



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 02:13 AM UTC

PDB ID : 9BA8 / pdb_00009ba8
Title : O-GlcNAcase (OGA) inhibitor complex for the Treatment of Alzheimer's Disease
Authors : Hendle, J.; Romero, R.
Deposited on : 2024-04-03
Resolution : 2.54 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp>

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:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

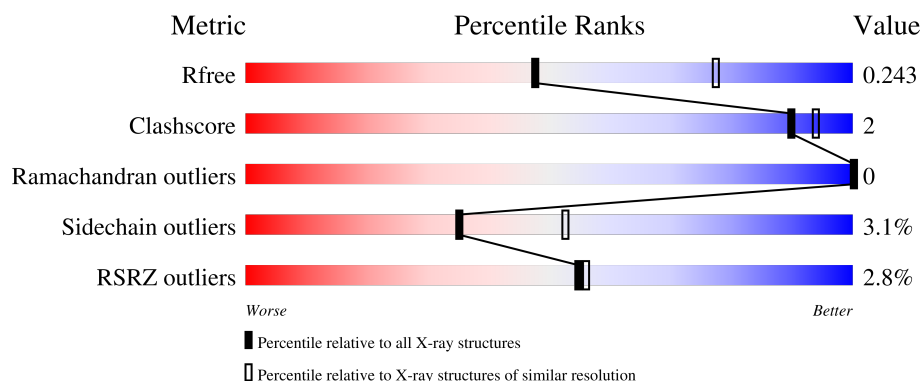
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

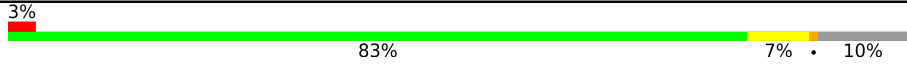
The reported resolution of this entry is 2.54 Å.

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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1091 (2.54-2.54)
Clashscore	190562	1120 (2.54-2.54)
Ramachandran outliers	187476	1106 (2.54-2.54)
Sidechain outliers	187428	1106 (2.54-2.54)
RSRZ outliers	180081	1091 (2.54-2.54)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	499	
1	B	499	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7412 atoms, of which 46 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Protein O-GlcNAcase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	451	Total	C	N	O	S	0	0	0
			3595	2322	593	658	22			
1	B	450	Total	C	N	O	S	0	0	0
			3615	2337	602	654	22			

There are 332 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	53	SER	-	expression tag	UNP O60502
A	54	LEU	-	expression tag	UNP O60502
A	?	-	GLY	deletion	UNP O60502
A	?	-	VAL	deletion	UNP O60502
A	?	-	ARG	deletion	UNP O60502
A	?	-	LYS	deletion	UNP O60502
A	?	-	ASP	deletion	UNP O60502
A	?	-	VAL	deletion	UNP O60502
A	?	-	VAL	deletion	UNP O60502
A	?	-	MET	deletion	UNP O60502
A	?	-	THR	deletion	UNP O60502
A	?	-	ASP	deletion	UNP O60502
A	?	-	SER	deletion	UNP O60502
A	?	-	GLU	deletion	UNP O60502
A	?	-	ASP	deletion	UNP O60502
A	?	-	SER	deletion	UNP O60502
A	?	-	THR	deletion	UNP O60502
A	?	-	VAL	deletion	UNP O60502
A	?	-	SER	deletion	UNP O60502
A	?	-	ILE	deletion	UNP O60502
A	?	-	GLN	deletion	UNP O60502
A	?	-	ILE	deletion	UNP O60502
A	?	-	LYS	deletion	UNP O60502
A	?	-	LEU	deletion	UNP O60502
A	?	-	GLU	deletion	UNP O60502

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ASN	deletion	UNP O60502
A	?	-	GLU	deletion	UNP O60502
A	?	-	GLY	deletion	UNP O60502
A	?	-	SER	deletion	UNP O60502
A	?	-	ASP	deletion	UNP O60502
A	?	-	GLU	deletion	UNP O60502
A	?	-	ASP	deletion	UNP O60502
A	?	-	ILE	deletion	UNP O60502
A	?	-	GLU	deletion	UNP O60502
A	?	-	THR	deletion	UNP O60502
A	?	-	ASP	deletion	UNP O60502
A	?	-	VAL	deletion	UNP O60502
A	?	-	LEU	deletion	UNP O60502
A	?	-	GLY	deletion	UNP O60502
A	?	-	THR	deletion	UNP O60502
A	?	-	PRO	deletion	UNP O60502
A	?	-	LEU	deletion	UNP O60502
A	?	-	VAL	deletion	UNP O60502
A	?	-	ALA	deletion	UNP O60502
A	?	-	ALA	deletion	UNP O60502
A	?	-	PRO	deletion	UNP O60502
A	?	-	SER	deletion	UNP O60502
A	?	-	LEU	deletion	UNP O60502
A	?	-	ASN	deletion	UNP O60502
A	?	-	ALA	deletion	UNP O60502
A	?	-	THR	deletion	UNP O60502
A	?	-	THR	deletion	UNP O60502
A	?	-	VAL	deletion	UNP O60502
A	?	-	VAL	deletion	UNP O60502
A	?	-	THR	deletion	UNP O60502
A	?	-	THR	deletion	UNP O60502
A	?	-	VAL	deletion	UNP O60502
A	?	-	TYR	deletion	UNP O60502
A	?	-	GLN	deletion	UNP O60502
A	?	-	GLU	deletion	UNP O60502
A	?	-	PRO	deletion	UNP O60502
A	?	-	ILE	deletion	UNP O60502
A	?	-	MET	deletion	UNP O60502
A	?	-	SER	deletion	UNP O60502
A	?	-	GLN	deletion	UNP O60502
A	?	-	GLY	deletion	UNP O60502
A	?	-	ALA	deletion	UNP O60502

