



wwPDB EM Validation Summary Report ⓘ

May 13, 2025 – 01:44 AM EDT

PDB ID : 7SUD / pdb_00007sud
EMDB ID : EMD-25440
Title : CryoEM structure of DNA-PK complex VIII
Authors : Chen, X.; Liu, L.; Gellert, M.; Yang, W.
Deposited on : 2021-11-16
Resolution : 3.60 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.dev118
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0rc1
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

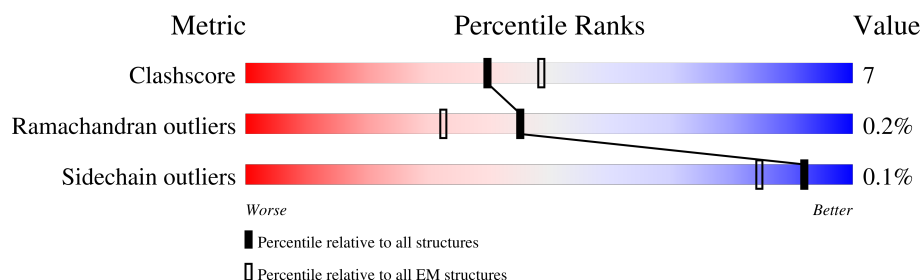
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	4128	<div> <div>21%</div> <div>74%</div> <div>17%</div> <div>9%</div> </div>
2	C	732	<div> <div>99%</div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 29980 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 DNA-dependent protein kinase catalytic subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3740	Total	C	N	O	P	S	
			29880	19157	5071	5454	4	194	4 0

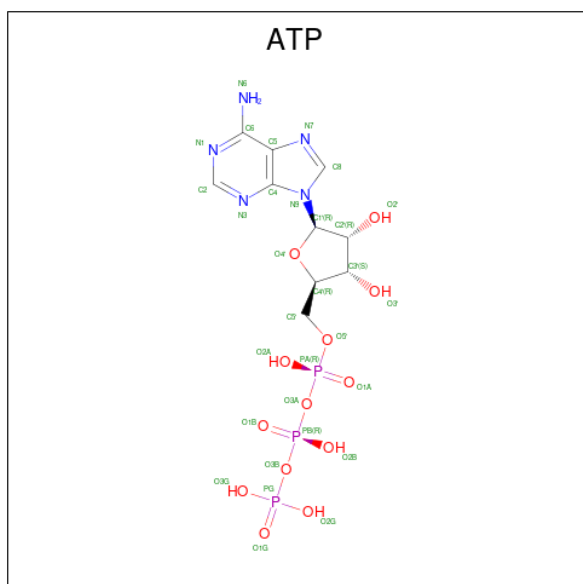
- Molecule 2 is a protein called X-ray repair cross-complementing protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	9	Total	C	N	O	S		
			68	43	9	15	1	0	0

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total	Mg	
			1	1	0

- Molecule 4 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃) (labeled as "Ligand of Interest" by depositor).

