



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 10:07 PM GMT

PDB ID : 1RYY
Title : Acetobacter turbidans alpha-amino acid ester hydrolase Y206A mutant
Authors : Barends, T.R.M.
Deposited on : 2003-12-23
Resolution : 2.80 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

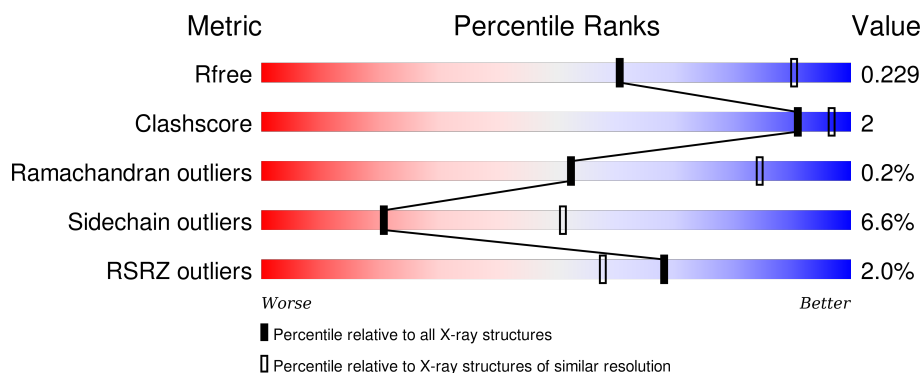
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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}	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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 ≥ 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></div> <div>84% 9% • 6%</div> </div>
1	B	652	<div> <div>2%</div> <div>82% 11% • 6%</div> </div>
1	C	652	<div> <div>2%</div> <div>82% 10% • 6%</div> </div>
1	D	652	<div> <div></div> <div>84% 9% • 6%</div> </div>
1	E	652	<div> <div>3%</div> <div>82% 11% • 6%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	652	<div><div><div></div><div></div><div></div></div><div><div></div><div></div><div></div></div><div>2%</div><div>81%</div><div>12%</div><div>• 6%</div></div>
1	G	652	<div><div><div></div><div></div><div></div></div><div><div></div><div></div><div></div></div><div>2%</div><div>83%</div><div>10%</div><div>• 6%</div></div>
1	H	652	<div><div><div></div><div></div><div></div></div><div><div></div><div></div><div></div></div><div>2%</div><div>81%</div><div>12%</div><div>• 6%</div></div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 39009 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	612	Total	C	N	O	S	0	0	0
			4836	3081	838	898	19			
1	B	612	Total	C	N	O	S	0	0	0
			4836	3081	838	898	19			
1	C	612	Total	C	N	O	S	0	0	0
			4836	3081	838	898	19			
1	D	612	Total	C	N	O	S	0	0	0
			4836	3081	838	898	19			
1	E	612	Total	C	N	O	S	0	0	0
			4836	3081	838	898	19			
1	F	612	Total	C	N	O	S	0	0	0
			4836	3081	838	898	19			
1	G	612	Total	C	N	O	S	0	0	0
			4836	3081	838	898	19			
1	H	612	Total	C	N	O	S	0	0	0
			4836	3081	838	898	19			

There are 208 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	206	ALA	TYR	engineered	UNP Q8VRK8
A	668	LYS	-	myc tag	UNP Q8VRK8
A	669	LEU	-	myc tag	UNP Q8VRK8
A	670	GLY	-	myc tag	UNP Q8VRK8
A	671	PRO	-	myc tag	UNP Q8VRK8
A	672	GLU	-	myc tag	UNP Q8VRK8
A	673	GLN	-	myc tag	UNP Q8VRK8
A	674	LYS	-	myc tag	UNP Q8VRK8
A	675	LEU	-	myc tag	UNP Q8VRK8
A	676	ILE	-	myc tag	UNP Q8VRK8
A	677	SER	-	myc tag	UNP Q8VRK8
A	678	GLU	-	myc tag	UNP Q8VRK8
A	679	GLU	-	myc tag	UNP Q8VRK8

