



wwPDB EM Validation Summary Report ⓘ

May 28, 2026 – 04:40 PM 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.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

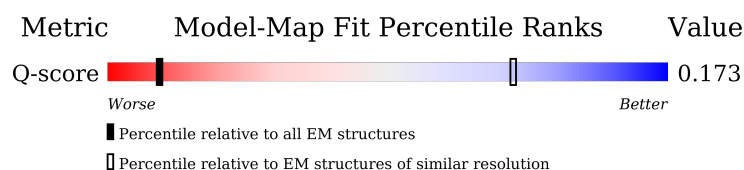
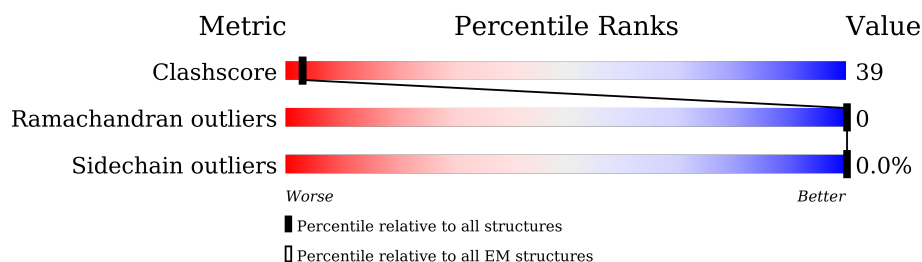
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 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.





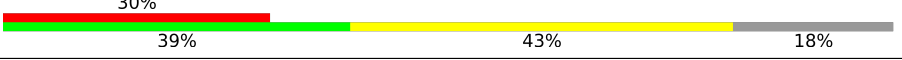
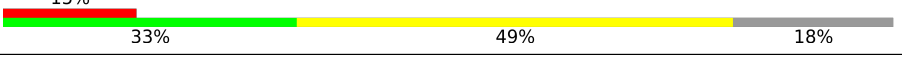
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	374 (7.04 - 8.01)

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	<div> <div>6%</div> <div>29%</div> <div>53%</div> <div>18%</div> </div>
1	B	2053	<div> <div>6%</div> <div>29%</div> <div>53%</div> <div>18%</div> </div>
1	C	2053	<div> <div>5%</div> <div>28%</div> <div>54%</div> <div>18%</div> </div>
1	D	2053	<div> <div>5%</div> <div>29%</div> <div>53%</div> <div>18%</div> </div>

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Mol	Chain	Length	Quality of chain
1	E	2053	
1	F	2053	
1	G	2053	
1	H	2053	

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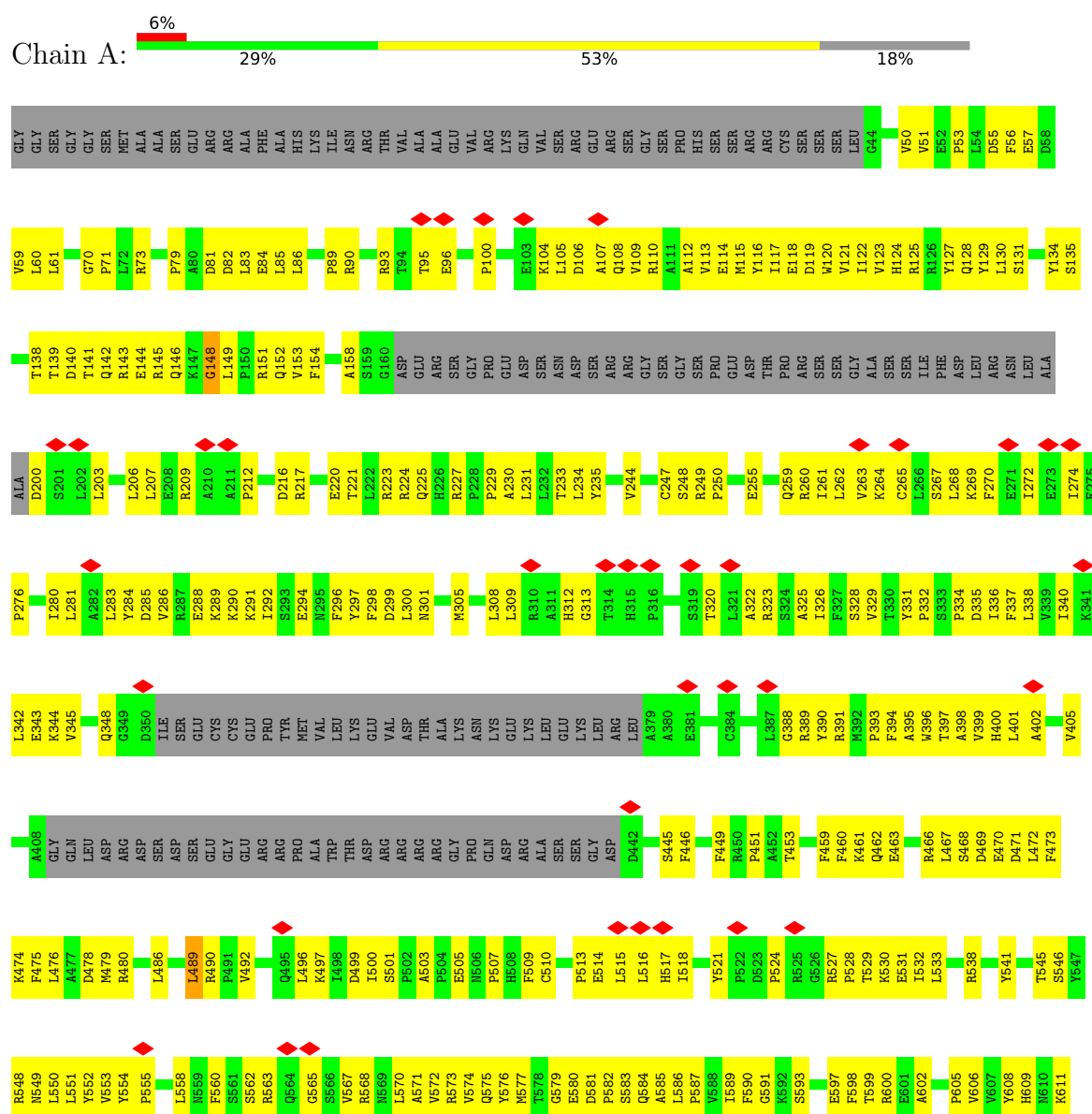
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Chain	Residue	Modelled	Actual	Comment	Reference
D	-3	SER	-	expression tag	UNP Q96HP0
D	-2	GLY	-	expression tag	UNP Q96HP0
D	-1	GLY	-	expression tag	UNP Q96HP0
D	0	SER	-	expression tag	UNP Q96HP0
B	-5	GLY	-	expression tag	UNP Q96HP0
B	-4	GLY	-	expression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

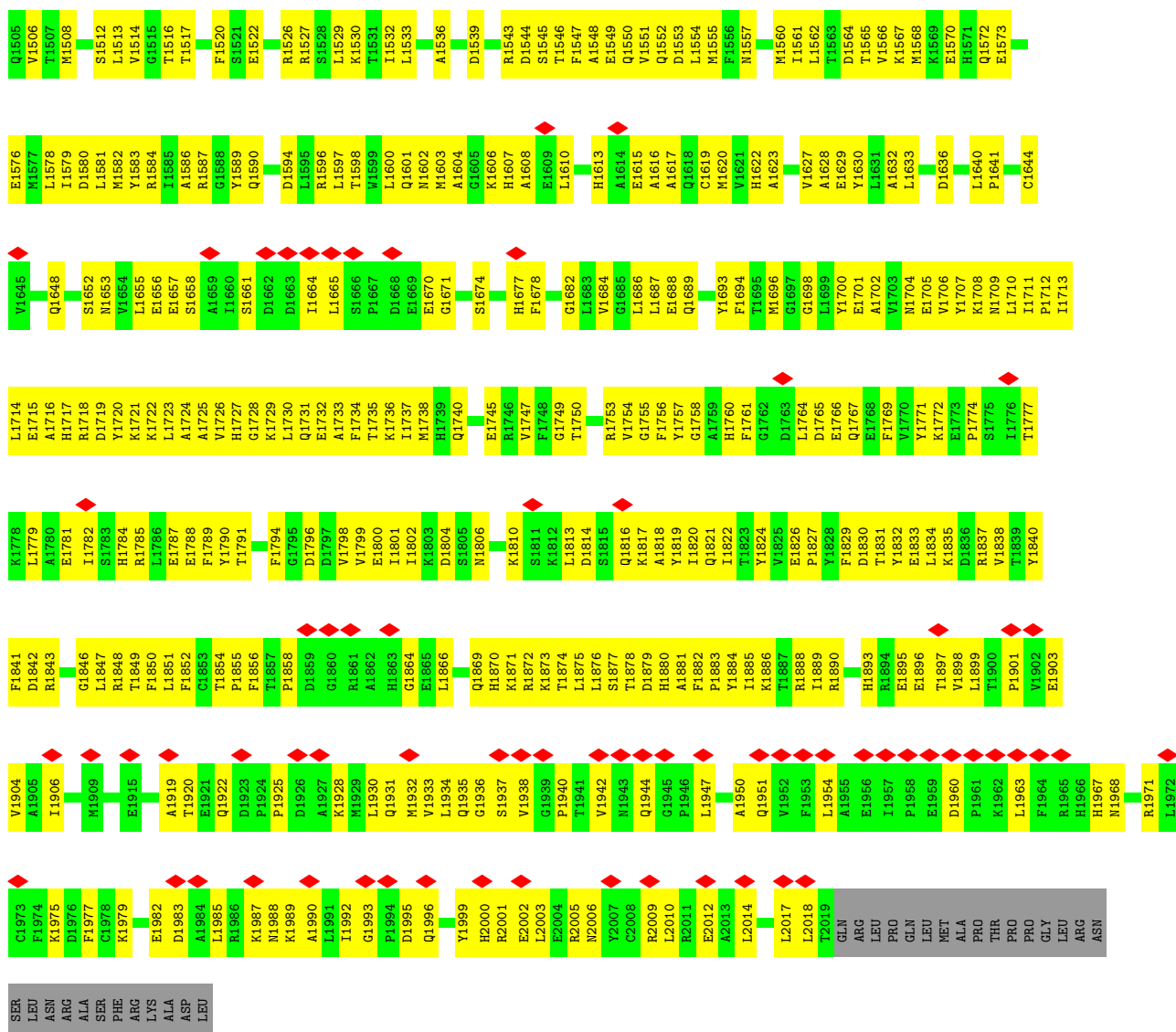
3 Residue-property plots

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.

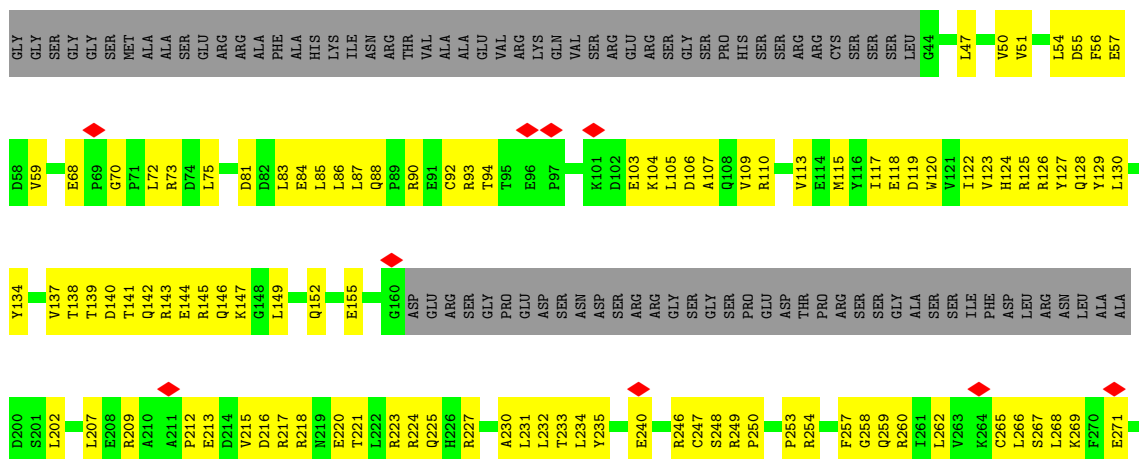
- Molecule 1: Dedicator of cytokinesis protein 6







