



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 09:25 AM UTC

PDB ID : 8EZ9 / pdb_00008ez9
EMDB ID : EMD-28731
Title : Dimeric complex of DNA-PKcs
Authors : Chen, S.; He, Y.
Deposited on : 2022-10-31
Resolution : 5.67 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

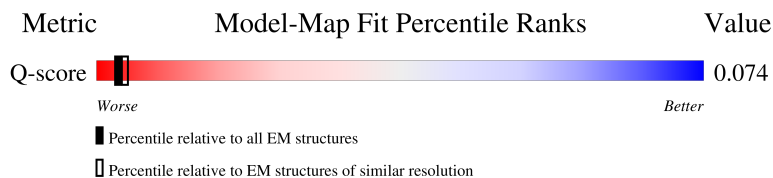
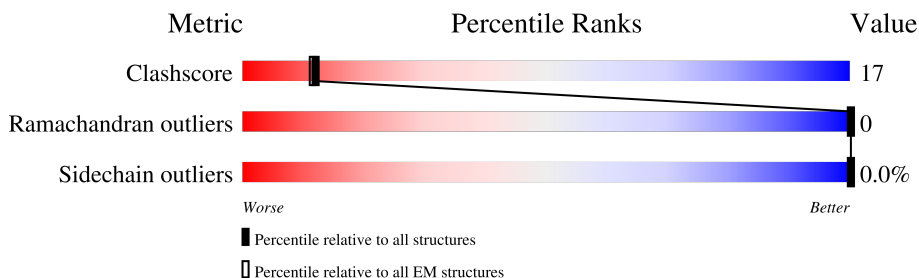
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.67 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	467 (5.18 - 6.17)

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	Q	20	25% 90% 10%
1	R	20	25% 90% 10%
2	C	4128	30% 58% 31% 11%
2	L	4128	31% 58% 31% 11%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 58770 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 unknown region of DNA-PKcs.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	R	20	Total	C	N	O	0	0
			101	60	20	21		
1	Q	20	Total	C	N	O	0	0
			101	60	20	21		

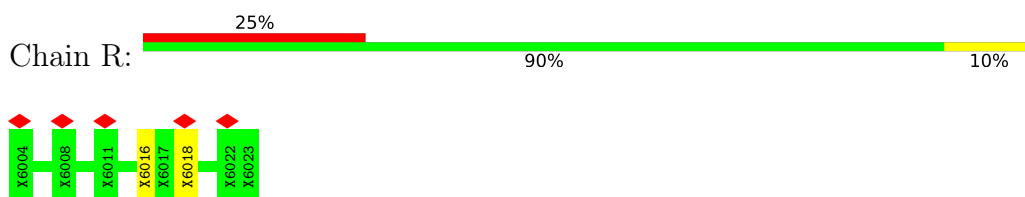
- Molecule 2 is a protein called DNA-dependent protein kinase catalytic subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L	3662	Total	C	N	O	S	0	0
			29284	18776	4946	5370	192		
2	C	3662	Total	C	N	O	S	0	0
			29284	18776	4946	5370	192		

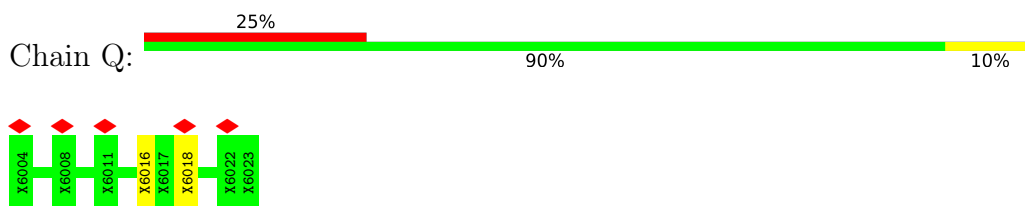
3 Residue-property plots

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.

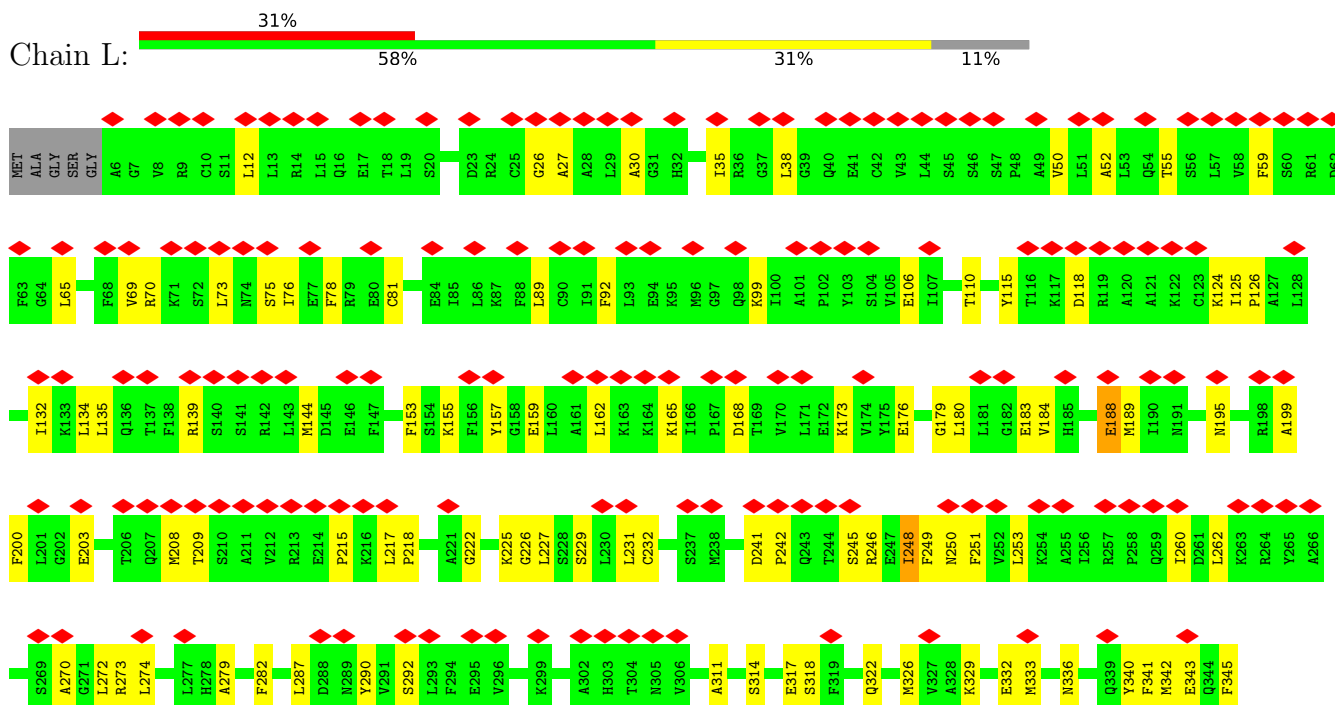
- Molecule 1: unknown region of DNA-PKcs

