



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 04:03 am GMT

PDB ID : 1NX9  
Title : Acetobacter turbidans alpha-amino acid ester hydrolase S205A mutant complexed with ampicillin  
Authors : Barends, T.R.M.; Polderman-Tijmes, J.J.; Jekel, P.A.; Janssen, D.B.; Dijkstra, B.W.  
Deposited on : 2003-02-10  
Resolution : 2.20 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

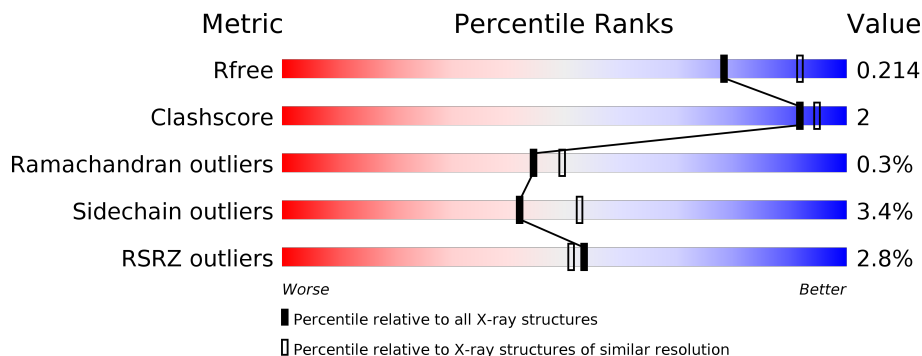
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	100719	4002 (2.20-2.20)
Clashscore	112137	4730 (2.20-2.20)
Ramachandran outliers	110173	4656 (2.20-2.20)
Sidechain outliers	110143	4657 (2.20-2.20)
RSRZ outliers	101464	4033 (2.20-2.20)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	652	<div> <div>2%</div> <div> <div></div> <div>83%</div> <div>11%</div> <div>5%</div> </div> </div>
1	B	652	<div> <div>2%</div> <div> <div></div> <div>82%</div> <div>12%</div> <div>5%</div> </div> </div>
1	C	652	<div> <div>3%</div> <div> <div></div> <div>84%</div> <div>11%</div> <div>5%</div> </div> </div>
1	D	652	<div> <div>4%</div> <div> <div></div> <div>83%</div> <div>12%</div> <div>5%</div> </div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	AIC	A	5001	X	-	-	X
2	AIC	B	5002	X	-	-	X
2	AIC	C	5003	X	-	-	X
2	AIC	D	5004	X	-	-	X
3	GOL	A	6002	-	-	-	X
3	GOL	B	6004	-	-	-	X
3	GOL	C	6006	-	-	-	X
3	GOL	D	6008	-	-	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 21877 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 alpha-amino acid ester hydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	617	Total	C	N	O	S	0	0	0
			4882	3111	845	906	20			
1	B	617	Total	C	N	O	S	0	0	0
			4882	3111	845	906	20			
1	C	617	Total	C	N	O	S	0	0	0
			4882	3111	845	906	20			
1	D	617	Total	C	N	O	S	0	0	0
			4882	3111	845	906	20			

There are 104 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	205	ALA	SER	ENGINEERED	UNP Q8VRK8
A	668	LYS	-	MYC EPITOPE	UNP Q8VRK8
A	669	LEU	-	MYC EPITOPE	UNP Q8VRK8
A	670	GLY	-	MYC EPITOPE	UNP Q8VRK8
A	671	PRO	-	MYC EPITOPE	UNP Q8VRK8
A	672	GLU	-	MYC EPITOPE	UNP Q8VRK8
A	673	GLN	-	MYC EPITOPE	UNP Q8VRK8
A	674	LYS	-	MYC EPITOPE	UNP Q8VRK8
A	675	LEU	-	MYC EPITOPE	UNP Q8VRK8
A	676	ILE	-	MYC EPITOPE	UNP Q8VRK8
A	677	SER	-	MYC EPITOPE	UNP Q8VRK8
A	678	GLU	-	MYC EPITOPE	UNP Q8VRK8
A	679	GLU	-	MYC EPITOPE	UNP Q8VRK8
A	680	ASP	-	MYC EPITOPE	UNP Q8VRK8
A	681	LEU	-	MYC EPITOPE	UNP Q8VRK8
A	682	ASN	-	MYC EPITOPE	UNP Q8VRK8
A	683	SER	-	MYC EPITOPE	UNP Q8VRK8
A	684	ALA	-	MYC EPITOPE	UNP Q8VRK8
A	685	VAL	-	MYC EPITOPE	UNP Q8VRK8
A	686	ASP	-	MYC EPITOPE	UNP Q8VRK8
A	687	HIS	-	EXPRESSION TAG	UNP Q8VRK8