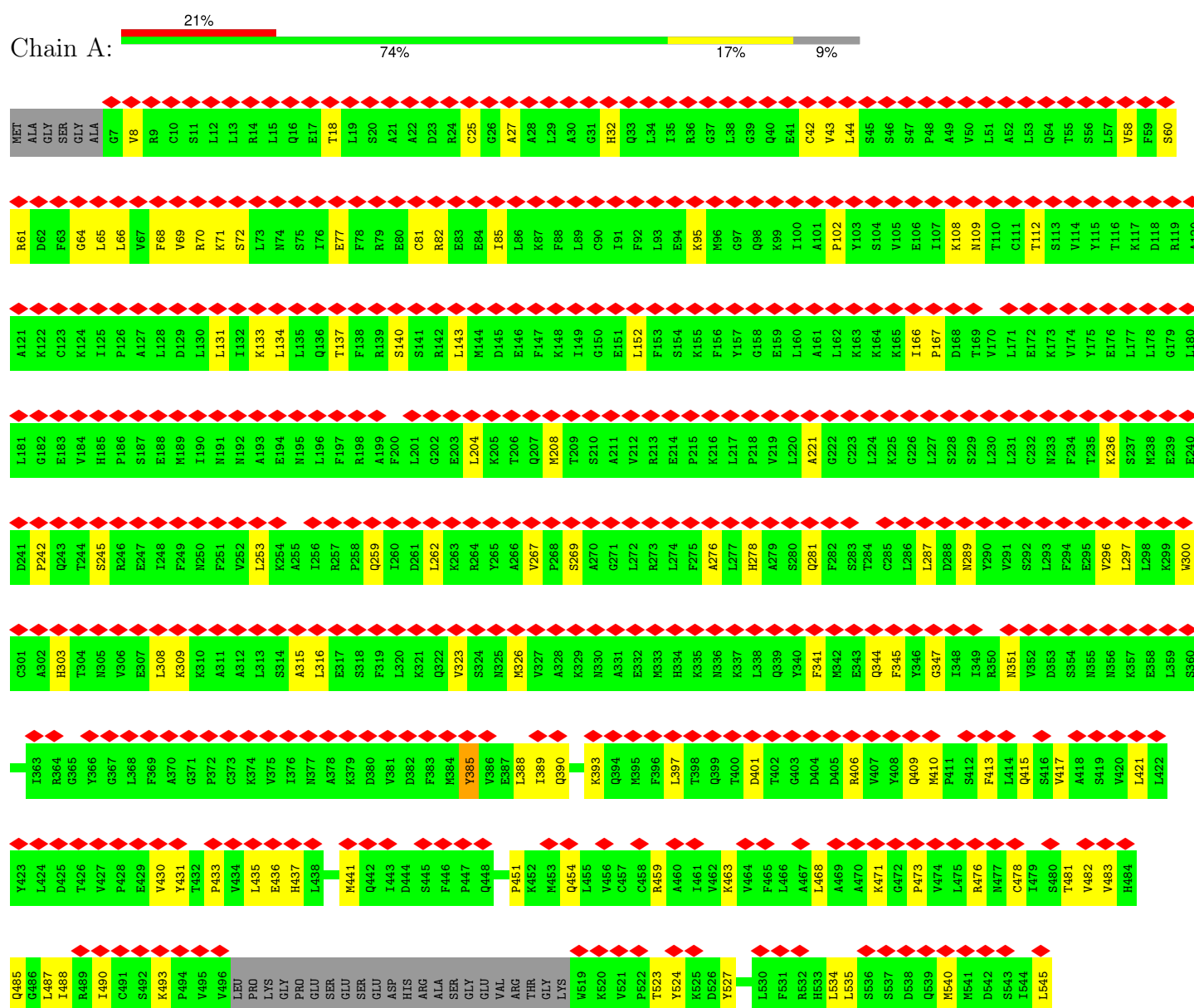


Mol	Chain	Residues	Atoms					AltConf
4	A	1	Total	C	N	O	P	0
			31	10	5	13	3	

3 Residue-property plots

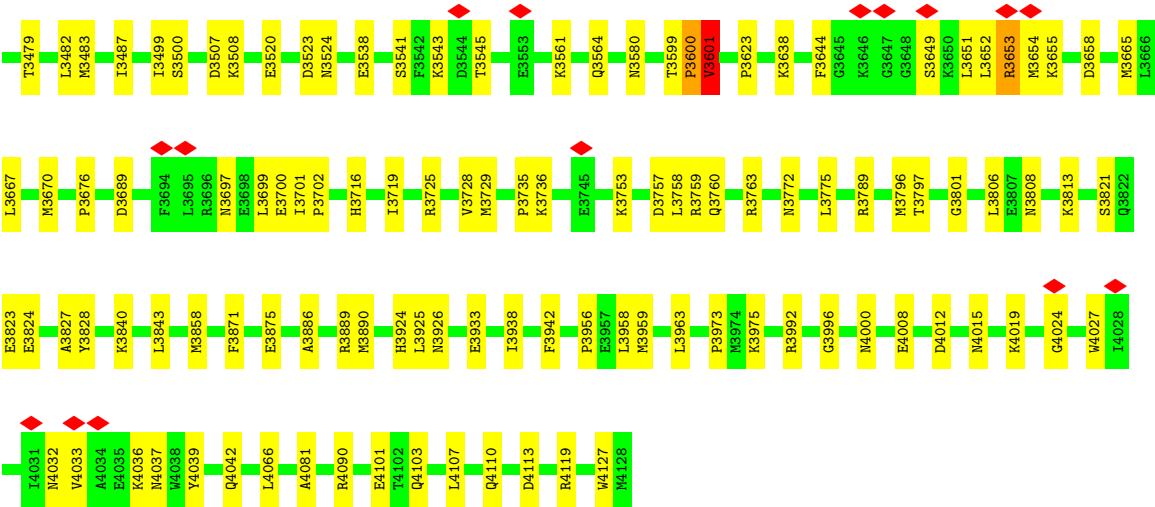
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: DNA-dependent protein kinase catalytic subunit

