



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 22, 2026 – 01:18 AM UTC

PDB ID : 6AZN / pdb_00006azn
Title : Structural and biochemical characterization of a non-canonical biuret hydrolase (BiuH) from the cyanuric acid catabolism pathway of *Rhizobium leguminosorum* bv. *viciae* 3841
Authors : Peat, T.S.; Esquirol, L.; Newman, J.; Scott, C.
Deposited on : 2017-09-11
Resolution : 1.75 Å(reported)

This is a wwPDB X-ray Structure 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/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
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

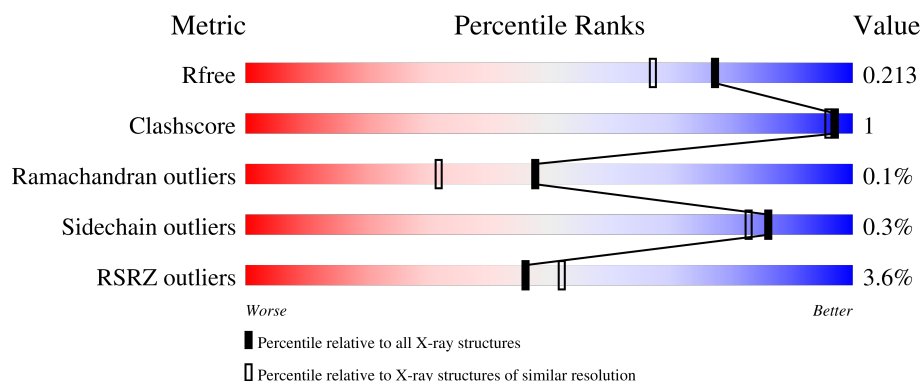
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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.



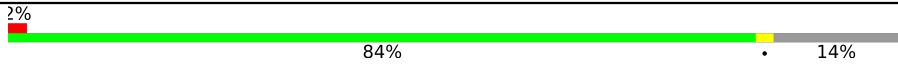
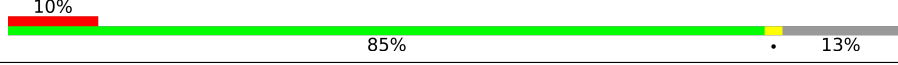
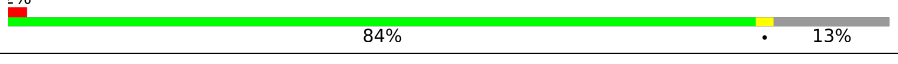
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3183 (1.76-1.76)
Clashscore	190562	3299 (1.76-1.76)
Ramachandran outliers	187476	3274 (1.76-1.76)
Sidechain outliers	187428	3274 (1.76-1.76)
RSRZ outliers	180081	3183 (1.76-1.76)

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	262	84% 14%
1	B	262	6% 82% 15%
1	C	262	84% 14%
1	D	262	2% 84% 14%
1	F	262	83% 14%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	G	262	
1	H	262	
1	I	262	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	PO4	A	302	-	X	-	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15574 atoms, of which 0 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 Putative amidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	226	Total	C	N	O	S	0	5	0
			1780	1116	318	333	13			
1	B	223	Total	C	N	O	S	0	3	0
			1721	1079	303	327	12			
1	C	226	Total	C	N	O	S	0	4	0
			1766	1111	313	329	13			
1	D	226	Total	C	N	O	S	0	5	0
			1776	1115	316	332	13			
1	F	226	Total	C	N	O	S	0	4	0
			1768	1110	314	331	13			
1	G	226	Total	C	N	O	S	0	2	0
			1748	1099	309	327	13			
1	H	229	Total	C	N	O	S	0	2	0
			1766	1109	313	331	13			
1	I	227	Total	C	N	O	S	0	4	0
			1773	1115	312	333	13			

There are 240 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP Q1M7F4
A	-18	GLY	-	expression tag	UNP Q1M7F4
A	-17	SER	-	expression tag	UNP Q1M7F4
A	-16	SER	-	expression tag	UNP Q1M7F4
A	-15	HIS	-	expression tag	UNP Q1M7F4
A	-14	HIS	-	expression tag	UNP Q1M7F4
A	-13	HIS	-	expression tag	UNP Q1M7F4
A	-12	HIS	-	expression tag	UNP Q1M7F4
A	-11	HIS	-	expression tag	UNP Q1M7F4
A	-10	HIS	-	expression tag	UNP Q1M7F4
A	-9	SER	-	expression tag	UNP Q1M7F4
A	-8	SER	-	expression tag	UNP Q1M7F4
A	-7	GLY	-	expression tag	UNP Q1M7F4

