



# wwPDB X-ray Structure Validation Summary Report

Apr 25, 2026 – 04:38 PM EDT


PDB ID : 3FEQ / pdb\_00003feq  
Title : Crystal structure of uncharacterized protein eah89906  
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Bain, K.; Wasserman, S.R.; Raushel, F.; Sauder, J.M.; Burley, S.K.; Almo,  
S.C.; New York SGX Research Center for Structural Genomics (NYSGXRC)  
Deposited on : 2008-11-30  
Resolution : 2.63 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

<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>.

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

MolProbity : 4-5-2 with Phenix2.0  
Xtrriage (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

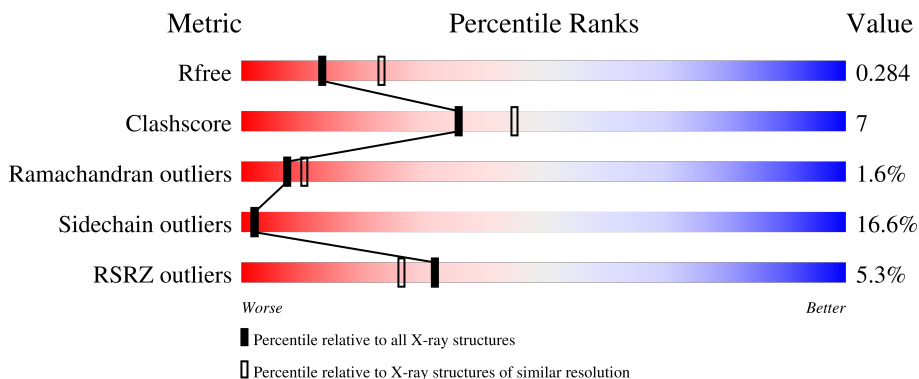
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.63 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	2053 (2.66-2.62)
Clashscore	190562	2097 (2.66-2.62)
Ramachandran outliers	187476	2066 (2.66-2.62)
Sidechain outliers	187428	2066 (2.66-2.62)
RSRZ outliers	180081	2052 (2.66-2.62)

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  $\geq 3$ , 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	423	
1	B	423	
1	C	423	
1	D	423	
1	E	423	

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Mol	Chain	Length	Quality of chain
1	F	423	 5% 72% 17% 6% . .
1	G	423	 2% 70% 21% . . .
1	H	423	 6% 68% 22% 5% .
1	I	423	 6% 67% 22% 6% .
1	J	423	 9% 70% 22% . 5%
1	K	423	 5% 69% 22% 5% 5%
1	L	423	 7% 69% 23% . .
1	M	423	 11% 68% 23% 5% .
1	N	423	 6% 67% 23% 5% .
1	O	423	 2% 68% 25% . 5%
1	P	423	 3% 70% 22% . .

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 48417 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 AMIDOHYDROLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	405	Total 3028	C 1886	N 547	O 580	S 15	0	4	0
1	B	405	Total 3040	C 1894	N 552	O 579	S 15	0	6	0
1	C	406	Total 3025	C 1883	N 550	O 577	S 15	0	2	0
1	D	405	Total 3035	C 1890	N 553	O 577	S 15	0	4	0
1	E	405	Total 3026	C 1883	N 550	O 578	S 15	0	4	0
1	F	405	Total 3016	C 1878	N 546	O 577	S 15	0	2	0
1	G	405	Total 3021	C 1881	N 549	O 576	S 15	0	2	0
1	H	405	Total 3016	C 1878	N 546	O 577	S 15	0	2	0
1	I	405	Total 3013	C 1876	N 546	O 576	S 15	0	1	0
1	J	402	Total 2994	C 1866	N 543	O 571	S 14	0	1	0
1	K	403	Total 3000	C 1869	N 544	O 572	S 15	0	1	0
1	L	404	Total 3005	C 1870	N 545	O 575	S 15	0	1	0
1	M	406	Total 3017	C 1878	N 547	O 577	S 15	0	1	0
1	N	404	Total 3003	C 1869	N 545	O 575	S 14	0	1	0
1	O	401	Total 2983	C 1857	N 542	O 570	S 14	0	1	0
1	P	405	Total 3018	C 1879	N 547	O 577	S 15	0	2	0

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total 2	Zn 2	0	0
2	B	2	Total 2	Zn 2	0	0
2	C	2	Total 2	Zn 2	0	0
2	D	2	Total 2	Zn 2	0	0
2	E	2	Total 2	Zn 2	0	0
2	F	2	Total 2	Zn 2	0	0
2	G	2	Total 2	Zn 2	0	0
2	H	2	Total 2	Zn 2	0	0
2	I	2	Total 2	Zn 2	0	0
2	J	2	Total 2	Zn 2	0	0
2	K	2	Total 2	Zn 2	0	0
2	L	2	Total 2	Zn 2	0	0
2	M	2	Total 2	Zn 2	0	0
2	N	2	Total 2	Zn 2	0	0
2	O	2	Total 2	Zn 2	0	0
2	P	2	Total 2	Zn 2	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	24	Total 24	O 24	0	0
3	B	27	Total 27	O 27	0	0
3	C	13	Total 13	O 13	0	0

