



wwPDB EM Validation Summary Report ⓘ

Jul 15, 2024 – 11:16 pm BST

PDB ID : 7Z8I
EMDB ID : EMD-14552
Title : The barbed end complex of dynactin bound to BICDR1 and the cytoplasmic dynein tails (A2, B1, B2)
Authors : Chaaban, S.; Carter, A.P.
Deposited on : 2022-03-17
Resolution : 3.30 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:

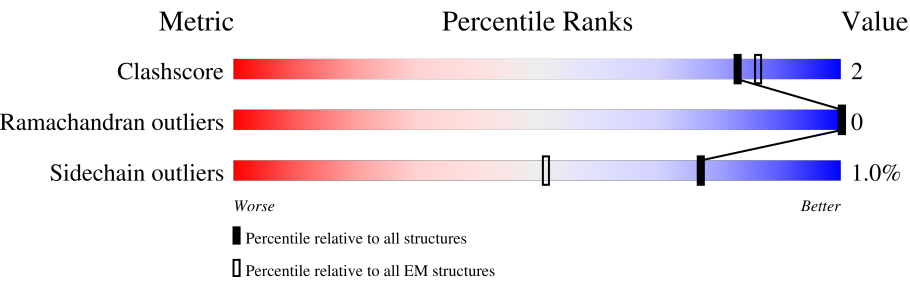
EMDB validation analysis	:	0.0.1.dev92
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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.






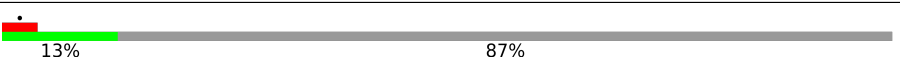
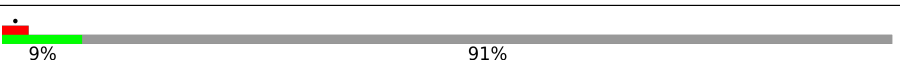

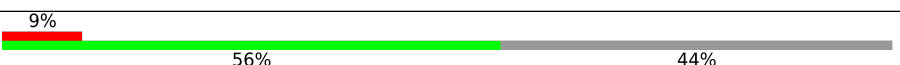

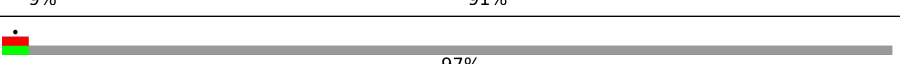
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	376	<div><div>6%</div><div>95%</div><div>5%</div><div>• •</div></div>
1	B	376	<div><div>•</div><div>93%</div><div>5%</div><div>•</div></div>
1	C	376	<div><div>•</div><div>95%</div><div>• •</div></div>
1	D	376	<div><div>•</div><div>93%</div><div>5%</div><div>•</div></div>
1	E	376	<div><div>•</div><div>93%</div><div>6%</div><div>•</div></div>
1	F	376	<div><div>10%</div><div>71%</div><div>26%</div><div>•</div></div>
2	K	286	<div><div>20%</div><div>88%</div><div>9%</div><div>•</div></div>
3	L	272	<div><div>9%</div><div>90%</div><div>9%</div><div>•</div></div>

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Mol	Chain	Length	Quality of chain
4	X	577	
4	x	577	
5	f	4646	
5	m	4646	
5	n	4646	
6	h	638	
6	o	638	
7	j	492	
7	r	492	

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 43425 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 ARP1 actin related protein 1 homolog A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	370	Total	C	N	O	S	0	0
			2944	1886	509	539	10		
1	B	370	Total	C	N	O	S	0	0
			2956	1892	509	545	10		
1	C	375	Total	C	N	O	S	0	0
			2998	1918	514	556	10		
1	D	370	Total	C	N	O	S	0	0
			2956	1892	509	545	10		
1	E	370	Total	C	N	O	S	0	0
			2944	1886	509	539	10		
1	F	279	Total	C	N	O	S	0	0
			2223	1429	385	400	9		

- Molecule 2 is a protein called Capping protein (Actin filament) muscle Z-line, alpha 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	K	278	Total	C	N	O	S	0	0
			2264	1428	396	434	6		

- Molecule 3 is a protein called F-actin capping protein beta subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L	269	Total	C	N	O	S	0	0
			2122	1323	370	418	11		

- Molecule 4 is a protein called BICD family-like cargo adapter 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	X	93	Total	C	N	O	S	0	0
			797	488	153	154	2		
4	x	93	Total	C	N	O	S	0	0
			797	488	153	154	2		

- Molecule 5 is a protein called Cytoplasmic dynein 1 heavy chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	f	720	Total	C	N	O	S	0	0
			5943	3766	1074	1083	20		
5	m	602	Total	C	N	O	S	0	0
			4963	3148	900	900	15		
5	n	409	Total	C	N	O	S	0	0
			3387	2137	623	616	11		

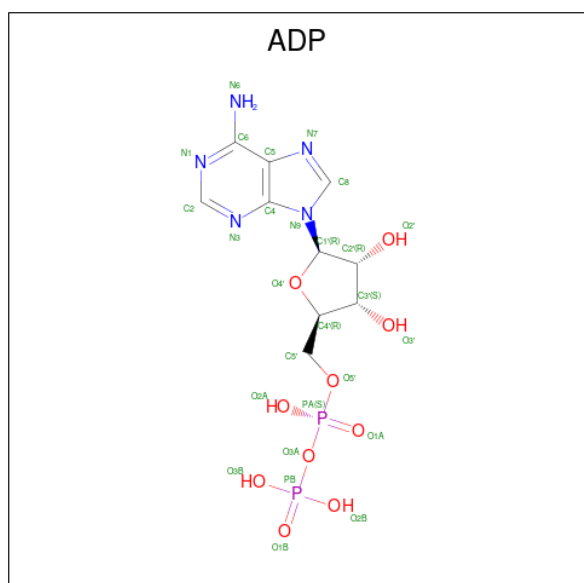
- Molecule 6 is a protein called Cytoplasmic dynein 1 intermediate chain 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	h	358	Total	C	N	O	S	0	0
			2808	1771	490	532	15		
6	o	358	Total	C	N	O	S	0	0
			2808	1771	490	532	15		

- Molecule 7 is a protein called Cytoplasmic dynein 1 light intermediate chain 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	j	44	Total	C	N	O	S	0	0
			291	176	53	61	1		
7	r	14	Total	C	N	O		0	0
			56	28	14	14			

- Molecule 8 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					AltConf
8	A	1	Total	C	N	O	P	0
			27	10	5	10	2	
8	B	1	Total	C	N	O	P	0
			27	10	5	10	2	
8	C	1	Total	C	N	O	P	0
			27	10	5	10	2	
8	D	1	Total	C	N	O	P	0
			27	10	5	10	2	
8	E	1	Total	C	N	O	P	0
			27	10	5	10	2	
8	F	1	Total	C	N	O	P	0
			27	10	5	10	2	

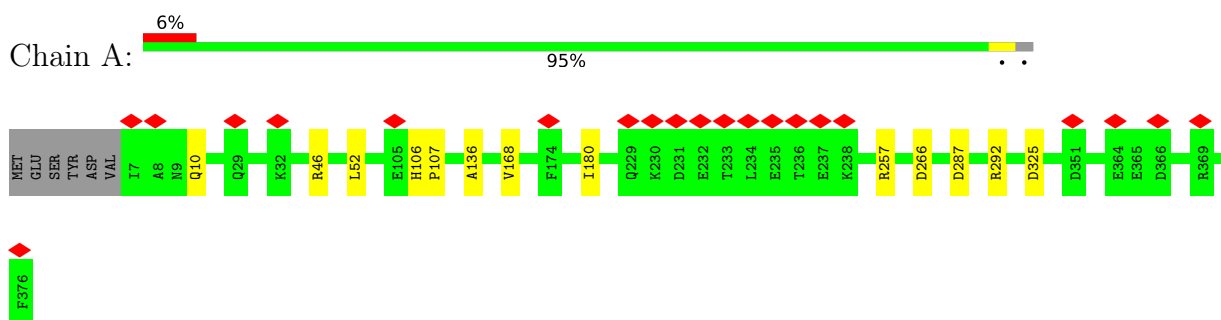
- Molecule 9 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
9	A	1	Total	Mg	0
			1	1	
9	B	1	Total	Mg	0
			1	1	
9	C	1	Total	Mg	0
			1	1	
9	D	1	Total	Mg	0
			1	1	
9	E	1	Total	Mg	0
			1	1	
9	F	1	Total	Mg	0
			1	1	

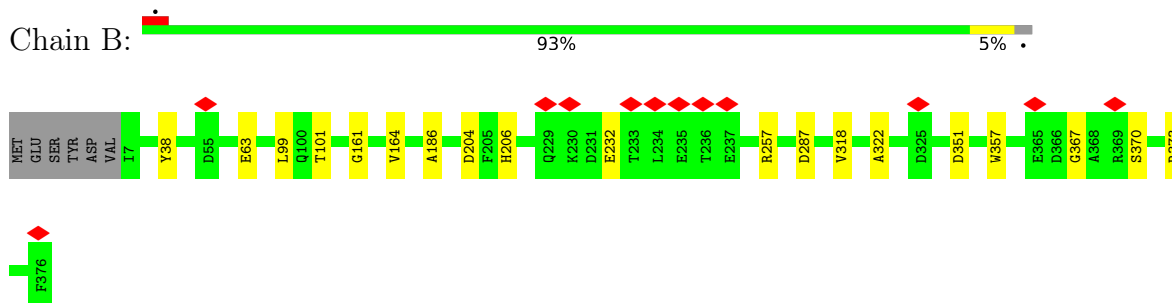
3 Residue-property plots

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.

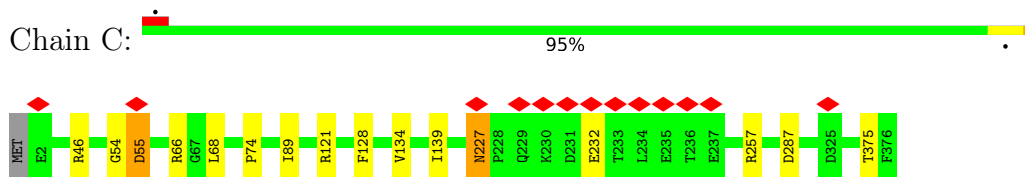
- Molecule 1: ARP1 actin related protein 1 homolog A



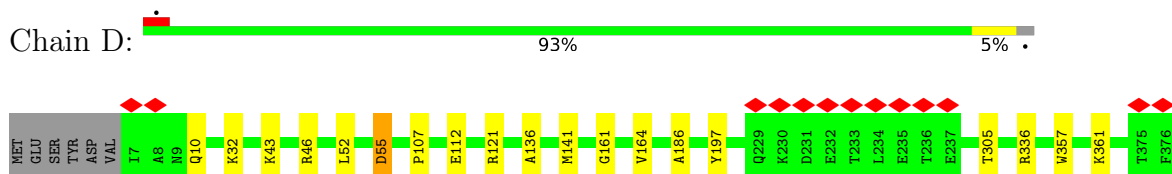
- Molecule 1: ARP1 actin related protein 1 homolog A