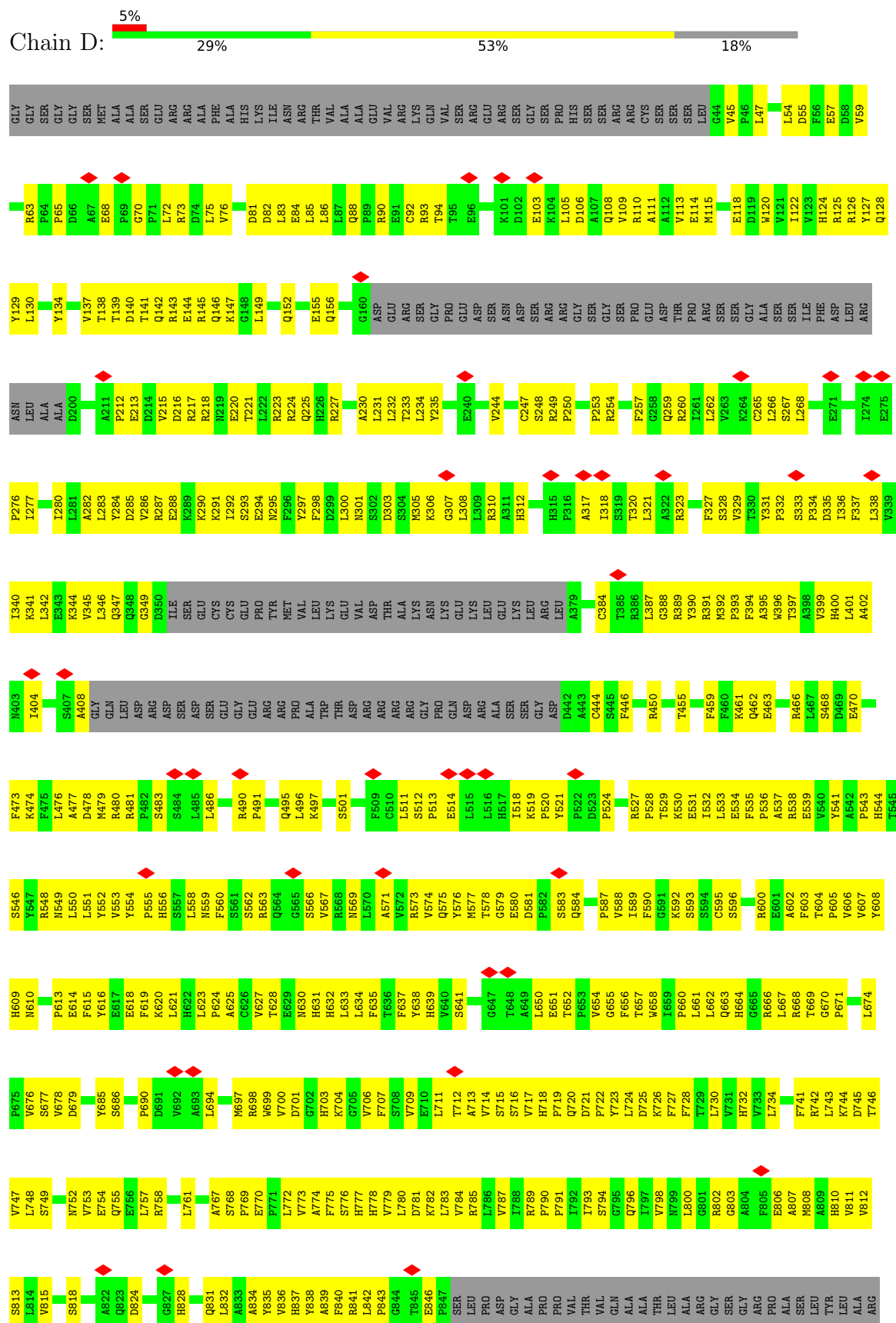
• Molecule 1: Dedicator of cytokinesis protein 6



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				
L1007	V1008	D1009	R1010	G1011	F1012	V1013	F1014	S1015	L1016	V1017	R1018	R1019	H1020	V1021	K1022	Q1023	F1024	A1025	T1026	R1027	L1028	V1029	S1030	S1031	F1032	M1033	P1034	A1035	A1036	L1037	L1038	T1039	R1040	V1041	R1042	E1043	F1044	T1045	R1046	T1047	L1048	H1051	E1052	H1053	L1057	N1058	L1059	C1062	P1063	L1064	S1065	PRO	PRO	ALA	SER	H1128	F1129	L1130	L1131	H1132	K1133
SER	PRO	SER	VAL	SER	SER	THR	THR	SER	GLN	SER	THR	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	N994	A995	S996	L997	A998	F999	F1000	L1001	S1002	D1003	L1004	L1005	S1006		
SER	SER	SER	ASN	PRO	ASP	LEU	ALA	VAL	ALA	ALA	GLY	SER	VAL	D896	D897	E898	R901	I902	L903	L907	L908	H909	E910	F911	L912	A913	L914	Q915	W916	V917	I918	PRO	PRO	VAL	THR	VAL	R924	E925	E926	I927	L928	Q929	A931	Q932	F933	F934	Q936	L937	N938	V939	K940	S941	N942	A943	L944	H945	L946				
A822	Q823	D824	G827	H828	C829	P830	Q831	L832	A833	H834	Y835	V836	H837	A838	A839	F840	R841	L842	P843	T844	E846	P847	LEU	PRO	ASP	GLY	ALA	ALA	ALA	ALA	THR	THR	LEU	ALA	ARG	GLY	SER	SER	GLY	ARG	ARG	PRO	ALA	ALA	LEU	LEU	TVR	H811	V812	S813	L814	V815	S818								
V753	E754	Q755	E756	L757	R758	A759	S760	L761	A767	S768	P769	E770	P771	L772	V773	A774	F775	S776	H777	F707	T708	V709	E710	L711	T712	A713	V714	S715	V716	L717	H718	P719	Q720	D721	P722	V723	L724	D725	K726	Q796	L797	F798	N799	L800	G801	R802	C803	E806	A807	N808	A809	H810	V811	H812	S813	L814	V815	S818			
E614	F615	Y616	E617	E618	F619	V620	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	Q658	T659	P660	L661	L662	Q663	H664	G665	R666	L667	R668	A602	F603	T604	P605	V606	V607	Y608	H609	N610	P613				
R480	R481	S482	S483	S484	L485	R486	R487	L488	R489	R490	T493	A494	Q495	L496	K497	S501	E505	F509	C510	L511	S512	P513	E514	L515	L516	H517	I518	K519	P520	Y521	P522	D523	P524	R525	G526	R527	P528	T529	K530	E531	I532	L533	E534	F535	P536	A537	R538	E539	A542	P543	H544	T545	S546	Y547							
R548	N549	L550	L551	Y552	V553	Y554	P555	H556	S557	L558	N559	S562	R563	Q564	G565	S566	V567	R568	N569	L570	A571	V572	R573	V574	Q575	Y576	N577	T578	G579	E580	S583	P587	V588	I589	F590	G591	R592	K593	S594	C595	S596	T599	R600	E601	A602	F603	T604	P605	V606	V607	Y608	H609	N610	P613							
R548	N549	L550	L551	Y552	V553	Y554	P555	H556	S557	L558	N559	S562	R563	Q564	G565	S566	V567	R568	N569	L570	A571	V572	R573	V574	Q575	Y576	N577	T578	G579	E580	S583	P587	V588	I589	F590	G591	R592	K593	S594	C595	S596	T599	R600	E601	A602	F603	T604	P605	V606	V607	Y608	H609	N610	P613							
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R548	N549	L550	L551	Y552	V553	Y554	P555	H556	S557	L558	N559	S562	R563	Q564	G565	S566	V567	R568	N569	L570	A571	V572	R573	V574	Q575	Y576	N577	T578	G579	E580	S583	P587	V588	I589	F590	G591	R592	K593	S594	C595	S596	T599	R600	E601	A602	F603	T604	P605	V606	V607	Y608	H609	N610	P613							
R548	N549	L550	L551	Y552	V553	Y554	P555	H556	S557	L558	N559	S562	R563	Q564	G565	S566	V567	R568	N569	L570	A571	V572	R573	V574	Q575	Y576	N577	T578	G579	E580	S583	P587	V588	I589	F590	G591	R592	K593	S594	C595	S596	T599	R600	E601	A602	F603	T604	P605	V606	V607	Y608	H609	N610	P613							
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R548	N549	L550	L551	Y552	V553	Y554	P555	H556	S557	L558	N559	S562	R563	Q564	G565	S566	V567	R568	N569	L570	A571	V572	R573	V574	Q575	Y576	N577	T578	G579	E580	S583	P587	V588	I589	F590	G591	R592	K593	S594	C595	S596	T599	R600	E601	A602	F603	T604	P605	V606	V607	Y608	H609	N610	P613							
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R548	N549	L550	L551	Y552	V553	Y554	P555	H556	S557	L558	N559	S562	R563	Q564	G565	S566	V567	R568	N569	L570	A571	V572	R573	V574	Q575	Y576	N577	T578	G579	E580	S583	P587	V588	I589	F590	G591	R592	K593	S594	C595	S596	T599	R600	E601	A602	F603	T604	P605	V606	V607	Y608	H609	N610	P613							
R548	N549	L550	L551	Y552	V553	Y554	P555	H556	S557	L558	N559	S562	R563	Q564	G565	S566	V567	R568	N569	L570	A571	V572	R573	V574	Q575	Y576	N577	T578	G579	E580	S583	P587	V588	I589	F590	G591	R592	K593	S594	C595	S596	T599	R600	E601	A602	F603	T604	P605	V606	V607	Y608	H609	N610	P613							
R548	N549	L550	L551	Y552	V553	Y554	P555	H556	S557	L558	N559	S562	R563	Q564	G565	S566	V567	R568	N569	L570	A571	V572	R573	V574	Q575	Y576	N577	T578	G579	E580	S583	P587	V588	I589	F590	G591	R592	K593	S594	C595	S596	T599	R600	E601	A602	F603	T604	P605	V606	V607	Y608	H609	N610	P613							
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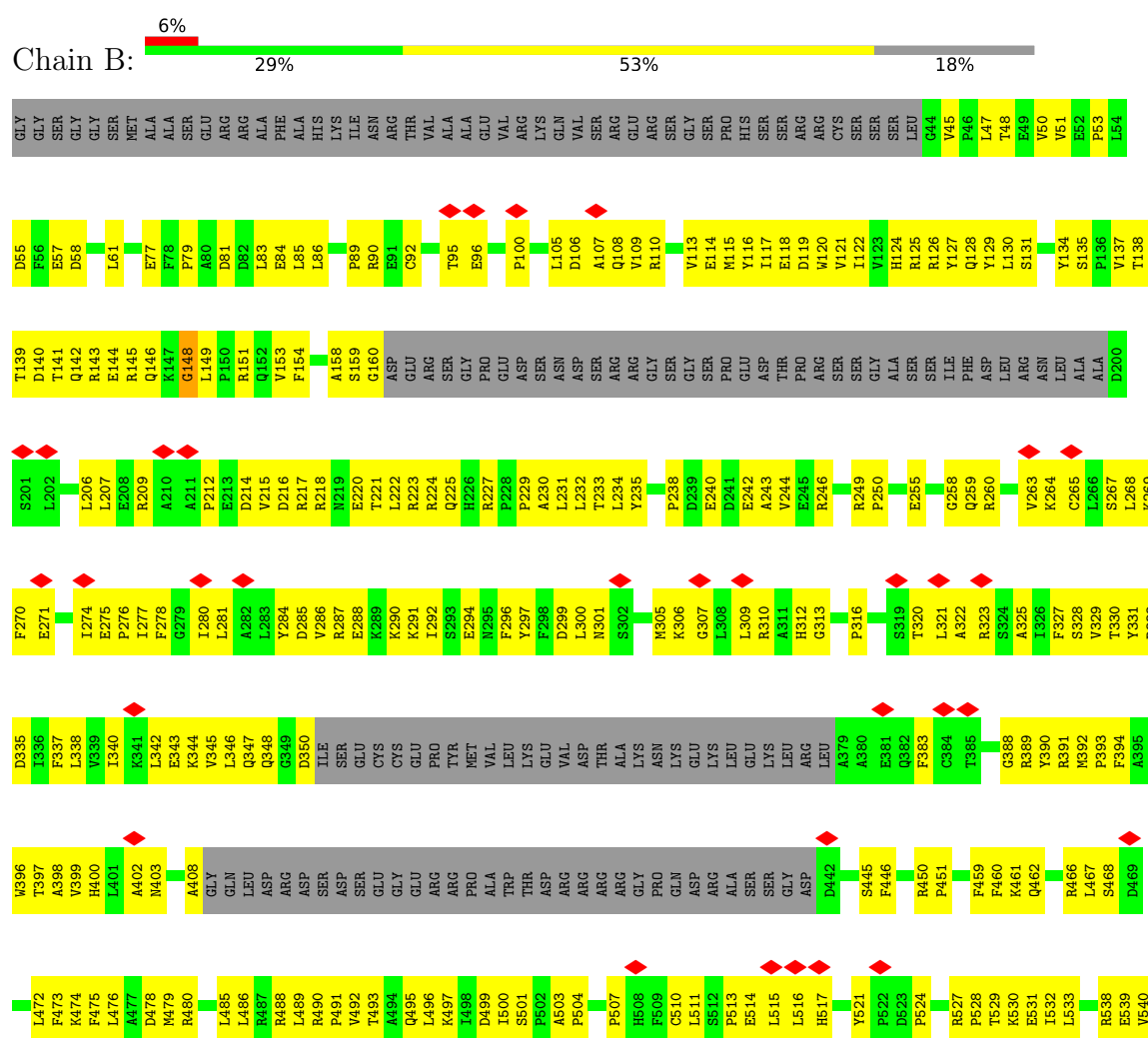


