



Full wwPDB EM Validation Report ⓘ

May 13, 2025 – 09:32 PM EDT

PDB ID : 9DHA / pdb_00009dha
EMDB ID : EMD-46861
Title : State-7-Post-1 of the motor domain from full-length human dynein-1 in 5mM AMPPNP with 5mM Mg2+
Authors : Chai, P.; Zhang, K.
Deposited on : 2024-09-03
Resolution : 3.60 Å(reported)

This is a Full wwPDB EM Validation 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

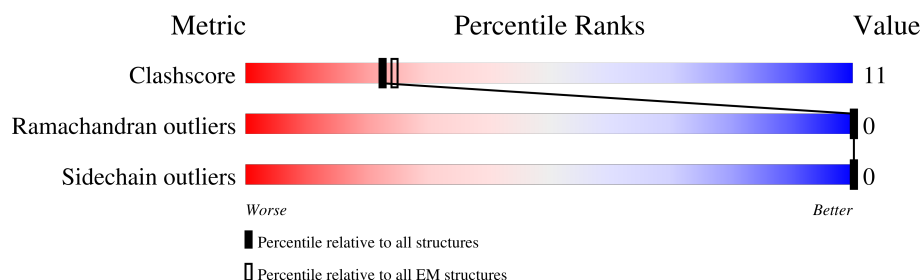
1 Overall quality at a glance

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	4646	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 24588 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 Cytoplasmic dynein 1 heavy chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	3038	24471	15586	4225	4538	122	0	0

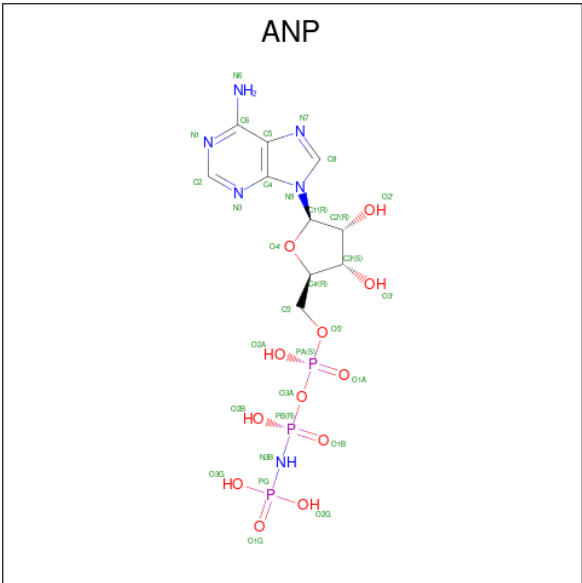
- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).





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

- Molecule 4 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula: $C_{10}H_{17}N_6O_{12}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
4	A	1	Total	C	N	O	P	0
			31	10	6	12	3	

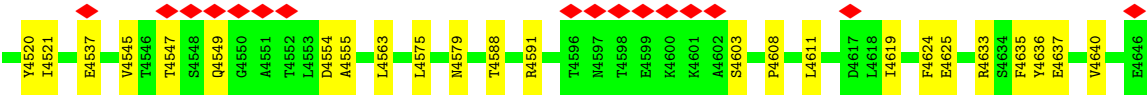
- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

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

K1992	T1993	S1994	A1995	P1996	I1997	L2001	L2002	N2003	V2006	K2007	V2008	D2011	N2012	M2018	G2021	TTR	ALA	GLY	ARG	S2026	N2027	D2030	K2033	S2038	P2044	Q2047	L2048	I2049	L2054	R2060	E2063	V2064	L2065	A2066	I2069	V2070	F2073	D2077	S2082	Q2083	Y2086																																																																																																																																																																																																																																																																																																
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GLN	Q3198	R3007	E2914	R2831	L2744	F2635	Y2517	E2406	T2301	R2091	GLN	GLN	R2091	R2092	L2093	L2097	K2104	R2107	T2111	R2112	R2113	E2114	K2115	E2116	E2117	R2118	G2119	E2120	A2121	V2122	D2123	E2124	G2125	E2126	T2127	A2128	P2129	E2133	T2136	L2137	L2138	P2147	K2148	L2149	V2150	L2157	L2161	R2172	G2173	E2174	N2175	L2182	L2191	W2203	L2208	G2209	L2210																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
GLU	K3199	M3008	V2915	Q2834	I2747	D2636	L2518	E2407	V2302	R2092	ILE	GLN	F3100	A3101	L3012	V3105	T3110	K3113	D3114	L3115	E3116	K3117	P3118	N3119	D3124	V3125	V3128	Y3129	Y3130	D3131	K3132	F3136	P3137	S3138	H3139	R3140	N3145	V3148	L3154	G3166	R3167	T3168	M3169	T3172	H3175	Y3176	T3180	SER	GLU	ASP	ARG	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	40983	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	45000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.956	Depositor
Minimum map value	-0.343	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.028	Depositor
Recommended contour level	0.25	Depositor
Map size (Å)	444.4032, 444.4032, 444.4032	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1573, 1.1573, 1.1573	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.12	0/24989	0.32	0/33856

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	24471	0	24527	545	0
2	A	54	0	24	10	0
3	A	31	0	12	6	0
4	A	31	0	13	5	0
5	A	1	0	0	0	0
All	All	24588	0	24576	546	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 11.

