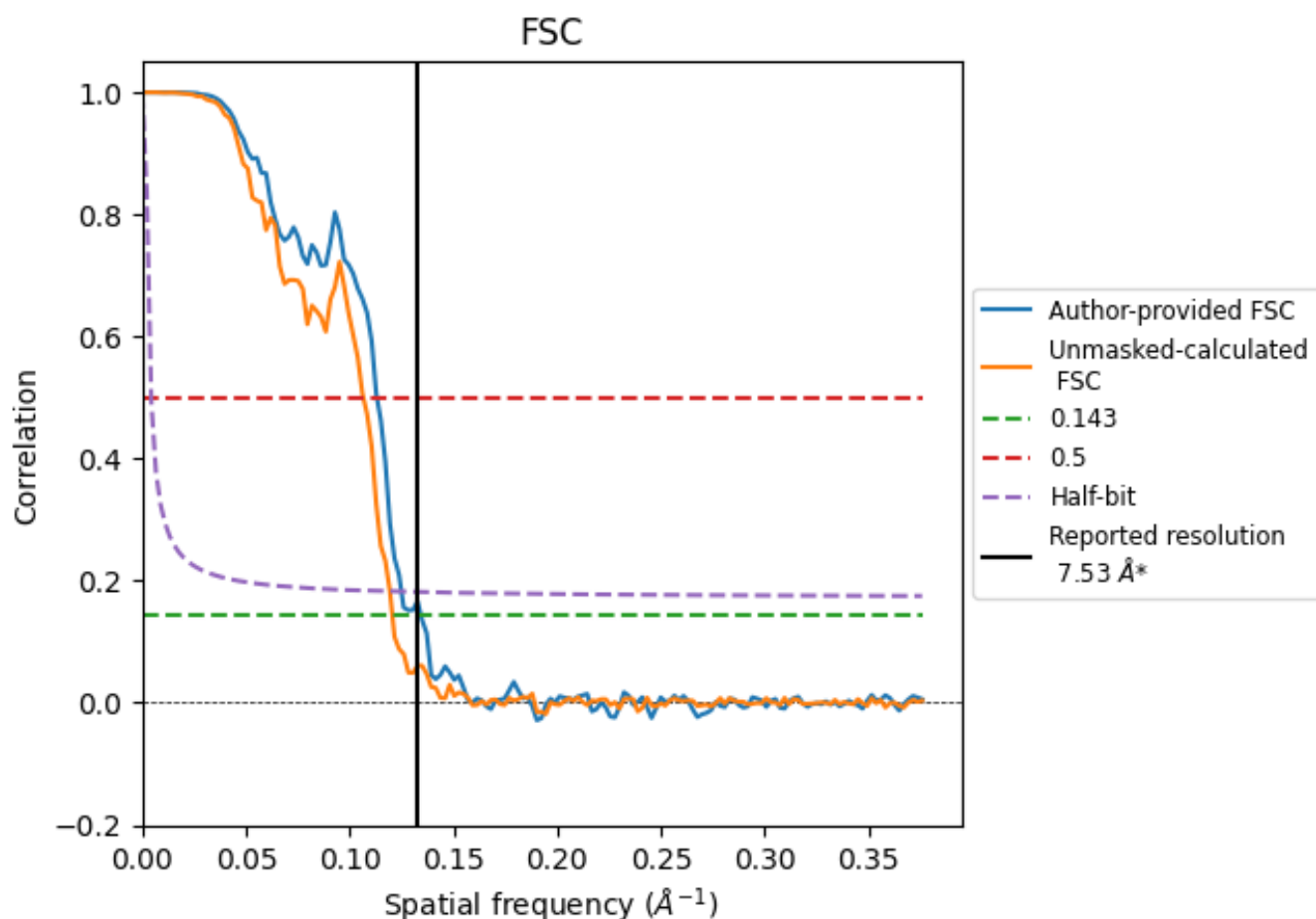


*Reported resolution corresponds to spatial frequency of 0.133 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.133 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