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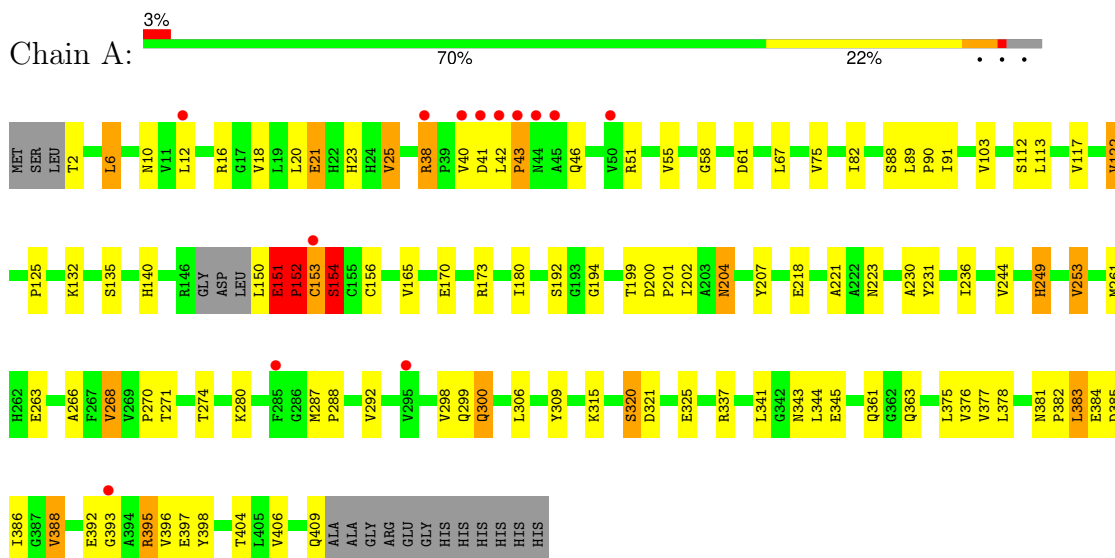
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>	<b>ZeroOcc</b>	<b>AltConf</b>
3	D	20	Total O 20 20	0	0
3	E	18	Total O 18 18	0	0
3	F	17	Total O 17 17	0	0
3	G	16	Total O 16 16	0	0
3	H	6	Total O 6 6	0	0
3	O	2	Total O 2 2	0	0
3	P	2	Total O 2 2	0	0

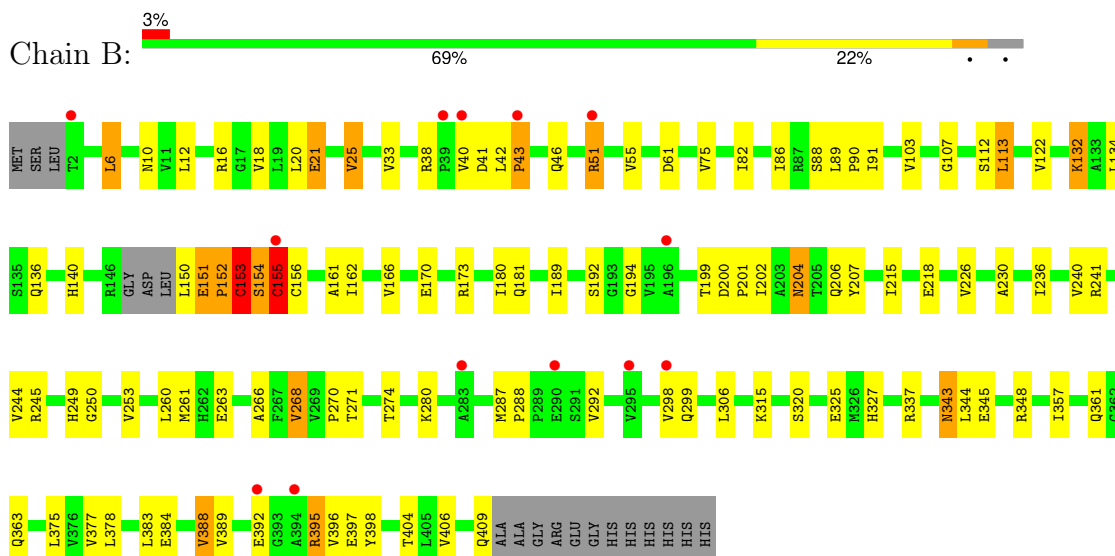
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: PUTATIVE AMIDOHYDROLASE