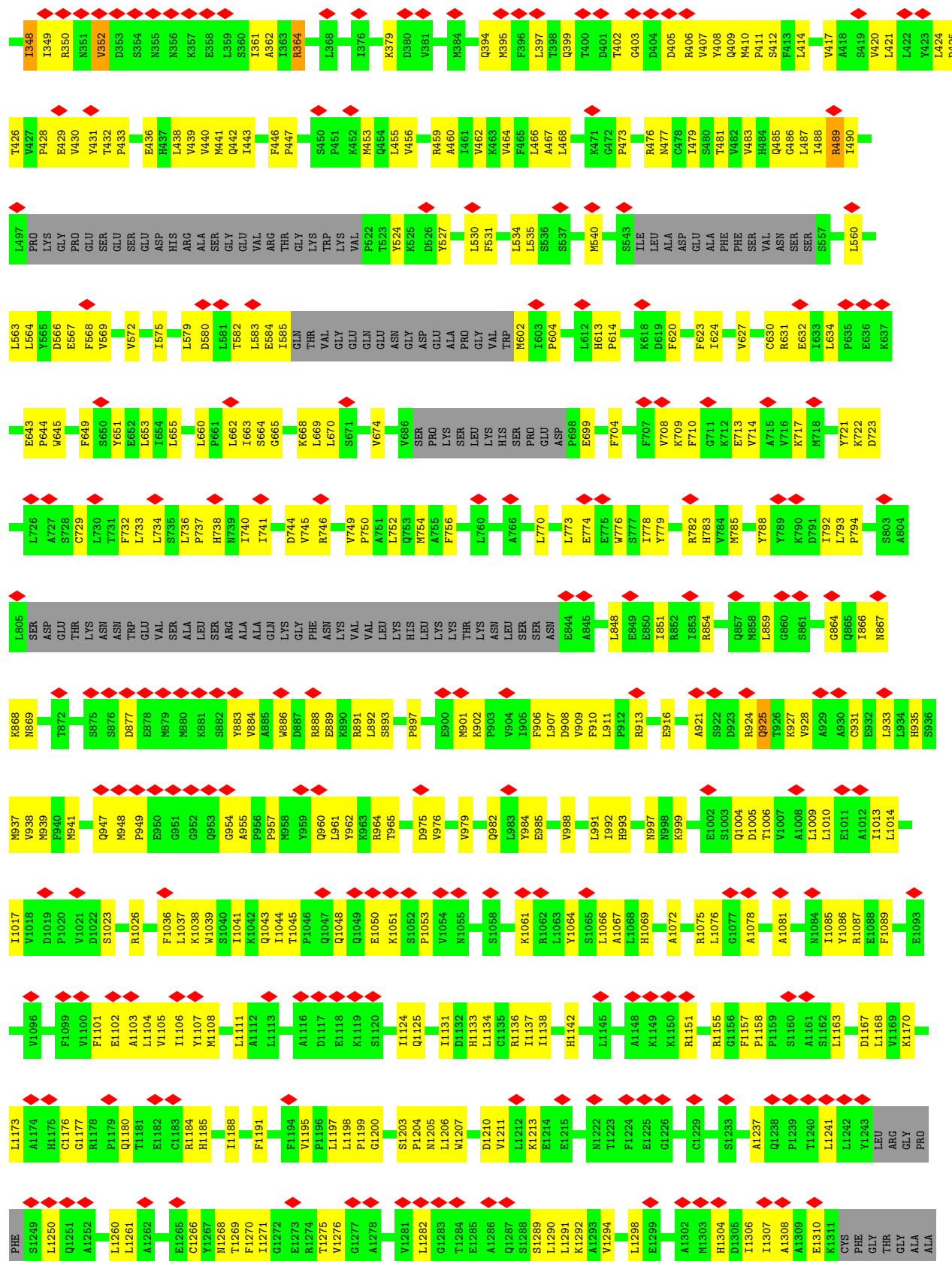


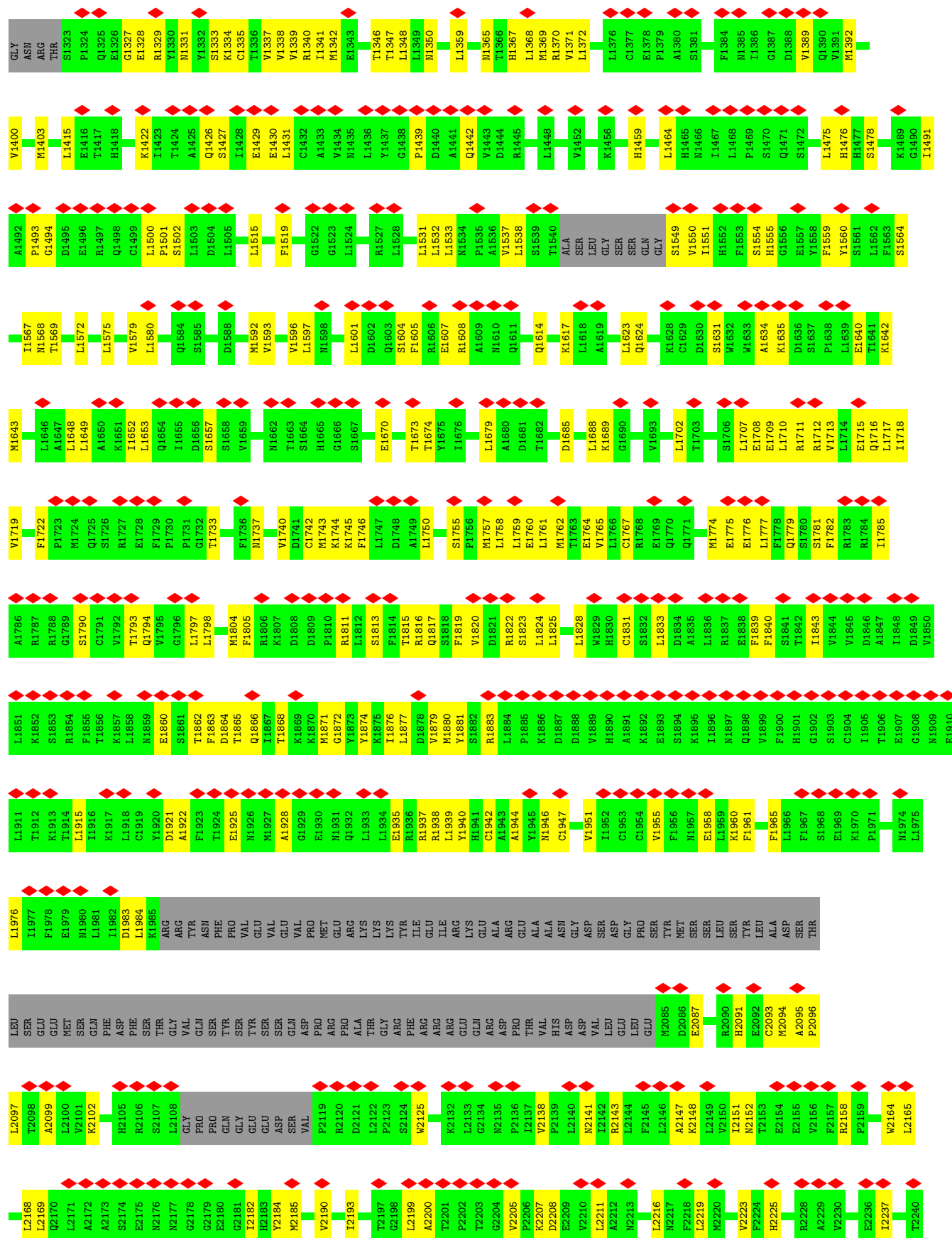
- Molecule 1: unknown region of DNA-PKcs