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Chain	Residue	Modelled	Actual	Comment	Reference
A	688	HIS	-	EXPRESSION TAG	UNP Q8VRK8
A	689	HIS	-	EXPRESSION TAG	UNP Q8VRK8
A	690	HIS	-	EXPRESSION TAG	UNP Q8VRK8
A	691	HIS	-	EXPRESSION TAG	UNP Q8VRK8
A	692	HIS	-	EXPRESSION TAG	UNP Q8VRK8
B	205	ALA	SER	ENGINEERED	UNP Q8VRK8
B	668	LYS	-	MYC EPITOPE	UNP Q8VRK8
B	669	LEU	-	MYC EPITOPE	UNP Q8VRK8
B	670	GLY	-	MYC EPITOPE	UNP Q8VRK8
B	671	PRO	-	MYC EPITOPE	UNP Q8VRK8
B	672	GLU	-	MYC EPITOPE	UNP Q8VRK8
B	673	GLN	-	MYC EPITOPE	UNP Q8VRK8
B	674	LYS	-	MYC EPITOPE	UNP Q8VRK8
B	675	LEU	-	MYC EPITOPE	UNP Q8VRK8
B	676	ILE	-	MYC EPITOPE	UNP Q8VRK8
B	677	SER	-	MYC EPITOPE	UNP Q8VRK8
B	678	GLU	-	MYC EPITOPE	UNP Q8VRK8
B	679	GLU	-	MYC EPITOPE	UNP Q8VRK8
B	680	ASP	-	MYC EPITOPE	UNP Q8VRK8
B	681	LEU	-	MYC EPITOPE	UNP Q8VRK8
B	682	ASN	-	MYC EPITOPE	UNP Q8VRK8
B	683	SER	-	MYC EPITOPE	UNP Q8VRK8
B	684	ALA	-	MYC EPITOPE	UNP Q8VRK8
B	685	VAL	-	MYC EPITOPE	UNP Q8VRK8
B	686	ASP	-	MYC EPITOPE	UNP Q8VRK8
B	687	HIS	-	EXPRESSION TAG	UNP Q8VRK8
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B	691	HIS	-	EXPRESSION TAG	UNP Q8VRK8
B	692	HIS	-	EXPRESSION TAG	UNP Q8VRK8
C	205	ALA	SER	ENGINEERED	UNP Q8VRK8
C	668	LYS	-	MYC EPITOPE	UNP Q8VRK8
C	669	LEU	-	MYC EPITOPE	UNP Q8VRK8
C	670	GLY	-	MYC EPITOPE	UNP Q8VRK8
C	671	PRO	-	MYC EPITOPE	UNP Q8VRK8
C	672	GLU	-	MYC EPITOPE	UNP Q8VRK8
C	673	GLN	-	MYC EPITOPE	UNP Q8VRK8
C	674	LYS	-	MYC EPITOPE	UNP Q8VRK8
C	675	LEU	-	MYC EPITOPE	UNP Q8VRK8
C	676	ILE	-	MYC EPITOPE	UNP Q8VRK8
C	677	SER	-	MYC EPITOPE	UNP Q8VRK8