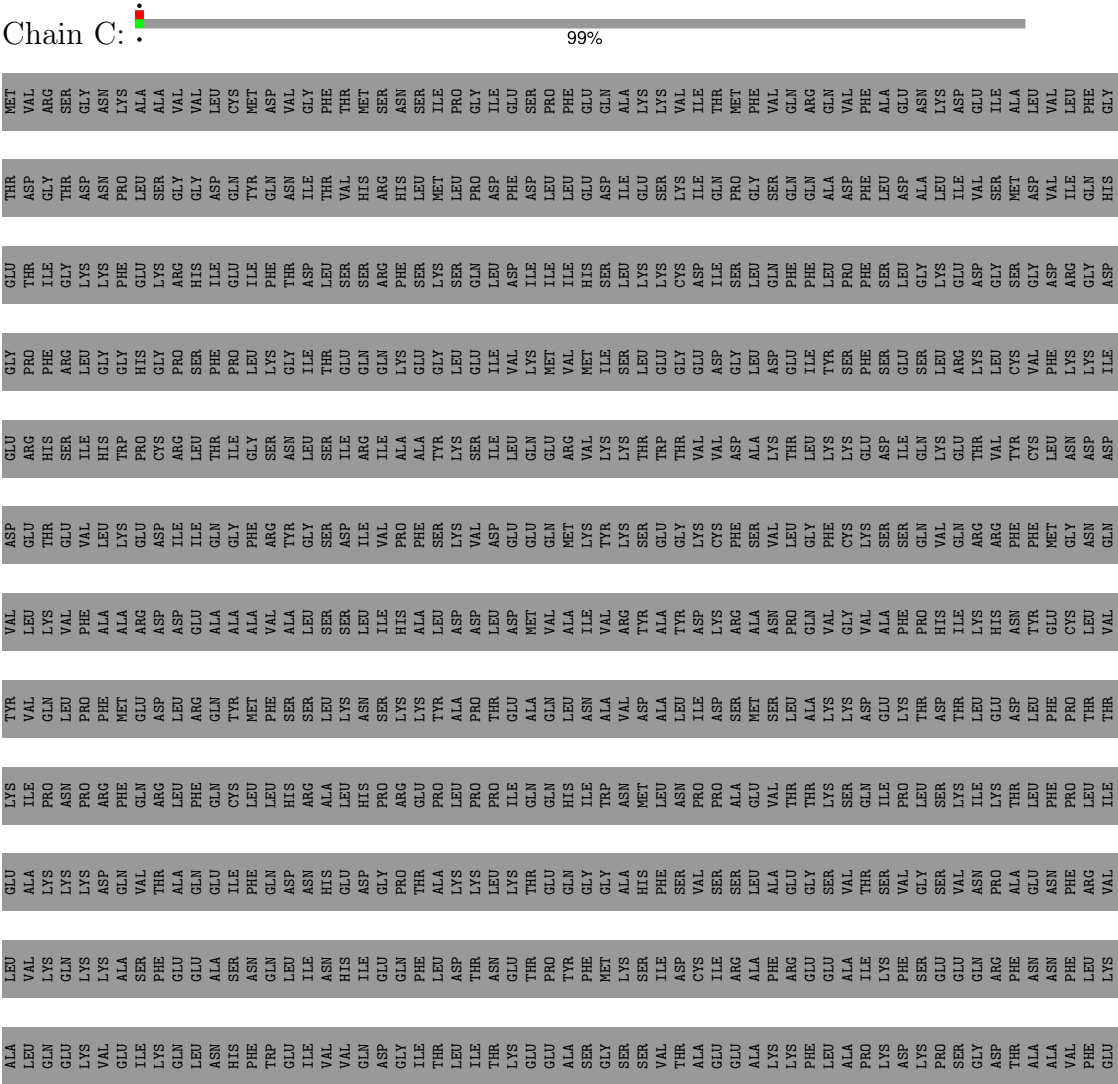




L3307	V3312	L3316	S3317	K3318	L3330	I3337	A3338	N3339	L3348	D3354	R3357	R3358	E3361	E3368	S3370	V3373	Y3378	E3394	ALA	GLN	PRO	PRO	TRP	CYS	GLY	PRO	A3406	N3414	ALA	VAL	ILE	ASP	SER	A3437	N3450	I3472																								
L3190	T3198	PRO	LEU	GLU	ASN	SER	ASP	ASP	ASP	ASP	PRO	SER	ARG	MET	GLU	VAL	GLN	GLN	K3235	K3239	D3244	R3247	K3257	K3260	E3261	L3262	T3268	R3269	L3283	R3287	S3288	Q3291	V3297	T3303																										
R2922	K2950	Q2954	R2962	D2980	L3005	I3019	D3020	ASN	ASP	S3021	E3022	N3023	N3028	E3033	Q3037	L3041	L3049	L3053	L3062	K3067	H3081	Y3082	S3083	Q3084	L3089	Y3090	L3091	D3097	I3107	Q3108	S3109	N3113	V3119	E3137	W3164	R3167	R3186																							
G2648																																																												
THR	ALA	ASP	GLY	VAL	ASN	SER	PHE	TRP	ALA	LEU	THR	GLY	THR	SER	THR	ASP	LEU	PRO	ARG	LEU	VAL	ASP	ARG	HIS	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR																									
E2406	G2407	M2408	F2413	Q2414	L2415	K2416	S2417	K2418	D2419	D2429	L2436	T2439	M2442	P2448	L2454	V2458	R2470	T2476	P2487	E2488	S2489	E2490	T2491	D2492	N2493	I2511	D2512	R2522	N2523	F2524	H2527	R2530	L2536	P2548	K2549	I2550	N2560	E2564																						
L2303	V2304	N2305	N2306	K2311	A2317	V2322	L2323	G2324	L2325	T2326	L2327	K2328	T2329	V2330	K2333	K2334	N2335	T2336	L2337	E2338	E2339	S2340	E2343	K2347	Q2348	L2349	K2350	Q2351	Q2352	N2354	T2355	N2356	K2359	K2366	S2370	F2371	P2372	A2375	K2379	N2380	A2381	F2384	K2394	V2401																
I2193	L2199	A2200	T2201	P2202	T2203	G2204	V2205	P2206	V2210	F2218	L2219	M2220	K2221	V2223	W2245	C2248	L2249	S2250	L2251	P2252	L2255	T2256	F2257	S2261	G2262	S2271	I2274	Q2275	L2279	V2280	M2281	D2284	L2285	D2289	P2290	G2293	I2294	Q2295	S2296	S2297	E2298	Q2301	A2302																	
ASP	SER	VAL	PRO	ARG	ASP	L2122	P2123	S2124	W2125	M2126	K2127	F2128	L2129	H2130	G2134	I2137	V2138	P2139	R2143	L2144	F2145	L2146	H2147	K2148	I2151	N2152	V2156	P2159	K2162	H2163	P2167	Q2170	L2171	A2172	E2175	N2176	N2177	G2178	L2179	E2180	G2181	L2182	H2183	V2184	N2185	E2188	I2189	V2190												
F1978	E1979	N1980	L1981	I1982	D1983	L1984	K1985	R1986	R1987	Y1988	N1989	F1990	P1991	C1919	Y1920	V1993	E1994	D1921	A1922	F1923	K2002	E2010	A2011	R2012	E2013	A2014	A2015	N2016	G2017	D2018	S2019	D2020	G2021	P2022	S2023	Y2024	M2025	SER	SER	SER	TYR	LEU	ALA	ASP	SER	THR	LEU	GLY	PRO	GLU	GLU	MET	SER	GLN	GLN	ASP	PHE	PHE	SER	THR
T1906	E1907	G1908	N1909	E1910	L1911	T1912	K1913	T1914	L1915	I1916	N1917	L1918	C1919	Y1920	V1993	E1994	D1921	A1922	F1923	N1926	M1927	A1928	G1929	E1930	N1931	Q1932	L1933	L1934	E1935	R1936	E1937	Y1940	H1941	Y1945	V1955	F1956	N1957	E1958	L1959	K1960	F1961	Y1962	N1963	G1964	F1965	L1966	F1967	S1968	E1969	K1970	P1971	E1972	K1973	N1974	L1975	L1976	I1977			



● Molecule 2: X-ray repair cross-complementing protein 5



GLU											
GLY											
GLY											
	D724	V725	D726	D727	L728	L729	D730	M731	I732		

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	42521	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.051	Depositor
Minimum map value	-0.024	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0095	Depositor
Map size (\AA)	399.84, 399.84, 399.84	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.833, 0.833, 0.833	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, TPO, ATP

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	0.39	0/30454	0.70	16/41158 (0.0%)
2	C	0.28	0/67	0.61	0/90
All	All	0.39	0/30521	0.70	16/41248 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	15

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	A	3369	ASP	CA-C-N	6.17	133.32	121.54
1	A	3369	ASP	C-N-CA	6.17	133.32	121.54
1	A	3599	THR	CA-C-N	5.53	140.27	127.00
1	A	3599	THR	C-N-CA	5.53	140.27	127.00
1	A	8	VAL	CA-C-N	5.50	132.04	121.54

There are no chirality outliers.

5 of 15 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1273	GLU	Peptide
1	A	1306	ILE	Peptide
1	A	166	ILE	Peptide

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Mol	Chain	Res	Type	Group
1	A	345	PHE	Peptide
1	A	385	TYR	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	29880	0	30201	415	0
2	C	68	0	64	2	0
3	A	1	0	0	0	0
4	A	31	0	12	0	0
All	All	29980	0	30277	416	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 7.

The worst 5 of 416 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:A:1837:ARG:O	1:A:1841:SER:HB3	1.64	0.98
1:A:1578:ALA:O	1:A:1582:LEU:HB2	1.83	0.78
1:A:1802:TYR:O	1:A:1806:ARG:HB2	1.84	0.76
1:A:2220:MET:HG2	1:A:2255:LEU:HD13	1.68	0.76
1:A:1717:LEU:O	1:A:1721:HIS:HB2	1.92	0.68

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	
1	A	3704/4128 (90%)	3338 (90%)	357 (10%)	9 (0%)	44	73
2	C	7/732 (1%)	7 (100%)	0	0	100	100
All	All	3711/4860 (76%)	3345 (90%)	357 (10%)	9 (0%)	45	73

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1307	ILE
1	A	3601	VAL
1	A	1275	THR
1	A	3083	SER
1	A	2871	LEU

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	3303/3667 (90%)	3300 (100%)	3 (0%)	92	97
2	C	8/649 (1%)	8 (100%)	0	100	100
All	All	3311/4316 (77%)	3308 (100%)	3 (0%)	92	97

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	430	VAL
1	A	1406	LEU
1	A	1678	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 56 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2275	GLN

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Mol	Chain	Res	Type
1	A	4087	HIS
1	A	2475	ASN
1	A	4042	GLN
1	A	3379	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
1	TPO	A	2638	1	8,10,11	1.70	1 (12%)	10,14,16	2.37	2 (20%)
1	TPO	A	2647	1	8,10,11	1.21	1 (12%)	10,14,16	1.18	0
1	TPO	A	2609	1	8,10,11	1.18	0	10,14,16	1.51	2 (20%)
1	TPO	A	2645	1	8,10,11	1.08	0	10,14,16	2.21	1 (10%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	TPO	A	2638	1	-	0/9/11/13	-
1	TPO	A	2647	1	-	5/9/11/13	-
1	TPO	A	2609	1	-	6/9/11/13	-
1	TPO	A	2645	1	-	1/9/11/13	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2638	TPO	P-O1P	3.49	1.61	1.50
1	A	2647	TPO	P-OG1	2.02	1.63	1.59

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2638	TPO	P-OG1-CB	-6.71	105.09	123.33
1	A	2645	TPO	P-OG1-CB	-6.48	105.71	123.33
1	A	2638	TPO	CG2-CB-CA	-2.48	108.43	113.26
1	A	2609	TPO	CG2-CB-CA	-2.28	108.81	113.26
1	A	2609	TPO	O3P-P-OG1	2.16	114.25	105.85

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	2609	TPO	N-CA-CB-OG1
1	A	2609	TPO	C-CA-CB-CG2
1	A	2609	TPO	O-C-CA-CB
1	A	2609	TPO	CG2-CB-OG1-P
1	A	2645	TPO	O-C-CA-CB

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	ATP	A	4202	3	28,33,33	0.83	0	34,52,52	1.06	1 (2%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	ATP	A	4202	3	-	5/18/38/38	0/3/3/3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	4202	ATP	N3-C2-N1	-3.84	123.46	128.67

There are no chirality outliers.