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ALA	deletion	UNP O60502
A	?	-	LEU	deletion	UNP O60502
A	?	-	SER	deletion	UNP O60502
A	?	-	GLY	deletion	UNP O60502
A	?	-	GLU	deletion	UNP O60502
A	?	-	PRO	deletion	UNP O60502
A	?	-	THR	deletion	UNP O60502
A	?	-	THR	deletion	UNP O60502
A	?	-	LEU	deletion	UNP O60502
A	?	-	THR	deletion	UNP O60502
A	?	-	LYS	deletion	UNP O60502
A	?	-	GLU	deletion	UNP O60502
A	?	-	GLU	deletion	UNP O60502
A	?	-	GLU	deletion	UNP O60502
A	?	-	LYS	deletion	UNP O60502
A	?	-	LYS	deletion	UNP O60502
A	?	-	GLN	deletion	UNP O60502
A	?	-	PRO	deletion	UNP O60502
A	?	-	ASP	deletion	UNP O60502
A	?	-	GLU	deletion	UNP O60502
A	?	-	GLU	deletion	UNP O60502
A	?	-	PRO	deletion	UNP O60502
A	?	-	MET	deletion	UNP O60502
A	?	-	ASP	deletion	UNP O60502
A	?	-	MET	deletion	UNP O60502
A	?	-	VAL	deletion	UNP O60502
A	?	-	VAL	deletion	UNP O60502
A	?	-	GLU	deletion	UNP O60502
A	?	-	LYS	deletion	UNP O60502
A	?	-	GLN	deletion	UNP O60502
A	?	-	GLU	deletion	UNP O60502
A	?	-	GLU	deletion	UNP O60502
A	?	-	THR	deletion	UNP O60502
A	?	-	ASP	deletion	UNP O60502
A	?	-	HIS	deletion	UNP O60502
A	?	-	LYS	deletion	UNP O60502
A	?	-	ASN	deletion	UNP O60502
A	?	-	ASP	deletion	UNP O60502
A	?	-	ASN	deletion	UNP O60502
A	?	-	GLN	deletion	UNP O60502
A	?	-	ILE	deletion	UNP O60502
A	?	-	LEU	deletion	UNP O60502

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	SER	deletion	UNP O60502
A	?	-	GLU	deletion	UNP O60502
A	?	-	ILE	deletion	UNP O60502
A	?	-	VAL	deletion	UNP O60502
A	?	-	GLU	deletion	UNP O60502
A	?	-	ALA	deletion	UNP O60502
A	?	-	LYS	deletion	UNP O60502
A	?	-	MET	deletion	UNP O60502
A	?	-	ALA	deletion	UNP O60502
A	?	-	GLU	deletion	UNP O60502
A	?	-	GLU	deletion	UNP O60502
A	?	-	LEU	deletion	UNP O60502
A	?	-	LYS	deletion	UNP O60502
A	?	-	PRO	deletion	UNP O60502
A	?	-	MET	deletion	UNP O60502
A	?	-	ASP	deletion	UNP O60502
A	?	-	THR	deletion	UNP O60502
A	?	-	ASP	deletion	UNP O60502
A	?	-	LYS	deletion	UNP O60502
A	?	-	GLU	deletion	UNP O60502
A	?	-	SER	deletion	UNP O60502
A	?	-	ILE	deletion	UNP O60502
A	?	-	ALA	deletion	UNP O60502
A	?	-	GLU	deletion	UNP O60502
A	?	-	SER	deletion	UNP O60502
A	?	-	LYS	deletion	UNP O60502
A	?	-	SER	deletion	UNP O60502
A	?	-	PRO	deletion	UNP O60502
A	?	-	GLU	deletion	UNP O60502
A	?	-	MET	deletion	UNP O60502
A	?	-	SER	deletion	UNP O60502
A	?	-	MET	deletion	UNP O60502
A	?	-	GLN	deletion	UNP O60502
A	?	-	GLU	deletion	UNP O60502
A	?	-	ASP	deletion	UNP O60502
A	?	-	CYS	deletion	UNP O60502
A	?	-	ILE	deletion	UNP O60502
A	?	-	SER	deletion	UNP O60502
A	?	-	ASP	deletion	UNP O60502
A	?	-	ILE	deletion	UNP O60502
A	?	-	ALA	deletion	UNP O60502
A	?	-	PRO	deletion	UNP O60502