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	LEU	-	expression tag	UNP Q1M7F4
A	-5	VAL	-	expression tag	UNP Q1M7F4
A	-4	PRO	-	expression tag	UNP Q1M7F4
A	-3	ARG	-	expression tag	UNP Q1M7F4
A	-2	GLY	-	expression tag	UNP Q1M7F4
A	-1	SER	-	expression tag	UNP Q1M7F4
A	0	HIS	-	expression tag	UNP Q1M7F4
A	175	SER	CYS	conflict	UNP Q1M7F4
A	234	GLY	-	expression tag	UNP Q1M7F4
A	235	LEU	-	expression tag	UNP Q1M7F4
A	236	VAL	-	expression tag	UNP Q1M7F4
A	237	PRO	-	expression tag	UNP Q1M7F4
A	238	ARG	-	expression tag	UNP Q1M7F4
A	239	GLY	-	expression tag	UNP Q1M7F4
A	240	SER	-	expression tag	UNP Q1M7F4
A	241	ILE	-	expression tag	UNP Q1M7F4
A	242	GLU	-	expression tag	UNP Q1M7F4
B	-19	MET	-	initiating methionine	UNP Q1M7F4
B	-18	GLY	-	expression tag	UNP Q1M7F4
B	-17	SER	-	expression tag	UNP Q1M7F4
B	-16	SER	-	expression tag	UNP Q1M7F4
B	-15	HIS	-	expression tag	UNP Q1M7F4
B	-14	HIS	-	expression tag	UNP Q1M7F4
B	-13	HIS	-	expression tag	UNP Q1M7F4
B	-12	HIS	-	expression tag	UNP Q1M7F4
B	-11	HIS	-	expression tag	UNP Q1M7F4
B	-10	HIS	-	expression tag	UNP Q1M7F4
B	-9	SER	-	expression tag	UNP Q1M7F4
B	-8	SER	-	expression tag	UNP Q1M7F4
B	-7	GLY	-	expression tag	UNP Q1M7F4
B	-6	LEU	-	expression tag	UNP Q1M7F4
B	-5	VAL	-	expression tag	UNP Q1M7F4
B	-4	PRO	-	expression tag	UNP Q1M7F4
B	-3	ARG	-	expression tag	UNP Q1M7F4
B	-2	GLY	-	expression tag	UNP Q1M7F4
B	-1	SER	-	expression tag	UNP Q1M7F4
B	0	HIS	-	expression tag	UNP Q1M7F4
B	175	SER	CYS	conflict	UNP Q1M7F4
B	234	GLY	-	expression tag	UNP Q1M7F4
B	235	LEU	-	expression tag	UNP Q1M7F4
B	236	VAL	-	expression tag	UNP Q1M7F4
B	237	PRO	-	expression tag	UNP Q1M7F4