- Molecule 2: DNA-dependent protein kinase catalytic subunit

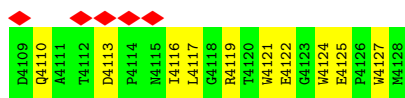




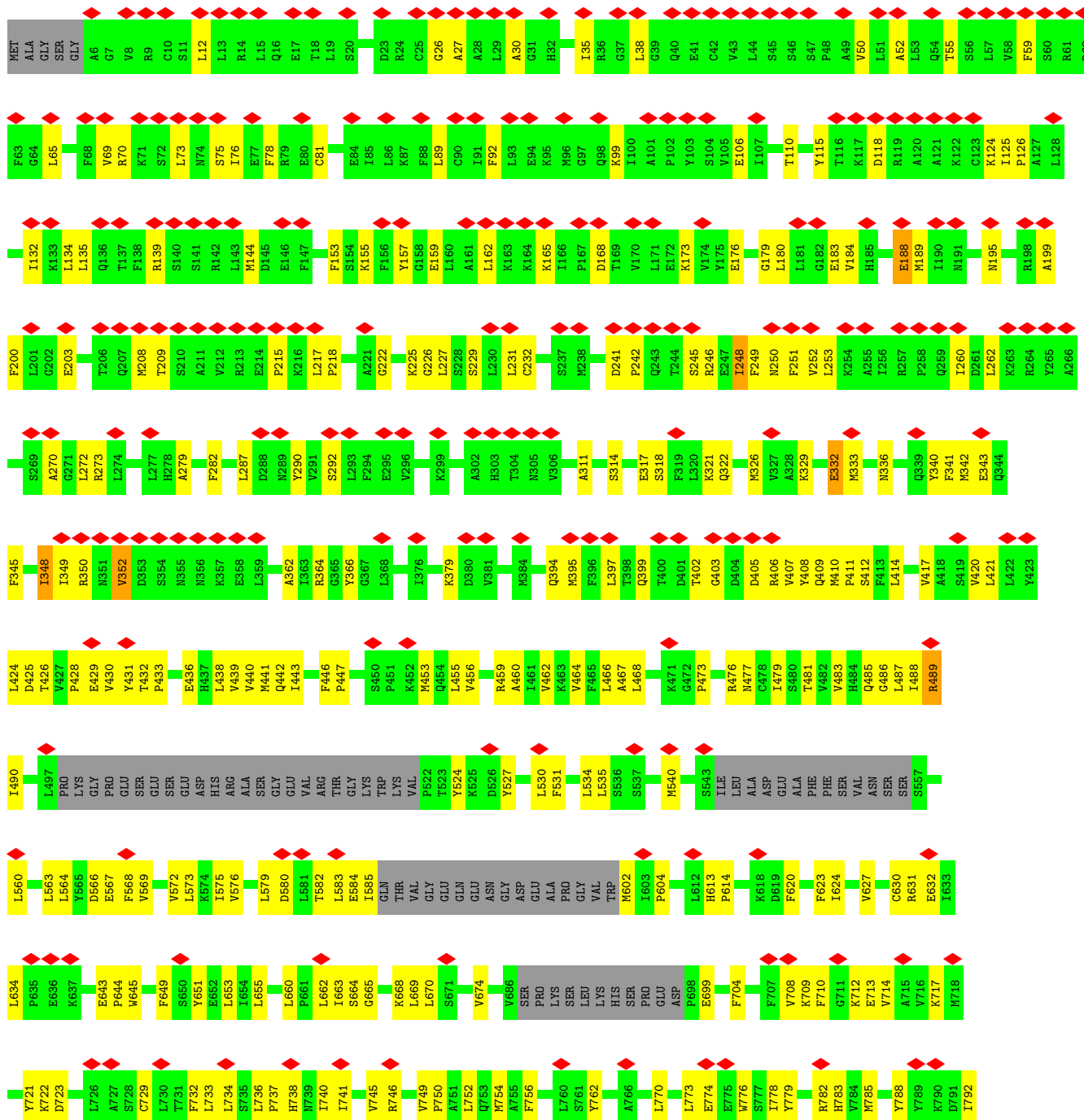




N4032	Q3951	R3874	N3908	D3723	R3653	R593	Q3515	E3438	V3373	V3304	R3232	N3170
K4036	F3952	E3875	T3809	E3724	M3654	R593	R5516	L3439	I3374	S3305	S3233	A3171
N4037	L3953	S3876	V3810	R3725	K3655	A3594	S3517	Q3440	A3375	L3306	K3234	K3172
N4038	P3954		T3811	V3726	E3595	E3595	V3518	Q3441	G3376	L3307	K3235	N3173
F4040	V3955	P3879	D3814	S3731	S3657	A3597	E3520	Y3442	L3377	D3308	F3236	N3174
F4041	P3956	A3880	L3815	L3732	P3658	K3598	T3521	V3446	Q3379	V3312	S3237	P3175
F4042	E3957	D3881	L3816	R3733	F3659	K3599	T3522	V3447	K3380	S3313	M3238	N3176
N4043	N3958	L3882	L3817	R3733	P3660	T3599	A3528	E3448	A3381	S3314	K3239	N3177
N4044	P3960	R3734	T3819	P3735	N3661	V3601	I3529	K3449	F3382	S3314	M3240	N3178
C4045	F3961	R3885	N3820	R3736	T3662	N3602	A3528	M3450	Q3384	Y3315	K3241	N3179
Y4046	R3962	A3886	Q3821	I3739	T3663	K3603	I3529	L3451	Q3384		M3242	D3180
A4047	L3963	F3887	Q3822	I3740	N3664	K3603	V3530		Q3384		I3243	D3181
K4048	T3964	V3888	E3823	R3741	N3665	K3604	F3531	L3455	Q3385	K3318	I3182	I3182
L4051	Q3965	R3889	A3826	G3742	L3666	P3604	P3532	K3454	V3389	N3319	I3183	I3183
A4052	R3966	N3890	A3827	H3743	L3667	N3605	I3535	R3462	Q3390	A3322	A3246	T3184
N4055	N3969	F3897	A3827	H3744	L3668	I3606	S3536	L3463	A3391	F3323	R3247	T3184
P4056	A4057		Y3828	E3745	K3669	E3607	S3537	K3464	A3392	K3248	Q3249	N3185
A4057			E3823	R3746	M3670	K3608	E3538	P3465	E3393	F3252	Q3249	C3187
T4060	L3972	H3903	P3832	R3746	N3671	Y3610	S3539	P3466	E3394	S3253	F3252	F3188
C4061	P3973	F3904	R3833	F3750	E3611	E3612	Y3540	R3467	ALA	K3257	K3257	S3191
D4062	M3974	A3905	C3837	L3751	S3674	R3612	S3541	L3468	GLN	L3258	L3258	S3191
E4063	K3975		E3838	V3752	K3675	M3613	F3542	P3470	PRO	L3259	K3260	K3192
L4064	Q3978	A3909	Y3839	G3753	P3676	Y3614	K3543	I3471	PRO	L3330	E3261	E3194
L4065	G3979	L3910	D3941	G3754	P3677	A3615	D3544	I3472	SER	T3332	E3261	E3195
L4065	M3980	I3913	N3942	E3755	P3678	A3615	T3545	R3473	TTP	T3333	L3262	K3196
N3981	Y3981	N3916	L3943	D3757	N3679	A3617	S3546	E3474	SER	Y3334	H3263	L3197
S3982	I3983	I3917	T3944	R3758	K3680	G3618	T3547	R3474	CYS	K3335	K3264	T3198
I3983		L3918	K3945	L3759	K3681	P3619	T3547	Y3475	GLY	I3336	K3267	P3199
H4068		G3921	N3946	R3760	C3682	P3620	H3549	P3476	PRO	I3337	K3267	LEU
E4069	L3997	G3921	G3948	D3761	S3684	K3621	K3550	T3479	A3406	L3341	T3268	PRO
P4072	L3998	D3922	C3948	V3764	M3687	A3622	V3555	L3482	A3407	E3344	D3271	GLU
R4075	T4001	D3922	K3949	L3767	K3687	P3623	I3558	K3485	G3408	F3345	W3272	ASP
D4076	M4002	R3923	H3950	L3767	F3690	G3624	T3558	K3485	D3411	E3344	S3275	ASN
A4079	D4003	H3924	D3951	I3774	K3691	L3625	I3559	S3489	A3412	P3345	S3275	SER
K4085	V4004	L3925	N3952		V3692	G3626	S3560	W3493	Y3413	A3346	Q3278	ASN
D4086	F4005	N3926	G3853	A3780	K3691	A3627	S3561	Q3494	K3414	C3347	Q3278	VAL
H4087	V4006	N3927	G3853	C3781	E3693	F3628	L3562	F3495	T3415	L3348	C3281	ASP
N4088	K4007	F3928	Y3855	S3782	F3694	R3629	D3563	S3497	L3416	A3349	R2822	GLN
I4089	F4011	N3930	M3856	R3783	N3697	K3630	K3564	W3498	F3419	E3350	H3285	ASP
R4090	D4012	A3931	L3857	A3785	K3697	F3632	Q3564		G3420	I3351	C3286	PRO
A4091	F4016	E3932	Y3859	A3785	E3700	Q3634	Q3564		E3352	E3352	R3287	SER
Q4092	E4017	E3933	K3860	L3786	I3701	T3633	C3565		D3421	E3353	S3288	ASP
S4096	V3937	V3937	C3861	R3789	Q3700	I3633	I3568	H3501	Q3422	D3354	Q3291	ARG
G4097	L3938	L3938	A3862	S3798	P3702	Q3634	Q3569	M3502	Q3422	K3355	G3292	MET
L4098	G3939	G3939	A3862	S3798	Q3703	Q3637	D3570	V3503	L3424	K3355	G3292	GLU
S4099	L3940	L3940	N3863	R3799	Q3704	T3635	F3571	A3504	R3425	A3356	C3293	VAL
N4099	D3941	D3941	R3864	L3800	K3708	K3638	I3572	A3504	K3426	R3357	S3294	GLN
K4023	F3942	F3942	T3865	G3801	R3709	E3639	N3573	L3506	E3427	I3359	Q3295	GLN
G4024	G3943	G3943	E3866	L3802	K3710	F3640	A3574	D3507		L3360	Q3296	GLU
E4100	F4101	F4101	T3867	I3803	P3711	H3643	L3575	K3508	N3430	E3361	V3297	GLU
T4102	A3945	A3945	V3868	E3804	H3716	F3644	L3576	D3509	A3431	G3364	L3298	ASP
Q4103	F3946	F3946	W3905	N3804	V3717	G3645	Q3577	Q3510	S3432	S3365	T3299	
N4105	G3947	G3947	K3871	E3807	R3718	K3646	L3578		V3433	S3366	K3302	
C4106	S3948	S3948	R3872		I3719	G3647	L3583	A3513	I3434	S3367	T3303	
L4107			A3720		I3719	G3648	L3584	V3514	D3435	E3368		
N4108	E4030	E4030	G3721		G3722	K3650	F3585		A3437	D3369		
			K3873			L3652	W3588			K3372		



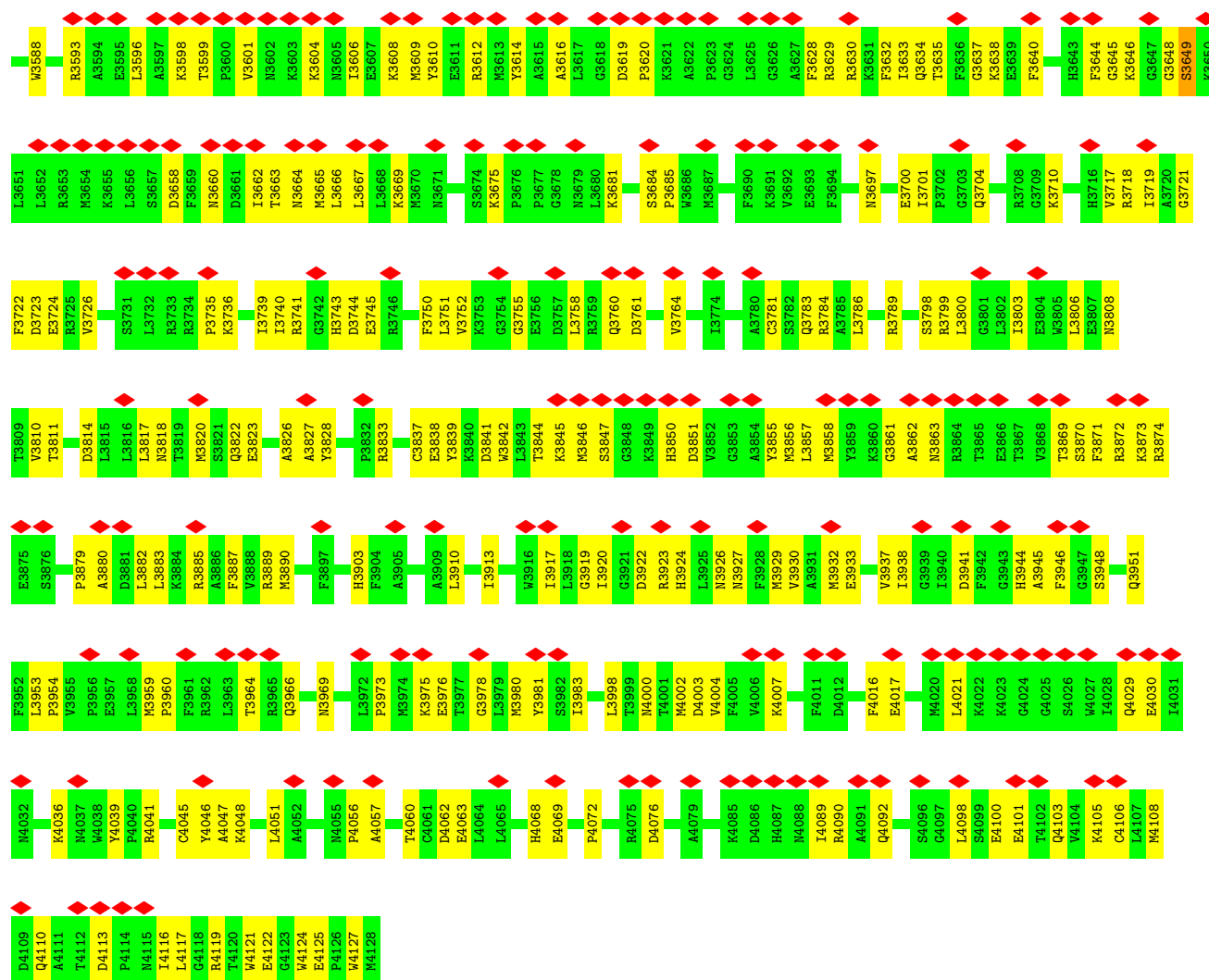
● Molecule 2: DNA-dependent protein kinase catalytic subunit