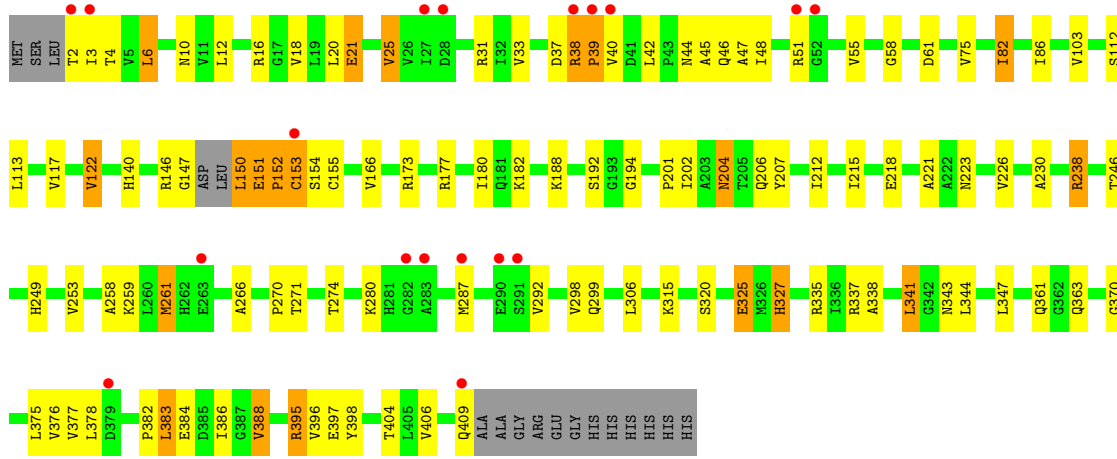


- Molecule 1: PUTATIVE AMIDOHYDROLASE

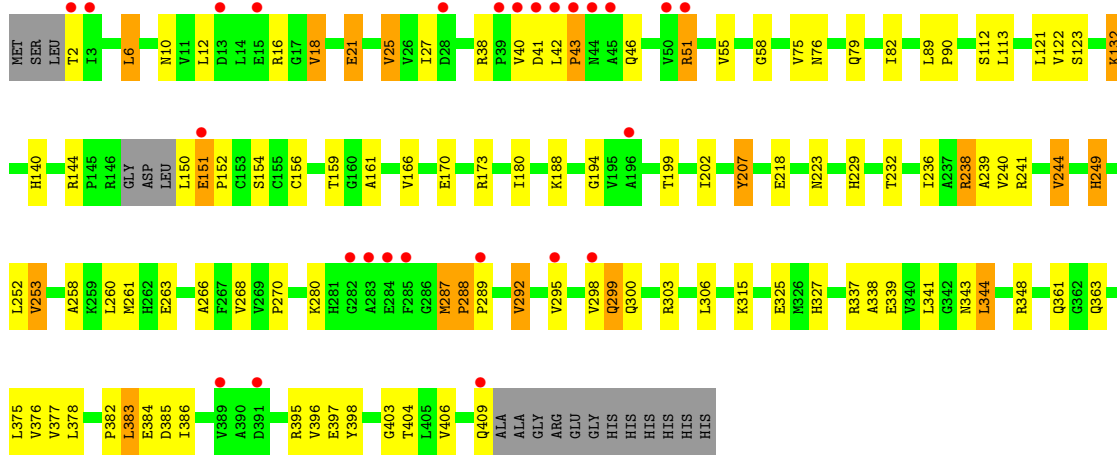


- Molecule 1: PUTATIVE AMIDOHYDROLASE

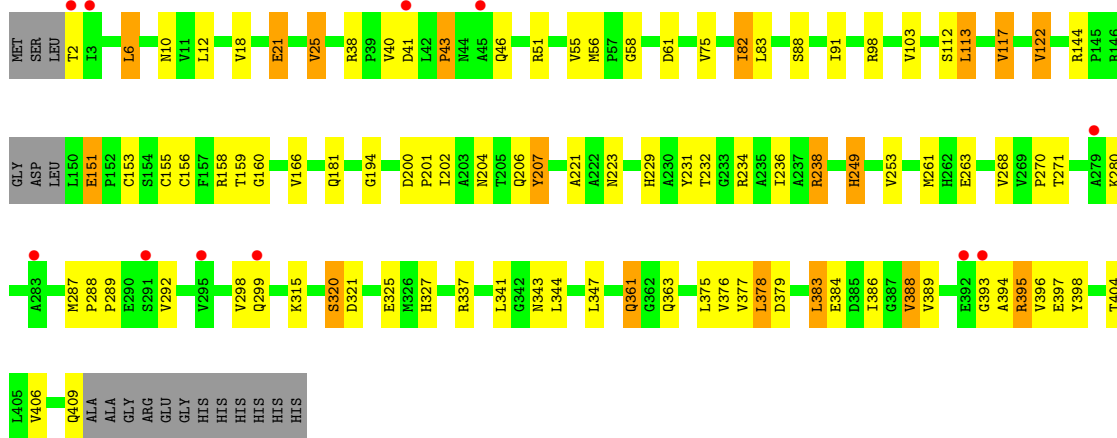
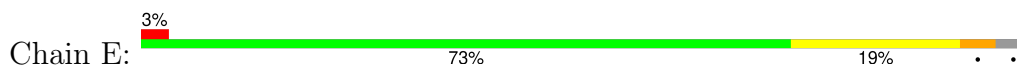