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Chain	Residue	Modelled	Actual	Comment	Reference
A	680	ASP	-	myc tag	UNP Q8VRK8
A	681	LEU	-	myc tag	UNP Q8VRK8
A	682	ASN	-	myc tag	UNP Q8VRK8
A	683	SER	-	myc tag	UNP Q8VRK8
A	684	ALA	-	myc tag	UNP Q8VRK8
A	685	VAL	-	myc tag	UNP Q8VRK8
A	686	ASP	-	myc tag	UNP Q8VRK8
A	687	HIS	-	EXPRESSION TAG	UNP Q8VRK8
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	206	ALA	TYR	engineered	UNP Q8VRK8
B	668	LYS	-	myc tag	UNP Q8VRK8
B	669	LEU	-	myc tag	UNP Q8VRK8
B	670	GLY	-	myc tag	UNP Q8VRK8
B	671	PRO	-	myc tag	UNP Q8VRK8
B	672	GLU	-	myc tag	UNP Q8VRK8
B	673	GLN	-	myc tag	UNP Q8VRK8
B	674	LYS	-	myc tag	UNP Q8VRK8
B	675	LEU	-	myc tag	UNP Q8VRK8
B	676	ILE	-	myc tag	UNP Q8VRK8
B	677	SER	-	myc tag	UNP Q8VRK8
B	678	GLU	-	myc tag	UNP Q8VRK8
B	679	GLU	-	myc tag	UNP Q8VRK8
B	680	ASP	-	myc tag	UNP Q8VRK8
B	681	LEU	-	myc tag	UNP Q8VRK8
B	682	ASN	-	myc tag	UNP Q8VRK8
B	683	SER	-	myc tag	UNP Q8VRK8
B	684	ALA	-	myc tag	UNP Q8VRK8
B	685	VAL	-	myc tag	UNP Q8VRK8
B	686	ASP	-	myc tag	UNP Q8VRK8
B	687	HIS	-	EXPRESSION TAG	UNP Q8VRK8
B	688	HIS	-	EXPRESSION TAG	UNP Q8VRK8
B	689	HIS	-	EXPRESSION TAG	UNP Q8VRK8
B	690	HIS	-	EXPRESSION TAG	UNP Q8VRK8
B	691	HIS	-	EXPRESSION TAG	UNP Q8VRK8
B	692	HIS	-	EXPRESSION TAG	UNP Q8VRK8
C	206	ALA	TYR	engineered	UNP Q8VRK8
C	668	LYS	-	myc tag	UNP Q8VRK8
C	669	LEU	-	myc tag	UNP Q8VRK8

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Chain	Residue	Modelled	Actual	Comment	Reference
C	670	GLY	-	myc tag	UNP Q8VRK8
C	671	PRO	-	myc tag	UNP Q8VRK8
C	672	GLU	-	myc tag	UNP Q8VRK8
C	673	GLN	-	myc tag	UNP Q8VRK8
C	674	LYS	-	myc tag	UNP Q8VRK8
C	675	LEU	-	myc tag	UNP Q8VRK8
C	676	ILE	-	myc tag	UNP Q8VRK8
C	677	SER	-	myc tag	UNP Q8VRK8
C	678	GLU	-	myc tag	UNP Q8VRK8
C	679	GLU	-	myc tag	UNP Q8VRK8
C	680	ASP	-	myc tag	UNP Q8VRK8
C	681	LEU	-	myc tag	UNP Q8VRK8
C	682	ASN	-	myc tag	UNP Q8VRK8
C	683	SER	-	myc tag	UNP Q8VRK8
C	684	ALA	-	myc tag	UNP Q8VRK8
C	685	VAL	-	myc tag	UNP Q8VRK8
C	686	ASP	-	myc tag	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	206	ALA	TYR	engineered	UNP Q8VRK8
D	668	LYS	-	myc tag	UNP Q8VRK8
D	669	LEU	-	myc tag	UNP Q8VRK8
D	670	GLY	-	myc tag	UNP Q8VRK8
D	671	PRO	-	myc tag	UNP Q8VRK8
D	672	GLU	-	myc tag	UNP Q8VRK8
D	673	GLN	-	myc tag	UNP Q8VRK8
D	674	LYS	-	myc tag	UNP Q8VRK8
D	675	LEU	-	myc tag	UNP Q8VRK8
D	676	ILE	-	myc tag	UNP Q8VRK8
D	677	SER	-	myc tag	UNP Q8VRK8
D	678	GLU	-	myc tag	UNP Q8VRK8
D	679	GLU	-	myc tag	UNP Q8VRK8
D	680	ASP	-	myc tag	UNP Q8VRK8
D	681	LEU	-	myc tag	UNP Q8VRK8
D	682	ASN	-	myc tag	UNP Q8VRK8
D	683	SER	-	myc tag	UNP Q8VRK8
D	684	ALA	-	myc tag	UNP Q8VRK8
D	685	VAL	-	myc tag	UNP Q8VRK8