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	238	ARG	-	expression tag	UNP Q1M7F4
B	239	GLY	-	expression tag	UNP Q1M7F4
B	240	SER	-	expression tag	UNP Q1M7F4
B	241	ILE	-	expression tag	UNP Q1M7F4
B	242	GLU	-	expression tag	UNP Q1M7F4
C	-19	MET	-	initiating methionine	UNP Q1M7F4
C	-18	GLY	-	expression tag	UNP Q1M7F4
C	-17	SER	-	expression tag	UNP Q1M7F4
C	-16	SER	-	expression tag	UNP Q1M7F4
C	-15	HIS	-	expression tag	UNP Q1M7F4
C	-14	HIS	-	expression tag	UNP Q1M7F4
C	-13	HIS	-	expression tag	UNP Q1M7F4
C	-12	HIS	-	expression tag	UNP Q1M7F4
C	-11	HIS	-	expression tag	UNP Q1M7F4
C	-10	HIS	-	expression tag	UNP Q1M7F4
C	-9	SER	-	expression tag	UNP Q1M7F4
C	-8	SER	-	expression tag	UNP Q1M7F4
C	-7	GLY	-	expression tag	UNP Q1M7F4
C	-6	LEU	-	expression tag	UNP Q1M7F4
C	-5	VAL	-	expression tag	UNP Q1M7F4
C	-4	PRO	-	expression tag	UNP Q1M7F4
C	-3	ARG	-	expression tag	UNP Q1M7F4
C	-2	GLY	-	expression tag	UNP Q1M7F4
C	-1	SER	-	expression tag	UNP Q1M7F4
C	0	HIS	-	expression tag	UNP Q1M7F4
C	175	SER	CYS	conflict	UNP Q1M7F4
C	234	GLY	-	expression tag	UNP Q1M7F4
C	235	LEU	-	expression tag	UNP Q1M7F4
C	236	VAL	-	expression tag	UNP Q1M7F4
C	237	PRO	-	expression tag	UNP Q1M7F4
C	238	ARG	-	expression tag	UNP Q1M7F4
C	239	GLY	-	expression tag	UNP Q1M7F4
C	240	SER	-	expression tag	UNP Q1M7F4
C	241	ILE	-	expression tag	UNP Q1M7F4
C	242	GLU	-	expression tag	UNP Q1M7F4
D	-19	MET	-	initiating methionine	UNP Q1M7F4
D	-18	GLY	-	expression tag	UNP Q1M7F4
D	-17	SER	-	expression tag	UNP Q1M7F4
D	-16	SER	-	expression tag	UNP Q1M7F4
D	-15	HIS	-	expression tag	UNP Q1M7F4
D	-14	HIS	-	expression tag	UNP Q1M7F4
D	-13	HIS	-	expression tag	UNP Q1M7F4

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	-12	HIS	-	expression tag	UNP Q1M7F4
D	-11	HIS	-	expression tag	UNP Q1M7F4
D	-10	HIS	-	expression tag	UNP Q1M7F4
D	-9	SER	-	expression tag	UNP Q1M7F4
D	-8	SER	-	expression tag	UNP Q1M7F4
D	-7	GLY	-	expression tag	UNP Q1M7F4
D	-6	LEU	-	expression tag	UNP Q1M7F4
D	-5	VAL	-	expression tag	UNP Q1M7F4
D	-4	PRO	-	expression tag	UNP Q1M7F4
D	-3	ARG	-	expression tag	UNP Q1M7F4
D	-2	GLY	-	expression tag	UNP Q1M7F4
D	-1	SER	-	expression tag	UNP Q1M7F4
D	0	HIS	-	expression tag	UNP Q1M7F4
D	175	SER	CYS	conflict	UNP Q1M7F4
D	234	GLY	-	expression tag	UNP Q1M7F4
D	235	LEU	-	expression tag	UNP Q1M7F4
D	236	VAL	-	expression tag	UNP Q1M7F4
D	237	PRO	-	expression tag	UNP Q1M7F4
D	238	ARG	-	expression tag	UNP Q1M7F4
D	239	GLY	-	expression tag	UNP Q1M7F4
D	240	SER	-	expression tag	UNP Q1M7F4
D	241	ILE	-	expression tag	UNP Q1M7F4
D	242	GLU	-	expression tag	UNP Q1M7F4
F	-19	MET	-	initiating methionine	UNP Q1M7F4
F	-18	GLY	-	expression tag	UNP Q1M7F4
F	-17	SER	-	expression tag	UNP Q1M7F4
F	-16	SER	-	expression tag	UNP Q1M7F4
F	-15	HIS	-	expression tag	UNP Q1M7F4
F	-14	HIS	-	expression tag	UNP Q1M7F4
F	-13	HIS	-	expression tag	UNP Q1M7F4
F	-12	HIS	-	expression tag	UNP Q1M7F4
F	-11	HIS	-	expression tag	UNP Q1M7F4
F	-10	HIS	-	expression tag	UNP Q1M7F4
F	-9	SER	-	expression tag	UNP Q1M7F4
F	-8	SER	-	expression tag	UNP Q1M7F4
F	-7	GLY	-	expression tag	UNP Q1M7F4
F	-6	LEU	-	expression tag	UNP Q1M7F4
F	-5	VAL	-	expression tag	UNP Q1M7F4
F	-4	PRO	-	expression tag	UNP Q1M7F4
F	-3	ARG	-	expression tag	UNP Q1M7F4
F	-2	GLY	-	expression tag	UNP Q1M7F4
F	-1	SER	-	expression tag	UNP Q1M7F4

