



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 05:19 AM GMT

PDB ID : 2Q43  
Title : Ensemble refinement of the protein crystal structure of IAA-aminoacid hydrolase from Arabidopsis thaliana gene At5g56660  
Authors : Levin, E.J.; Kondrashov, D.A.; Wesenberg, G.E.; Phillips Jr., G.N.; Center for Eukaryotic Structural Genomics (CESG)  
Deposited on : 2007-05-31  
Resolution : 2.00 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 (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

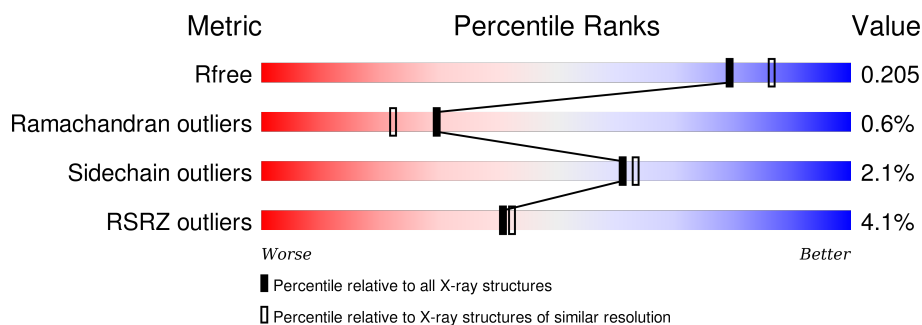
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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.






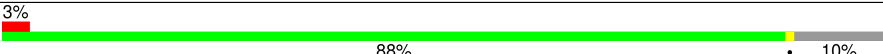
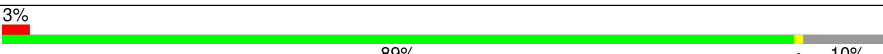
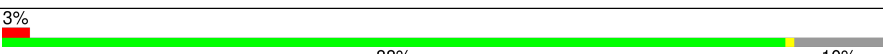
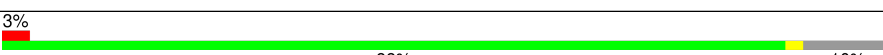
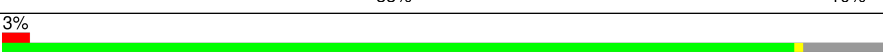

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	6249 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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	1-A	418	<div> <div>3%</div> <div>88%</div> <div>10%</div> </div>
1	10-A	418	<div> <div>3%</div> <div>88%</div> <div>10%</div> </div>
1	11-A	418	<div> <div>3%</div> <div>88%</div> <div>10%</div> </div>
1	12-A	418	<div> <div>3%</div> <div>87%</div> <div>10%</div> </div>
1	13-A	418	<div> <div>3%</div> <div>87%</div> <div>10%</div> </div>
1	14-A	418	<div> <div>3%</div> <div>87%</div> <div>10%</div> </div>
1	15-A	418	<div> <div>3%</div> <div>86%</div> <div>10%</div> </div>

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Mol	Chain	Length	Quality of chain
1	16-A	418	
1	2-A	418	
1	3-A	418	
1	4-A	418	
1	5-A	418	
1	6-A	418	
1	7-A	418	
1	8-A	418	
1	9-A	418	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 50784 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.