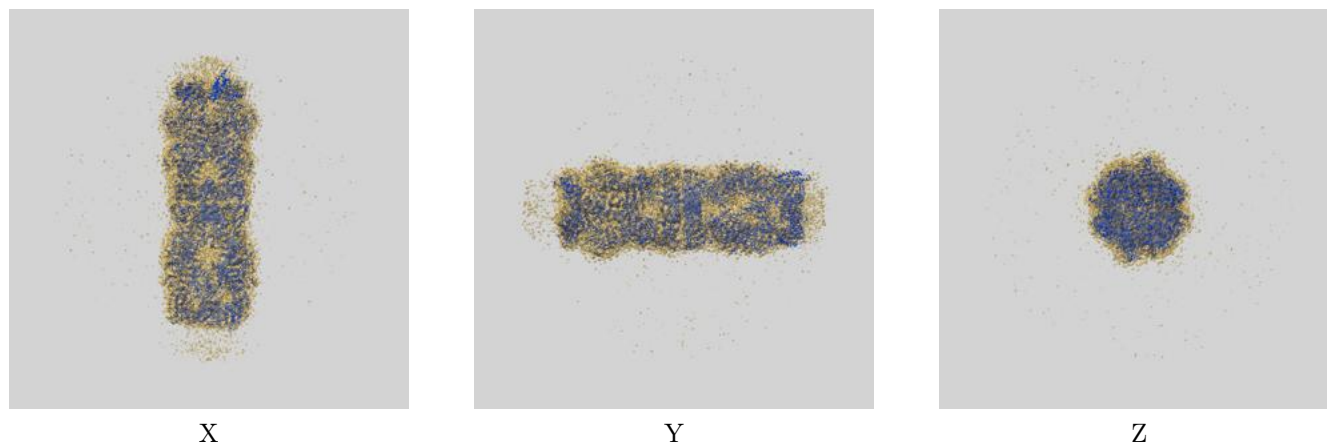
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.53	-	-
Author-provided FSC curve	7.44	8.84	8.00
Unmasked-calculated*	8.29	9.38	8.38

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 8.29 differs from the reported value 7.53 by more than 10 %

9 Map-model fit [i](#)

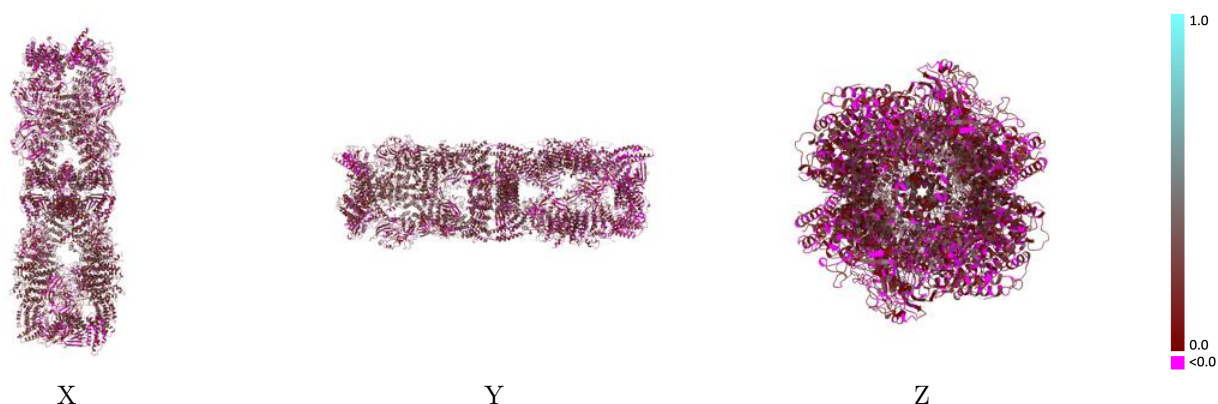
This section contains information regarding the fit between EMDB map EMD-65180 and PDB model 9VM8. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



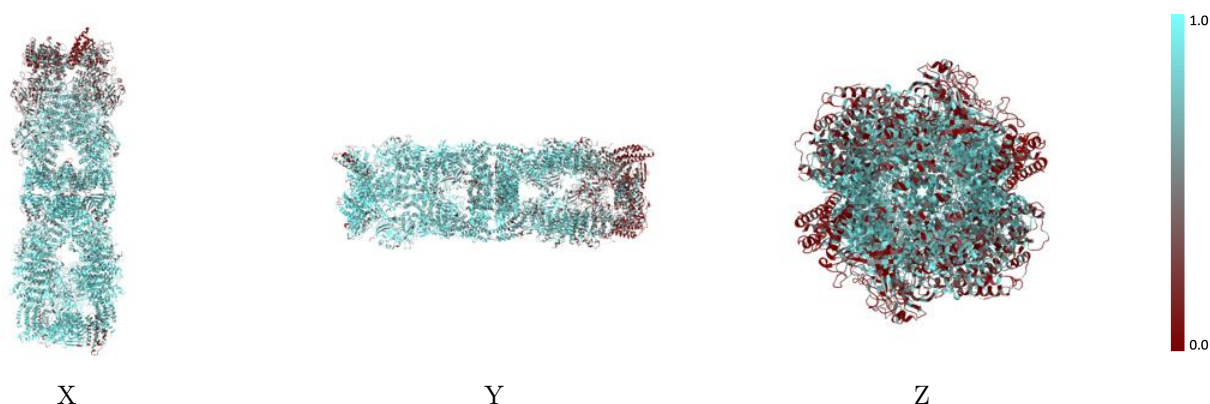
The images above show the 3D surface view of the map at the recommended contour level 0.008 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