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Chain	Residue	Modelled	Actual	Comment	Reference
D	686	ASP	-	myc tag	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
E	206	ALA	TYR	engineered	UNP Q8VRK8
E	668	LYS	-	myc tag	UNP Q8VRK8
E	669	LEU	-	myc tag	UNP Q8VRK8
E	670	GLY	-	myc tag	UNP Q8VRK8
E	671	PRO	-	myc tag	UNP Q8VRK8
E	672	GLU	-	myc tag	UNP Q8VRK8
E	673	GLN	-	myc tag	UNP Q8VRK8
E	674	LYS	-	myc tag	UNP Q8VRK8
E	675	LEU	-	myc tag	UNP Q8VRK8
E	676	ILE	-	myc tag	UNP Q8VRK8
E	677	SER	-	myc tag	UNP Q8VRK8
E	678	GLU	-	myc tag	UNP Q8VRK8
E	679	GLU	-	myc tag	UNP Q8VRK8
E	680	ASP	-	myc tag	UNP Q8VRK8
E	681	LEU	-	myc tag	UNP Q8VRK8
E	682	ASN	-	myc tag	UNP Q8VRK8
E	683	SER	-	myc tag	UNP Q8VRK8
E	684	ALA	-	myc tag	UNP Q8VRK8
E	685	VAL	-	myc tag	UNP Q8VRK8
E	686	ASP	-	myc tag	UNP Q8VRK8
E	687	HIS	-	EXPRESSION TAG	UNP Q8VRK8
E	688	HIS	-	EXPRESSION TAG	UNP Q8VRK8
E	689	HIS	-	EXPRESSION TAG	UNP Q8VRK8
E	690	HIS	-	EXPRESSION TAG	UNP Q8VRK8
E	691	HIS	-	EXPRESSION TAG	UNP Q8VRK8
E	692	HIS	-	EXPRESSION TAG	UNP Q8VRK8
F	206	ALA	TYR	engineered	UNP Q8VRK8
F	668	LYS	-	myc tag	UNP Q8VRK8
F	669	LEU	-	myc tag	UNP Q8VRK8
F	670	GLY	-	myc tag	UNP Q8VRK8
F	671	PRO	-	myc tag	UNP Q8VRK8
F	672	GLU	-	myc tag	UNP Q8VRK8
F	673	GLN	-	myc tag	UNP Q8VRK8
F	674	LYS	-	myc tag	UNP Q8VRK8
F	675	LEU	-	myc tag	UNP Q8VRK8

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Chain	Residue	Modelled	Actual	Comment	Reference
F	676	ILE	-	myc tag	UNP Q8VRK8
F	677	SER	-	myc tag	UNP Q8VRK8
F	678	GLU	-	myc tag	UNP Q8VRK8
F	679	GLU	-	myc tag	UNP Q8VRK8
F	680	ASP	-	myc tag	UNP Q8VRK8
F	681	LEU	-	myc tag	UNP Q8VRK8
F	682	ASN	-	myc tag	UNP Q8VRK8
F	683	SER	-	myc tag	UNP Q8VRK8
F	684	ALA	-	myc tag	UNP Q8VRK8
F	685	VAL	-	myc tag	UNP Q8VRK8
F	686	ASP	-	myc tag	UNP Q8VRK8
F	687	HIS	-	EXPRESSION TAG	UNP Q8VRK8
F	688	HIS	-	EXPRESSION TAG	UNP Q8VRK8
F	689	HIS	-	EXPRESSION TAG	UNP Q8VRK8
F	690	HIS	-	EXPRESSION TAG	UNP Q8VRK8
F	691	HIS	-	EXPRESSION TAG	UNP Q8VRK8
F	692	HIS	-	EXPRESSION TAG	UNP Q8VRK8
G	206	ALA	TYR	engineered	UNP Q8VRK8
G	668	LYS	-	myc tag	UNP Q8VRK8
G	669	LEU	-	myc tag	UNP Q8VRK8
G	670	GLY	-	myc tag	UNP Q8VRK8
G	671	PRO	-	myc tag	UNP Q8VRK8
G	672	GLU	-	myc tag	UNP Q8VRK8
G	673	GLN	-	myc tag	UNP Q8VRK8
G	674	LYS	-	myc tag	UNP Q8VRK8
G	675	LEU	-	myc tag	UNP Q8VRK8
G	676	ILE	-	myc tag	UNP Q8VRK8
G	677	SER	-	myc tag	UNP Q8VRK8
G	678	GLU	-	myc tag	UNP Q8VRK8
G	679	GLU	-	myc tag	UNP Q8VRK8
G	680	ASP	-	myc tag	UNP Q8VRK8
G	681	LEU	-	myc tag	UNP Q8VRK8
G	682	ASN	-	myc tag	UNP Q8VRK8
G	683	SER	-	myc tag	UNP Q8VRK8
G	684	ALA	-	myc tag	UNP Q8VRK8
G	685	VAL	-	myc tag	UNP Q8VRK8
G	686	ASP	-	myc tag	UNP Q8VRK8
G	687	HIS	-	EXPRESSION TAG	UNP Q8VRK8
G	688	HIS	-	EXPRESSION TAG	UNP Q8VRK8
G	689	HIS	-	EXPRESSION TAG	UNP Q8VRK8
G	690	HIS	-	EXPRESSION TAG	UNP Q8VRK8
G	691	HIS	-	EXPRESSION TAG	UNP Q8VRK8