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	MET	deletion	UNP O60502
A	?	-	GLN	deletion	UNP O60502
A	?	-	THR	deletion	UNP O60502
A	?	-	ASP	deletion	UNP O60502
A	?	-	GLU	deletion	UNP O60502
A	?	-	GLN	deletion	UNP O60502
A	?	-	THR	deletion	UNP O60502
A	?	-	ASN	deletion	UNP O60502
A	?	-	LYS	deletion	UNP O60502
A	?	-	GLU	deletion	UNP O60502
A	?	-	GLN	deletion	UNP O60502
A	?	-	PHE	deletion	UNP O60502
A	?	-	VAL	deletion	UNP O60502
A	596	SER	CYS	conflict	UNP O60502
A	663	GLU	CYS	conflict	UNP O60502
B	53	SER	-	expression tag	UNP O60502
B	54	LEU	-	expression tag	UNP O60502
B	?	-	GLY	deletion	UNP O60502
B	?	-	VAL	deletion	UNP O60502
B	?	-	ARG	deletion	UNP O60502
B	?	-	LYS	deletion	UNP O60502
B	?	-	ASP	deletion	UNP O60502
B	?	-	VAL	deletion	UNP O60502
B	?	-	VAL	deletion	UNP O60502
B	?	-	MET	deletion	UNP O60502
B	?	-	THR	deletion	UNP O60502
B	?	-	ASP	deletion	UNP O60502
B	?	-	SER	deletion	UNP O60502
B	?	-	GLU	deletion	UNP O60502
B	?	-	ASP	deletion	UNP O60502
B	?	-	SER	deletion	UNP O60502
B	?	-	THR	deletion	UNP O60502
B	?	-	VAL	deletion	UNP O60502
B	?	-	SER	deletion	UNP O60502
B	?	-	ILE	deletion	UNP O60502
B	?	-	GLN	deletion	UNP O60502
B	?	-	ILE	deletion	UNP O60502
B	?	-	LYS	deletion	UNP O60502
B	?	-	LEU	deletion	UNP O60502
B	?	-	GLU	deletion	UNP O60502
B	?	-	ASN	deletion	UNP O60502
B	?	-	GLU	deletion	UNP O60502

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	GLY	deletion	UNP O60502
B	?	-	SER	deletion	UNP O60502
B	?	-	ASP	deletion	UNP O60502
B	?	-	GLU	deletion	UNP O60502
B	?	-	ASP	deletion	UNP O60502
B	?	-	ILE	deletion	UNP O60502
B	?	-	GLU	deletion	UNP O60502
B	?	-	THR	deletion	UNP O60502
B	?	-	ASP	deletion	UNP O60502
B	?	-	VAL	deletion	UNP O60502
B	?	-	LEU	deletion	UNP O60502
B	?	-	GLY	deletion	UNP O60502
B	?	-	THR	deletion	UNP O60502
B	?	-	PRO	deletion	UNP O60502
B	?	-	LEU	deletion	UNP O60502
B	?	-	VAL	deletion	UNP O60502
B	?	-	ALA	deletion	UNP O60502
B	?	-	ALA	deletion	UNP O60502
B	?	-	PRO	deletion	UNP O60502
B	?	-	SER	deletion	UNP O60502
B	?	-	LEU	deletion	UNP O60502
B	?	-	ASN	deletion	UNP O60502
B	?	-	ALA	deletion	UNP O60502
B	?	-	THR	deletion	UNP O60502
B	?	-	THR	deletion	UNP O60502
B	?	-	VAL	deletion	UNP O60502
B	?	-	VAL	deletion	UNP O60502
B	?	-	THR	deletion	UNP O60502
B	?	-	THR	deletion	UNP O60502
B	?	-	VAL	deletion	UNP O60502
B	?	-	TYR	deletion	UNP O60502
B	?	-	GLN	deletion	UNP O60502
B	?	-	GLU	deletion	UNP O60502
B	?	-	PRO	deletion	UNP O60502
B	?	-	ILE	deletion	UNP O60502
B	?	-	MET	deletion	UNP O60502
B	?	-	SER	deletion	UNP O60502
B	?	-	GLN	deletion	UNP O60502
B	?	-	GLY	deletion	UNP O60502
B	?	-	ALA	deletion	UNP O60502
B	?	-	ALA	deletion	UNP O60502
B	?	-	LEU	deletion	UNP O60502

