



## wwPDB EM Validation Summary Report ⓘ

Nov 6, 2022 – 01:52 AM EST

PDB ID : 6AP1  
EMDB ID : EMD-8887  
Title : Vps4p-Vta1p complex with peptide binding to the central pore of Vps4p  
Authors : Han, H.; Monroe, N.; Shen, P.; Sundquist, W.I.; Hill, C.P.  
Deposited on : 2017-08-16  
Resolution : 3.20 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev43  
Mogul : 1.8.5 (274361), 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 : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

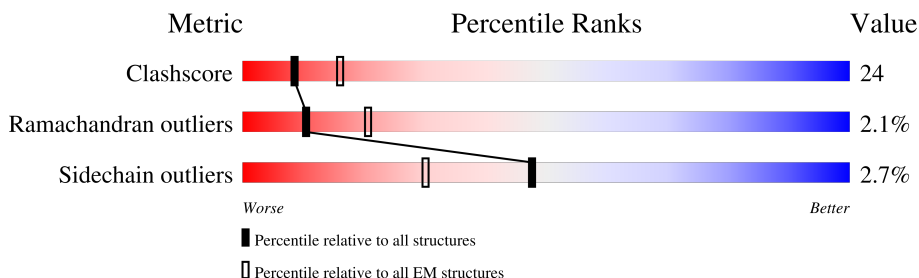
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.20 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  $\geq 3$ , 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	519	33% (Upper red bar) 49% (Red), 9% (Orange), 39% (Green), 9% (Yellow), 0% (Grey)
1	B	519	18% (Upper red bar) 50% (Red), 11% (Orange), 38% (Green), 11% (Yellow), 0% (Grey)
1	C	519	18% (Upper red bar) 50% (Red), 11% (Orange), 38% (Green), 11% (Yellow), 0% (Grey)
1	D	519	23% (Upper red bar) 51% (Red), 9% (Orange), 38% (Green), 9% (Yellow), 0% (Grey)
1	E	519	41% (Upper red bar) 45% (Red), 12% (Orange), 41% (Green), 12% (Yellow), 0% (Grey)
1	F	519	59% (Upper red bar) 35% (Red), 22% (Orange), 41% (Green), 22% (Yellow), 0% (Grey)
2	G	10	60% (Upper red bar) 90% (Red), 10% (Green), 0% (Yellow), 0% (Grey)
3	H	330	13% (Upper red bar) 5% (Red), 8% (Orange), 87% (Green), 0% (Yellow), 0% (Grey)

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Mol	Chain	Length	Quality of chain
3	I	330	13% 8% 5% 87%
3	J	330	13% 5% 8% 87%
3	K	330	13% 8% . 87%
3	L	330	13% 5% 8% 87%
3	M	330	13% 8% 5% 87%
3	N	330	13% 5% 8% 87%
3	O	330	13% 8% 5% 87%
3	P	330	13% 5% 8% 87%
3	Q	330	13% 8% . 87%
3	R	330	13% 5% 8% 87%
3	S	330	13% 8% . 87%

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 18838 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 Vacuolar protein sorting-associated protein 4, Protein hcp1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	314	2427	1530	414	474	9	0	0
1	B	322	2491	1568	427	487	9	0	0
1	C	322	2491	1568	427	487	9	0	0
1	D	322	2491	1568	427	487	9	0	0
1	E	304	2360	1489	401	461	9	0	0
1	F	308	2387	1507	405	466	9	0	0

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	100	GLY	-	expression tag	UNP P52917
A	438	GLY	-	linker	UNP P52917
A	439	GLY	-	linker	UNP P52917
A	440	GLY	-	linker	UNP P52917
A	441	GLY	-	linker	UNP P52917
A	442	SER	-	linker	UNP P52917
A	443	GLY	-	linker	UNP P52917
A	444	GLY	-	linker	UNP P52917
A	445	GLY	-	linker	UNP P52917
A	446	GLY	-	linker	UNP P52917
A	447	SER	-	linker	UNP P52917
A	448	GLY	-	linker	UNP P52917
A	449	GLY	-	linker	UNP P52917
A	450	GLY	-	linker	UNP P52917
A	451	GLY	-	linker	UNP P52917
A	452	SER	-	linker	UNP P52917
A	453	GLY	-	linker	UNP P52917
A	454	GLY	-	linker	UNP P52917

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Chain	Residue	Modelled	Actual	Comment	Reference
A	455	GLY	-	linker	UNP P52917
A	618	GLY	-	expression tag	UNP Q9I747
B	100	GLY	-	expression tag	UNP P52917
B	438	GLY	-	linker	UNP P52917
B	439	GLY	-	linker	UNP P52917
B	440	GLY	-	linker	UNP P52917
B	441	GLY	-	linker	UNP P52917
B	442	SER	-	linker	UNP P52917
B	443	GLY	-	linker	UNP P52917
B	444	GLY	-	linker	UNP P52917
B	445	GLY	-	linker	UNP P52917
B	446	GLY	-	linker	UNP P52917
B	447	SER	-	linker	UNP P52917
B	448	GLY	-	linker	UNP P52917
B	449	GLY	-	linker	UNP P52917
B	450	GLY	-	linker	UNP P52917
B	451	GLY	-	linker	UNP P52917
B	452	SER	-	linker	UNP P52917
B	453	GLY	-	linker	UNP P52917
B	454	GLY	-	linker	UNP P52917
B	455	GLY	-	linker	UNP P52917
B	618	GLY	-	expression tag	UNP Q9I747
C	100	GLY	-	expression tag	UNP P52917
C	438	GLY	-	linker	UNP P52917
C	439	GLY	-	linker	UNP P52917
C	440	GLY	-	linker	UNP P52917
C	441	GLY	-	linker	UNP P52917
C	442	SER	-	linker	UNP P52917
C	443	GLY	-	linker	UNP P52917
C	444	GLY	-	linker	UNP P52917
C	445	GLY	-	linker	UNP P52917
C	446	GLY	-	linker	UNP P52917
C	447	SER	-	linker	UNP P52917
C	448	GLY	-	linker	UNP P52917
C	449	GLY	-	linker	UNP P52917
C	450	GLY	-	linker	UNP P52917
C	451	GLY	-	linker	UNP P52917
C	452	SER	-	linker	UNP P52917
C	453	GLY	-	linker	UNP P52917
C	454	GLY	-	linker	UNP P52917
C	455	GLY	-	linker	UNP P52917
C	618	GLY	-	expression tag	UNP Q9I747

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Chain	Residue	Modelled	Actual	Comment	Reference
D	100	GLY	-	expression tag	UNP P52917
D	438	GLY	-	linker	UNP P52917
D	439	GLY	-	linker	UNP P52917
D	440	GLY	-	linker	UNP P52917
D	441	GLY	-	linker	UNP P52917
D	442	SER	-	linker	UNP P52917
D	443	GLY	-	linker	UNP P52917
D	444	GLY	-	linker	UNP P52917
D	445	GLY	-	linker	UNP P52917
D	446	GLY	-	linker	UNP P52917
D	447	SER	-	linker	UNP P52917
D	448	GLY	-	linker	UNP P52917
D	449	GLY	-	linker	UNP P52917
D	450	GLY	-	linker	UNP P52917
D	451	GLY	-	linker	UNP P52917
D	452	SER	-	linker	UNP P52917
D	453	GLY	-	linker	UNP P52917
D	454	GLY	-	linker	UNP P52917
D	455	GLY	-	linker	UNP P52917
D	618	GLY	-	expression tag	UNP Q9I747
E	100	GLY	-	expression tag	UNP P52917
E	438	GLY	-	linker	UNP P52917
E	439	GLY	-	linker	UNP P52917
E	440	GLY	-	linker	UNP P52917
E	441	GLY	-	linker	UNP P52917
E	442	SER	-	linker	UNP P52917
E	443	GLY	-	linker	UNP P52917
E	444	GLY	-	linker	UNP P52917
E	445	GLY	-	linker	UNP P52917
E	446	GLY	-	linker	UNP P52917
E	447	SER	-	linker	UNP P52917
E	448	GLY	-	linker	UNP P52917
E	449	GLY	-	linker	UNP P52917
E	450	GLY	-	linker	UNP P52917
E	451	GLY	-	linker	UNP P52917
E	452	SER	-	linker	UNP P52917
E	453	GLY	-	linker	UNP P52917
E	454	GLY	-	linker	UNP P52917
E	455	GLY	-	linker	UNP P52917
E	618	GLY	-	expression tag	UNP Q9I747
F	100	GLY	-	expression tag	UNP P52917
F	438	GLY	-	linker	UNP P52917

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Chain	Residue	Modelled	Actual	Comment	Reference
F	439	GLY	-	linker	UNP P52917
F	440	GLY	-	linker	UNP P52917
F	441	GLY	-	linker	UNP P52917
F	442	SER	-	linker	UNP P52917
F	443	GLY	-	linker	UNP P52917
F	444	GLY	-	linker	UNP P52917
F	445	GLY	-	linker	UNP P52917
F	446	GLY	-	linker	UNP P52917
F	447	SER	-	linker	UNP P52917
F	448	GLY	-	linker	UNP P52917
F	449	GLY	-	linker	UNP P52917
F	450	GLY	-	linker	UNP P52917
F	451	GLY	-	linker	UNP P52917
F	452	SER	-	linker	UNP P52917
F	453	GLY	-	linker	UNP P52917
F	454	GLY	-	linker	UNP P52917
F	455	GLY	-	linker	UNP P52917
F	618	GLY	-	expression tag	UNP Q9I747

- Molecule 2 is a protein called ACE-ASP-GLU-ILE-VAL-ASN-LYS-VAL-LEU-NH2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	G	10	68	43	11	14	1	1

- Molecule 3 is a protein called Vacuolar protein sorting-associated protein VTA1.