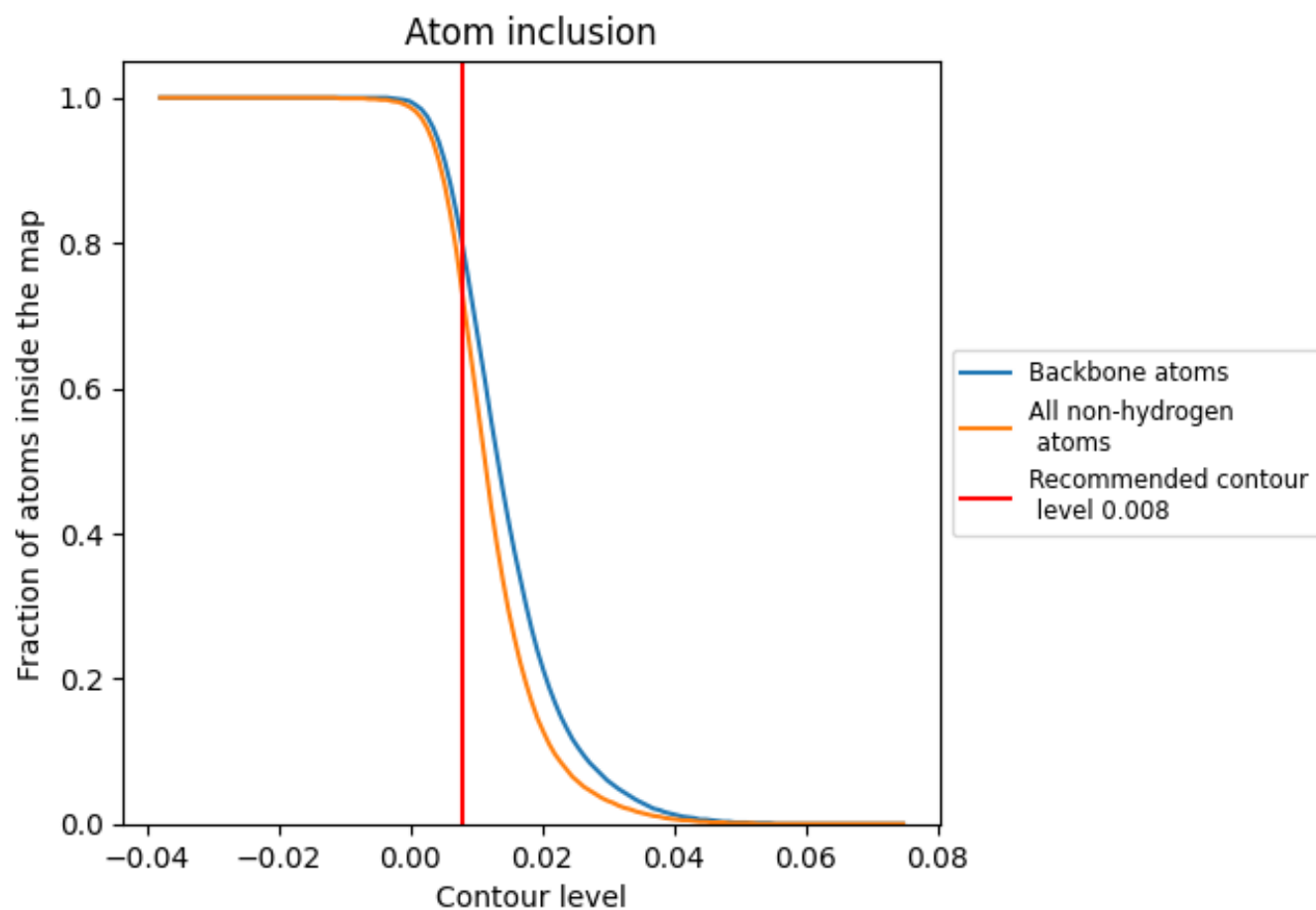
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.008).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 72% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.008) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7230	0.1730
A	0.8230	0.1890
B	0.8210	0.1870
C	0.8300	0.1980
D	0.8290	0.1970
E	0.7050	0.1670
F	0.5370	0.1400
G	0.5370	0.1410
H	0.7040	0.1680