L793	P794	S803	A804	L805	SER	ASP	GLU	THR	LYS	ASN	ASN	TRP	GLU	VAL	SER	ALA	LEU	SER	ARG	ALA	ALA	GLN	LYS	GLY	PHE	ASN	LYS	VAL	SER	SER	ASN	E944	A845	L848	E849	E850	I851	P852	I853	R854	Q857	M858	L859	G860	S861										
		G864	Q865	I866	N867	K868	N869	T872	S875	S876	D877	E878	M879	M880	K881	S882	Y883	V884	A885	D886	D887	R888	E889	K890	R891	L892	S893	P897	E900	M901	K902	P903	V904	I905	F906	L907	D908	V909	F910	L911	P912	R913	E916	A921	S922	D923	R924	Q925	T926	K927	V928	A929	A930	C931	
		E932	L933	L934	H935	S936	N937	V938	M939	F940	M941	Q947	M948	P949	E950	G951	G952	Q953	G954	A955	P956	P957	M958	Y959	Q960	L961	Y962	K963	R964	T965	D975	V976	V979	Q982	L983	Y984	E985	V988	L991	T992	H993	N997	E1002	S1003	I1004	D1005	T1006	V1007	A1008	L1009	L1010	F1011	A1012		
		I1013	L1014	I1017	V1018	D1019	D1020	V1021	D1022	S1023	R1026	F1036	L1037	K1038	S1040	I1041	K1042	Q1043	I1044	T1045	P1046	Q1047	Q1048	Q1049	Y1050	K1051	S1052	P1053	V1054	N1055	S1058	K1061	R1062	L1063	Y1064	S1065	L1066	A1067	H1068	A1072	R1075	L1076	G1077	A1078	A1081	N1084	I1085	Y1086	R1087	E1088					
		F1089	E1093	V1096	F1099	V1100	F1101	E1102	A1103	L1104	V1105	L1106	Y1107	C1183	M1108	L1111	A1112	L1113	A1116	D1117	E1118	P1196	L1197	L1198	P1199	G1200	S1203	P1204	N1205	L1206	W1207	L1208	K1209	D1210	L1211	L1212	K1213	E1214	E1215	F1219	N1222	T1223	F1224	E1225	G1226	G1229	S1233	A1237	Q1238	P1239					
		T1240	L1241	L1242	L1243	LEU	ARG	GLY	PRO	PHE	S1249	L1250	Q1251	A1252	L1260	L1261	A1262	E1265	C1266	N1268	T1269	F1270	I1271	G1272	E1273	R1274	T1275	V1276	G1277	A1278	V1281	L1282	G1283	T1284	E1285	A1286	Q1287	S1288	L1289	L1290	L1291	K1292	A1293	V1294	L1298	E1299	A1302	M1303	H1304	I1306	L1307	A1308	E1310		
		K1311	CYS	PHE	GLY	THR	GLY	ALA	ALA	GLY	ASN	ARG	THR	S1323	P1324	Q1325	E1326	E1327	E1328	R1329	Y1330	N1331	Y1332	S1333	K1334	C1335	T1336	V1337	V1338	V1339	R1340	I1341	M1342	E1343	T1346	T1347	L1348	L1349	N1350	L1359	N1365	T1366	L1367	M1369	R1370	V1371	L1372	L1376	C1377	E1378	V1379	A1380	S1381	F1384	N1385
		I1386	G1387	D1388	V1389	Q1390	V1391	M1392	V1400	M1403	L1415	E1416	T1417	H1418	K1422	T1423	T1424	A1425	Q1426	S1427	I1428	E1429	E1430	L1431	C1432	A1433	V1434	N1435	L1436	V1437	G1438	P1439	A1441	Q1442	V1443	D1444	R1445	L1448	V1452	K1456	H1459	L1464	H1465	L1466	I1467	L1468	P1469	S1470	Q1471	S1472					
		L1475	H1476	H1477	S1478	K1489	G1490	I1491	A1492	P1493	G1494	D1495	E1496	R1497	Q1498	C1499	L1500	P1501	L1502	S1503	D1504	L1505	L1515	F1519	G1522	G1523	L1524	A1527	L1528	L1531	L1532	L1533	M1534	P1535	A1536	V1537	L1538	S1539	T1540	ALA	SER	LEU	GLY	SER	SER	GLN	SER	V1549	V1550	I1551	H1552	F1553	S1554	G1555	
		E1557	Y1558	F1559	Y1560	S1561	L1562	F1563	S1564	T1567	N1568	T1569	L1572	L1575	V1579	L1580	Q1584	S1585	D1588	M1592	V1593	T1663	S1664	H1665	G1666	S1667	N1662	T1673	T1674	V1675	I1676	L1679	L1759	M1757	L1758	A1609	M1610	Q1611	Q1614	K1617	L1618	A1619	L1623	Q1624	K1628	C1629	D1630	S1631	V1632	F1633	A1634				
		K1635	D1636	S1637	P1638	L1639	K1642	M1643	L1646	A1647	L1648	L1649	A1650	K1651	L1652	L1653	Q1654	I1655	D1656	S1657	G1658	V1659	N1662	T1663	S1664	H1665	G1666	S1667	E1670	T1673	T1674	V1675	I1676	L1679	L1759	M1757	L1758	A1680	D1681	T1682	E1685	L1688	K1689	G1690	V1693	T1703	S1706	L1707	E1708	F1709	L1710	R1711	R1712		
		V1713	L1714	E1715	Q1716	L1717	L1718	V1719	F1722	P1723	M1724	Q1725	L1726	R1727	E1728	F1729	P1730	P1731	G1732	T1733	F1736	N1737	V1740	D1741	M1742	K1743	K1744	K1745	F1746	L1747	D1748	A1749	L1750	S1755	P1756	L1757	L1758	A1680	D1681	T1682	E1685	L1688	K1689	G1690	V1693	T1703	S1706	L1707	E1708	F1709	L1710	R1711	R1712		







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	64775	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 ($e^-/\text{\AA}^2$)	65	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.031	Depositor
Minimum map value	-0.017	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.006	Depositor
Map size (Å)	356.6592, 356.6592, 356.6592	wwPDB
Map dimensions	432, 432, 432	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8256, 0.8256, 0.8256	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	$\# Z > 5$
2	C	0.25	1/29884 (0.0%)	0.65	20/40387 (0.0%)
2	L	0.25	1/29884 (0.0%)	0.65	16/40387 (0.0%)
All	All	0.25	2/59768 (0.0%)	0.65	36/80774 (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
2	C	0	3
2	L	0	2
All	All	0	5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	580	ASP	CA-CB	5.07	1.60	1.53
2	L	580	ASP	CA-CB	5.04	1.60	1.53

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	352	VAL	N-CA-C	10.45	124.15	111.09
2	C	352	VAL	N-CA-C	10.42	124.11	111.09
2	C	348	ILE	CA-C-N	8.10	135.36	122.56
2	C	348	ILE	C-N-CA	8.10	135.36	122.56
2	L	348	ILE	CA-C-N	8.08	135.33	122.56

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	364	ARG	Sidechain
2	C	366	TYR	Sidechain
2	C	489	ARG	Sidechain
2	L	364	ARG	Sidechain
2	L	489	ARG	Sidechain

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Q	101	0	25	3	0
1	R	101	0	25	3	0
2	C	29284	0	29680	1017	0
2	L	29284	0	29680	1031	0
All	All	58770	0	59410	2020	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 17.