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	SER	deletion	UNP O60502
B	?	-	GLY	deletion	UNP O60502
B	?	-	GLU	deletion	UNP O60502
B	?	-	PRO	deletion	UNP O60502
B	?	-	THR	deletion	UNP O60502
B	?	-	THR	deletion	UNP O60502
B	?	-	LEU	deletion	UNP O60502
B	?	-	THR	deletion	UNP O60502
B	?	-	LYS	deletion	UNP O60502
B	?	-	GLU	deletion	UNP O60502
B	?	-	GLU	deletion	UNP O60502
B	?	-	GLU	deletion	UNP O60502
B	?	-	LYS	deletion	UNP O60502
B	?	-	LYS	deletion	UNP O60502
B	?	-	GLN	deletion	UNP O60502
B	?	-	PRO	deletion	UNP O60502
B	?	-	ASP	deletion	UNP O60502
B	?	-	GLU	deletion	UNP O60502
B	?	-	GLU	deletion	UNP O60502
B	?	-	PRO	deletion	UNP O60502
B	?	-	MET	deletion	UNP O60502
B	?	-	ASP	deletion	UNP O60502
B	?	-	MET	deletion	UNP O60502
B	?	-	VAL	deletion	UNP O60502
B	?	-	VAL	deletion	UNP O60502
B	?	-	GLU	deletion	UNP O60502
B	?	-	LYS	deletion	UNP O60502
B	?	-	GLN	deletion	UNP O60502
B	?	-	GLU	deletion	UNP O60502
B	?	-	GLU	deletion	UNP O60502
B	?	-	THR	deletion	UNP O60502
B	?	-	ASP	deletion	UNP O60502
B	?	-	HIS	deletion	UNP O60502
B	?	-	LYS	deletion	UNP O60502
B	?	-	ASN	deletion	UNP O60502
B	?	-	ASP	deletion	UNP O60502
B	?	-	ASN	deletion	UNP O60502
B	?	-	GLN	deletion	UNP O60502
B	?	-	ILE	deletion	UNP O60502
B	?	-	LEU	deletion	UNP O60502
B	?	-	SER	deletion	UNP O60502
B	?	-	GLU	deletion	UNP O60502

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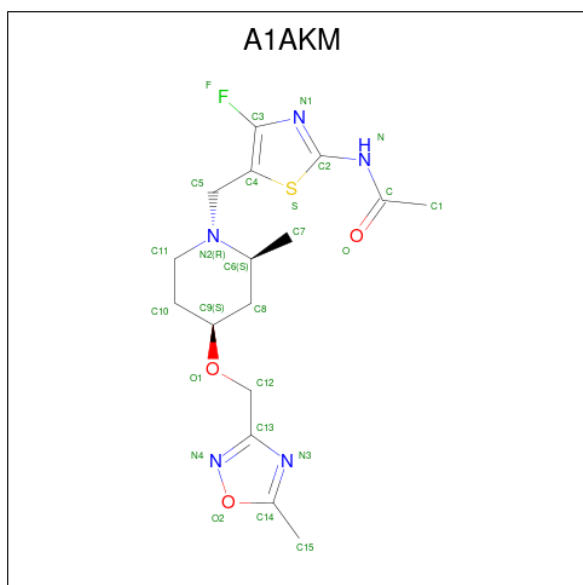
Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	ILE	deletion	UNP O60502
B	?	-	VAL	deletion	UNP O60502
B	?	-	GLU	deletion	UNP O60502
B	?	-	ALA	deletion	UNP O60502
B	?	-	LYS	deletion	UNP O60502
B	?	-	MET	deletion	UNP O60502
B	?	-	ALA	deletion	UNP O60502
B	?	-	GLU	deletion	UNP O60502
B	?	-	GLU	deletion	UNP O60502
B	?	-	LEU	deletion	UNP O60502
B	?	-	LYS	deletion	UNP O60502
B	?	-	PRO	deletion	UNP O60502
B	?	-	MET	deletion	UNP O60502
B	?	-	ASP	deletion	UNP O60502
B	?	-	THR	deletion	UNP O60502
B	?	-	ASP	deletion	UNP O60502
B	?	-	LYS	deletion	UNP O60502
B	?	-	GLU	deletion	UNP O60502
B	?	-	SER	deletion	UNP O60502
B	?	-	ILE	deletion	UNP O60502
B	?	-	ALA	deletion	UNP O60502
B	?	-	GLU	deletion	UNP O60502
B	?	-	SER	deletion	UNP O60502
B	?	-	LYS	deletion	UNP O60502
B	?	-	SER	deletion	UNP O60502
B	?	-	PRO	deletion	UNP O60502
B	?	-	GLU	deletion	UNP O60502
B	?	-	MET	deletion	UNP O60502
B	?	-	SER	deletion	UNP O60502
B	?	-	MET	deletion	UNP O60502
B	?	-	GLN	deletion	UNP O60502
B	?	-	GLU	deletion	UNP O60502
B	?	-	ASP	deletion	UNP O60502
B	?	-	CYS	deletion	UNP O60502
B	?	-	ILE	deletion	UNP O60502
B	?	-	SER	deletion	UNP O60502
B	?	-	ASP	deletion	UNP O60502
B	?	-	ILE	deletion	UNP O60502
B	?	-	ALA	deletion	UNP O60502
B	?	-	PRO	deletion	UNP O60502
B	?	-	MET	deletion	UNP O60502
B	?	-	GLN	deletion	UNP O60502