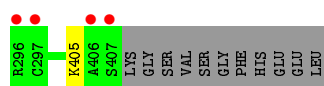
- Molecule 1 is a protein called IAA-amino acid hydrolase ILR1-like 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1-A	375	Total	C	N	O	S	0	0	0
			2889	1841	501	536	11			
1	2-A	375	Total	C	N	O	S	0	0	0
			2889	1841	501	536	11			
1	3-A	375	Total	C	N	O	S	0	0	0
			2889	1841	501	536	11			
1	4-A	375	Total	C	N	O	S	0	0	0
			2889	1841	501	536	11			
1	5-A	375	Total	C	N	O	S	0	0	0
			2889	1841	501	536	11			
1	6-A	375	Total	C	N	O	S	0	0	0
			2889	1841	501	536	11			
1	7-A	375	Total	C	N	O	S	0	0	0
			2889	1841	501	536	11			
1	8-A	375	Total	C	N	O	S	0	0	0
			2889	1841	501	536	11			
1	9-A	375	Total	C	N	O	S	0	0	0
			2889	1841	501	536	11			
1	10-A	375	Total	C	N	O	S	0	0	0
			2889	1841	501	536	11			
1	11-A	375	Total	C	N	O	S	0	0	0
			2889	1841	501	536	11			
1	12-A	375	Total	C	N	O	S	0	0	0
			2889	1841	501	536	11			
1	13-A	375	Total	C	N	O	S	0	0	0
			2889	1841	501	536	11			
1	14-A	375	Total	C	N	O	S	0	0	0
			2889	1841	501	536	11			
1	15-A	375	Total	C	N	O	S	0	0	0
			2889	1841	501	536	11			
1	16-A	375	Total	C	N	O	S	0	0	0
			2889	1841	501	536	11			

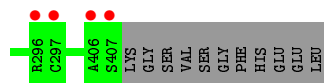
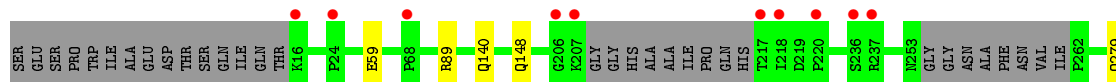
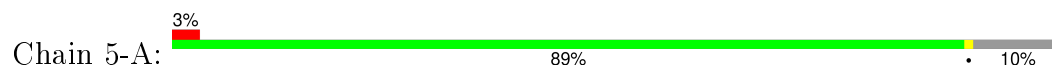
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	1-A	285	Total O 285 285	0	0
2	2-A	285	Total O 285 285	0	0
2	3-A	285	Total O 285 285	0	0
2	4-A	285	Total O 285 285	0	0
2	5-A	285	Total O 285 285	0	0
2	6-A	285	Total O 285 285	0	0
2	7-A	285	Total O 285 285	0	0
2	8-A	285	Total O 285 285	0	0
2	9-A	285	Total O 285 285	0	0
2	10-A	285	Total O 285 285	0	0
2	11-A	285	Total O 285 285	0	0
2	12-A	285	Total O 285 285	0	0
2	13-A	285	Total O 285 285	0	0
2	14-A	285	Total O 285 285	0	0
2	15-A	285	Total O 285 285	0	0
2	16-A	285	Total O 285 285	0	0

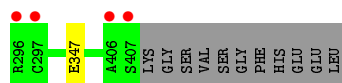
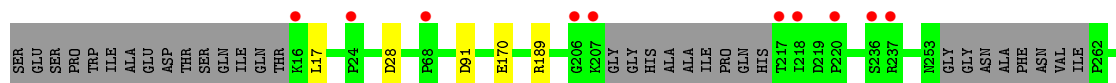
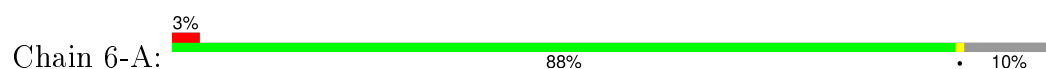