The worst 5 of 2020 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)
2:L:3606:ILE:O	2:L:3610:TYR:HB2	1.53	1.08
2:C:3606:ILE:O	2:C:3610:TYR:HB2	1.53	1.07
2:L:26:GLY:C	2:C:76:ILE:HD12	1.84	1.01
2:L:76:ILE:HD12	2:C:26:GLY:C	1.86	1.01
2:C:2890:ILE:HG12	2:C:2929:LEU:HD21	1.47	0.95

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	
2	C	3632/4128 (88%)	3344 (92%)	288 (8%)	0	100	100
2	L	3632/4128 (88%)	3343 (92%)	289 (8%)	0	100	100
All	All	7264/8256 (88%)	6687 (92%)	577 (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	
2	C	3266/3671 (89%)	3265 (100%)	1 (0%)	100	100
2	L	3266/3671 (89%)	3265 (100%)	1 (0%)	100	100
All	All	6532/7342 (89%)	6530 (100%)	2 (0%)	100	100

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	L	925	GLN
2	C	925	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 79 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	1772	HIS
2	C	3249	GLN
2	C	2135	ASN
2	C	2553	HIS
2	C	3743	HIS

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 [i](#)

There are no chain breaks in this entry.

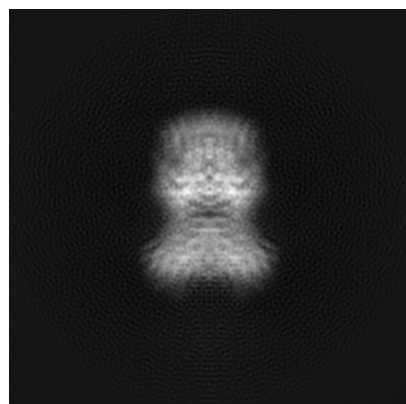
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-28731. These allow visual inspection of the internal detail of the map and identification of artifacts.

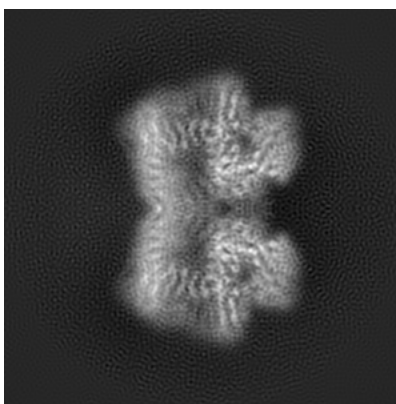
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

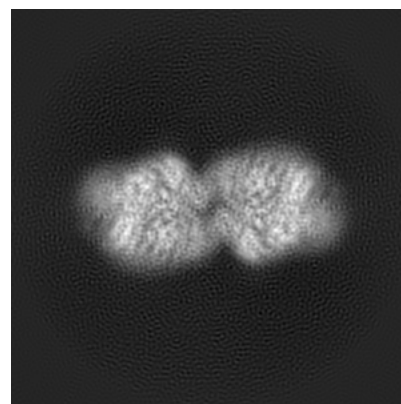
6.1.1 Primary map



X

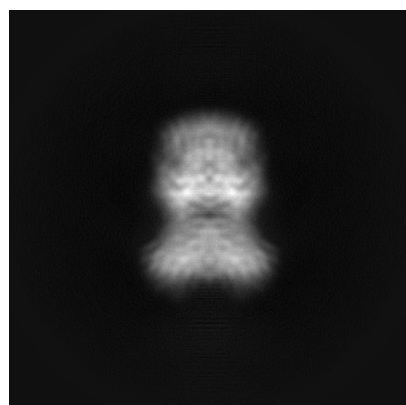


Y

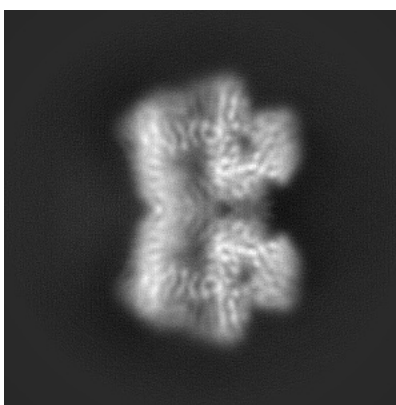


Z

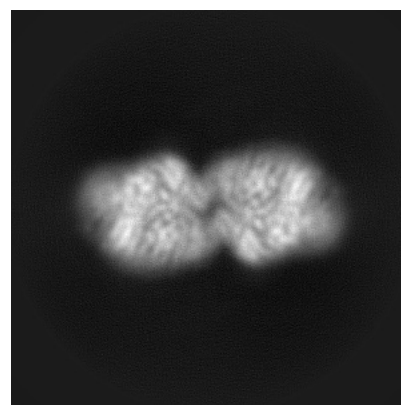
6.1.2 Raw map



X



Y

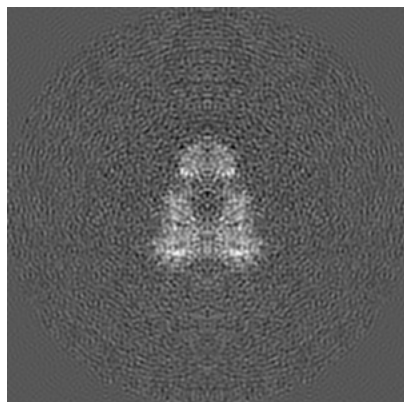


Z

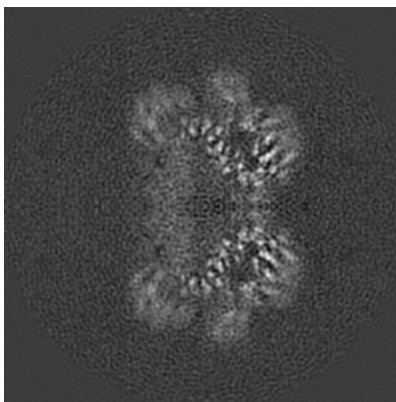
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

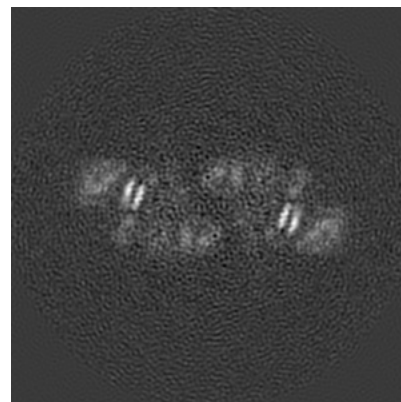
6.2.1 Primary map



X Index: 216

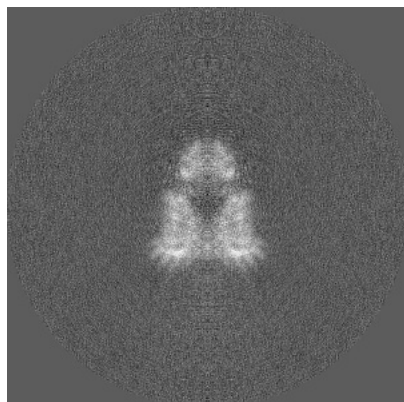


Y Index: 216

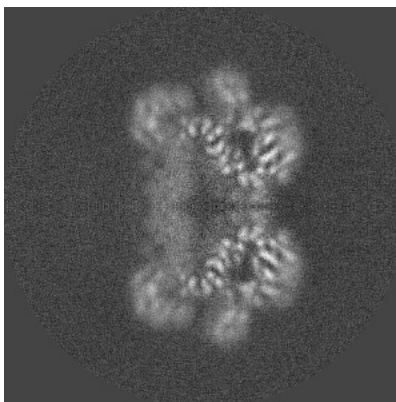


Z Index: 216

6.2.2 Raw map



X Index: 216



Y Index: 216

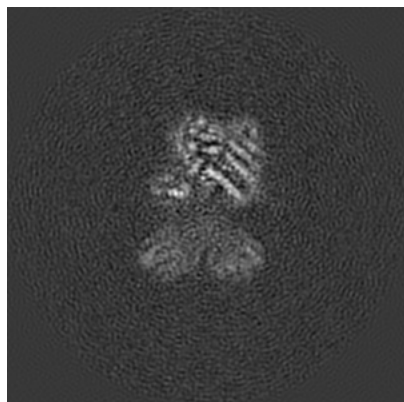


Z Index: 216

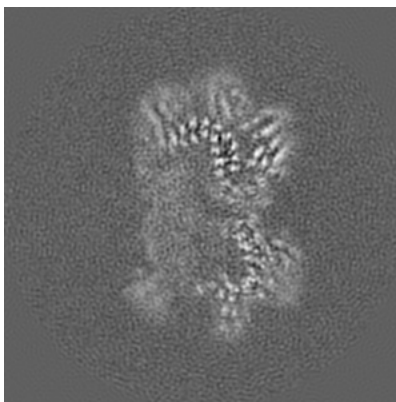
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