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Chain	Residue	Modelled	Actual	Comment	Reference
G	692	HIS	-	EXPRESSION TAG	UNP Q8VRK8
H	206	ALA	TYR	engineered	UNP Q8VRK8
H	668	LYS	-	myc tag	UNP Q8VRK8
H	669	LEU	-	myc tag	UNP Q8VRK8
H	670	GLY	-	myc tag	UNP Q8VRK8
H	671	PRO	-	myc tag	UNP Q8VRK8
H	672	GLU	-	myc tag	UNP Q8VRK8
H	673	GLN	-	myc tag	UNP Q8VRK8
H	674	LYS	-	myc tag	UNP Q8VRK8
H	675	LEU	-	myc tag	UNP Q8VRK8
H	676	ILE	-	myc tag	UNP Q8VRK8
H	677	SER	-	myc tag	UNP Q8VRK8
H	678	GLU	-	myc tag	UNP Q8VRK8
H	679	GLU	-	myc tag	UNP Q8VRK8
H	680	ASP	-	myc tag	UNP Q8VRK8
H	681	LEU	-	myc tag	UNP Q8VRK8
H	682	ASN	-	myc tag	UNP Q8VRK8
H	683	SER	-	myc tag	UNP Q8VRK8
H	684	ALA	-	myc tag	UNP Q8VRK8
H	685	VAL	-	myc tag	UNP Q8VRK8
H	686	ASP	-	myc tag	UNP Q8VRK8
H	687	HIS	-	EXPRESSION TAG	UNP Q8VRK8
H	688	HIS	-	EXPRESSION TAG	UNP Q8VRK8
H	689	HIS	-	EXPRESSION TAG	UNP Q8VRK8
H	690	HIS	-	EXPRESSION TAG	UNP Q8VRK8
H	691	HIS	-	EXPRESSION TAG	UNP Q8VRK8
H	692	HIS	-	EXPRESSION TAG	UNP Q8VRK8

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	66	Total O 66 66	0	0
2	B	56	Total O 56 56	0	0
2	C	43	Total O 43 43	0	0
2	D	55	Total O 55 55	0	0
2	E	15	Total O 15 15	0	0
2	F	22	Total O 22 22	0	0

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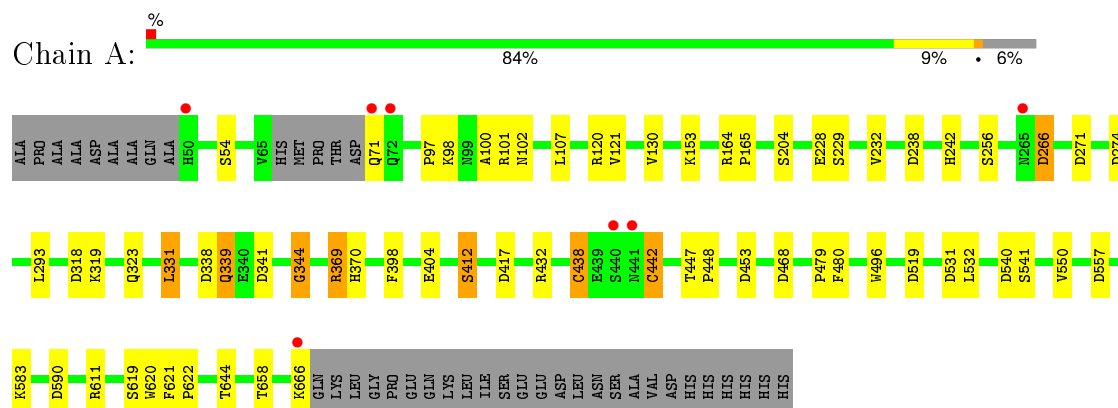
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	G	32	Total 32	O 32	0	0
2	H	32	Total 32	O 32	0	0