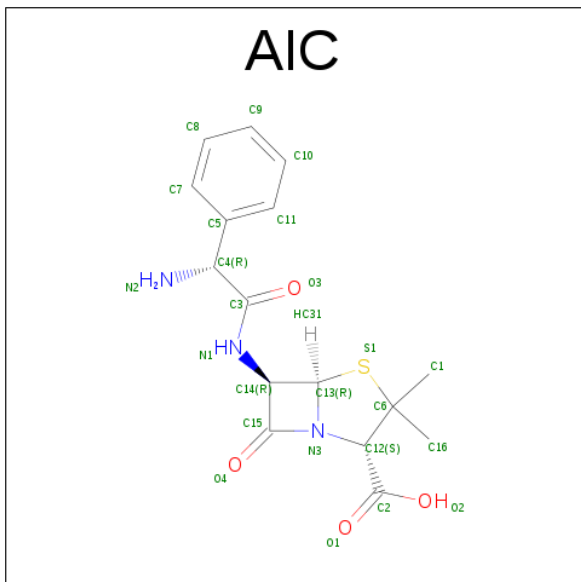
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Chain	Residue	Modelled	Actual	Comment	Reference
C	678	GLU	-	MYC EPITOPE	UNP Q8VRK8
C	679	GLU	-	MYC EPITOPE	UNP Q8VRK8
C	680	ASP	-	MYC EPITOPE	UNP Q8VRK8
C	681	LEU	-	MYC EPITOPE	UNP Q8VRK8
C	682	ASN	-	MYC EPITOPE	UNP Q8VRK8
C	683	SER	-	MYC EPITOPE	UNP Q8VRK8
C	684	ALA	-	MYC EPITOPE	UNP Q8VRK8
C	685	VAL	-	MYC EPITOPE	UNP Q8VRK8
C	686	ASP	-	MYC EPITOPE	UNP Q8VRK8
C	687	HIS	-	EXPRESSION TAG	UNP Q8VRK8
C	688	HIS	-	EXPRESSION TAG	UNP Q8VRK8
C	689	HIS	-	EXPRESSION TAG	UNP Q8VRK8
C	690	HIS	-	EXPRESSION TAG	UNP Q8VRK8
C	691	HIS	-	EXPRESSION TAG	UNP Q8VRK8
C	692	HIS	-	EXPRESSION TAG	UNP Q8VRK8
D	205	ALA	SER	ENGINEERED	UNP Q8VRK8
D	668	LYS	-	MYC EPITOPE	UNP Q8VRK8
D	669	LEU	-	MYC EPITOPE	UNP Q8VRK8
D	670	GLY	-	MYC EPITOPE	UNP Q8VRK8
D	671	PRO	-	MYC EPITOPE	UNP Q8VRK8
D	672	GLU	-	MYC EPITOPE	UNP Q8VRK8
D	673	GLN	-	MYC EPITOPE	UNP Q8VRK8
D	674	LYS	-	MYC EPITOPE	UNP Q8VRK8
D	675	LEU	-	MYC EPITOPE	UNP Q8VRK8
D	676	ILE	-	MYC EPITOPE	UNP Q8VRK8
D	677	SER	-	MYC EPITOPE	UNP Q8VRK8
D	678	GLU	-	MYC EPITOPE	UNP Q8VRK8
D	679	GLU	-	MYC EPITOPE	UNP Q8VRK8
D	680	ASP	-	MYC EPITOPE	UNP Q8VRK8
D	681	LEU	-	MYC EPITOPE	UNP Q8VRK8
D	682	ASN	-	MYC EPITOPE	UNP Q8VRK8
D	683	SER	-	MYC EPITOPE	UNP Q8VRK8
D	684	ALA	-	MYC EPITOPE	UNP Q8VRK8
D	685	VAL	-	MYC EPITOPE	UNP Q8VRK8
D	686	ASP	-	MYC EPITOPE	UNP Q8VRK8
D	687	HIS	-	EXPRESSION TAG	UNP Q8VRK8
D	688	HIS	-	EXPRESSION TAG	UNP Q8VRK8
D	689	HIS	-	EXPRESSION TAG	UNP Q8VRK8
D	690	HIS	-	EXPRESSION TAG	UNP Q8VRK8
D	691	HIS	-	EXPRESSION TAG	UNP Q8VRK8
D	692	HIS	-	EXPRESSION TAG	UNP Q8VRK8