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	THR	deletion	UNP O60502
B	?	-	ASP	deletion	UNP O60502
B	?	-	GLU	deletion	UNP O60502
B	?	-	GLN	deletion	UNP O60502
B	?	-	THR	deletion	UNP O60502
B	?	-	ASN	deletion	UNP O60502
B	?	-	LYS	deletion	UNP O60502
B	?	-	GLU	deletion	UNP O60502
B	?	-	GLN	deletion	UNP O60502
B	?	-	PHE	deletion	UNP O60502
B	?	-	VAL	deletion	UNP O60502
B	596	SER	CYS	conflict	UNP O60502
B	663	GLU	CYS	conflict	UNP O60502

- Molecule 2 is N-[4-fluoro-5-((2S,4S)-2-methyl-4-[(5-methyl-1,2,4-oxadiazol-3-yl)methoxy]piperidin-1-yl)methyl]-1,3-thiazol-2-yl]acetamide (CCD ID: A1AKM) (formula: C₁₆H₂₂FN₅O₃S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
2	A	1	Total	C	F	H	N	O	S	0	0
			49	16	1	23	5	3	1		
2	B	1	Total	C	F	H	N	O	S	0	0
			49	16	1	23	5	3	1		

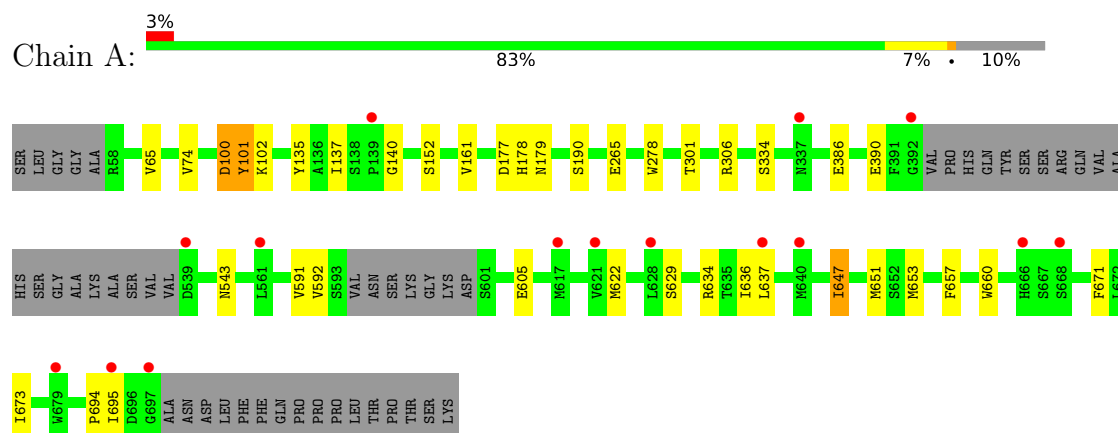
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	47	Total 47	O 47	0	0
3	B	57	Total 57	O 57	0	0

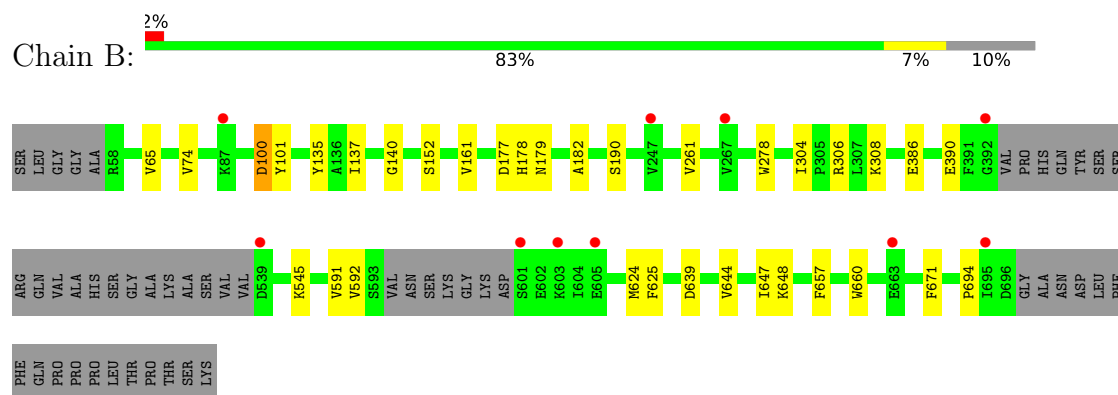
3 Residue-property plots [i](#)