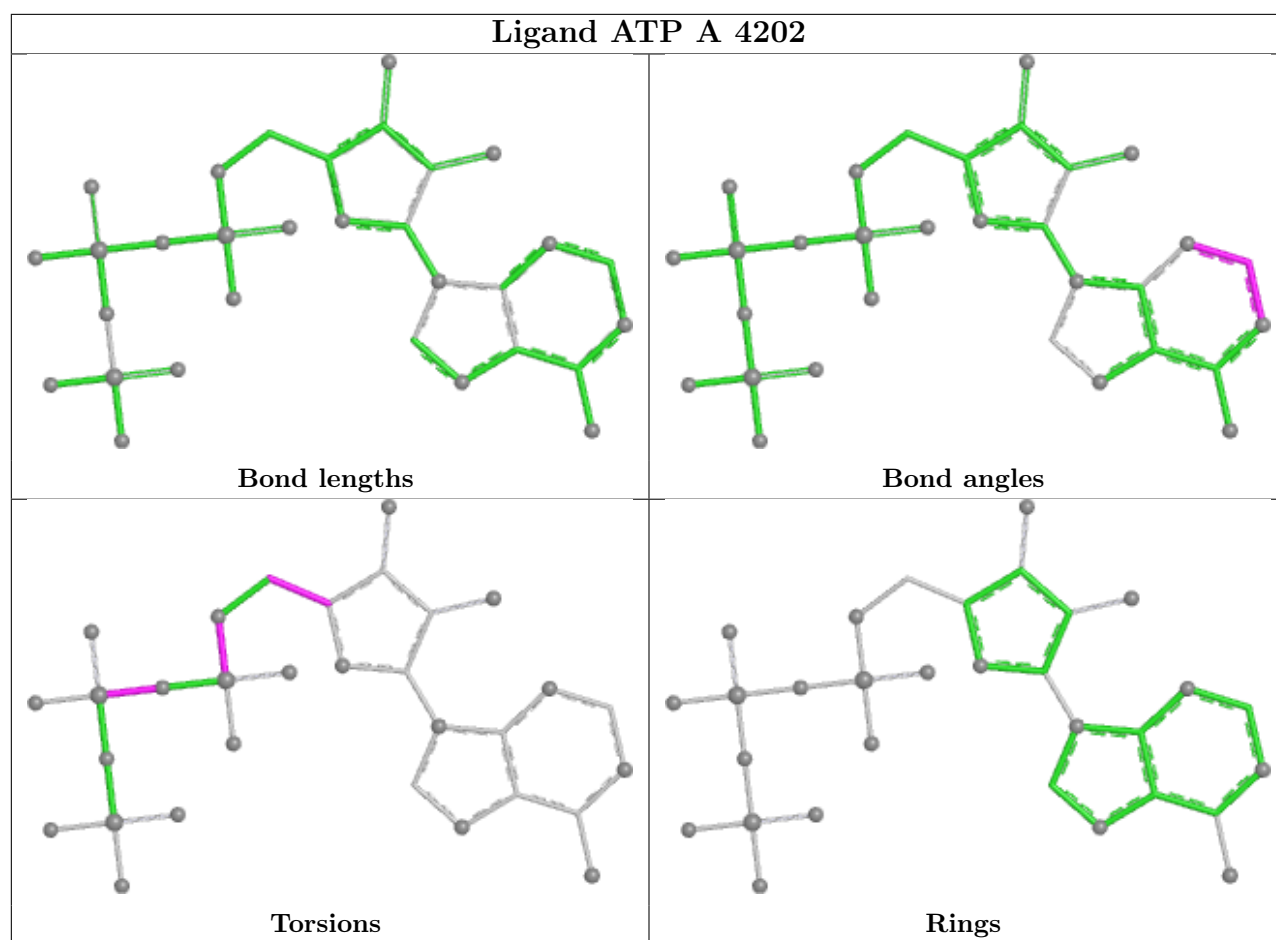
All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	4202	ATP	C5'-O5'-PA-O1A
4	A	4202	ATP	C5'-O5'-PA-O2A
4	A	4202	ATP	C5'-O5'-PA-O3A
4	A	4202	ATP	O4'-C4'-C5'-O5'
4	A	4202	ATP	PA-O3A-PB-O2B

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

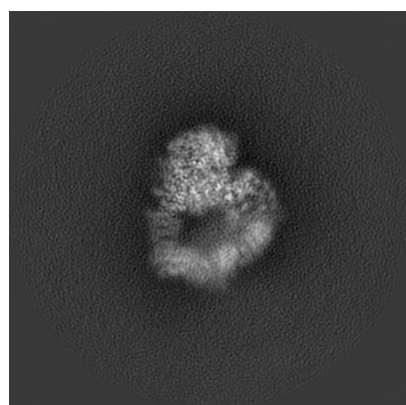
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25440. These allow visual inspection of the internal detail of the map and identification of artifacts.

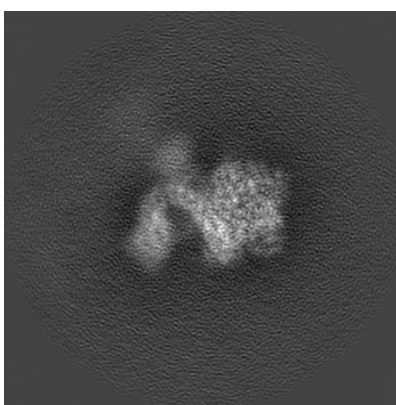
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