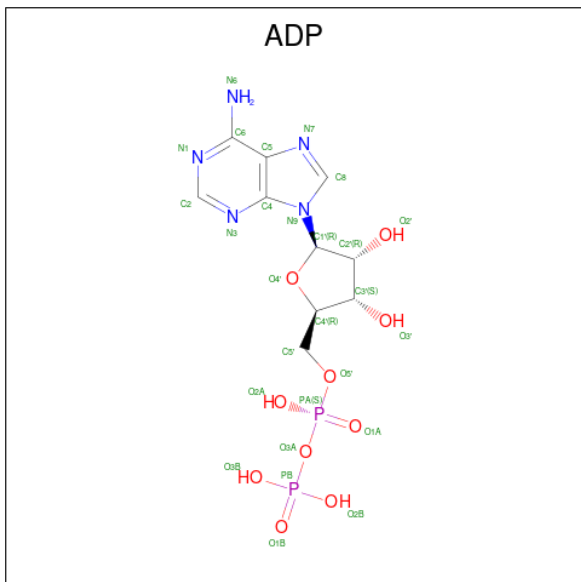
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	H	42	331	209	54	68	0	0
3	I	42	331	209	54	68	0	0
3	J	42	331	209	54	68	0	0
3	K	42	331	209	54	68	0	0
3	L	42	331	209	54	68	0	0
3	M	42	331	209	54	68	0	0
3	N	42	331	209	54	68	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
3	O	42	Total	C	N	O	0	0
			331	209	54	68		
3	P	42	Total	C	N	O	0	0
			331	209	54	68		
3	Q	42	Total	C	N	O	0	0
			331	209	54	68		
3	R	42	Total	C	N	O	0	0
			331	209	54	68		
3	S	42	Total	C	N	O	0	0
			331	209	54	68		

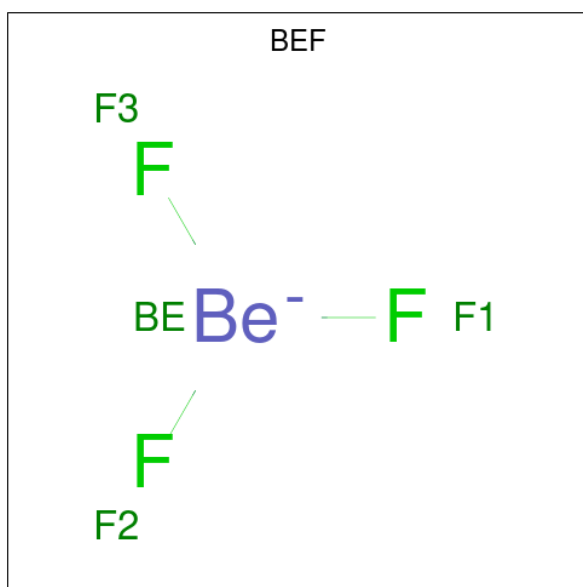
- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula:  $C_{10}H_{15}N_5O_{10}P_2$ ).



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

- Molecule 5 is BERYLLIUM TRIFLUORIDE ION (three-letter code: BEF) (formula:  $BeF_3$ ).





Mol	Chain	Residues	Atoms			AltConf
			Total	Be	F	
5	A	1	4	1	3	0
5	B	1	4	1	3	0
5	C	1	4	1	3	0

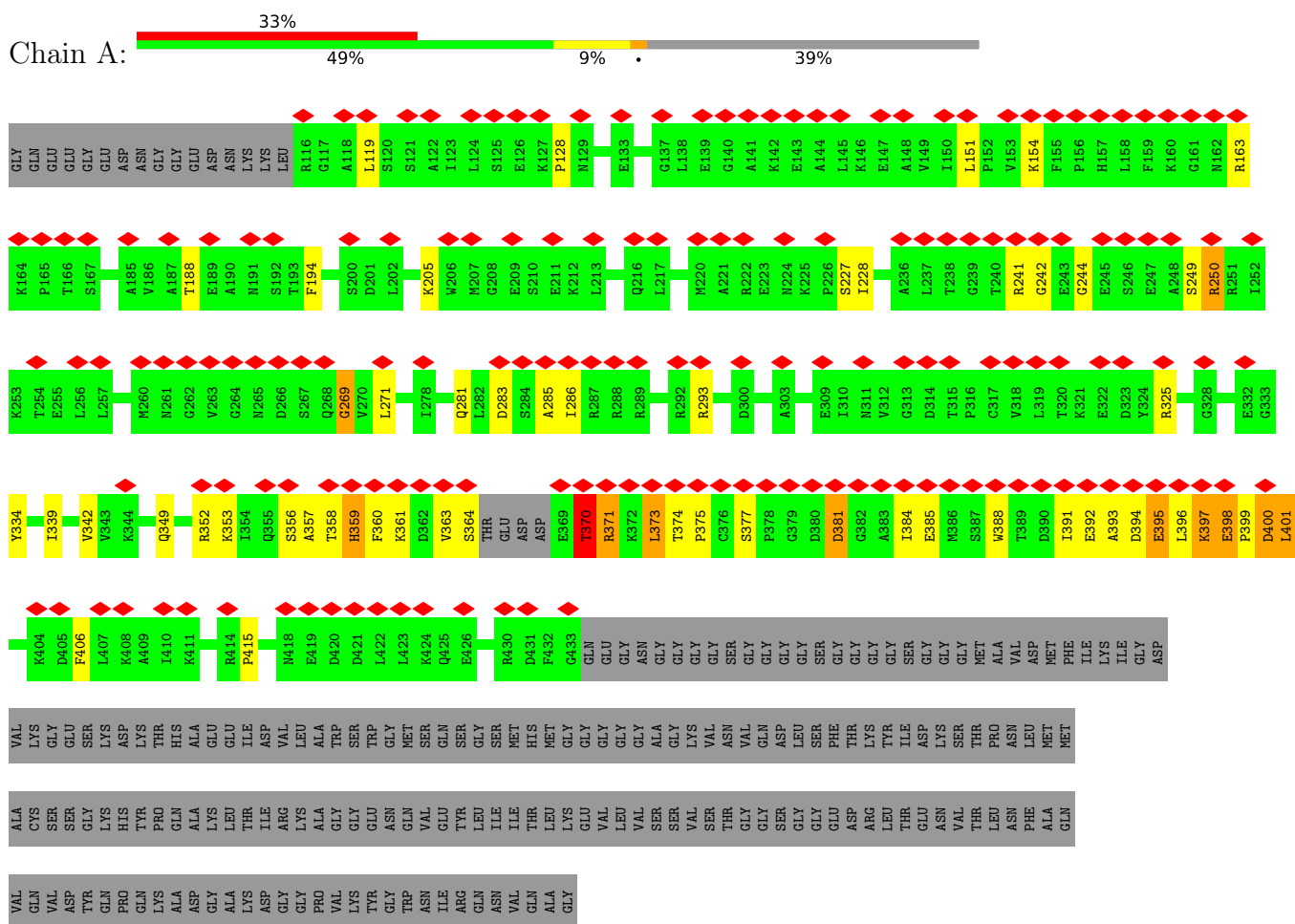
- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
6	A	1	1	1	0
6	B	1	1	1	0
6	C	1	1	1	0
6	D	1	1	1	0

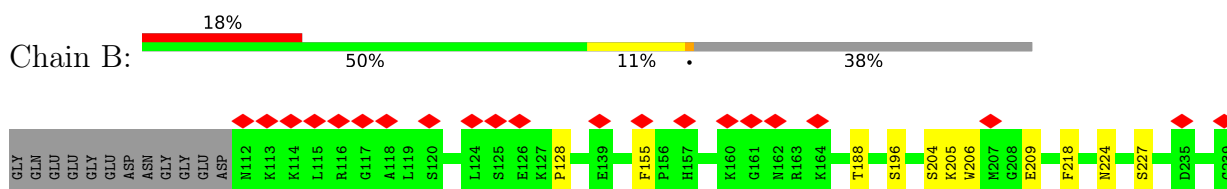
### 3 Residue-property plots [i](#)

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.

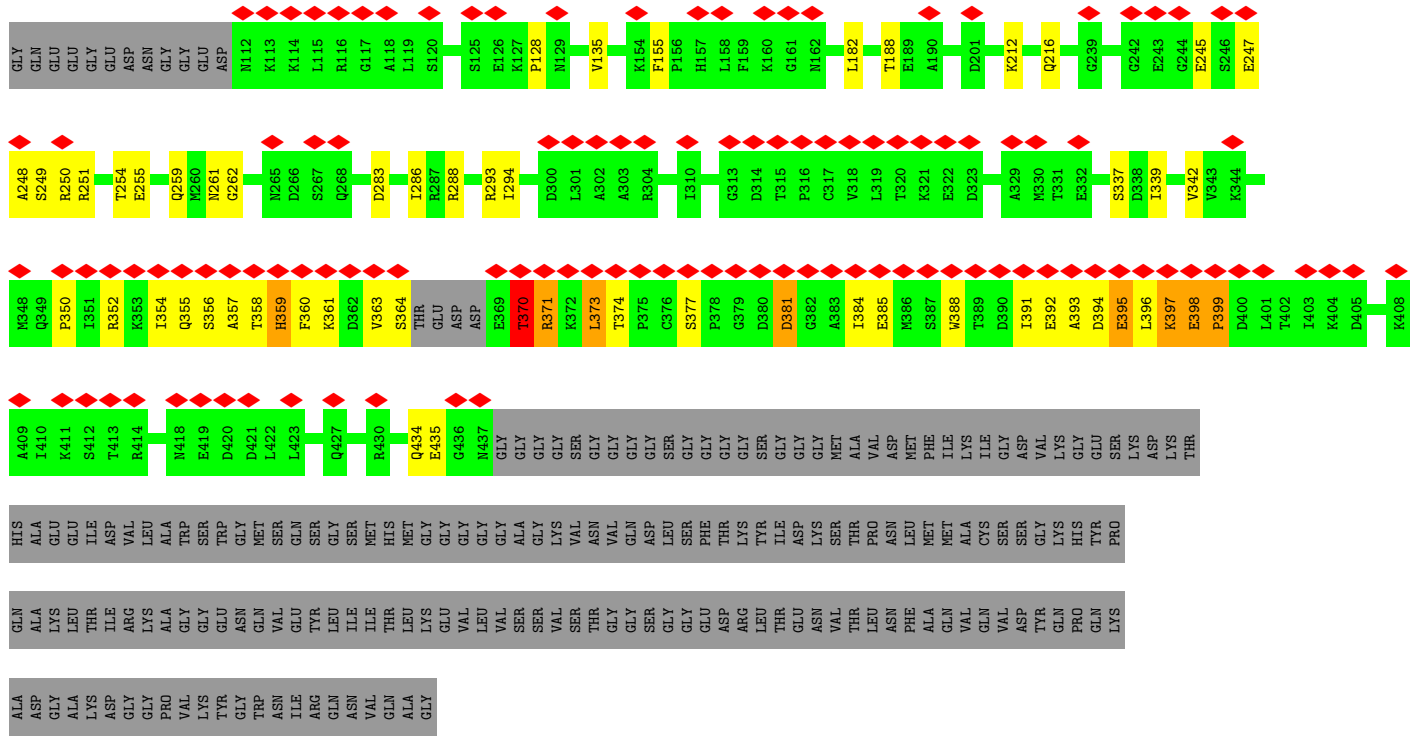
- Molecule 1: Vacuolar protein sorting-associated protein 4,Protein hcp1