All (546) 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:3211:THR:HG21	1:A:3753:LEU:HD21	1.51	0.93
1:A:3208:ILE:HD11	1:A:3482:LEU:HD22	1.55	0.88
1:A:3202:ASN:HB3	1:A:3206:ARG:HH12	1.37	0.86
1:A:1511:PRO:O	1:A:1514:LYS:NZ	2.11	0.81
1:A:2481:MET:HE3	1:A:2485:GLN:HG2	1.61	0.81
1:A:3167:ARG:NH2	1:A:3169:MET:SD	2.55	0.79
1:A:3585:ARG:HB2	1:A:3697:THR:HG23	1.66	0.77
1:A:2386:PRO:HA	1:A:2416:GLN:HE22	1.51	0.76
1:A:3502:THR:HG21	1:A:3544:ARG:HG2	1.68	0.75
1:A:3167:ARG:NH1	1:A:3168:THR:O	2.20	0.75
1:A:2910:VAL:HG21	1:A:3105:VAL:HG22	1.68	0.74
1:A:2834:GLN:HE21	1:A:2843:ARG:HB3	1.51	0.74
1:A:3167:ARG:HH21	1:A:3687:GLU:HA	1.53	0.74
1:A:2804:ARG:HD3	1:A:2929:PRO:HG2	1.70	0.74
1:A:3817:SER:HB3	1:A:4349:LEU:HD21	1.71	0.73
1:A:2773:MET:HG2	1:A:2825:TRP:HE1	1.53	0.72
1:A:3202:ASN:HB3	1:A:3206:ARG:NH1	2.04	0.72
1:A:3654:ARG:HH11	1:A:3661:LEU:HD11	1.55	0.72
1:A:4192:GLU:OE1	1:A:4195:ARG:NH1	2.24	0.70
1:A:2994:MET:HE1	1:A:3008:MET:HE1	1.72	0.70
1:A:2601:LYS:NZ	4:A:4703:ANP:O3G	2.25	0.70
1:A:2221:MET:HG2	1:A:2343:PHE:HB2	1.73	0.70
1:A:2839:GLU:HG3	1:A:2841:GLU:HG3	1.74	0.70
1:A:3724:VAL:HG11	1:A:3797:VAL:HG21	1.72	0.69
1:A:1397:ASN:O	1:A:1401:ILE:HD12	1.91	0.69
1:A:4193:ARG:NH2	1:A:4637:GLU:O	2.26	0.68
1:A:2148:LYS:HG2	1:A:2361:MET:HB3	1.75	0.68
1:A:2581:LEU:HD13	1:A:2591:LEU:HD21	1.73	0.68
1:A:2660:VAL:HG12	1:A:2707:GLN:HB2	1.75	0.68
1:A:4042:LEU:HD13	1:A:4139:LEU:HD23	1.74	0.68
1:A:2798:GLU:OE1	1:A:2836:ARG:NH2	2.26	0.68
1:A:2481:MET:HE2	1:A:2486:LEU:HA	1.77	0.67
1:A:4505:LYS:NZ	1:A:4554:ASP:O	2.25	0.66
1:A:4068:SER:HA	1:A:4095:MET:HB3	1.77	0.66
1:A:2446:ILE:HG23	1:A:2447:MET:HG2	1.77	0.66
1:A:2768:PRO:HB2	1:A:2858:PHE:HE1	1.59	0.66
1:A:2793:ILE:O	1:A:2836:ARG:NH1	2.26	0.66
1:A:4545:VAL:HG22	1:A:4588:THR:HG22	1.75	0.66
1:A:2684:ARG:NH1	1:A:2688:GLU:OE1	2.29	0.65
1:A:3767:ILE:HA	1:A:3770:LEU:HD13	1.79	0.65
1:A:4107:MET:HE1	1:A:4137:ASN:HD21	1.61	0.65
1:A:2505:ASP:HB3	1:A:2733:VAL:HG13	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2563:ALA:O	1:A:2804:ARG:NH2	2.29	0.65
1:A:2773:MET:HB3	1:A:2799:MET:HE1	1.79	0.65
1:A:1360:ARG:HB3	1:A:1397:ASN:HD21	1.62	0.64
1:A:4176:ARG:NH1	1:A:4220:ASP:OD1	2.30	0.64
1:A:2065:LEU:HD11	1:A:2133:GLU:HB3	1.79	0.64
1:A:4385:SER:O	1:A:4389:HIS:ND1	2.31	0.64
1:A:3044:LEU:HD11	1:A:3049:GLU:HB2	1.79	0.64
1:A:1438:ASP:OD1	1:A:1440:GLN:NE2	2.31	0.63
1:A:2287:ILE:HD12	1:A:2299:GLN:HG3	1.79	0.63
1:A:2413:LEU:HA	1:A:2416:GLN:HE21	1.63	0.63
1:A:1698:ILE:HD13	1:A:1701:TRP:HE1	1.63	0.63
1:A:3508:LEU:HD23	1:A:3536:LEU:HD21	1.80	0.63
1:A:1579:MET:HE2	1:A:1579:MET:HA	1.81	0.63
1:A:3584:ASN:O	1:A:3651:ARG:NH1	2.31	0.63
1:A:2918:HIS:O	1:A:2922:ILE:HG12	1.99	0.62
1:A:4099:VAL:HB	1:A:4106:LEU:HD21	1.80	0.62
1:A:4611:LEU:HB2	1:A:4619:ILE:HD11	1.81	0.62
1:A:2149:LEU:HD11	1:A:2157:LEU:HD13	1.82	0.62
1:A:2915:VAL:HG13	1:A:2946:LEU:HD11	1.80	0.62
1:A:3638:VAL:HG22	1:A:3681:THR:HB	1.81	0.62
1:A:2485:GLN:HA	1:A:2488:ARG:HE	1.65	0.61
1:A:4326:ASN:ND2	1:A:4579:ASN:O	2.33	0.61
1:A:1491:ASP:O	1:A:1495:ASN:ND2	2.33	0.61
1:A:2665:GLU:HB3	1:A:2668:LEU:HD23	1.81	0.61
1:A:4554:ASP:OD2	1:A:4591:ARG:NH2	2.33	0.61
1:A:1766:LEU:HD13	1:A:1833:ALA:HA	1.83	0.60
1:A:3172:THR:HG21	1:A:3694:SER:HB2	1.81	0.60
1:A:1792:LEU:HB3	1:A:1812:ILE:HD11	1.81	0.60
1:A:3114:ASP:OD2	1:A:3191:ARG:NH2	2.34	0.60
1:A:4437:VAL:HG21	1:A:4444:GLN:HB3	1.84	0.60
1:A:4226:THR:HG21	1:A:4239:PRO:HD3	1.83	0.60
1:A:1486:LEU:HB3	1:A:1541:GLN:NE2	2.17	0.60
1:A:1395:LYS:NZ	1:A:1440:GLN:OE1	2.33	0.60
1:A:1905:PHE:HB3	1:A:2018:MET:HB3	1.82	0.60
1:A:2728:LEU:HA	1:A:2731:VAL:HG12	1.83	0.60
1:A:3835:ILE:HG12	1:A:3870:ARG:HD2	1.83	0.60
1:A:2138:ILE:HG23	1:A:2161:LEU:HD21	1.84	0.59
1:A:2488:ARG:NH1	1:A:2543:GLY:O	2.35	0.59
1:A:1531:MET:HE3	1:A:1535:ASP:HB2	1.85	0.59
1:A:4496:ALA:HB2	1:A:4504:LEU:HD21	1.84	0.59
1:A:1728:GLY:O	1:A:1784:ASN:ND2	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4266:ASN:O	1:A:4270:GLU:HG2	2.03	0.59
1:A:1985:HIS:HD2	1:A:1997:ILE:HD12	1.67	0.59
1:A:2729:ARG:NH2	3:A:4702:ATP:O2A	2.33	0.59
1:A:3931:GLN:O	1:A:3935:VAL:HG23	2.03	0.59
1:A:3113:MET:O	1:A:3140:ARG:NH2	2.26	0.58
1:A:3808:CYS:HB3	1:A:3832:PHE:HZ	1.67	0.58
1:A:2488:ARG:O	1:A:2492:ARG:HG2	2.03	0.58
1:A:3544:ARG:NH2	1:A:3735:GLN:OE1	2.37	0.58
1:A:2875:ASN:OD1	1:A:2927:ARG:NH2	2.36	0.58
1:A:1721:VAL:HA	1:A:1724:VAL:HG12	1.84	0.58
1:A:2112:LYS:HG3	1:A:2122:VAL:HG21	1.84	0.58
1:A:2593:LEU:HD12	1:A:2605:LEU:HG	1.86	0.58
1:A:3128:VAL:HG23	1:A:3145:ASN:HD21	1.68	0.58
1:A:3873:ARG:HH21	1:A:4020:ILE:HG22	1.68	0.58
1:A:2994:MET:O	1:A:3067:THR:OG1	2.20	0.58
1:A:1497:VAL:HG23	1:A:1527:LEU:HD12	1.85	0.58
1:A:2115:LYS:HE3	1:A:2122:VAL:HG12	1.86	0.57
1:A:3130:TYR:CZ	1:A:3132:LYS:HB2	2.39	0.57
1:A:1882:THR:HG22	1:A:1885:THR:HG23	1.85	0.57
1:A:4105:TRP:HZ3	1:A:4109:LEU:HD12	1.69	0.57
1:A:2275:TRP:NE1	1:A:2277:ASP:OD1	2.38	0.57
1:A:1396:ILE:HB	1:A:1439:LEU:HD12	1.86	0.57
1:A:1769:MET:HB3	1:A:1831:ASP:HB2	1.86	0.57
1:A:4100:HIS:NE2	1:A:4129:GLU:OE2	2.38	0.57
1:A:1376:ARG:NH1	1:A:1379:GLN:OE1	2.38	0.57
1:A:1486:LEU:HB3	1:A:1541:GLN:HE22	1.70	0.57
1:A:1985:HIS:CD2	1:A:1997:ILE:HD12	2.40	0.57
1:A:4377:MET:SD	1:A:4438:CYS:HA	2.45	0.57
1:A:1861:MET:HG2	1:A:1862:ALA:H	1.70	0.56
1:A:2257:LYS:NZ	1:A:2676:THR:OG1	2.29	0.56
1:A:1360:ARG:HB3	1:A:1397:ASN:ND2	2.20	0.56
1:A:2265:TYR:OH	1:A:2311:TRP:O	2.19	0.56
1:A:1414:LYS:HA	1:A:1417:MET:HE2	1.88	0.56
1:A:4554:ASP:OD1	1:A:4555:ALA:N	2.38	0.56
1:A:3947:LEU:O	1:A:3951:VAL:HG23	2.06	0.56
1:A:1763:GLU:OE2	1:A:1838:TRP:NE1	2.37	0.56
1:A:1574:GLU:OE1	1:A:1603:ARG:NH1	2.39	0.56
1:A:3766:ILE:O	1:A:3769:THR:OG1	2.24	0.56
1:A:1487:ILE:HD11	1:A:1579:MET:HE1	1.88	0.56
1:A:4129:GLU:O	1:A:4131:ASN:ND2	2.39	0.56
1:A:4537:GLU:OE2	1:A:4537:GLU:N	2.31	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3708:LEU:HD23	1:A:3809:SER:HA	1.87	0.55
1:A:1523:TRP:HA	1:A:1526:LYS:HE3	1.89	0.55
1:A:1911:GLY:HA2	2:A:4701:ADP:H5'1	1.89	0.55
1:A:1409:LYS:HD2	1:A:1410:ASP:N	2.22	0.55
1:A:1429:LEU:HD21	1:A:1434:ILE:HD11	1.88	0.55
1:A:2729:ARG:NH1	3:A:4702:ATP:O3B	2.39	0.55
1:A:3824:LEU:HD11	1:A:4130:ILE:HG12	1.89	0.55
1:A:1911:GLY:HA3	2:A:4701:ADP:H8	1.71	0.55
1:A:4448:LEU:HD13	1:A:4451:LEU:HD23	1.88	0.55
1:A:2277:ASP:OD2	1:A:2285:ARG:NE	2.34	0.55
1:A:3194:LEU:O	1:A:3198:GLN:HG2	2.07	0.55
1:A:3817:SER:O	1:A:3820:GLN:NE2	2.40	0.55
1:A:3193:GLU:O	1:A:3196:GLU:HG3	2.07	0.54
1:A:3215:VAL:HG21	1:A:3478:LEU:HD22	1.89	0.54
1:A:1750:VAL:HG12	1:A:1811:LEU:HD21	1.90	0.54
1:A:1547:LEU:HD21	1:A:1612:GLN:HG3	1.88	0.54
1:A:2971:ASP:O	1:A:2974:GLU:HG2	2.06	0.54
1:A:2885:ASP:OD1	1:A:2886:GLN:N	2.40	0.54
1:A:3198:GLN:OE1	1:A:3496:PHE:HB3	2.08	0.54
1:A:4413:PHE:HE2	1:A:4504:LEU:HB3	1.72	0.54
1:A:2890:ARG:NH2	1:A:2913:ASN:OD1	2.41	0.54
1:A:4377:MET:HB3	1:A:4378:ARG:HH11	1.72	0.54
1:A:4603:SER:OG	1:A:4625:GLU:OE2	2.23	0.54
1:A:4071:ILE:HG13	1:A:4099:VAL:HG12	1.90	0.54
1:A:1578:LEU:O	1:A:1582:VAL:HG23	2.07	0.54
1:A:2283:VAL:O	1:A:2287:ILE:HG12	2.08	0.54
1:A:2499:LEU:O	1:A:2503:SER:OG	2.24	0.54
1:A:3688:PHE:HB3	1:A:3692:LEU:HD23	1.90	0.54
1:A:1363:LEU:O	1:A:1367:LEU:HG	2.08	0.54
1:A:1946:VAL:HG13	1:A:2006:VAL:HG21	1.89	0.54
1:A:3873:ARG:NH2	1:A:4020:ILE:O	2.41	0.53
1:A:4547:THR:O	1:A:4549:GLN:NE2	2.40	0.53
1:A:2628:PRO:HB3	1:A:2682:PHE:CD2	2.43	0.53
1:A:3484:ALA:HA	1:A:3487:GLU:OE1	2.09	0.53
1:A:4460:LEU:HD12	1:A:4461:PRO:HD2	1.89	0.53
1:A:1879:LEU:HB2	2:A:4701:ADP:C6	2.43	0.53
1:A:4002:LEU:O	1:A:4005:ALA:HB3	2.09	0.53
1:A:1701:TRP:O	1:A:1705:VAL:HG23	2.08	0.53
1:A:2231:SER:OG	1:A:2344:GLU:OE2	2.26	0.53
1:A:2601:LYS:NZ	4:A:4703:ANP:O2B	2.41	0.53
1:A:4350:GLU:N	1:A:4350:GLU:OE1	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1351:TRP:O	1:A:1404:LYS:NZ	2.40	0.53
1:A:1892:MET:HE3	1:A:1892:MET:HA	1.90	0.53
1:A:3889:ARG:HH22	1:A:4347:GLN:HE22	1.56	0.53
1:A:1910:THR:HG22	1:A:2044:PRO:HD3	1.90	0.53
1:A:2865:LYS:HD2	1:A:2865:LYS:O	2.09	0.53
1:A:3553:LEU:HB2	1:A:3578:ILE:HD13	1.90	0.53
1:A:4425:GLN:OE1	1:A:4429:GLN:NE2	2.41	0.53
1:A:3767:ILE:O	1:A:3770:LEU:HB2	2.08	0.52
1:A:4105:TRP:CZ3	1:A:4109:LEU:HD12	2.43	0.52
1:A:4160:THR:HG23	1:A:4212:LEU:HD21	1.91	0.52
1:A:2729:ARG:HD3	1:A:2730:HIS:NE2	2.25	0.52
1:A:3558:GLU:HA	1:A:3561:ARG:NH1	2.25	0.52
1:A:2464:GLN:HG2	1:A:2583:THR:HA	1.90	0.52
1:A:3661:LEU:HD13	1:A:3668:ASP:HB3	1.91	0.52
1:A:4030:ILE:HG21	1:A:4145:PHE:HZ	1.74	0.52
1:A:4436:GLN:HG2	1:A:4441:LYS:HE2	1.91	0.52
1:A:2894:LYS:HG2	1:A:2911:LEU:HD23	1.91	0.52
1:A:3967:GLU:HB2	1:A:4004:MET:HB2	1.90	0.52
1:A:3558:GLU:HA	1:A:3561:ARG:HH12	1.74	0.52
1:A:3638:VAL:HG11	1:A:3679:LEU:HB3	1.92	0.52
1:A:3113:MET:SD	1:A:3184:ALA:HA	2.50	0.52
1:A:4088:VAL:HG21	1:A:4116:LEU:HD21	1.92	0.52
1:A:4452:ILE:O	1:A:4456:VAL:HG23	2.09	0.52
1:A:1880:VAL:HB	1:A:2049:ILE:HG12	1.92	0.52
1:A:3916:LEU:HD21	1:A:3936:VAL:HG13	1.91	0.52
1:A:4434:VAL:HA	1:A:4437:VAL:HG12	1.91	0.51
1:A:4055:VAL:HG11	1:A:4095:MET:SD	2.51	0.51
1:A:4271:ARG:HG3	1:A:4633:ARG:HH22	1.74	0.51
1:A:4469:VAL:HB	1:A:4473:MET:HE3	1.91	0.51
1:A:2996:GLU:HA	1:A:2999:VAL:HG22	1.91	0.51
1:A:4412:PHE:HE1	1:A:4516:VAL:HG23	1.75	0.51
1:A:1685:MET:HE3	1:A:1685:MET:HA	1.92	0.51
1:A:2218:HIS:HA	1:A:2340:ARG:HD3	1.93	0.51
1:A:2922:ILE:HB	1:A:2950:VAL:HG11	1.92	0.51
1:A:4431:LEU:HA	1:A:4434:VAL:HG12	1.91	0.51
1:A:2755:MET:HG2	1:A:2756:LEU:HD23	1.91	0.51
1:A:1952:GLY:HA2	1:A:2012:MET:HB3	1.93	0.50
1:A:2577:HIS:O	1:A:2581:LEU:HD23	2.10	0.50
1:A:2592:VAL:HG23	1:A:2731:VAL:HG21	1.93	0.50
1:A:4100:HIS:HB3	1:A:4128:MET:HG3	1.92	0.50
1:A:2729:ARG:HH22	3:A:4702:ATP:PA	2.35	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4008:PHE:O	1:A:4011:THR:OG1	2.27	0.50
1:A:1351:TRP:HZ3	1:A:1400:VAL:HG13	1.77	0.50
1:A:1832:ASN:OD1	1:A:1833:ALA:N	2.45	0.50
1:A:3514:ILE:HD11	1:A:3553:LEU:HD13	1.94	0.50
1:A:2363:TRP:CD1	1:A:2365:SER:HG	2.30	0.50
1:A:3846:LEU:HB3	1:A:3855:ARG:HH21	1.77	0.50
1:A:1800:GLN:OE1	1:A:1804:ARG:NH1	2.44	0.50
1:A:1947:GLY:O	1:A:1951:VAL:HG12	2.12	0.50
1:A:2026:SER:OG	1:A:2027:ASN:N	2.44	0.50
1:A:2925:ILE:HG12	1:A:2933:LEU:HB2	1.93	0.50
1:A:4274:THR:O	1:A:4277:SER:OG	2.27	0.50
1:A:1357:ARG:HD3	1:A:1357:ARG:N	2.27	0.50
1:A:2566:ASP:OD1	1:A:2566:ASP:N	2.45	0.50
1:A:2901:TYR:OH	1:A:2909:LEU:O	2.30	0.50
1:A:2335:LEU:HD12	1:A:2336:PRO:HD2	1.94	0.50
1:A:1447:LYS:O	1:A:1451:LEU:HG	2.13	0.49
1:A:3497:LYS:HD2	1:A:3497:LYS:O	2.13	0.49
1:A:1335:GLU:HG3	1:A:1377:LEU:HD13	1.94	0.49
1:A:3757:LYS:HB2	1:A:3759:ARG:HE	1.78	0.49
1:A:1408:LEU:O	1:A:1413:TRP:HD1	1.96	0.49
1:A:1459:LEU:HD22	1:A:1507:MET:HE2	1.94	0.49
1:A:1706:GLU:OE2	1:A:1710:ARG:NH2	2.45	0.49
1:A:3591:ASP:HB3	1:A:3701:PHE:HB2	1.92	0.49
1:A:4002:LEU:HD21	1:A:4336:GLY:HA2	1.93	0.49
1:A:1385:PHE:HA	1:A:1388:ARG:NH1	2.28	0.49
1:A:2175:MET:HE2	1:A:2208:LEU:HB3	1.94	0.49
1:A:3026:TYR:CE1	1:A:3030:MET:HE3	2.47	0.49
1:A:2302:VAL:HG12	1:A:2342:MET:HE3	1.95	0.49
1:A:2759:ILE:HG21	1:A:2762:LEU:HD12	1.95	0.49
1:A:3966:PRO:HD2	1:A:4000:ARG:HG3	1.94	0.49
1:A:3762:ASP:OD1	1:A:3763:ASP:N	2.42	0.49
1:A:1463:LEU:O	1:A:1467:ARG:HG3	2.13	0.48
1:A:1910:THR:N	2:A:4701:ADP:O1B	2.46	0.48
1:A:1984:GLU:HG2	1:A:1997:ILE:HD13	1.94	0.48
1:A:3954:ASP:OD1	1:A:3957:PHE:N	2.46	0.48
1:A:3961:LEU:O	1:A:3997:ARG:NH1	2.42	0.48
1:A:1478:VAL:HG21	1:A:1488:ARG:HH21	1.78	0.48
1:A:2324:LEU:HD11	1:A:2332:ARG:HB3	1.94	0.48
1:A:3113:MET:HE3	1:A:3115:LEU:HD11	1.94	0.48
1:A:2527:PRO:HD3	1:A:2545:TRP:CE2	2.48	0.48
1:A:3196:GLU:HA	1:A:3199:MET:HG3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4353:ASP:OD1	1:A:4375:ALA:N	2.46	0.48
1:A:2150:VAL:HG12	1:A:2363:TRP:CE2	2.48	0.48
1:A:2299:GLN:O	1:A:2339:VAL:HA	2.13	0.48
1:A:4068:SER:OG	1:A:4097:LYS:NZ	2.37	0.48
1:A:2104:LYS:HA	1:A:2136:ILE:HD13	1.94	0.48
1:A:2395:GLN:HB2	1:A:2396:ARG:HH21	1.78	0.48
1:A:2999:VAL:HB	1:A:3005:LEU:HD21	1.95	0.48
1:A:4407:ASP:OD2	1:A:4410:PHE:N	2.45	0.48
1:A:1548:GLU:O	1:A:1552:THR:OG1	2.22	0.48
1:A:1378:ARG:HG2	1:A:1383:TYR:CZ	2.49	0.48
1:A:2964:HIS:NE2	1:A:2967:TYR:HA	2.28	0.48
1:A:3783:LYS:O	1:A:3787:THR:OG1	2.27	0.48
1:A:2796:PRO:O	1:A:2800:THR:HG23	2.14	0.47
1:A:2944:THR:OG1	2:A:4704:ADP:O2A	2.32	0.47
1:A:4563:LEU:HD12	1:A:4588:THR:HG21	1.95	0.47
1:A:3026:TYR:CZ	1:A:3030:MET:HE3	2.49	0.47
1:A:3110:THR:O	1:A:3140:ARG:NH2	2.46	0.47
1:A:4088:VAL:HG13	1:A:4118:PRO:HA	1.95	0.47
1:A:1509:LEU:HB3	1:A:3608:LYS:HG2	1.97	0.47
1:A:2222:MET:HG2	1:A:2364:PHE:HE2	1.80	0.47
1:A:2752:ASN:HA	1:A:2755:MET:HB3	1.96	0.47
1:A:3659:ARG:NE	1:A:3670:ASP:OD2	2.46	0.47
1:A:3769:THR:O	1:A:3772:ASN:HB3	2.14	0.47
1:A:1359:LEU:HD11	1:A:1435:TRP:HZ2	1.80	0.47
1:A:2422:ILE:HD13	1:A:2487:GLU:HA	1.97	0.47