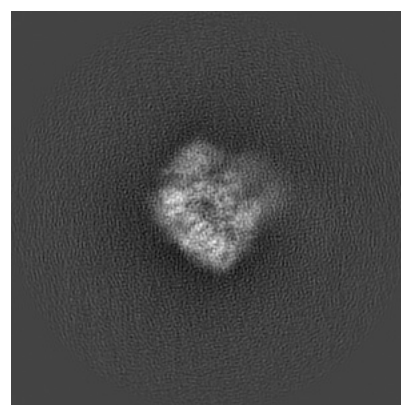
6.1.1 Primary map



X



Y

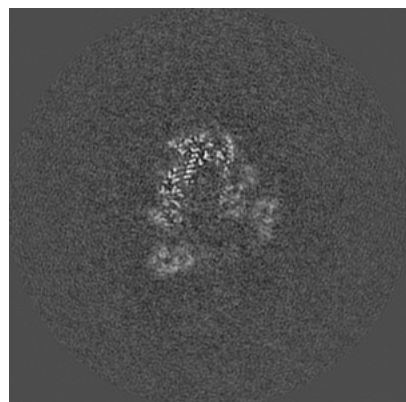


Z

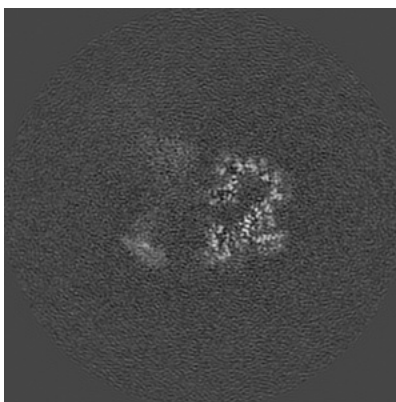
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

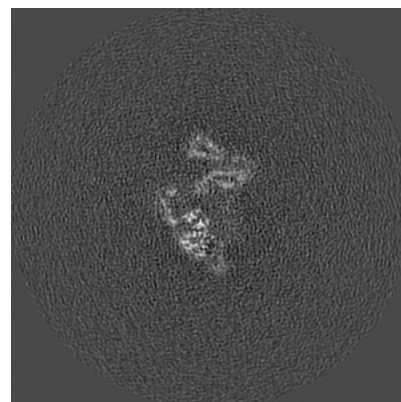
6.2.1 Primary map



X Index: 240



Y Index: 240

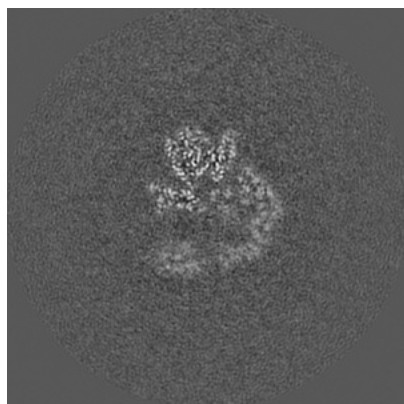


Z Index: 240

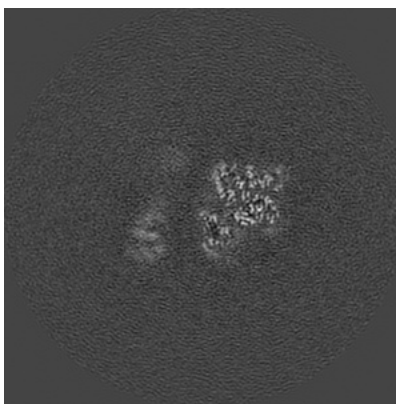
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

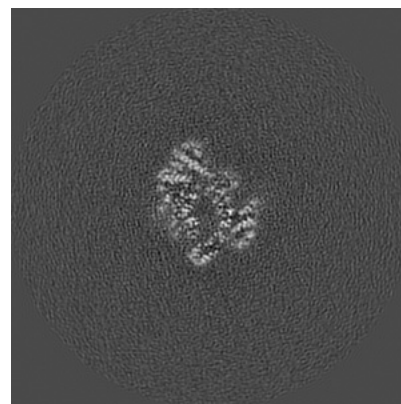
6.3.1 Primary map



X Index: 225



Y Index: 223

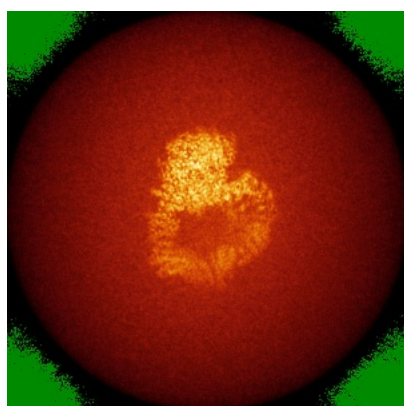


Z Index: 262

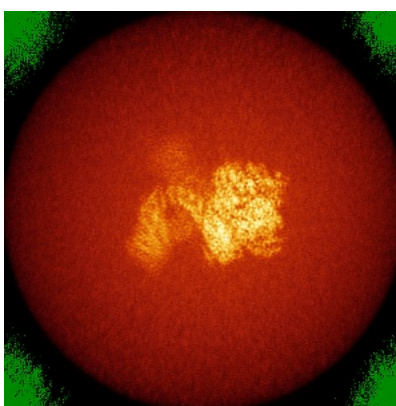
The images above show the largest variance slices of the map in three orthogonal directions.

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

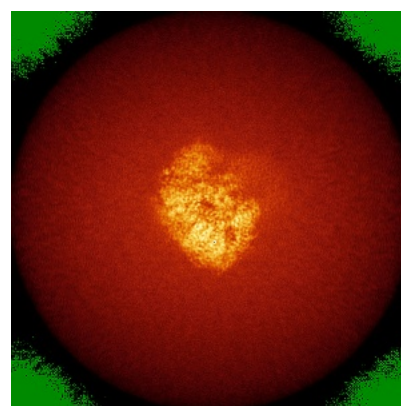
6.4.1 Primary map



X



Y

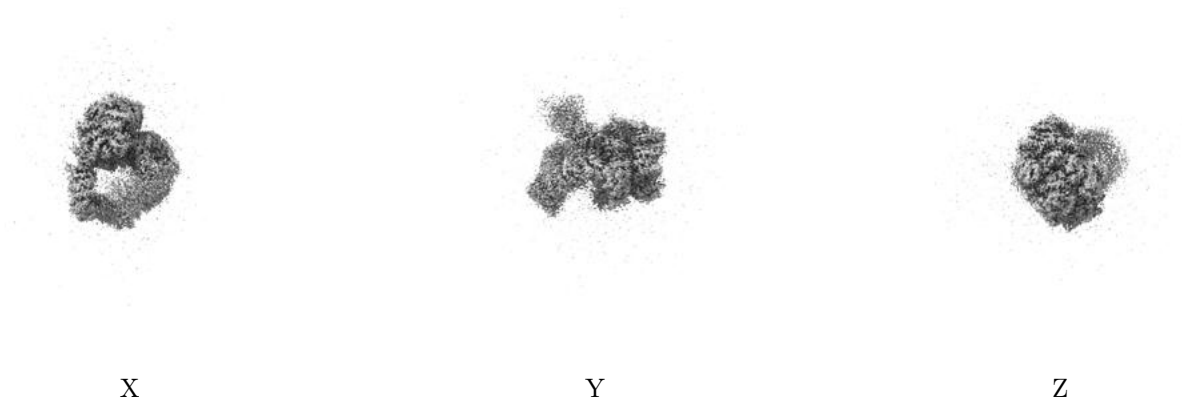


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0095. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