- Molecule 2 is (2S,5R,6R)-6-{[(2R)-2-AMINO-2-PHENYLETHANOYL]AMINO}-3,3-DI

METHYL-7-OXO-4-THIA-1-AZABICYCLO[3.2.0]HEPTANE-2-CARBOXYLIC ACID  
(three-letter code: AIC) (formula:  $C_{16}H_{19}N_3O_4S$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			24	16	3	4	1		
2	B	1	Total	C	N	O	S	0	0
			24	16	3	4	1		
2	C	1	Total	C	N	O	S	0	0
			24	16	3	4	1		
2	D	1	Total	C	N	O	S	0	0
			24	16	3	4	1		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is water.

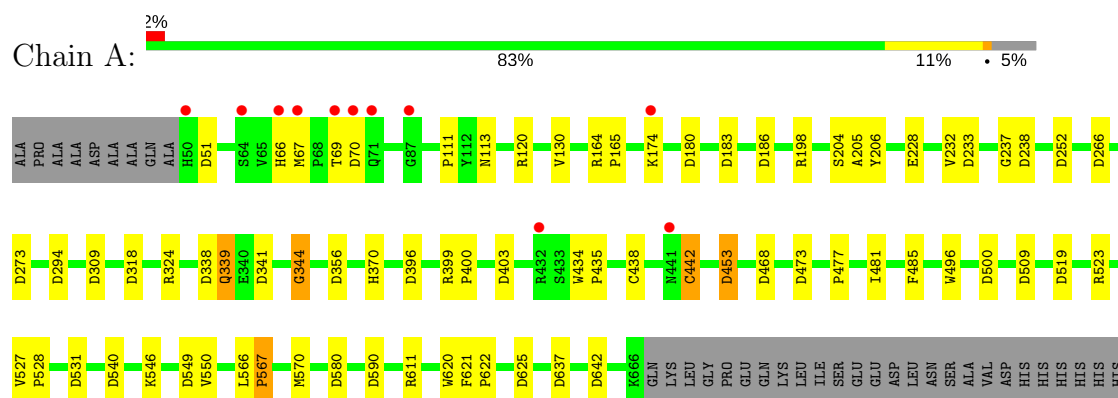
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	571	Total	O	0	0
			571	571		
4	B	573	Total	O	0	0
			573	573		
4	C	589	Total	O	0	0
			589	589		
4	D	496	Total	O	0	0
			496	496		



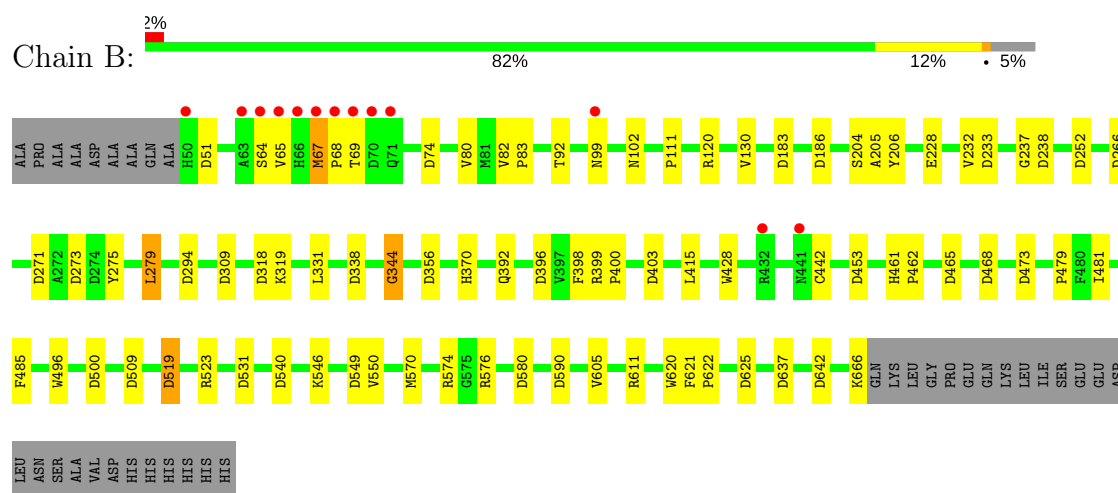
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