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I1711	C1644	E1670	V1506	L1384	ARG	V1257	ASP	F1129	ALA	V1008	SER	L944
P1712	F1647	E1573	T1507	A1385	LEU	L1258	SER	L1130	SER	D1009	LYS	L947
L1714			M1508	T1386	GLU	V1259	ASP	L1131	PRO	R1010	ILE	L948
E1715	I1650	L1578	M1509	E1387	ALA	W1260	THR	H1132	SER	G1011	SER	
H1716		L1579	L1510	A1388	ILE	K1261	GLY	K1133	PRO	F1012	SER	
H1717	M1653	D1580	L1513	S1389	GLY	K1262	GLY	K1134	SER	V1013	SER	
D1718		L1581	L1514	L1450	LEU	N1263	GLY	A1135	VAL	F1014	ASN	L952
R1719		L1582	V1514	L1390	GLY	N1264	GLY	A1136	SER	S1015	ASN	D953
D1720	E1656	M1582	G1515	V1391	THR	T1265	ASP	S1137	SER	L1016	PRO	T954
K1721	E1657	Y1583	T1516	L1393	ILE	P1266	ILE	A1138	THR	R1017	ASP	R955
K1722	S1658	R1584	L1517	D1394	GLY	A1267	ALA	V1139	THR	V1018	LEU	R956
K1723	I1659	I1585	Q1518	L1395	ALA	L1268	GLY	L1141	SER	A1019	ALA	
L1724	I1660	R1586	M1519	T1396	ARG	L1269	THR	S1141	GLN	H1020	VAL	R959
A1725	S1661	G1588	F1520	E1397	GLN	Q1270	ILE	L1142	SER	Y1021	ALA	F960
V1726	D1662	Y1589	S1521	I1398	GLU	W1271	ASN	H1146	SER	Q1022	PRO	P961
H1727	G1663	E1522	E1523	I1399	MET	T1272	PRO		THR	K1023	GLY	G962
G1728	I1664	D1461	H1524	V1400	VAL	W1273	SER		PHE	V1024	SER	R963
K1729	L1665	L1462	H1524	Q1401	ARG		VAL	D1149	SER	A1025		F964
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F1734	D1668	L1467	S1406	ARG	GLY	L1281	GLY	K1158	D1090	S1030		T969
T1735		R1468	E1407	SER	GLY	G1282	GLY	A1159	P1091	P1031		L970
K1736	G1671	H1469	A1408	PRO	PRO	R1283	GLY	R1160	K1092	L1037		L971
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M1738	C1673	E1410	E1410	GLY	GLY	L1285	LEU	A1162	T1094	P1034		S973
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			T1476	ARG	ARG	C1291	ALA	L1168	S1100	R1041		V979
			T1477	TRP	TRP	L1292	SER	L1169	G1101	M1042		T980
			R1478	ARG	ARG	A1293	ILE	S1170	P1102	R982		T981
			H1479	GLY	GLY	L1294	GLN	I1171	F1103	A1043		L912
			H1480	VAL	VAL	F1295	GLY	A1172	K1104	F1044		A913
			L1481	THR	THR	E1296	GLY	R1173	Q1105	T1045		L914
			S1482	HIS	HIS	Y1297	PRO	D1174	Q1106	R1046		Q915
			A1483	TRP	TRP		THR	T1175	H1107	I1047		W916
			L1484	LYS	LYS	K1300	ALA	P1177	F1108	L1048		V917
			L1485	GLN	GLN	A1302	SER	R1178	L1109	C1049		V918
			Y1486	SER	SER	F1303	ARG	L1179	A1110	S1050		S919
			L1487	THR	THR		ALA		G1111	H1051		R924
			L1488	SER	SER	K1301	GLY	F1182	L1112	E1052		E925
			M1489	ASP	ASP	A1302	GLY	A1183	L1113	H1053		A926
			R1490	VAL	VAL	F1303	ASP	E1184	L1114	N993		L927
			Q1428	LYS	LYS		ASP	GLY	T1115	V1055		L928
			L1431	LYS	LYS		ASP	PRO	E1116	T1056		
			F1432	THR	THR		THR	GLY	L1117	L1057		A931
			L1433	PHE	PHE		THR	GLN	A1118	N1058		W932
			Q1434	LEU	LEU		THR	GLN	A1119	L1059		F933
			H1435	LEU	LEU		THR	GLN	A1120	P1060		F934
			G1436	LEU	LEU		THR	GLN	A1121	C1061		F935
			L1437	LEU	LEU		THR	GLN	A1122	D1002		Q936
			L1438	LEU	LEU		THR	GLN	A1123	L1003		L937
			A1438	LEU	LEU		THR	GLN	A1124	L1004		M938
			T1439	LEU	LEU		THR	GLN	A1125	S1006		V939
			Q1440	LEU	LEU		THR	GLN	A1126	L1007		K940
			R1441	LEU	LEU		THR	GLN	A1127			S941
			L1442	LEU	LEU		THR	GLN	A1128			
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S1389	ALA	M1263	GLU	S1441	SER	L1007	L944	A807	K744	V676	V607	Y641
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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	THR	G1145	THR	G1011		V811	L748	Q680	K611	R548
D1394	ILE	H1146	ALA	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	GLN	T1148	GLN	F1014	L952	S813	G751	Y685	E614	L551
E1397	ARG	D1149	ASN	D1149	SER	S1015	D953	V815	V753	Y686	F615	Y552
I1398	GLN	R1150	PRO	R1150	PRO	L1016	T954	H816	E754	Y687	E616	V553
V1399	GLY	P1151	THR	P1151	THR	V1017	P955	R817	ASP	Y688	E617	
V1400	VAL	R1152	THR	R1152	PHE	R1018	R956	S818	ASP	L688	E618	L558
Q1401	VAL	A1153	SER	A1153	SER	H1020	K957	L819	T755	T689	F619	N559
T1402	ARG	E1154	SER	E1154	SER	H1020	L958		L757	P690	K820	F560
V1403	ARG	V1157	ALA	V1157	ALA	Y1021	R959	G826	R758	V691	L621	S561
M1404	SER	K1158	ILE	K1158	ILE	K1022	F960	G827	L761	V692	H622	S562
S1406	GLU	A1159	ALA	A1159	ALA	V1024	P961	H828			L623	R563
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A1408	SER	V1161	PRO	V1161	PRO	T1026	L965	P930	R765	R698	E629	G565
R1409	LEU	A1162	LEU	A1162	LEU	R1027	D966	Q831	L766	V699	N630	S566
E1410	PHE	L1163	ALA	L1163	ALA	L1028	D967	L832	A767	V700	H631	R568
S1411	GLY	L1164	PRO	L1164	PRO	Q1029	D968	A833		D701	H632	
V1412	ASN	Y1165	GLY	Y1165	ASN	N1033	T969	Y835	E770	G702	L633	N569
L1413	PRO	L1166	SER	L1166	SER	P1034	A970	H836	P771	H703	L634	L570
G1414	GLU	P1167	ARG	P1167	ARG	A1035	L971	H837	L772	K704		A571
A1415	ASN	L1168	ALA	L1168	ASN	A1036	V972	H837	L773	F707	Y638	V572
L1416	VAL	L1169	SER	L1169	SER	G1036	G973	Y838	A774		H639	R573
L1417	TRP	S1170	ILE	S1170	ILE	L1037	S974	A839	F775	S708	V640	V574
K1418	ARG	T1171	SER	T1171	SER	L1038	V975	F840	S776	V709	Q541	Q575
V1419	LYS	A1172	GLN	A1172	GLN	T1039	G976		H777	E710	C642	Y576
S1420	GLY	R1173	GLY	R1173	GLY	L1040	L977	P947	H778			M577
E1421	PRO	D1174	PRO	D1174	PRO	R1041	S978	LEU	T779	T712	R645	T578
T1422	VAL	T1175	PRO	T1175	VAL	E1042	V979	PRO	D781	A713	P646	E580
S1423	THR	L1176	THR	L1176	THR	F1044	T981	ASP	K782	S715	G647	D581
G1299	ALA	P1177	ALA	P1177	ALA	T1045	R982	GLY	L783	S716	T648	P582
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K1301	ARG	L1179	ARG	L1179	ARG	L1047	H984	PRO	H785	V717		Q584
A1302	ALA	F1182	ALA	F1182	ALA	T1048	K985	PRO	L786	H718	T652	A585
F1303	GLY	E1183	GLY	E1183	GLY	C1049	D986	VAL	L787	P719	P653	L586
GLU	ASP	A1184	ASP	A1184	ASP	S1050	V987	THR	I788	Q720	V654	P587
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VAL	SER	GLY	VAL	GLY	SER	H1053	A990	GLN	I792	P722	G656	I589
ASP	LEU	GLY	ASP	GLY	LEU	V1054	E991	ALA	L793	L724	F657	F590
THR	ARG	GLN	THR	GLN	ARG	T1055	H992	THR	D725	W658	I659	G591
PHE	SER	SER	PHE	SER	SER	L1056	L993	ALA	K726	F727	P660	K592
LYS	ARG	ARG	LYS	ARG	ARG	L1057	N994	ARG	G795	F728	C595	S593
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SER	ALA	ALA	SER	ALA	SER	L1064	S996	GLY	Q796	L661	Q663	C595
LEU	SER	L1130	LEU	L1130	SER	S1065	A997	GLY	I797	T729	Q663	S596
ASP	MET	H1132	ASP	H1132	ASP	PRO	A998	ARG	N799	L730	H664	E597
MET	LEU	K1133	MET	K1133	MET	PRO	F999	ARG	L800	V731	G665	F598
V1257	ASP	L1134	V1257	L1134	ASP	ALA	F1000	PRO	G801	V732	R666	T599
L1258	ALA	A1135	L1258	A1135	ALA	ALA	Q935	ALA	R802	V733	R667	R600
W1259	SER	I1136	W1259	I1136	SER	SER	Q936	SER	G803	L734	L667	E601
V1260	THR	S1137	V1260	S1137	THR	PRO	L937	LEU	E735	E736	R668	A602
L1261	GLU	A1138	L1261	A1138	GLU	SER	M938	THR	A804		T669	F603
V1139	GLY	H1139	V1139	H1139	GLY	PRO	L1004	LEU	F805		C673	T604
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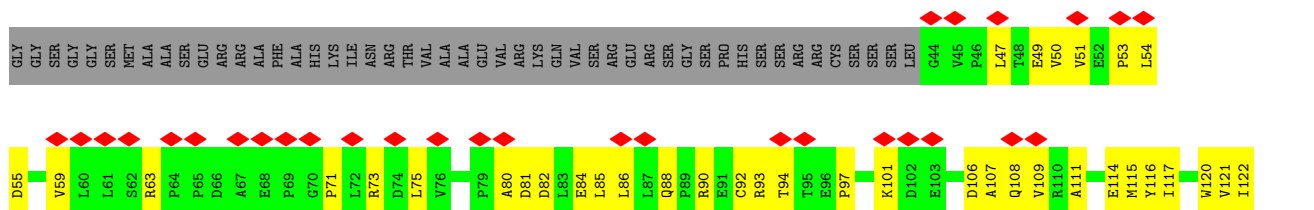
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H909	L977	F1000	ILE	Y390	T456	P520	Q584	E651	S715	W784	SER	H909
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L914	T981	L1005	ARG	A396	F459	P524	V589	G655	Y723	L788	ALA	L914