• Molecule 1: PUTATIVE AMIDOHYDROLASE

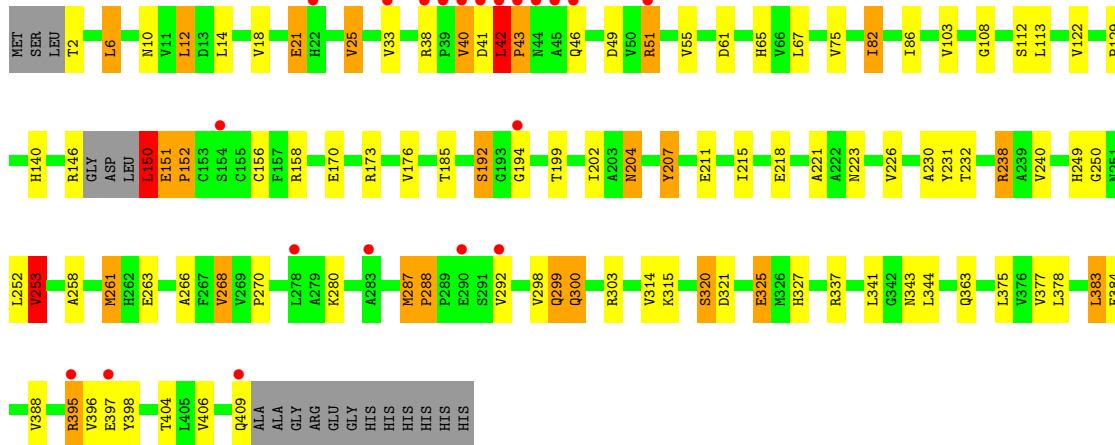


• Molecule 1: PUTATIVE AMIDOHYDROLASE



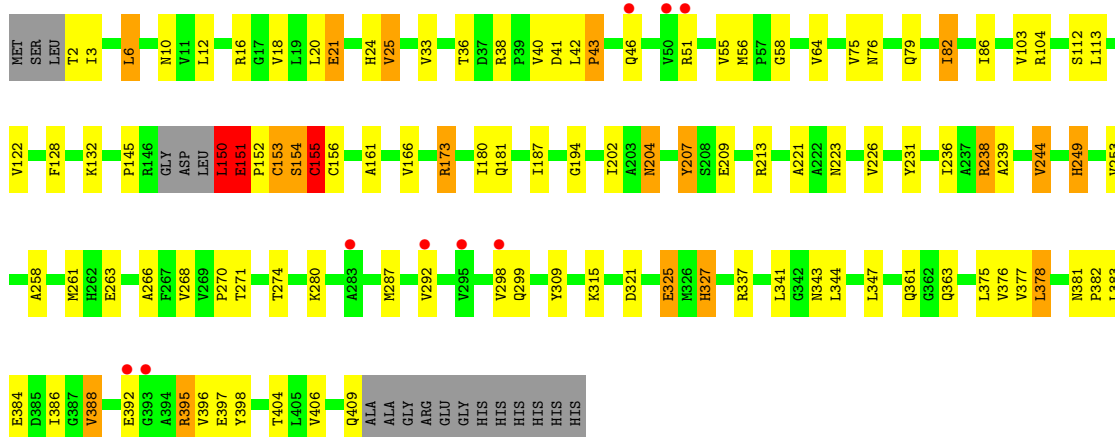
• Molecule 1: PUTATIVE AMIDOHYDROLASE

Chain F: 5% 72% 17% 6%



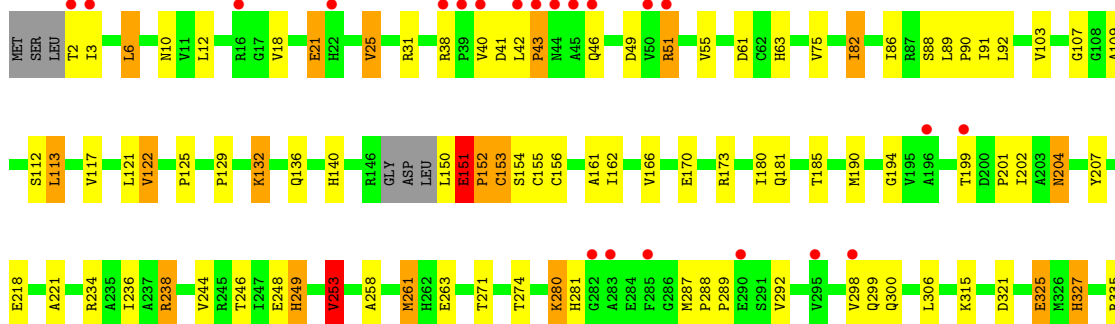
• Molecule 1: PUTATIVE AMIDOHYDROLASE

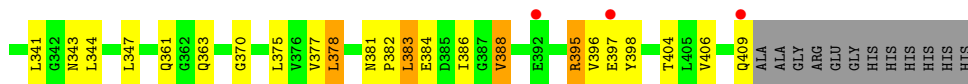
Chain G: 2% 70% 21%



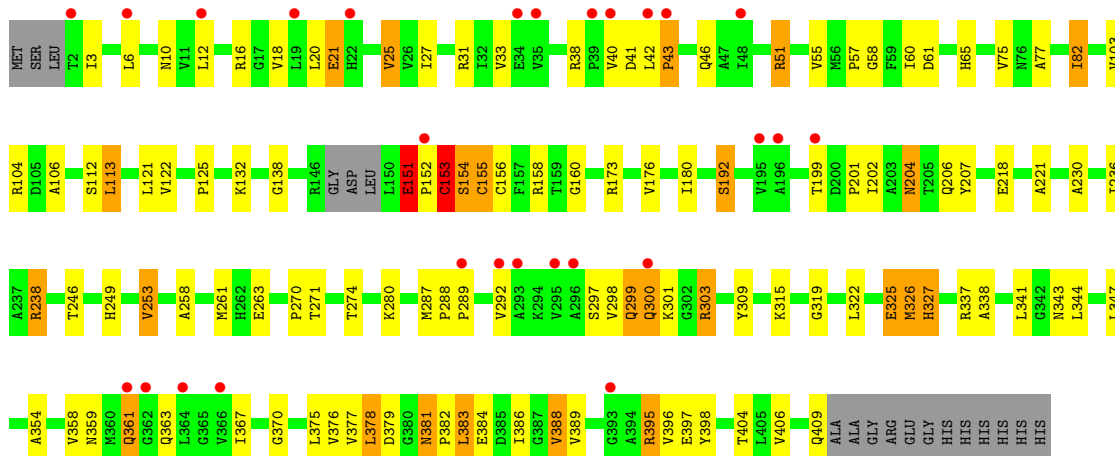
• Molecule 1: PUTATIVE AMIDOHYDROLASE

Chain H: 6% 68% 22% 5%

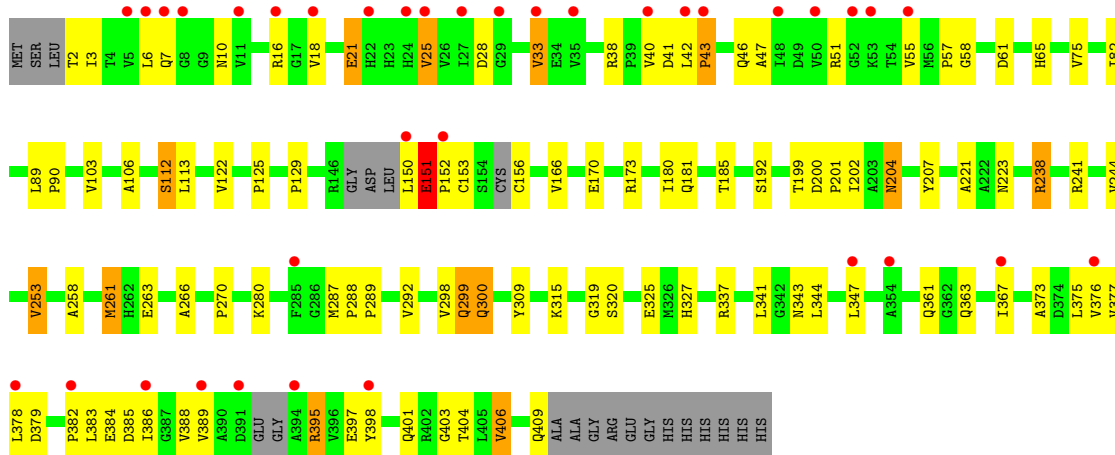




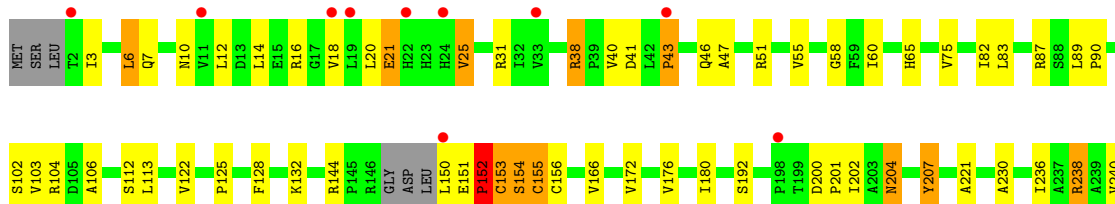
• Molecule 1: PUTATIVE AMIDOHYDROLASE

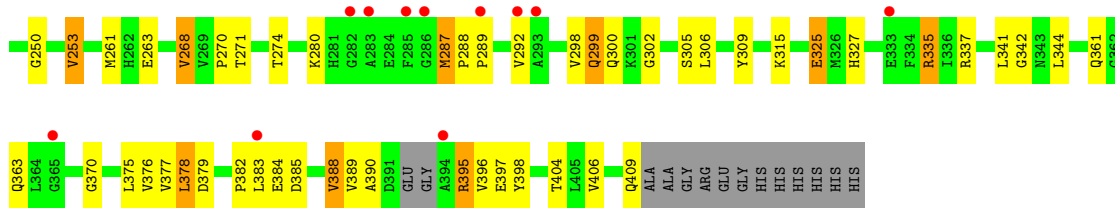


• Molecule 1: PUTATIVE AMIDOHYDROLASE