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 electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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: Protein O-GlcNAcase



• Molecule 1: Protein O-GlcNAcase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	132.10Å 134.58Å 61.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.38 – 2.54 35.38 – 2.54	Depositor EDS
% Data completeness (in resolution range)	98.7 (35.38-2.54) 98.6 (35.38-2.54)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.23 (at 2.55Å)	Xtriage
Refinement program	BUSTER 2.11.6	Depositor
R, R_{free}	0.200 , 0.231 0.209 , 0.243	Depositor DCC
R_{free} test set	1783 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	56.6	Xtriage
Anisotropy	0.013	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 39.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.050 for k,h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7412	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.35% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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: A1AKM

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	0.84	0/3693	1.30	9/5016 (0.2%)
1	B	0.86	2/3714 (0.1%)	1.30	5/5041 (0.1%)
All	All	0.85	2/7407 (0.0%)	1.30	14/10057 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	304	ILE	CA-CB	6.40	1.57	1.54
1	B	304	ILE	CA-C	6.18	1.58	1.52

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	100	ASP	N-CA-C	-7.42	97.16	108.67
1	B	190	SER	CA-C-N	6.39	128.84	120.28
1	B	190	SER	C-N-CA	6.39	128.84	120.28
1	B	100	ASP	N-CA-C	-6.21	97.06	107.99
1	A	140	GLY	N-CA-C	5.88	121.51	113.99
1	A	647	ILE	CA-C-N	5.78	128.35	120.54
1	A	647	ILE	C-N-CA	5.78	128.35	120.54
1	B	140	GLY	N-CA-C	5.73	121.33	113.99
1	A	636	ILE	N-CA-C	-5.70	104.38	110.36
1	A	190	SER	CA-C-N	5.61	127.79	120.28
1	A	190	SER	C-N-CA	5.61	127.79	120.28
1	A	278	TRP	N-CA-C	-5.41	97.69	107.75
1	A	695	ILE	N-CA-C	-5.19	102.81	109.30
1	B	278	TRP	N-CA-C	-5.11	98.25	107.75

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	3595	0	3427	18	0
1	B	3615	0	3483	11	0
2	A	26	23	0	0	0
2	B	26	23	0	1	0
3	A	47	0	0	0	0
3	B	57	0	0	0	0
All	All	7366	46	6910	26	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.

All (26) 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:622:MET:HE1	1:A:651:MET:HB3	1.84	0.59
1:A:74:VAL:HG21	1:B:74:VAL:HG11	1.87	0.56
1:A:265:GLU:CG	1:A:306:ARG:HH12	2.19	0.55
1:A:653:MET:HE1	1:A:673:ILE:HG23	1.92	0.51
1:B:591:VAL:HG23	1:B:592:VAL:HG13	1.94	0.50
1:A:543:ASN:HB3	1:B:182:ALA:HB3	1.94	0.49
1:A:591:VAL:HG23	1:A:592:VAL:HG13	1.96	0.48
1:A:694:PRO:HG3	1:B:657:PHE:CE1	2.49	0.48
2:B:801:A1AKM:S	2:B:801:A1AKM:O	2.72	0.46
1:A:647:ILE:HG13	1:A:651:MET:HE2	1.98	0.46
1:B:135:TYR:CG	1:B:161:VAL:HG11	2.52	0.44
1:B:624:MET:HE3	1:B:644:VAL:HG13	1.99	0.43
1:A:637:LEU:O	1:A:637:LEU:HG	2.17	0.43
1:A:647:ILE:O	1:A:651:MET:HB2	2.19	0.43
1:B:660:TRP:CD2	1:B:671:PHE:HB2	2.54	0.42
1:A:301:THR:HG21	1:A:334:SER:OG	2.20	0.42
1:A:177:ASP:OD1	1:A:179:ASN:HB2	2.19	0.42
1:B:625:PHE:CG	1:B:648:LYS:HG3	2.55	0.42
1:A:657:PHE:CE1	1:B:694:PRO:HG3	2.55	0.42
1:A:660:TRP:CD2	1:A:671:PHE:HB2	2.55	0.41
1:A:135:TYR:CG	1:A:161:VAL:HG11	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:261:VAL:HG13	1:B:306:ARG:HD3	2.02	0.41
1:A:653:MET:CE	1:A:673:ILE:HG23	2.51	0.41
1:A:265:GLU:HG3	1:A:306:ARG:NH1	2.36	0.41
1:B:177:ASP:OD1	1:B:179:ASN:HB2	2.21	0.41
1:A:101:TYR:CZ	1:A:102:LYS:HE3	2.56	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 X-ray entries followed by that with respect to entries of similar resolution.

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	445/499 (89%)	432 (97%)	13 (3%)	0	100	100
1	B	444/499 (89%)	431 (97%)	13 (3%)	0	100	100
All	All	889/998 (89%)	863 (97%)	26 (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 X-ray entries followed by that with respect to entries of similar resolution.