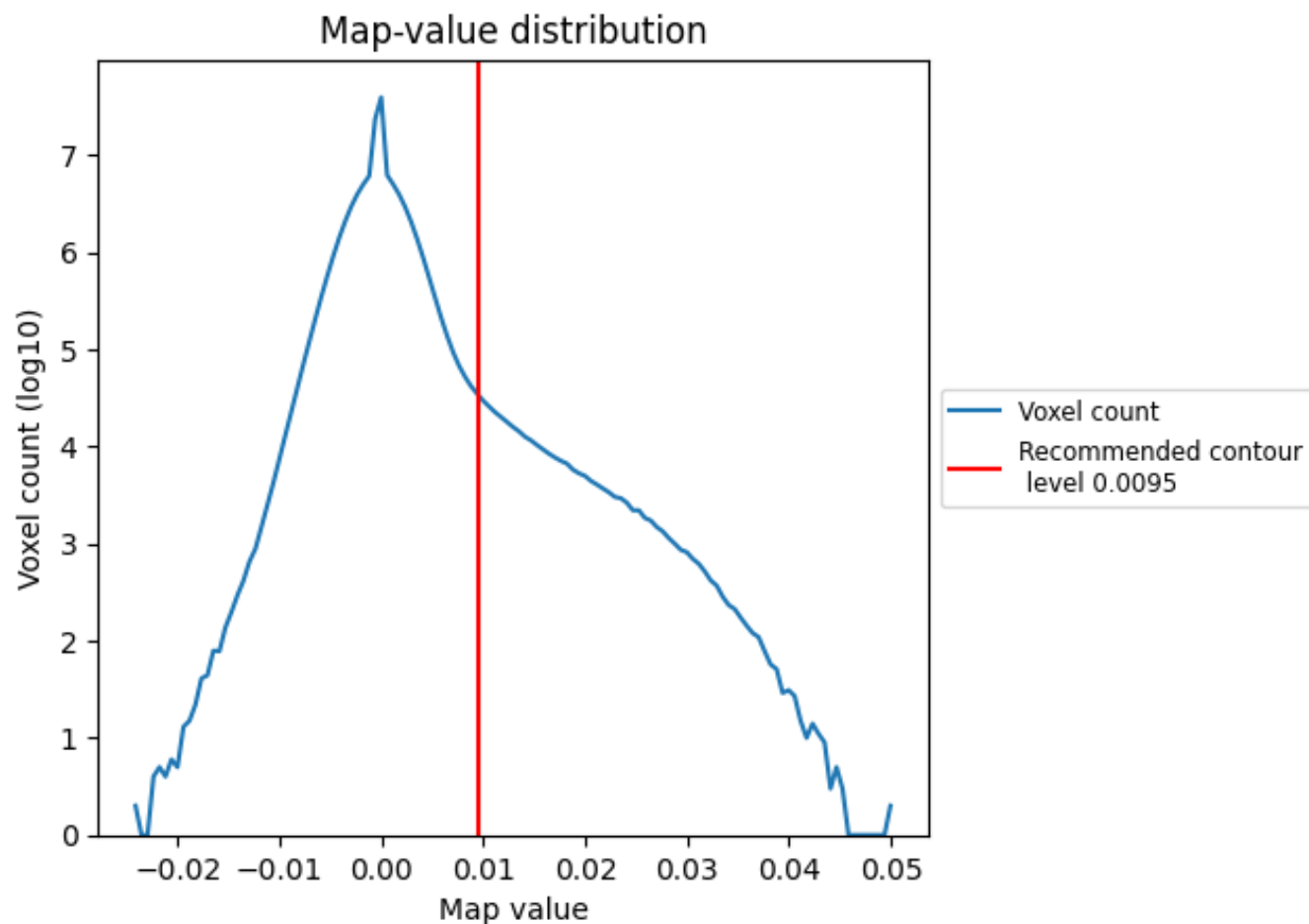
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

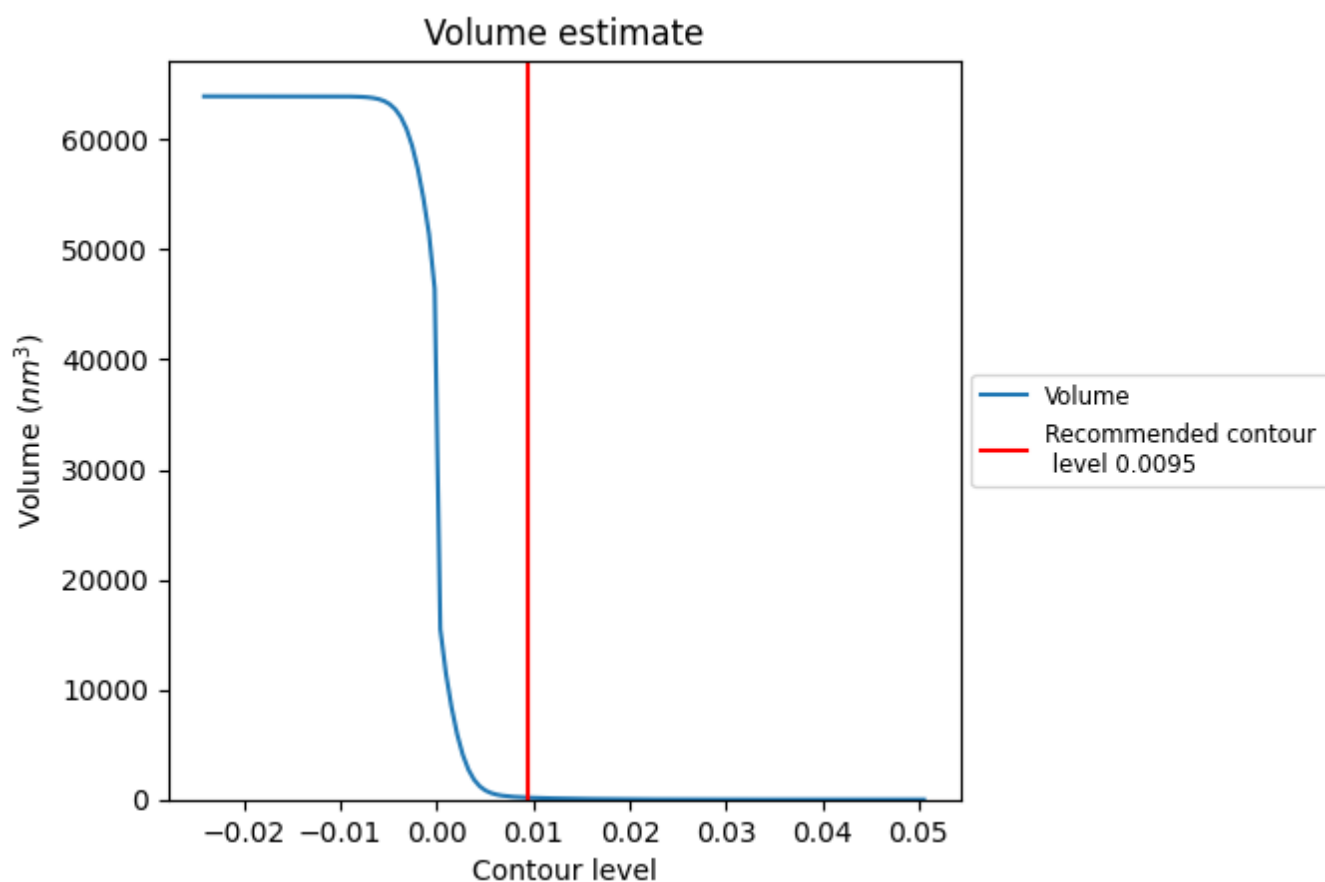
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