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
F	0	HIS	-	expression tag	UNP Q1M7F4
F	175	SER	CYS	conflict	UNP Q1M7F4
F	234	GLY	-	expression tag	UNP Q1M7F4
F	235	LEU	-	expression tag	UNP Q1M7F4
F	236	VAL	-	expression tag	UNP Q1M7F4
F	237	PRO	-	expression tag	UNP Q1M7F4
F	238	ARG	-	expression tag	UNP Q1M7F4
F	239	GLY	-	expression tag	UNP Q1M7F4
F	240	SER	-	expression tag	UNP Q1M7F4
F	241	ILE	-	expression tag	UNP Q1M7F4
F	242	GLU	-	expression tag	UNP Q1M7F4
G	-19	MET	-	initiating methionine	UNP Q1M7F4
G	-18	GLY	-	expression tag	UNP Q1M7F4
G	-17	SER	-	expression tag	UNP Q1M7F4
G	-16	SER	-	expression tag	UNP Q1M7F4
G	-15	HIS	-	expression tag	UNP Q1M7F4
G	-14	HIS	-	expression tag	UNP Q1M7F4
G	-13	HIS	-	expression tag	UNP Q1M7F4
G	-12	HIS	-	expression tag	UNP Q1M7F4
G	-11	HIS	-	expression tag	UNP Q1M7F4
G	-10	HIS	-	expression tag	UNP Q1M7F4
G	-9	SER	-	expression tag	UNP Q1M7F4
G	-8	SER	-	expression tag	UNP Q1M7F4
G	-7	GLY	-	expression tag	UNP Q1M7F4
G	-6	LEU	-	expression tag	UNP Q1M7F4
G	-5	VAL	-	expression tag	UNP Q1M7F4
G	-4	PRO	-	expression tag	UNP Q1M7F4
G	-3	ARG	-	expression tag	UNP Q1M7F4
G	-2	GLY	-	expression tag	UNP Q1M7F4
G	-1	SER	-	expression tag	UNP Q1M7F4
G	0	HIS	-	expression tag	UNP Q1M7F4
G	175	SER	CYS	conflict	UNP Q1M7F4
G	234	GLY	-	expression tag	UNP Q1M7F4
G	235	LEU	-	expression tag	UNP Q1M7F4
G	236	VAL	-	expression tag	UNP Q1M7F4
G	237	PRO	-	expression tag	UNP Q1M7F4
G	238	ARG	-	expression tag	UNP Q1M7F4
G	239	GLY	-	expression tag	UNP Q1M7F4
G	240	SER	-	expression tag	UNP Q1M7F4
G	241	ILE	-	expression tag	UNP Q1M7F4
G	242	GLU	-	expression tag	UNP Q1M7F4
H	-19	MET	-	initiating methionine	UNP Q1M7F4

Continued on next page...

Continued from previous page...