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	374/438 (85%)	363 (97%)	11 (3%)	37	55
1	B	379/438 (86%)	367 (97%)	12 (3%)	34	51
All	All	753/876 (86%)	730 (97%)	23 (3%)	35	53

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	65	VAL
1	A	100	ASP
1	A	101	TYR
1	A	137	ILE
1	A	152	SER
1	A	178	HIS
1	A	386	GLU
1	A	390	GLU
1	A	605	GLU
1	A	629	SER
1	A	634	ARG
1	B	65	VAL
1	B	100	ASP
1	B	101	TYR
1	B	137	ILE
1	B	152	SER
1	B	178	HIS
1	B	308	LYS
1	B	386	GLU
1	B	390	GLU
1	B	545	LYS
1	B	639	ASP
1	B	647	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	204	GLN
1	A	389	GLN
1	A	676	GLN
1	B	204	GLN
1	B	377	GLN
1	B	389	GLN
1	B	670	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	A1AKM	A	801	-	27,28,28	1.25	3 (11%)	26,39,39	0.95	1 (3%)
2	A1AKM	B	801	-	27,28,28	0.73	1 (3%)	26,39,39	0.93	2 (7%)

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
2	A1AKM	A	801	-	-	2/13/26/26	0/3/3/3
2	A1AKM	B	801	-	-	0/13/26/26	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	A1AKM	C3-C4	4.35	1.39	1.36
2	A	801	A1AKM	C5-C4	-3.57	1.45	1.50
2	B	801	A1AKM	C11-N2	2.11	1.51	1.47
2	A	801	A1AKM	C11-N2	2.03	1.50	1.47

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	801	A1AKM	C8-C6-N2	-2.73	106.12	110.59
2	A	801	A1AKM	C7-C6-C8	-2.72	106.83	112.69
2	B	801	A1AKM	C7-C6-C8	-2.07	108.23	112.69

There are no chirality outliers.

All (2) torsion outliers are listed below:

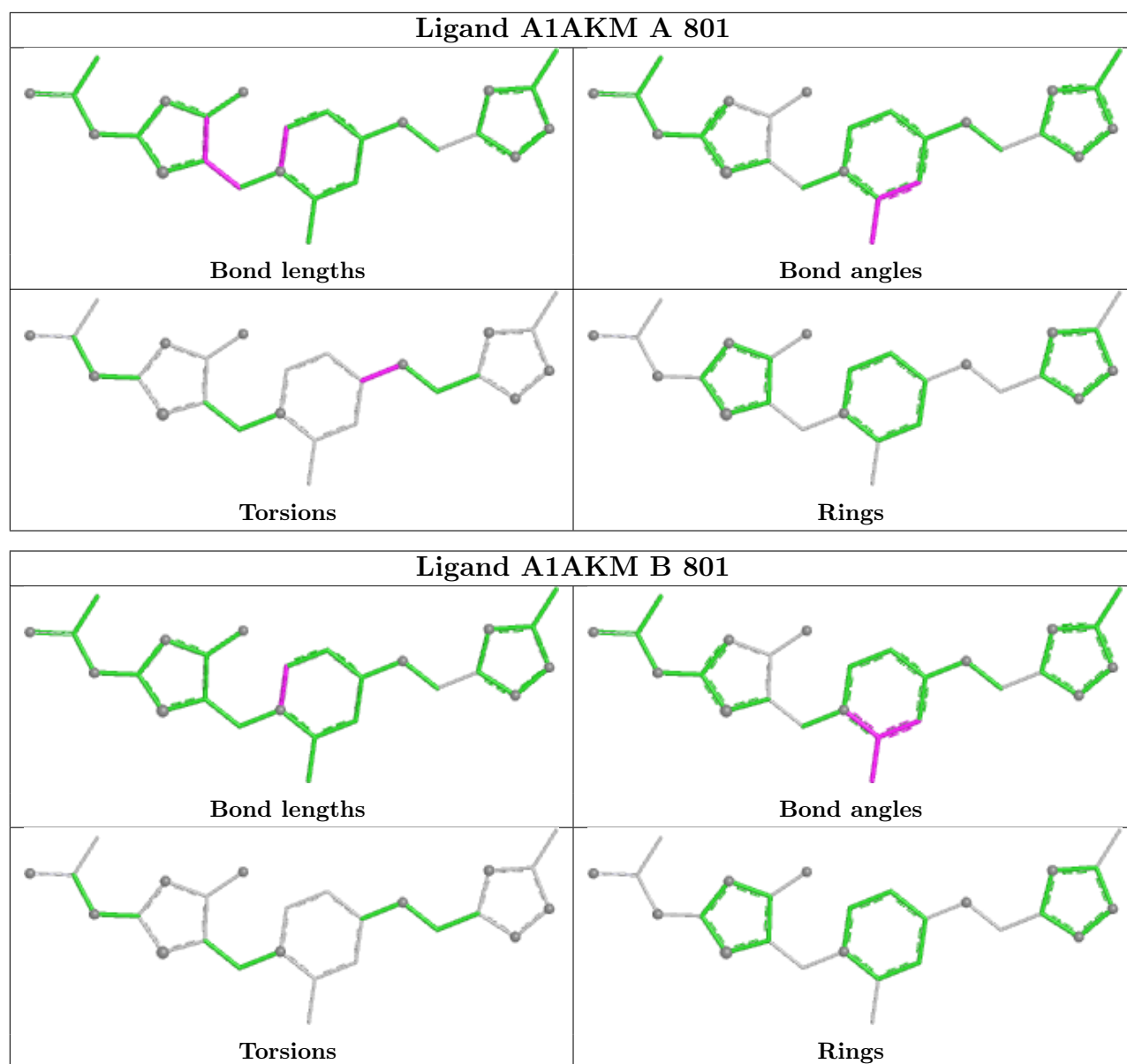
Mol	Chain	Res	Type	Atoms
2	A	801	A1AKM	C10-C9-O1-C12
2	A	801	A1AKM	C8-C9-O1-C12