- Molecule 1: ARP1 actin related protein 1 homolog A

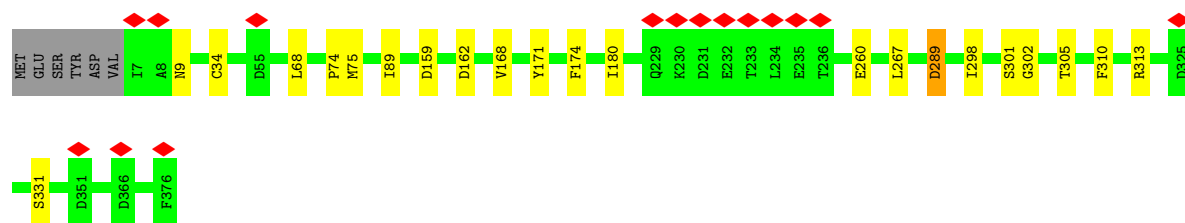


- Molecule 1: ARP1 actin related protein 1 homolog A



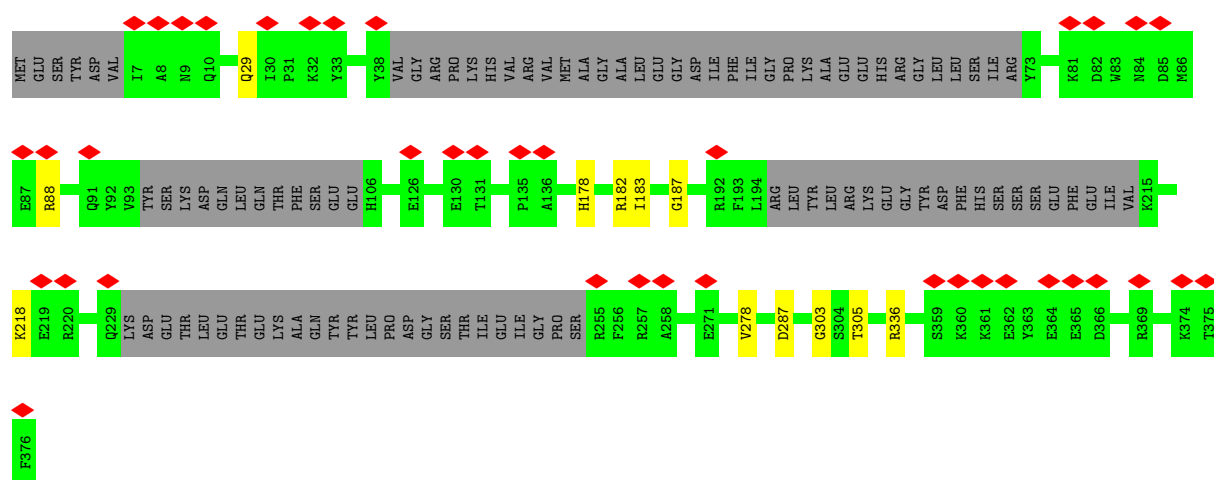
- Molecule 1: ARP1 actin related protein 1 homolog A

Chain E:  93% 6%




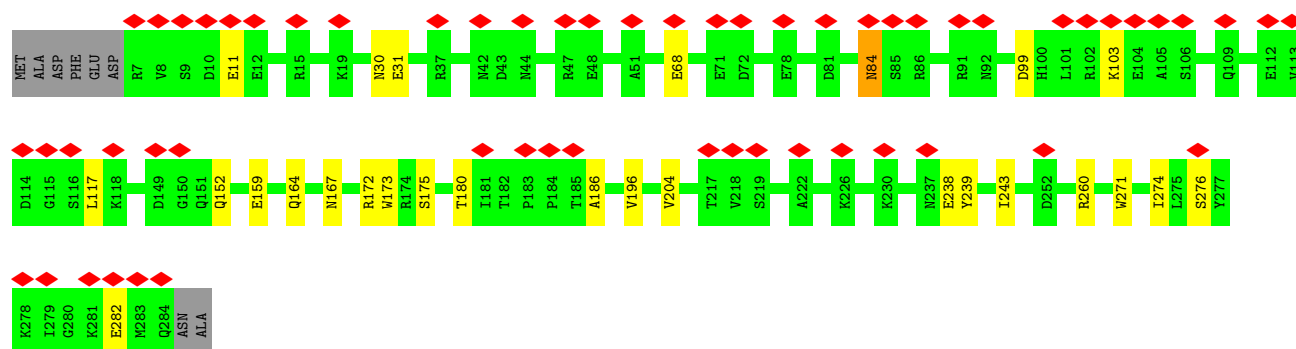
- Molecule 1: ARP1 actin related protein 1 homolog A

Chain F:  10% 71% 26%




- Molecule 2: Capping protein (Actin filament) muscle Z-line, alpha 1

Chain K:  20% 88% 9%



- Molecule 3: F-actin capping protein beta subunit

Chain L:  9% 90% 9%







[illegible]

- Molecule 5: Cytoplasmic dynein 1 heavy chain 1

Chain m: 13% 87%

+	R704	+	K394	+	SER	VAL	THR	ARG	ALA	SER
+	E520	+	K400	+	VAL	GLU	PRO	THR	LEU	SER
+	E532	+	H403	+	LYS	LYS	ILE	MET	GLN	PRO
+	D534	+	E407	+	ALA	GLU	ASP	ARG	GLY	GLY
+	G535	+	D436	+	LEU	LEU	PRO	PHE	LYS	GLY
+	L536	+	K441	+	GLU	GLU	VAL	SER	ASP	GLY
+	S539	+	R442	+	MET	GLY	SER	PRO	GLY	ASP
+	K540	+	R443	+	LEU	LEU	SER	GLN	GLN	SER
+	E541	+	E443	+	LEU	LEU	GLN	VAL	ALA	GLY
+	E544	+	E444	+	GLN	GLN	ARG	THR	LEU	GLY
+	A545	+	N445	+	LEU	VAL	VAL	VAL	GLU	GLU
+	R552	+	L446	+	ASN	GLN	THR	VAL	LEU	VAL
+	E555	+	K447	+	ILE	ILE	SER	LEU	GLU	SER
+	R559	+	M448	+	GLU	GLU	SER	ARG	ALA	VAL
+	D570	+	R451	+	PRO	PRO	ASP	THR	ASN	ASN
+	G573	+	T452	+	ILE	ILE	PRO	LEU	VAL	ALA
+	T574	+	N453	+	SER	SER	TYR	GLU	ASP	ASP
+	A575	+	R482	+	PRO	PRO	THR	VAL	SER	VAL
+	R583	+	R485	+	ILE	ILE	LEU	GLY	VAL	VAL
+	K734	+	PRO	+	H210	HIS	HIS	ASP	ASP	LEU
+	L735	+	GLN	+	A217	SER	PHE	GLY	GLU	GLN
+	K736	+	VAL	+	K218	ILE	ILE	GLU	GLY	LYS
+	V737	+	ALA	+	Y221	ASN	ALA	LYS	GLU	ARG
+	N738	+	VAL	+	E222	VAL	VAL	GLU	LEU	LYS
+	F739	+	ALA	+	R223	PRO	ALA	ILE	VAL	LEU
+	L740	+	GLN	+	G224	PHE	PHE	TYR	THR	LEU
+	F741	+	ASN	+	E225	ASN	ASN	LYS	ASN	LEU
+	E742	+	GLY	+	G233	SER	SER	ILE	ILE	GLU
+	I743	+	GLU	+	D234	TYR	TYR	ASN	ASN	ASP
+	S747	+	VAL	+	D263	ILE	ILE	ILE	ILE	GLY
+	K754	+	PRO	+	R264	ARG	ARG	ASP	ASP	GLY
+	R759	+	GLU	+	D265	GLU	GLU	ILE	ILE	ALA
+	V760	+	GLN	+	D266	SER	SER	TYR	TYR	PRO
+	P761	+	ASP	+	A267	LYS	LYS	GLY	GLY	ALA
+	L762	+	MET	+	D319	ALA	ASP	VAL	VAL	ALA
+	R759	+	LYS	+	E327	LYS	ASP	ASP	ASN	LEU
+	V760	+	VAL	+	N342	ASP	ARG	ARG	SER	GLU
+	P761	+	ALA	+	D343	GLU	ASP	ASP	ASN	ALA
+	L762	+	GLU	+	D351	GLY	GLY	GLY	SER	LEU
+	A768	+	VAL	+	D387	ASP	ASP	ASP	LEU	GLU
+	H769	+	PHE	+	D513	LYS	LYS	MET	PHE	GLU
+	Q770	+	D685	+	A514	ALA	ALA	ALA	ILE	LYS
+	A771	+	G686	+	A515	ALA	ALA	ALA	ILE	SER
+	N772	+	D687	+	D516	ALA	ALA	ALA	ILE	SER
+	Q773	+	R690	+	A517	ALA	ALA	ALA	ILE	SER
+	F777	+	H691	+	N518	ALA	ALA	ALA	ILE	SER
+	A778	+	F699	+	A519	ALA	ALA	ALA	ILE	SER
+	I779	+	D700	+						
+	F750	+	D701	+						

L781	L782	E783	S784	V785	R786	T787	Y788	E789	R790	T791	C792	E793	K794	V795	E796	E797	R798	N799	T800	I801	S802	L803	L804	V805	A806	G807	L808	K809	K810	E811	V812	Q813	A814	L815	I816	A817	E818	G819	I820	A821	L822	V823	E824	S825	Y827	K828	L829	D830	V833	Q834	R835	L836	A837	E838	T839	V840	F841
N842	F843	Q844	E845	K846	V847	D848	D849	L850	L851	ILE	ILE	GLU	GLU	LYS	ILE	ASP	GLY	VAL	ARG	SER	LEU	GLY	THR	GLN	CYS	ALA	GLY	THR	GLY	VAL	GLN	ASP	ASN	ARG	PRO	GLN	VAL	SER	GLY	PRO	GLY	GLY	LEU	ASN	GLY	THR	GLY	THR	VAL	ASN							
LYS	LEU	ASP	ILE	THR	ASP	ILE	THR	GLY	VAL	PRO	ILE	GLN	ALA	GLY	ASP	THR	GLY	VAL	GLY	LEU	LEU	THR	GLN	CYS	ALA	GLY	ASP	GLY	GLU	ILE	ILE	ASP	ASN	ARG	PRO	VAL	GLN	LYS	ALA	VAL	VAL	ASP	ASP	GLY	LEU	ASN	GLY	THR	GLY	THR	ASN						
LEU	ARG	ILE	THR	ASN	VAL	ILE	THR	LEU	ASN	PRO	ILE	GLU	ALA	GLY	THR	GLY	VAL	GLN	VAL	PHE	LEU	GLY	ALA	VAL	VAL	VAL	LEU	SER	GLY	VAL	GLN	SER	GLN	TRP	TYR	GLN	VAL	GLY	HIS	GLY	VAL	VAL	ASP	GLY	LEU	THR	GLY	GLY	THR	ASN							
ALA	LEU	THR	MET	PRO	ASP	GLY	VAL	ALA	LEU	GLU	GLU	SER	TYR	VAL	MET	GLY	VAL	VAL	SER	GLY	VAL	VAL	VAL	LYS	TRP	THR	GLN	TYR	ALA	GLY	TRP	MET	ARG	PRO	VAL	GLN	VAL	SER	GLY	HIS	VAL	VAL	ASP	ILE	THR	GLY	THR	ASN									
LEU	VAL	GLN	ILE	ARG	LYS	ALA	THR	GLY	PHE	ASN	ASN	ALA	THR	LYS	GLY	PHE	GLY	PRO	VAL	VAL	ILE	ILE	GLN	VAL	GLN	SER	LYS	ASN	LEU	LYS	TYR	SER	HIS	GLY	VAL	GLY	GLU	LYS	VAL	GLN	GLY	GLN	GLY	GLN	THR	GLY	THR	GLY	ALA								
PHE	HIS	SER	GLN	ILE	SER	LYS	SER	GLY	LEU	GLN	HIS	SER	VAL	ASP	ALA	THR	ASP	GLY	ALA	ALA	VAL	THR	LYS	VAL	GLN	VAL	GLN	SER	LYS	ARG	ILE	LYS	ASP	TRP	PHE	GLY	VAL	VAL	GLY	VAL	GLY	GLN	GLY	GLY	GLY	THR	THR	THR	ARG								
PHE	GLN	PHE	PRO	PRO	SER	TRP	LEU	TYR	ASN	ILE	GLY	GLY	THR	ALA	PHE	ARG	LYS	ARG	GLY	THR	VAL	GLN	GLY	ASP	GLY	GLN	GLY	VAL	ASN	LEU	GLN	ALA	VAL	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	THR	THR	THR	TRP	TRP									
GLY	LYS	THR	LYS	VAL	THR	GLY	THR	LEU	PRO	GLY	GLY	ALA	THR	LEU	PHE	GLY	GLY	GLY	GLY	THR	GLY	ASP	LYS	ASP	GLY	GLY	GLY	VAL	ALA	LYS	ALA	ALA	LYS	ALA	LEU	GLY	GLY	LEU	LEU	SER	SER	GLY	GLY	GLY	VAL	VAL											
ALA	LEU	GLY	GLY	GLN	ASP	LYS	VAL	GLY	TRP	SER	GLY	LEU	SER	VAL	GLY	GLN	ASP	GLN	MET	LYS	PHE	GLY	THR	GLY	VAL	SER	VAL	GLN	PRO	LYS	LYS	ARG	LEU	HIS	VAL	TRP	VAL	VAL	SER	GLY	PRO	ARG	GLY	PRO	ALA	GLY	GLY	GLY	ALA								
SER	TYR	GLY	PHE	VAL	GLN	ARG	LEU	GLY	TYR	MET	LYS	ILE	MET	LEU	ILE	GLY	LEU	SER	GLY	ALA	ALA	LYS	GLY	VAL	SER	VAL	GLN	LEU	MET	LYS	ARG	LEU	HIS	VAL	TRP	VAL	VAL	SER	GLY	GLY	ILE	GLY	GLY	ILE	LYS												
ASN	GLY	ALA	ILE	LYS	ASP	VAL	LEU	VAL	ALA	GLY	GLY	GLY	MET	LEU	GLY	GLY	LYS	GLN	GLY	GLY	GLY	TRP	ASN	THR	GLY	VAL	LEU	VAL	VAL	ILE	TYR	ASN	LYS	VAL	ARG	LEU	ILE	ASP	PHE	GLY	ILE	THR	GLY	GLY	GLY	GLY	GLY	ILE									
ASN	SER	VAL	SER	MET	LYS	LEU	TYR	VAL	TYR	LYS	VAL	PHE	GLY	GLY	LEU	SER	GLY	GLY	ASP	ALA	LEU	LEU	LYS	VAL	ASN	PHE	VAL	TRP	ILE	ASP	VAL	GLN	ARG	GLY	VAL	ALA	ASP	LEU	GLY	GLN	GLY	THR	GLY	GLY	GLY	GLY	GLY	GLY	LEU								
PRO	VAL	GLY	THR	GLN	PHE	GLN	SER	ILE	PRO	GLY	THR	ALA	ALA	MET	LYS	VAL	LYS	SER	ASP	LYS	LEU	VAL	VAL	VAL	ASP	ASN	GLY	VAL	VAL	PRO	ARG	GLY	GLY	ARG	VAL	ALA	ASP	LEU	GLY	GLN	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	ARG							
GLY	ARG	SER	PHE	PRO	ARG	PHE	THR	VAL	GLY	ASP	HIS	PRO	VAL	ILE	GLY	THR	GLY	ASN	VAL	VAL	VAL	GLY	GLY	LYS	ALA	PHE	PHE	ALA	ALA	GLY	VAL	VAL	THR	ILE	LEU	ASN	VAL	PHE	ASN	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	GLY									
GLY	VAL	MET	PHE	LYS	THR	PRO	SER	ILE	LEU	HIS	PRO	LYS	ILE	GLY	TRP	THR	THR	ASN	VAL	THR	LEU	THR	VAL	GLY	LYS	ALA	GLY	PRO	LEU	HIS	GLY	VAL	VAL	THR	ILE	LEU	ASN	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	TRP								
ILE	ASP	LYS	GLN	ALA	GLN	LEU	VAL	VAL	LEU	GLN	ILE	ILE	THR	SER	ASN	VAL	THR	GLY	ALA	GLY	SER	GLY	GLY	GLY	GLY	GLY	GLY	PRO	LEU	HIS	GLY	VAL	VAL	ASN	VAL	GLY	THR	VAL	LEU	LEU	VAL	VAL	VAL	VAL	VAL	VAL	VAL	PRO									
PRO	LEU	ARG	ARG	LYS	LEU	GLY	HIS	ILE	THR	LEU	VAL	VAL	GLN	ARG	VAL	THR	SER	ILE	ILE	LYS	LYS	SER	GLY	GLY	GLY	GLY	GLY	GLY	TRP	LEU	SER	GLN	MET	GLY	PRO	TYR	PHE	ASP	VAL	VAL	VAL	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY					
ALA	ASN	ALA	LYS	ASN	TYR	GLY	VAL	GLY	GLY	VAL	GLN	GLN	LYS	VAL	GLN	CYS	TYR	THR	THR	GLN	THR	GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	ARG	LEU	GLY	GLY	PRO	PHE	GLY	GLY	LYS	THR	THR	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	HIS						
GLN	LEU	ARG	PHE	VAL	LEU	VAL	CYS	ASP	GLY	THR	PHE	ASP	PHE	ALA	MET	GLY	ILE	VAL	VAL	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	ASP	GLY	PHE	ASN	ASN	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA					