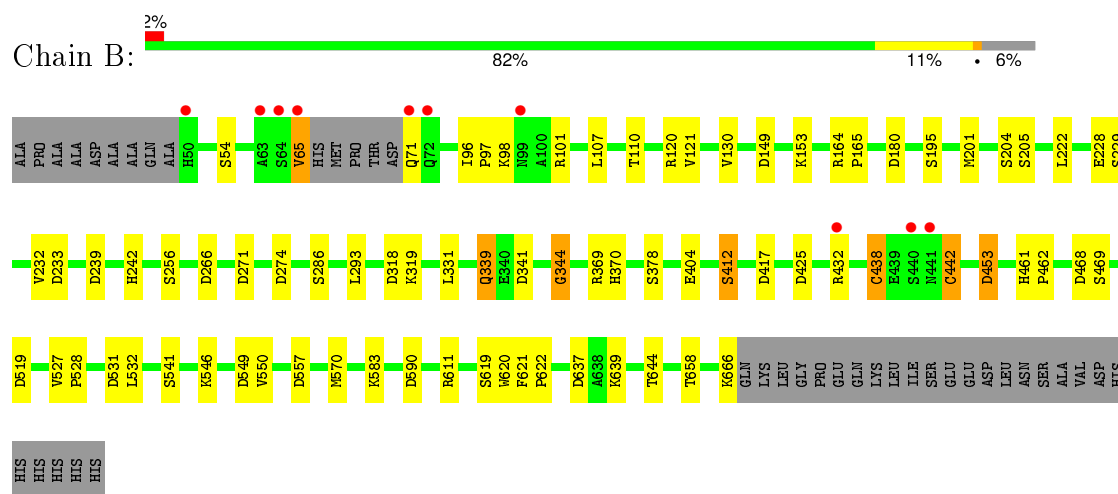
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

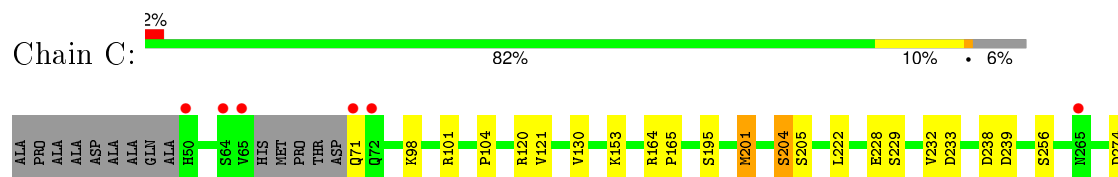
- Molecule 1: alpha-amino acid ester hydrolase