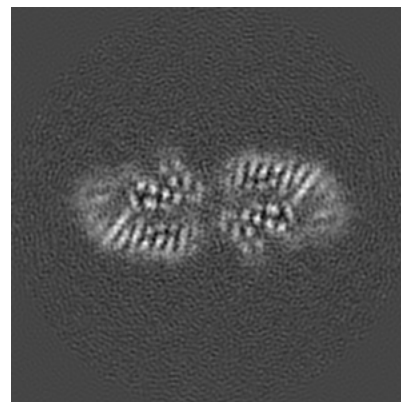
6.3.1 Primary map



X Index: 174

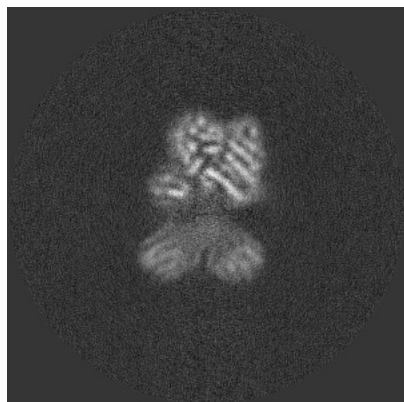


Y Index: 204

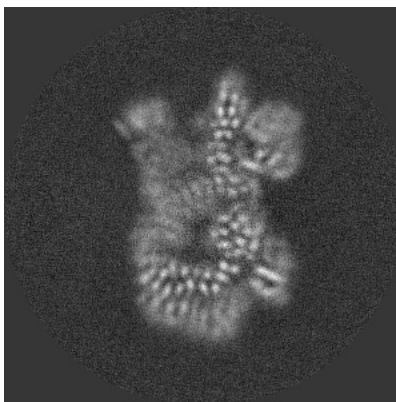


Z Index: 234

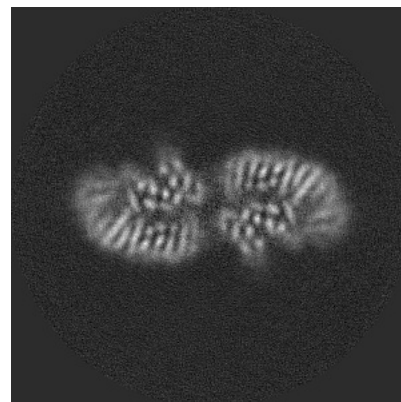
6.3.2 Raw map



X Index: 174



Y Index: 239

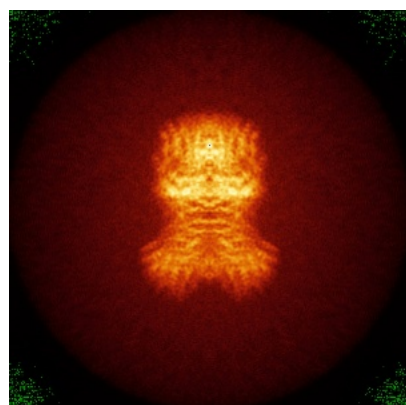


Z Index: 234

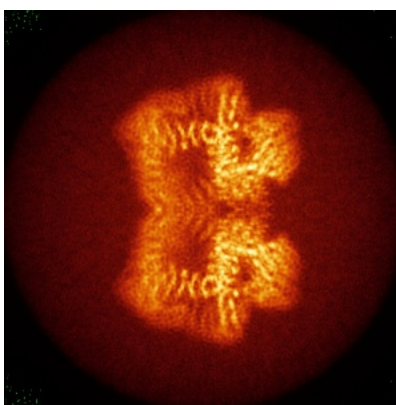
The images above show the largest variance slices of the map in three orthogonal directions.

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

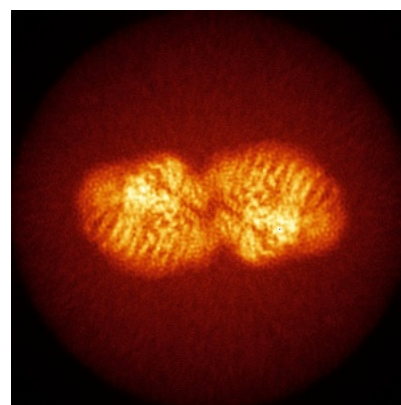
6.4.1 Primary map



X

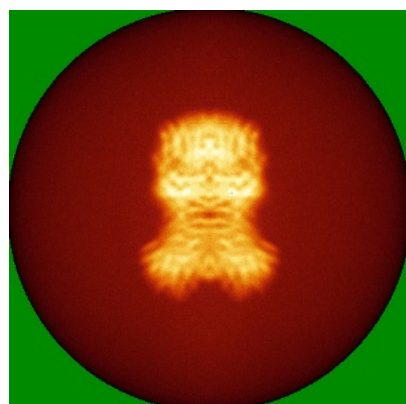


Y

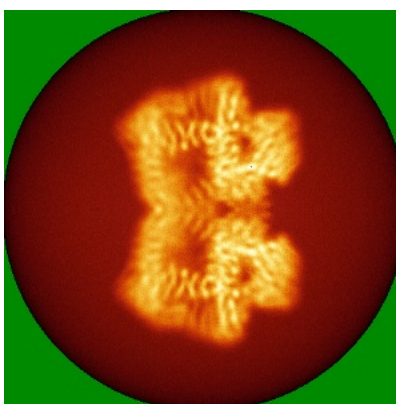


Z

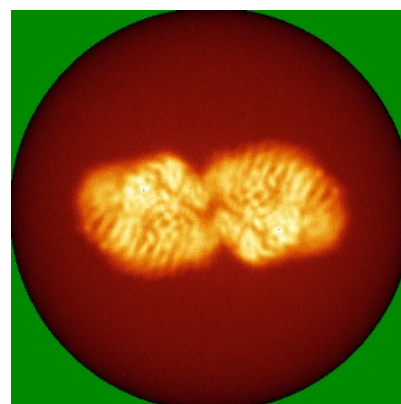
6.4.2 Raw map



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](#)

This section was not generated.

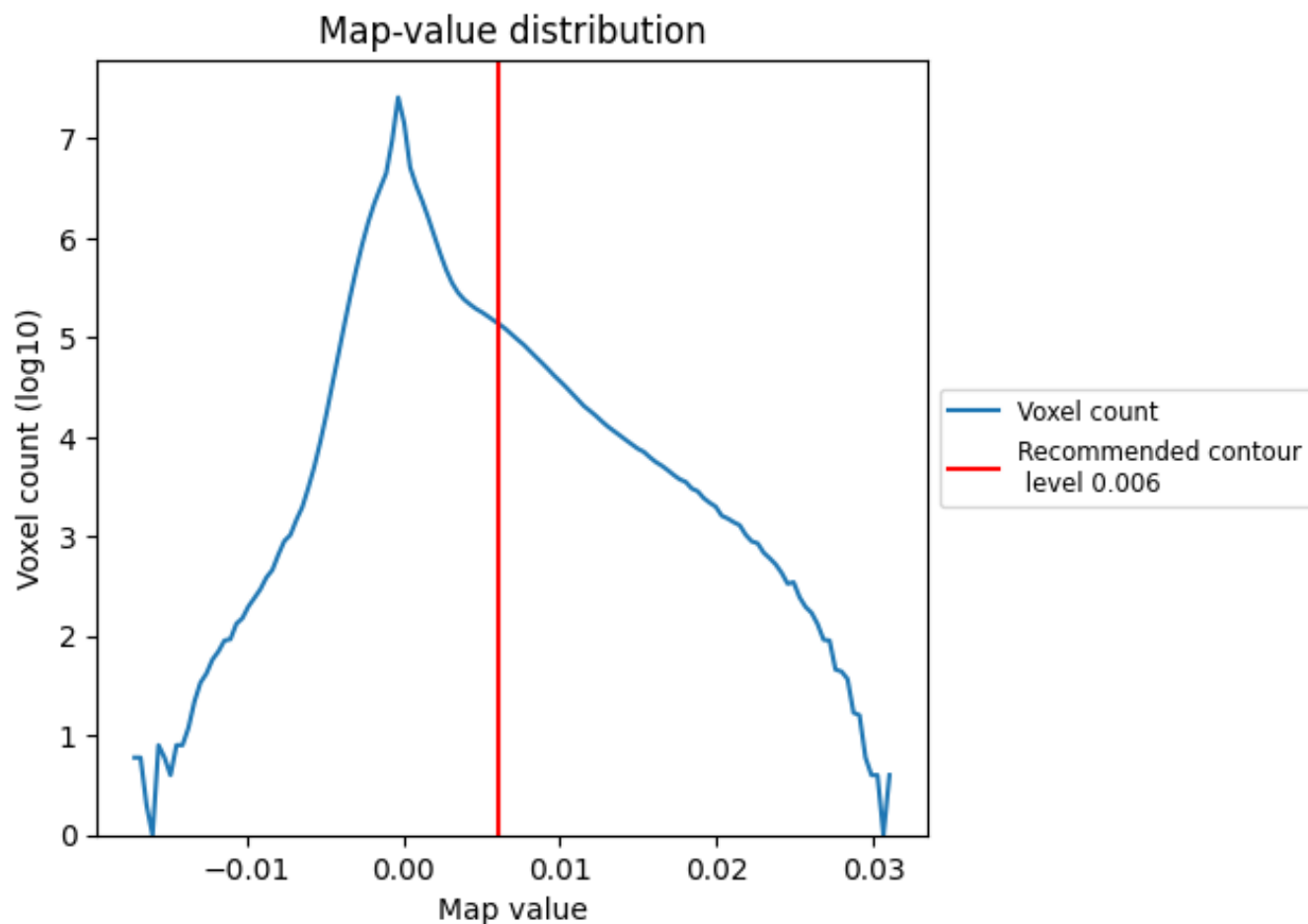
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