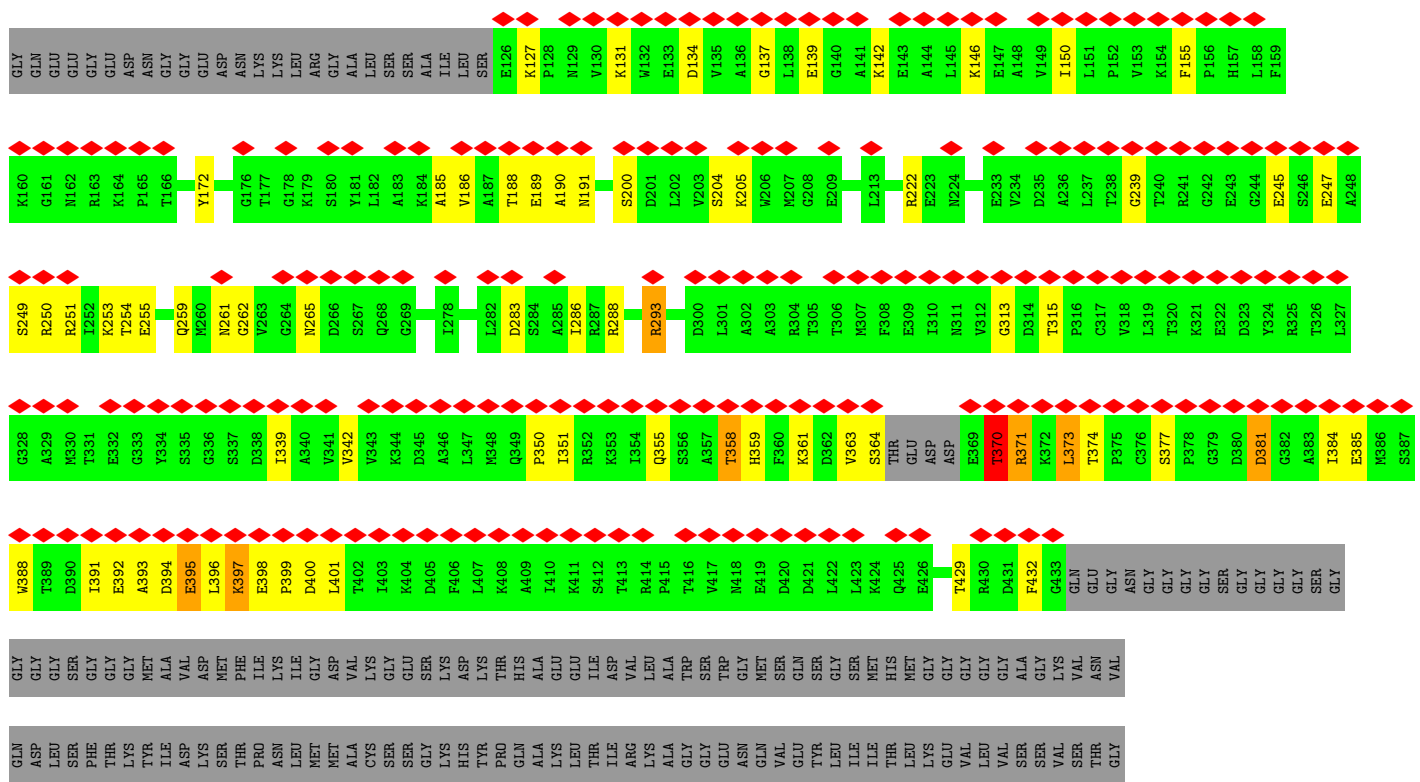
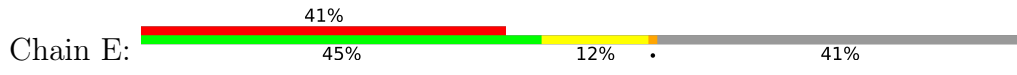
- Molecule 1: Vacuolar protein sorting-associated protein 4,Protein hcp1





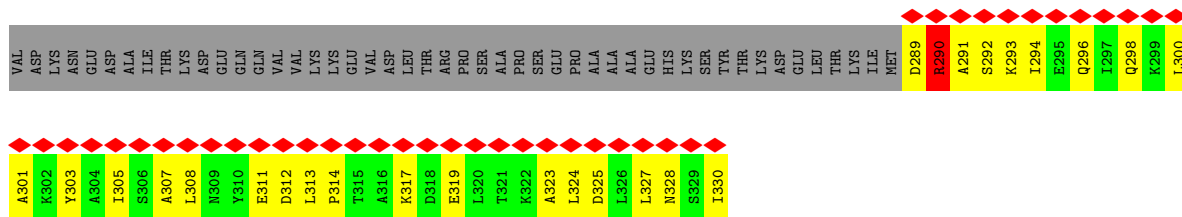


● Molecule 1: Vacuolar protein sorting-associated protein 4, Protein hep1









• Molecule 3: Vacuolar protein sorting-associated protein VTA1



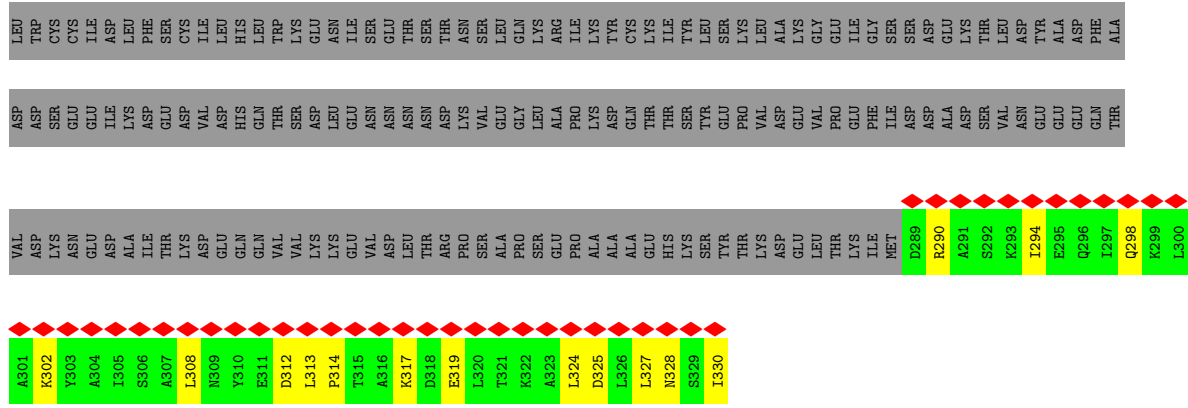
• Molecule 3: Vacuolar protein sorting-associated protein VTA1



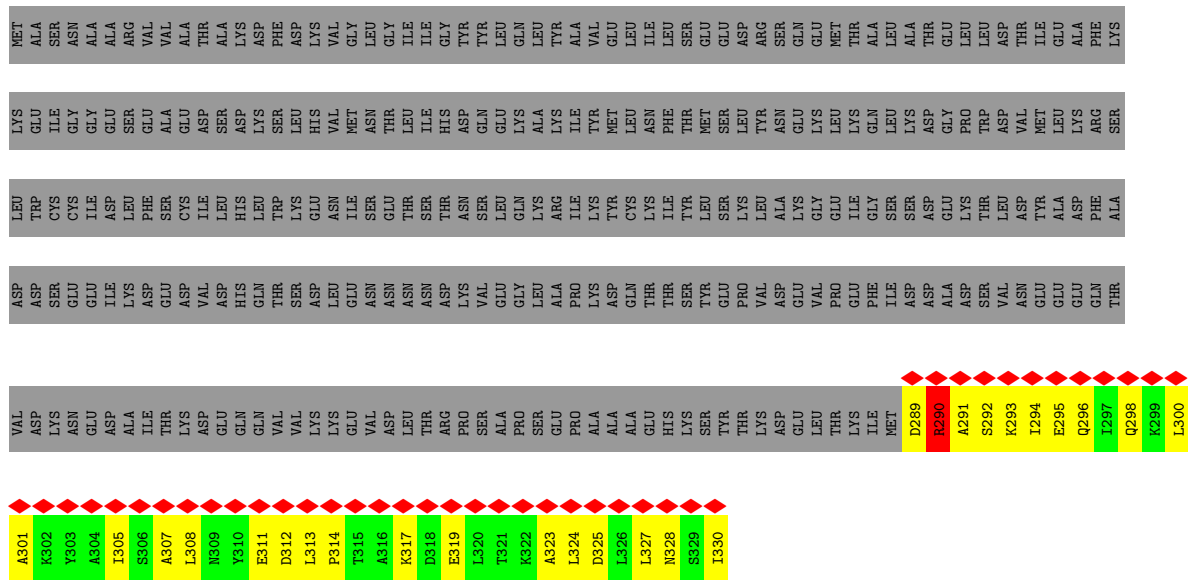
• Molecule 3: Vacuolar protein sorting-associated protein VTA1







• Molecule 3: Vacuolar protein sorting-associated protein VTA1



• Molecule 3: Vacuolar protein sorting-associated protein VTA1





• Molecule 3: Vacuolar protein sorting-associated protein VTA1



MET	ALA	SER	ASN	ALA	ARG	VAL	ALA	THR	ALA	LYS	ASP	PHE	ASP	D312	L313	P314	T315	A316	K317	D318	E319	L320	T321	K322	A323	L324	D325	L326	L327	N328	S329	I330			
LYS	ILE	GLY	GLY	GLU	SER	GLU	VAL	ALA	ASP	LYS	SER	LEU	LEU	HIS	VAL	VAL	GLY	LEU	GLY	ILE	GLY	TYR	LEU	GLN	LEU	ALA	VAL	GLU	LEU	LEU	GLU	GLU	LYS		
LEU	TRP	CYS	ILE	ASP	LEU	PHE	LEU	SER	ASP	LEU	TRP	THR	THR	GLU	ASN	ILE	SER	ASN	GLY	THR	ASN	SER	GLN	LEU	GLN	LYS	ARG	ILE	TYR	SER	LEU	SER	PRO	ASP	
ASP	ASP	SER	ASN	GLY	ILE	LYS	ASP	THR	VAL	GLN	HIS	GLN	GLN	THR	VAL	LYS	VAL	ASP	ASN	ASN	ASN	LYS	VAL	GLY	GLY	ALA	PRO	LYS	ASP	GLN	THR	PRO	VAL	ASP	
VAL	ASP	LYS	ASN	GLU	ALA	ILE	THR	LYS	ASP	GLU	GLN	GLN	VAL	VAL	VAL	LYS	GLU	VAL	ASP	LEU	THR	ARG	PRO	SER	ALA	PRO	ALA	ALA	ALA	GLU	HIS	THR	THR	LYS	SER