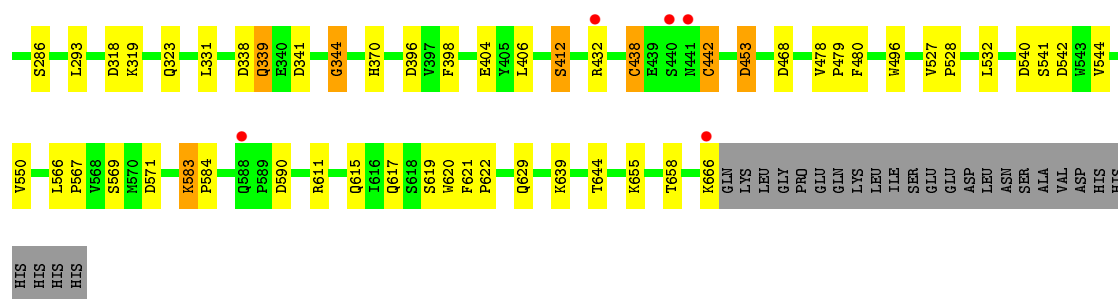


- Molecule 1: alpha-amino acid ester hydrolase

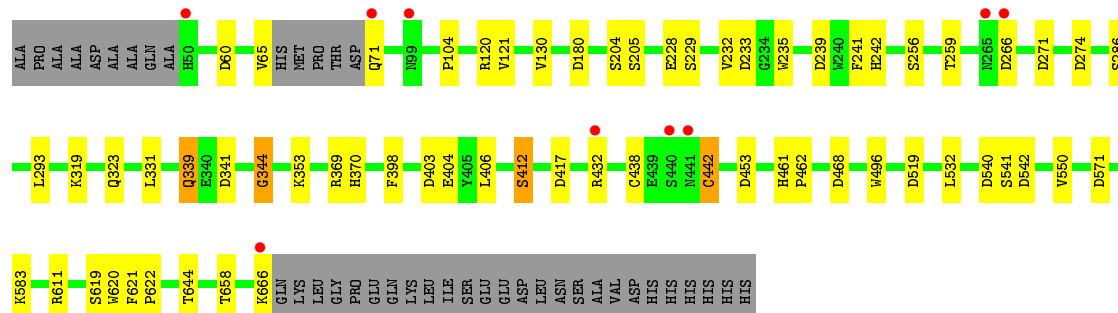
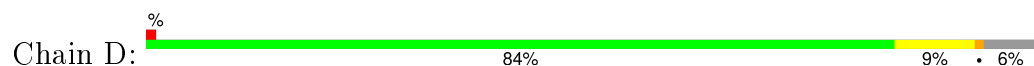


- Molecule 1: alpha-amino acid ester hydrolase

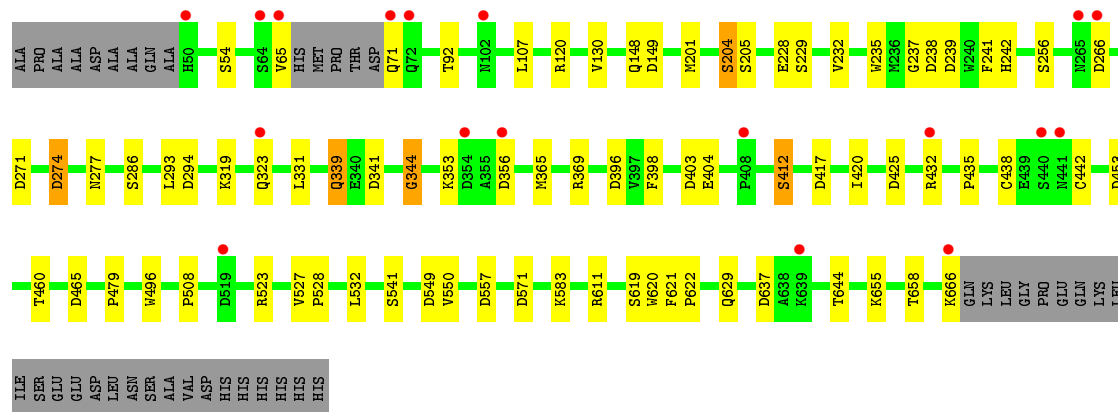
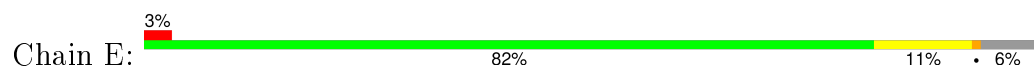




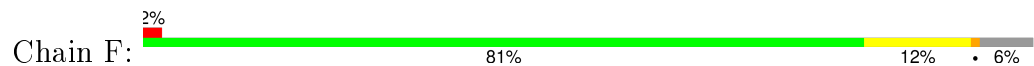
- Molecule 1: alpha-amino acid ester hydrolase