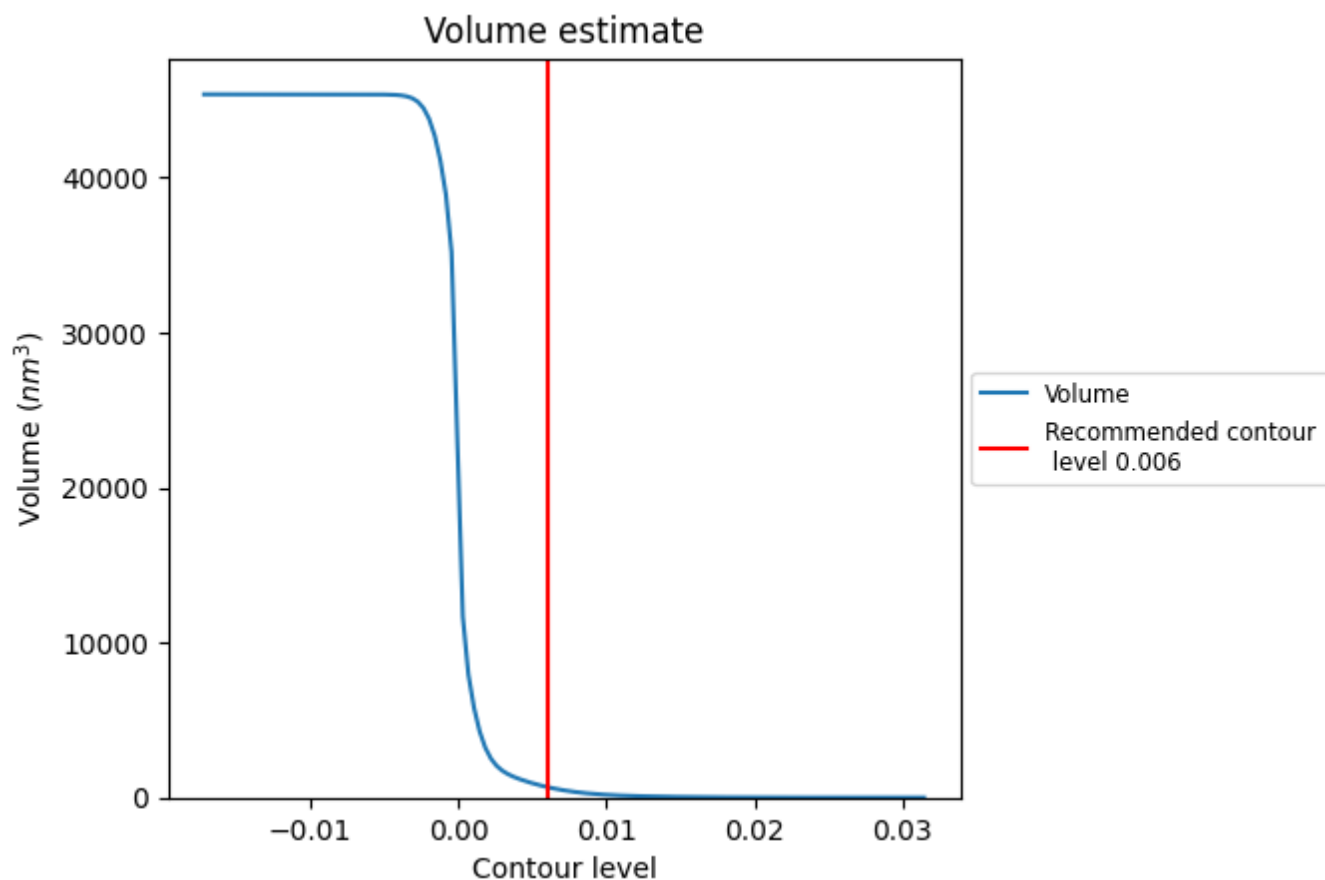
This section contains the results of statistical analysis of the map.

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.

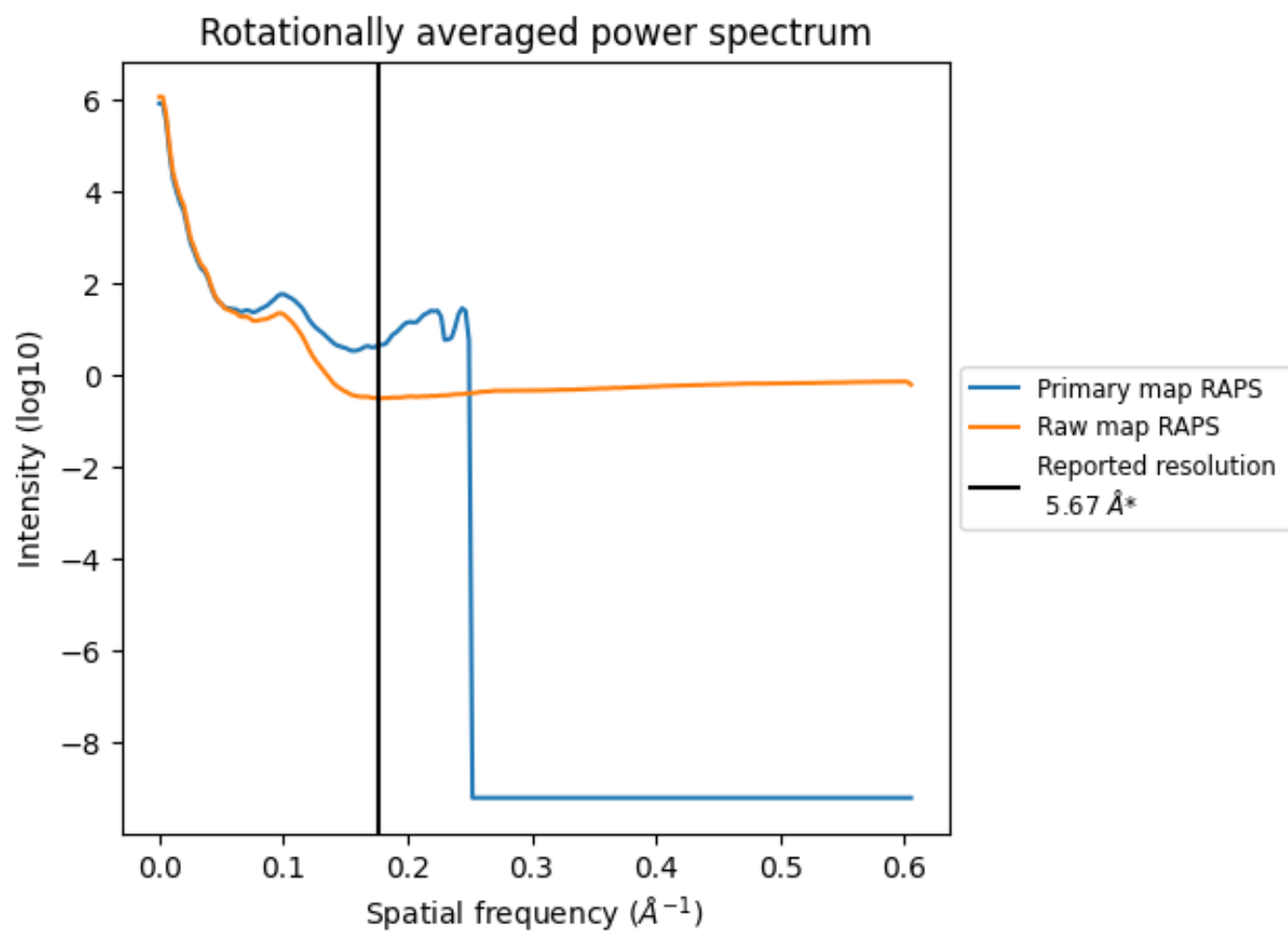
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 677 nm³; this corresponds to an approximate mass of 612 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 ⓘ