VAL	GLY	LYS	LYS	THR
ASP	LEU	GLU	LEU	THR
PHE	LYS	GLU	LYS	THR
GLU	LEU	ASN	ASN	ASN
ILE	GLN	ASN	ILE	TRP
ALA	GLY	ILE	LEU	LEU
THR	ALA	HIS	VAL	HIS
LYS	THR	VAL	VAL	ARG
GLU	CYS	CYS	LEU	LEU
ASP	ASN	LEU	CYS	THR
PRO	ASN	GLY	LEU	ILE
ARG	ASN	GLY	ASN	GLN
SER	LYS	LEU	GLU	THR
PHE	LEU	PHE	LEU	LEU
TYR	SER	VAL	VAL	SER
GLU	LEU	PRO	GLY	HIS
ARG	SER	GLU	GLY	LYS
GLY	ASN	ALA	ILE	LYS
VAL	ALA	TYR	ALA	ARG
ALA	ILE	ILE	THR	VAL
VAL	SER	THR	ALA	GLU
LEU	THR	ALA	THR	ASN
CYS	ALA	ARG	ARG	ILE
THR	LEU	GLN	GLN	LYS
GLU	PRO	GLN	THR	LYS
	LEU	TYR	TYR	ASP
	THR	VAL	THR	PRO
	GLN	ALA	VAL	PHE
	LEU	GLN	PRO	PHE
	ARG	ALA	ALA	ARG
	TRP	ASN	GLY	ARG
	VAL	SER	MET	PHE
	LYS	TRP	THR	GLU
	GLN	SER	VAL	ARG
	THR	LEU	ILE	GLU
	ASN	GLU	GLN	VAL
	THR	GLU	TRP	LYS
	GLU	LEU	VAL	GLY
	LYS	CYS	SER	GLY
	LYS	LEU	ASP	ALA
	ALA	GLU	PHE	LYS
	SER	VAL	SER	LEU
	VAL	ASN	GLU	LEU
	VAL	VAL	ARG	GLN
	THR	THR	ILE	ASP
	LEU	SER	GLN	ARG
	VAL	GLN	LEU	GLN
	TYR	GLY	GLN	ASP
	LEU	ALA	ASN	LEU
	ASN	THR	ILE	ALA
	PHE	LEU	SER	ASP
	THR	ASP	LEU	VAL
	ARG	ALA	ALA	VAL
	ALA	CYS	ALA	GLN
	ASP	SER	ALA	VAL
	LEU	PHE	SER	CYS
	ILE	GLY	GLY	GLY
	PHE	VAL	ALA	LYS
	THR	THR	THR	ALA

- Molecule 5: Cytoplasmic dynein 1 heavy chain 1

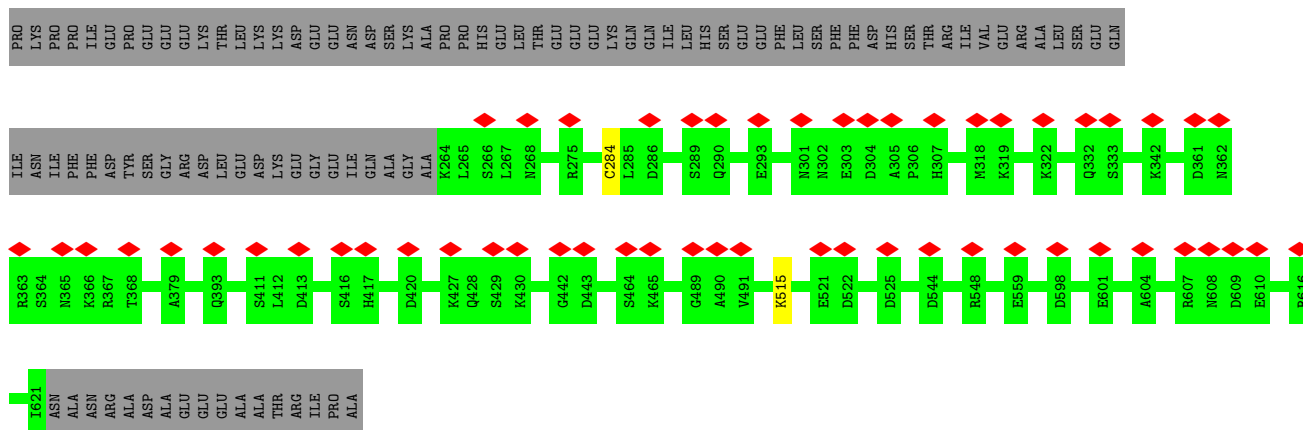
Chain n: 9% 91%

[illegible]

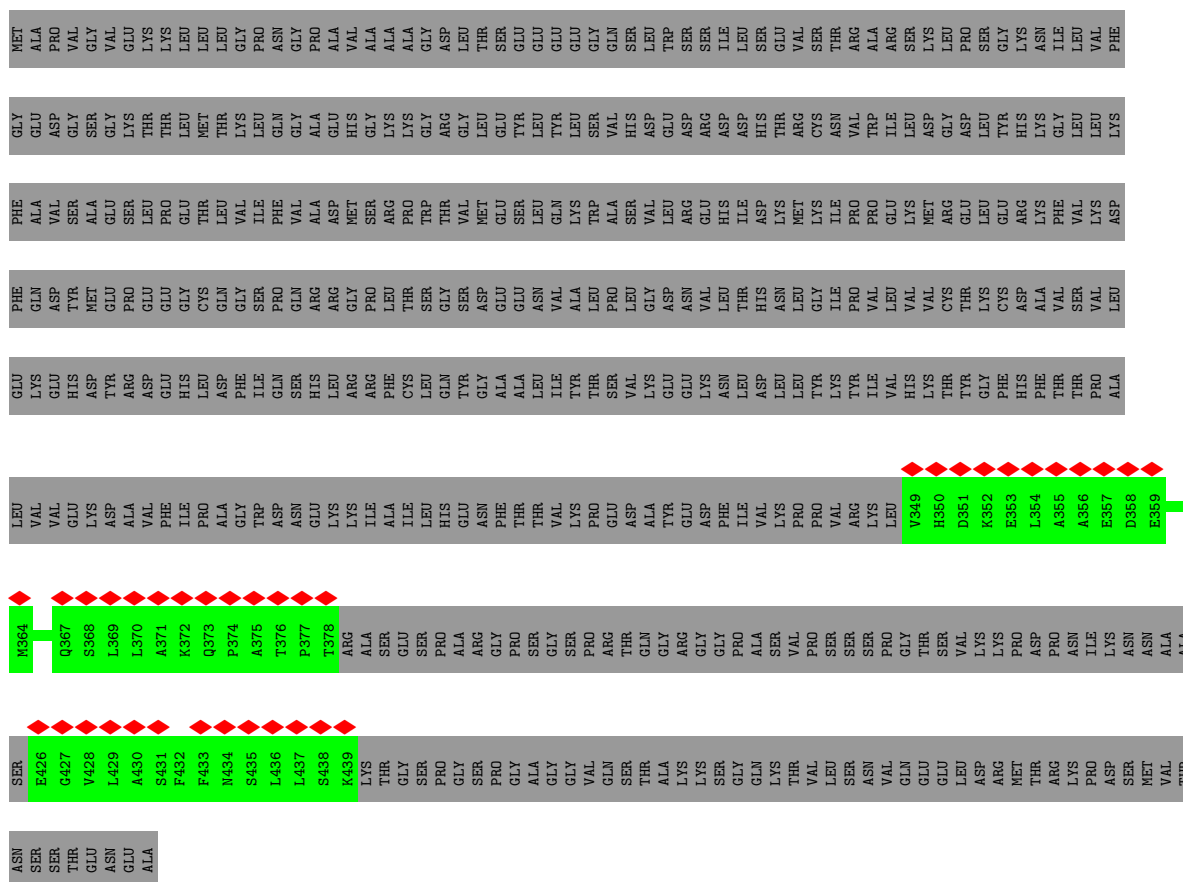




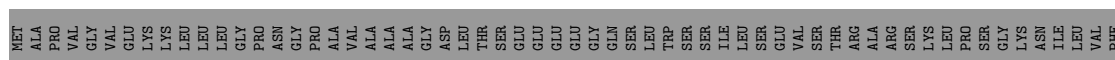




- Molecule 7: Cytoplasmic dynein 1 light intermediate chain 2



- Molecule 7: Cytoplasmic dynein 1 light intermediate chain 2



[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	179660	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 ($e^-/\text{\AA}^2$)	53	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.160	Depositor
Minimum map value	-0.076	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0244	Depositor
Map size (Å)	955.776, 955.776, 955.776	wwPDB
Map dimensions	768, 768, 768	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.2445, 1.2445, 1.2445	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: MG, ADP