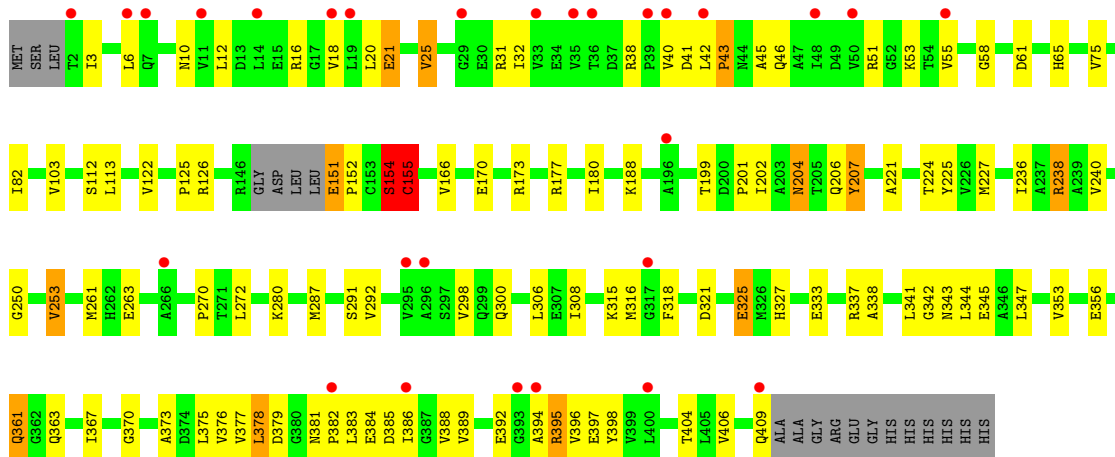


• Molecule 1: PUTATIVE AMIDOHYDROLASE

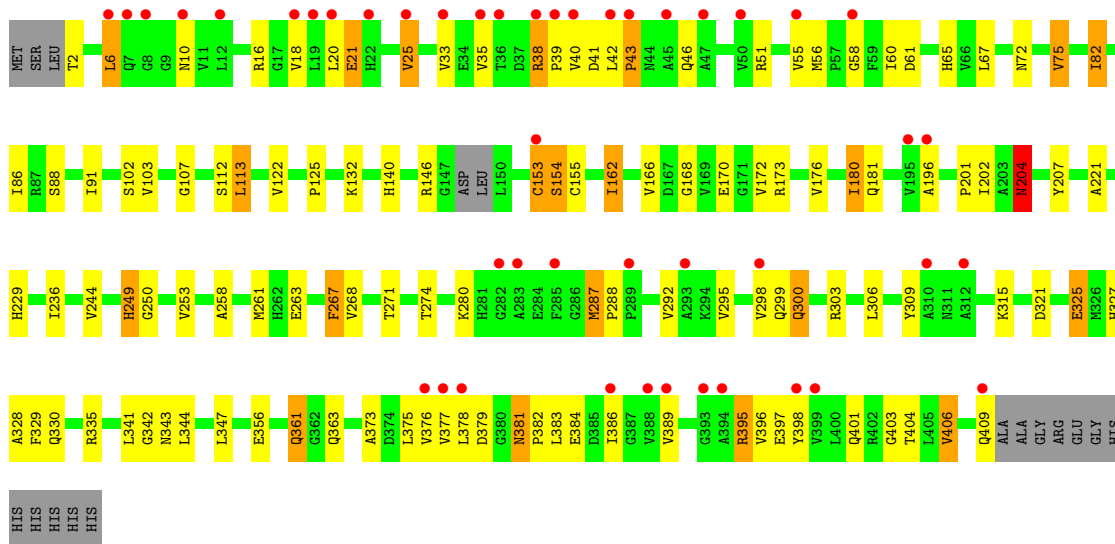




● Molecule 1: PUTATIVE AMIDOHYDROLASE

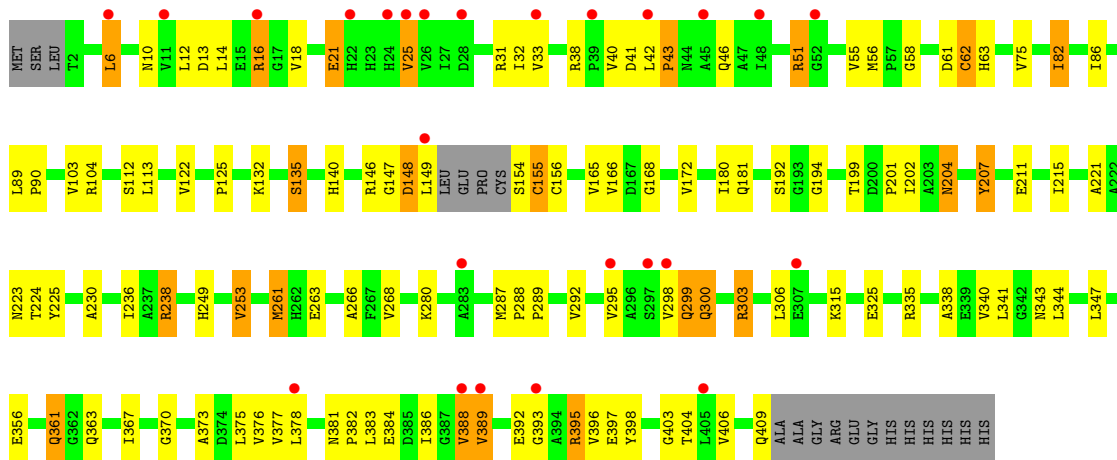


● Molecule 1: PUTATIVE AMIDOHYDROLASE

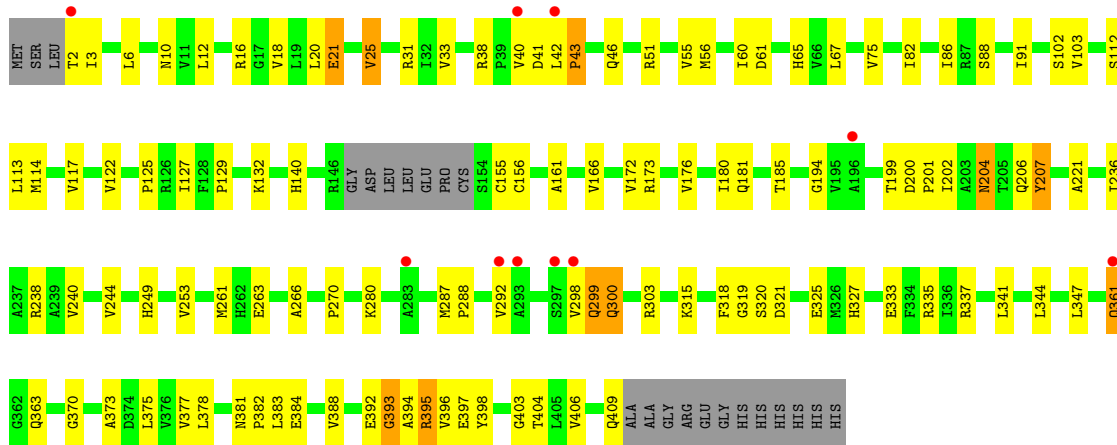


● Molecule 1: PUTATIVE AMIDOHYDROLASE

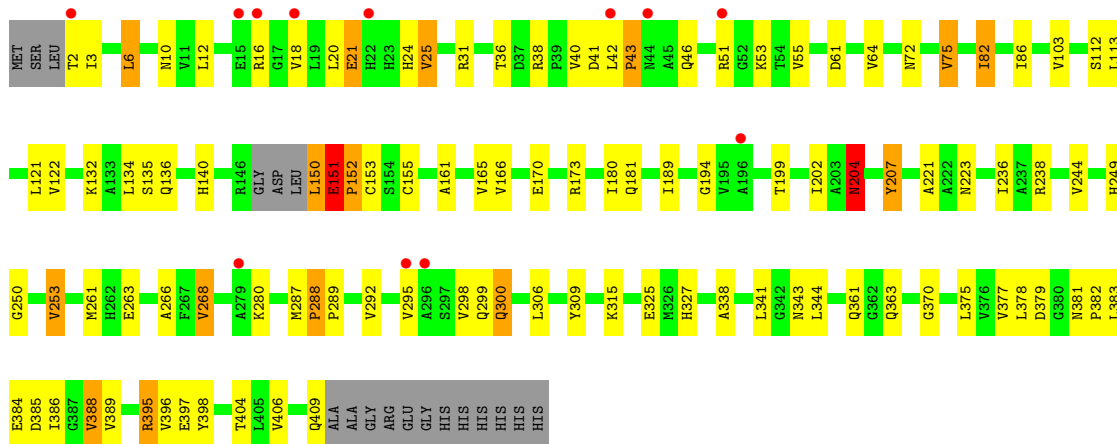




• Molecule 1: PUTATIVE AMIDOHYDROLASE



• Molecule 1: PUTATIVE AMIDOHYDROLASE



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	113.21Å 108.05Å 171.13Å 81.75° 80.36° 74.40°	Depositor
Resolution (Å)	20.00 – 2.63 20.00 – 2.63	Depositor EDS
% Data completeness (in resolution range)	96.4 (20.00-2.63) 96.2 (20.00-2.63)	Depositor EDS
$R_{merge}$	0.21	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.42 (at 2.65Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.238 , 0.281 0.242 , 0.284	Depositor DCC
$R_{free}$ test set	6591 reflections (2.90%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	41.7	Xtrriage
Anisotropy	0.071	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 50.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	0.011 for -k,-h,-l	Xtrriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	48417	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	58.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.46% 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:  
ZN

