



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 15, 2026 – 12:49 AM UTC

PDB ID : 6AZQ / pdb_00006azq
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 : 2.22 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
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

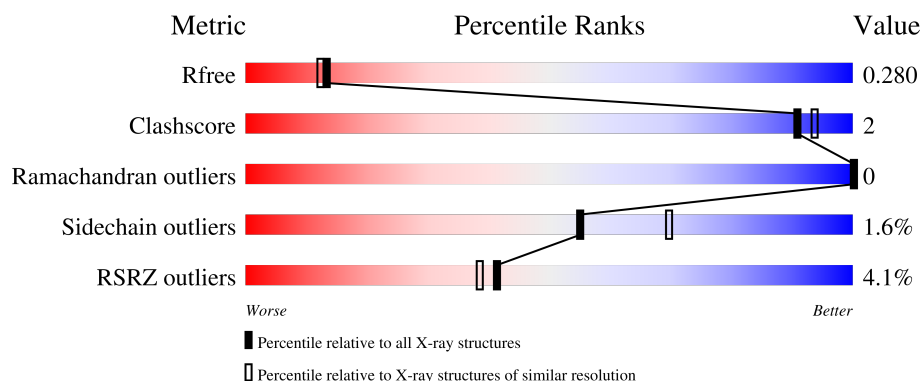
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.22 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	7682 (2.24-2.20)
Clashscore	190562	8402 (2.24-2.20)
Ramachandran outliers	187476	8303 (2.24-2.20)
Sidechain outliers	187428	8304 (2.24-2.20)
RSRZ outliers	180081	7683 (2.24-2.20)

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	83% 14%
1	B	262	83% 14%
1	C	262	5% 80% 5% 14%
1	D	262	3% 84% 14%
1	E	262	6% 82% 14%

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Mol	Chain	Length	Quality of chain
1	F	262	10% 81% 14%
1	G	262	% 84% 14%
1	H	262	% 82% 14%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 14376 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	G	226	Total	C	N	O	S	0	2	0
			1749	1098	308	330	13			
1	H	226	Total	C	N	O	S	0	2	0
			1748	1099	309	327	13			
1	A	226	Total	C	N	O	S	0	0	0
			1732	1090	305	325	12			
1	B	226	Total	C	N	O	S	0	1	0
			1738	1093	306	326	13			
1	C	225	Total	C	N	O	S	0	2	0
			1743	1096	308	326	13			
1	D	226	Total	C	N	O	S	0	0	0
			1732	1090	305	325	12			
1	E	226	Total	C	N	O	S	0	1	0
			1738	1093	306	326	13			
1	F	225	Total	C	N	O	S	0	1	0
			1733	1090	305	325	13			

There are 240 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
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

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Chain	Residue	Modelled	Actual	Comment	Reference
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
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

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Chain	Residue	Modelled	Actual	Comment	Reference
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
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
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

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Chain	Residue	Modelled	Actual	Comment	Reference
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
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

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Chain	Residue	Modelled	Actual	Comment	Reference
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
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
E	-19	MET	-	initiating methionine	UNP Q1M7F4

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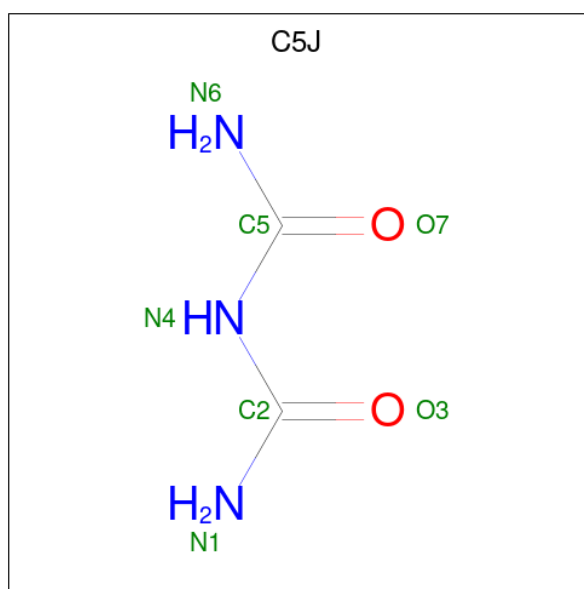
Chain	Residue	Modelled	Actual	Comment	Reference
E	-18	GLY	-	expression tag	UNP Q1M7F4
E	-17	SER	-	expression tag	UNP Q1M7F4
E	-16	SER	-	expression tag	UNP Q1M7F4
E	-15	HIS	-	expression tag	UNP Q1M7F4
E	-14	HIS	-	expression tag	UNP Q1M7F4
E	-13	HIS	-	expression tag	UNP Q1M7F4
E	-12	HIS	-	expression tag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