1:A:4454:GLU:OE2	1:A:4461:PRO:HG3	2.15	0.47
1:A:1351:TRP:H	1:A:1430:THR:HA	1.80	0.47
1:A:1477:LEU:O	1:A:1485:ARG:NH2	2.40	0.47
1:A:1880:VAL:N	2:A:4701:ADP:N1	2.60	0.47
1:A:2278:GLY:N	1:A:2281:THR:OG1	2.48	0.47
1:A:1399:LEU:HD22	1:A:1439:LEU:HB3	1.97	0.47
1:A:1460:GLU:HG2	1:A:1464:LYS:HE3	1.96	0.47
1:A:1661:VAL:HG22	1:A:1676:ILE:HD12	1.96	0.47
1:A:2590:PRO:HB3	1:A:2708:PHE:HB2	1.97	0.46
1:A:3879:ASP:OD1	1:A:4342:LYS:NZ	2.45	0.46
1:A:1343:ILE:HG22	1:A:1347:LYS:HD3	1.98	0.46
1:A:2191:LEU:HD21	1:A:2232:MET:HE3	1.96	0.46
1:A:2737:ASP:OD1	1:A:2738:TYR:N	2.44	0.46
1:A:2755:MET:HE2	1:A:2807:PHE:HB2	1.97	0.46
1:A:3117:LYS:NZ	1:A:3119:ASN:OD1	2.36	0.46
1:A:3176:TYR:O	1:A:3180:ILE:HG12	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2752:ASN:OD1	1:A:2770:THR:OG1	2.21	0.46
1:A:3476:THR:O	1:A:3480:LYS:NZ	2.48	0.46
1:A:1396:ILE:O	1:A:1400:VAL:HG23	2.16	0.46
1:A:1741:TRP:CH2	1:A:1750:VAL:HG13	2.50	0.46
1:A:1843:ARG:NH1	1:A:1845:TYR:OH	2.48	0.46
1:A:1978:ILE:HD11	1:A:2001:LEU:HD11	1.97	0.46
1:A:2066:ALA:HA	1:A:2069:ILE:HG22	1.96	0.46
1:A:4451:LEU:HD12	1:A:4454:GLU:OE2	2.15	0.46
1:A:1781:VAL:O	1:A:1785:VAL:HG23	2.15	0.46
1:A:1911:GLY:HA3	2:A:4701:ADP:C8	2.51	0.46
1:A:2666:ILE:HB	1:A:2712:CYS:SG	2.56	0.46
1:A:2797:ARG:NH2	4:A:4703:ANP:O1A	2.49	0.46
1:A:3886:LEU:O	1:A:3890:ILE:HG12	2.15	0.46
1:A:4388:LEU:HD11	1:A:4435:VAL:HG21	1.97	0.46
1:A:4461:PRO:HD3	1:A:4475:VAL:HG12	1.97	0.46
1:A:1671:SER:HA	1:A:1692:ILE:HD12	1.97	0.46
1:A:4267:THR:HG21	1:A:4636:TYR:HD2	1.80	0.46
1:A:4603:SER:OG	1:A:4603:SER:O	2.34	0.46
1:A:1546:TYR:O	1:A:1550:ILE:HG12	2.16	0.46
1:A:1627:PRO:HB3	1:A:1950:GLN:HB3	1.96	0.46
1:A:1911:GLY:N	2:A:4701:ADP:O1B	2.48	0.46
1:A:4031:VAL:O	1:A:4123:ARG:NH2	2.44	0.46
1:A:4297:PRO:HB3	1:A:4308:TRP:CD1	2.51	0.46
1:A:1523:TRP:O	1:A:1527:LEU:HD23	2.16	0.46
1:A:2063:GLU:HG2	1:A:2064:VAL:N	2.31	0.46
1:A:4485:ARG:NH1	1:A:4513:GLY:O	2.49	0.46
1:A:4178:ARG:CZ	1:A:4296:MET:HE1	2.45	0.45
1:A:1609:GLY:O	1:A:1613:LYS:HG2	2.16	0.45
1:A:2593:LEU:HD23	1:A:2734:VAL:HB	1.99	0.45
1:A:3601:MET:CE	1:A:3611:ARG:HB2	2.47	0.45
1:A:2231:SER:HA	1:A:2234:TRP:NE1	2.31	0.45
1:A:2614:ASP:O	1:A:2615:MET:HE2	2.16	0.45
1:A:2729:ARG:HD3	1:A:2730:HIS:CD2	2.50	0.45
1:A:1455:GLY:O	1:A:1459:LEU:HG	2.16	0.45
1:A:2299:GLN:HB2	1:A:2339:VAL:HG22	1.98	0.45
1:A:4423:LEU:HD13	1:A:4466:HIS:ND1	2.31	0.45
1:A:2594:CYS:O	1:A:2735:TYR:HA	2.15	0.45
1:A:2808:GLU:OE2	1:A:2808:GLU:HA	2.16	0.45
1:A:4517:PRO:HG3	1:A:4611:LEU:HD13	1.98	0.45
1:A:1888:CYS:O	1:A:1892:MET:HG2	2.16	0.45
1:A:2571:THR:O	1:A:2575:VAL:HG22	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3485:GLU:CD	1:A:3488:ARG:HH22	2.25	0.45
1:A:1653:HIS:HA	1:A:1656:LYS:HE2	1.98	0.45
1:A:3851:ASP:O	1:A:3855:ARG:HG3	2.16	0.45
1:A:2509:LYS:HE2	1:A:2509:LYS:HB3	1.67	0.45
1:A:2616:GLU:HG3	1:A:2657:LYS:HD3	1.99	0.45
1:A:2963:VAL:HG22	1:A:2998:ASN:HB3	1.98	0.45
1:A:1373:PHE:HD2	1:A:1383:TYR:HE1	1.64	0.45
1:A:1409:LYS:HD2	1:A:1410:ASP:H	1.82	0.45
1:A:1464:LYS:O	1:A:1468:GLU:HG2	2.17	0.45
1:A:1539:ASP:CG	1:A:1543:ARG:HE	2.25	0.45
1:A:2239:LYS:HE2	1:A:2239:LYS:HB3	1.91	0.45
1:A:4086:THR:OG1	1:A:4092:ARG:NH2	2.50	0.45
1:A:4482:PHE:O	1:A:4486:ILE:HG12	2.17	0.45
1:A:1914:GLU:CD	2:A:4701:ADP:H3'	2.42	0.45
1:A:2182:LEU:HD23	1:A:2236:VAL:HG22	1.99	0.45
1:A:2361:MET:HE2	1:A:2361:MET:HB2	1.90	0.45
1:A:4387:TRP:HZ2	1:A:4476:ILE:HG22	1.82	0.45
1:A:1598:GLN:O	1:A:1602:GLU:HG2	2.16	0.44
1:A:2518:ILE:O	1:A:2522:THR:N	2.51	0.44
1:A:3554:SER:OG	1:A:3555:ASN:N	2.50	0.44
1:A:3779:GLU:O	1:A:3782:ARG:HG2	2.17	0.44
1:A:2210:LEU:O	1:A:2214:THR:HG23	2.18	0.44
1:A:2658:TRP:CE3	1:A:2705:ARG:HA	2.53	0.44
1:A:2822:ILE:HD12	1:A:2861:ILE:HG21	1.99	0.44
1:A:3101:ALA:O	1:A:3105:VAL:HG23	2.16	0.44
1:A:3618:ALA:HA	1:A:3621:LYS:HE2	2.00	0.44
1:A:3983:ILE:HD12	1:A:4012:ASN:ND2	2.31	0.44
1:A:1903:SER:O	1:A:1903:SER:OG	2.29	0.44
1:A:2813:LEU:HD21	1:A:2816:LEU:HG	2.00	0.44
1:A:2232:MET:O	1:A:2236:VAL:HG12	2.18	0.44
1:A:2943:LYS:NZ	2:A:4704:ADP:O3B	2.48	0.44
1:A:3813:PHE:O	1:A:3816:GLU:HG3	2.18	0.44
1:A:4336:GLY:O	1:A:4340:ILE:HG12	2.17	0.44
1:A:4575:LEU:HG	1:A:4624:PHE:HB3	1.99	0.44
1:A:1788:THR:O	1:A:1792:LEU:HD23	2.18	0.44
1:A:2030:ASP:OD1	1:A:2030:ASP:N	2.47	0.44
1:A:2107:ARG:O	1:A:2111:ILE:HG12	2.17	0.44
1:A:2451:ARG:O	1:A:2455:LEU:HD23	2.18	0.44
1:A:3030:MET:HE1	1:A:3047:HIS:O	2.18	0.44
1:A:3175:HIS:CD2	1:A:3585:ARG:HH12	2.35	0.44
1:A:1356:PRO:HD3	1:A:1404:LYS:HD2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1698:ILE:HA	1:A:1701:TRP:NE1	2.32	0.44
1:A:2540:SER:OG	1:A:2542:SER:O	2.32	0.44
1:A:2827:HIS:O	1:A:2831:ARG:HG2	2.18	0.44
1:A:2868:SER:OG	1:A:2870:PRO:O	2.35	0.44
1:A:3875:MET:HE3	1:A:3879:ASP:HB2	1.99	0.44
1:A:4153:VAL:O	1:A:4157:MET:HG3	2.18	0.44
1:A:4412:PHE:CE2	1:A:4520:TYR:HB2	2.53	0.44
1:A:1382:SER:O	1:A:1386:VAL:HG22	2.18	0.44
1:A:1905:PHE:HE2	1:A:2038:SER:HB3	1.82	0.44
1:A:3502:THR:HG23	1:A:3543:PHE:HA	1.99	0.44
1:A:3904:GLU:OE2	1:A:3904:GLU:N	2.40	0.44
1:A:2214:THR:HG22	1:A:2220:LEU:HD21	1.99	0.43
1:A:2230:LYS:HG2	1:A:2364:PHE:CD2	2.53	0.43
1:A:2449:LEU:HA	1:A:2453:ARG:NH2	2.32	0.43
1:A:2589:LYS:NZ	1:A:2730:HIS:O	2.45	0.43
1:A:2802:TRP:CZ2	1:A:2829:ALA:HB2	2.53	0.43
1:A:3099:THR:HG23	1:A:3148:VAL:HG11	2.00	0.43
1:A:4635:PHE:HD2	1:A:4640:VAL:HG11	1.83	0.43
1:A:1861:MET:HE1	1:A:1889:TYR:HB3	2.00	0.43
1:A:2485:GLN:HG3	1:A:2488:ARG:HH21	1.83	0.43
1:A:2301:ILE:HB	1:A:2341:ILE:HD13	2.00	0.43
1:A:2924:ARG:O	1:A:2928:GLN:HG2	2.18	0.43
1:A:1402:GLU:HG3	1:A:3655:ARG:HH22	1.83	0.43
1:A:1467:ARG:NH1	1:A:1523:TRP:HE1	2.16	0.43
1:A:2787:ASP:OD1	1:A:2787:ASP:N	2.51	0.43
1:A:3839:VAL:HG21	1:A:3863:LEU:HA	2.00	0.43
1:A:2919:VAL:HG13	1:A:2950:VAL:HG22	2.00	0.43
1:A:4031:VAL:HA	1:A:4035:VAL:HG12	2.01	0.43
1:A:4077:PHE:HB3	1:A:4105:TRP:HE1	1.83	0.43
1:A:1335:GLU:O	1:A:1339:VAL:HG13	2.18	0.43
1:A:1415:GLN:HA	1:A:1418:LYS:HG2	2.01	0.43
1:A:2600:GLY:HA2	4:A:4703:ANP:H5'1	2.00	0.43
1:A:2884:VAL:HG13	1:A:2889:LEU:HD11	1.99	0.43
1:A:3485:GLU:HA	1:A:3488:ARG:NH1	2.34	0.43
1:A:3776:GLU:O	1:A:3779:GLU:HB3	2.18	0.43
1:A:4077:PHE:HB3	1:A:4105:TRP:NE1	2.33	0.43
1:A:4347:GLN:HA	1:A:4350:GLU:HB2	1.99	0.43
1:A:1460:GLU:O	1:A:1463:LEU:HG	2.19	0.43
1:A:2930:GLN:NE2	1:A:3012:LEU:O	2.46	0.43
1:A:3928:THR:HB	1:A:3931:GLN:HB2	2.01	0.43
1:A:1354:VAL:HG11	1:A:1431:LEU:HD22	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2047:GLN:HA	1:A:2070:VAL:HG21	2.01	0.43
1:A:2295:LEU:HA	1:A:2338:ASN:HD21	1.83	0.43
1:A:2914:GLU:OE1	1:A:2914:GLU:N	2.44	0.43
1:A:3138:SER:OG	1:A:3139:HIS:N	2.52	0.43
1:A:4107:MET:HE1	1:A:4137:ASN:ND2	2.32	0.43
3:A:4702:ATP:O5'	3:A:4702:ATP:H8	2.02	0.43
1:A:1659:ALA:HB2	1:A:1926:PHE:CD1	2.54	0.43
1:A:1933:ASP:HB3	1:A:1962:ARG:NH2	2.34	0.43
1:A:2213:ILE:HG22	1:A:2220:LEU:HD22	2.01	0.43
1:A:2668:LEU:HD12	1:A:3006:GLU:OE1	2.19	0.43
1:A:2930:GLN:HB2	1:A:3059:ILE:HG23	1.99	0.43
1:A:3510:SER:HB2	1:A:3553:LEU:HD21	2.01	0.43
1:A:3893:LYS:HE2	1:A:3893:LYS:HB3	1.73	0.43
1:A:4193:ARG:NH1	1:A:4321:LEU:O	2.52	0.43
1:A:2230:LYS:NZ	3:A:4702:ATP:O3G	2.44	0.43
1:A:2348:LEU:HB3	1:A:2351:ALA:HB3	2.01	0.43
1:A:2445:HIS:NE2	1:A:2449:LEU:HD22	2.34	0.43
1:A:2775:GLU:O	1:A:2778:THR:OG1	2.34	0.43
1:A:2847:ASP:CG	1:A:2869:ARG:HH22	2.26	0.43
1:A:3088:ARG:NH1	4:A:4703:ANP:O1G	2.51	0.43
1:A:3876:LEU:HD23	1:A:4146:VAL:HG11	2.00	0.43
1:A:4071:ILE:HD11	1:A:4096:LEU:HD22	2.01	0.43
1:A:1329:LEU:HA	1:A:1332:VAL:HG12	2.00	0.42
1:A:1843:ARG:NH2	1:A:1861:MET:O	2.52	0.42
1:A:2083:GLN:N	1:A:2083:GLN:OE1	2.52	0.42
1:A:2287:ILE:HD13	1:A:2294:GLU:HG2	2.01	0.42
1:A:2635:PHE:HB3	1:A:2650:LEU:HD21	2.00	0.42
1:A:2831:ARG:HA	1:A:2835:ASP:OD1	2.18	0.42
1:A:2927:ARG:HG3	1:A:2928:GLN:HE21	1.84	0.42
1:A:2934:LEU:HB2	1:A:3089:CYS:SG	2.59	0.42
1:A:4185:TRP:O	1:A:4189:ILE:HG12	2.19	0.42
1:A:2229:GLY:N	3:A:4702:ATP:O2B	2.52	0.42
1:A:2512:ALA:O	1:A:2516:GLU:HG2	2.19	0.42
1:A:2569:VAL:HB	1:A:2747:ILE:HG12	2.00	0.42
1:A:2592:VAL:O	1:A:2733:VAL:HA	2.19	0.42
1:A:4031:VAL:HG21	1:A:4058:LEU:HD21	2.02	0.42
1:A:1969:SER:O	1:A:1973:GLN:HG2	2.20	0.42
1:A:2630:LEU:O	1:A:2634:THR:HG23	2.19	0.42
1:A:4080:ALA:O	1:A:4084:ILE:HG13	2.19	0.42
1:A:4474:THR:OG1	1:A:4477:GLN:HG3	2.19	0.42
1:A:4517:PRO:O	1:A:4521:ILE:HG12	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1671:SER:O	1:A:1692:ILE:N	2.50	0.42
1:A:2784:PHE:HB3	1:A:2792:TYR:CD2	2.53	0.42
1:A:3212:VAL:HG21	1:A:3486:ARG:HH12	1.84	0.42
1:A:4169:ILE:HD12	1:A:4302:ARG:HE	1.84	0.42
1:A:4431:LEU:O	1:A:4435:VAL:HG23	2.19	0.42
1:A:4476:ILE:HA	1:A:4479:VAL:HG22	2.02	0.42
1:A:2759:ILE:HG22	1:A:2762:LEU:H	1.85	0.42
1:A:3200:HIS:NE2	1:A:3747:LYS:HD3	2.34	0.42
1:A:4635:PHE:CD2	1:A:4640:VAL:HG11	2.55	0.42
1:A:1485:ARG:HE	1:A:1485:ARG:HB3	1.74	0.42
1:A:1949:CYS:HB3	1:A:2008:VAL:HA	2.02	0.42
1:A:2437:LEU:HD22	1:A:2455:LEU:HD21	2.01	0.42
1:A:2981:ARG:O	1:A:2985:CYS:HB3	2.19	0.42
1:A:3597:THR:O	1:A:3600:ILE:HG22	2.20	0.42
1:A:4257:ASP:OD1	1:A:4257:ASP:N	2.52	0.42
1:A:2569:VAL:HG11	1:A:2747:ILE:HA	2.00	0.42
1:A:2870:PRO:HB2	1:A:2872:LEU:HD11	2.01	0.42
1:A:2967:TYR:HE1	1:A:2972:PHE:HB2	1.85	0.42
1:A:3928:THR:O	1:A:3932:ALA:N	2.39	0.42
1:A:4379:THR:O	1:A:4383:THR:HG23	2.20	0.42
1:A:2054:LEU:HG	1:A:2097:LEU:HD22	2.02	0.42
1:A:2972:PHE:CE2	1:A:2976:LEU:HD11	2.55	0.42
1:A:4490:GLN:O	1:A:4494:LEU:HG	2.20	0.42
1:A:2238:LEU:HD11	1:A:2249:GLY:HA3	2.02	0.41
1:A:2775:GLU:HG3	1:A:2779:MET:HE3	2.02	0.41
1:A:2994:MET:HB3	1:A:2998:ASN:OD1	2.20	0.41
1:A:3208:ILE:O	1:A:3212:VAL:HG23	2.20	0.41
1:A:3477:ALA:HA	1:A:3480:LYS:HG2	2.01	0.41
1:A:3567:LEU:HB2	1:A:3599:PHE:CD1	2.55	0.41
1:A:4265:LEU:O	1:A:4269:LEU:HD23	2.20	0.41
1:A:1356:PRO:HA	1:A:1359:LEU:HB3	2.02	0.41
1:A:1450:LEU:O	1:A:1454:GLN:HG2	2.21	0.41
1:A:2147:PRO:HB3	1:A:2362:VAL:HG12	2.01	0.41
1:A:2323:LYS:HE2	1:A:2323:LYS:HB3	1.85	0.41
1:A:2933:LEU:HD11	1:A:3092:ASN:HB2	2.02	0.41
1:A:3003:GLY:HA2	1:A:3006:GLU:HG2	2.02	0.41
1:A:3500:MET:O	1:A:3503:ILE:HG22	2.20	0.41
1:A:3586:TYR:HA	1:A:3587:PRO:HD3	1.96	0.41
1:A:3909:LEU:HD21	1:A:4343:MET:HE3	2.03	0.41
1:A:4088:VAL:HG11	1:A:4116:LEU:HD11	2.02	0.41
1:A:3570:ASP:O	1:A:3574:THR:HG23	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3716:VAL:HG23	1:A:3836:TYR:OH	2.20	0.41
1:A:4235:PRO:HB3	1:A:4278:PHE:CD2	2.55	0.41
1:A:1391:LYS:HE2	1:A:1391:LYS:HB3	1.93	0.41
1:A:1587:LEU:O	1:A:1591:VAL:HG22	2.20	0.41
1:A:2395:GLN:HB2	1:A:2396:ARG:NH2	2.35	0.41
1:A:2739:PRO:HB2	1:A:2744:LEU:HG	2.03	0.41
1:A:3488:ARG:NH2	1:A:3489:TRP:HE1	2.19	0.41
1:A:4113:LEU:HD23	1:A:4116:LEU:HD23	2.02	0.41
1:A:1961:ASN:HB3	1:A:2018:MET:HE1	2.03	0.41
1:A:2294:GLU:N	1:A:2294:GLU:OE1	2.53	0.41
1:A:2900:PHE:CE1	1:A:2904:GLU:HG3	2.56	0.41
1:A:2922:ILE:HA	1:A:2925:ILE:HG22	2.02	0.41
1:A:3684:PRO:HB3	1:A:3702:THR:HG21	2.02	0.41
1:A:4018:MET:SD	1:A:4018:MET:N	2.93	0.41
1:A:4113:LEU:HD23	1:A:4113:LEU:HA	1.89	0.41
1:A:4377:MET:HB3	1:A:4378:ARG:NH1	2.35	0.41
1:A:1518:GLU:HG2	1:A:1519:ASP:N	2.36	0.41
1:A:1521:LEU:O	1:A:1524:GLU:HG3	2.21	0.41
1:A:2203:TRP:CH2	1:A:2236:VAL:HG11	2.55	0.41
1:A:2486:LEU:O	1:A:2490:ILE:HG12	2.21	0.41
1:A:1393:TYR:HE2	1:A:1435:TRP:CG	2.38	0.41
1:A:1691:SER:OG	1:A:1694:GLU:OE1	2.37	0.41
1:A:4133:LYS:HB2	1:A:4133:LYS:HE3	1.89	0.41
1:A:2082:SER:HA	1:A:2086:TYR:CD2	2.55	0.41
1:A:2396:ARG:HA	1:A:2399:LYS:HG3	2.02	0.41
1:A:2412:MET:HE1	1:A:2467:ARG:HA	2.02	0.41
1:A:2496:TYR:CE1	1:A:2500:TRP:HD1	2.39	0.41
1:A:2879:LYS:HB3	1:A:2879:LYS:HE3	1.88	0.41
1:A:4425:GLN:O	1:A:4426:ASP:C	2.64	0.41
1:A:1447:LYS:HE3	1:A:1447:LYS:HB2	1.79	0.41
1:A:1452:VAL:O	1:A:1456:GLU:HG2	2.20	0.41
1:A:1481:GLN:HE21	1:A:2273:ARG:NH1	2.18	0.41
1:A:1491:ASP:OD1	1:A:1492:ASP:N	2.53	0.41
1:A:2123:ASP:O	1:A:2127:ILE:HG13	2.21	0.41
1:A:2514:LEU:O	1:A:2518:ILE:HG12	2.20	0.41
1:A:2863:ARG:HD2	1:A:2863:ARG:HA	1.87	0.41
1:A:3485:GLU:OE1	1:A:3773:LEU:HD23	2.21	0.41
1:A:3757:LYS:HE3	1:A:3757:LYS:HB3	1.83	0.41
1:A:3871:VAL:O	1:A:3875:MET:HB2	2.21	0.41
1:A:1739:ILE:HG23	1:A:1804:ARG:HD3	2.02	0.41
1:A:2772:ALA:HA	1:A:2857:HIS:CE1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3498:ASN:O	1:A:3501:SER:OG	2.30	0.41
1:A:4157:MET:HE2	1:A:4157:MET:HB3	1.88	0.41
1:A:2668:LEU:HD21	1:A:2720:ARG:NH1	2.36	0.40
1:A:4260:PHE:CE2	1:A:4608:PRO:HB3	2.56	0.40
1:A:3203:VAL:O	1:A:3207:LYS:HG2	2.21	0.40
1:A:2912:PHE:CE1	1:A:2915:VAL:HG23	2.57	0.40
1:A:2073:PHE:HE2	1:A:2093:LEU:HA	1.86	0.40
1:A:2300:TRP:CE3	1:A:2342:MET:HE1	2.57	0.40
1:A:2648:VAL:HG11	1:A:2694:ARG:NH2	2.36	0.40
1:A:1399:LEU:O	1:A:1403:LEU:HD23	2.21	0.40
1:A:2686:MET:HG2	1:A:2703:LEU:HD11	2.04	0.40
1:A:3154:LEU:HG	1:A:3516:TYR:CD1	2.57	0.40