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	0.53	0/3083	0.86	5/4180 (0.1%)
1	B	0.60	0/3102	0.87	5/4205 (0.1%)
1	C	0.58	0/3074	0.86	3/4167 (0.1%)
1	D	0.61	0/3090	0.87	5/4188 (0.1%)
1	E	0.57	0/3081	0.87	2/4177 (0.0%)
1	F	0.56	0/3065	0.89	7/4156 (0.2%)
1	G	0.54	0/3070	0.88	7/4162 (0.2%)
1	H	0.60	0/3065	0.86	5/4156 (0.1%)
1	I	0.61	0/3059	0.89	5/4148 (0.1%)
1	J	0.56	0/3038	0.86	6/4117 (0.1%)
1	K	0.56	0/3045	0.89	2/4128 (0.0%)
1	L	0.56	0/3051	0.90	6/4137 (0.1%)
1	M	0.56	0/3063	0.89	5/4153 (0.1%)
1	N	0.58	1/3048 (0.0%)	0.86	4/4132 (0.1%)
1	O	0.56	0/3028	0.86	4/4105 (0.1%)
1	P	0.55	0/3067	0.89	5/4159 (0.1%)
All	All	0.57	1/49029 (0.0%)	0.87	76/66470 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	4
1	B	0	2
1	C	0	3
1	D	0	2
1	E	0	3
1	F	0	2
1	G	0	6

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	H	0	4
1	I	0	2
1	J	0	3
1	K	0	2
1	L	0	2
1	M	0	2
1	N	0	1
1	O	0	3
1	P	0	5
All	All	0	46

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	N	63	HIS	CA-C	-6.20	1.47	1.53

The worst 5 of 76 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	381	ASN	CA-C-N	6.83	126.46	119.56
1	L	381	ASN	C-N-CA	6.83	126.46	119.56
1	H	156	CYS	N-CA-C	6.82	119.53	109.24
1	L	287	MET	CA-C-N	6.61	127.19	120.38
1	L	287	MET	C-N-CA	6.61	127.19	120.38

There are no chirality outliers.

5 of 46 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	151	GLU	Peptide
1	A	152	PRO	Peptide
1	A	2	THR	Peptide
1	A	38	ARG	Peptide
1	B	38	ARG	Peptide

## 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	3028	0	3044	48	0
1	B	3040	0	3063	47	0
1	C	3025	0	3041	47	1
1	D	3035	0	3059	45	0
1	E	3026	0	3040	43	0
1	F	3016	0	3030	46	0
1	G	3021	0	3038	43	0
1	H	3016	0	3030	53	0
1	I	3013	0	3025	62	1
1	J	2994	0	3009	41	0
1	K	3000	0	3015	43	0
1	L	3005	0	3014	43	0
1	M	3017	0	3028	56	0
1	N	3003	0	3014	56	0
1	O	2983	0	2996	38	0
1	P	3018	0	3031	43	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
2	E	2	0	0	0	0
2	F	2	0	0	0	0
2	G	2	0	0	0	0
2	H	2	0	0	0	0
2	I	2	0	0	0	0
2	J	2	0	0	0	0
2	K	2	0	0	0	0
2	L	2	0	0	0	0
2	M	2	0	0	0	0
2	N	2	0	0	0	0
2	O	2	0	0	0	0
2	P	2	0	0	0	0
3	A	24	0	0	0	0
3	B	27	0	0	1	0
3	C	13	0	0	1	0
3	D	20	0	0	1	0
3	E	18	0	0	3	0
3	F	17	0	0	1	0
3	G	16	0	0	1	0
3	H	6	0	0	1	0
3	O	2	0	0	0	0
3	P	2	0	0	0	0
All	All	48417	0	48477	704	1

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 7.

The worst 5 of 704 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:H:263:GLU:OE2	1:M:38:ARG:HD2	1.55	1.07
1:I:221:ALA:O	1:K:204:ASN:HB2	1.60	1.01
1:A:16:ARG:HH12	1:A:20:LEU:HD21	1.27	0.97
1:C:221:ALA:O	1:F:204:ASN:HB2	1.72	0.88
1:C:3:ILE:HG23	1:C:45:ALA:HA	1.59	0.85

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:45:ALA:O	1:I:301:LYS:NZ[1_546]	1.98	0.22

## 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	405/423 (96%)	385 (95%)	13 (3%)	7 (2%)	7 9
1	B	407/423 (96%)	384 (94%)	16 (4%)	7 (2%)	7 9
1	C	404/423 (96%)	380 (94%)	18 (4%)	6 (2%)	8 11
1	D	405/423 (96%)	383 (95%)	17 (4%)	5 (1%)	10 15
1	E	405/423 (96%)	378 (93%)	23 (6%)	4 (1%)	12 18
1	F	403/423 (95%)	379 (94%)	19 (5%)	5 (1%)	10 15
1	G	403/423 (95%)	380 (94%)	18 (4%)	5 (1%)	10 15
1	H	403/423 (95%)	374 (93%)	21 (5%)	8 (2%)	6 8
1	I	402/423 (95%)	374 (93%)	20 (5%)	8 (2%)	6 8

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	J	395/423 (93%)	368 (93%)	22 (6%)	5 (1%)	9	14
1	K	398/423 (94%)	369 (93%)	22 (6%)	7 (2%)	6	9
1	L	401/423 (95%)	371 (92%)	21 (5%)	9 (2%)	5	7
1	M	403/423 (95%)	378 (94%)	17 (4%)	8 (2%)	6	8
1	N	401/423 (95%)	367 (92%)	28 (7%)	6 (2%)	8	11
1	O	398/423 (94%)	373 (94%)	18 (4%)	7 (2%)	6	9
1	P	403/423 (95%)	380 (94%)	17 (4%)	6 (2%)	8	11
All	All	6436/6768 (95%)	6023 (94%)	310 (5%)	103 (2%)	7	10

5 of 103 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	151	GLU
1	A	152	PRO
1	A	153	CYS
1	B	151	GLU
1	B	152	PRO