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	0.27	0/3013	0.56	0/4070
1	B	0.29	0/3025	0.57	0/4085
1	C	0.28	0/3068	0.57	0/4144
1	D	0.29	0/3025	0.58	0/4085
1	E	0.27	0/3013	0.58	0/4070
1	F	0.27	0/2272	0.58	0/3065
2	K	0.30	0/2316	0.58	0/3135
3	L	0.27	0/2156	0.56	0/2906
4	X	0.30	0/805	0.63	0/1072
4	x	0.29	0/805	0.64	0/1072
5	f	0.27	0/6045	0.58	0/8149
5	m	0.26	0/5048	0.57	0/6801
5	n	0.27	0/3442	0.60	0/4632
6	h	0.27	0/2887	0.54	0/3938
6	o	0.26	0/2887	0.54	0/3938
7	j	0.44	0/293	0.58	0/388
7	r	0.83	0/55	0.72	0/67
All	All	0.28	0/44155	0.58	0/59617

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	2944	0	2938	6	0
1	B	2956	0	2950	8	0
1	C	2998	0	2983	12	0
1	D	2956	0	2950	8	0
1	E	2944	0	2938	12	0
1	F	2223	0	2233	8	0
2	K	2264	0	2186	17	0
3	L	2122	0	2113	12	0
4	X	797	0	797	2	0
4	x	797	0	797	0	0
5	f	5943	0	6059	0	0
5	m	4963	0	5069	0	0
5	n	3387	0	3444	0	0
6	h	2808	0	2673	0	0
6	o	2808	0	2673	0	0
7	j	291	0	251	0	0
7	r	56	0	15	0	0
8	A	27	0	12	0	0
8	B	27	0	12	0	0
8	C	27	0	12	0	0
8	D	27	0	12	0	0
8	E	27	0	12	1	0
8	F	27	0	12	1	0
9	A	1	0	0	0	0
9	B	1	0	0	0	0
9	C	1	0	0	0	0
9	D	1	0	0	0	0
9	E	1	0	0	0	0
9	F	1	0	0	0	0
All	All	43425	0	43141	77	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 2.

The worst 5 of 77 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:K:84:ASN:O	2:K:84:ASN:ND2	2.18	0.77
1:B:232:GLU:OE1	1:B:257:ARG:NH2	2.24	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:287:ASP:OD2	2:K:260:ARG:NH2	2.24	0.70
3:L:163:ARG:O	3:L:203:VAL:N	2.25	0.70
1:A:46:ARG:NH2	1:A:52:LEU:O	2.25	0.69

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	368/376 (98%)	359 (98%)	9 (2%)	0	100	100
1	B	368/376 (98%)	359 (98%)	9 (2%)	0	100	100
1	C	373/376 (99%)	362 (97%)	11 (3%)	0	100	100
1	D	368/376 (98%)	358 (97%)	10 (3%)	0	100	100
1	E	368/376 (98%)	355 (96%)	13 (4%)	0	100	100
1	F	269/376 (72%)	263 (98%)	6 (2%)	0	100	100
2	K	276/286 (96%)	264 (96%)	12 (4%)	0	100	100
3	L	267/272 (98%)	260 (97%)	7 (3%)	0	100	100
4	X	91/577 (16%)	91 (100%)	0	0	100	100
4	x	91/577 (16%)	91 (100%)	0	0	100	100
5	f	714/4646 (15%)	700 (98%)	14 (2%)	0	100	100
5	m	596/4646 (13%)	591 (99%)	5 (1%)	0	100	100
5	n	403/4646 (9%)	394 (98%)	9 (2%)	0	100	100
6	h	356/638 (56%)	347 (98%)	9 (2%)	0	100	100
6	o	356/638 (56%)	347 (98%)	9 (2%)	0	100	100
7	j	40/492 (8%)	39 (98%)	1 (2%)	0	100	100
7	r	12/492 (2%)	12 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	5316/20166 (26%)	5192 (98%)	124 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	315/324 (97%)	313 (99%)	2 (1%)	86	91
1	B	318/324 (98%)	314 (99%)	4 (1%)	69	82
1	C	323/324 (100%)	320 (99%)	3 (1%)	78	87
1	D	318/324 (98%)	311 (98%)	7 (2%)	52	74
1	E	315/324 (97%)	310 (98%)	5 (2%)	62	79
1	F	239/324 (74%)	238 (100%)	1 (0%)	91	95
2	K	247/254 (97%)	244 (99%)	3 (1%)	71	83
3	L	238/241 (99%)	235 (99%)	3 (1%)	69	82
4	X	87/503 (17%)	86 (99%)	1 (1%)	73	85
4	x	87/503 (17%)	86 (99%)	1 (1%)	73	85
5	f	651/4125 (16%)	645 (99%)	6 (1%)	78	87
5	m	539/4125 (13%)	535 (99%)	4 (1%)	84	90
5	n	365/4125 (9%)	362 (99%)	3 (1%)	81	89
6	h	309/557 (56%)	306 (99%)	3 (1%)	76	86
6	o	309/557 (56%)	307 (99%)	2 (1%)	86	91
7	j	26/422 (6%)	26 (100%)	0	100	100
All	All	4686/17356 (27%)	4638 (99%)	48 (1%)	77	86

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	X	178	LYS

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Mol	Chain	Res	Type
6	h	275	ARG
5	f	215	ASN
5	f	338	ASP
6	h	437	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
2	K	84	ASN
2	K	167	ASN
3	L	209	HIS
5	m	311	HIS
5	m	769	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 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
8	ADP	C	800	9	24,29,29	0.90	1 (4%)	29,45,45	1.49	4 (13%)
8	ADP	A	800	9	24,29,29	0.91	1 (4%)	29,45,45	1.51	4 (13%)
8	ADP	D	800	9	24,29,29	0.91	1 (4%)	29,45,45	1.51	4 (13%)
8	ADP	E	800	9	24,29,29	0.91	1 (4%)	29,45,45	1.47	4 (13%)
8	ADP	F	800	9	24,29,29	0.93	1 (4%)	29,45,45	1.53	4 (13%)
8	ADP	B	800	9	24,29,29	0.90	1 (4%)	29,45,45	1.51	4 (13%)

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
8	ADP	C	800	9	-	3/12/32/32	0/3/3/3
8	ADP	A	800	9	-	0/12/32/32	0/3/3/3
8	ADP	D	800	9	-	3/12/32/32	0/3/3/3
8	ADP	E	800	9	-	3/12/32/32	0/3/3/3
8	ADP	F	800	9	-	3/12/32/32	0/3/3/3
8	ADP	B	800	9	-	0/12/32/32	0/3/3/3

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	F	800	ADP	C5-C4	2.33	1.47	1.40
8	A	800	ADP	C5-C4	2.30	1.47	1.40
8	E	800	ADP	C5-C4	2.29	1.47	1.40
8	C	800	ADP	C5-C4	2.29	1.47	1.40
8	B	800	ADP	C5-C4	2.28	1.47	1.40

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	F	800	ADP	PA-O3A-PB	-3.80	119.79	132.83
8	D	800	ADP	N3-C2-N1	-3.61	123.04	128.68
8	B	800	ADP	N3-C2-N1	-3.53	123.16	128.68
8	F	800	ADP	N3-C2-N1	-3.50	123.22	128.68
8	E	800	ADP	N3-C2-N1	-3.47	123.25	128.68

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

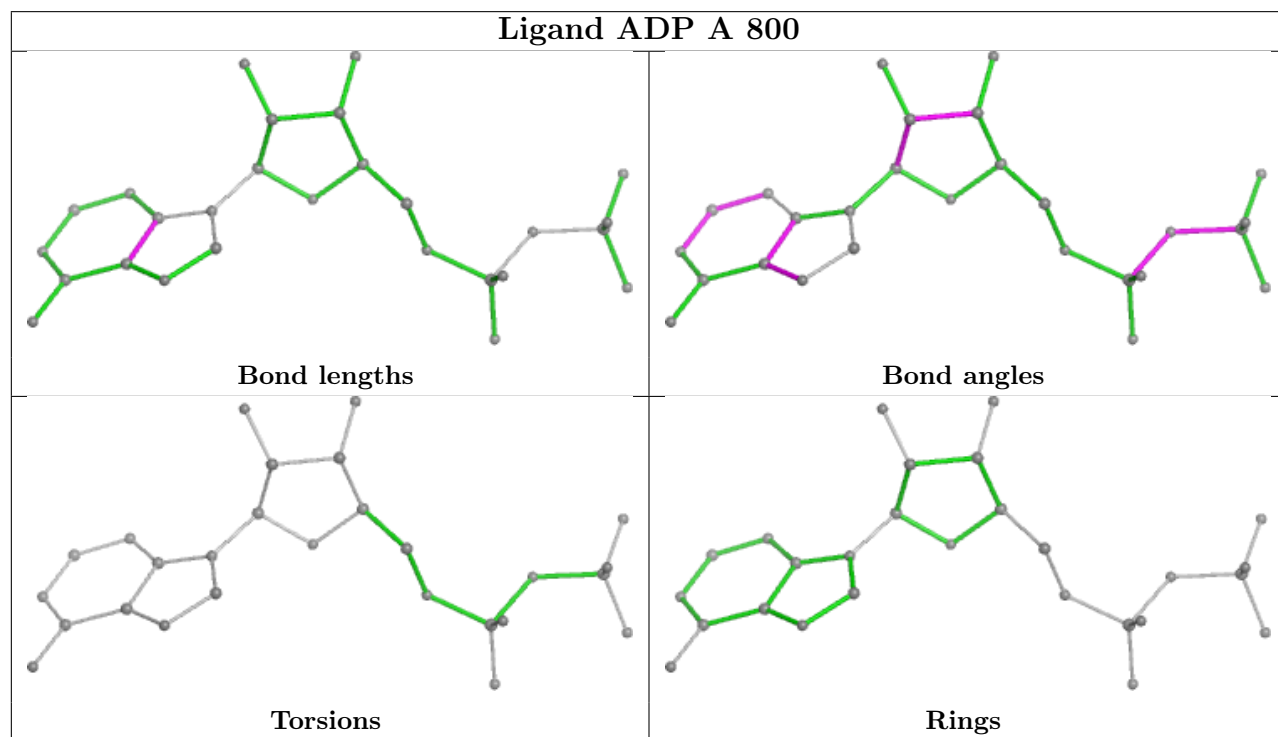
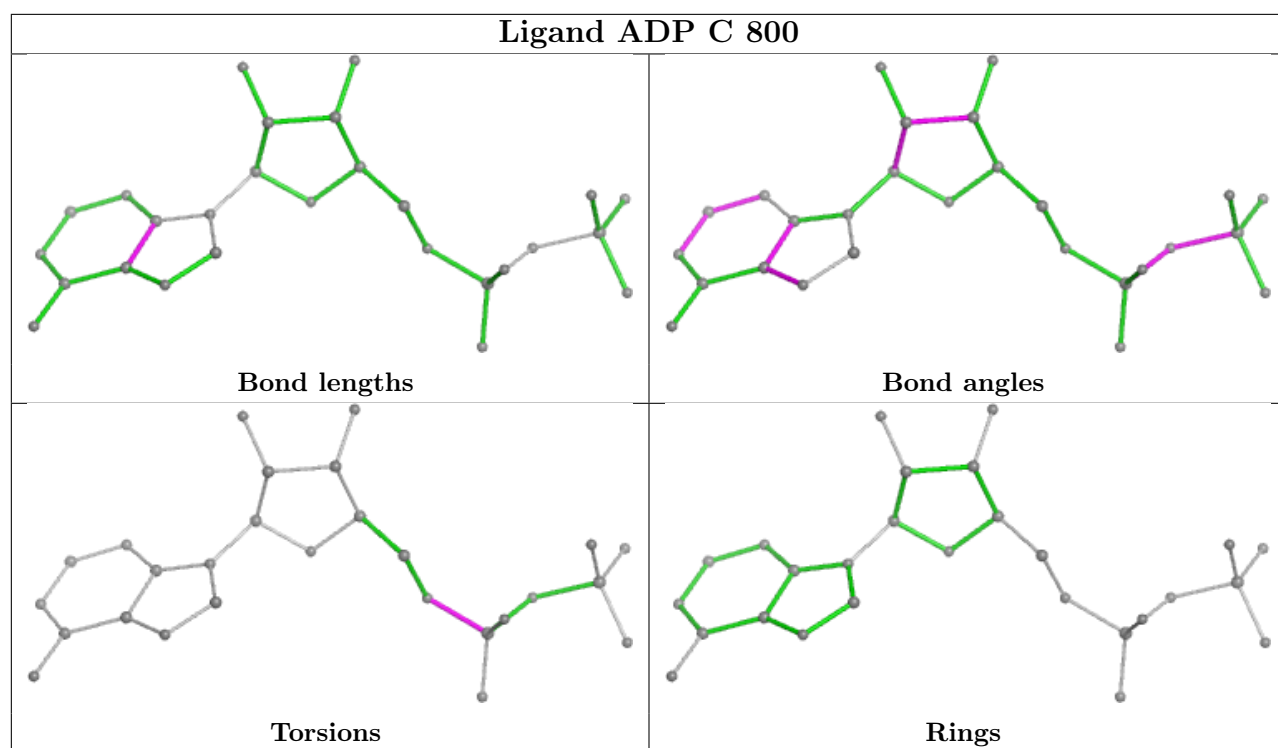
Mol	Chain	Res	Type	Atoms
8	C	800	ADP	C5'-O5'-PA-O1A
8	D	800	ADP	C5'-O5'-PA-O1A
8	E	800	ADP	C5'-O5'-PA-O1A
8	E	800	ADP	C5'-O5'-PA-O2A
8	F	800	ADP	C5'-O5'-PA-O1A