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Chain	Residue	Modelled	Actual	Comment	Reference
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
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

- Molecule 2 is dicarbonimidic diamide (CCD ID: C5J) (formula: $\text{C}_2\text{H}_5\text{N}_3\text{O}_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	G	1	Total	C	N	O	0	0
			7	2	3	2		
2	H	1	Total	C	N	O	0	0
			7	2	3	2		
2	A	1	Total	C	N	O	0	0
			7	2	3	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	N	O	0	0
			7	2	3	2		
2	C	1	Total	C	N	O	0	0
			7	2	3	2		
2	D	1	Total	C	N	O	0	0
			7	2	3	2		
2	E	1	Total	C	N	O	0	0
			7	2	3	2		

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	G	1	Total	Ca	0	0
			1	1		
3	B	1	Total	Ca	0	0
			1	1		
3	C	2	Total	Ca	0	0
			2	2		
3	F	1	Total	Ca	0	0
			1	1		

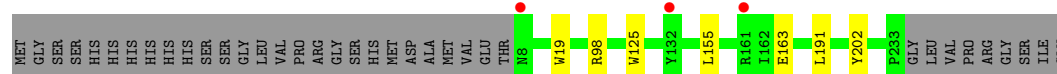
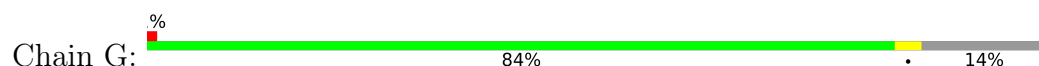
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	G	60	Total	O	0	0
			60	60		
4	H	64	Total	O	0	0
			64	64		
4	A	49	Total	O	0	0
			49	49		
4	B	61	Total	O	0	0
			61	61		
4	C	62	Total	O	0	0
			62	62		
4	D	54	Total	O	0	0
			54	54		
4	E	32	Total	O	0	0
			32	32		
4	F	27	Total	O	0	0
			27	27		

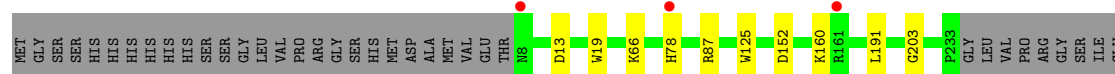
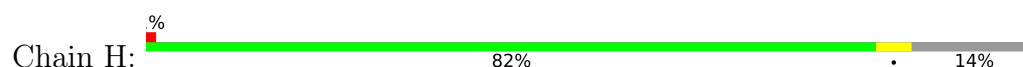
3 Residue-property plots [i](#)

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.

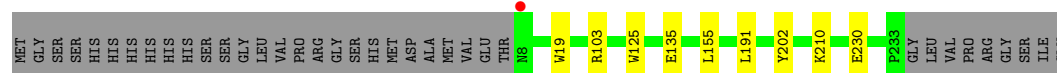
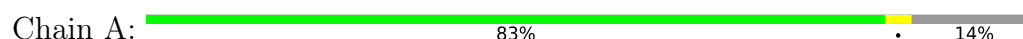
- Molecule 1: Putative amidase