• Molecule 3: Vacuolar protein sorting-associated protein VTA1



MET	ALA	SER	ASN	ALA	ARG	VAL	ALA	THR	ALA	LYS	ASP	PHE	ASP	D312	L313	P314	T315	A316	K317	D318	E319	L320	T321	K322	A323	L324	D325	L326	L327	N328	S329	I330			
LYS	ILE	GLY	GLY	GLU	SER	GLU	VAL	ALA	ASP	LYS	SER	LEU	LEU	HIS	VAL	VAL	GLY	LEU	GLY	ILE	GLY	TYR	LEU	GLN	LEU	ALA	VAL	GLU	LEU	LEU	GLU	GLU	LYS		
LEU	TRP	CYS	ILE	ASP	LEU	PHE	LEU	SER	ASP	LEU	TRP	THR	THR	GLU	ASN	ILE	SER	ASN	GLY	THR	ASN	SER	GLN	LEU	GLN	LYS	ARG	ILE	TYR	SER	LEU	SER	PRO	ASP	
ASP	ASP	SER	ASN	GLY	ILE	LYS	ASP	THR	VAL	GLN	HIS	GLN	GLN	THR	VAL	LYS	VAL	ASP	ASN	ASN	ASN	LYS	VAL	GLY	GLY	ALA	PRO	LYS	ASP	GLN	THR	PRO	VAL	ASP	
VAL	ASP	LYS	ASN	GLU	ALA	ILE	THR	LYS	ASP	GLU	GLN	GLN	VAL	VAL	VAL	LYS	GLU	VAL	ASP	LEU	THR	ARG	PRO	SER	ALA	PRO	ALA	ALA	ALA	GLU	HIS	THR	THR	LYS	SER



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	82225	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 ( $e^-/\text{\AA}^2$ )	1.55	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.388	Depositor
Minimum map value	-0.195	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.0749	Depositor
Map size (Å)	280.6016, 280.6016, 280.6016	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0961, 1.0961, 1.0961	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: BEF, NH2, ACE, ADP, MG

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	0.71	0/2468	0.81	2/3334 (0.1%)
1	B	0.78	0/2532	0.79	0/3418
1	C	0.79	1/2532 (0.0%)	0.83	2/3418 (0.1%)
1	D	0.75	0/2532	0.78	0/3418
1	E	0.70	0/2401	0.79	0/3244
1	F	0.59	0/2428	0.70	2/3281 (0.1%)
2	G	1.02	0/64	1.07	0/86
3	H	0.53	0/333	0.75	0/447
3	I	0.54	0/333	0.69	0/447
3	J	0.53	0/333	0.75	0/447
3	K	0.54	0/333	0.69	0/447
3	L	0.52	0/333	0.75	0/447
3	M	0.54	0/333	0.70	0/447
3	N	0.53	0/333	0.75	0/447
3	O	0.54	0/333	0.70	0/447
3	P	0.52	0/333	0.74	0/447
3	Q	0.54	0/333	0.69	0/447
3	R	0.53	0/333	0.75	0/447
3	S	0.54	0/333	0.69	0/447
All	All	0.69	1/18953 (0.0%)	0.77	6/25563 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	C	0	1
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	211	GLU	CG-CD	-5.85	1.43	1.51

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	250	ARG	NE-CZ-NH1	-6.81	116.89	120.30
1	C	138	LEU	CB-CG-CD2	-6.21	100.45	111.00
1	A	119	LEU	CB-CG-CD1	-5.34	101.92	111.00
1	F	269	GLY	N-CA-C	5.18	126.06	113.10
1	F	287	ARG	NE-CZ-NH1	5.16	122.88	120.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	269	GLY	Peptide
1	B	205	LYS	Peptide
1	C	125	SER	Mainchain

## 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	2427	0	2449	107	0
1	B	2491	0	2516	71	0
1	C	2491	0	2516	86	0
1	D	2491	0	2516	78	0
1	E	2360	0	2377	124	0
1	F	2387	0	2409	340	0
2	G	68	0	71	1	0
3	H	331	0	344	33	0
3	I	331	0	344	17	0
3	J	331	0	344	33	0
3	K	331	0	344	22	0
3	L	331	0	344	34	0
3	M	331	0	344	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	N	331	0	344	34	0
3	O	331	0	344	19	0
3	P	331	0	344	33	0
3	Q	331	0	344	18	0
3	R	331	0	344	36	0
3	S	331	0	344	29	0
4	A	27	0	12	1	0
4	B	27	0	12	1	0
4	C	27	0	12	1	0
4	D	27	0	12	0	0
4	E	27	0	12	0	0
5	A	4	0	0	1	0
5	B	4	0	0	1	0
5	C	4	0	0	1	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
All	All	18838	0	19042	904	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 24.

The worst 5 of 904 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:F:172:TYR:CZ	1:F:428:PHE:CD2	1.78	1.63
1:F:172:TYR:CZ	1:F:428:PHE:HD2	0.93	1.57
1:F:295:TYR:CE1	1:F:425:GLN:HB3	1.37	1.54
1:F:199:SER:HB3	1:F:237:LEU:CG	1.39	1.53
1:E:388:TRP:CZ3	1:F:151:LEU:CD1	1.90	1.52

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	310/519 (60%)	274 (88%)	31 (10%)	5 (2%)	9	43
1	B	318/519 (61%)	284 (89%)	29 (9%)	5 (2%)	9	43
1	C	318/519 (61%)	280 (88%)	33 (10%)	5 (2%)	9	43
1	D	318/519 (61%)	279 (88%)	33 (10%)	6 (2%)	8	39
1	E	300/519 (58%)	260 (87%)	36 (12%)	4 (1%)	12	47
1	F	304/519 (59%)	277 (91%)	20 (7%)	7 (2%)	6	34
2	G	8/10 (80%)	6 (75%)	2 (25%)	0	100	100
3	H	40/330 (12%)	31 (78%)	7 (18%)	2 (5%)	2	16
3	I	40/330 (12%)	34 (85%)	5 (12%)	1 (2%)	5	32
3	J	40/330 (12%)	31 (78%)	7 (18%)	2 (5%)	2	16
3	K	40/330 (12%)	34 (85%)	5 (12%)	1 (2%)	5	32
3	L	40/330 (12%)	31 (78%)	7 (18%)	2 (5%)	2	16
3	M	40/330 (12%)	34 (85%)	5 (12%)	1 (2%)	5	32
3	N	40/330 (12%)	31 (78%)	7 (18%)	2 (5%)	2	16
3	O	40/330 (12%)	34 (85%)	5 (12%)	1 (2%)	5	32
3	P	40/330 (12%)	31 (78%)	7 (18%)	2 (5%)	2	16
3	Q	40/330 (12%)	34 (85%)	5 (12%)	1 (2%)	5	32
3	R	40/330 (12%)	31 (78%)	7 (18%)	2 (5%)	2	16
3	S	40/330 (12%)	34 (85%)	5 (12%)	1 (2%)	5	32
All	All	2356/7084 (33%)	2050 (87%)	256 (11%)	50 (2%)	10	37

5 of 50 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	359	HIS
1	A	371	ARG
1	A	395	GLU
1	B	371	ARG
1	B	395	GLU

### 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	266/418 (64%)	258 (97%)	8 (3%)	41	73
1	B	273/418 (65%)	269 (98%)	4 (2%)	65	85
1	C	273/418 (65%)	269 (98%)	4 (2%)	65	85
1	D	273/418 (65%)	268 (98%)	5 (2%)	59	82
1	E	259/418 (62%)	254 (98%)	5 (2%)	57	81
1	F	262/418 (63%)	251 (96%)	11 (4%)	30	65
2	G	8/8 (100%)	8 (100%)	0	100	100
3	H	36/294 (12%)	34 (94%)	2 (6%)	21	57
3	I	36/294 (12%)	35 (97%)	1 (3%)	43	74
3	J	36/294 (12%)	34 (94%)	2 (6%)	21	57
3	K	36/294 (12%)	35 (97%)	1 (3%)	43	74
3	L	36/294 (12%)	34 (94%)	2 (6%)	21	57
3	M	36/294 (12%)	35 (97%)	1 (3%)	43	74
3	N	36/294 (12%)	34 (94%)	2 (6%)	21	57
3	O	36/294 (12%)	35 (97%)	1 (3%)	43	74
3	P	36/294 (12%)	34 (94%)	2 (6%)	21	57
3	Q	36/294 (12%)	35 (97%)	1 (3%)	43	74
3	R	36/294 (12%)	34 (94%)	2 (6%)	21	57
3	S	36/294 (12%)	35 (97%)	1 (3%)	43	74
All	All	2046/6044 (34%)	1991 (97%)	55 (3%)	48	75

5 of 55 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	200	SER
1	F	412	SER
3	S	319	GLU
3	P	290	ARG

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Mol	Chain	Res	Type
1	F	209	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
3	J	296	GLN
3	M	298	GLN
3	L	296	GLN
3	N	296	GLN
1	F	157	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, 4 are monoatomic - leaving 8 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	ADP	A	701	5,6	24,29,29	1.29	2 (8%)	29,45,45	1.71	8 (27%)
5	BEF	A	702	4	0,3,3	-	-	-		

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	BEF	B	702	4	0,3,3	-	-	-		
4	ADP	D	701	6	24,29,29	1.16	1 (4%)	29,45,45	1.75	8 (27%)
4	ADP	B	701	5,6	24,29,29	1.41	4 (16%)	29,45,45	1.70	7 (24%)
4	ADP	E	701	-	24,29,29	0.94	1 (4%)	29,45,45	1.58	4 (13%)
4	ADP	C	701	5,6	24,29,29	1.45	4 (16%)	29,45,45	1.71	10 (34%)
5	BEF	C	702	4	0,3,3	-	-	-		

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	ADP	A	701	5,6	-	6/12/32/32	0/3/3/3
4	ADP	D	701	6	-	1/12/32/32	0/3/3/3
4	ADP	B	701	5,6	-	4/12/32/32	0/3/3/3
4	ADP	E	701	-	-	3/12/32/32	0/3/3/3
4	ADP	C	701	5,6	-	2/12/32/32	0/3/3/3

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	701	ADP	C8-N7	-3.20	1.29	1.34
4	B	701	ADP	C8-N7	-2.88	1.29	1.34
4	A	701	ADP	C8-N7	-2.66	1.30	1.34
4	D	701	ADP	C2'-C1'	-2.65	1.49	1.53
4	B	701	ADP	PA-O2A	-2.56	1.43	1.55

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	701	ADP	C3'-C2'-C1'	4.32	107.48	100.98
4	B	701	ADP	O3B-PB-O1B	-4.17	94.35	110.68
4	D	701	ADP	PA-O3A-PB	-4.12	118.69	132.83
4	A	701	ADP	C2'-C3'-C4'	-4.01	94.84	102.64
4	C	701	ADP	O2B-PB-O3A	3.60	116.71	104.64