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	3028/4646 (65%)	2940 (97%)	88 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	2703/4125 (66%)	2703 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (38) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1355	GLN
1	A	1397	ASN
1	A	1495	ASN
1	A	1569	GLN
1	A	1598	GLN
1	A	1670	ASN
1	A	1736	ASN
1	A	1985	HIS
1	A	2057	GLN
1	A	2085	HIS
1	A	2212	GLN
1	A	2416	GLN
1	A	2439	HIS
1	A	2549	GLN
1	A	2637	HIS
1	A	2834	GLN
1	A	2954	ASN
1	A	3145	ASN
1	A	3185	ASN
1	A	3214	GLN
1	A	3526	GLN
1	A	3540	ASN
1	A	3595	GLN
1	A	3622	ASN
1	A	3931	GLN
1	A	4062	GLN
1	A	4078	ASN
1	A	4137	ASN
1	A	4156	ASN
1	A	4174	ASN
1	A	4191	GLN
1	A	4231	GLN
1	A	4347	GLN
1	A	4381	HIS
1	A	4530	GLN
1	A	4532	ASN

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Mol	Chain	Res	Type
1	A	4549	GLN
1	A	4566	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 ⓘ

Of 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 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	ANP	A	4703	-	29,33,33	1.12	4 (13%)	31,52,52	0.88	1 (3%)
3	ATP	A	4702	5	28,33,33	0.67	0	34,52,52	0.60	1 (2%)
2	ADP	A	4704	-	24,29,29	0.90	0	29,45,45	1.23	2 (6%)
2	ADP	A	4701	-	24,29,29	0.95	1 (4%)	29,45,45	1.18	2 (6%)

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	ANP	A	4703	-	-	2/14/38/38	0/3/3/3
3	ATP	A	4702	5	-	3/18/38/38	0/3/3/3
2	ADP	A	4704	-	-	4/12/32/32	0/3/3/3
2	ADP	A	4701	-	-	5/12/32/32	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	4703	ANP	PG-O1G	2.45	1.49	1.46
4	A	4703	ANP	PG-N3B	2.41	1.69	1.63
4	A	4703	ANP	PB-O1B	2.35	1.49	1.46
4	A	4703	ANP	PB-O3A	-2.32	1.56	1.59
2	A	4701	ADP	PA-O3A	2.27	1.61	1.59

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	4704	ADP	N3-C2-N1	-3.69	123.67	128.67
2	A	4701	ADP	N3-C2-N1	-3.60	123.79	128.67
2	A	4704	ADP	C4-C5-N7	-2.65	106.53	109.34
2	A	4701	ADP	C4-C5-N7	-2.46	106.74	109.34
4	A	4703	ANP	C5-C6-N6	2.33	123.86	120.31
3	A	4702	ATP	C5-C6-N6	2.29	123.79	120.31

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	4701	ADP	C5'-O5'-PA-O1A
2	A	4701	ADP	C5'-O5'-PA-O2A
2	A	4704	ADP	C5'-O5'-PA-O1A
2	A	4704	ADP	C5'-O5'-PA-O3A
3	A	4702	ATP	C5'-O5'-PA-O3A
4	A	4703	ANP	PG-N3B-PB-O1B
3	A	4702	ATP	O4'-C4'-C5'-O5'
3	A	4702	ATP	C3'-C4'-C5'-O5'
2	A	4701	ADP	C5'-O5'-PA-O3A
2	A	4701	ADP	PB-O3A-PA-O1A
2	A	4701	ADP	PB-O3A-PA-O2A
4	A	4703	ANP	C4'-C5'-O5'-PA
2	A	4704	ADP	PA-O3A-PB-O2B