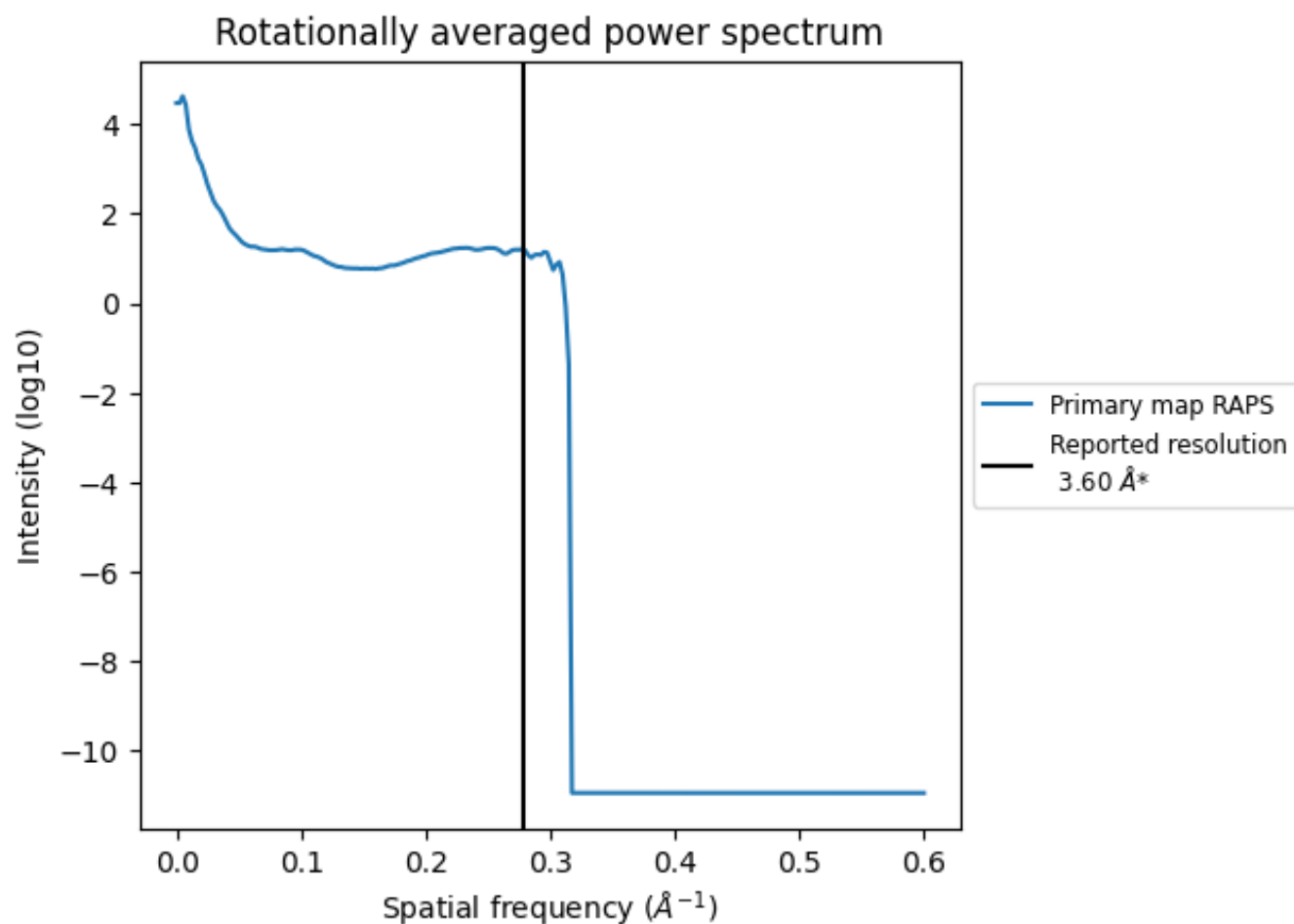
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 177 nm³; this corresponds to an approximate mass of 160 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 0.278 Å⁻¹

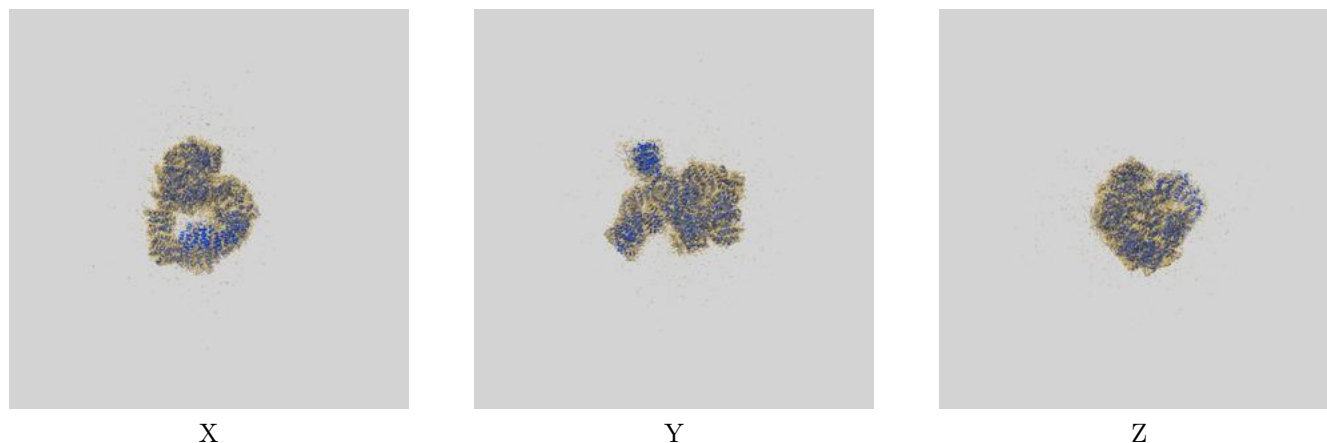
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