Q915	T982	L1006	ASN	W396	F460	R525	L589	F656	W724	R789	PRO	Q915
W916	T983	L1007	LEU	T397	F461	R526	L590	T657	L724	P790	PRO	W916
V917	T984	L1008	ALA	A398	K462	G526	G591	W658	D725	P791	VAL	V917
W918	T985	L1009	D200	V399	E463	R527	S593	L659	K726	L792	THR	W918
S919	T986	L1010	S901	H400	R466	P528	S594	P660	F727	L793	VAL	S919
S920	T987	L1011	ALA	L401	L467	T529	C595	L661	W728	S794	GLN	S920
V923	T988	L1012	L202	A402	S468	K530	S596	L662	L729	G795	ALA	V923
R924	T989	L1013	L203	I404	D469	E531	T599	Q663	L730	Q796	ALA	R924
E925	T990	L1014	L204	N403	E470	L532	R600	L664	W731	L797	THR	E925
A926	T991	L1015	L205	I404	D471	L533	E601	L665	H732	W798	LEU	A926
L927	T992	L1016	L206	A408	F473	E534	A602	L666	W733	L799	ALA	L927
L928	T993	L1017	L207	A408	K474	P535	L605	L667	L734	E736	ARG	L928
Q929	T994	L1018	L208	A408	F475	P536	P605	L668	L735	E737	GLY	Q929
H930	T995	L1019	L209	A408	L476	E537	H609	T669	F741	G737	GLY	H930
A931	T996	L1020	P212	A408	A477	R538	H609	G670	L742	F742	ARG	A931
W932	T997	L1021	E213	A408	D478	E539	K611	P671	L743	L743	PRO	W932
F933	T998	L1022	D216	A408	M479	H544	K611	C673	W744	K744	ALA	F933
L934	T999	L1023	N219	A408	R480	Y547	S612	L674	D745	D745	LEU	L934
F935	T1000	L1024	E220	A408	R481	R548	P613	P675	L746	L746	LEU	F935
Q936	T1001	L1025	T221	A408	P482	L550	E614	V676	L747	S749	ALA	Q936
L937	T1002	L1026	T222	A408	L485	L551	F615	Q677	E750	E750	ARG	L937
M938	T1003	L1027	R224	A408	L486	Y552	V616	Q680	W752	G751	SER	M938
V939	T1004	L1028	R227	A408	L487	L553	S617	P681	N753	W753	SER	V939
K940	T1005	L1029	L231	A408	L488	V554	K620	P682	W754	E754	SER	K940
S941	T1006	L1030	L232	A408	L489	L555	L621	P683	W755	Q755	ASN	S941
M942	T1007	L1031	L233	A408	L489	P555	H622	S684	E756	L757	PRO	M942
G1011	T1008	L1032	L234	A408	L489	H556	L623	V685	L757	W757	ASP	G1011
L1016	T1009	L1033	Y235	A408	L489	S557	A625	S686	R758	L758	LEU	L1016
V1017	T1010	L1034	L300	A408	L489	L558	L624	V687	A759	L759	ALA	V1017
R1018	T1011	L1035	N301	A408	L489	L559	A626	L687	W760	S760	ALA	R1018
A1019	T1012	L1036	S302	A408	L489	P559	C626	L688	L761	L761	VAL	A1019
H1020	T1013	L1037	D303	A408	L489	F560	V627	L689	L762	L762	ALA	H1020
P955	T1014	L1038	S304	A408	L489	S561	T628	T689	L763	L763	PRO	P955
R956	T1015	L1039	M305	A408	L489	Q495	A494	E629	L764	L764	GLY	R956
K957	T1016	L1040	K306	A408	L489	S562	L496	N630	L765	L765	SER	K957
L958	T1017	L1041	L307	A408	L489	Q564	L497	L631	L766	L766	VAL	L958
R959	T1018	L1042	L308	A408	L489	G565	L498	H632	L767	L767	VAL	R959
P960	T1019	L1043	L309	A408	L489	S566	V567	L633	L768	L768	VAL	P960
G961	T1020	L1044	ARG	A408	L489	R568	R568	F635	L769	L769	VAL	G961
R962	T1021	L1045	ASP	A408	L489	N569	N569	Y638	L770	L770	VAL	R962
R963	T1022	L1046	ASP	A408	L489	L570	L570	H639	L771	L771	VAL	R963
P964	T1023	L1047	ASP	A408	L489	A571	A571	V640	L772	L772	VAL	P964
D967	T1024	L1048	ASP	A408	L489	V572	V572	H641	L773	L773	VAL	D967
G962	T1025	L1049	ASP	A408	L489	L511	L511	S642	L774	L774	VAL	G962
R963	T1026	L1050	ASP	A408	L489	S512	S512	C643	L775	L775	VAL	R963
P964	T1027	L1051	ASP	A408	L489	P513	P513	Q646	L776	L776	VAL	P964
D967	T1028	L1052	ASP	A408	L489	L515	L515	P646	L777	L777	VAL	D967
G962	T1029	L1053	ASP	A408	L489	L516	L516	H647	L778	L778	VAL	G962
R963	T1030	L1054	ASP	A408	L489	H517	H517	T648	L779	L779	VAL	R963
P964	T1031	L1055	ASP	A408	L489	D581	D581	L712	L780	L780	VAL	P964
D967	T1032	L1056	ASP	A408	L489			L711	L781	L781	VAL	D967
G962	T1033	L1057	ASP	A408	L489			L712	L782	L782	VAL	G962
R963	T1034	L1058	ASP	A408	L489			L713	L783	L783	VAL	R963
P964	T1035	L1059	ASP	A408	L489			L714	L784	L784	VAL	P964
D967	T1036	L1060	ASP	A408	L489			L715	L785	L785	VAL	D967
G962	T1037	L1061	ASP	A408	L489			L716	L786	L786	VAL	G962
R963	T1038	L1062	ASP	A408	L489			L717	L787	L787	VAL	R963
P964	T1039	L1063	ASP	A408	L489			L718	L788	L788	VAL	P964
D967	T1040	L1064	ASP	A408	L489			L719	L789	L789	VAL	D967
G962	T1041	L1065	ASP	A408	L489			L720	L790	L790	VAL	G962
R963	T1042	L1066	ASP	A408	L489			L721	L791	L791	VAL	R963
P964	T1043	L1067	ASP	A408	L489			L722	L792	L792	VAL	P964
D967	T1044	L1068	ASP	A408	L489			L723	L793	L793	VAL	D967
G962	T1045	L1069	ASP	A408	L489			L724	L794	L794	VAL	G962
R963	T1046	L1070	ASP	A408	L489			L725	L795	L795	VAL	R963
P964	T1047	L1071	ASP	A408	L489			L726	L796	L796	VAL	P964
D967	T1048	L1072	ASP	A408	L489			L727	L797	L797	VAL	D967
G962	T1049	L1073	ASP	A408	L489			L728	L798	L798	VAL	G962
R963	T1050	L1074	ASP	A408	L489			L729	L799	L799	VAL	R963
P964	T1051	L1075	ASP	A408	L489			L730	L800	L800	VAL	P964
D967	T1052	L1076	ASP	A408	L489			L731	L801	L801	VAL	D967
G962	T1053	L1077	ASP	A408	L489			L732	L802	L802	VAL	G962
R963	T1054	L1078	ASP	A408	L489			L733	L803	L803	VAL	R963
P964	T1055	L1079	ASP	A408	L489			L734	L804	L804	VAL	P964
D967	T1056	L1080	ASP	A408	L489			L735	L805	L805	VAL	D967
G962	T1057	L1081	ASP	A408	L489			L736	L806	L806	VAL	G962
R963	T1058	L1082	ASP	A408	L489			L737	L807	L807	VAL	R963
P964	T1059	L1083	ASP	A408	L489			L738	L808	L808	VAL	P964
D967	T1060	L1084	ASP	A408	L489			L739	L809	L809	VAL	D967
G962	T1061	L1085	ASP	A408	L489			L740	L810	L810	VAL	G962
R963	T1062	L1086	ASP	A408	L489			L741	L811	L811	VAL	R963
P964	T1063	L1087	ASP	A408	L489			L742	L812	L812	VAL	P964
D967	T1064	L1088	ASP	A408	L489			L743	L813	L813	VAL	D967
G962	T1065	L1089	ASP	A408	L489			L744	L814	L814	VAL	G962
R963	T1066	L1090	ASP	A408	L489			L745	L815	L815	VAL	R963
P964	T1067	L1091	ASP	A408	L489			L746	L816	L816	VAL	P964
D967	T1068	L1092	ASP	A408	L489			L747	L817	L817	VAL	D967
G962	T1069	L1093	ASP	A408	L489			L748	L818	L818	VAL	G962
R963	T1070	L1094	ASP	A408	L489			L749	L819	L819	VAL	R963
P964	T1071	L1095	ASP	A408	L489			L750	L820	L820	VAL	P964
D967	T1072	L1096	ASP	A408	L489			L751	L821	L821	VAL	D967
G962	T1073	L1097	ASP	A408	L489			L752	L822	L822	VAL	G962
R963	T1074	L1098	ASP	A408	L489			L753	L823	L823	VAL	R963
P964	T1075	L1099	ASP	A408	L489			L754	L824	L824	VAL	P964
D967	T1076	L1100	ASP	A408	L489			L755	L825	L825	VAL	D967
G962	T1077	L1101	ASP	A408	L489			L756	L826	L826	VAL	G962
R963	T1078	L1102	ASP	A408	L489			L757	L827	L827	VAL	R963
P964	T1079	L1103	ASP	A408	L489			L758	L828	L828	VAL	P964
D967	T1080	L1104	ASP	A408	L489			L759	L829	L829	VAL	D967
G962	T1081	L1105	ASP	A408	L489			L760	L830	L830	VAL	G962
R963	T1082	L1106	ASP	A408	L489			L761	L831	L831	VAL	R963
P964	T1083	L1107	ASP	A408	L489			L762	L832	L832	VAL	P964
D967	T1084	L1108	ASP	A408	L489			L763	L833	L833	VAL	D967
G962	T1085	L1109	ASP	A408	L489			L764	L834	L834	VAL	G962
R963	T1086	L1110	ASP	A408	L489			L765	L835	L835	VAL	R963
P964	T1087	L1111	ASP	A408	L489			L766	L836	L836	VAL	P964
D967	T1088	L1112	ASP	A408	L489			L767	L837	L837	VAL	D967
G962	T1089	L1113	ASP	A408	L489			L768	L838	L838	VAL	G962
R963	T1090	L1114	ASP	A408	L489			L769	L839	L839	VAL	R963
P964	T1091	L1115	ASP	A408	L489			L770	L840	L840	VAL	P964
D967	T1092	L1116	ASP	A408	L489			L771	L841	L841	VAL	D967
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R963	T109											