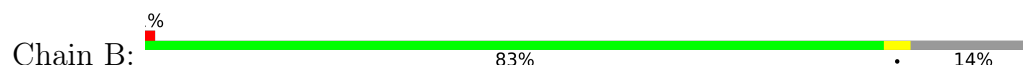
- Molecule 1: Putative amidase



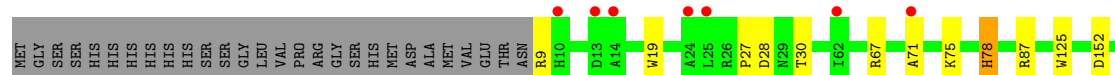
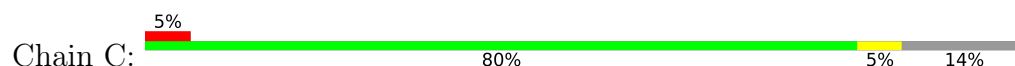
- Molecule 1: Putative amidase

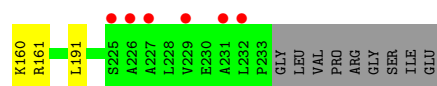


- Molecule 1: Putative amidase

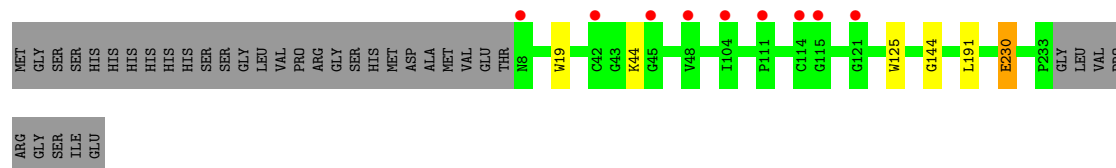
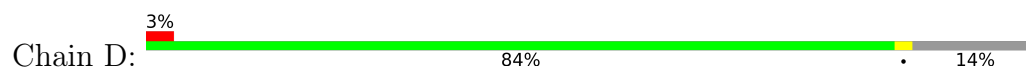


- Molecule 1: Putative amidase

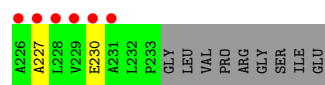
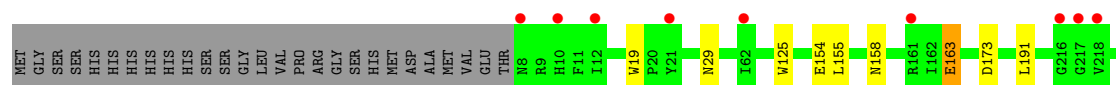
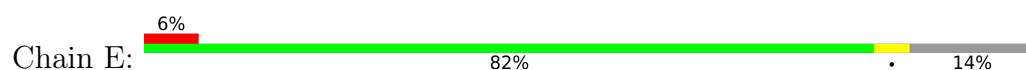




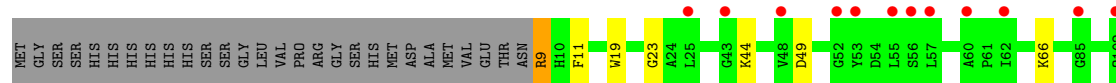
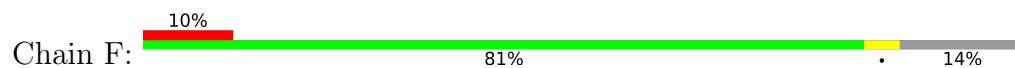
- Molecule 1: Putative amidase



- Molecule 1: Putative amidase



- Molecule 1: Putative amidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	73.70Å 87.30Å 341.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.85 – 2.22 42.85 – 2.22	Depositor EDS
% Data completeness (in resolution range)	99.9 (42.85-2.22) 99.9 (42.85-2.22)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.26 (at 2.22Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.249 , 0.277 0.252 , 0.280	Depositor DCC
R_{free} test set	5462 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	30.5	Xtriage
Anisotropy	0.030	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 33.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	14376	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.80% 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: C5J, CA