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

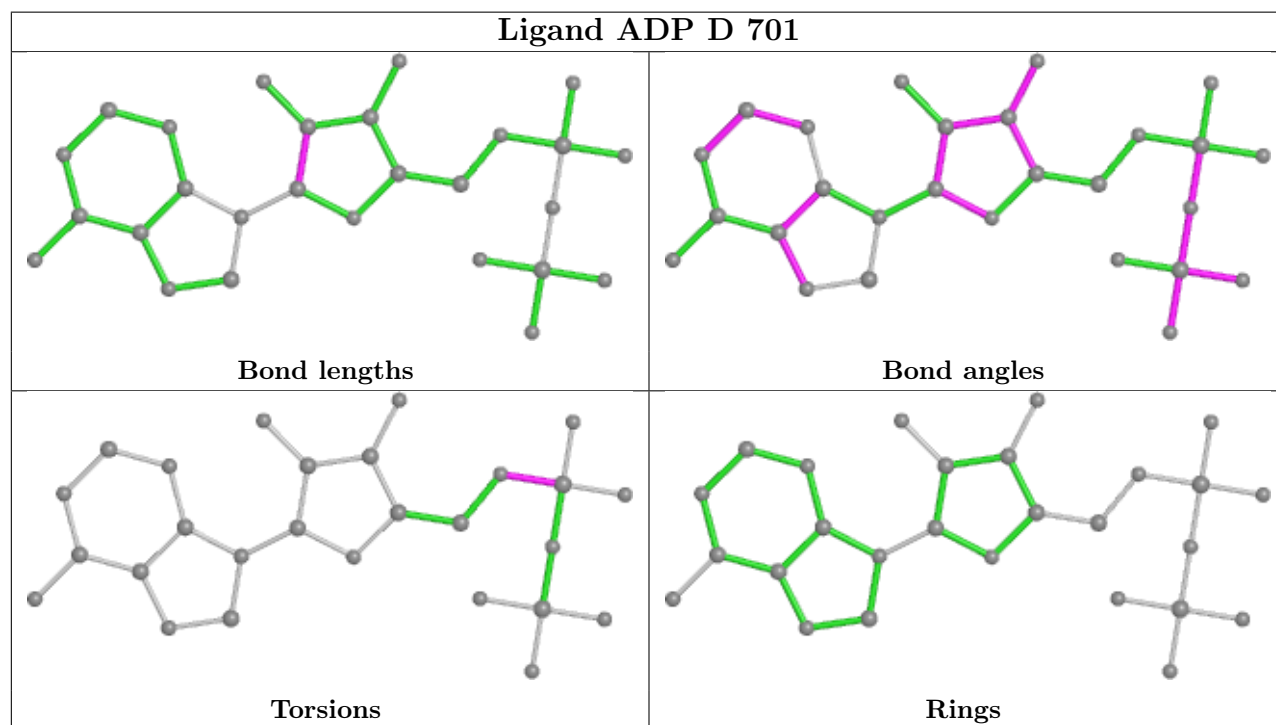
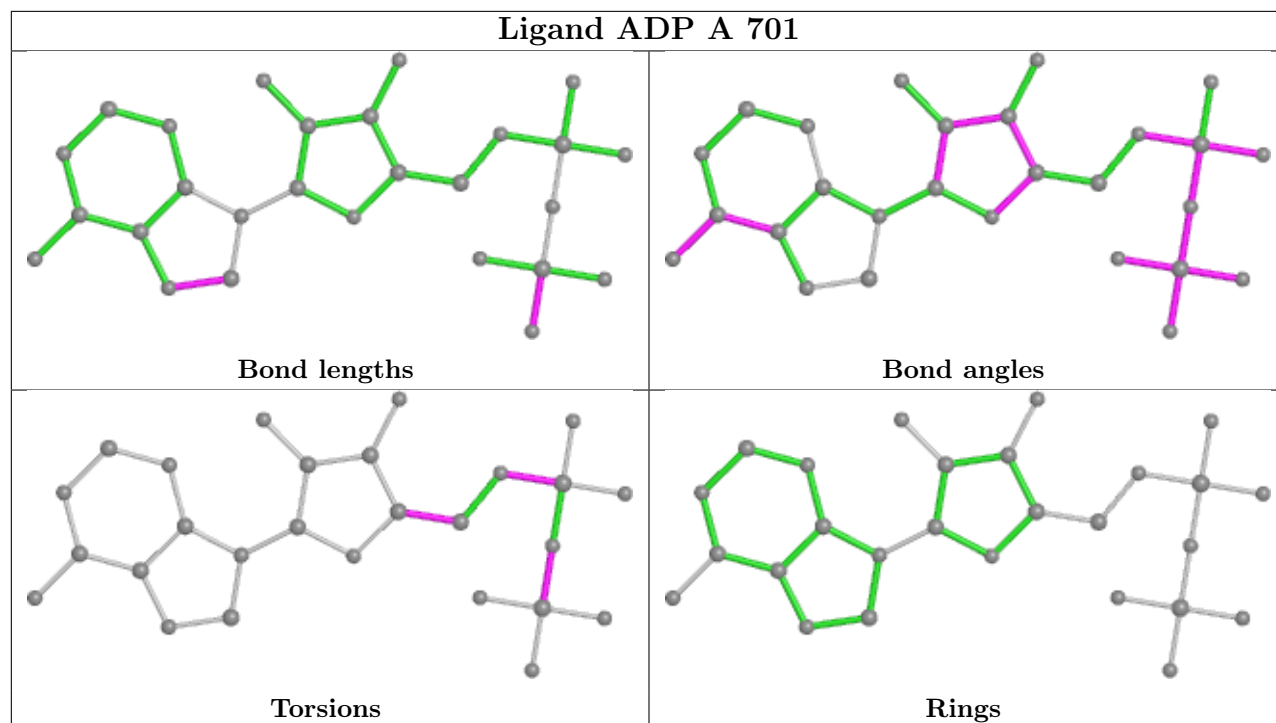
Mol	Chain	Res	Type	Atoms
4	A	701	ADP	PA-O3A-PB-O2B
4	A	701	ADP	C5'-O5'-PA-O2A
4	B	701	ADP	PA-O3A-PB-O2B
4	E	701	ADP	C5'-O5'-PA-O2A
4	B	701	ADP	C3'-C4'-C5'-O5'

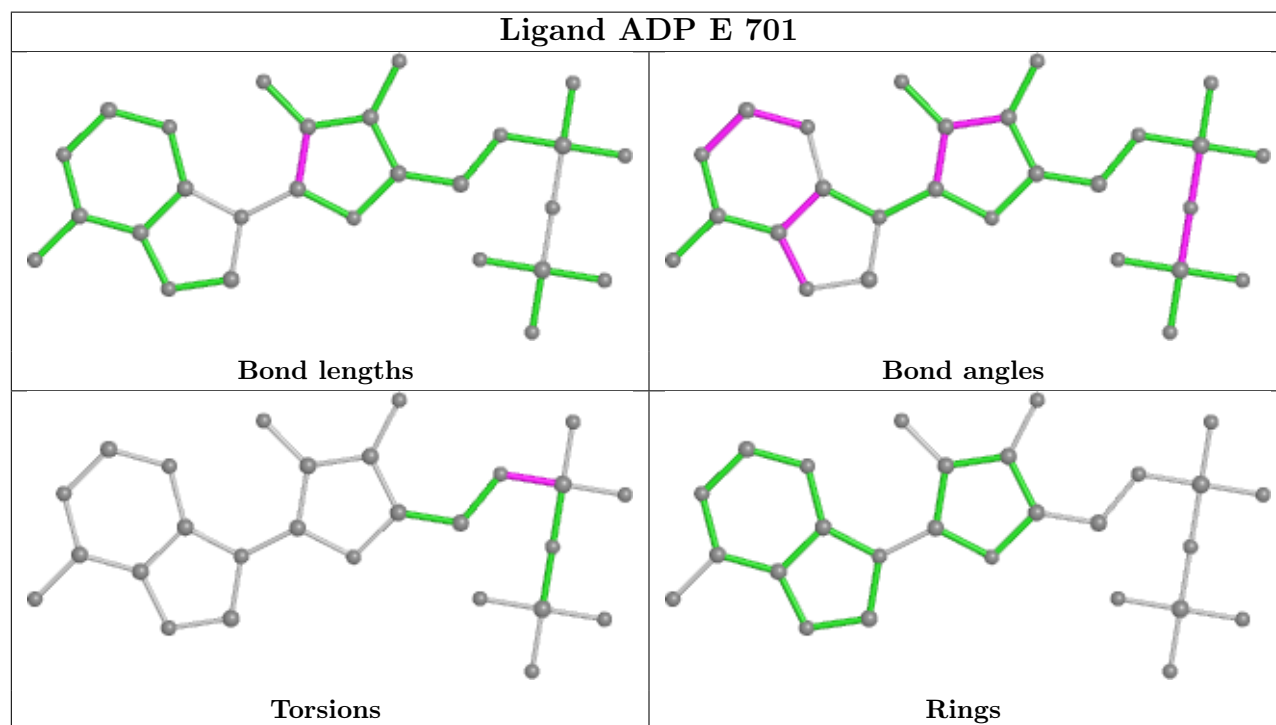
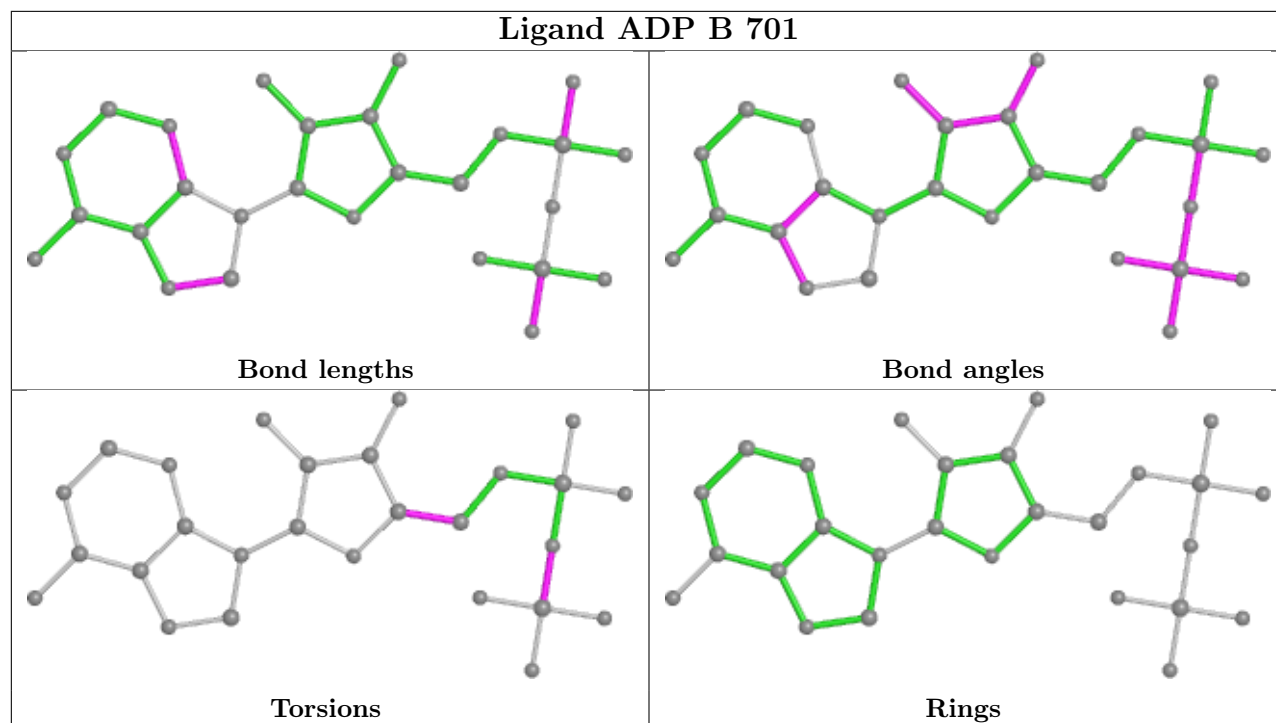
There are no ring outliers.