- Molecule 1: Dedicator of cytokinesis protein 6

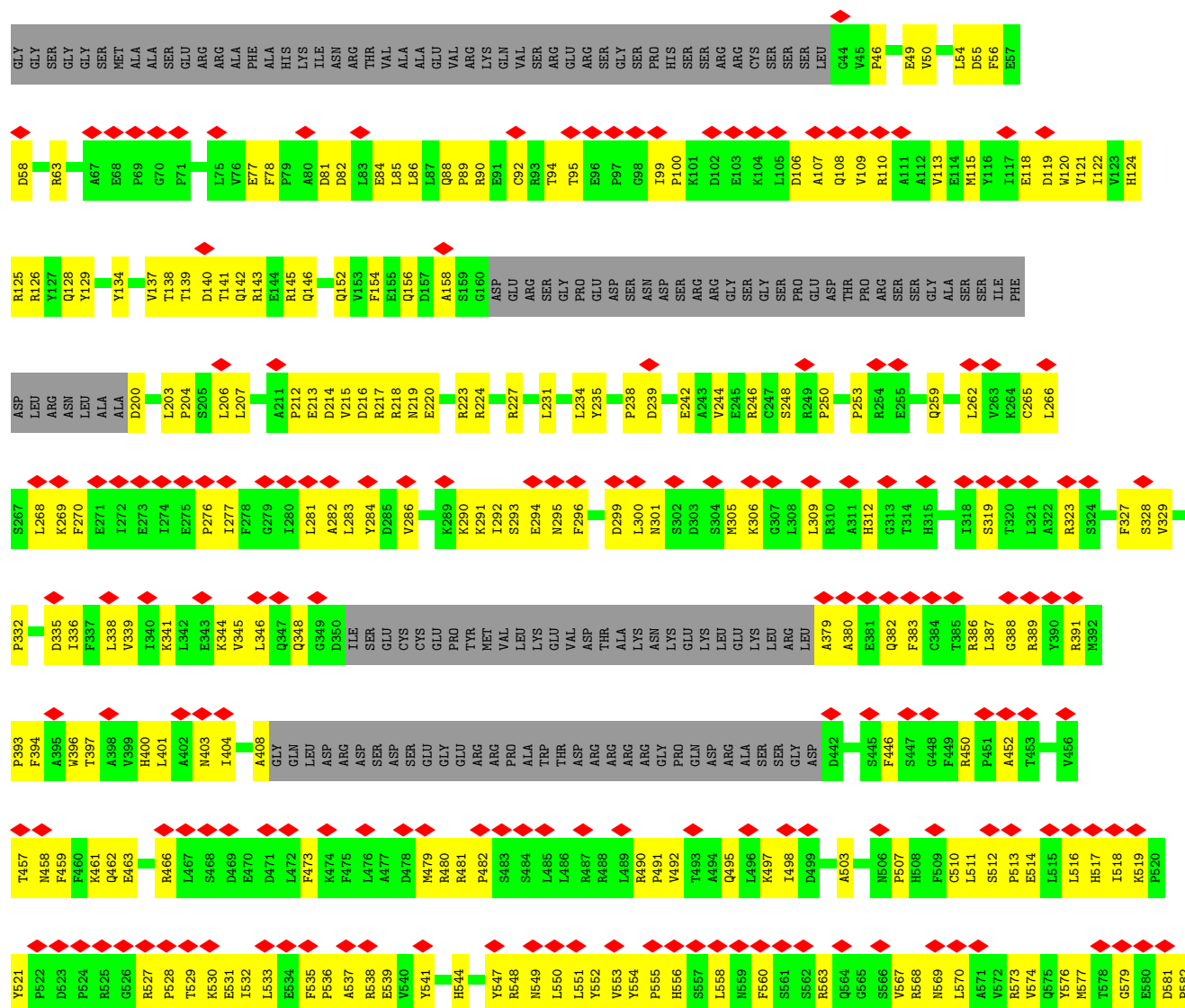


V123	H124	R125	Y127	Q128	Y129	L130	S131	A132	A133	Y134	V137	T138	T139	D140	Q141	Q142	R143	E144	R145	Q146	K147	G148	L149	P150	R151	Q152	V153	F154	E155	Q156	D157	A158	S159	G160	ASP	GLU	ARG	SER	GLY	PRO	GLU	ASP	SER	ASN	ASP	SER	ARG	ARG	GLY	SER	GLY	SER	PRO	GLU	ASP	THR	PRO
ARG	SER	GLY	ALA	SER	SER	ILE	PHE	ASP	LEU	ARG	ASN	ALA	ALA	D200	S201	L202	L203	P204	S205	L206	L207	E208	R209	A210	A211	P212	E213	D214	V215	D216	R217	R218	K290	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	R286	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	E343	K344	V345	Q347	Q348	G349	D350	ILE	SER	GLU	CYS	CYS	GLU	PRO	TYR	MET	THR	VAL	LEU	LYS	GLU	VAL	ARG	ASP	THR	L511	ALA	LYS	ASN	LYS	GLU	LEU	LEU	ARG	A379	A380	F383	C384	T385					
R386	L387	G388	R389	Y390	R391	M392	P393	F394	A395	V396	H400	L401	A402	N403	A408	GLY	LEU	ASP	ARG	ASP	SER	ASP	SER	GLU	GLY	GLY	ARG	ALA	THR	THR	LEU	LYS	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	P482	S483	S484	L485	R488	A494	Q495	L496	K497	L498	D499	T500	S501	F502	A503	P504	TRP	VAL	LEU	LYS	ARG	ARG	ARG	ARG	GLY	PRO	GLN	ASP	ARG	ALA	ARG	ALA	D442	A443	C444	S445	A452	T453	V456						
F535	P536	A537	R538	E539	H544	Y547	R548	N549	L550	L551	F552	V553	Y554	P555	H556	S557	L558	N559	F560	S561	S562	R563	Q564	S565	L566	V567	R568	N569	A571	V572	R573	V574	Q575	Y576	M577	T578	C579	L511	S512	P513	E514	L515	L516	H517	L518	R519	P520	P524	R525	T529	X530	E531	L532	L533	E534		
T604	F605	V606	V607	Y608	N610	K611	S612	P613	E614	F615	Y616	E617	S618	F619	R620	L621	H622	S623	L624	F624	A625	T628	E629	H630	H631	H632	L633	L634	T636	F637	V638	H639	V640	S641	C642	Q643	G647	T648	A649	L650	E651	G655	F656	T657	W658	T659	F660	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	Q796	F722	Y723	L724	D725	K726	F727	F728	T729	L730	W731	H732	W733	W734	E735	E736	G737	A738	F739	F740	F741				
R742	L743	T746	Y747	L748	S749	E750	V753	E754	Q755	E756	L757	R758	L761	R762	A763	L764	R765	V773	S776	H777	L780	D781	L783	V784	R785	L786	V787	I788	R789	P790	F791	I792	Q796	F722	Y723	L724	D725	K726	F727	F728	T729	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	L846	R847	SER	LEU	PRO	ASP	GLY	ALA	PRO	PRO	VAL	THR	VAL	GLN	ALA	ALA	THR	LEU	ALA	ARG	GLY	GLY	ARG	PRO	ALA	SER	LEU	TYR	ALA	ALA	ARG	ARG	SER	LYS	SER	ILE	SER	SER	ASN	PRO	ASP				
LEU	ALA	VAL	ALA	PRO	GLY	SER	VAL	D896	D897	E898	V899	S900	R901	L902	L903	A904	S905	K906	L907	L908	H909	E910	E911	A912	A913	L914	Q915	W916	V917	R924	E925	A926	I927	L928	Q929	H930	A931	W932	F933	M938	M942	A943	L944	L947	R951	L952	D953	T954	A1025	P955	R956	R959	F960	P961			
G962	R963	F964	L965	D966	D967	L968	T969	A970	L971	V972	G973	S974	Y975	G976	L977	E978	V979	L980	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	Q1023	V1024	A1025	T1026	R1027	L1028	Q1029	S1030	S1031		

G1795	D1796	D1797	V1798	V1799	E1800	I1801	I1802	K1803	D1804	S1805	N1806	P1807	V1808	D1809	K1810	S1811	K1812	L1813	D1814	S1815	Q1816	L1817	A1818	I1819	I1820	Q1821	I1822	I1823	Y1824	V1825	E1826	P1827	Y1828	V1770	Y1771	F1829	T1830	T1831	Y1832	E1833	L1834	R1837	V1838	T1839	F1841	D1842	R1843	N1844	Y1845	G1846	L1847	R1848	F1849	F1850	L1851	F1852	C1853																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
T1735	K1736	I1737	M1738	H1739	Q1740	S1741	S1742	G1743	W1744	E1745	R1746	V1747	F1748	G1749	T1750	Y1751	F1752	R1753	V1754	G1755	F1756	Y1757	G1758	A1759	H1760	F1761	D1762	D1763	L1764	D1765	E1766	Q1767	E1768	F1769	Y1770	Y1771	K1772	E1773	P1774	S1775	I1776	T1777	K1778	L1779	A1780	E1781	I1782	S1783	H1784	R1785	L1786	G1787	E1788	R1848	Y1790	T1791	E1792	R1793	F1794																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
F1672	C1673	S1674	G1675	H1676	H1677	F1678	T1679	E1680	L1681	G1682	L1683	V1684	G1685	L1686	L1687	E1688	Q1689	A1690	A1691	G1692	Y1693	F1694	T1695	M1696	L1699	Y1700	E1701	A1702	V1703	V1704	E1705	V1706	N1709	L1710	I1711	P1712	I1713	L1714	H1717	R1718	D1719	Y1720	K1721	K1722	L1723	A1724	A1725	V1726	H1727	G1728	K1729	L1730	Q1731	E1732	Y1733	F1734																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
A1608	E1609	L1610	G1611	M1612	H1613	A1614	E1615	A1616	A1617	M1620	V1621	H1622	A1623	A1624	A1625	L1626	V1627	Y1630	L1631	A1632	L1633	L1634	E1635	D1636	H1637	R1638	H1639	L1640	P1641	G1642	G1643	C1644	V1645	S1646	Q1647	F1648	N1649	I1650	M1653	V1654	L1655	E1656	A1659	I1660	S1661	D1662	D1663	I1664	L1665	S1666	P1667	D1668	E1669	E1670	L1671																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
F1547	A1548	E1549	Q1550	V1551	Q1552	D1553	L1554	M1555	F1556	M1557	H1558	H1559	M1560	I1561	L1562	T1563	D1564	T1565	V1566	K1567	M1568	K1569	E1570	H1571	Q1572	E1573	D1574	P1575	E1576	M1577	L1578	I1579	D1580	L1581	M1582	Y1583	R1584	I1585	G1588	Y1589	Q1590	G1591	S1592	P1593	D1594	L1595	R1596	L1597	T1598	V1599	L1600	Q1601	M1602	M1603	A1604	G1605	K1606	H1607																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
L1487	L1488	M1489	R1490	Q1491	N1492	F1493	E1494	F1495	G1496	H1497	N1498	F1499	A1500	R1501	V1502	K1503	M1504	V1505	V1506	T1507	M1508	S1509	L1510	S1511	S1512	L1513	G1514	T1515	L1516	T1517	Q1518	N1519	F1520	S1521	E1522	E1523	H1524	L1525	R1526	R1527	S1528	L1529	T1530	I1531	I1532	L1533	T1534	Y1535	A1536	E1537	E1538	D1539	M1540	G1541	L1542	R1543	D1544	T1545																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
L1424	G1425	S1426	A1427	Q1428	S1429	A1430	L1431	F1432	L1433	Q1434	H1435	G1436	L1437	A1438	T1439	Q1440	R1441	A1442	L1443	V1444	S1445	K1446	F1447	L1450	L1451	F1452	D1455	E1457	L1458	C1459	A1460	D1461	L1464	R1465	L1466	R1468	H1469	C1470	G1471	S1472	R1473	L1474	S1475	T1476	I1477	R1478	T1479	H1480	A1481	S1482	A1483	S1484	L1485	Y1486																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
H1S	TRP	LYS	GLN	THR	SER	ASN	VAL	ASP	ASP	ASP	ARG	VAL	ASP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR



• 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 ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

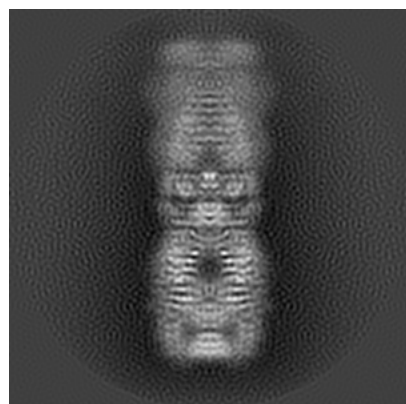
6 Map visualisation [i](#)

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.

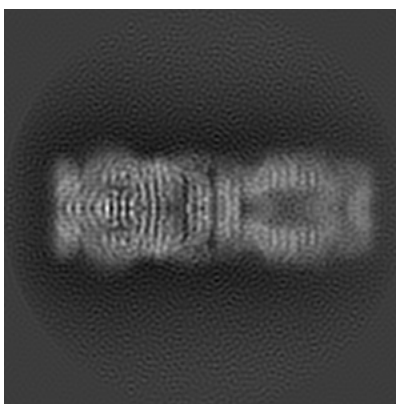
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

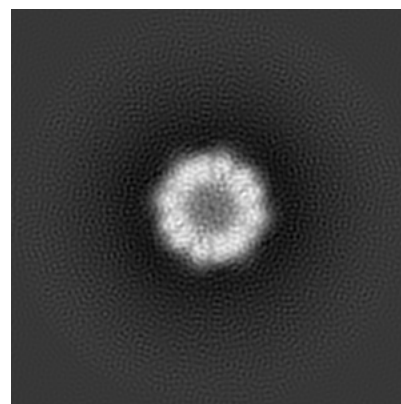
6.1.1 Primary map



X

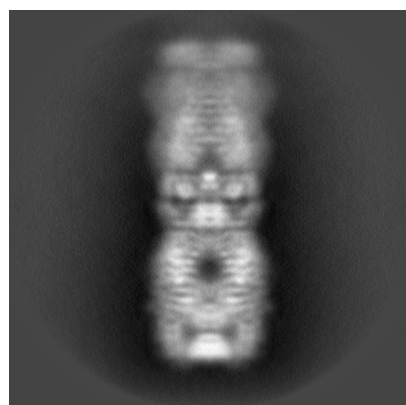


Y

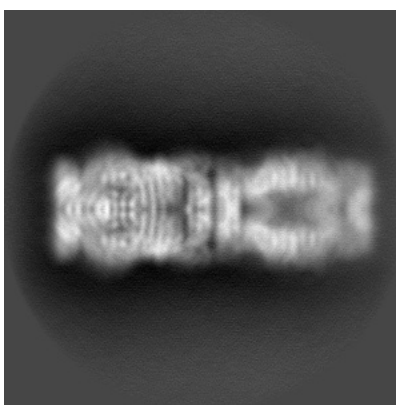


Z

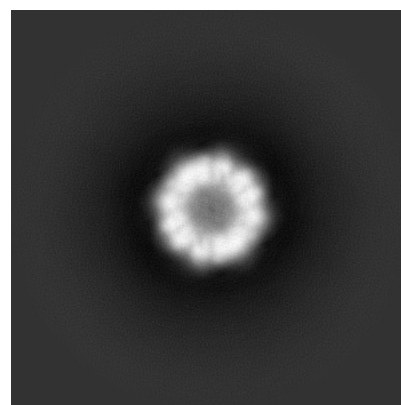
6.1.2 Raw map



X



Y

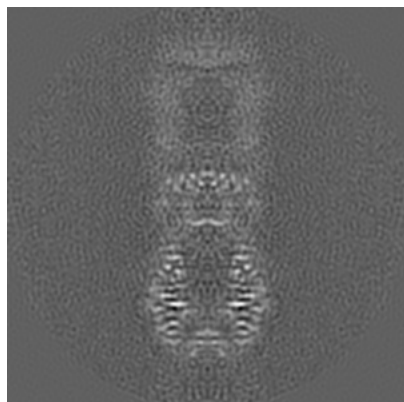


Z

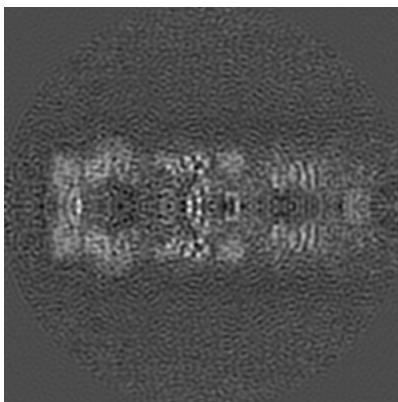
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

