



# Full wwPDB X-ray Structure Validation Report

May 29, 2020 – 05:05 am BST

PDB ID : 4IC5  
Title : Crystal structure of Deg5  
Authors : Gong, W.; Sun, W.; Fan, H.; Gao, F.; Liu, L.  
Deposited on : 2012-12-10  
Resolution : 2.61 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](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.

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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  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

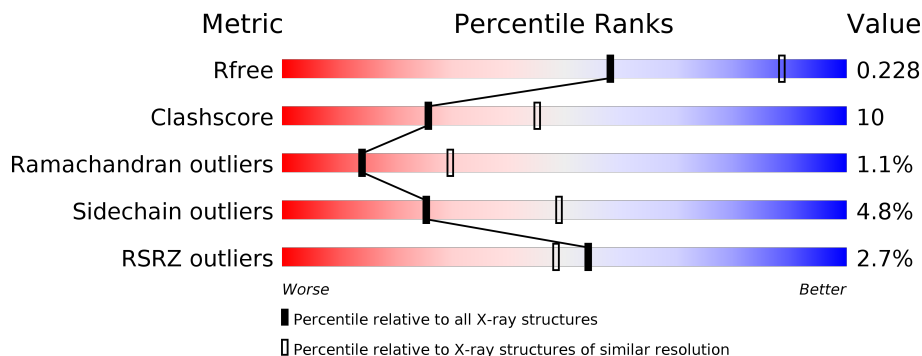
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.61 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))
$R_{free}$	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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 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	291	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 2px;"></div> <div style="width: 56%; height: 10px; background-color: green; margin-right: 2px;"></div> <div style="width: 14%; height: 10px; background-color: yellow; margin-right: 2px;"></div> <div style="width: 28%; height: 10px; background-color: grey; margin-right: 2px;"></div> </div> <p style="font-size: small; margin-top: 5px;">2%      56%      14%      •      28%</p>
1	B	291	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 2px;"></div> <div style="width: 57%; height: 10px; background-color: green; margin-right: 2px;"></div> <div style="width: 13%; height: 10px; background-color: yellow; margin-right: 2px;"></div> <div style="width: 28%; height: 10px; background-color: grey; margin-right: 2px;"></div> </div> <p style="font-size: small; margin-top: 5px;">2%      57%      13%      •      28%</p>
1	C	291	<div style="display: flex; align-items: center;"> <div style="width: 0%; height: 10px; background-color: red; margin-right: 2px;"></div> <div style="width: 56%; height: 10px; background-color: green; margin-right: 2px;"></div> <div style="width: 14%; height: 10px; background-color: yellow; margin-right: 2px;"></div> <div style="width: 28%; height: 10px; background-color: grey; margin-right: 2px;"></div> </div> <p style="font-size: small; margin-top: 5px;">%      56%      14%      •      28%</p>

## 2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 4946 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 Protease Do-like 5, chloroplastic.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	210	Total 1609	C 1015	N 271	O 321	S 2	0	3	0
1	B	210	Total 1601	C 1010	N 268	O 321	S 2	0	2	0
1	C	209	Total 1600	C 1010	N 270	O 318	S 2	0	3	0