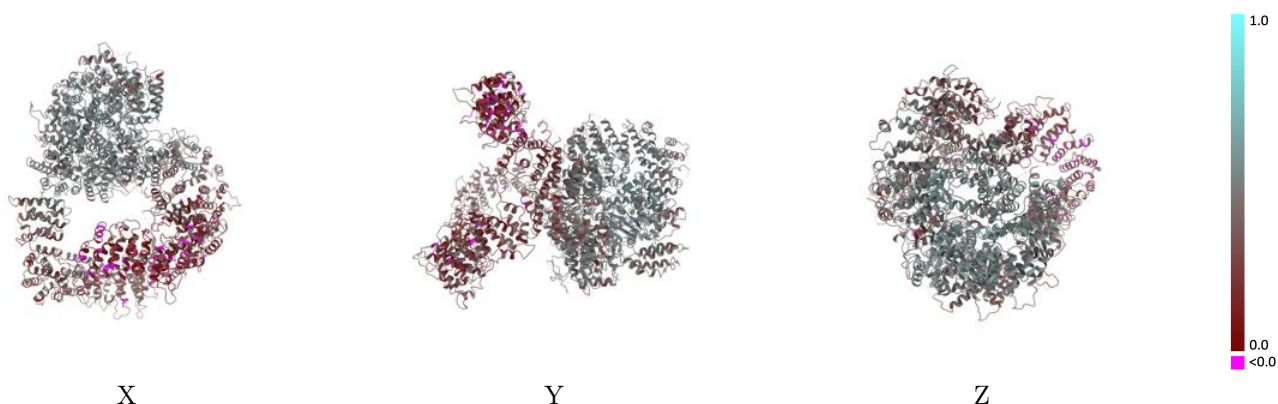
This section contains information regarding the fit between EMDB map EMD-25440 and PDB model 7SUD. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



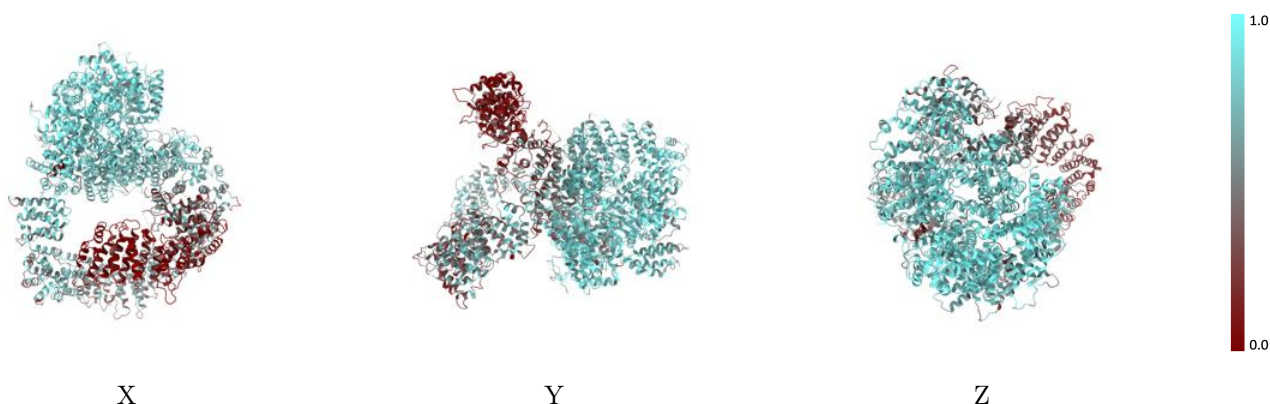
The images above show the 3D surface view of the map at the recommended contour level 0.0095 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



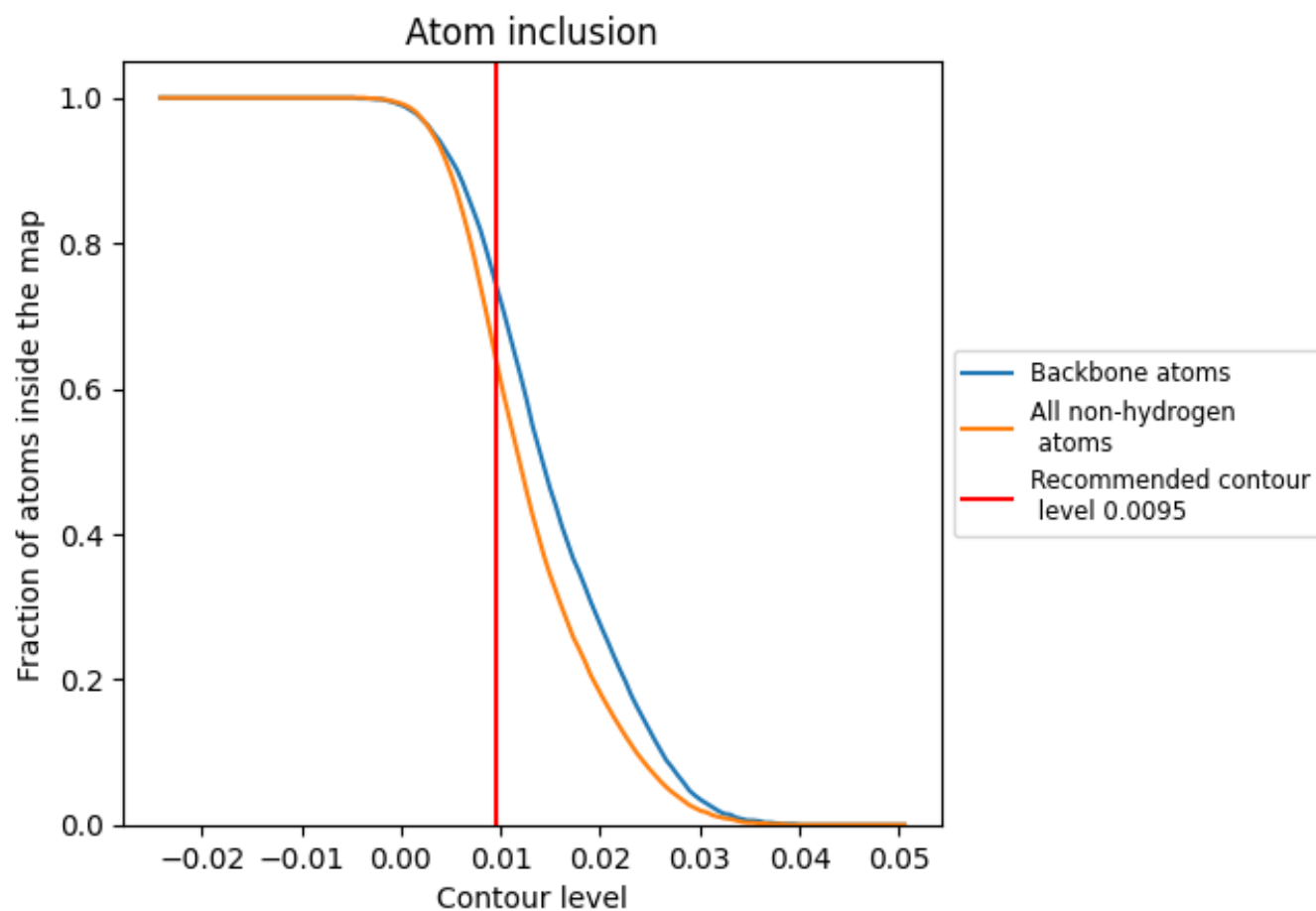
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0095).

9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 64% 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 (0.0095) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6420	<div></div> 0.4030
A	<div></div> 0.6440	<div></div> 0.4030
C	<div></div> 0.1180	<div></div> 0.2840