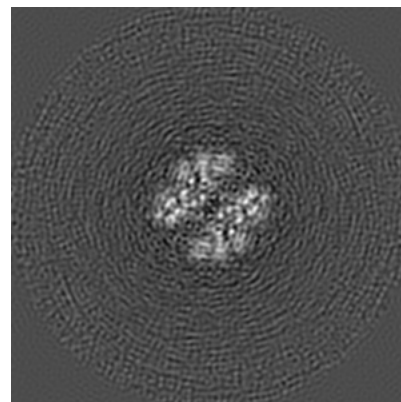
6.2.1 Primary map



X Index: 170

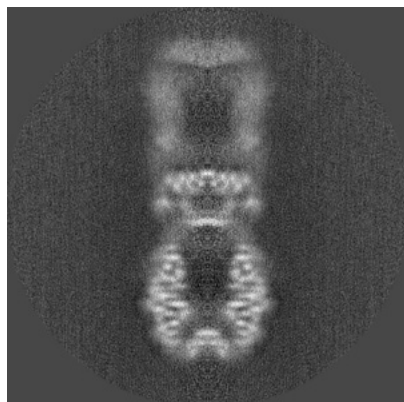


Y Index: 170

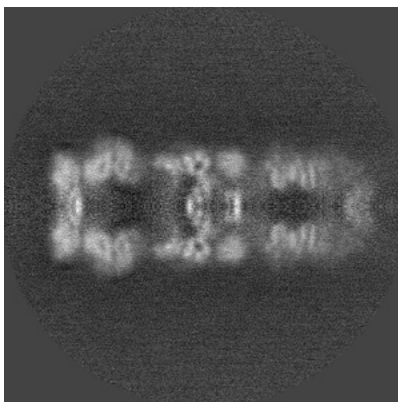


Z Index: 170

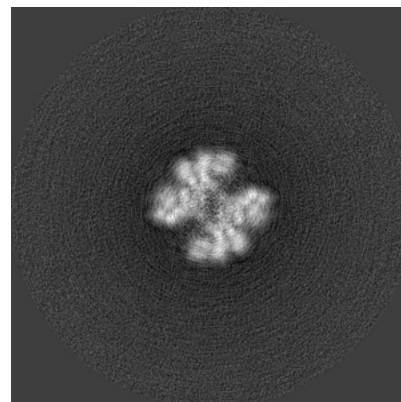
6.2.2 Raw map



X Index: 170



Y Index: 170



Z Index: 170

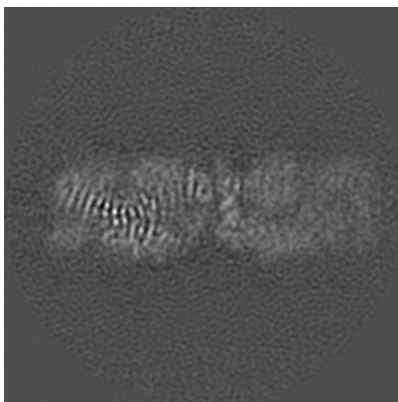
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

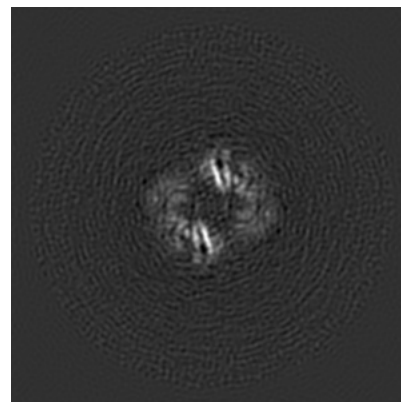
6.3.1 Primary map



X Index: 166

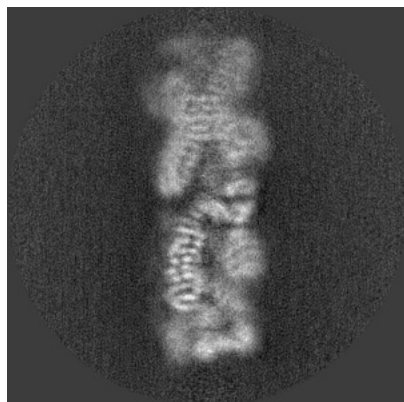


Y Index: 143

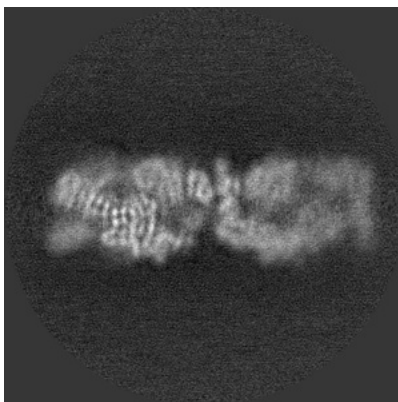


Z Index: 94

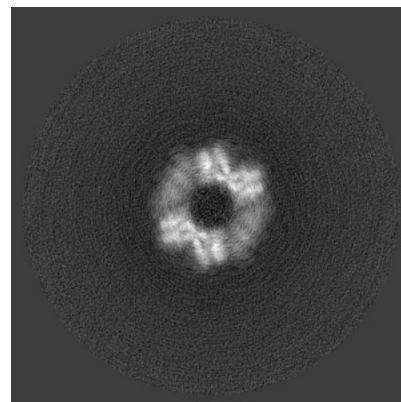
6.3.2 Raw map



X Index: 146



Y Index: 144

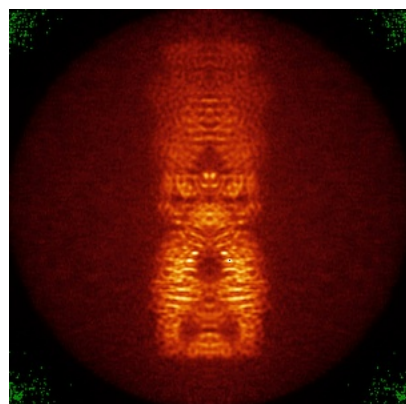


Z Index: 110

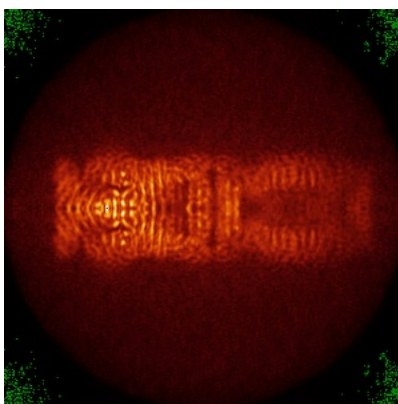
The images above show the largest variance slices of the map in three orthogonal directions.

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

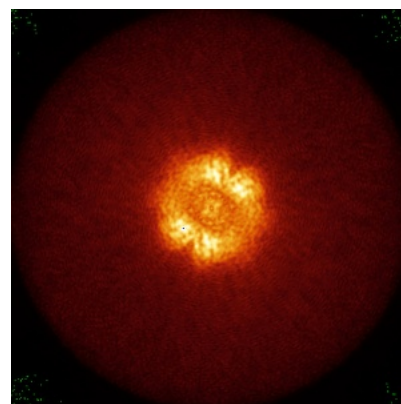
6.4.1 Primary map



X

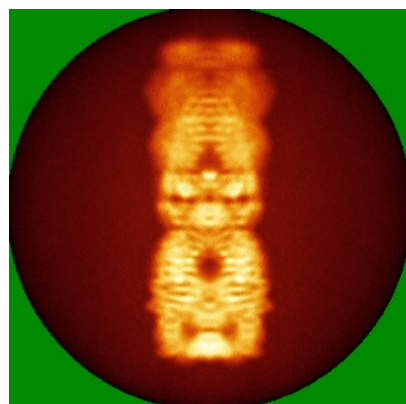


Y

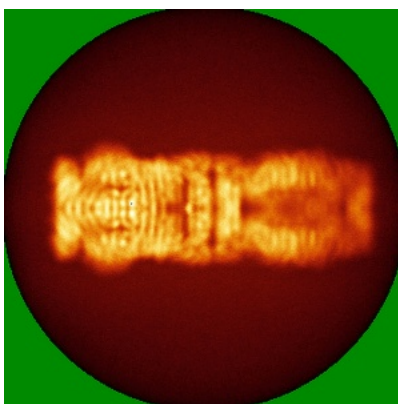


Z

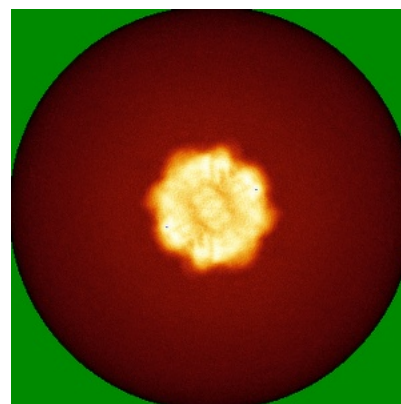
6.4.2 Raw map



X



Y

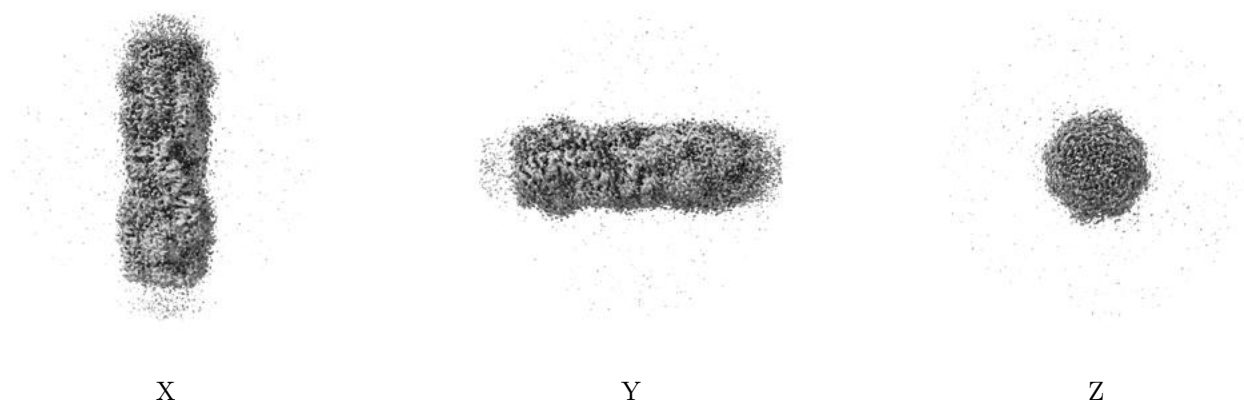


Z

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.

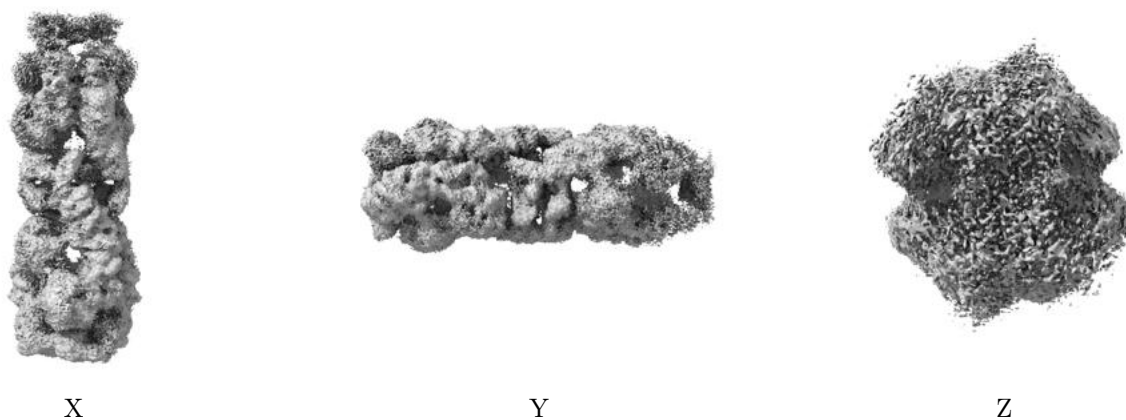
6.5 Orthogonal surface views [i](#)

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.