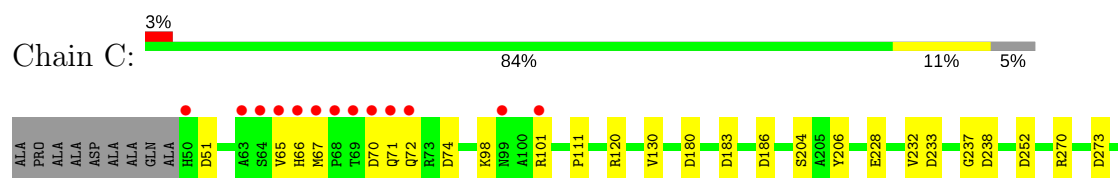
- Molecule 1: alpha-amino acid ester hydrolase

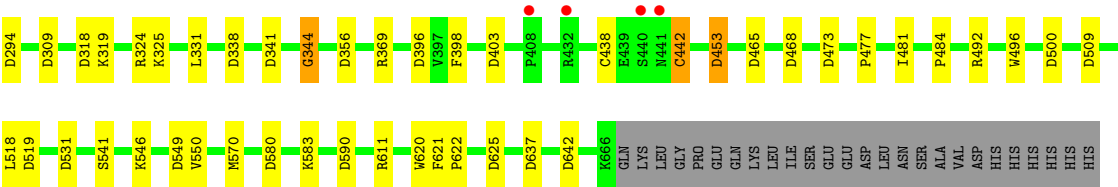


- Molecule 1: alpha-amino acid ester hydrolase

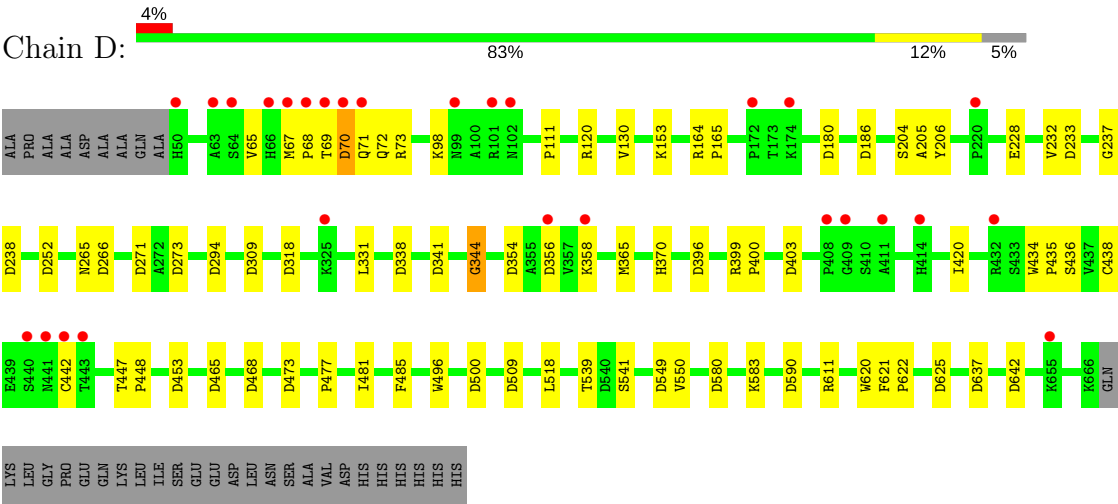


- Molecule 1: alpha-amino acid ester hydrolase





● Molecule 1: alpha-amino acid ester hydrolase



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 2 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	341.83Å 341.83Å 341.83Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.20 19.94 – 2.20	Depositor EDS
% Data completeness (in resolution range)	96.9 (15.00-2.20) 96.9 (19.94-2.20)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.90 (at 2.19Å)	Xtriage
Refinement program	REFMAC 5.1.19	Depositor
R, $R_{free}$	0.166 , 0.184 0.200 , 0.214	Depositor DCC
$R_{free}$ test set	16096 reflections (5.01%)	DCC
Wilson B-factor (Å <sup>2</sup> )	29.4	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 47.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.53$ , $\langle L^2 \rangle = 0.37$	Xtriage
Estimated twinning fraction	0.000 for -l,-k,-h	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	21877	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.78% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: GOL, AIC

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	0.34	0/5041	0.74	32/6886 (0.5%)
1	B	0.34	0/5041	0.74	32/6886 (0.5%)
1	C	0.34	0/5041	0.74	32/6886 (0.5%)
1	D	0.33	0/5041	0.73	30/6886 (0.4%)
All	All	0.34	0/20164	0.74	126/27544 (0.5%)

There are no bond length outliers.

The worst 5 of 126 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	625	ASP	CB-CG-OD2	6.64	124.28	118.30
1	B	625	ASP	CB-CG-OD2	6.62	124.26	118.30
1	A	625	ASP	CB-CG-OD2	6.61	124.25	118.30
1	D	625	ASP	CB-CG-OD2	6.51	124.16	118.30