### 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	317/326 (97%)	263 (83%)	54 (17%)	2	2
1	B	319/326 (98%)	263 (82%)	56 (18%)	2	2
1	C	315/326 (97%)	262 (83%)	53 (17%)	2	2
1	D	317/326 (97%)	264 (83%)	53 (17%)	2	2
1	E	316/326 (97%)	267 (84%)	49 (16%)	2	2
1	F	315/326 (97%)	261 (83%)	54 (17%)	2	2
1	G	315/326 (97%)	262 (83%)	53 (17%)	2	2
1	H	315/326 (97%)	262 (83%)	53 (17%)	2	2
1	I	314/326 (96%)	262 (83%)	52 (17%)	2	2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	J	312/326 (96%)	262 (84%)	50 (16%)	2	2
1	K	313/326 (96%)	261 (83%)	52 (17%)	2	2
1	L	313/326 (96%)	265 (85%)	48 (15%)	3	3
1	M	314/326 (96%)	261 (83%)	53 (17%)	2	2
1	N	312/326 (96%)	256 (82%)	56 (18%)	2	1
1	O	310/326 (95%)	257 (83%)	53 (17%)	2	2
1	P	315/326 (97%)	265 (84%)	50 (16%)	2	2
All	All	5032/5216 (96%)	4193 (83%)	839 (17%)	2	2

5 of 839 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	344	LEU
1	K	395	ARG
1	P	55	VAL
1	I	409	GLN
1	I	341	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 112 such sidechains are listed below:

Mol	Chain	Res	Type
1	I	299	GLN
1	P	299	GLN
1	K	223	ASN
1	P	281	HIS
1	N	361	GLN

### 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 32 ligands modelled in this entry, 32 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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 [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	405/423 (95%)	-0.07	13 (3%)	50	44	16, 50, 100, 117	4 (0%)
1	B	405/423 (95%)	-0.07	13 (3%)	50	44	11, 48, 102, 119	6 (1%)
1	C	406/423 (95%)	0.01	18 (4%)	39	32	14, 49, 104, 118	2 (0%)
1	D	405/423 (95%)	0.07	26 (6%)	25	21	14, 44, 98, 116	4 (0%)
1	E	405/423 (95%)	-0.02	11 (2%)	56	51	14, 47, 102, 119	4 (0%)
1	F	405/423 (95%)	0.00	21 (5%)	33	27	15, 49, 99, 119	2 (0%)
1	G	405/423 (95%)	-0.09	9 (2%)	62	58	13, 50, 103, 136	2 (0%)
1	H	405/423 (95%)	0.02	25 (6%)	26	22	12, 46, 100, 119	2 (0%)
1	I	405/423 (95%)	0.55	27 (6%)	24	19	28, 58, 106, 123	1 (0%)
1	J	402/423 (95%)	0.57	36 (8%)	15	12	27, 60, 103, 121	1 (0%)
1	K	403/423 (95%)	0.53	21 (5%)	33	27	25, 59, 103, 119	1 (0%)
1	L	404/423 (95%)	0.65	28 (6%)	23	19	22, 61, 106, 133	1 (0%)
1	M	406/423 (95%)	0.53	45 (11%)	10	8	23, 60, 107, 130	1 (0%)
1	N	404/423 (95%)	0.40	25 (6%)	26	22	21, 58, 106, 121	1 (0%)
1	O	401/423 (94%)	-0.02	10 (2%)	58	54	22, 53, 103, 121	1 (0%)
1	P	405/423 (95%)	-0.02	12 (2%)	52	47	13, 51, 100, 121	2 (0%)
All	All	6471/6768 (95%)	0.19	340 (5%)	32	26	11, 53, 103, 136	35 (0%)

The worst 5 of 340 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	44	ASN	6.0
1	F	43	PRO	5.3
1	D	409	GLN	5.0
1	A	42	LEU	4.5
1	M	393	GLY	4.3

## 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, 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	B-factors(Å <sup>2</sup> )	Q<0.9
2	ZN	J	426	1/1	0.79	0.13	68,68,68,68	1
2	ZN	J	425	1/1	0.83	0.11	60,60,60,60	1
2	ZN	O	426	1/1	0.84	0.17	58,58,58,58	1
2	ZN	N	425	1/1	0.85	0.11	41,41,41,41	1
2	ZN	I	426	1/1	0.87	0.14	58,58,58,58	1
2	ZN	P	425	1/1	0.87	0.11	47,47,47,47	1
2	ZN	F	426	1/1	0.88	0.16	51,51,51,51	1
2	ZN	N	426	1/1	0.89	0.16	55,55,55,55	1
2	ZN	F	425	1/1	0.90	0.10	52,52,52,52	1
2	ZN	K	426	1/1	0.90	0.09	68,68,68,68	1
2	ZN	P	426	1/1	0.90	0.13	59,59,59,59	1
2	ZN	L	425	1/1	0.91	0.06	55,55,55,55	1
2	ZN	E	425	1/1	0.91	0.10	43,43,43,43	1
2	ZN	H	426	1/1	0.91	0.12	39,39,39,39	1
2	ZN	M	425	1/1	0.92	0.06	50,50,50,50	1
2	ZN	K	425	1/1	0.92	0.10	55,55,55,55	1
2	ZN	M	426	1/1	0.93	0.13	63,63,63,63	1
2	ZN	L	426	1/1	0.93	0.10	63,63,63,63	1
2	ZN	A	425	1/1	0.93	0.10	51,51,51,51	1
2	ZN	G	425	1/1	0.94	0.10	40,40,40,40	1
2	ZN	E	426	1/1	0.94	0.17	45,45,45,45	1
2	ZN	I	425	1/1	0.95	0.07	42,42,42,42	1
2	ZN	B	425	1/1	0.95	0.11	44,44,44,44	1
2	ZN	O	425	1/1	0.95	0.09	50,50,50,50	1
2	ZN	C	425	1/1	0.96	0.11	42,42,42,42	1
2	ZN	D	426	1/1	0.96	0.11	33,33,33,33	1
2	ZN	B	426	1/1	0.97	0.08	44,44,44,44	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	ZN	A	426	1/1	0.97	0.07	52,52,52,52	1
2	ZN	G	426	1/1	0.97	0.08	37,37,37,37	1
2	ZN	C	426	1/1	0.97	0.08	38,38,38,38	1
2	ZN	D	425	1/1	0.97	0.08	34,34,34,34	1
2	ZN	H	425	1/1	0.98	0.08	40,40,40,40	1

## 6.5 Other polymers [i](#)

There are no such residues in this entry.