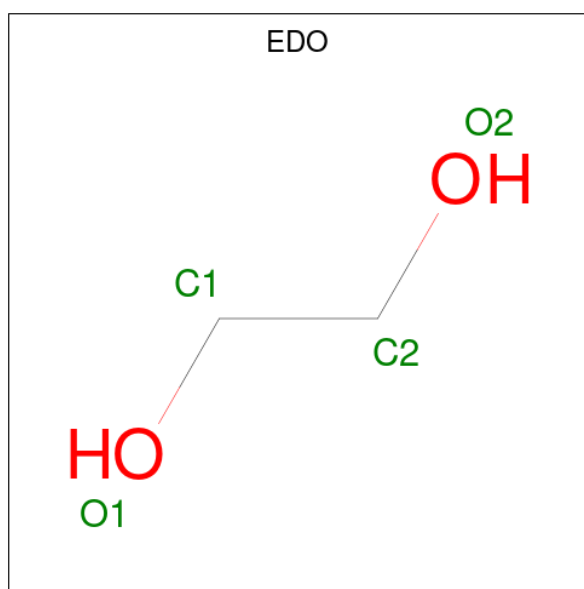
Chain	Residue	Modelled	Actual	Comment	Reference
H	-18	GLY	-	expression tag	UNP Q1M7F4
H	-17	SER	-	expression tag	UNP Q1M7F4
H	-16	SER	-	expression tag	UNP Q1M7F4
H	-15	HIS	-	expression tag	UNP Q1M7F4
H	-14	HIS	-	expression tag	UNP Q1M7F4
H	-13	HIS	-	expression tag	UNP Q1M7F4
H	-12	HIS	-	expression tag	UNP Q1M7F4
H	-11	HIS	-	expression tag	UNP Q1M7F4
H	-10	HIS	-	expression tag	UNP Q1M7F4
H	-9	SER	-	expression tag	UNP Q1M7F4
H	-8	SER	-	expression tag	UNP Q1M7F4
H	-7	GLY	-	expression tag	UNP Q1M7F4
H	-6	LEU	-	expression tag	UNP Q1M7F4
H	-5	VAL	-	expression tag	UNP Q1M7F4
H	-4	PRO	-	expression tag	UNP Q1M7F4
H	-3	ARG	-	expression tag	UNP Q1M7F4
H	-2	GLY	-	expression tag	UNP Q1M7F4
H	-1	SER	-	expression tag	UNP Q1M7F4
H	0	HIS	-	expression tag	UNP Q1M7F4
H	175	SER	CYS	conflict	UNP Q1M7F4
H	234	GLY	-	expression tag	UNP Q1M7F4
H	235	LEU	-	expression tag	UNP Q1M7F4
H	236	VAL	-	expression tag	UNP Q1M7F4
H	237	PRO	-	expression tag	UNP Q1M7F4
H	238	ARG	-	expression tag	UNP Q1M7F4
H	239	GLY	-	expression tag	UNP Q1M7F4
H	240	SER	-	expression tag	UNP Q1M7F4
H	241	ILE	-	expression tag	UNP Q1M7F4
H	242	GLU	-	expression tag	UNP Q1M7F4
I	-19	MET	-	initiating methionine	UNP Q1M7F4
I	-18	GLY	-	expression tag	UNP Q1M7F4
I	-17	SER	-	expression tag	UNP Q1M7F4
I	-16	SER	-	expression tag	UNP Q1M7F4
I	-15	HIS	-	expression tag	UNP Q1M7F4
I	-14	HIS	-	expression tag	UNP Q1M7F4
I	-13	HIS	-	expression tag	UNP Q1M7F4
I	-12	HIS	-	expression tag	UNP Q1M7F4
I	-11	HIS	-	expression tag	UNP Q1M7F4
I	-10	HIS	-	expression tag	UNP Q1M7F4
I	-9	SER	-	expression tag	UNP Q1M7F4
I	-8	SER	-	expression tag	UNP Q1M7F4
I	-7	GLY	-	expression tag	UNP Q1M7F4

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
I	-6	LEU	-	expression tag	UNP Q1M7F4
I	-5	VAL	-	expression tag	UNP Q1M7F4
I	-4	PRO	-	expression tag	UNP Q1M7F4
I	-3	ARG	-	expression tag	UNP Q1M7F4
I	-2	GLY	-	expression tag	UNP Q1M7F4
I	-1	SER	-	expression tag	UNP Q1M7F4
I	0	HIS	-	expression tag	UNP Q1M7F4
I	175	SER	CYS	conflict	UNP Q1M7F4
I	234	GLY	-	expression tag	UNP Q1M7F4
I	235	LEU	-	expression tag	UNP Q1M7F4
I	236	VAL	-	expression tag	UNP Q1M7F4
I	237	PRO	-	expression tag	UNP Q1M7F4
I	238	ARG	-	expression tag	UNP Q1M7F4
I	239	GLY	-	expression tag	UNP Q1M7F4
I	240	SER	-	expression tag	UNP Q1M7F4
I	241	ILE	-	expression tag	UNP Q1M7F4
I	242	GLU	-	expression tag	UNP Q1M7F4