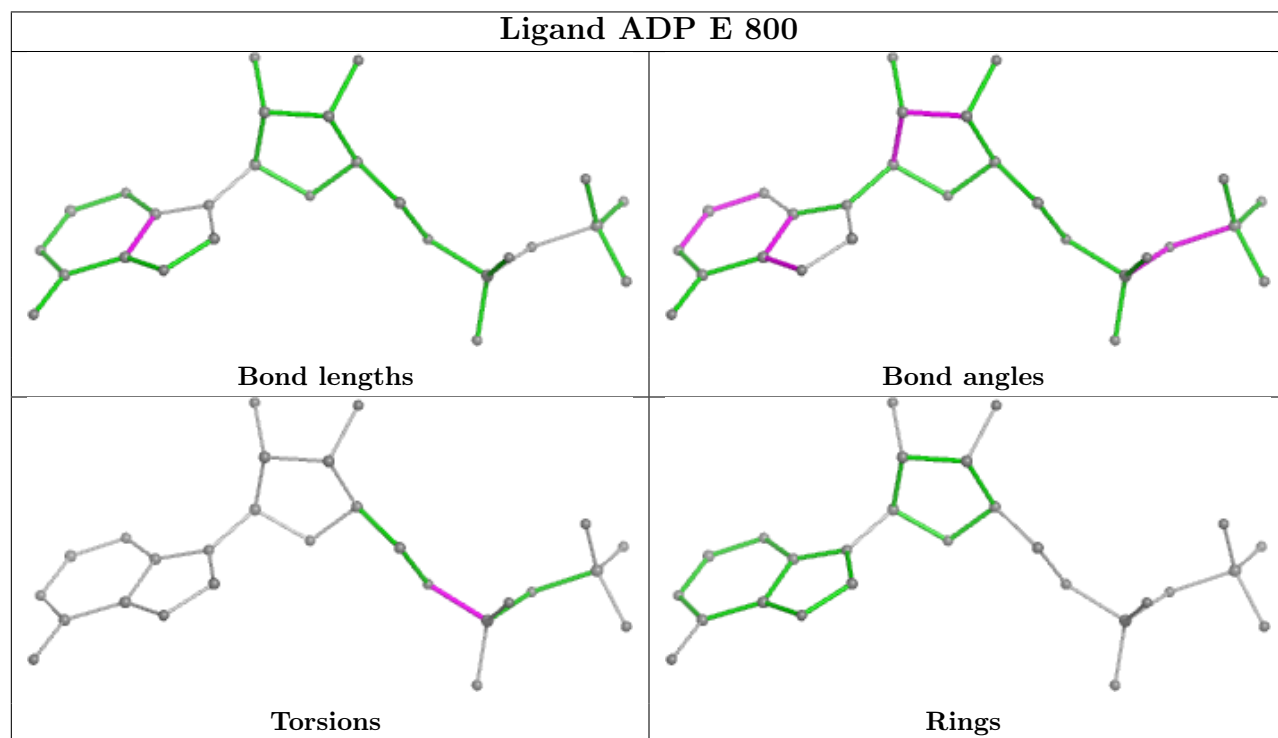
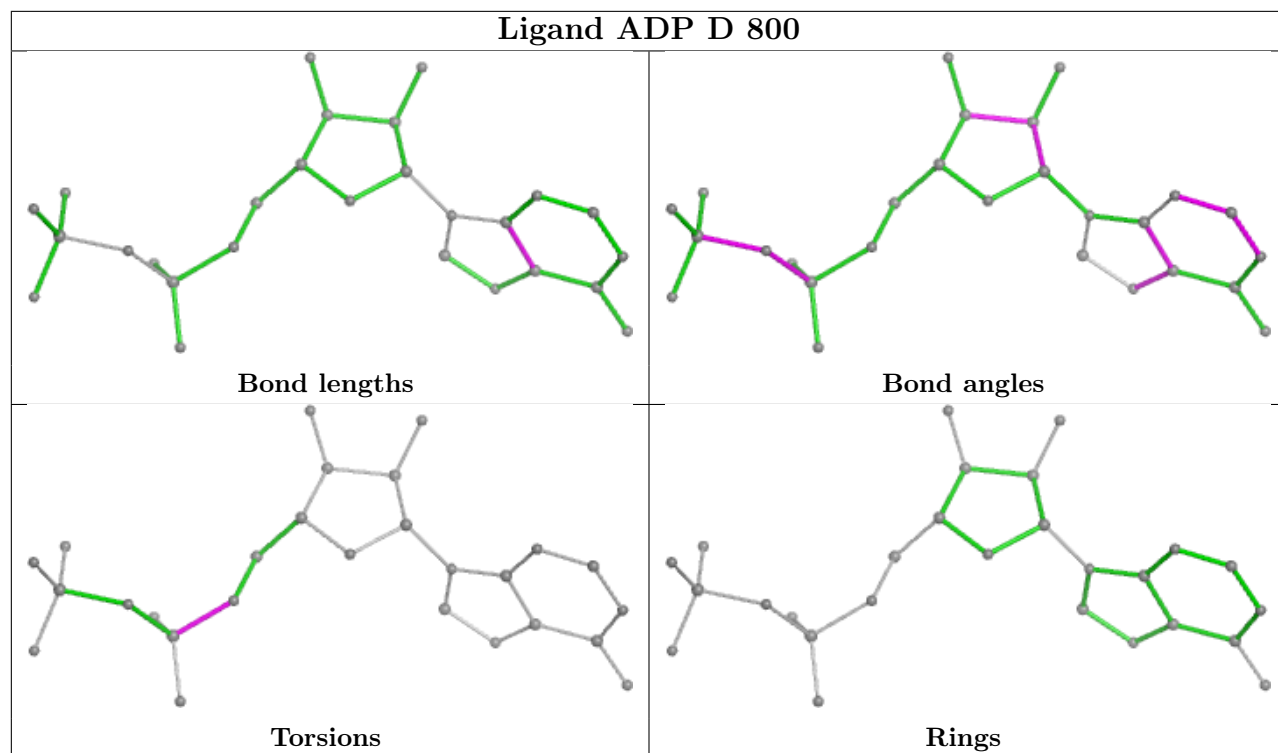
There are no ring outliers.

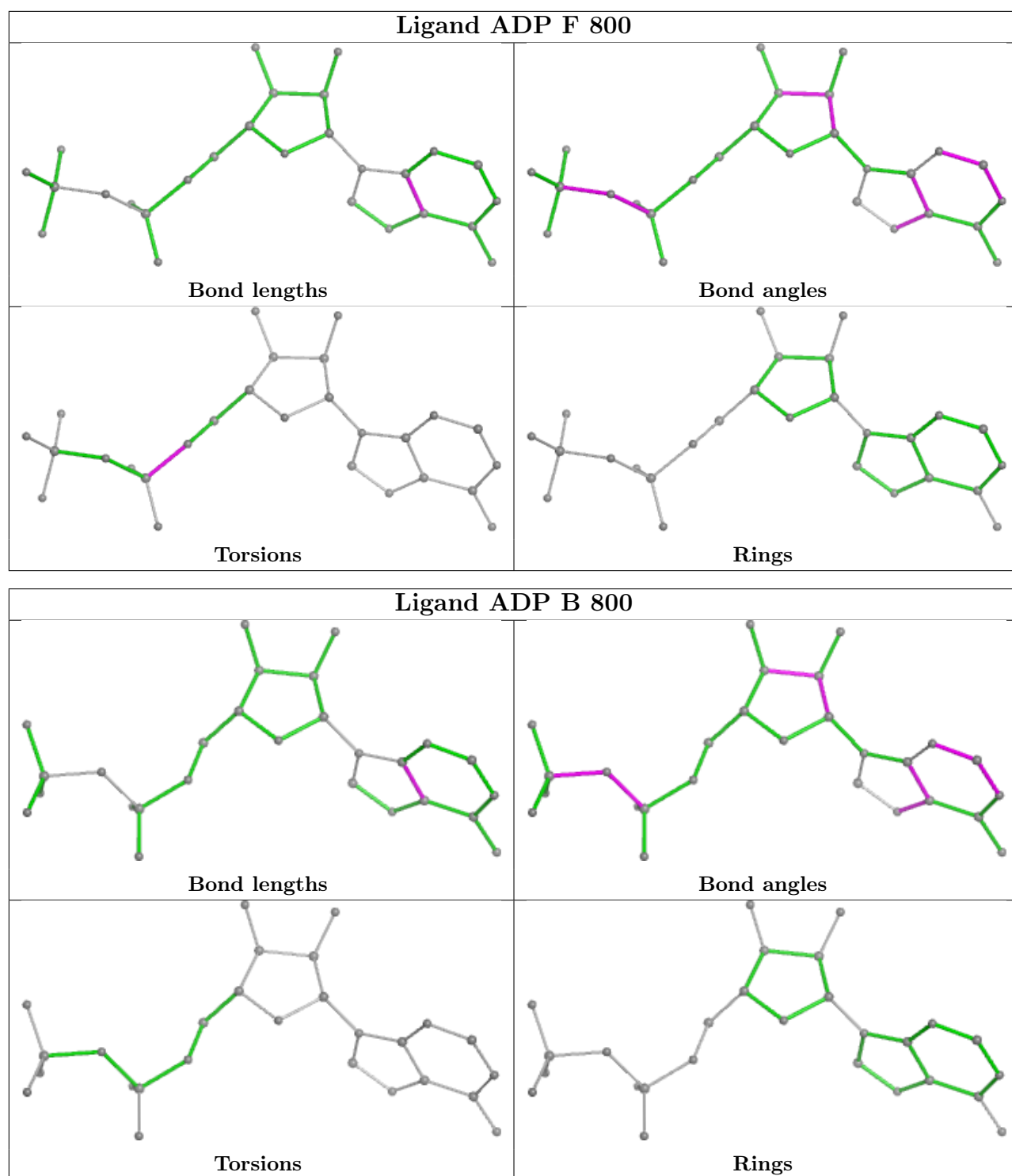
2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	E	800	ADP	1	0
8	F	800	ADP	1	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 ⓘ

There are no chain breaks in this entry.