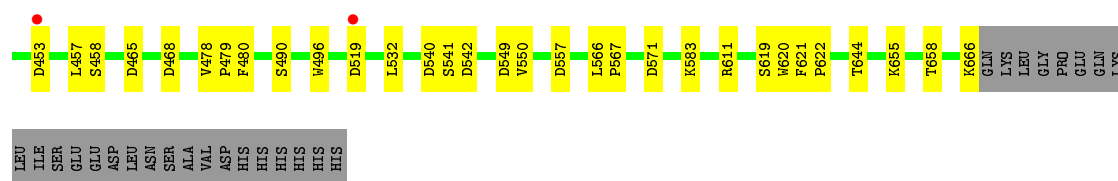


- Molecule 1: alpha-amino acid ester hydrolase

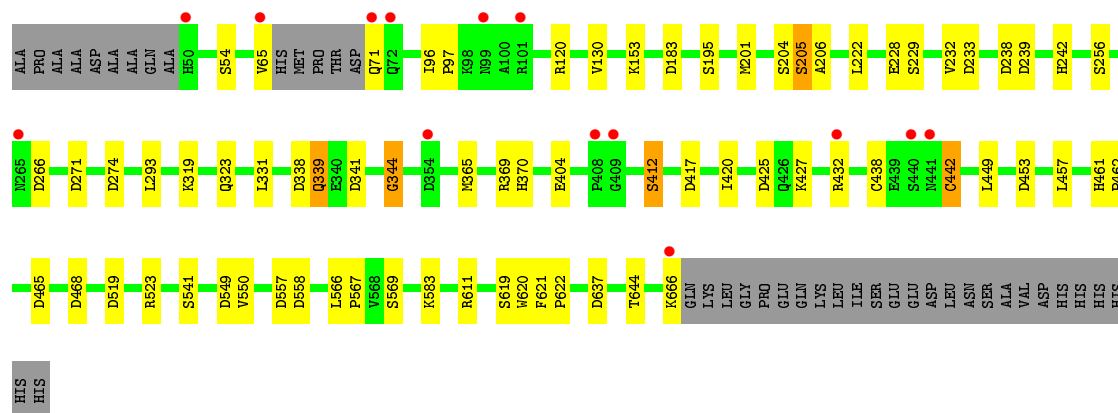
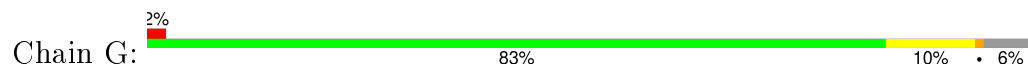


- Molecule 1: alpha-amino acid ester hydrolase

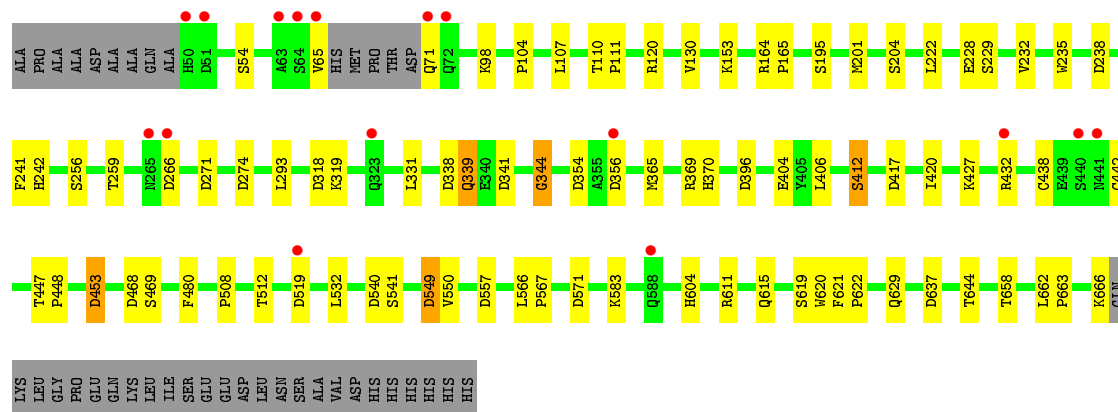
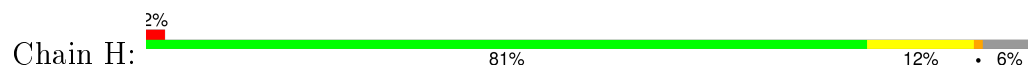




- Molecule 1: alpha-amino acid ester hydrolase



- Molecule 1: alpha-amino acid ester hydrolase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	91.65Å 177.51Å 169.97Å 90.00° 91.03° 90.00°	Depositor
Resolution (Å)	15.00 – 2.80 15.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.5 (15.00-2.80) 99.5 (15.00-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.60 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.1.19	Depositor
R, R_{free}	0.210 , 0.236 0.204 , 0.229	Depositor DCC
R_{free} test set	6623 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	36.9	Xtriage
Anisotropy	0.033	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 18.0	EDS
Estimated twinning fraction	0.006 for -h,-l,-k 0.000 for -h,l,k 0.015 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 131827 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	39009	wwPDB-VP
Average B, all atoms (Å ²)	19.0	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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.24	0/4991	0.80	13/6815 (0.2%)
1	B	0.24	0/4991	0.80	17/6815 (0.2%)
1	C	0.24	0/4991	0.79	14/6815 (0.2%)
1	D	0.24	0/4991	0.80	14/6815 (0.2%)
1	E	0.23	0/4991	0.78	15/6815 (0.2%)
1	F	0.23	0/4991	0.79	16/6815 (0.2%)
1	G	0.23	0/4991	0.79	15/6815 (0.2%)
1	H	0.23	0/4991	0.78	16/6815 (0.2%)
All	All	0.24	0/39928	0.79	120/54520 (0.2%)

There are no bond length outliers.