- Molecule 2 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



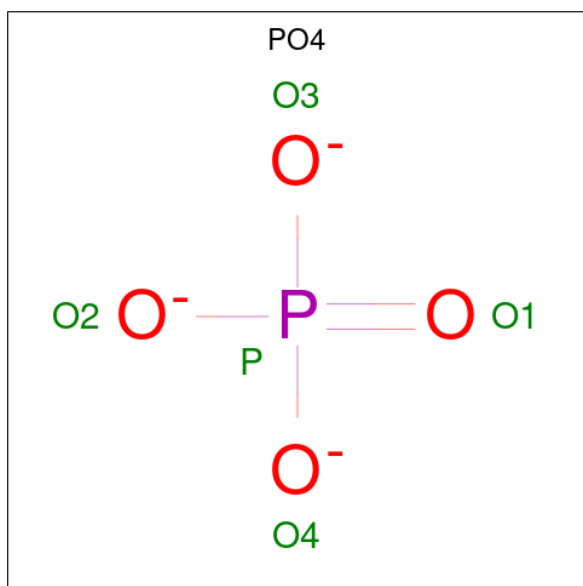
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		
2	C	1	Total	C	O	0	0
			4	2	2		
2	I	1	Total	C	O	0	0
			4	2	2		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	I	1	Total	C	O	0	0
			4	2	2		

- Molecule 3 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	P	0	0
			5	4	1		
3	F	1	Total	O	P	0	0
			5	4	1		
3	I	1	Total	O	P	0	0
			5	4	1		

- Molecule 4 is water.

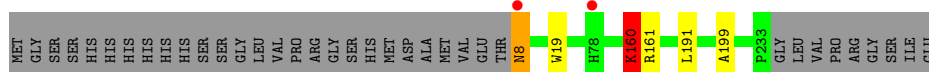
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	200	Total	O	0	0
			200	200		
4	B	187	Total	O	0	0
			187	187		
4	C	197	Total	O	0	0
			197	197		
4	D	194	Total	O	0	0
			194	194		
4	F	189	Total	O	0	0
			189	189		

Continued on next page...

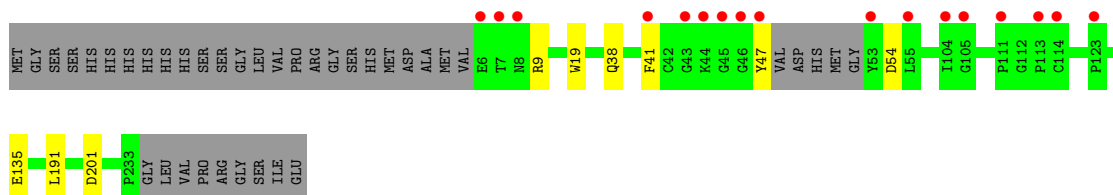
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	G	163	Total 163	O 163	0	0
4	H	112	Total 112	O 112	0	0
4	I	203	Total 203	O 203	0	0

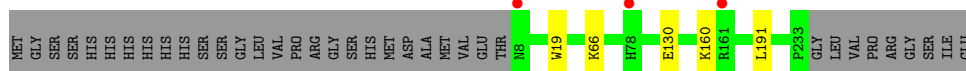
- Molecule 1: Putative amidase

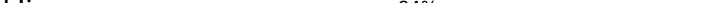


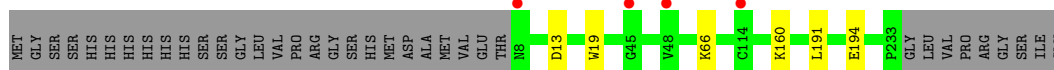
- Chain B:  6% 82% 15%



- Chain C:  84% 14% 2%



- Chain D:  2% 84% 14%

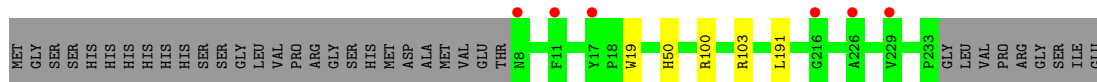


- Chain F:  83% 14% 3%



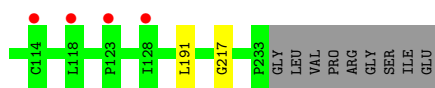
- Molecule 1: Putative amidase

Chain G:  2% 84% 14%



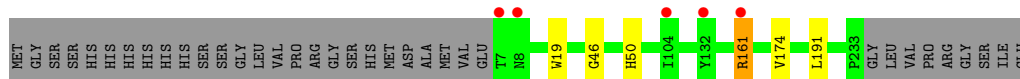
- Molecule 1: Putative amidase

Chain H:  10% 85% 13%



- Molecule 1: Putative amidase

Chain I:  2% 84% 13%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	74.18Å 86.92Å 342.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.48 – 1.75 44.48 – 1.75	Depositor EDS
% Data completeness (in resolution range)	99.1 (44.48-1.75) 99.1 (44.48-1.75)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.80 (at 1.75Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.174 , 0.204 0.185 , 0.213	Depositor DCC
R_{free} test set	11028 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	25.6	Xtriage
Anisotropy	0.025	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 30.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	15574	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.58% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: PO4, EDO