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	0.66	0/1770	0.83	0/2403
1	B	0.71	0/1776	0.85	1/2411 (0.0%)
1	C	0.70	0/1782	0.86	0/2419
1	D	0.69	0/1770	0.89	3/2403 (0.1%)
1	E	0.68	0/1776	0.86	0/2411
1	F	0.64	0/1771	0.83	0/2404
1	G	0.69	0/1787	0.85	1/2426 (0.0%)
1	H	0.76	1/1787 (0.1%)	0.87	0/2426
All	All	0.69	1/14219 (0.0%)	0.86	5/19303 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	13	ASP	CB-CG	-5.68	1.37	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	44	LYS	CA-CB-CG	7.35	128.79	114.10
1	D	230	GLU	CB-CA-C	-7.21	99.27	110.81
1	B	104	ILE	CB-CG1-CD1	6.53	127.52	113.80
1	G	98	ARG	NE-CZ-NH1	-5.43	116.06	121.50
1	D	230	GLU	N-CA-C	5.11	117.24	111.11

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	1732	0	1713	5	0
1	B	1738	0	1717	4	0
1	C	1743	0	1721	17	0
1	D	1732	0	1713	2	0
1	E	1738	0	1717	10	0
1	F	1733	0	1715	8	0
1	G	1749	0	1724	4	0
1	H	1748	0	1723	6	0
2	A	7	0	0	0	0
2	B	7	0	0	0	0
2	C	7	0	0	0	0
2	D	7	0	0	0	0
2	E	7	0	0	0	0
2	G	7	0	0	0	0
2	H	7	0	0	0	0
3	B	1	0	0	0	0
3	C	2	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
4	A	49	0	0	1	0
4	B	61	0	0	0	0
4	C	62	0	0	2	0
4	D	54	0	0	0	0
4	E	32	0	0	1	0
4	F	27	0	0	0	0
4	G	60	0	0	1	0
4	H	64	0	0	0	0
All	All	14376	0	13743	46	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 (46) 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:C:78[A]:HIS:H	1:C:78[A]:HIS:CD2	1.95	0.79
1:H:203:GLY:HA3	1:A:202:TYR:CD1	2.23	0.73
1:C:27:PRO:O	1:C:78[B]:HIS:CE1	2.45	0.70
1:F:44:LYS:HA	1:F:49:ASP:OD2	1.93	0.69
1:G:202:TYR:CD1	1:B:203:GLY:HA3	2.28	0.68
1:F:9:ARG:HG3	1:F:23:GLY:HA3	1.76	0.68
1:C:67:ARG:HD2	4:C:405:HOH:O	1.96	0.66
1:H:78[B]:HIS:CE1	1:H:160:LYS:HE3	2.31	0.66
1:C:78[B]:HIS:HD2	1:C:160:LYS:HD2	1.61	0.65
1:H:152:ASP:OD2	1:C:87:ARG:NH2	2.28	0.62
1:C:27:PRO:O	1:C:78[B]:HIS:HE1	1.81	0.62
1:C:78[A]:HIS:H	1:C:78[A]:HIS:HD2	1.44	0.61
1:F:66:LYS:HG3	1:F:131:LEU:HD21	1.85	0.59
1:C:78[A]:HIS:CD2	1:C:78[A]:HIS:N	2.67	0.59
1:E:154:GLU:O	1:E:158:ASN:ND2	2.36	0.57
1:E:29:ASN:HD22	1:E:163:GLU:HG3	1.71	0.55
1:E:154:GLU:HG2	1:E:158:ASN:HD21	1.70	0.55
1:C:71:ALA:O	1:C:75:LYS:HD3	2.10	0.52
1:E:227:ALA:HA	1:E:230:GLU:HG2	1.92	0.51
1:B:51:MET:SD	1:B:104:ILE:HD13	2.51	0.51
1:A:103:ARG:NH1	4:A:403:HOH:O	2.38	0.50
1:G:163:GLU:HG2	1:C:161:ARG:HH21	1.77	0.50