1	C	500	ASP	CB-CG-OD2	6.26	123.94	118.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4882	0	4648	21	0
1	B	4882	0	4648	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	4882	0	4648	12	0
1	D	4882	0	4648	17	0
2	A	24	0	17	1	0
2	B	24	0	17	1	0
2	C	24	0	17	0	0
2	D	24	0	17	0	0
3	A	6	0	8	0	0
3	B	6	0	8	0	0
3	C	6	0	8	0	0
3	D	6	0	8	0	0
4	A	571	0	0	2	0
4	B	573	0	0	1	0
4	C	589	0	0	0	0
4	D	496	0	0	0	0
All	All	21877	0	18692	71	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

The worst 5 of 71 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:339:GLN:HE22	1:A:370:HIS:H	1.43	0.64
1:B:550:VAL:HB	1:B:611:ARG:HB2	1.80	0.63
1:A:232:VAL:HB	1:A:344:GLY:HA2	1.83	0.60
1:A:550:VAL:HB	1:A:611:ARG:HB2	1.84	0.59
1:D:550:VAL:HB	1:D:611:ARG:HB2	1.84	0.58

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	615/652 (94%)	586 (95%)	27 (4%)	2 (0%)	44	49
1	B	615/652 (94%)	591 (96%)	22 (4%)	2 (0%)	44	49
1	C	615/652 (94%)	585 (95%)	28 (5%)	2 (0%)	44	49
1	D	615/652 (94%)	584 (95%)	29 (5%)	2 (0%)	44	49
All	All	2460/2608 (94%)	2346 (95%)	106 (4%)	8 (0%)	44	49

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	344	GLY
1	B	344	GLY
1	C	344	GLY
1	D	344	GLY
1	B	237	GLY

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	516/543 (95%)	502 (97%)	14 (3%)	50	62
1	B	516/543 (95%)	499 (97%)	17 (3%)	43	54
1	C	516/543 (95%)	495 (96%)	21 (4%)	35	44
1	D	516/543 (95%)	498 (96%)	18 (4%)	41	51
All	All	2064/2172 (95%)	1994 (97%)	70 (3%)	42	53

5 of 70 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	65	VAL
1	C	130	VAL
1	D	442	CYS
1	C	66	HIS
1	C	72	GLN

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

Mol	Chain	Res	Type
1	B	72	GLN
1	B	99	ASN
1	B	392	GLN
1	A	339	GLN
1	B	391	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 ⓘ

There are no carbohydrates in this entry.