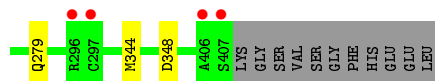
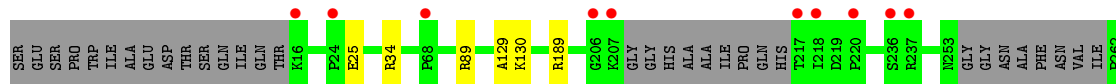
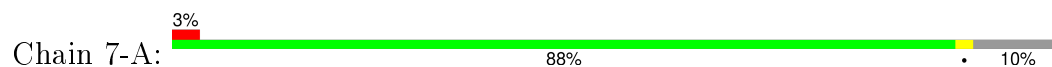
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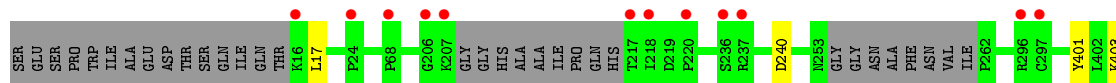
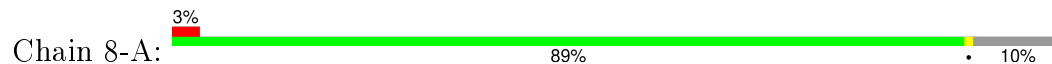
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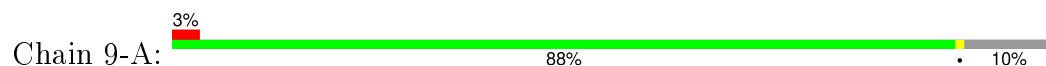
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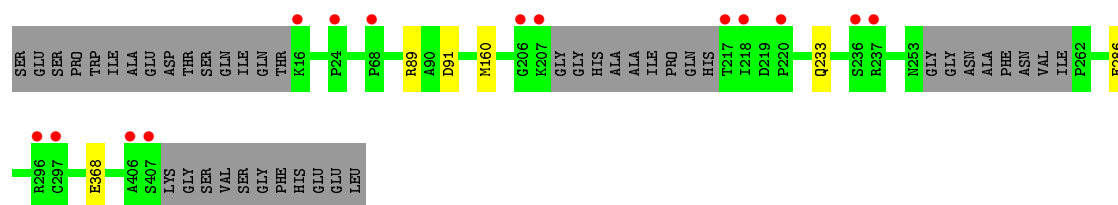


- Molecule 1: IAA-amino acid hydrolase ILR1-like 2

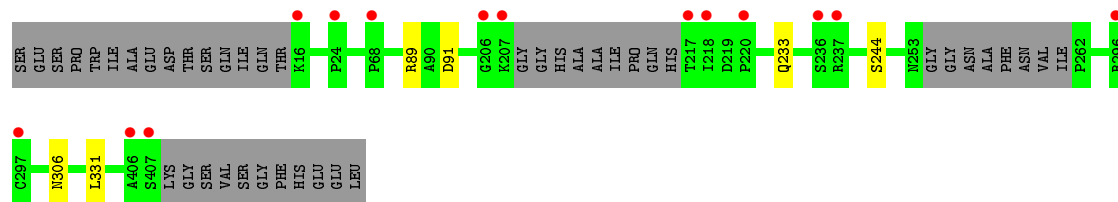


- Molecule 1: IAA-amino acid hydrolase ILR1-like 2

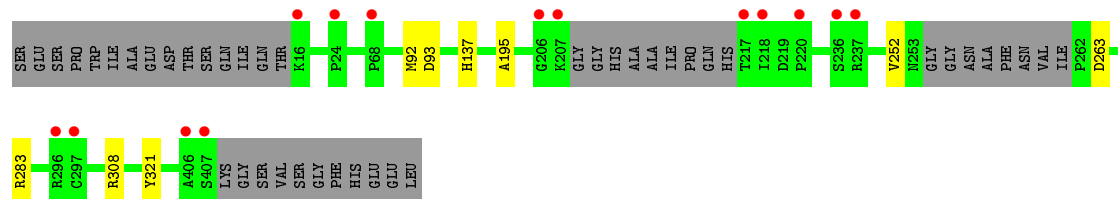
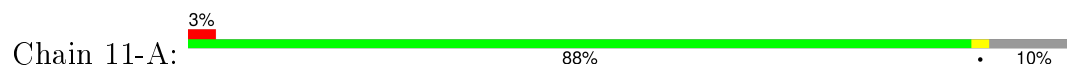