The worst 5 of 120 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	571	ASP	CB-CG-OD2	5.84	123.56	118.30
1	B	239	ASP	CB-CG-OD2	5.80	123.53	118.30
1	C	274	ASP	CB-CG-OD2	5.78	123.50	118.30
1	C	341	ASP	CB-CG-OD2	5.73	123.46	118.30
1	A	341	ASP	CB-CG-OD2	5.69	123.42	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	4836	0	4609	21	0
1	B	4836	0	4609	22	0
1	C	4836	0	4609	22	0
1	D	4836	0	4609	16	0
1	E	4836	0	4609	17	0
1	F	4836	0	4609	22	0
1	G	4836	0	4609	19	0
1	H	4836	0	4609	28	0
2	A	66	0	0	0	0
2	B	56	0	0	0	0
2	C	43	0	0	0	0
2	D	55	0	0	0	0
2	E	15	0	0	0	0
2	F	22	0	0	0	0
2	G	32	0	0	0	0
2	H	32	0	0	0	0
All	All	39009	0	36872	164	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 164 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:G:550:VAL:HB	1:G:611:ARG:HB2	1.68	0.75
1:C:550:VAL:HB	1:C:611:ARG:HB2	1.69	0.74
1:C:339:GLN:HE21	1:C:339:GLN:H	1.38	0.71
1:A:550:VAL:HB	1:A:611:ARG:HB2	1.73	0.70
1:H:550:VAL:HB	1:H:611:ARG:HB2	1.75	0.69

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	608/652 (93%)	571 (94%)	36 (6%)	1 (0%)	52	84
1	B	608/652 (93%)	574 (94%)	33 (5%)	1 (0%)	52	84
1	C	608/652 (93%)	580 (95%)	27 (4%)	1 (0%)	52	84
1	D	608/652 (93%)	576 (95%)	31 (5%)	1 (0%)	52	84
1	E	608/652 (93%)	573 (94%)	33 (5%)	2 (0%)	46	79
1	F	608/652 (93%)	578 (95%)	29 (5%)	1 (0%)	52	84
1	G	608/652 (93%)	574 (94%)	33 (5%)	1 (0%)	52	84
1	H	608/652 (93%)	571 (94%)	36 (6%)	1 (0%)	52	84
All	All	4864/5216 (93%)	4597 (94%)	258 (5%)	9 (0%)	52	84

5 of 9 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	E	344	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	511/543 (94%)	479 (94%)	32 (6%)	22	53
1	B	511/543 (94%)	476 (93%)	35 (7%)	20	49
1	C	511/543 (94%)	476 (93%)	35 (7%)	20	49
1	D	511/543 (94%)	482 (94%)	29 (6%)	25	58
1	E	511/543 (94%)	473 (93%)	38 (7%)	17	43
1	F	511/543 (94%)	473 (93%)	38 (7%)	17	43
1	G	511/543 (94%)	481 (94%)	30 (6%)	24	57
1	H	511/543 (94%)	480 (94%)	31 (6%)	23	55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	4088/4344 (94%)	3820 (93%)	268 (7%)	21 51

5 of 268 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	432	ARG
1	E	353	LYS
1	H	256	SER
1	D	496	TRP
1	E	130	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	339	GLN
1	E	339	GLN
1	H	133	GLN
1	E	133	GLN
1	F	99	ASN

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 ⓘ

There are no ligands in this entry.

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	612/652 (93%)	-0.43	7 (1%) 82 74	20, 20, 20, 20	0
1	B	612/652 (93%)	-0.40	10 (1%) 74 66	20, 20, 20, 20	0
1	C	612/652 (93%)	-0.37	11 (1%) 71 61	20, 20, 20, 20	0
1	D	612/652 (93%)	-0.37	9 (1%) 76 68	20, 20, 20, 20	0
1	E	612/652 (93%)	-0.06	18 (2%) 55 43	20, 20, 20, 20	0
1	F	612/652 (93%)	-0.16	14 (2%) 64 52	20, 20, 20, 20	0
1	G	612/652 (93%)	-0.25	14 (2%) 64 52	20, 20, 20, 20	0
1	H	612/652 (93%)	-0.17	16 (2%) 59 47	20, 20, 20, 20	0
All	All	4896/5216 (93%)	-0.28	99 (2%) 68 58	20, 20, 20, 20	0

The worst 5 of 99 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	50	HIS	6.4
1	H	50	HIS	5.9
1	D	50	HIS	5.0
1	A	441	ASN	5.0
1	F	71	GLN	4.9

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.