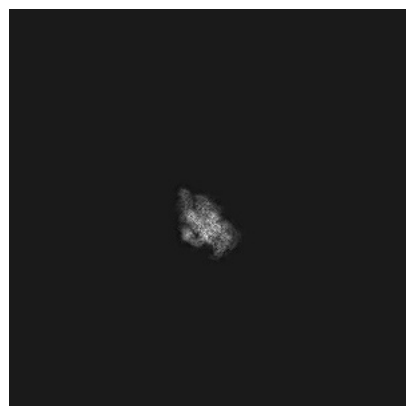
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14552. These allow visual inspection of the internal detail of the map and identification of artifacts.

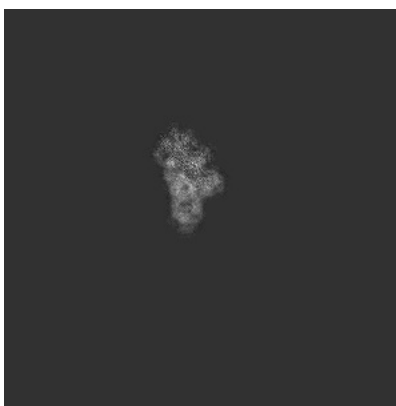
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X

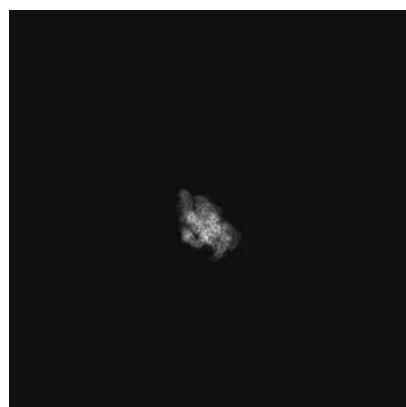


Y

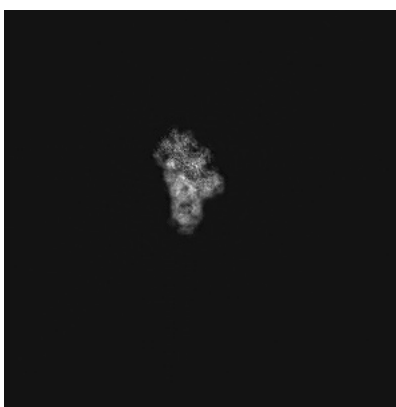


Z

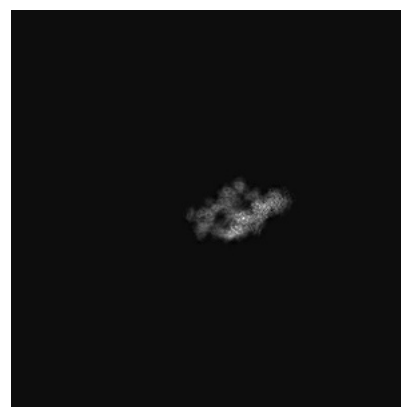
6.1.2 Raw map



X



Y

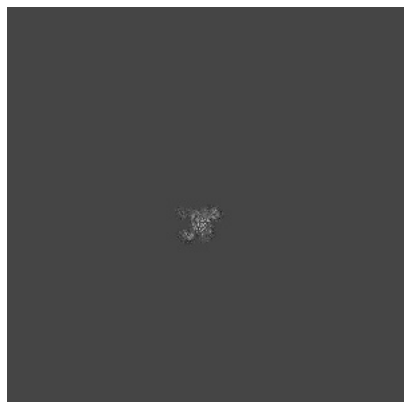


Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 384

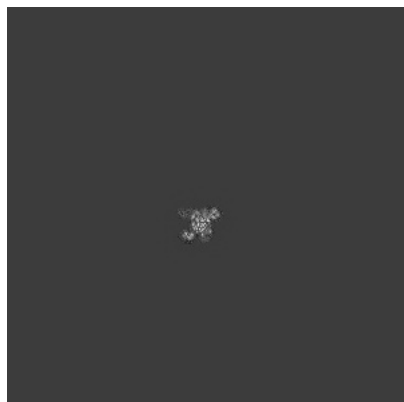


Y Index: 384

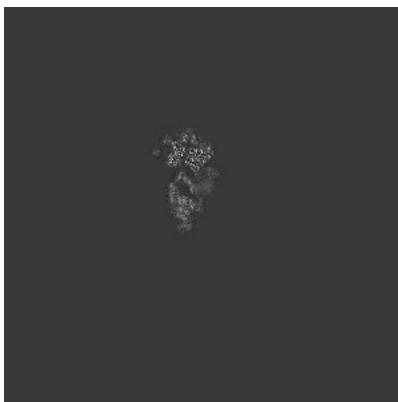


Z Index: 384

6.2.2 Raw map



X Index: 384



Y Index: 384

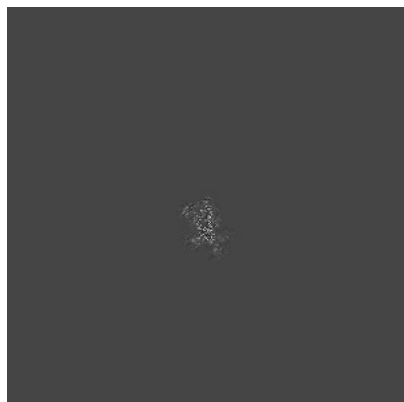


Z Index: 384

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: 478

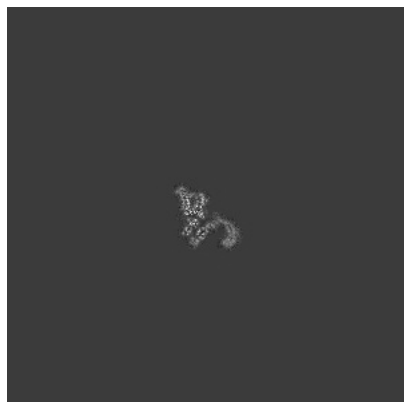


Y Index: 388



Z Index: 349

6.3.2 Raw map



X Index: 440



Y Index: 388

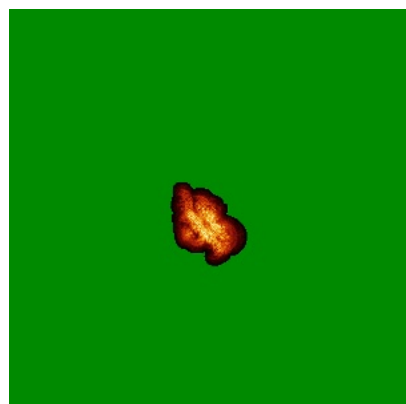


Z Index: 343

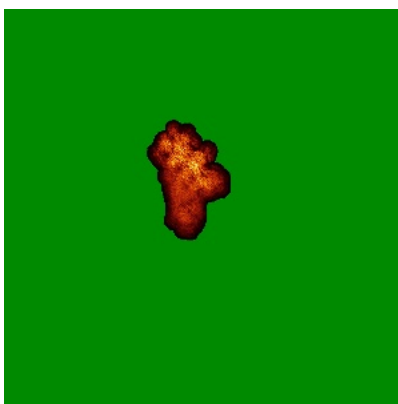
The images above show the largest variance slices of the map in three orthogonal directions.

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

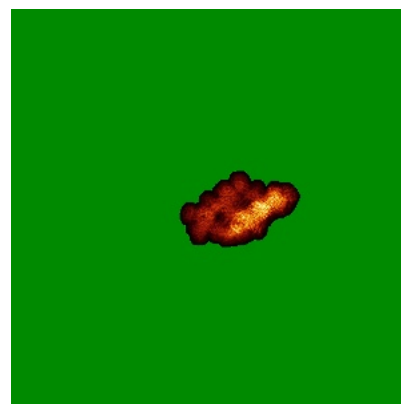
6.4.1 Primary map



X

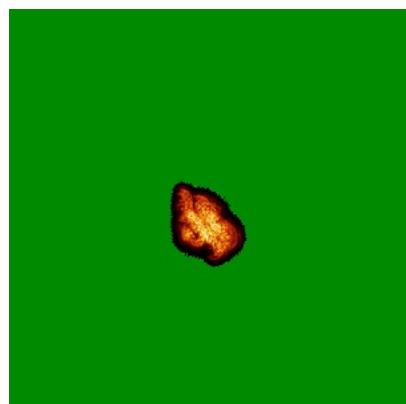


Y

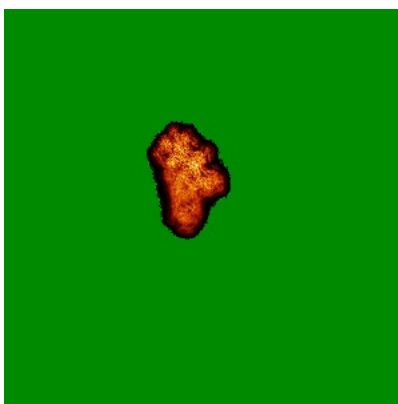


Z

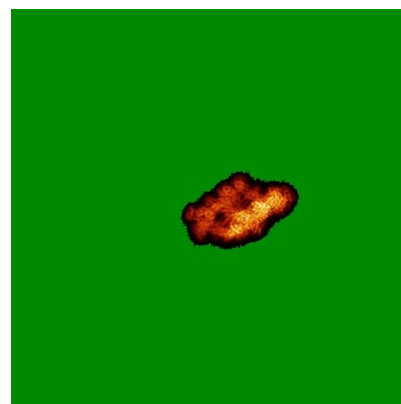
6.4.2 Raw map



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 0.0244. 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.

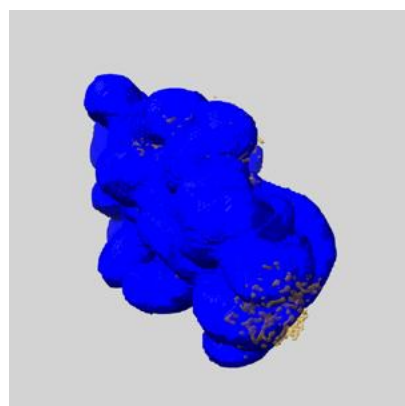
6.6 Mask visualisation [i](#)

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

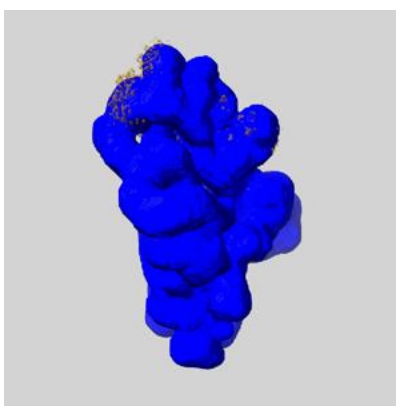
A mask typically either:

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

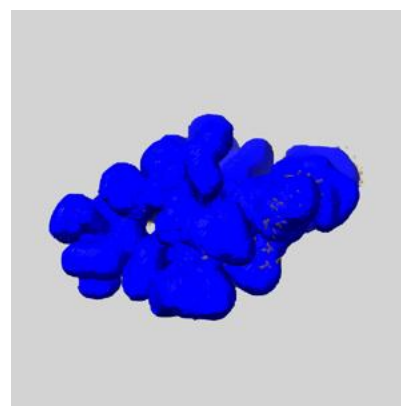
6.6.1 emd_14552_msk_1.map [i](#)