1:H:203:GLY:HA3	1:A:202:TYR:CE1	2.47	0.48
1:E:173:ASP:CB	1:F:211:MET:HE2	2.45	0.47
1:C:27:PRO:O	1:C:78[A]:HIS:NE2	2.48	0.47
1:G:202:TYR:CE1	1:B:203:GLY:HA3	2.51	0.46
1:C:78[B]:HIS:ND1	1:C:78[B]:HIS:N	2.58	0.46
4:G:402:HOH:O	1:A:210:LYS:HE2	2.16	0.45
1:C:27:PRO:O	1:C:78[A]:HIS:CD2	2.70	0.45
1:B:19:TRP:CE2	1:B:191:LEU:HB2	2.52	0.44
1:E:158:ASN:ND2	4:E:402:HOH:O	2.50	0.44
1:H:19:TRP:CE2	1:H:191:LEU:HB2	2.52	0.44
1:G:19:TRP:CE2	1:G:191:LEU:HB2	2.53	0.44
1:F:9:ARG:HG2	1:F:11:PHE:CE2	2.53	0.44
1:C:19:TRP:CE2	1:C:191:LEU:HB2	2.53	0.44
1:F:19:TRP:CE2	1:F:191:LEU:HB2	2.53	0.44
1:E:154:GLU:CG	1:E:158:ASN:HD21	2.31	0.44
1:D:19:TRP:CE2	1:D:191:LEU:HB2	2.52	0.43
1:E:19:TRP:CE2	1:E:191:LEU:HB2	2.52	0.43
1:H:87:ARG:NH2	1:C:152:ASP:OD2	2.43	0.43
1:A:19:TRP:CE2	1:A:191:LEU:HB2	2.52	0.43
1:E:173:ASP:HB2	1:F:211:MET:HE2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:173:ASP:HB3	1:F:211:MET:HE2	2.03	0.41
1:C:28:ASP:C	1:C:78[A]:HIS:HE2	2.29	0.41
1:C:30:THR:O	1:C:78[A]:HIS:CD2	2.74	0.41
4:C:444:HOH:O	1:D:144:GLY:HA2	2.21	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	224/262 (86%)	220 (98%)	4 (2%)	0	100	100
1	B	225/262 (86%)	221 (98%)	4 (2%)	0	100	100
1	C	225/262 (86%)	221 (98%)	4 (2%)	0	100	100
1	D	224/262 (86%)	220 (98%)	4 (2%)	0	100	100
1	E	225/262 (86%)	221 (98%)	4 (2%)	0	100	100
1	F	224/262 (86%)	220 (98%)	4 (2%)	0	100	100
1	G	226/262 (86%)	222 (98%)	4 (2%)	0	100	100
1	H	226/262 (86%)	222 (98%)	4 (2%)	0	100	100
All	All	1799/2096 (86%)	1767 (98%)	32 (2%)	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	183/214 (86%)	179 (98%)	4 (2%)	45	59
1	B	184/214 (86%)	179 (97%)	5 (3%)	39	52
1	C	185/214 (86%)	181 (98%)	4 (2%)	45	59
1	D	183/214 (86%)	181 (99%)	2 (1%)	65	78
1	E	184/214 (86%)	181 (98%)	3 (2%)	55	70
1	F	184/214 (86%)	181 (98%)	3 (2%)	55	70
1	G	186/214 (87%)	184 (99%)	2 (1%)	65	78
1	H	185/214 (86%)	183 (99%)	2 (1%)	65	78
All	All	1474/1712 (86%)	1449 (98%)	25 (2%)	55	68

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	125	TRP
1	G	155	LEU
1	H	66	LYS
1	H	125	TRP
1	A	125	TRP
1	A	135	GLU
1	A	155	LEU
1	A	230	GLU
1	B	66	LYS
1	B	104	ILE
1	B	125	TRP
1	B	155	LEU
1	B	160	LYS
1	C	9	ARG
1	C	78[A]	HIS
1	C	78[B]	HIS
1	C	125	TRP
1	D	125	TRP
1	D	230	GLU
1	E	125	TRP
1	E	155	LEU
1	E	163	GLU
1	F	9	ARG
1	F	125	TRP
1	F	155	LEU