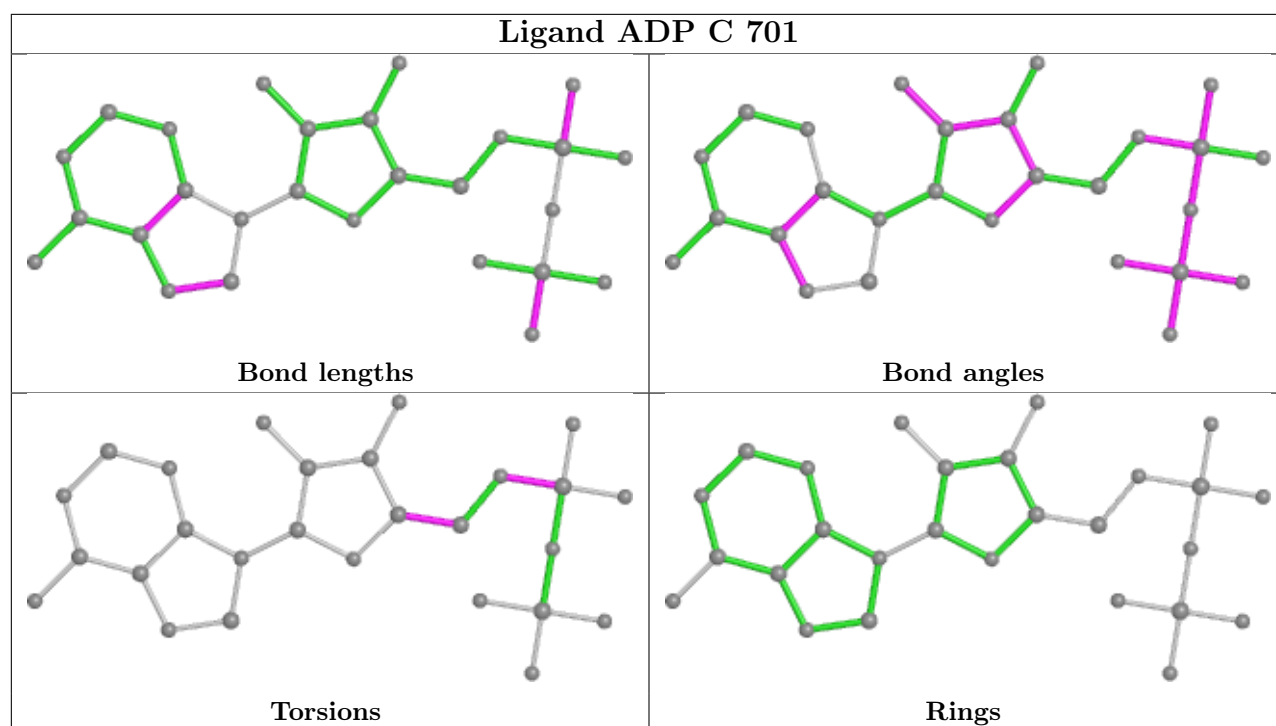
6 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	701	ADP	1	0
5	A	702	BEF	1	0
5	B	702	BEF	1	0
4	B	701	ADP	1	0
4	C	701	ADP	1	0
5	C	702	BEF	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 [i](#)

There are no chain breaks in this entry.

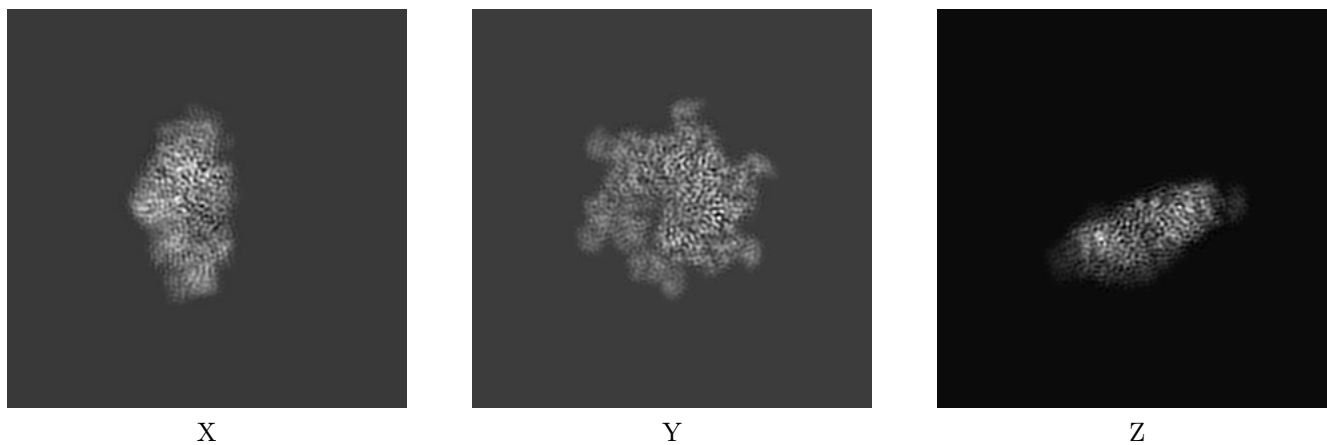
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8887. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

### 6.1 Orthogonal projections [i](#)

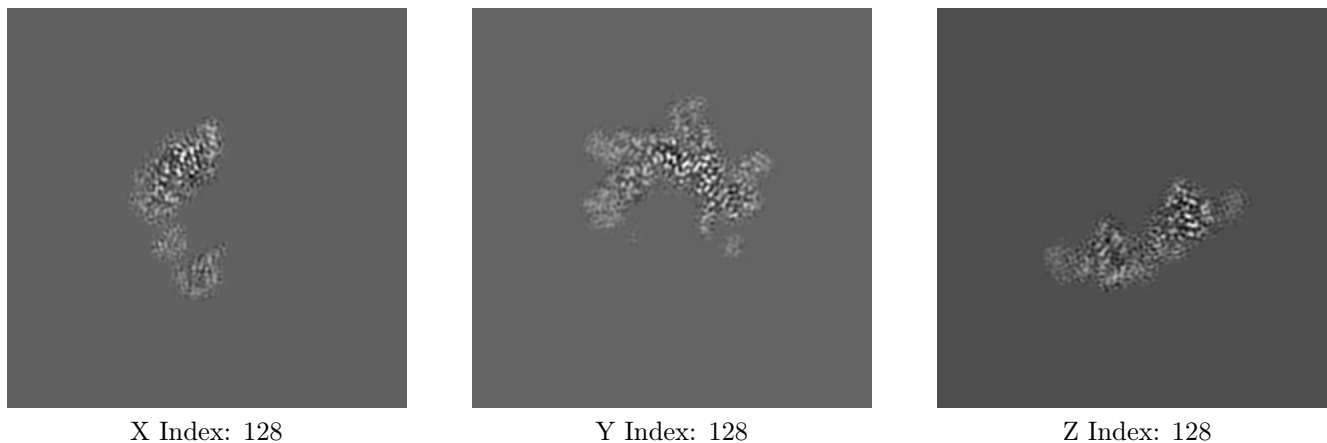
#### 6.1.1 Primary map



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

### 6.2 Central slices [i](#)

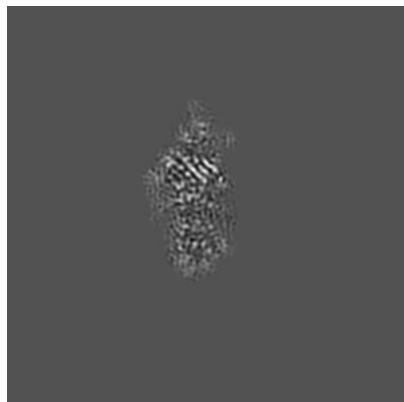
#### 6.2.1 Primary map



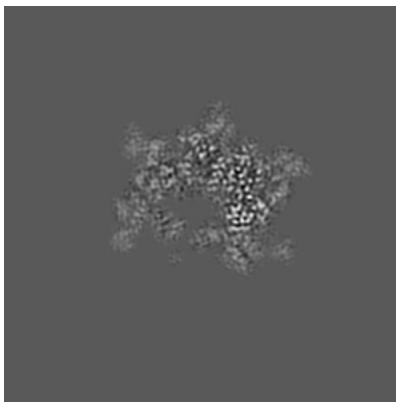
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

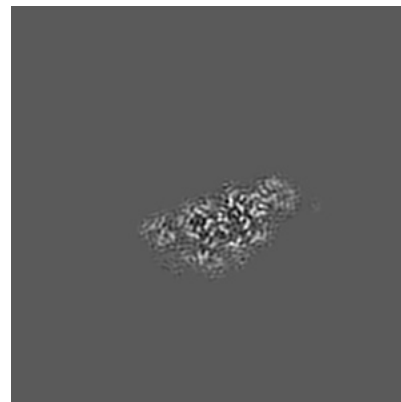
### 6.3.1 Primary map



X Index: 147



Y Index: 118



Z Index: 150

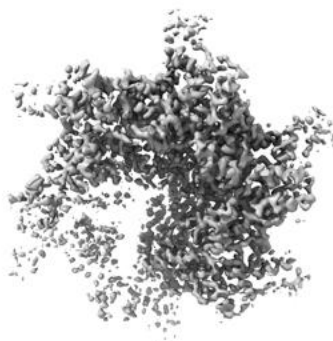
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0749. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.