### 5.6 Ligand geometry ⓘ

8 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	AIC	A	5001	-	22,26,26	2.60	7 (31%)	32,40,40	2.43	7 (21%)
3	GOL	A	6002	-	5,5,5	0.33	0	5,5,5	0.21	0
2	AIC	B	5002	-	22,26,26	2.60	7 (31%)	32,40,40	2.42	8 (25%)
3	GOL	B	6004	-	5,5,5	0.34	0	5,5,5	0.19	0
2	AIC	C	5003	-	22,26,26	2.64	7 (31%)	32,40,40	2.46	7 (21%)
3	GOL	C	6006	-	5,5,5	0.32	0	5,5,5	0.24	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	AIC	D	5004	-	22,26,26	2.62	7 (31%)	32,40,40	2.43	7 (21%)
3	GOL	D	6008	-	5,5,5	0.30	0	5,5,5	0.22	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	AIC	A	5001	-	1/1/9/10	0/12/47/47	0/3/3/3
3	GOL	A	6002	-	-	0/4/4/4	0/0/0/0
2	AIC	B	5002	-	1/1/9/10	0/12/47/47	0/3/3/3
3	GOL	B	6004	-	-	0/4/4/4	0/0/0/0
2	AIC	C	5003	-	1/1/9/10	0/12/47/47	0/3/3/3
3	GOL	C	6006	-	-	0/4/4/4	0/0/0/0
2	AIC	D	5004	-	1/1/9/10	0/12/47/47	0/3/3/3
3	GOL	D	6008	-	-	0/4/4/4	0/0/0/0

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	5003	AIC	C14-C15	-5.97	1.39	1.54
2	D	5004	AIC	C14-C15	-5.94	1.39	1.54
2	B	5002	AIC	C14-C15	-5.92	1.39	1.54
2	A	5001	AIC	C14-C15	-5.92	1.39	1.54
2	D	5004	AIC	C14-N1	-5.81	1.33	1.45

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	5003	AIC	C14-C13-S1	-5.76	110.36	119.40
2	D	5004	AIC	C14-C13-S1	-5.65	110.53	119.40
2	A	5001	AIC	C14-C13-S1	-5.60	110.61	119.40
2	B	5002	AIC	C14-C13-S1	-5.45	110.85	119.40
2	C	5003	AIC	C13-N3-C15	-3.80	88.93	93.92

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	C	5003	AIC	C14
2	D	5004	AIC	C14
2	A	5001	AIC	C14

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Mol	Chain	Res	Type	Atom
2	B	5002	AIC	C14

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	5001	AIC	1	0
2	B	5002	AIC	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	617/652 (94%)	-0.49	11 (1%) 69 66	13, 18, 32, 77	0
1	B	617/652 (94%)	-0.49	13 (2%) 64 61	14, 18, 33, 86	0
1	C	617/652 (94%)	-0.46	17 (2%) 53 51	14, 18, 32, 79	0
1	D	617/652 (94%)	-0.33	28 (4%) 34 32	13, 18, 32, 82	0
All	All	2468/2608 (94%)	-0.44	69 (2%) 53 51	13, 18, 32, 86	0

The worst 5 of 69 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	66	HIS	7.0
1	A	66	HIS	6.0
1	B	99	ASN	5.9
1	D	50	HIS	5.7
1	A	50	HIS	5.7

### 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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	AIC	C	5003	24/24	0.81	0.22	11.03	48,60,66,68	0
2	AIC	B	5002	24/24	0.77	0.24	9.92	47,63,66,68	0
3	GOL	D	6008	6/6	0.87	0.21	7.87	36,59,63,63	0
2	AIC	D	5004	24/24	0.80	0.23	7.40	53,62,67,68	0
2	AIC	A	5001	24/24	0.83	0.22	5.69	49,63,71,73	0
3	GOL	A	6002	6/6	0.81	0.22	5.46	35,57,59,59	0
3	GOL	B	6004	6/6	0.85	0.22	4.52	33,53,59,67	0
3	GOL	C	6006	6/6	0.91	0.18	4.18	30,50,50,53	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.