X



Y

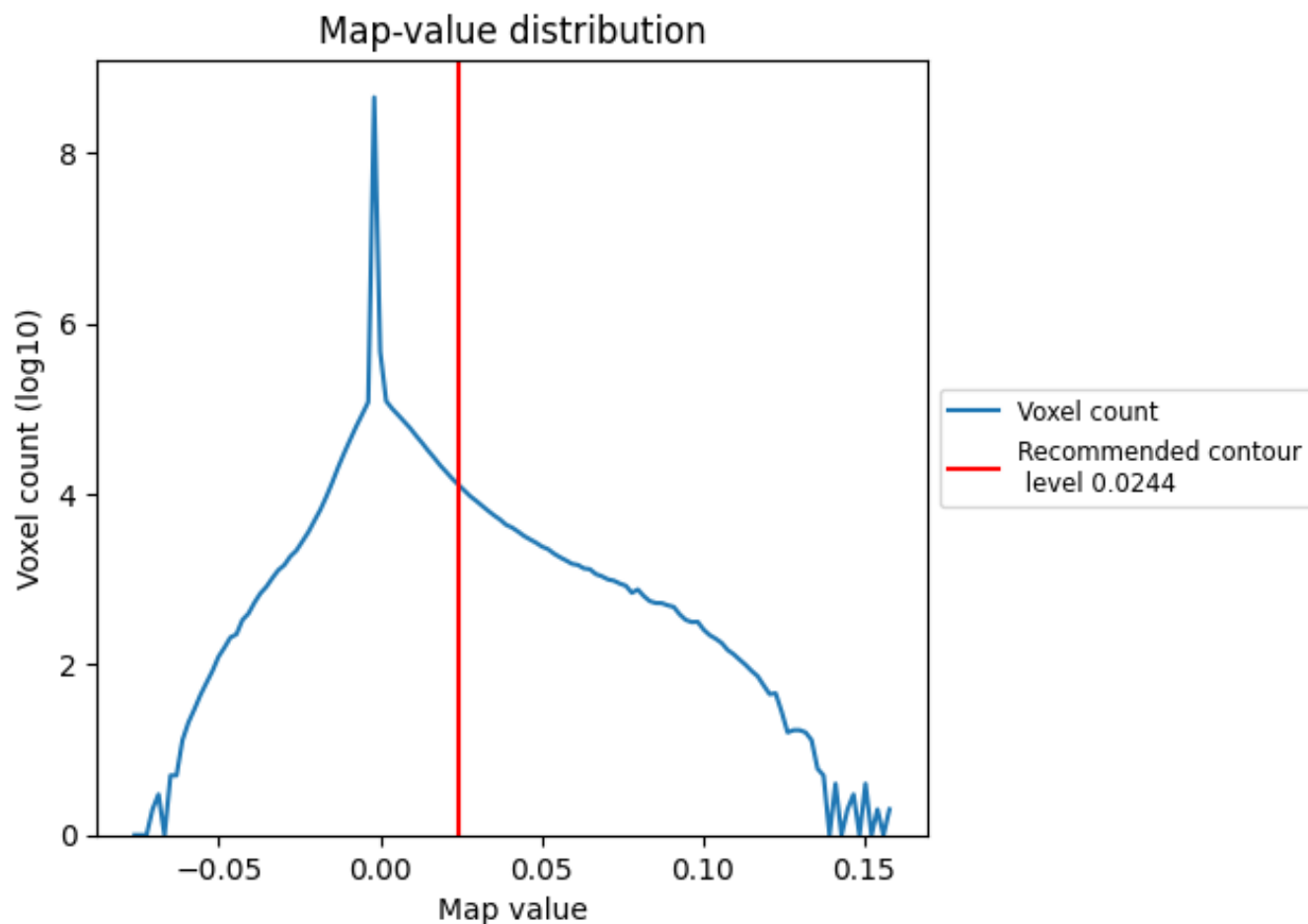


Z

7 Map analysis [i](#)

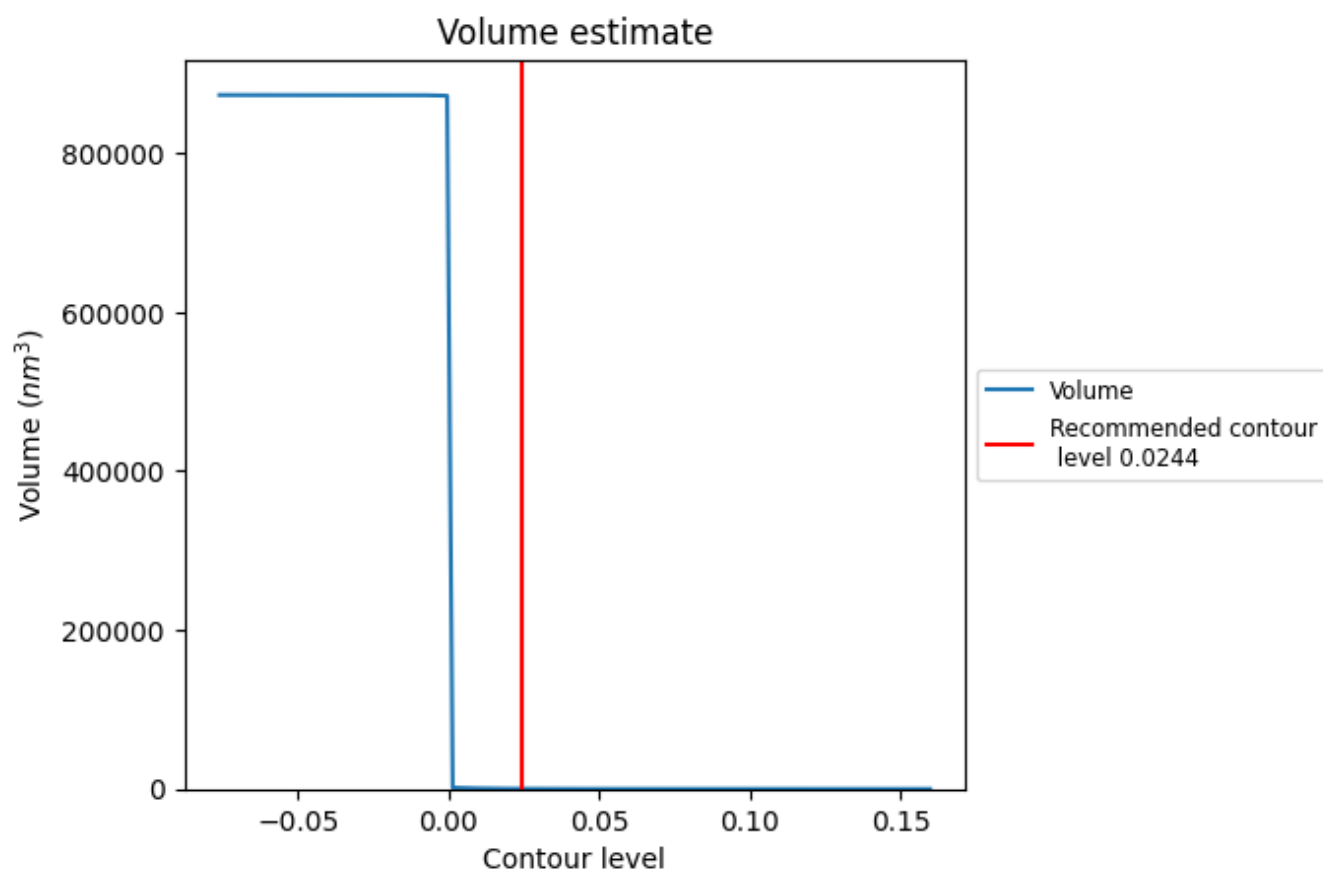
This section contains the results of statistical analysis of the map.

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.

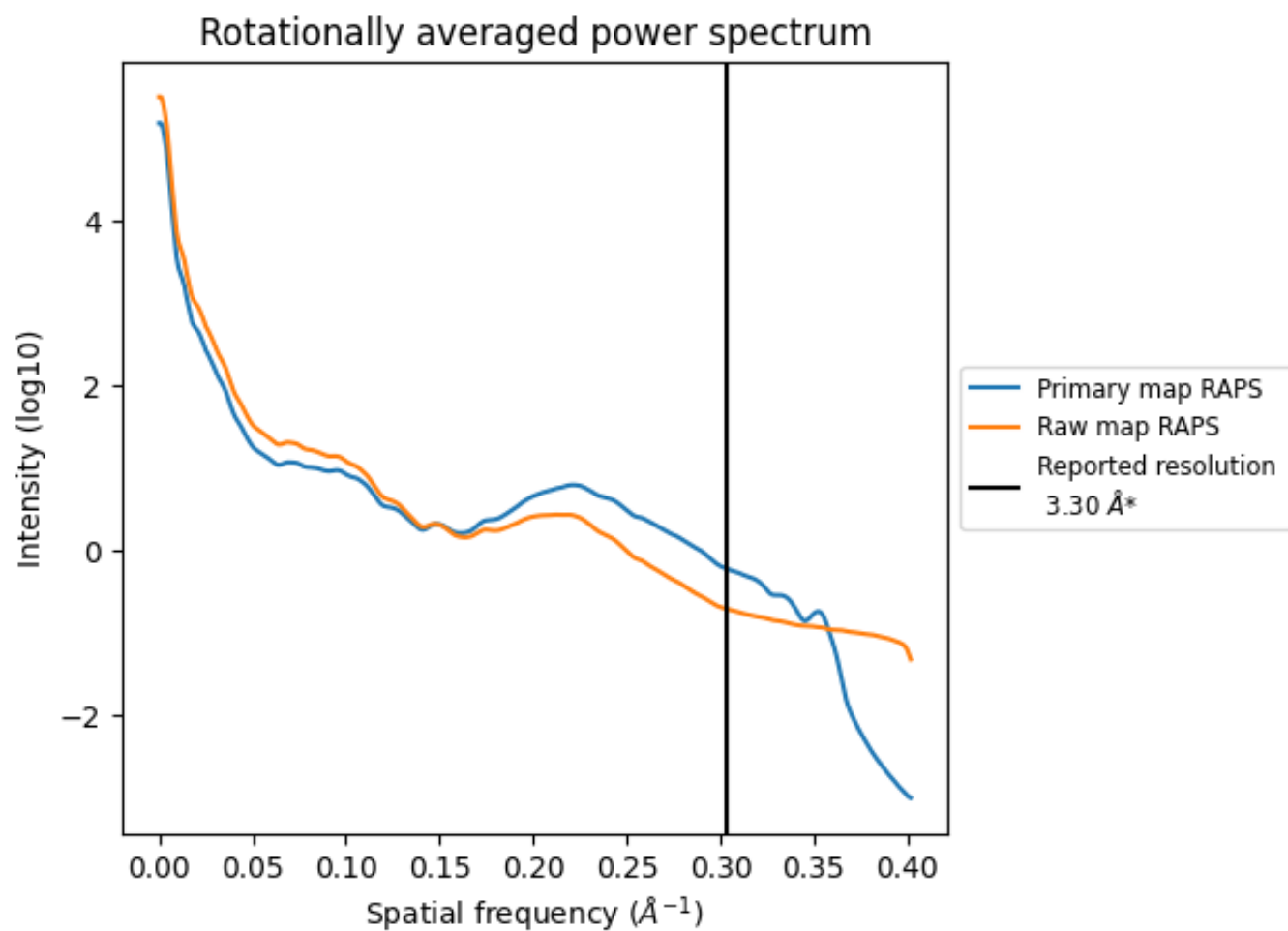
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 222 nm^3 ; this corresponds to an approximate mass of 201 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 ⓘ