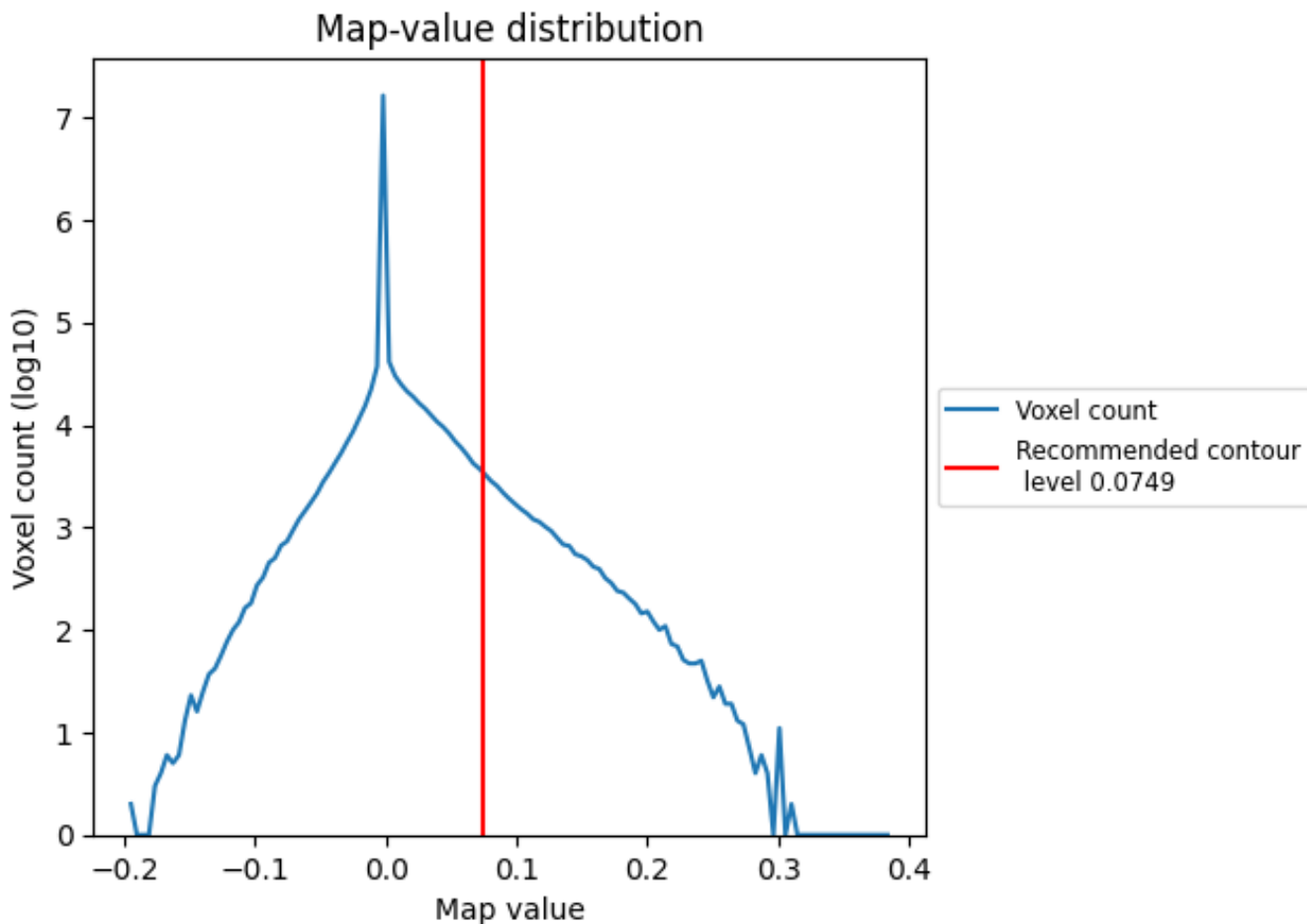
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

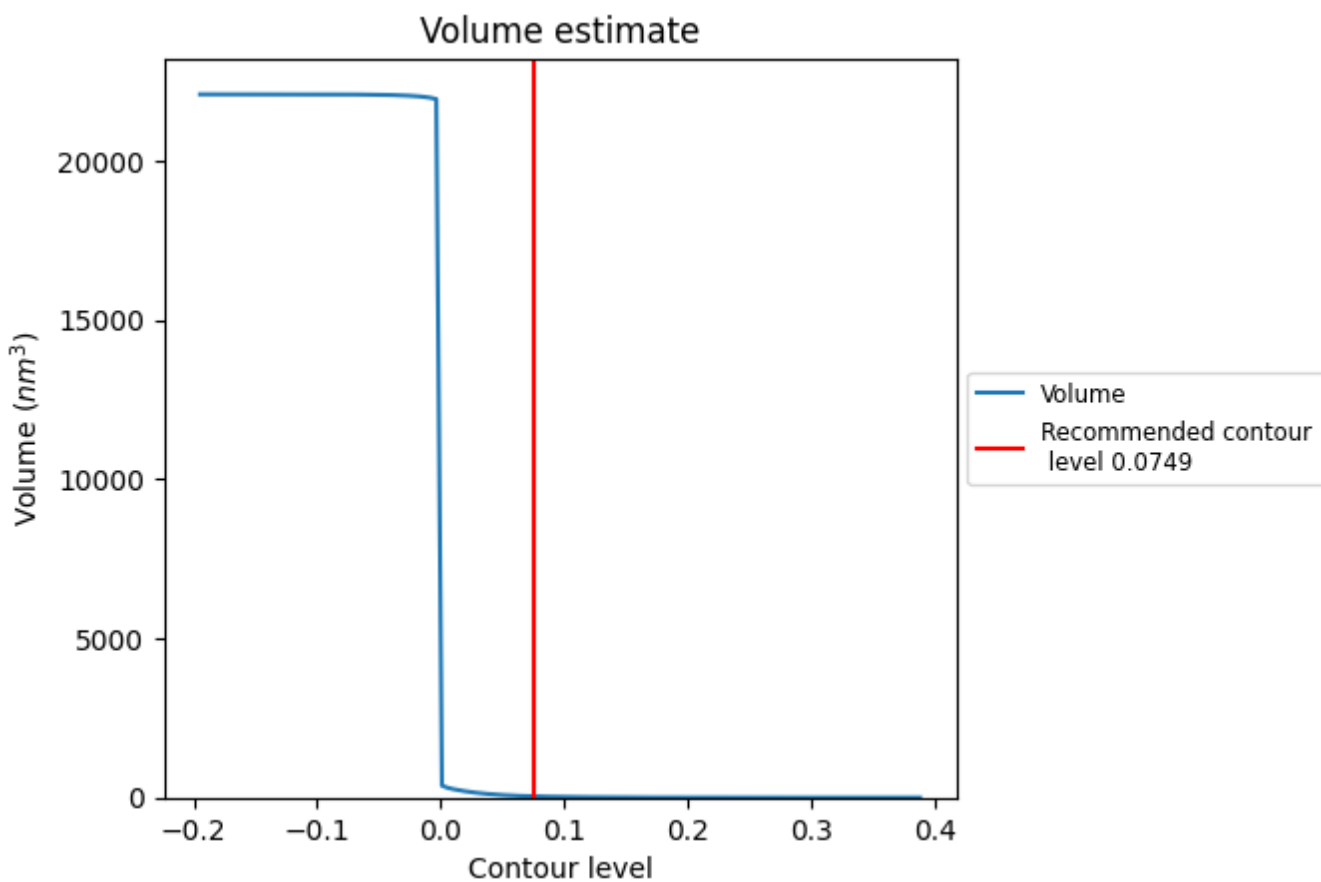
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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

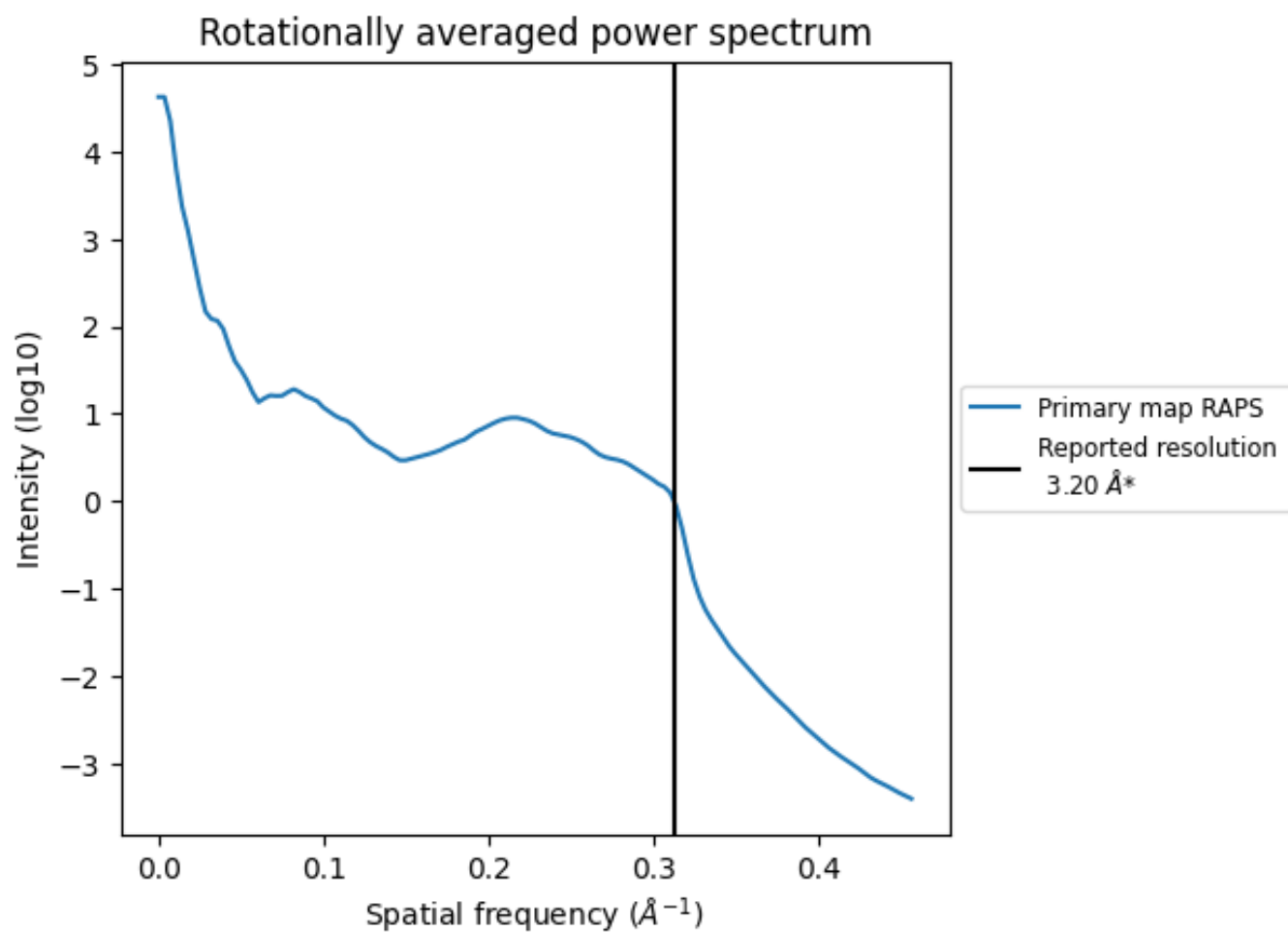
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 39 nm<sup>3</sup>; this corresponds to an approximate mass of 35 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 [i](#)