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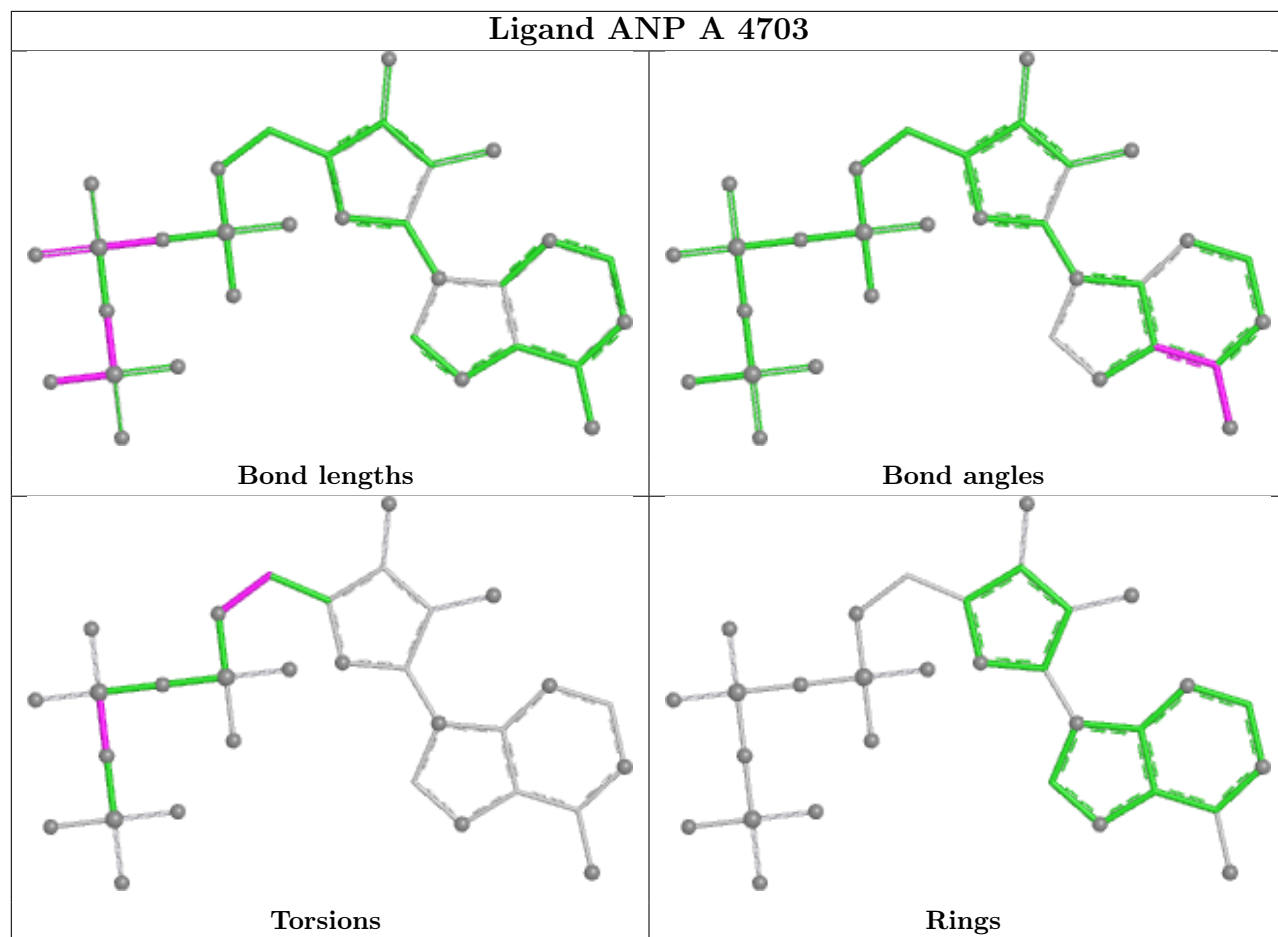
Mol	Chain	Res	Type	Atoms
2	A	4704	ADP	C4'-C5'-O5'-PA

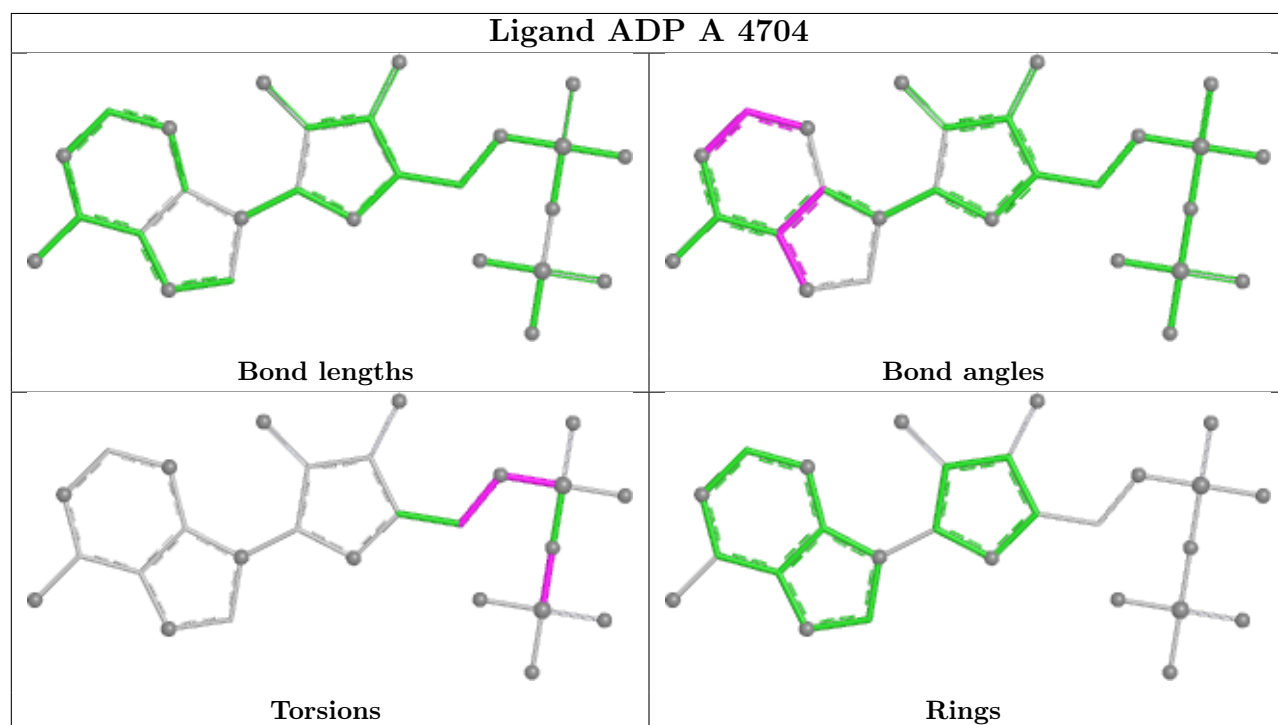
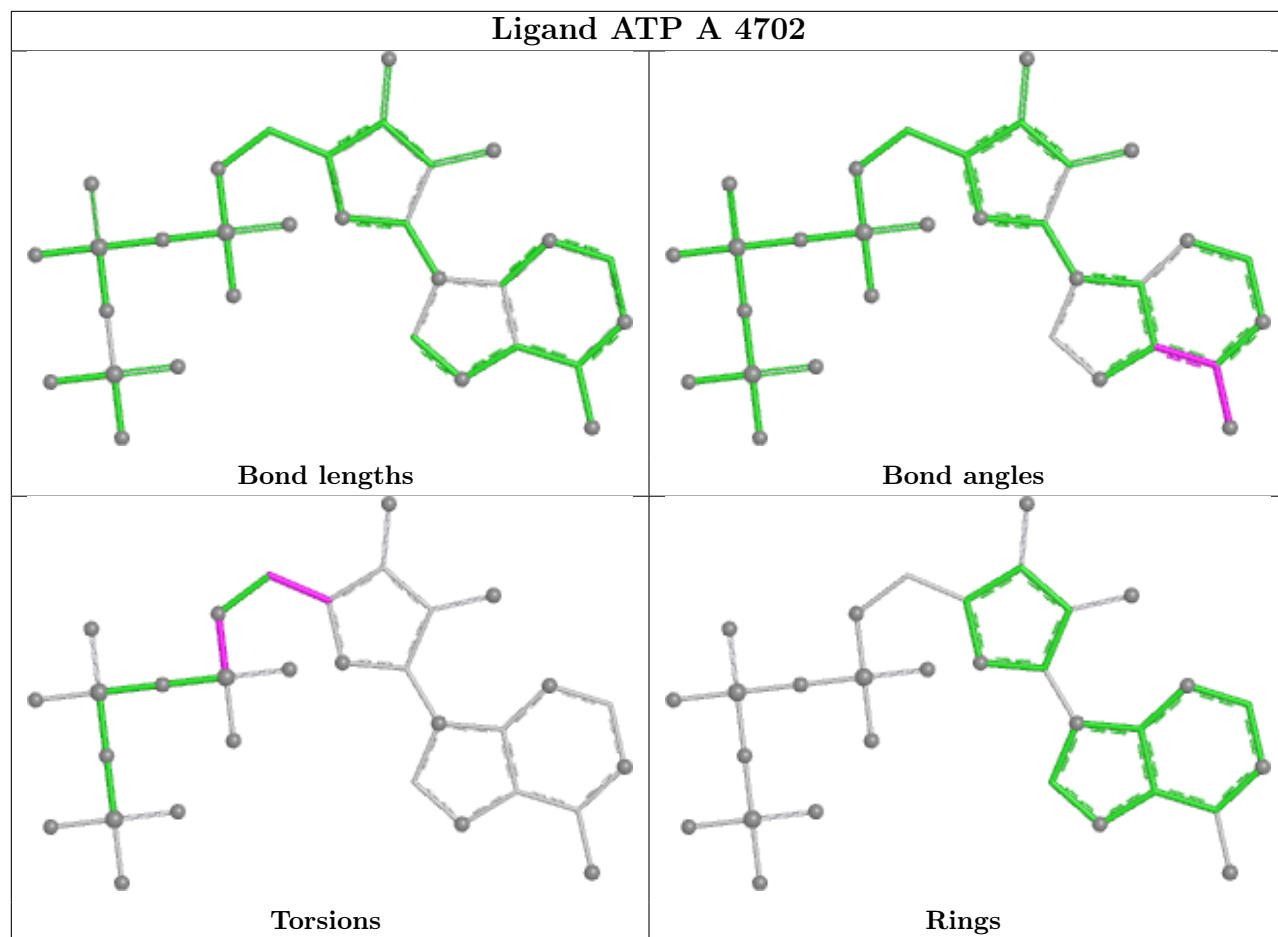
There are no ring outliers.

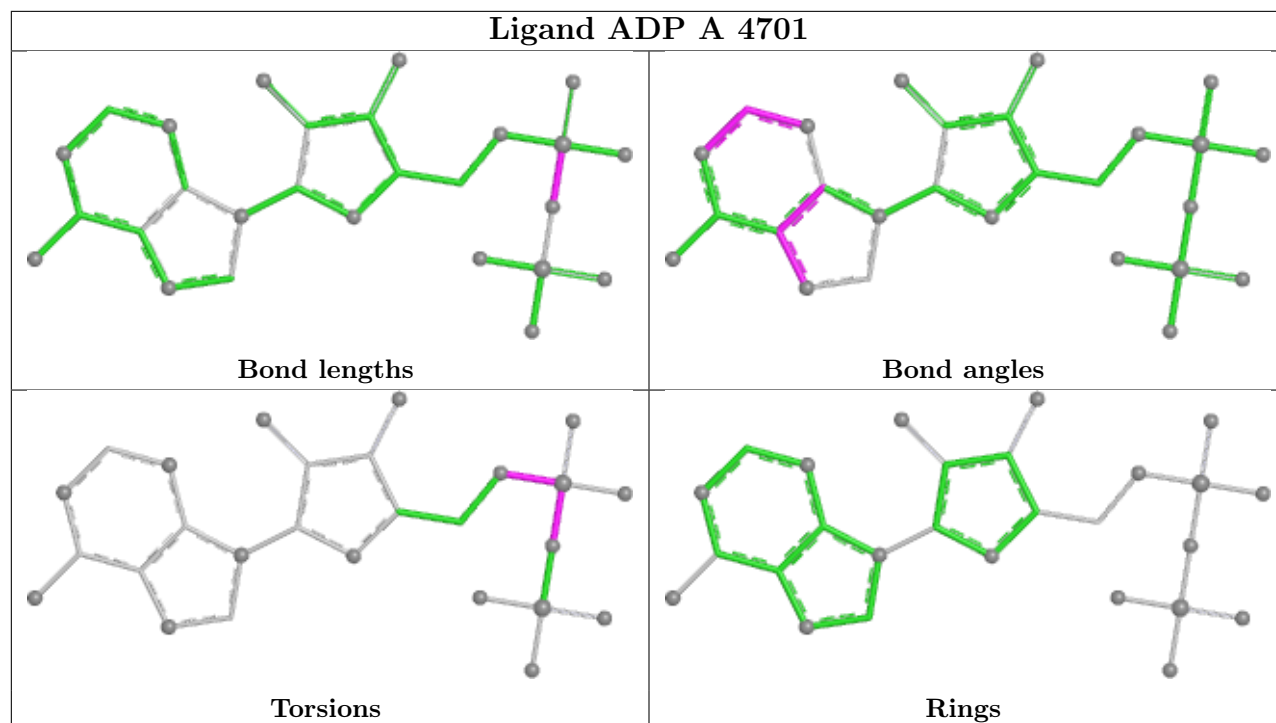
4 monomers are involved in 21 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	4703	ANP	5	0
3	A	4702	ATP	6	0
2	A	4704	ADP	2	0
2	A	4701	ADP	8	0

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.

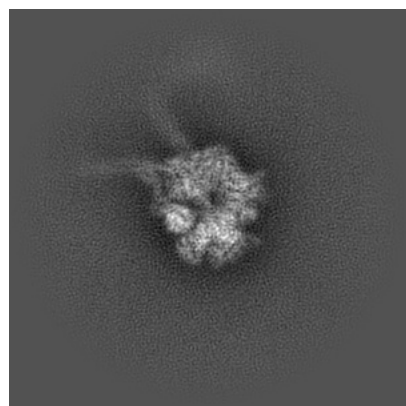
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-46861. These allow visual inspection of the internal detail of the map and identification of artifacts.