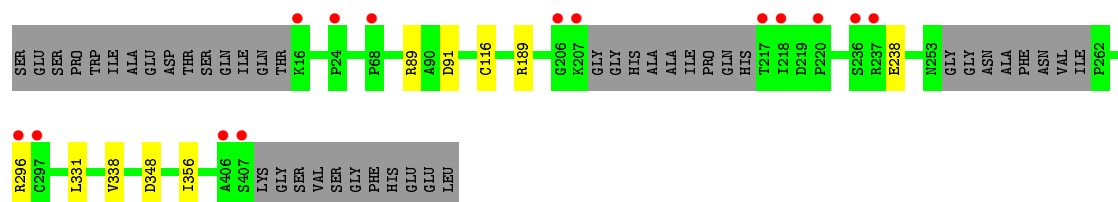
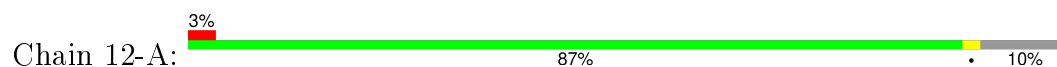
- Molecule 1: IAA-amino acid hydrolase ILR1-like 2



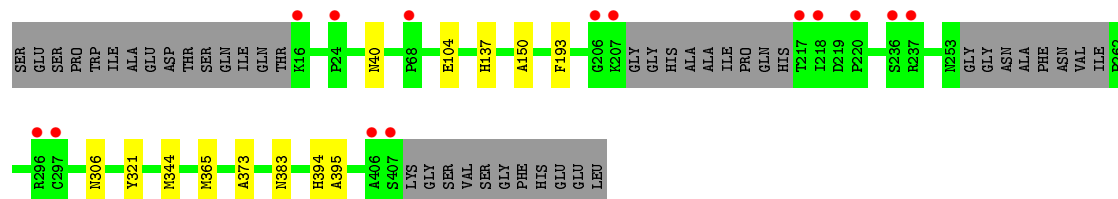
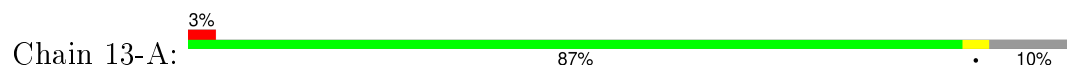
- Molecule 1: IAA-amino acid hydrolase ILR1-like 2



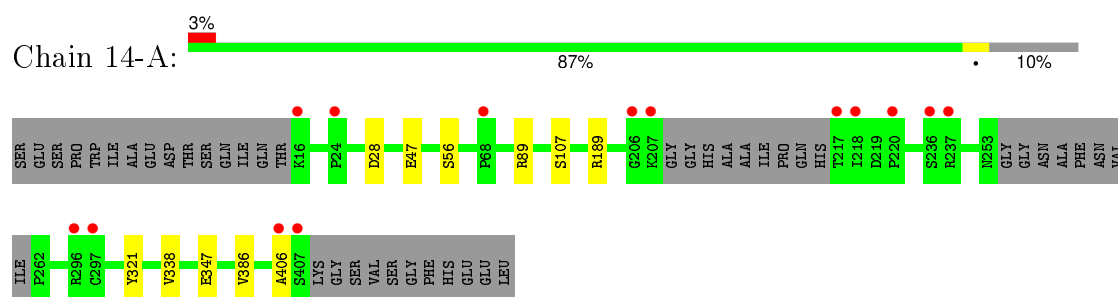
- Molecule 1: IAA-amino acid hydrolase ILR1-like 2