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	1.11	0/1820	1.03	2/2470 (0.1%)
1	B	1.25	5/1756 (0.3%)	1.06	2/2384 (0.1%)
1	C	1.15	0/1806	1.01	0/2452
1	D	1.11	0/1815	0.98	0/2462
1	F	1.06	1/1807 (0.1%)	0.99	1/2452 (0.0%)
1	G	1.06	0/1787	0.95	1/2426 (0.0%)
1	H	1.04	1/1805 (0.1%)	0.95	1/2451 (0.0%)
1	I	1.06	0/1813	1.00	1/2463 (0.0%)
All	All	1.10	7/14409 (0.0%)	1.00	8/19560 (0.0%)

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	38	GLN	C-O	-6.46	1.16	1.23
1	B	9	ARG	N-CA	6.14	1.53	1.46
1	F	60	ALA	C-N	6.01	1.39	1.33
1	H	7	THR	CA-C	5.74	1.60	1.52
1	B	38	GLN	CA-C	5.62	1.59	1.52

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	161	ARG	NE-CZ-NH2	8.22	126.60	119.20
1	H	8	ASN	N-CA-C	7.42	126.60	110.80
1	A	160	LYS	CB-CG-CD	7.27	128.02	111.30
1	B	9	ARG	N-CA-CB	6.52	121.05	110.43
1	G	103	ARG	NE-CZ-NH2	5.88	124.49	119.20

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	1780	0	1748	5	0
1	B	1721	0	1684	2	0
1	C	1766	0	1739	3	0
1	D	1776	0	1750	4	0
1	F	1768	0	1740	3	0
1	G	1748	0	1723	3	0
1	H	1766	0	1733	3	0
1	I	1773	0	1737	3	0
2	A	4	0	6	0	0
2	C	4	0	6	0	0
2	I	8	0	12	1	0
3	A	5	0	0	1	0
3	F	5	0	0	0	0
3	I	5	0	0	0	0
4	A	200	0	0	1	0
4	B	187	0	0	1	0
4	C	197	0	0	1	0
4	D	194	0	0	3	0
4	F	189	0	0	1	0
4	G	163	0	0	1	0
4	H	112	0	0	1	0
4	I	203	0	0	0	0
All	All	15574	0	13878	25	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 1.

The worst 5 of 25 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:194[A]:GLU:OE2	4:F:401:HOH:O	1.99	0.79
1:H:5:VAL:CB	4:H:405:HOH:O	2.33	0.76
1:B:135[B]:GLU:OE2	4:B:301:HOH:O	2.15	0.63
1:A:8:ASN:C	1:A:8:ASN:ND2	2.57	0.63
1:I:161:ARG:NH2	2:I:302:EDO:O1	2.41	0.54

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	229/262 (87%)	225 (98%)	4 (2%)	0	100	100
1	B	222/262 (85%)	215 (97%)	7 (3%)	0	100	100
1	C	228/262 (87%)	223 (98%)	5 (2%)	0	100	100
1	D	229/262 (87%)	224 (98%)	5 (2%)	0	100	100
1	F	228/262 (87%)	224 (98%)	3 (1%)	1 (0%)	30	15
1	G	226/262 (86%)	223 (99%)	3 (1%)	0	100	100
1	H	229/262 (87%)	223 (97%)	6 (3%)	0	100	100
1	I	229/262 (87%)	225 (98%)	3 (1%)	1 (0%)	30	15
All	All	1820/2096 (87%)	1782 (98%)	36 (2%)	2 (0%)	48	32

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	174	VAL
1	I	174	VAL

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	189/214 (88%)	187 (99%)	2 (1%)	65	52