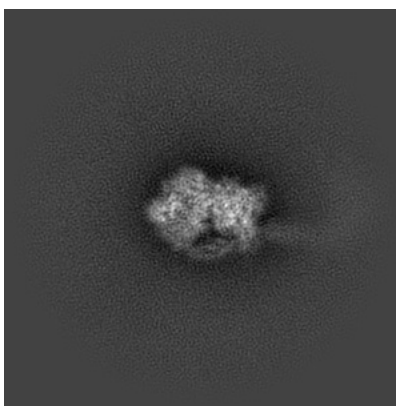
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

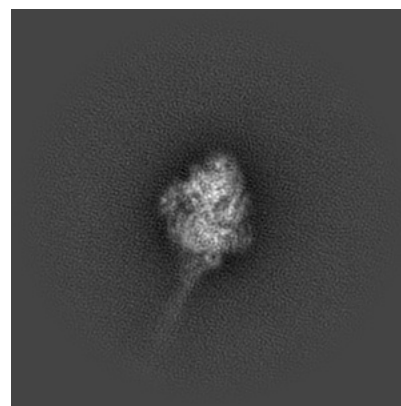
6.1.1 Primary map



X

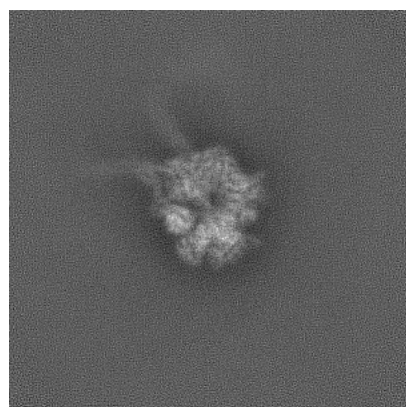


Y

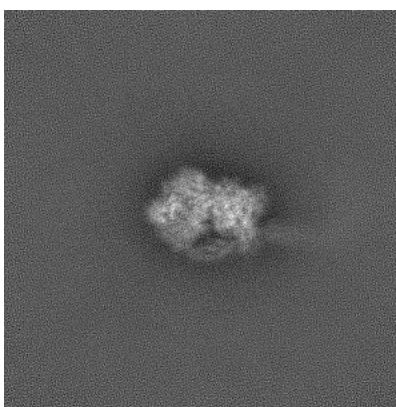


Z

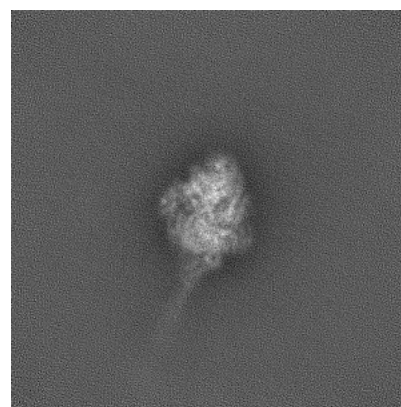
6.1.2 Raw map



X



Y

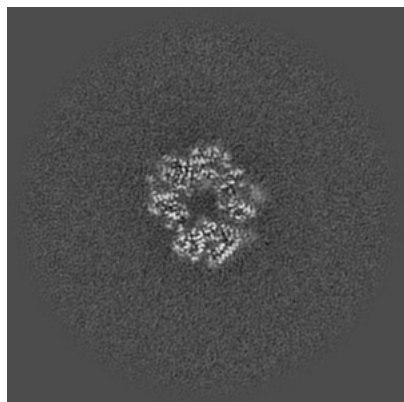


Z

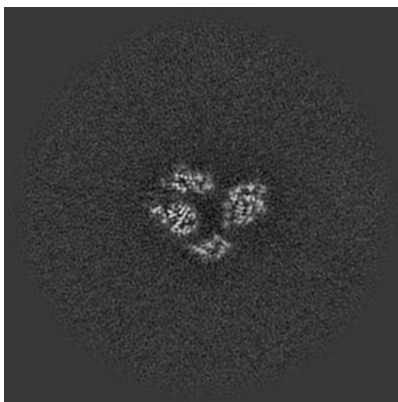
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

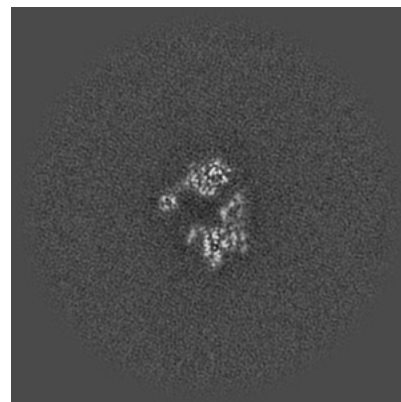
6.2.1 Primary map



X Index: 192

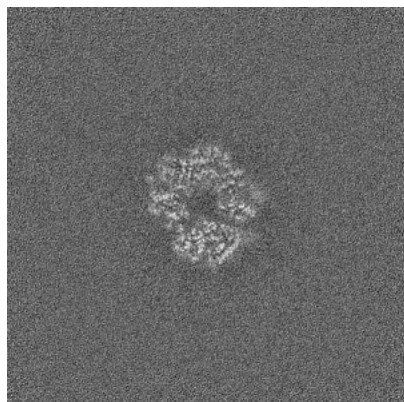


Y Index: 192

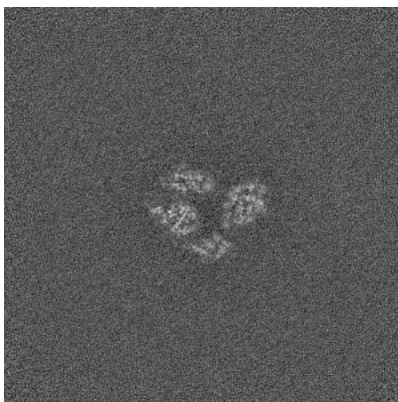


Z Index: 192

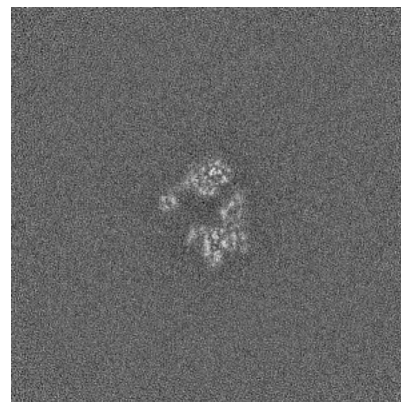
6.2.2 Raw map



X Index: 192



Y Index: 192

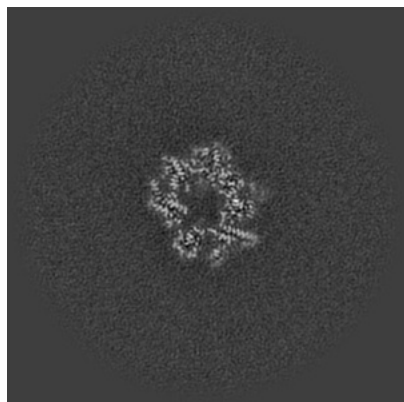


Z Index: 192

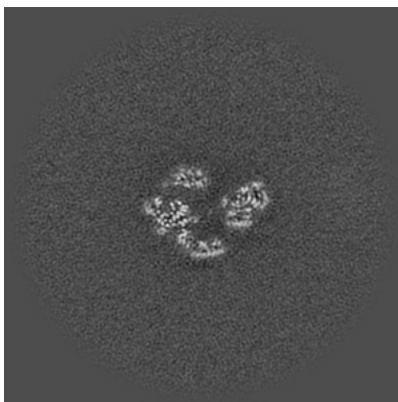
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

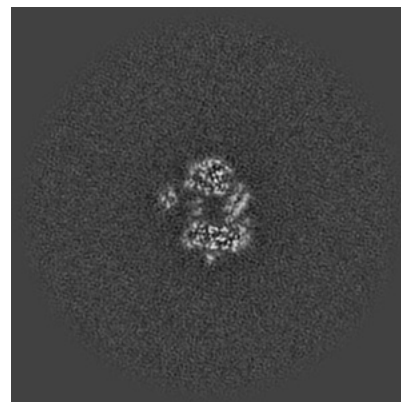
6.3.1 Primary map



X Index: 196

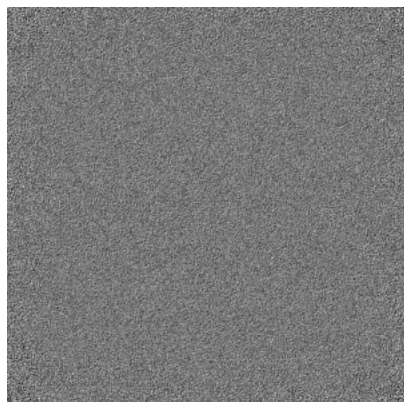


Y Index: 199

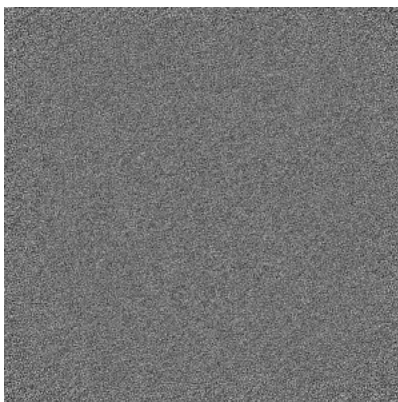


Z Index: 186

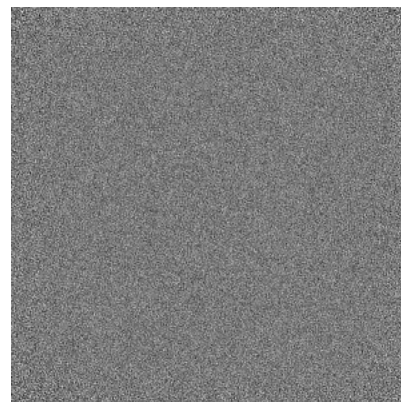
6.3.2 Raw map



X Index: 0



Y Index: 0

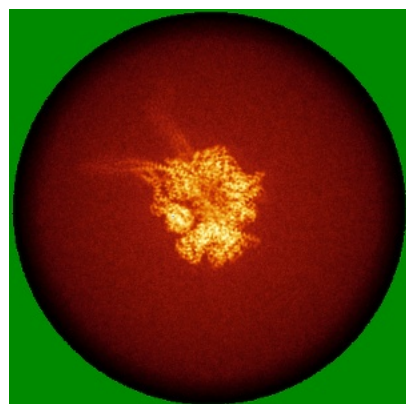


Z Index: 0

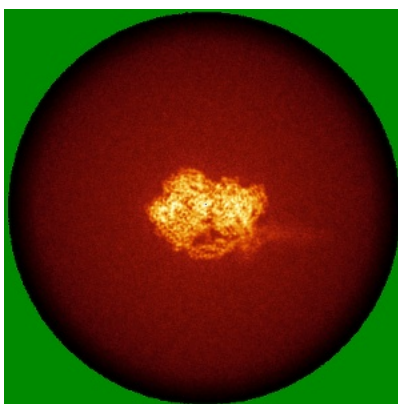
The images above show the largest variance slices of the map in three orthogonal directions.

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

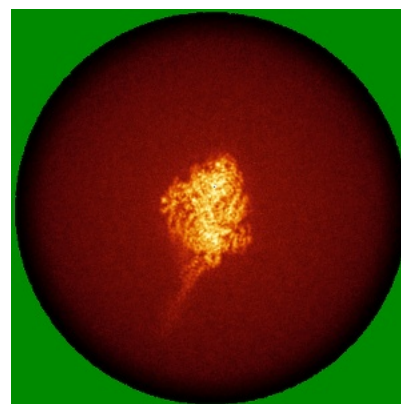
6.4.1 Primary map



X

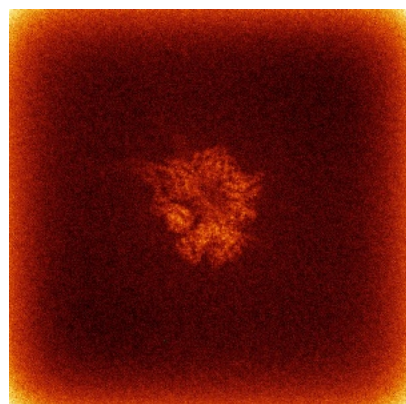


Y

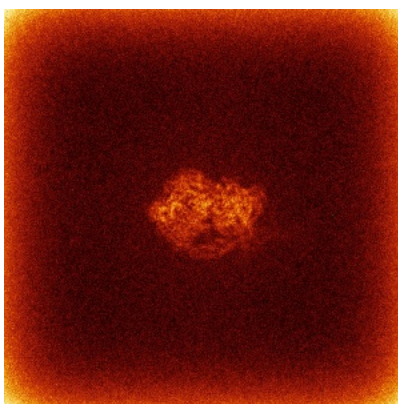


Z

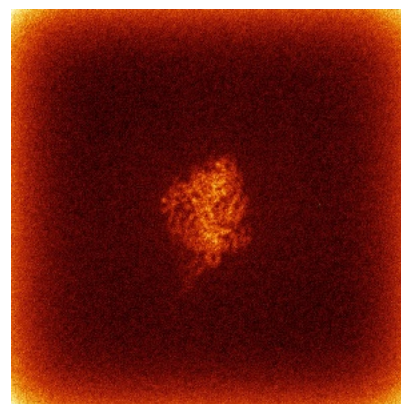
6.4.2 Raw map



X



Y

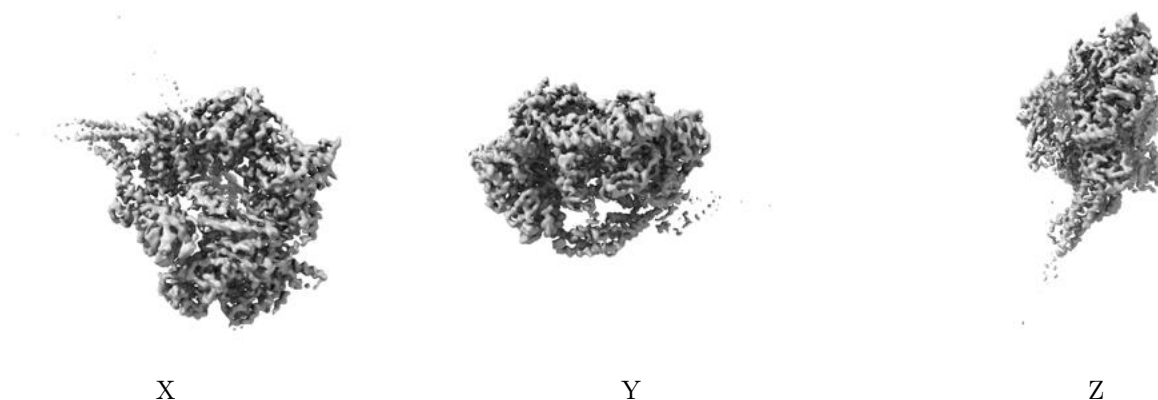


Z

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.