\*Reported resolution corresponds to spatial frequency of  $0.312 \text{\AA}^{-1}$

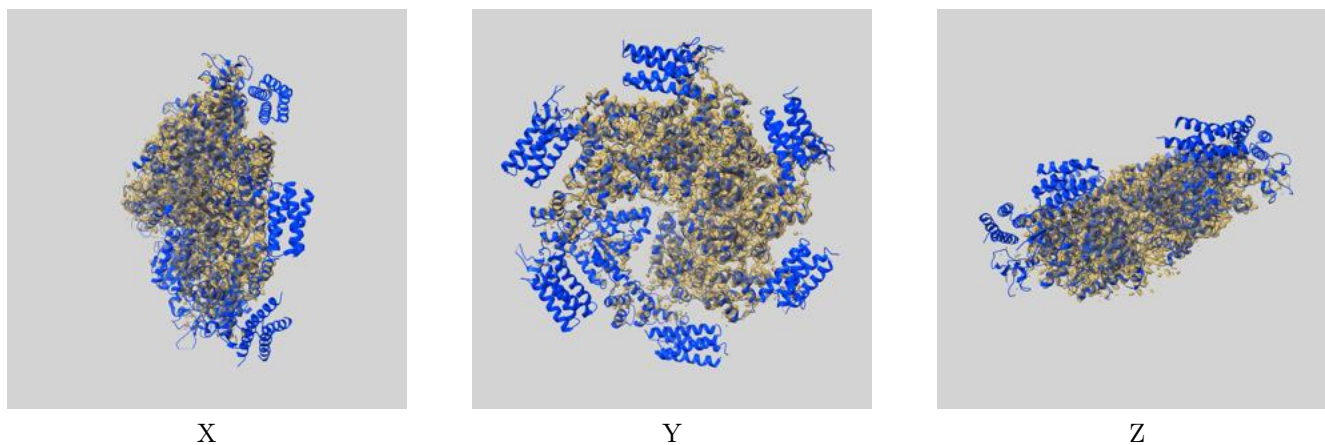
## 8 Fourier-Shell correlation

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

## 9 Map-model fit [i](#)

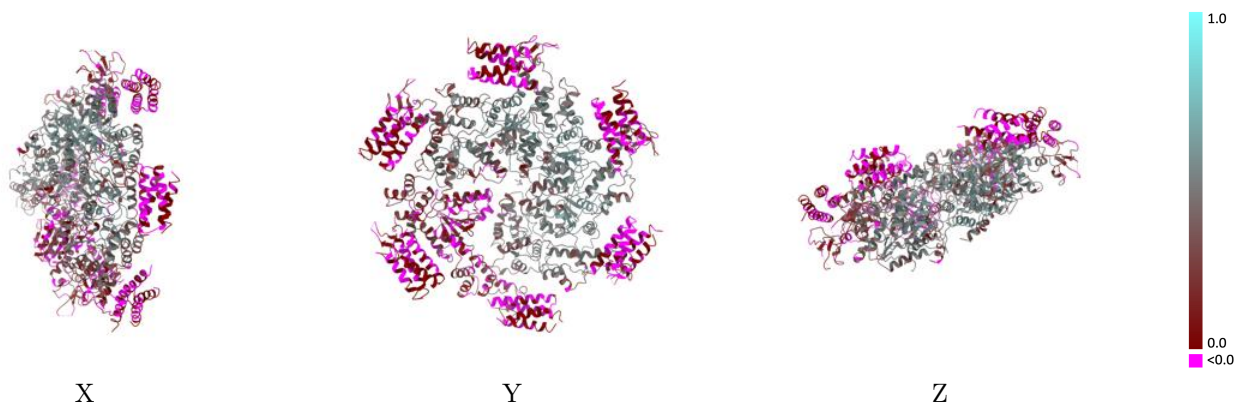
This section contains information regarding the fit between EMDB map EMD-8887 and PDB model 6AP1. Per-residue inclusion information can be found in section 3 on page 10.

### 9.1 Map-model overlay [i](#)



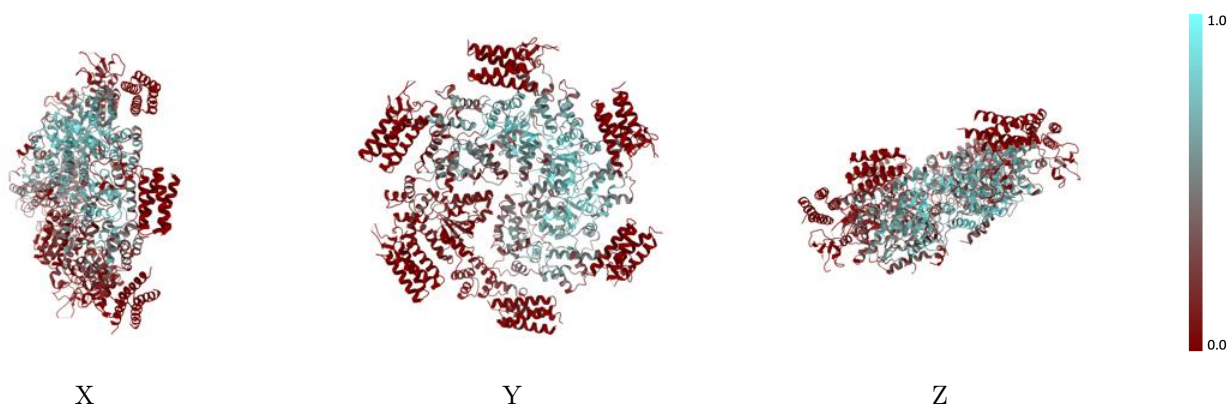
The images above show the 3D surface view of the map at the recommended contour level 0.0749 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



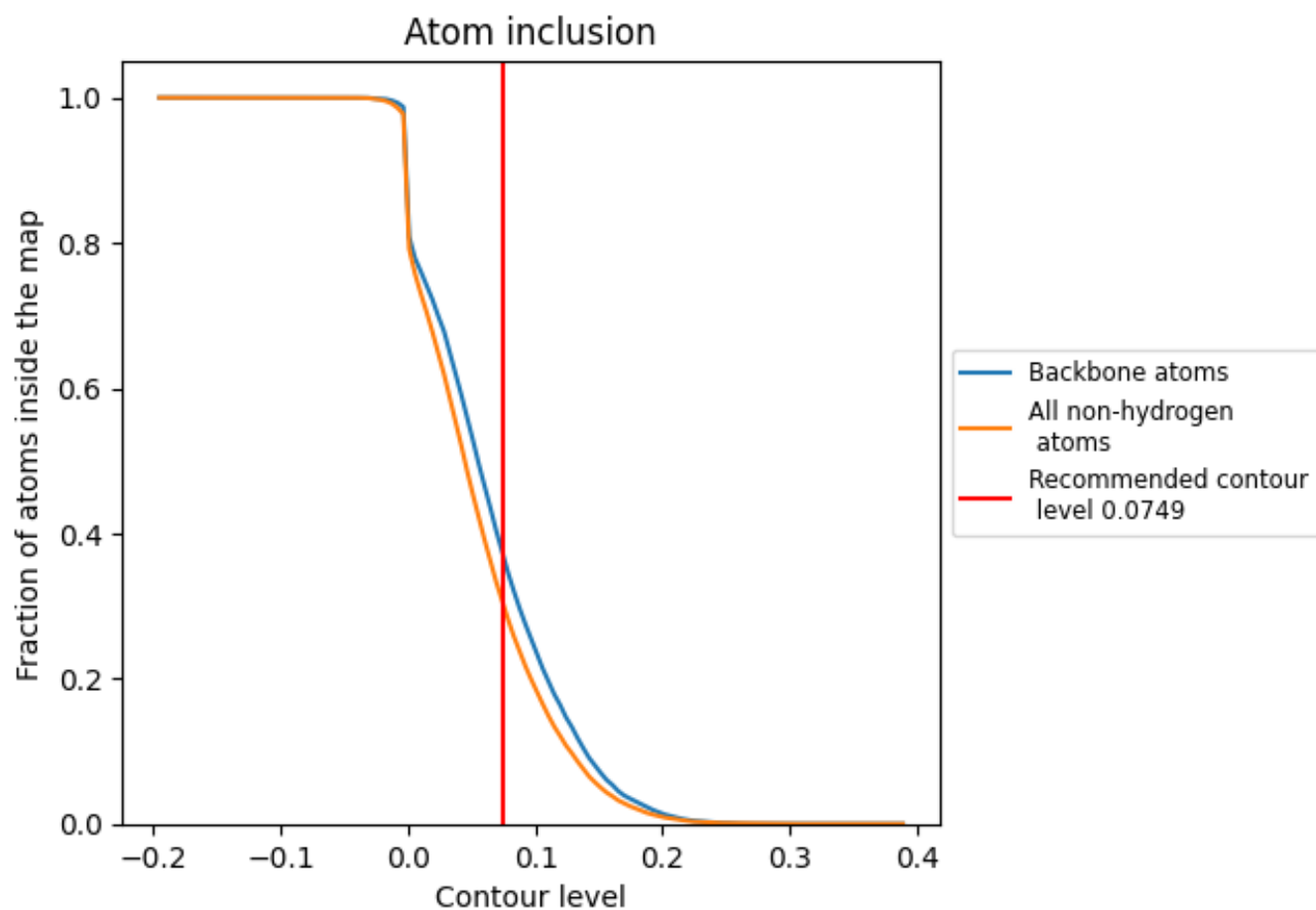
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0749).

## 9.4 Atom inclusion [i](#)











































At the recommended contour level, 37% of all backbone atoms, 30% of all non-hydrogen atoms, are inside the map.



## 9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (0.0749) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3023	 0.2740
A	 0.3750	 0.3850
B	 0.5536	 0.4520
C	 0.5629	 0.4620
D	 0.4947	 0.4220
E	 0.2643	 0.3250
F	 0.0251	 0.0570
G	 0.3433	 0.4940
H	 0.0000	 -0.0030
I	 0.0031	 -0.0450
J	 0.0000	 0.0020
K	 0.0000	 -0.0460
L	 0.0000	 -0.0200
M	 0.0000	 -0.0280
N	 0.0000	 -0.0130
O	 0.0000	 -0.0150
P	 0.0000	 -0.0400
Q	 0.0000	 -0.0400
R	 0.0000	 -0.0290
S	 0.0000	 -0.0310