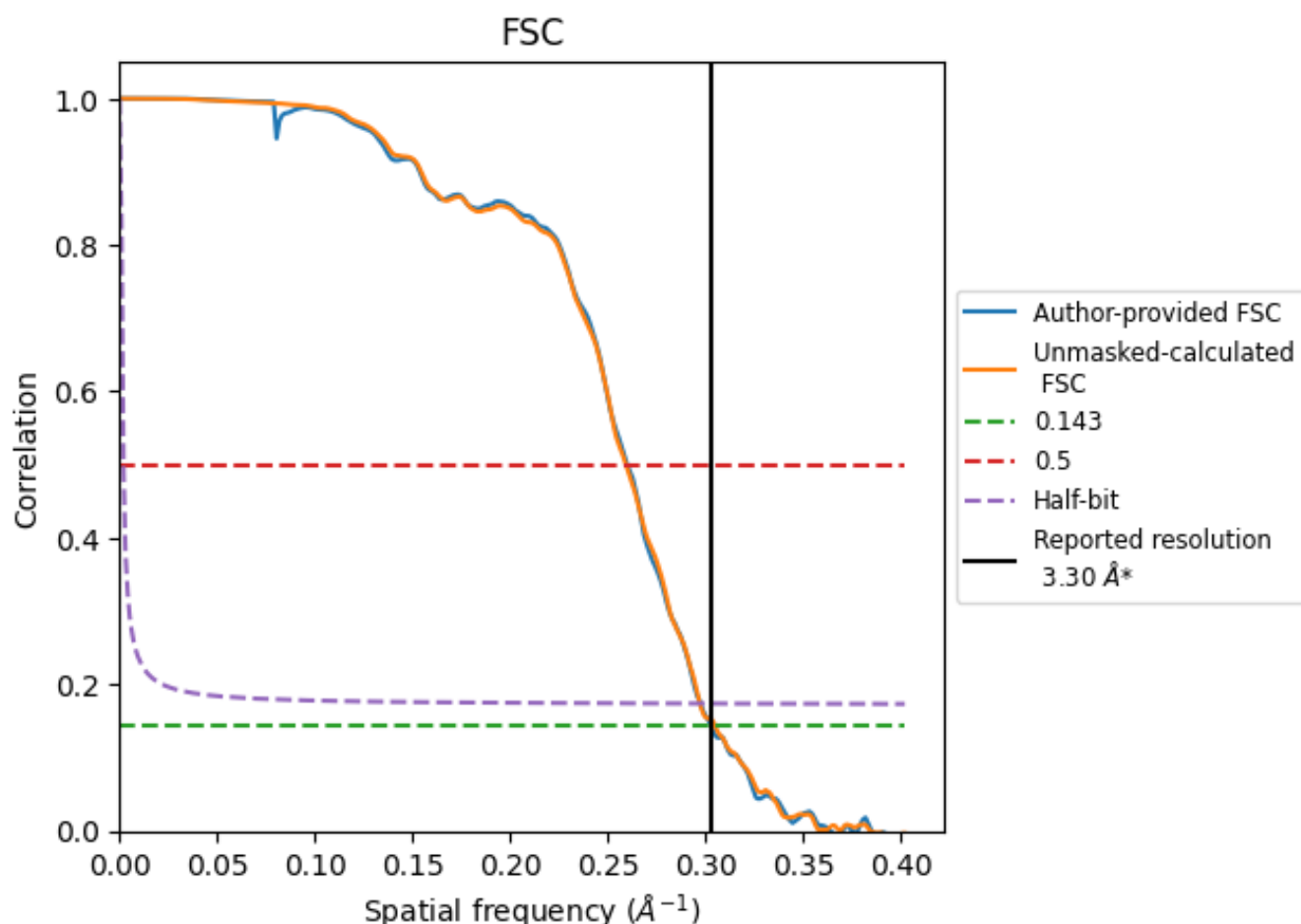


*Reported resolution corresponds to spatial frequency of 0.303 \AA^{-1}

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 0.303 Å⁻¹

8.2 Resolution estimates [i](#)

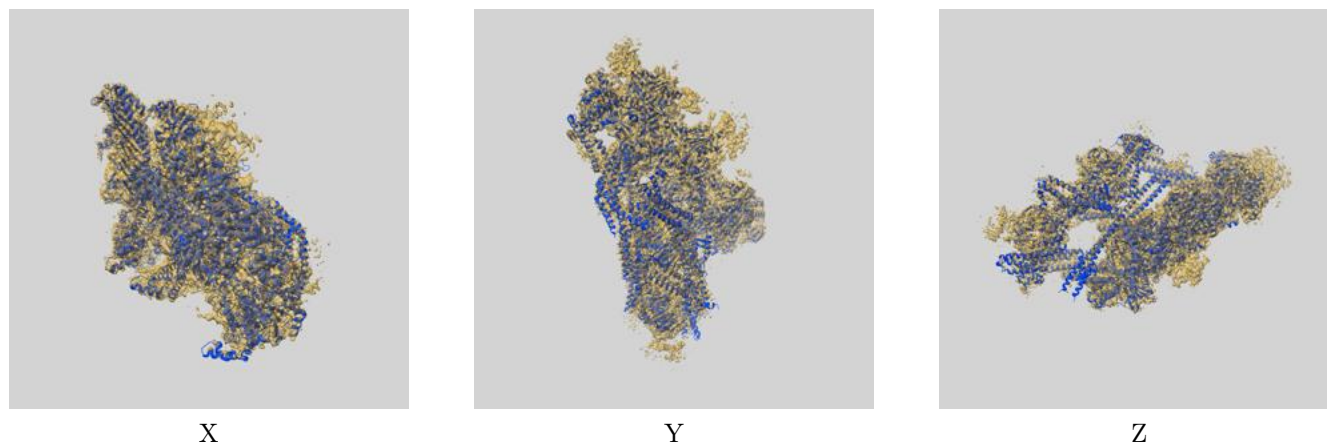
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.30	3.85	3.36
Unmasked-calculated*	3.28	3.86	3.37

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

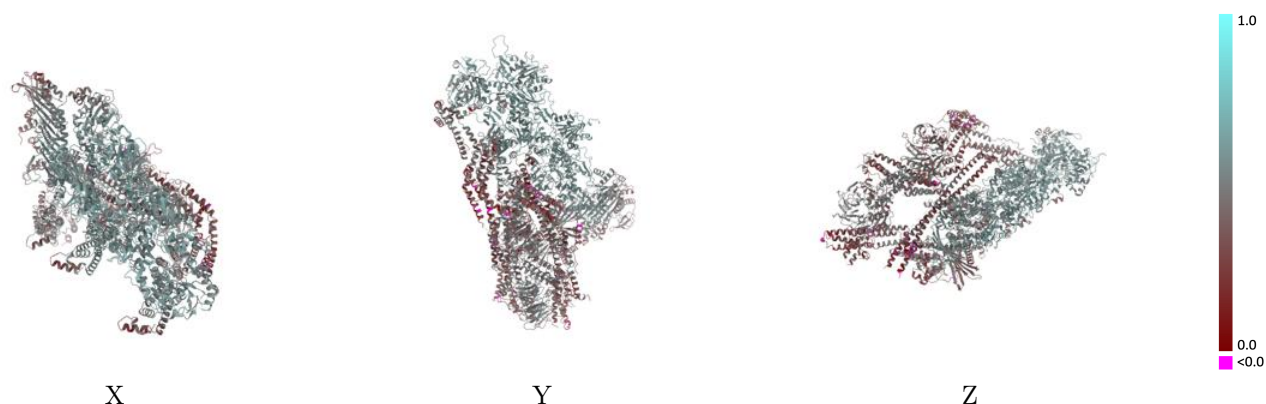
This section contains information regarding the fit between EMDB map EMD-14552 and PDB model 7Z8I. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



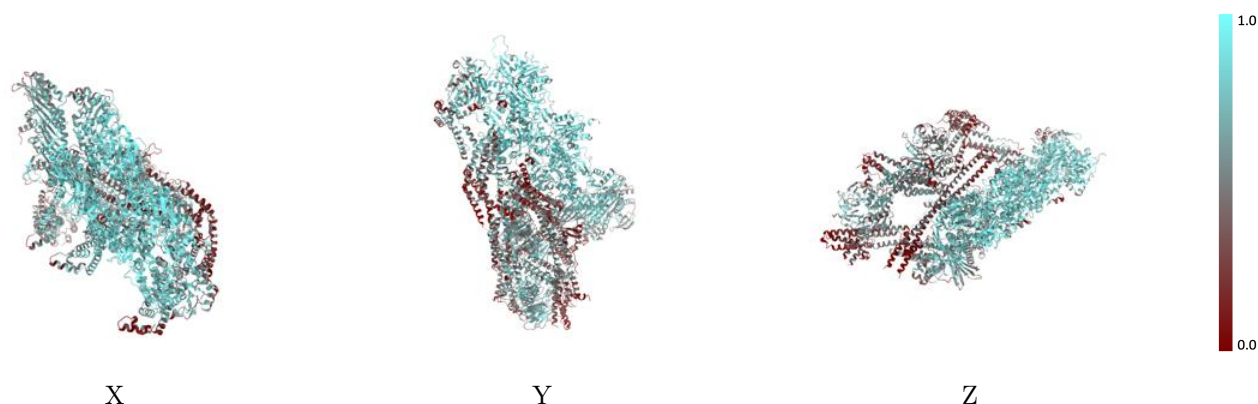
The images above show the 3D surface view of the map at the recommended contour level 0.0244 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



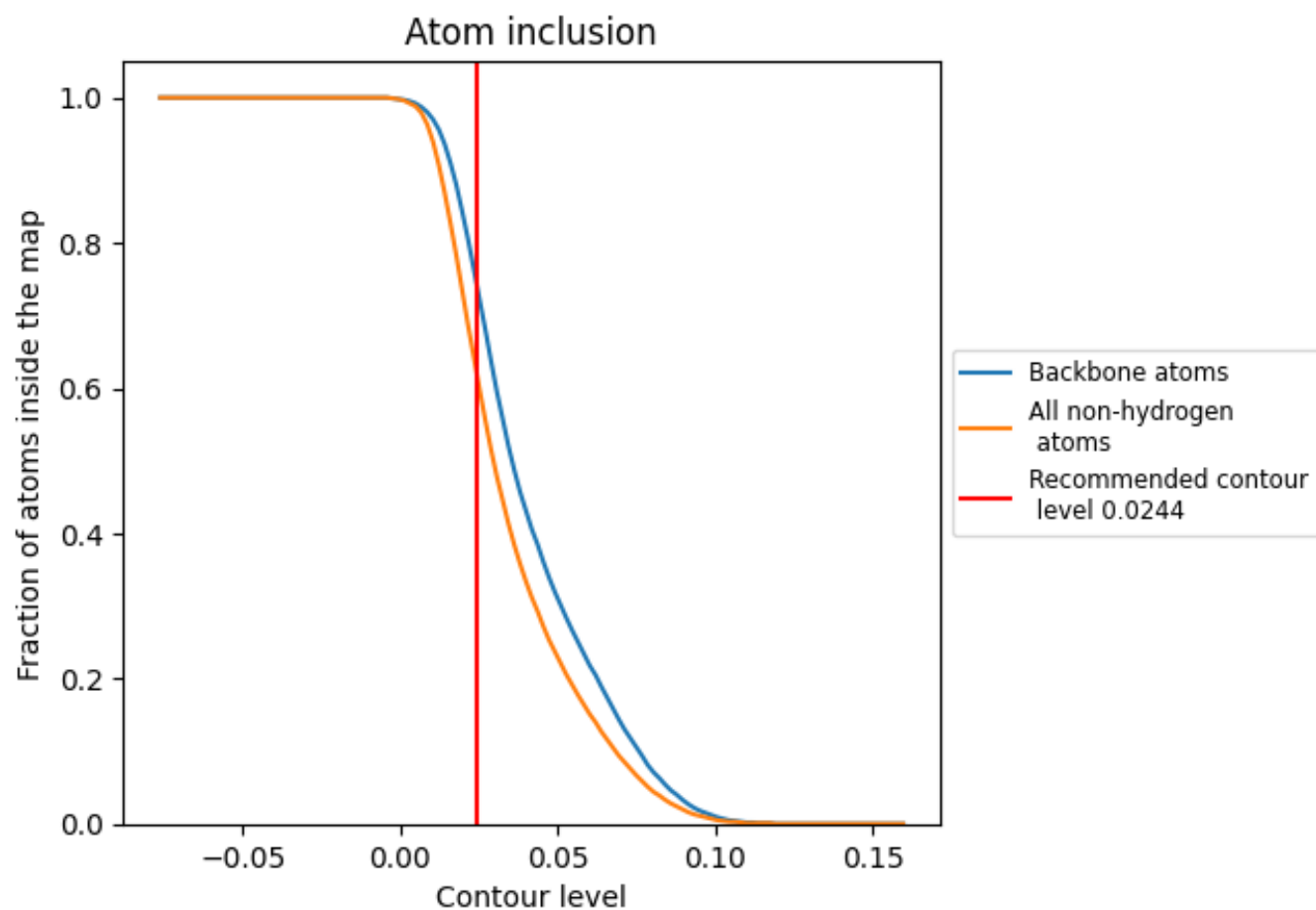
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0244).





































9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 62% 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 (0.0244) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6180	 0.4660
A	 0.7690	 0.5260
B	 0.8420	 0.5740
C	 0.8330	 0.5680
D	 0.8400	 0.5680
E	 0.8140	 0.5580
F	 0.6940	 0.5430
K	 0.6070	 0.4370
L	 0.7070	 0.5050
X	 0.2520	 0.3140
f	 0.3780	 0.3520
h	 0.5100	 0.4130
j	 0.1550	 0.2620
m	 0.5450	 0.4330
n	 0.4780	 0.3890
o	 0.6160	 0.4620
r	 0.0180	 0.2060
x	 0.2350	 0.2950