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

Mol	Chain	Res	Type
1	H	10	HIS
1	B	10	HIS
1	D	102	GLN
1	E	158	ASN
1	F	10	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 5 are monoatomic - leaving 7 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	$\# Z > 2$
2	C5J	G	301	-	6,6,6	1.65	1 (16%)	6,7,7	1.44	0
2	C5J	E	301	-	6,6,6	1.62	1 (16%)	6,7,7	1.47	1 (16%)
2	C5J	B	301	-	6,6,6	1.28	1 (16%)	6,7,7	1.60	2 (33%)
2	C5J	C	301	-	6,6,6	2.13	2 (33%)	6,7,7	1.79	2 (33%)
2	C5J	H	301	-	6,6,6	1.65	2 (33%)	6,7,7	0.91	0
2	C5J	D	301	-	6,6,6	1.25	0	6,7,7	1.42	2 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	C5J	A	301	-	6,6,6	1.51	1 (16%)	6,7,7	1.86	2 (33%)

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	C5J	G	301	-	-	2/4/4/4	-
2	C5J	E	301	-	-	2/4/4/4	-
2	C5J	B	301	-	-	2/4/4/4	-
2	C5J	C	301	-	-	2/4/4/4	-
2	C5J	H	301	-	-	2/4/4/4	-
2	C5J	D	301	-	-	2/4/4/4	-
2	C5J	A	301	-	-	2/4/4/4	-

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	301	C5J	C5-N4	-4.36	1.34	1.40
2	A	301	C5J	C5-N4	-3.24	1.35	1.40
2	E	301	C5J	O7-C5	-2.69	1.20	1.24
2	G	301	C5J	C2-N4	-2.49	1.36	1.40
2	H	301	C5J	C5-N4	-2.29	1.37	1.40
2	H	301	C5J	C5-N6	2.10	1.38	1.33
2	C	301	C5J	O7-C5	-2.06	1.21	1.24
2	B	301	C5J	C5-N4	-2.01	1.37	1.40

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	301	C5J	N1-C2-N4	-3.27	108.31	115.45
2	A	301	C5J	O7-C5-N4	2.76	126.72	120.39
2	C	301	C5J	O3-C2-N4	2.62	126.40	120.39
2	E	301	C5J	O3-C2-N1	-2.54	118.06	123.18
2	D	301	C5J	O3-C2-N4	2.52	126.18	120.39
2	A	301	C5J	O3-C2-N1	-2.50	118.16	123.18
2	D	301	C5J	N1-C2-N4	-2.23	110.57	115.45
2	B	301	C5J	O3-C2-N4	2.22	125.48	120.39
2	B	301	C5J	O7-C5-N4	2.18	125.39	120.39

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	G	301	C5J	N6-C5-N4-C2
2	G	301	C5J	O7-C5-N4-C2
2	H	301	C5J	N6-C5-N4-C2
2	H	301	C5J	O7-C5-N4-C2
2	A	301	C5J	N6-C5-N4-C2
2	A	301	C5J	O7-C5-N4-C2
2	B	301	C5J	N6-C5-N4-C2
2	B	301	C5J	O7-C5-N4-C2
2	C	301	C5J	O3-C2-N4-C5
2	D	301	C5J	N1-C2-N4-C5
2	D	301	C5J	O3-C2-N4-C5
2	E	301	C5J	N6-C5-N4-C2
2	E	301	C5J	O7-C5-N4-C2
2	C	301	C5J	N1-C2-N4-C5

There are no ring outliers.

No monomer is involved in short contacts.