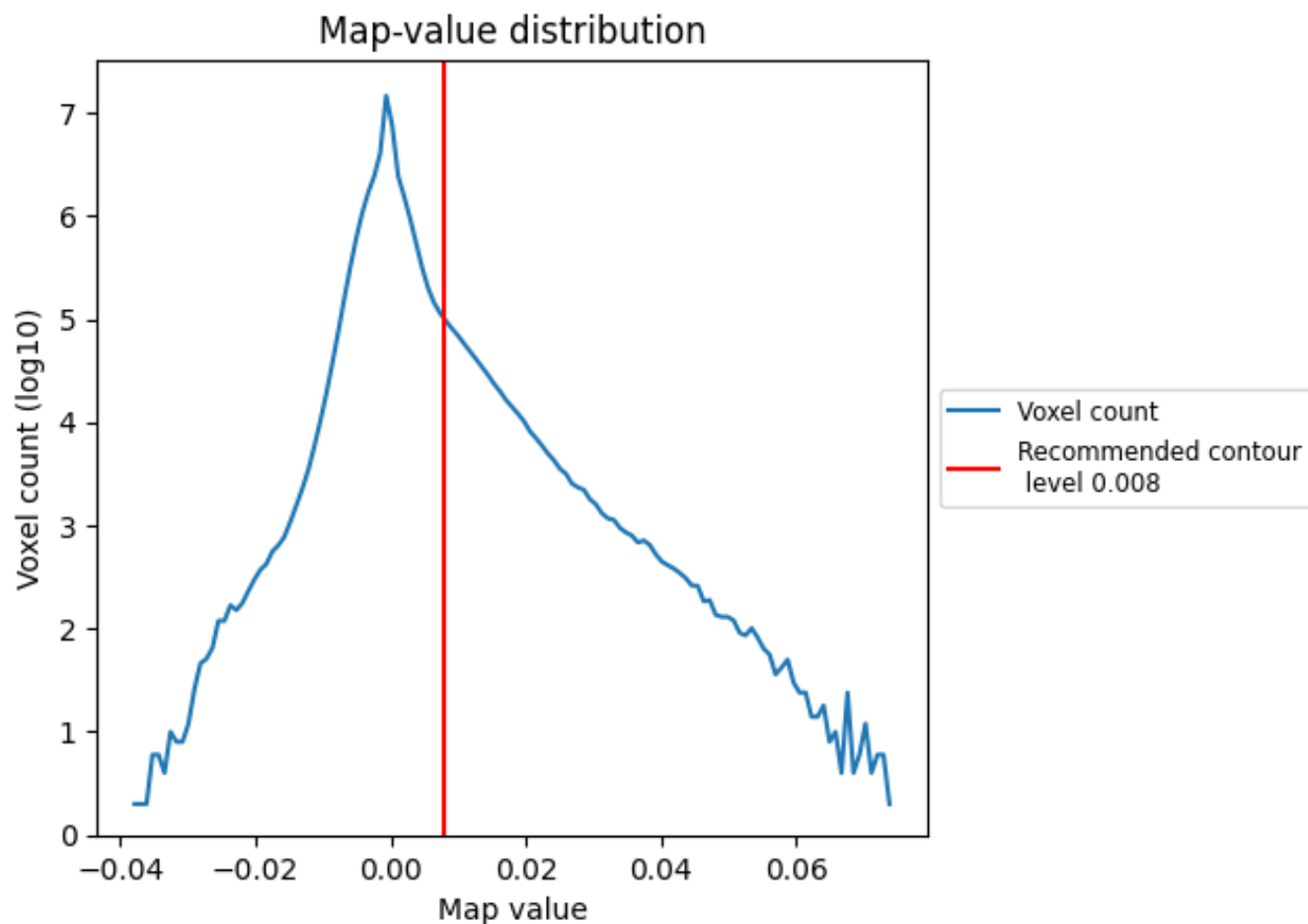
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

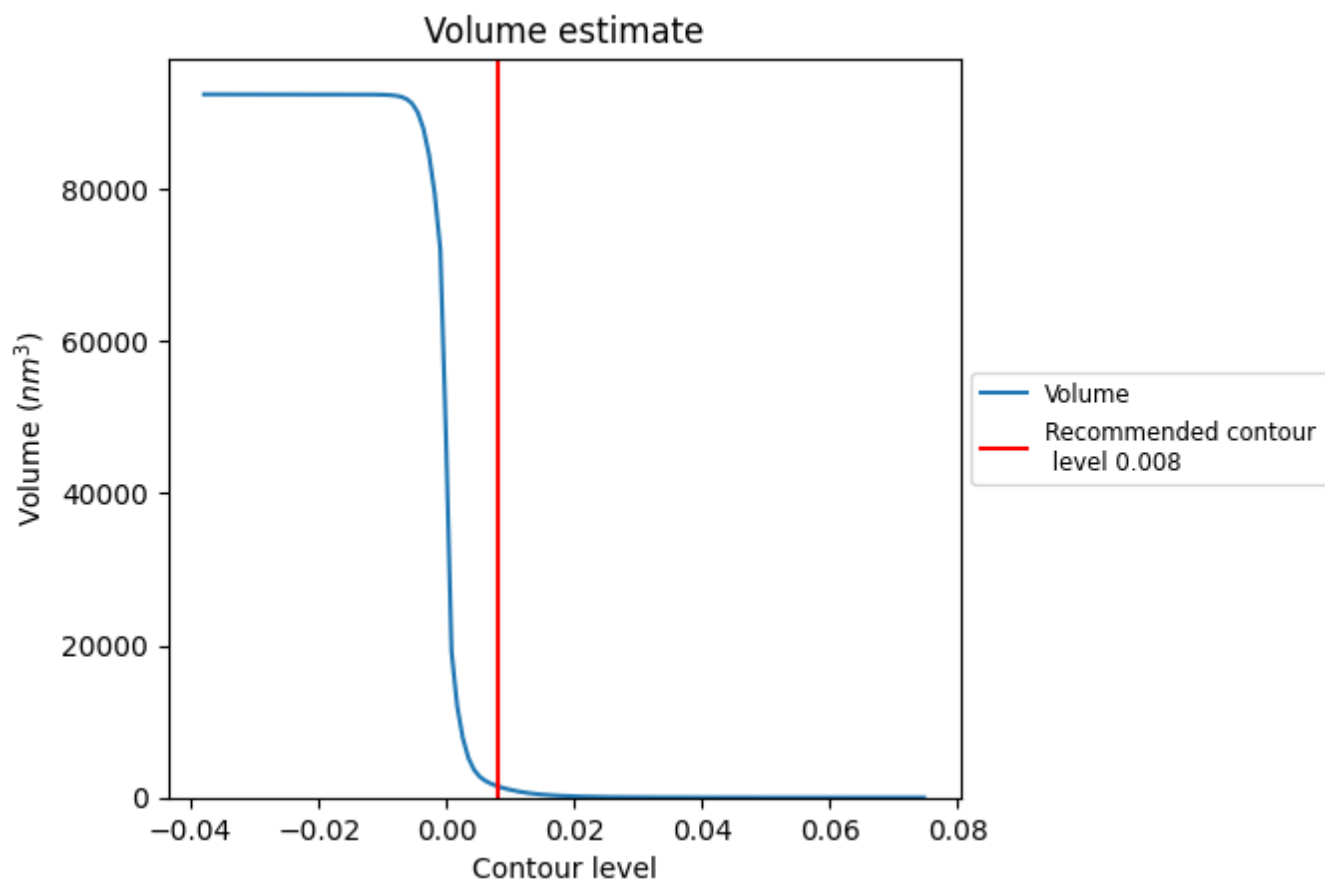
This section contains the results of statistical analysis of the map.

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.

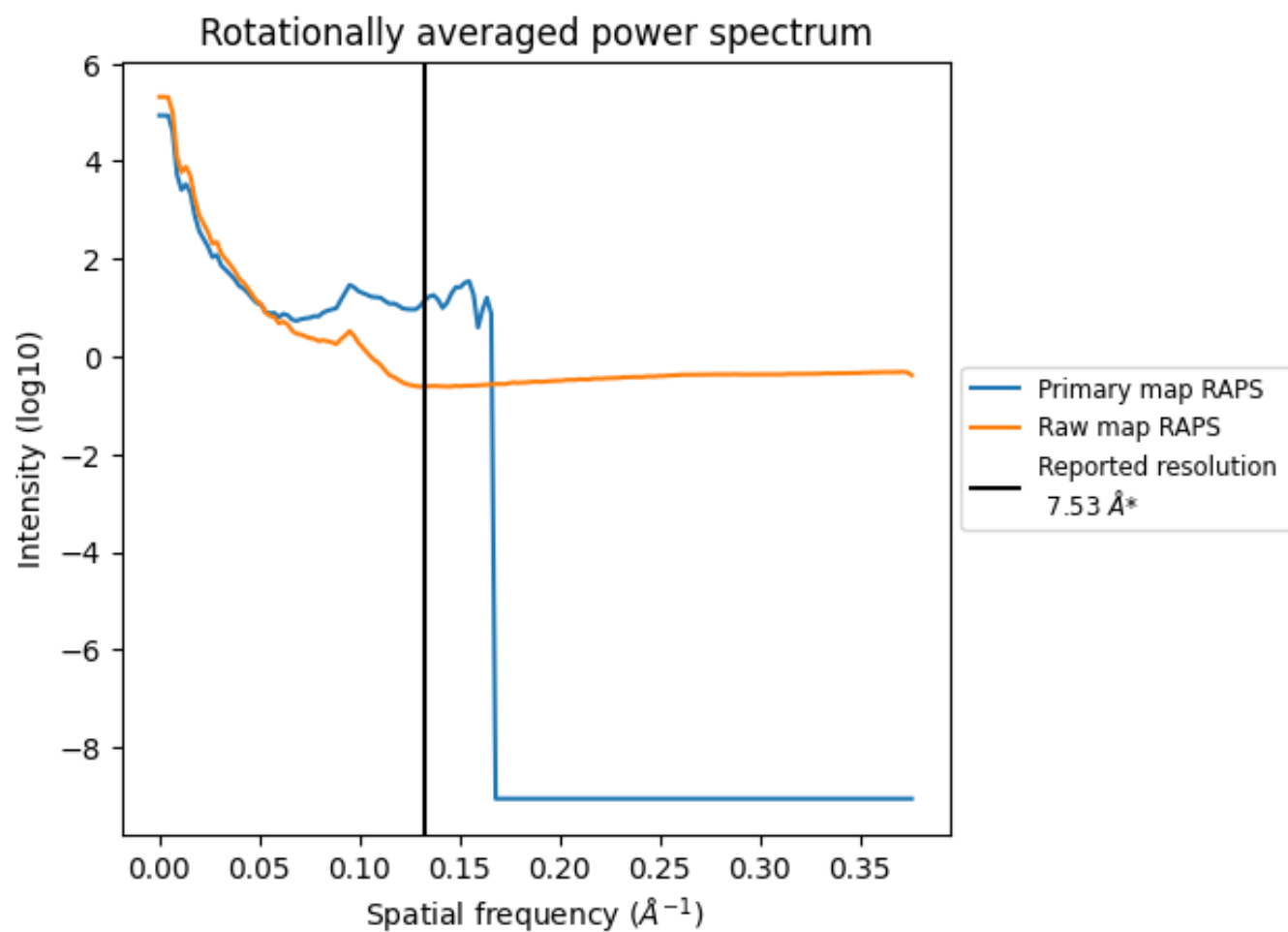
7.2 Volume estimate [i](#)