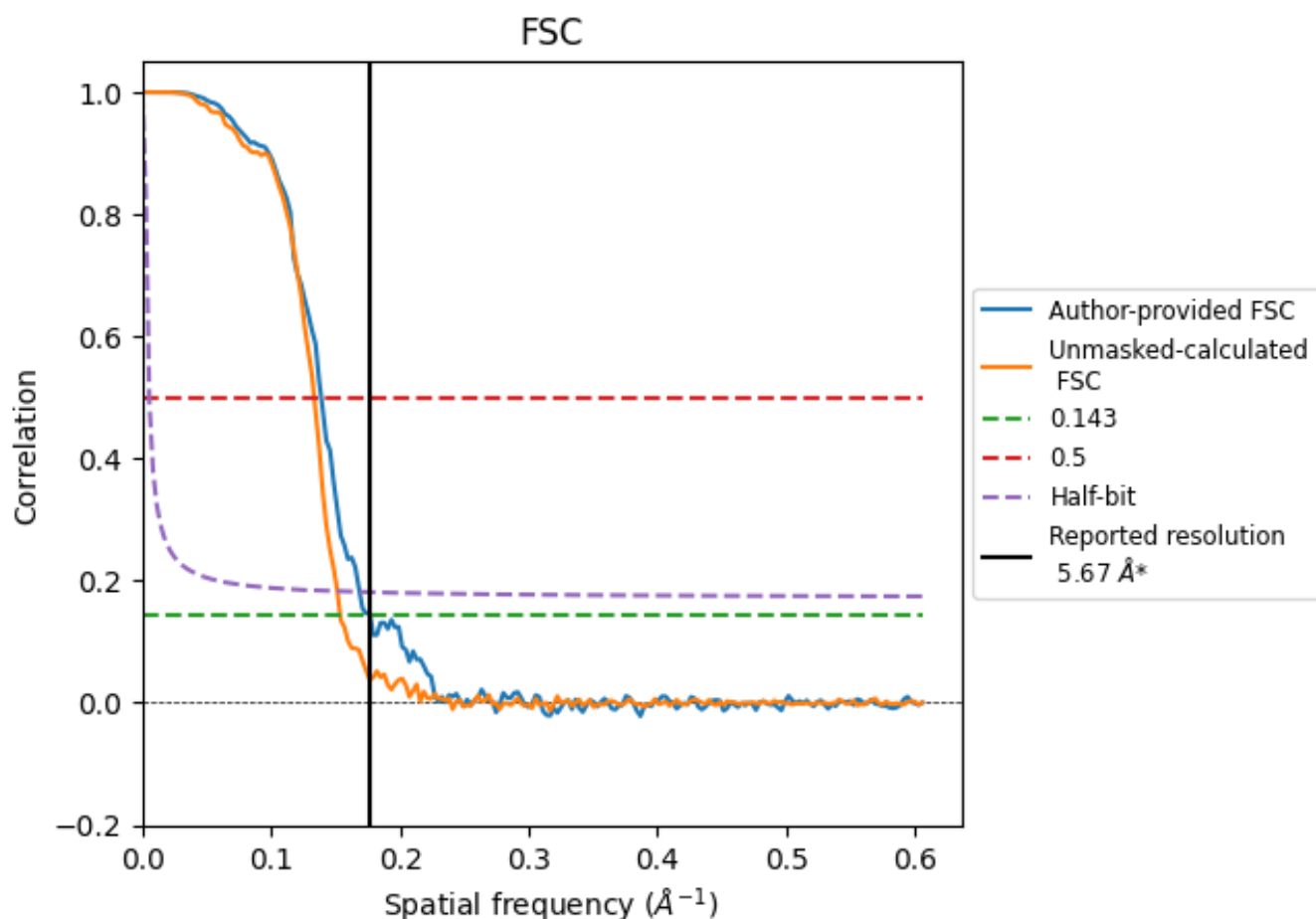


*Reported resolution corresponds to spatial frequency of 0.176 $\text{\AA}^{-1}$

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 0.176 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.67	-	-
Author-provided FSC curve	5.65	7.19	5.92
Unmasked-calculated*	6.50	7.49	6.60

*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 6.50 differs from the reported value 5.67 by more than 10 %

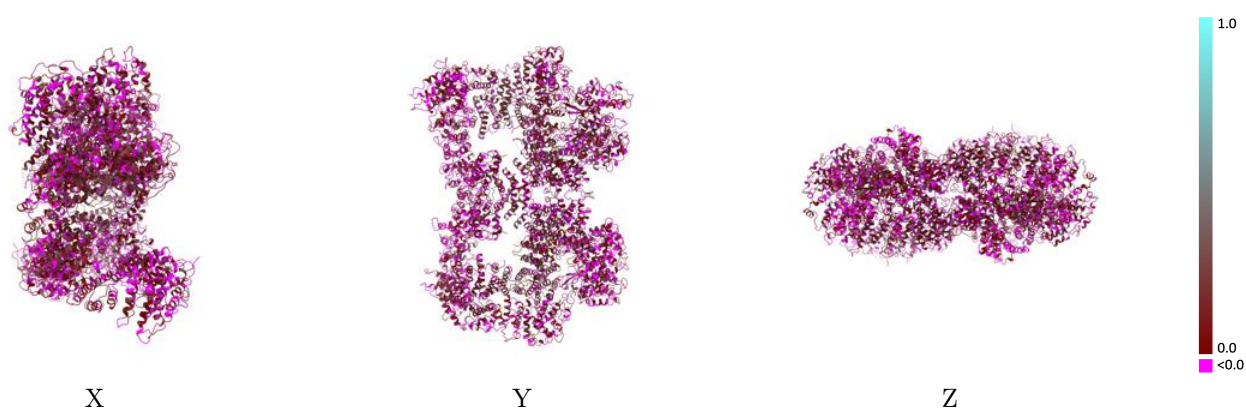
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-28731 and PDB model 8EZ9. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)

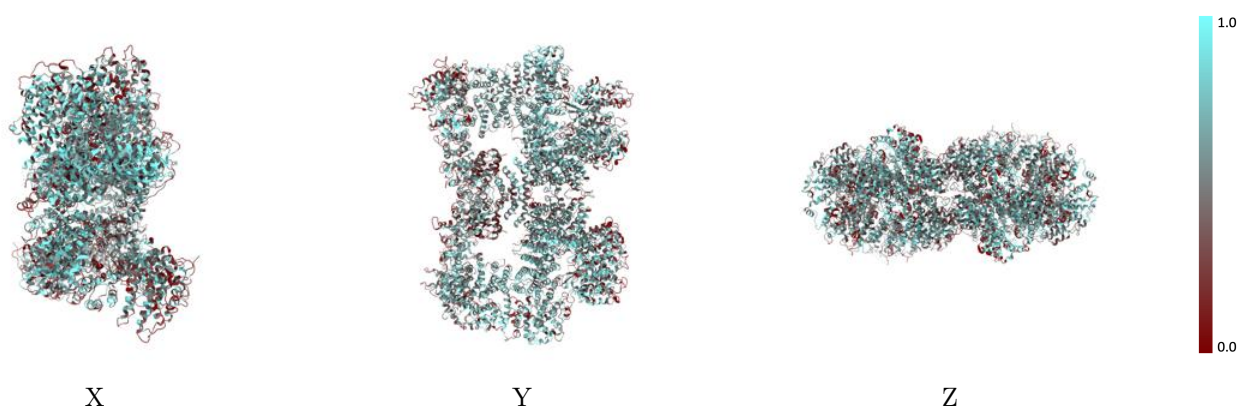
This section was not generated.

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



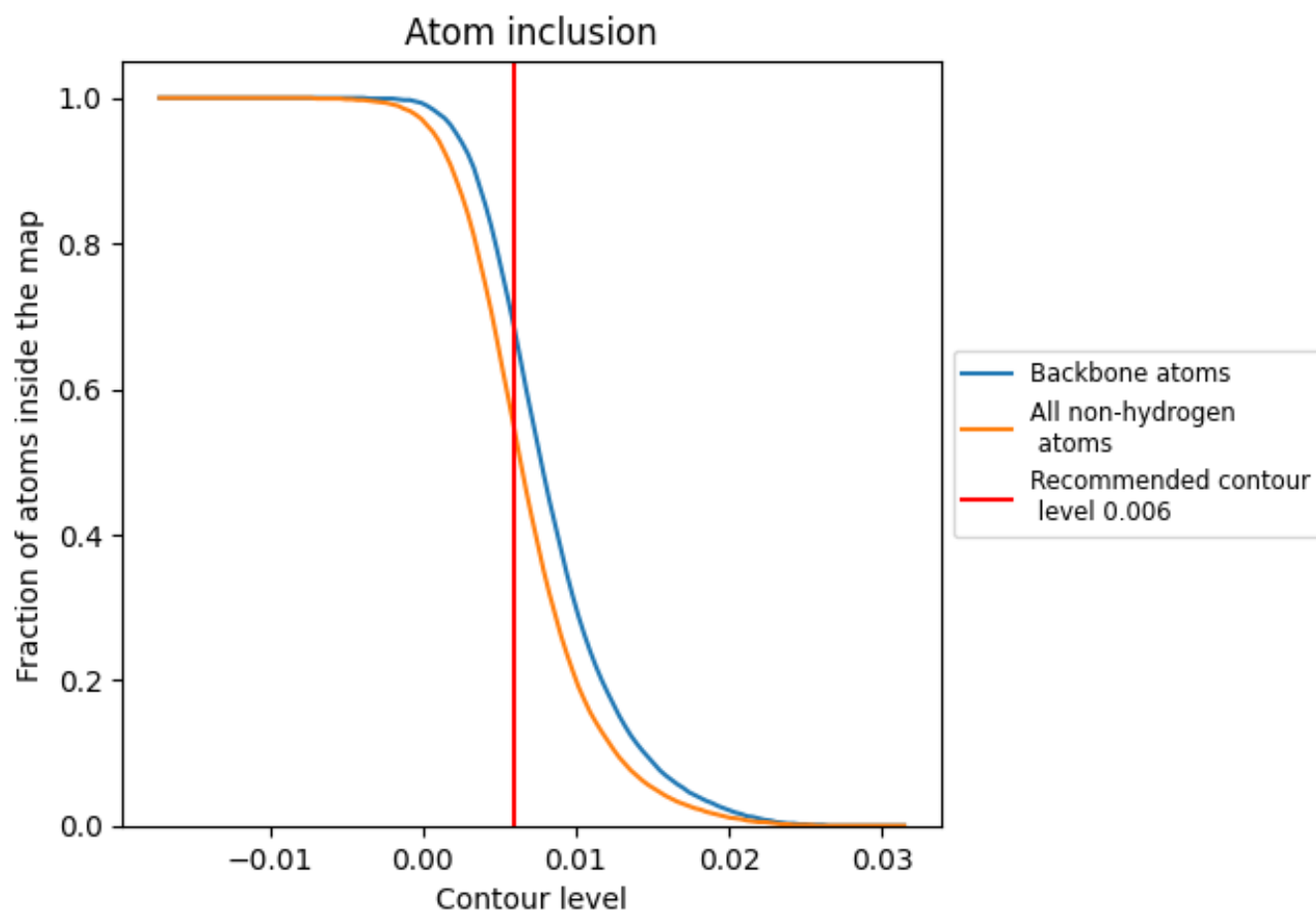
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.006).

9.4 Atom inclusion [i](#)



At the recommended contour level, 68% of all backbone atoms, 54% 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 (0.006) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5420	0.0740
C	0.5420	0.0740
L	0.5420	0.0720
Q	0.6040	0.2000
R	0.6240	0.1960