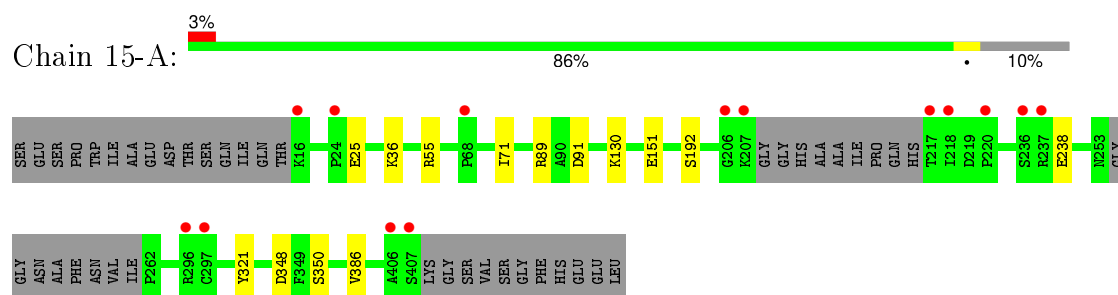
- Molecule 1: IAA-amino acid hydrolase ILR1-like 2



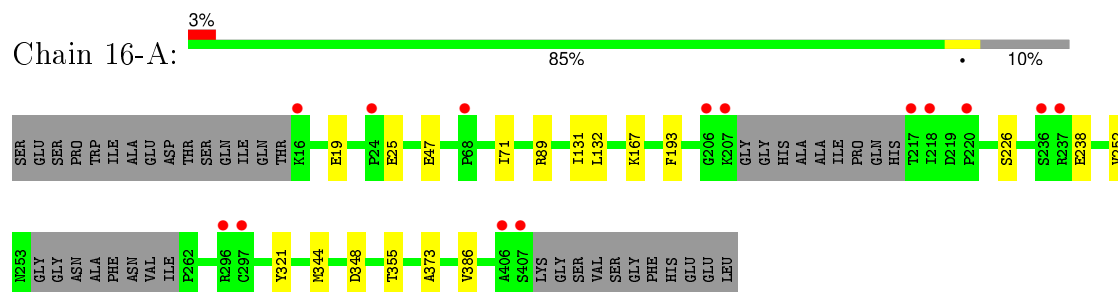
- Molecule 1: IAA-amino acid hydrolase ILR1-like 2



- Molecule 1: IAA-amino acid hydrolase ILR1-like 2



- Molecule 1: IAA-amino acid hydrolase ILR1-like 2



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	75.26 Å 75.26 Å 130.88 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	23.09 – 2.00 24.21 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (23.09-2.00) 99.9 (24.21-2.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.16 (at 1.99 Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.149 , 0.204 0.155 , 0.205	Depositor DCC
$R_{free}$ test set	1504 reflections (5.35%)	DCC
Wilson B-factor (Å <sup>2</sup> )	28.4	Xtriage
Anisotropy	0.041	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.26 , 68.1	EDS
Estimated twinning fraction	0.027 for -h,-k,l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 29630 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	50784	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.88% 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, 0.375 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	1-A	0.45	0/2948	0.63	0/3984
1	2-A	0.45	0/2948	0.63	0/3984
1	3-A	0.45	0/2948	0.63	0/3984
1	4-A	0.45	0/2948	0.63	0/3984
1	5-A	0.46	0/2948	0.62	0/3984
1	6-A	0.46	0/2948	0.62	0/3984
1	7-A	0.46	0/2948	0.61	0/3984
1	8-A	0.46	0/2948	0.61	0/3984
1	9-A	0.45	0/2948	0.61	0/3984
1	10-A	0.46	0/2948	0.62	0/3984
1	11-A	0.45	0/2948	0.62	0/3984
1	12-A	0.44	0/2948	0.62	0/3984
1	13-A	0.54	0/2948	0.70	0/3984
1	14-A	0.52	0/2948	0.71	1/3984 (0.0%)
1	15-A	0.52	0/2948	0.70	0/3984
1	16-A	0.51	0/2948	0.70	0/3984
All	All	0.47	0/47168	0.64	1/63744 (0.0%)