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	226/262 (86%)	0.44	1 (0%) 88 87	19, 31, 44, 57	0
1	B	226/262 (86%)	0.29	3 (1%) 75 73	16, 28, 39, 55	1 (0%)
1	C	225/262 (85%)	0.66	13 (5%) 29 26	17, 32, 48, 60	2 (0%)
1	D	226/262 (86%)	0.57	9 (3%) 42 39	16, 32, 50, 70	0
1	E	226/262 (86%)	0.79	15 (6%) 24 21	18, 37, 58, 68	1 (0%)
1	F	225/262 (85%)	1.05	27 (12%) 9 7	20, 42, 64, 72	1 (0%)
1	G	226/262 (86%)	0.41	3 (1%) 75 73	14, 29, 44, 60	2 (0%)
1	H	226/262 (86%)	0.18	3 (1%) 75 73	11, 25, 39, 63	2 (0%)
All	All	1806/2096 (86%)	0.55	74 (4%) 41 38	11, 31, 52, 72	9 (0%)

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	8	ASN	5.0
1	F	106	ALA	4.8
1	H	8	ASN	4.4
1	D	45	GLY	4.1
1	C	232	LEU	3.6
1	C	226	ALA	3.6
1	F	48	VAL	3.5
1	E	226	ALA	3.5
1	F	104	ILE	3.4
1	F	134	ILE	3.3
1	F	62	ILE	3.3
1	E	229	VAL	3.2
1	C	227	ALA	3.1
1	F	108	ILE	3.0
1	A	8	ASN	3.0
1	F	43	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
1	F	102	GLN	2.9
1	F	57	LEU	2.9
1	B	132	TYR	2.9
1	E	227	ALA	2.9
1	F	109	GLY	2.9
1	G	8	ASN	2.8
1	C	24	ALA	2.8
1	B	8	ASN	2.7
1	E	228	LEU	2.7
1	C	71	ALA	2.7
1	D	104	ILE	2.7
1	F	117	ILE	2.7
1	F	25	LEU	2.7
1	D	114	CYS	2.6
1	F	55	LEU	2.6
1	C	14	ALA	2.6
1	E	230	GLU	2.6
1	H	78[A]	HIS	2.6
1	E	217	GLY	2.6
1	C	10	HIS	2.6
1	F	85	GLY	2.5
1	D	48	VAL	2.5
1	F	128	ILE	2.5
1	D	8	ASN	2.5
1	F	113	PRO	2.5
1	F	60	ALA	2.5
1	E	231	ALA	2.5
1	D	111	PRO	2.5
1	D	121	GLY	2.5
1	F	114	CYS	2.4
1	C	225	SER	2.4
1	F	56	SER	2.4
1	E	21	TYR	2.4
1	E	216	GLY	2.4
1	E	12	ILE	2.4
1	F	105	GLY	2.3
1	E	218	VAL	2.3
1	B	161	ARG	2.3
1	C	13	ASP	2.3
1	F	127	ILE	2.3
1	F	229	VAL	2.3
1	F	123	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
1	G	132	TYR	2.3
1	H	161	ARG	2.3
1	F	52	GLY	2.2
1	C	62	ILE	2.2
1	G	161	ARG	2.2
1	E	10	HIS	2.2
1	F	53	TYR	2.2
1	C	229	VAL	2.1
1	E	161	ARG	2.1
1	C	231	ALA	2.1
1	C	25	LEU	2.1
1	D	115	GLY	2.1
1	E	62	ILE	2.1
1	F	118	LEU	2.0
1	D	42	CYS	2.0
1	F	201	ASP	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(Å ²)	Q<0.9
3	CA	C	303	1/1	0.87	0.16	67,67,67,67	0
3	CA	C	302	1/1	0.93	0.14	57,57,57,57	0
2	C5J	H	301	7/7	0.94	0.07	13,15,17,19	0
2	C5J	C	301	7/7	0.95	0.08	21,25,26,27	0
3	CA	F	301	1/1	0.95	0.10	52,52,52,52	0
2	C5J	D	301	7/7	0.96	0.06	25,26,28,28	0
2	C5J	E	301	7/7	0.96	0.07	19,21,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	C5J	A	301	7/7	0.96	0.06	20,22,23,25	0
2	C5J	B	301	7/7	0.96	0.07	23,26,28,30	0
2	C5J	G	301	7/7	0.96	0.07	24,25,27,30	0
3	CA	G	302	1/1	0.97	0.11	51,51,51,51	0
3	CA	B	302	1/1	0.98	0.11	50,50,50,50	0

6.5 Other polymers [i](#)

There are no such residues in this entry.