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 ⓘ

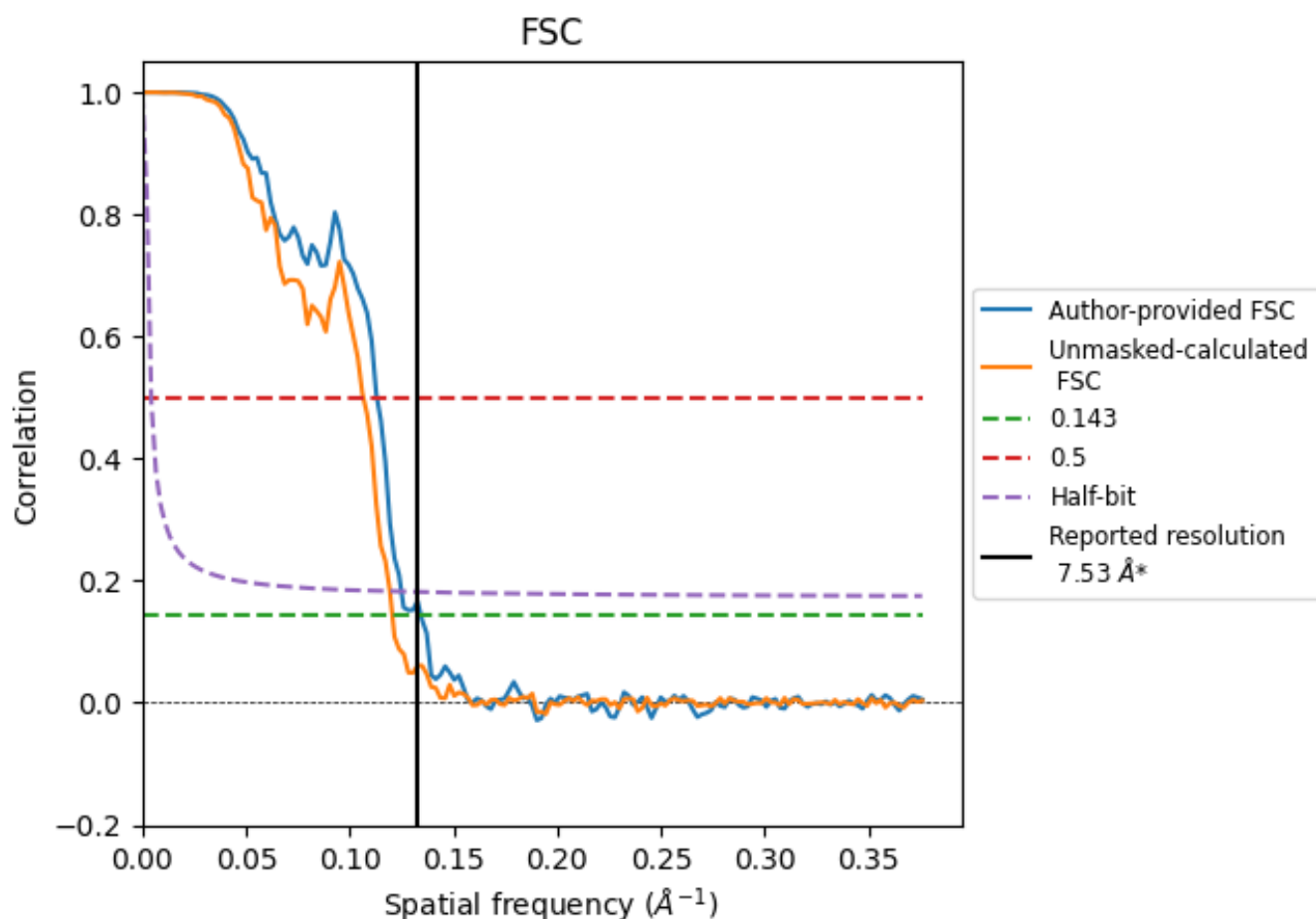


*Reported resolution corresponds to spatial frequency of 0.133 Å⁻¹

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 \AA^{-1}

8.2 Resolution estimates [i](#)

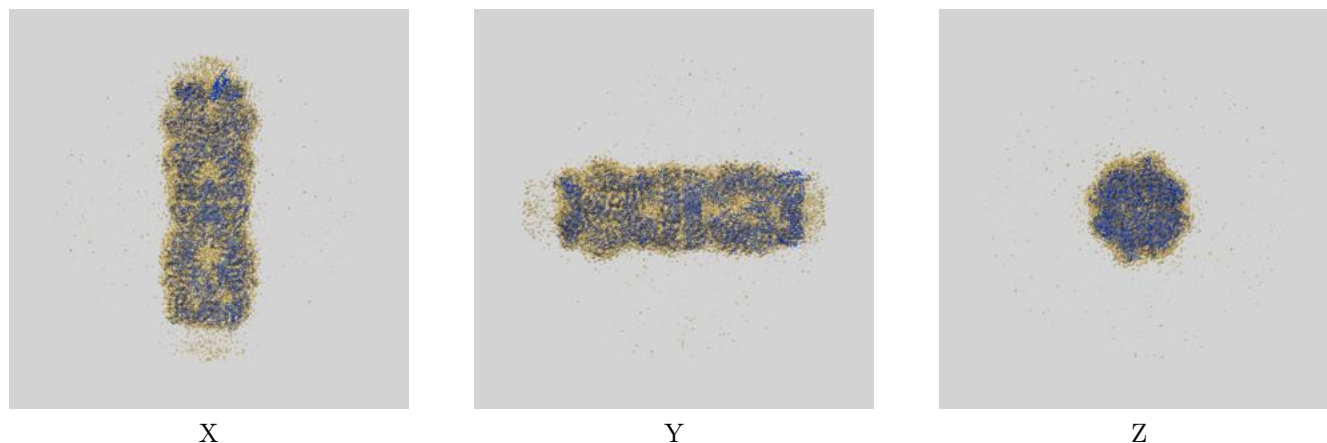
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.53	-	-
Author-provided FSC curve	7.44	8.84	8.00
Unmasked-calculated*	8.29	9.38	8.38

*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](#)

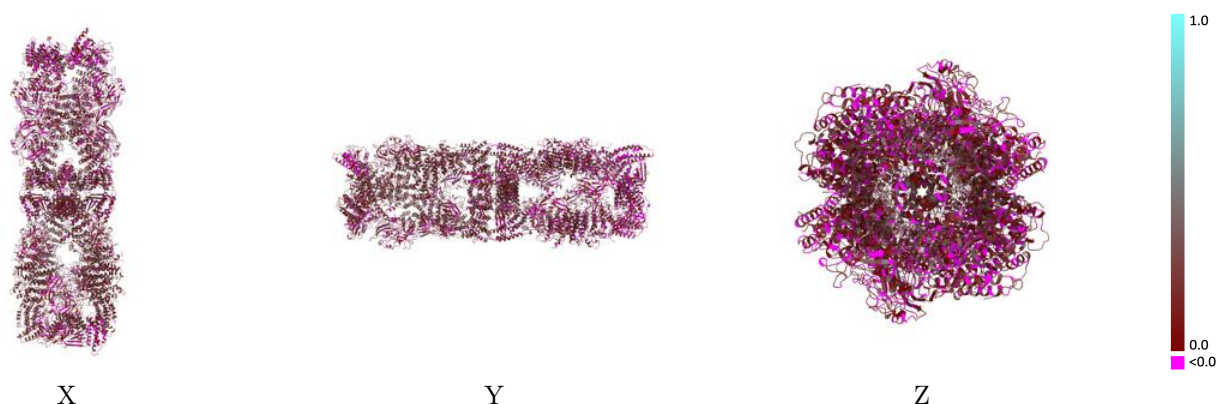
This section contains information regarding the fit between EMDB map EMD-65180 and PDB model 9VM8. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



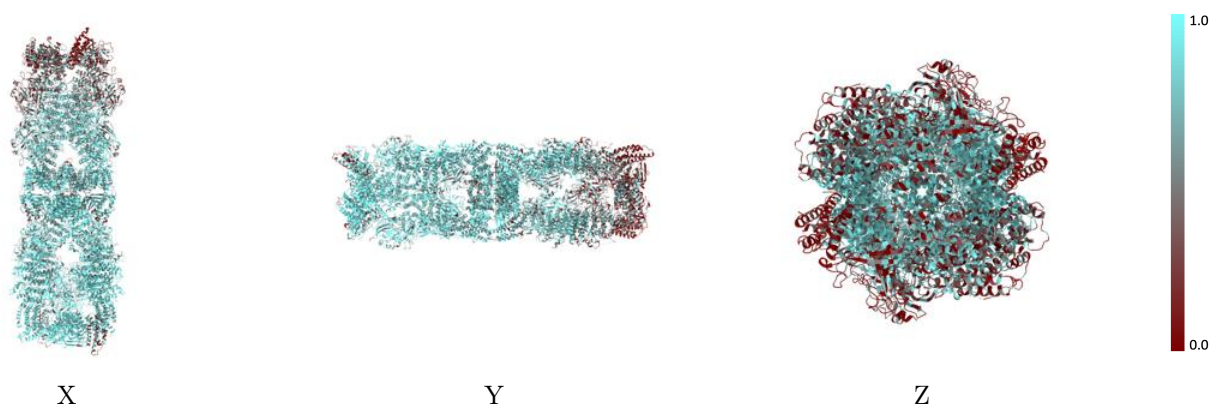
The images above show the 3D surface view of the map at the recommended contour level 0.008 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



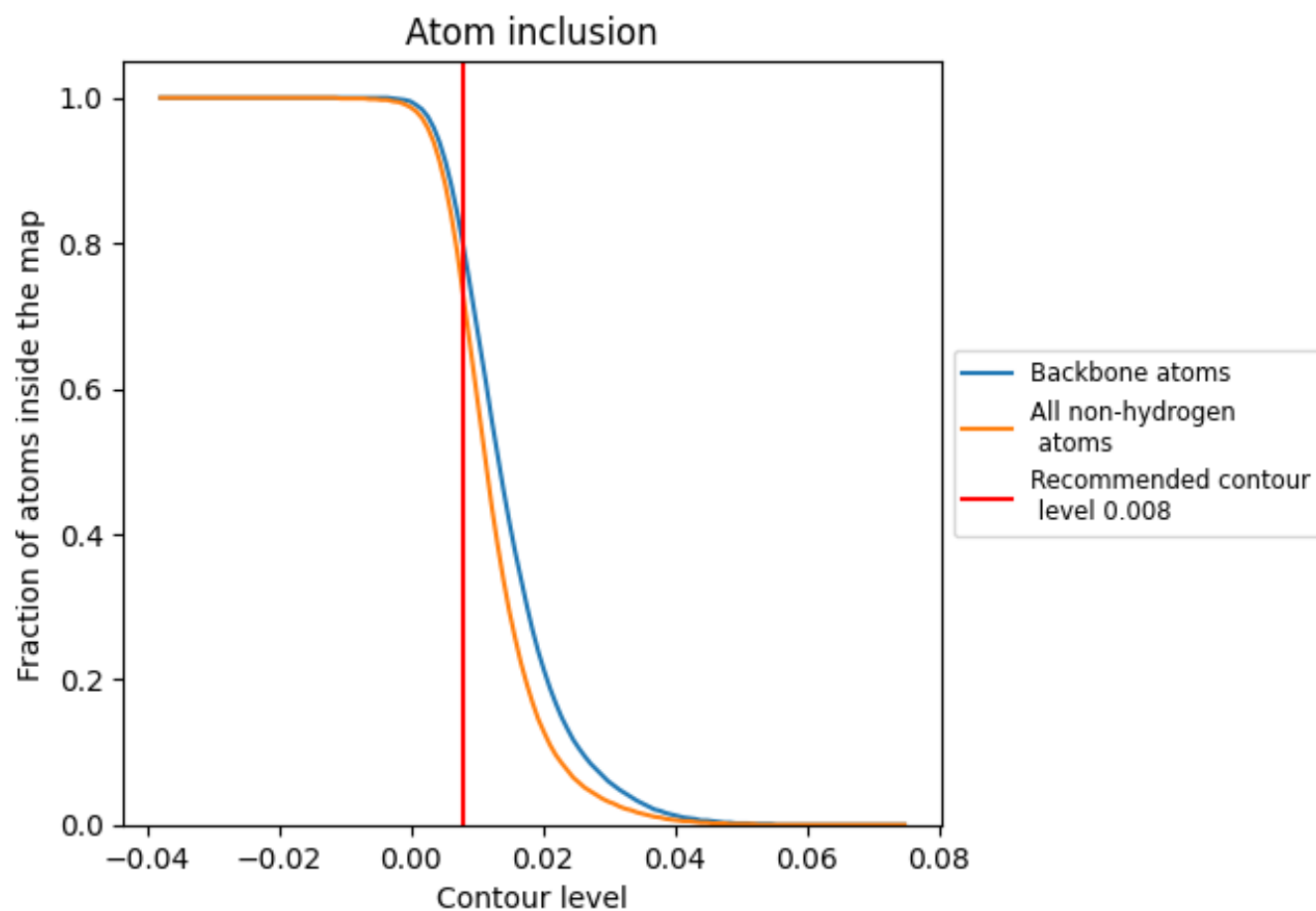
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	<div></div> 0.7230	<div></div> 0.1730
A	<div></div> 0.8230	<div></div> 0.1890
B	<div></div> 0.8210	<div></div> 0.1870
C	<div></div> 0.8300	<div></div> 0.1980
D	<div></div> 0.8290	<div></div> 0.1970
E	<div></div> 0.7050	<div></div> 0.1670
F	<div></div> 0.5370	<div></div> 0.1400
G	<div></div> 0.5370	<div></div> 0.1410
H	<div></div> 0.7040	<div></div> 0.1680

1.0

0.0

<0.0