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	16-A	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	14-A	189	ARG	NE-CZ-NH1	-5.11	117.74	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	16-A	321	TYR	Sidechain

## 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	1-A	2889	0	2919	0	0
1	2-A	2889	0	2919	0	0
1	3-A	2889	0	2919	0	0
1	4-A	2889	0	2919	0	0
1	5-A	2889	0	2919	0	0
1	6-A	2889	0	2919	0	0
1	7-A	2889	0	2919	0	0
1	8-A	2889	0	2919	0	0
1	9-A	2889	0	2919	0	0
1	10-A	2889	0	2919	0	0
1	11-A	2889	0	2919	0	0
1	12-A	2889	0	2919	0	0
1	13-A	2889	0	2919	0	0
1	14-A	2889	0	2919	0	0
1	15-A	2889	0	2919	0	0
1	16-A	2889	0	2919	0	0
2	1-A	285	0	0	0	0
2	2-A	285	0	0	0	0
2	3-A	285	0	0	0	0
2	4-A	285	0	0	0	0
2	5-A	285	0	0	0	0
2	6-A	285	0	0	0	0
2	7-A	285	0	0	0	0
2	8-A	285	0	0	0	0
2	9-A	285	0	0	0	0
2	10-A	285	0	0	0	0
2	11-A	285	0	0	0	0
2	12-A	285	0	0	0	0
2	13-A	285	0	0	0	0
2	14-A	285	0	0	0	0
2	15-A	285	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	16-A	285	0	0	0	0
All	All	50784	0	46704	0	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). Clashscore could not be calculated for this entry.

There are no clashes within the asymmetric unit.

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	1-A	369/418 (88%)	348 (94%)	20 (5%)	1 (0%)	46	41
1	2-A	369/418 (88%)	348 (94%)	20 (5%)	1 (0%)	46	41
1	3-A	369/418 (88%)	338 (92%)	27 (7%)	4 (1%)	17	9
1	4-A	369/418 (88%)	354 (96%)	15 (4%)	0	100	100
1	5-A	369/418 (88%)	357 (97%)	12 (3%)	0	100	100
1	6-A	369/418 (88%)	352 (95%)	17 (5%)	0	100	100
1	7-A	369/418 (88%)	340 (92%)	27 (7%)	2 (0%)	34	26
1	8-A	369/418 (88%)	354 (96%)	13 (4%)	2 (0%)	34	26
1	9-A	369/418 (88%)	356 (96%)	13 (4%)	0	100	100
1	10-A	369/418 (88%)	355 (96%)	13 (4%)	1 (0%)	46	41
1	11-A	369/418 (88%)	348 (94%)	16 (4%)	5 (1%)	14	6
1	12-A	369/418 (88%)	345 (94%)	23 (6%)	1 (0%)	46	41
1	13-A	369/418 (88%)	341 (92%)	23 (6%)	5 (1%)	14	6
1	14-A	369/418 (88%)	349 (95%)	16 (4%)	4 (1%)	17	9
1	15-A	369/418 (88%)	347 (94%)	21 (6%)	1 (0%)	46	41
1	16-A	369/418 (88%)	340 (92%)	21 (6%)	8 (2%)	8	3

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	5904/6688 (88%)	5572 (94%)	297 (5%)	35 (1%)	30	22

5 of 35 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	2-A	150	ALA
1	11-A	195	ALA
1	11-A	263	ASP
1	11-A	308	ARG
1	13-A	373	ALA