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	181/214 (85%)	180 (99%)	1 (1%)	78	71
1	C	187/214 (87%)	187 (100%)	0	100	100
1	D	188/214 (88%)	186 (99%)	2 (1%)	65	52
1	F	187/214 (87%)	186 (100%)	1 (0%)	81	75
1	G	185/214 (86%)	185 (100%)	0	100	100
1	H	186/214 (87%)	186 (100%)	0	100	100
1	I	187/214 (87%)	187 (100%)	0	100	100
All	All	1490/1712 (87%)	1484 (100%)	6 (0%)	86	80

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	66[A]	LYS
1	D	66[B]	LYS
1	F	230	GLU
1	A	160	LYS
1	A	8	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	159	GLN
1	H	10	HIS
1	I	159	GLN
1	H	159	GLN
1	C	10	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

7 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	$\# Z > 2$
3	PO4	A	302	-	4,4,4	1.68	1 (25%)	6,6,6	2.65	3 (50%)
2	EDO	C	301	-	3,3,3	0.64	0	2,2,2	1.37	0
3	PO4	F	301	-	4,4,4	1.47	1 (25%)	6,6,6	1.58	2 (33%)
2	EDO	I	301	-	3,3,3	0.54	0	2,2,2	1.17	0
3	PO4	I	303	-	4,4,4	0.96	0	6,6,6	1.76	2 (33%)
2	EDO	A	301	-	3,3,3	0.78	0	2,2,2	0.85	0
2	EDO	I	302	-	3,3,3	0.26	0	2,2,2	1.08	0

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	EDO	A	301	-	-	1/1/1/1	-
2	EDO	C	301	-	-	0/1/1/1	-
2	EDO	I	302	-	-	1/1/1/1	-
2	EDO	I	301	-	-	0/1/1/1	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	302	PO4	P-O3	-3.31	1.45	1.54
3	F	301	PO4	P-O2	-2.37	1.47	1.54

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	302	PO4	O4-P-O3	-4.06	95.27	107.91
3	A	302	PO4	O4-P-O1	3.71	124.08	110.95
3	I	303	PO4	O4-P-O3	2.63	116.11	107.91
3	A	302	PO4	O2-P-O1	-2.28	102.89	110.95
3	I	303	PO4	O3-P-O1	-2.24	103.02	110.95

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	I	302	EDO	O1-C1-C2-O2
2	A	301	EDO	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	302	PO4	1	0
2	I	302	EDO	1	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	226/262 (86%)	-0.26	2 (0%) 81 86	10, 23, 35, 64	5 (2%)
1	B	223/262 (85%)	0.16	17 (7%) 20 23	12, 24, 52, 75	3 (1%)
1	C	226/262 (86%)	0.13	3 (1%) 75 81	10, 27, 39, 63	4 (1%)
1	D	226/262 (86%)	0.11	4 (1%) 67 74	12, 26, 40, 66	5 (2%)
1	F	226/262 (86%)	0.04	2 (0%) 81 86	12, 27, 40, 60	4 (1%)
1	G	226/262 (86%)	0.40	6 (2%) 56 62	15, 31, 47, 67	2 (0%)
1	H	229/262 (87%)	0.89	26 (11%) 10 11	19, 35, 61, 81	2 (0%)
1	I	227/262 (86%)	-0.16	5 (2%) 62 69	10, 24, 33, 75	4 (1%)
All	All	1809/2096 (86%)	0.16	65 (3%) 46 52	10, 27, 48, 81	29 (1%)

The worst 5 of 65 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	7	THR	6.5
1	B	53	TYR	5.7
1	H	7	THR	5.1
1	H	6	GLU	5.0
1	H	5	VAL	4.9

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(Å ²)	Q<0.9
3	PO4	A	302	5/5	0.76	0.24	43,45,48,61	5
3	PO4	F	301	5/5	0.81	0.18	49,50,55,69	5
2	EDO	A	301	4/4	0.84	0.16	39,46,47,51	0
2	EDO	C	301	4/4	0.85	0.19	43,53,53,55	0
2	EDO	I	302	4/4	0.85	0.18	50,52,56,59	0
3	PO4	I	303	5/5	0.87	0.20	44,49,56,60	5
2	EDO	I	301	4/4	0.90	0.10	34,35,36,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.