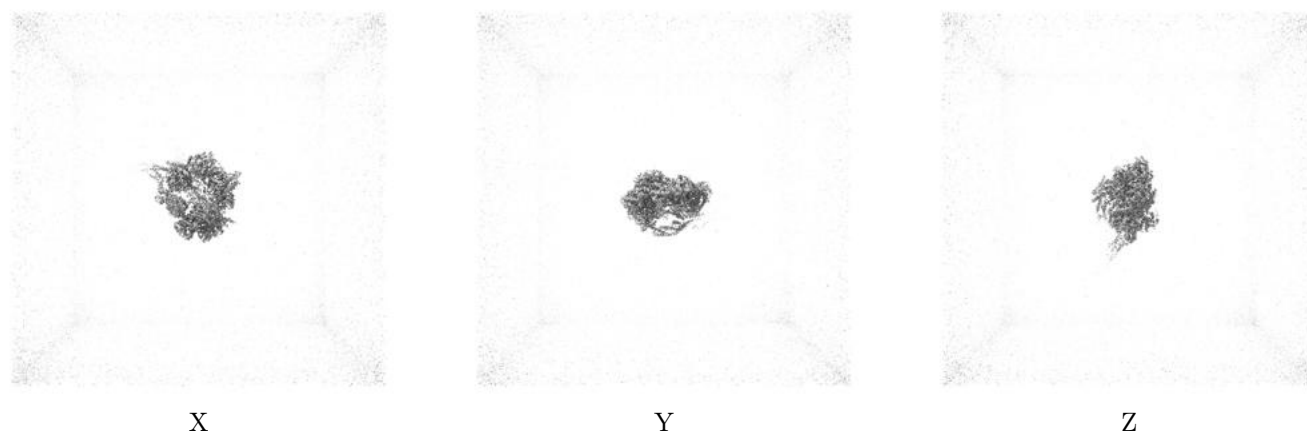
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.25. 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.

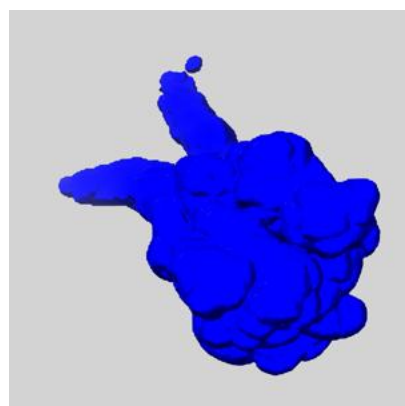
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

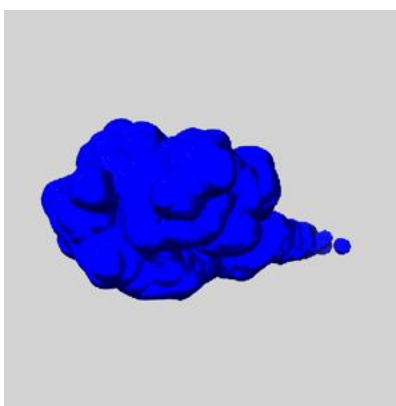
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

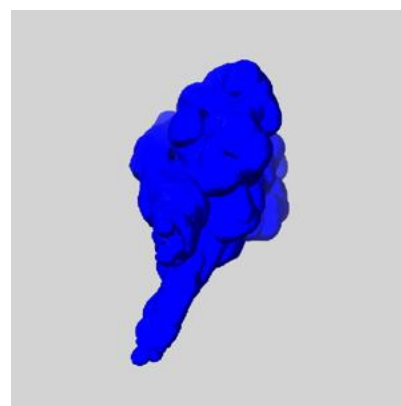
6.6.1 emd_46861_msk_1.map [i](#)



X



Y

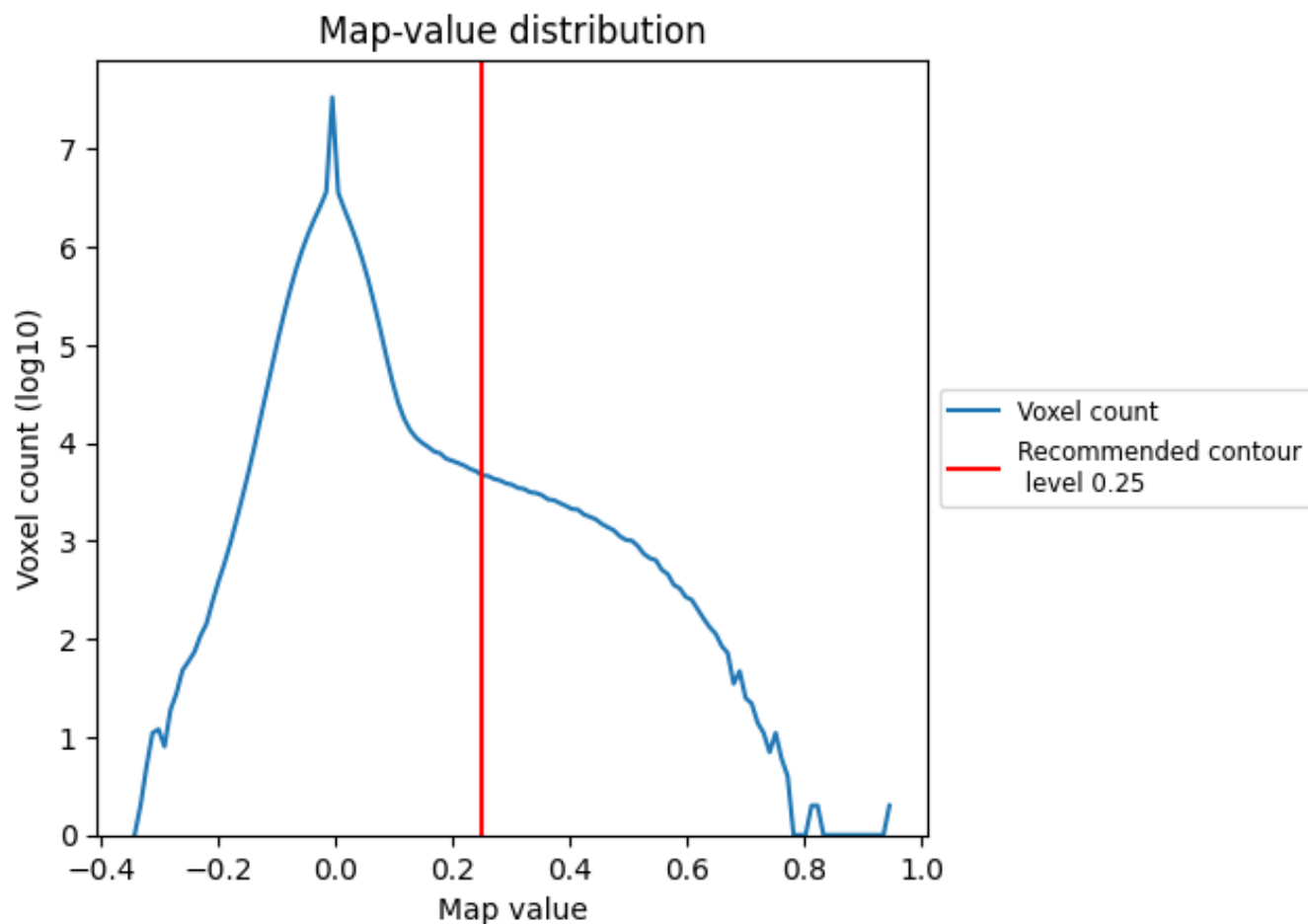


Z

7 Map analysis [i](#)

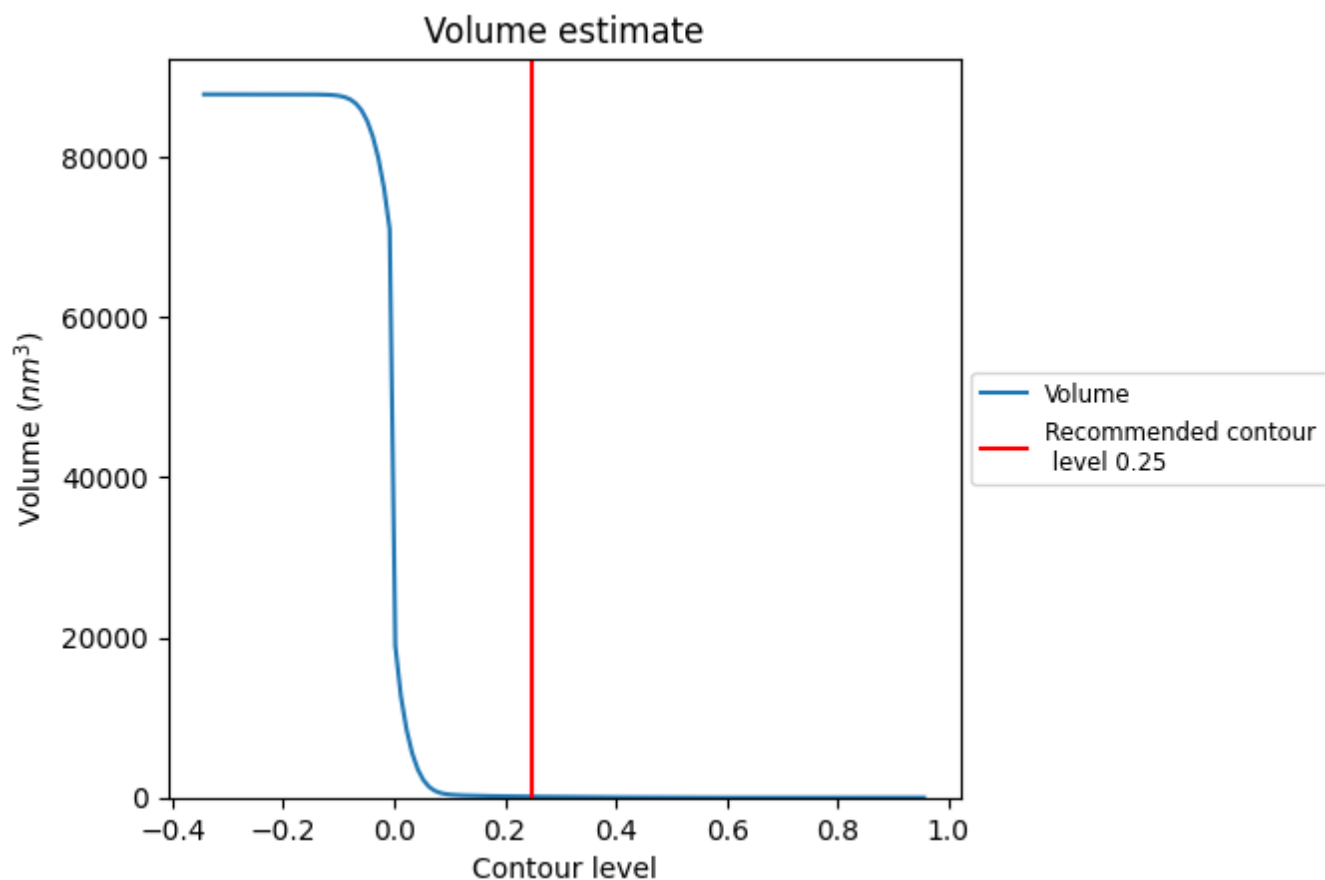
This section contains the results of statistical analysis of the map.

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.

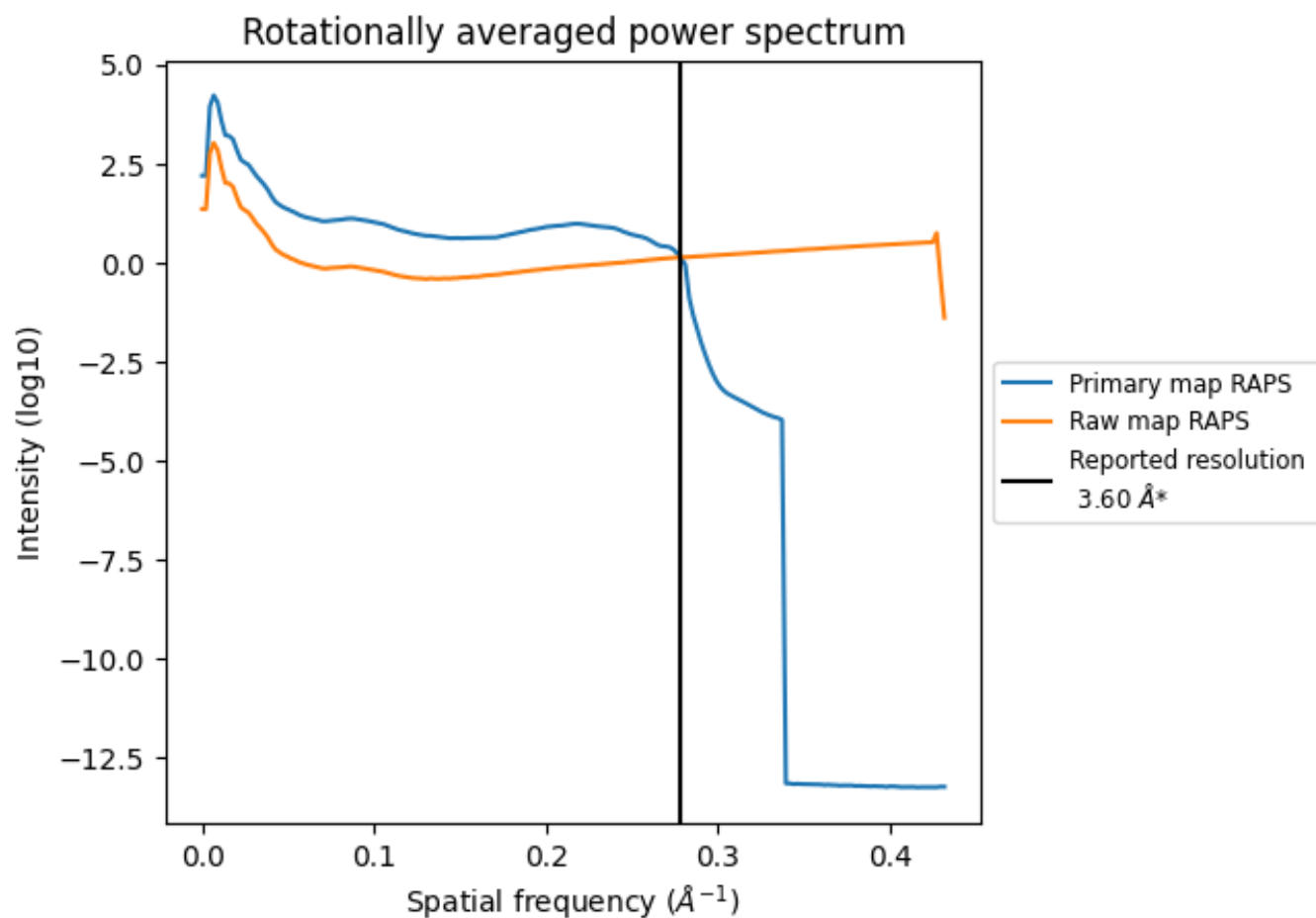
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 116 nm³; this corresponds to an approximate mass of 105 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 ⓘ