### 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	1-A	308/341 (90%)	303 (98%)	5 (2%)	70	73
1	2-A	308/341 (90%)	305 (99%)	3 (1%)	82	85
1	3-A	308/341 (90%)	297 (96%)	11 (4%)	42	39
1	4-A	308/341 (90%)	302 (98%)	6 (2%)	65	67
1	5-A	308/341 (90%)	303 (98%)	5 (2%)	70	73
1	6-A	308/341 (90%)	302 (98%)	6 (2%)	65	67
1	7-A	308/341 (90%)	301 (98%)	7 (2%)	58	60
1	8-A	308/341 (90%)	306 (99%)	2 (1%)	90	93
1	9-A	308/341 (90%)	302 (98%)	6 (2%)	65	67
1	10-A	308/341 (90%)	303 (98%)	5 (2%)	70	73
1	11-A	308/341 (90%)	304 (99%)	4 (1%)	76	79
1	12-A	308/341 (90%)	299 (97%)	9 (3%)	50	49
1	13-A	308/341 (90%)	300 (97%)	8 (3%)	54	54
1	14-A	308/341 (90%)	302 (98%)	6 (2%)	65	67
1	15-A	308/341 (90%)	295 (96%)	13 (4%)	36	31
1	16-A	308/341 (90%)	299 (97%)	9 (3%)	50	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	4928/5456 (90%)	4823 (98%)	105 (2%)	61 63

5 of 105 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	9-A	160	MET
1	11-A	283	ARG
1	16-A	25	GLU
1	9-A	233	GLN
1	10-A	233	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 117 such sidechains are listed below:

Mol	Chain	Res	Type
1	8-A	334	GLN
1	10-A	370	ASN
1	16-A	140	GLN
1	9-A	281	GLN
1	10-A	140	GLN

### 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, 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	1-A	375/418 (89%)	-0.16	14 (3%)	45	47	10, 23, 47, 66	375 (100%)
1	2-A	375/418 (89%)	-0.16	14 (3%)	45	47	10, 23, 47, 66	375 (100%)
1	3-A	375/418 (89%)	-0.16	14 (3%)	45	47	10, 23, 47, 66	375 (100%)
1	4-A	375/418 (89%)	-0.16	14 (3%)	45	47	10, 23, 47, 66	375 (100%)
1	5-A	375/418 (89%)	-0.16	14 (3%)	45	47	10, 23, 47, 66	375 (100%)
1	6-A	375/418 (89%)	-0.16	14 (3%)	45	47	10, 23, 47, 66	375 (100%)
1	7-A	375/418 (89%)	-0.16	14 (3%)	45	47	10, 23, 47, 66	375 (100%)
1	8-A	375/418 (89%)	-0.16	14 (3%)	45	47	10, 23, 47, 66	375 (100%)
1	9-A	375/418 (89%)	-0.16	14 (3%)	45	47	10, 23, 47, 66	375 (100%)
1	10-A	375/418 (89%)	-0.16	14 (3%)	45	47	10, 23, 47, 66	375 (100%)
1	11-A	375/418 (89%)	-0.16	14 (3%)	45	47	10, 23, 47, 66	375 (100%)
1	12-A	375/418 (89%)	-0.16	14 (3%)	45	47	10, 23, 47, 66	375 (100%)
1	13-A	375/418 (89%)	-0.16	14 (3%)	45	47	10, 23, 47, 66	375 (100%)
1	14-A	375/418 (89%)	-0.16	14 (3%)	45	47	10, 23, 47, 66	375 (100%)
1	15-A	375/418 (89%)	-0.16	14 (3%)	45	47	10, 23, 47, 66	375 (100%)
1	16-A	375/418 (89%)	-0.16	14 (3%)	45	47	10, 23, 47, 66	375 (100%)
All	All	6000/6688 (89%)	-0.16	224 (3%)	41	47	10, 23, 48, 66	6000 (100%)

The worst 5 of 224 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	1-A	218	ILE	5.8
1	2-A	218	ILE	5.8
1	3-A	218	ILE	5.8
1	4-A	218	ILE	5.8
1	5-A	218	ILE	5.8

## 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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.