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	801	A1AKM	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 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	451/499 (90%)	0.25	15 (3%) 49 50	40, 61, 92, 119	0
1	B	450/499 (90%)	0.19	10 (2%) 62 63	38, 57, 86, 101	0
All	All	901/998 (90%)	0.22	25 (2%) 55 56	38, 58, 91, 119	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	392	GLY	5.3
1	A	337	ASN	3.9
1	B	392	GLY	3.6
1	B	247	VAL	3.5
1	A	695	ILE	3.1
1	A	139	PRO	2.9
1	A	539	ASP	2.8
1	B	601	SER	2.8
1	A	617	MET	2.6
1	A	561	LEU	2.6
1	B	605	GLU	2.5
1	A	666	HIS	2.5
1	A	628	LEU	2.5
1	A	637	LEU	2.4
1	A	679	TRP	2.4
1	A	640	MET	2.4
1	A	668	SER	2.4
1	A	697	GLY	2.3
1	B	663	GLU	2.3
1	A	621	VAL	2.2
1	B	695	ILE	2.1
1	B	267	VAL	2.1
1	B	539	ASP	2.0
1	B	87	LYS	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	603	LYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

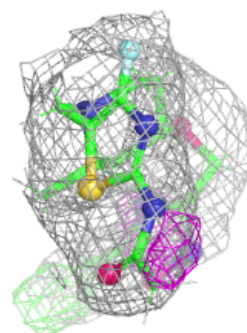
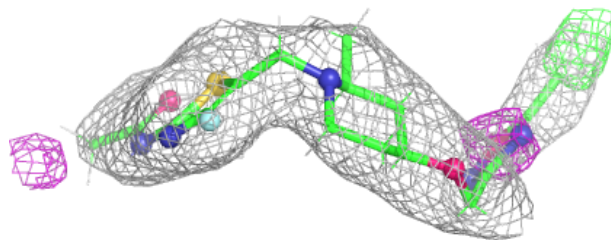
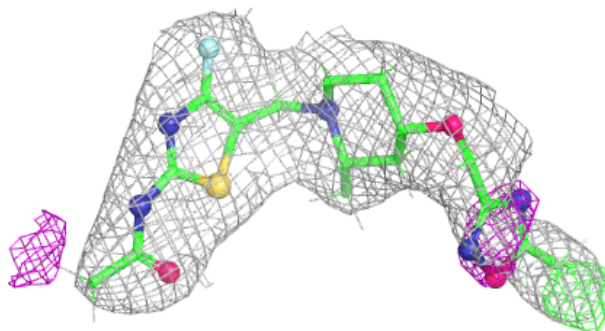
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	A1AKM	B	801	26/26	0.91	0.11	39,58,92,94	0
2	A1AKM	A	801	26/26	0.92	0.09	43,49,89,89	0

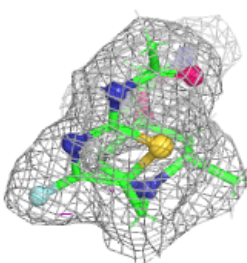
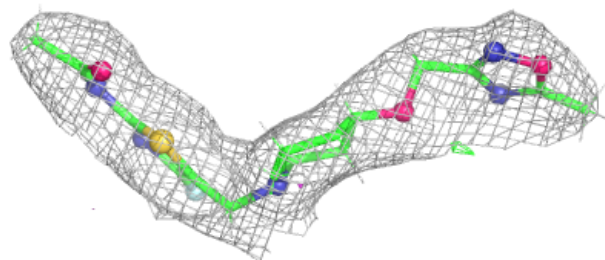
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around A1AKM B 801:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around A1AKM A 801:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.