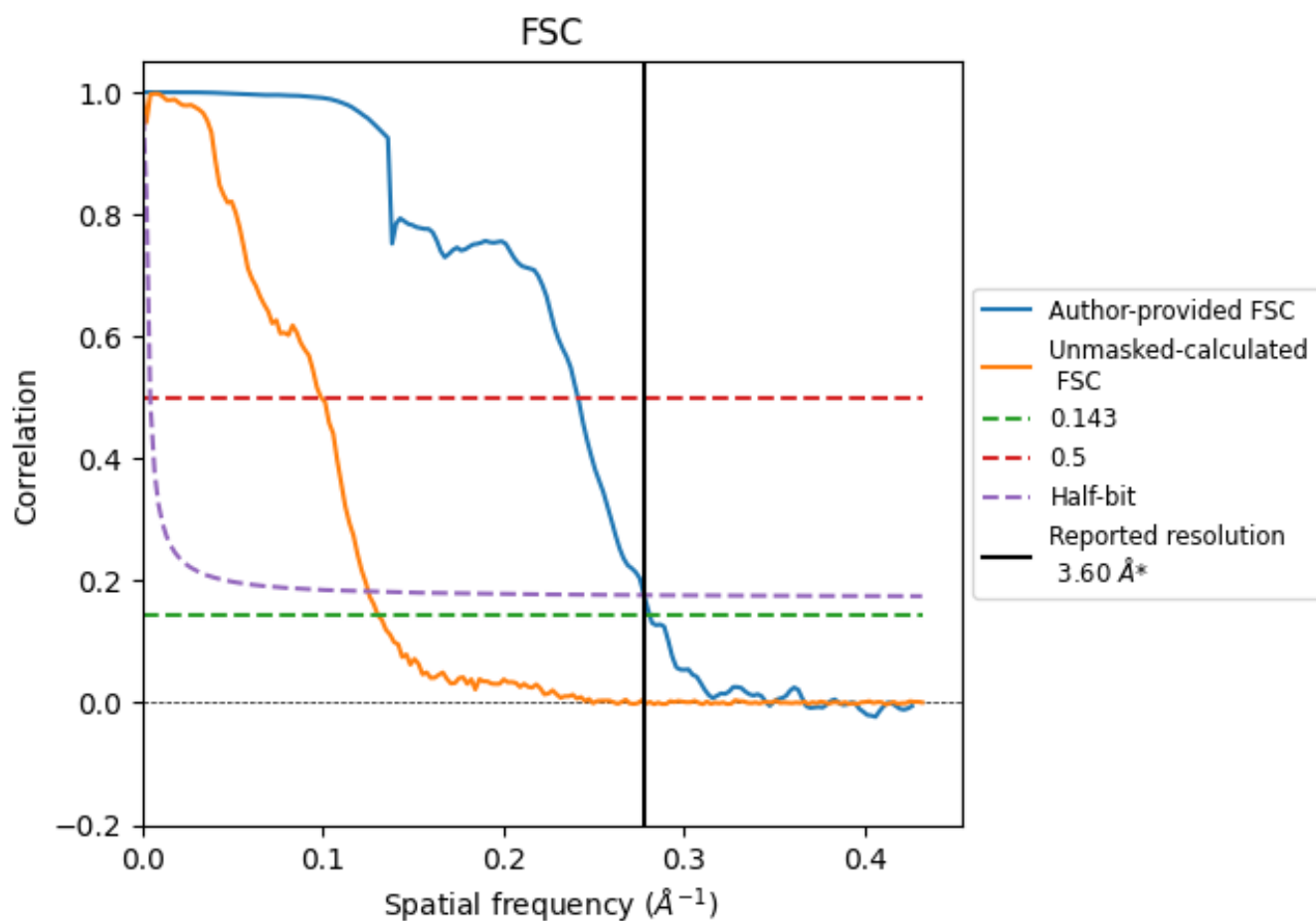


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

8 Fourier-Shell correlation [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 0.278 \AA^{-1}

8.2 Resolution estimates [i](#)

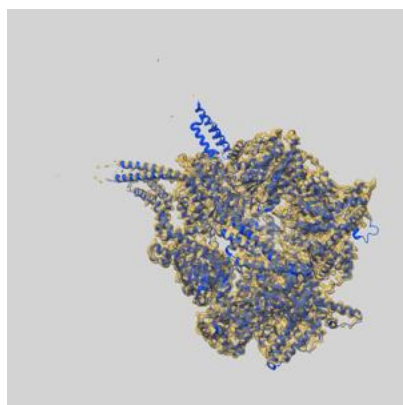
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.56	4.14	3.60
Unmasked-calculated*	7.65	10.09	7.99

*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 7.65 differs from the reported value 3.6 by more than 10 %

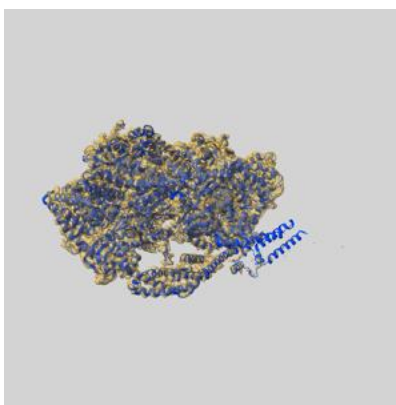
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-46861 and PDB model 9DHA. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

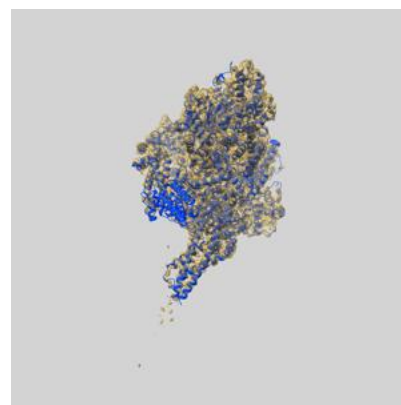
9.1 Map-model overlay [i](#)



X



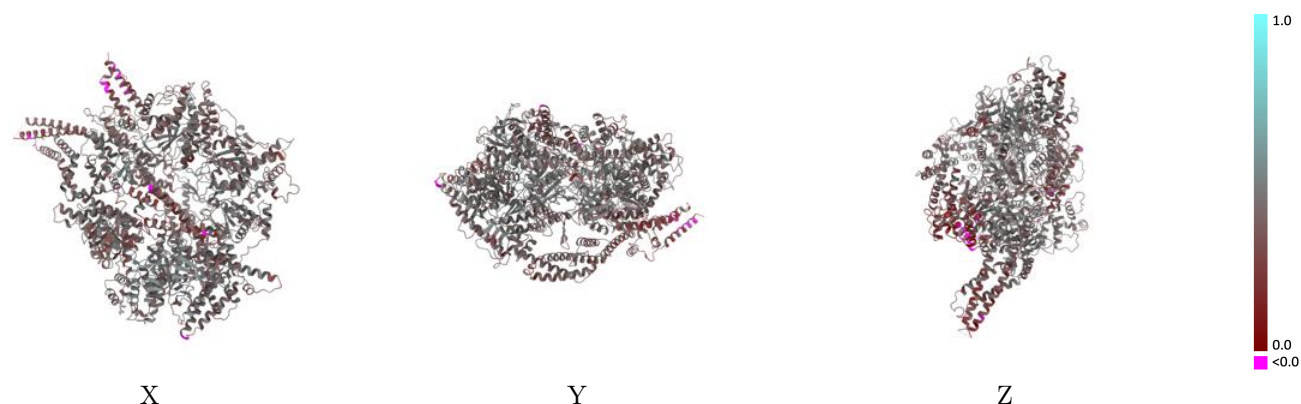
Y



Z

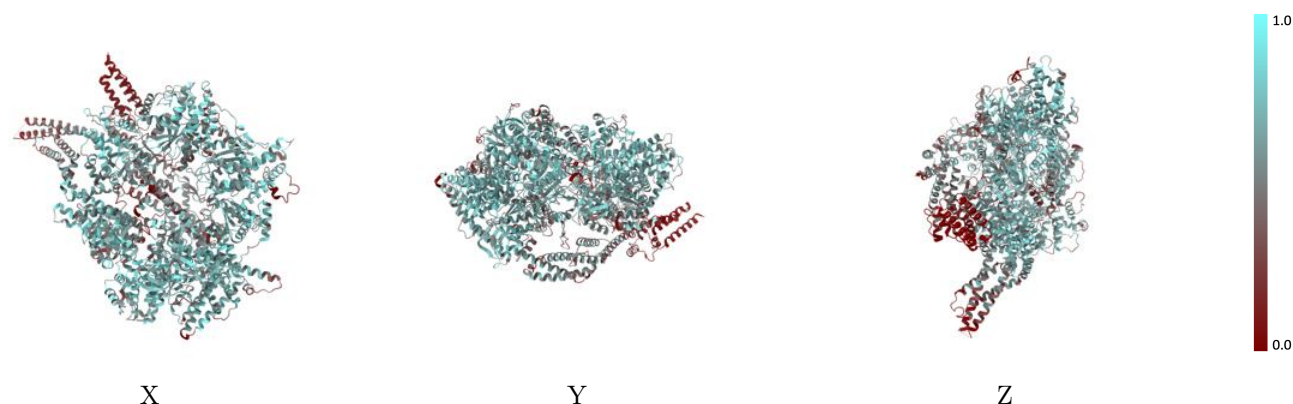
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



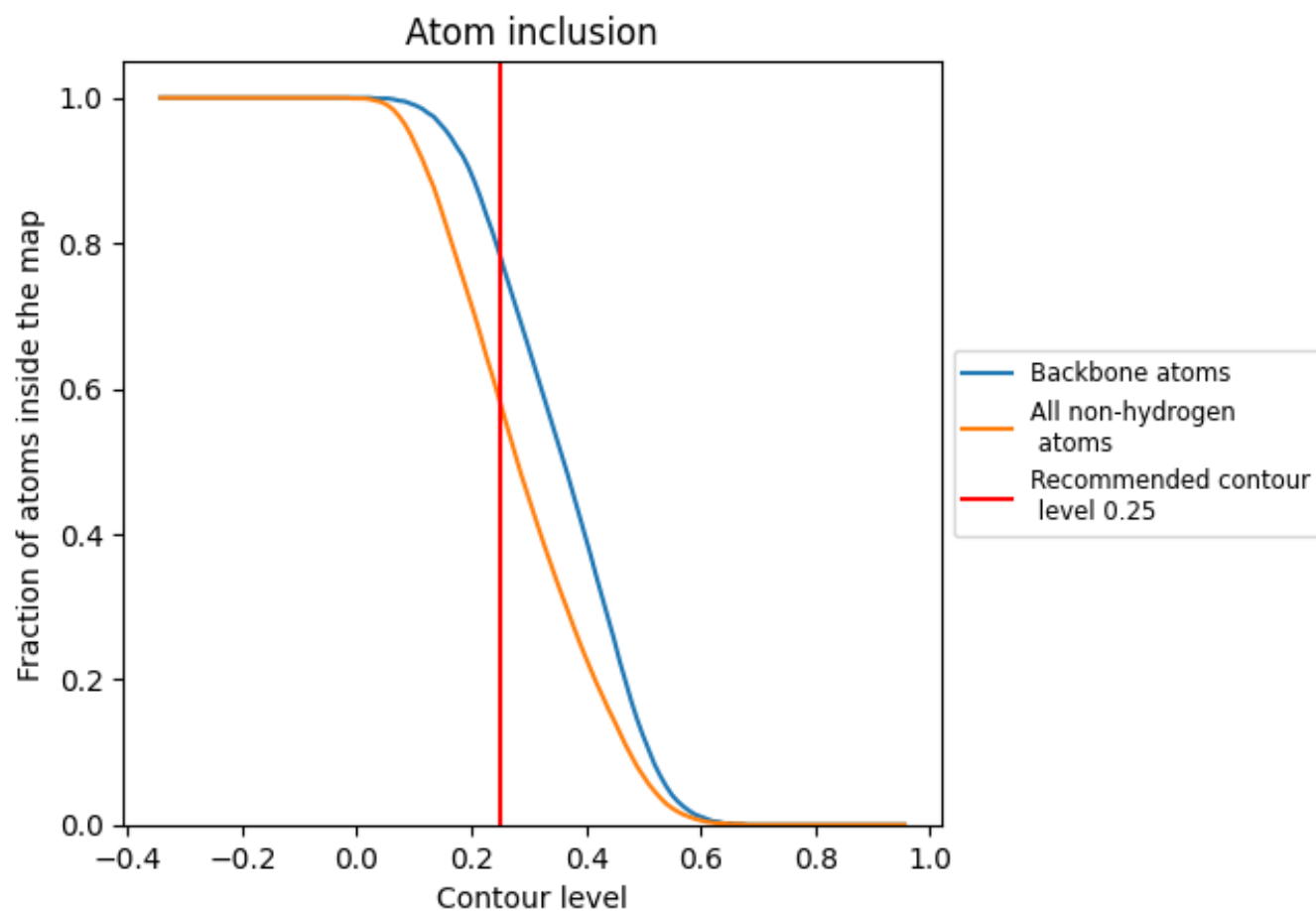
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.25).

9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 58% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.5810	<div></div> 0.4120
A	<div></div> 0.5810	<div></div> 0.4120