There are 126 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	50	MET	-	EXPRESSION TAG	UNP Q9SEL7
A	51	GLY	-	EXPRESSION TAG	UNP Q9SEL7
A	52	SER	-	EXPRESSION TAG	UNP Q9SEL7
A	53	SER	-	EXPRESSION TAG	UNP Q9SEL7
A	54	HIS	-	EXPRESSION TAG	UNP Q9SEL7
A	55	HIS	-	EXPRESSION TAG	UNP Q9SEL7
A	56	HIS	-	EXPRESSION TAG	UNP Q9SEL7
A	57	HIS	-	EXPRESSION TAG	UNP Q9SEL7
A	58	HIS	-	EXPRESSION TAG	UNP Q9SEL7
A	59	HIS	-	EXPRESSION TAG	UNP Q9SEL7
A	60	SER	-	EXPRESSION TAG	UNP Q9SEL7
A	61	SER	-	EXPRESSION TAG	UNP Q9SEL7
A	62	GLY	-	EXPRESSION TAG	UNP Q9SEL7
A	63	LEU	-	EXPRESSION TAG	UNP Q9SEL7
A	64	VAL	-	EXPRESSION TAG	UNP Q9SEL7
A	65	PRO	-	EXPRESSION TAG	UNP Q9SEL7
A	66	ARG	-	EXPRESSION TAG	UNP Q9SEL7
A	67	GLY	-	EXPRESSION TAG	UNP Q9SEL7
A	68	SER	-	EXPRESSION TAG	UNP Q9SEL7
A	69	HIS	-	EXPRESSION TAG	UNP Q9SEL7
A	70	MET	-	EXPRESSION TAG	UNP Q9SEL7
A	71	ALA	-	EXPRESSION TAG	UNP Q9SEL7
A	72	SER	-	EXPRESSION TAG	UNP Q9SEL7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	266	ALA	SER	ENGINEERED MUTATION	UNP Q9SEL7
A	323	LEU	-	EXPRESSION TAG	UNP Q9SEL7
A	324	SER	-	EXPRESSION TAG	UNP Q9SEL7
A	325	SER	-	EXPRESSION TAG	UNP Q9SEL7
A	326	VAL	-	EXPRESSION TAG	UNP Q9SEL7
A	327	ASP	-	EXPRESSION TAG	UNP Q9SEL7
A	328	LYS	-	EXPRESSION TAG	UNP Q9SEL7
A	329	LEU	-	EXPRESSION TAG	UNP Q9SEL7
A	330	ALA	-	EXPRESSION TAG	UNP Q9SEL7
A	331	ALA	-	EXPRESSION TAG	UNP Q9SEL7
A	332	ALA	-	EXPRESSION TAG	UNP Q9SEL7
A	333	LEU	-	EXPRESSION TAG	UNP Q9SEL7
A	334	GLU	-	EXPRESSION TAG	UNP Q9SEL7
A	335	HIS	-	EXPRESSION TAG	UNP Q9SEL7
A	336	HIS	-	EXPRESSION TAG	UNP Q9SEL7
A	337	HIS	-	EXPRESSION TAG	UNP Q9SEL7
A	338	HIS	-	EXPRESSION TAG	UNP Q9SEL7
A	339	HIS	-	EXPRESSION TAG	UNP Q9SEL7
A	340	HIS	-	EXPRESSION TAG	UNP Q9SEL7
B	50	MET	-	EXPRESSION TAG	UNP Q9SEL7
B	51	GLY	-	EXPRESSION TAG	UNP Q9SEL7
B	52	SER	-	EXPRESSION TAG	UNP Q9SEL7
B	53	SER	-	EXPRESSION TAG	UNP Q9SEL7
B	54	HIS	-	EXPRESSION TAG	UNP Q9SEL7
B	55	HIS	-	EXPRESSION TAG	UNP Q9SEL7
B	56	HIS	-	EXPRESSION TAG	UNP Q9SEL7
B	57	HIS	-	EXPRESSION TAG	UNP Q9SEL7
B	58	HIS	-	EXPRESSION TAG	UNP Q9SEL7
B	59	HIS	-	EXPRESSION TAG	UNP Q9SEL7
B	60	SER	-	EXPRESSION TAG	UNP Q9SEL7
B	61	SER	-	EXPRESSION TAG	UNP Q9SEL7
B	62	GLY	-	EXPRESSION TAG	UNP Q9SEL7
B	63	LEU	-	EXPRESSION TAG	UNP Q9SEL7
B	64	VAL	-	EXPRESSION TAG	UNP Q9SEL7
B	65	PRO	-	EXPRESSION TAG	UNP Q9SEL7
B	66	ARG	-	EXPRESSION TAG	UNP Q9SEL7
B	67	GLY	-	EXPRESSION TAG	UNP Q9SEL7
B	68	SER	-	EXPRESSION TAG	UNP Q9SEL7
B	69	HIS	-	EXPRESSION TAG	UNP Q9SEL7
B	70	MET	-	EXPRESSION TAG	UNP Q9SEL7
B	71	ALA	-	EXPRESSION TAG	UNP Q9SEL7
B	72	SER	-	EXPRESSION TAG	UNP Q9SEL7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	266	ALA	SER	ENGINEERED MUTATION	UNP Q9SEL7
B	323	LEU	-	EXPRESSION TAG	UNP Q9SEL7
B	324	SER	-	EXPRESSION TAG	UNP Q9SEL7
B	325	SER	-	EXPRESSION TAG	UNP Q9SEL7
B	326	VAL	-	EXPRESSION TAG	UNP Q9SEL7
B	327	ASP	-	EXPRESSION TAG	UNP Q9SEL7
B	328	LYS	-	EXPRESSION TAG	UNP Q9SEL7
B	329	LEU	-	EXPRESSION TAG	UNP Q9SEL7
B	330	ALA	-	EXPRESSION TAG	UNP Q9SEL7
B	331	ALA	-	EXPRESSION TAG	UNP Q9SEL7
B	332	ALA	-	EXPRESSION TAG	UNP Q9SEL7
B	333	LEU	-	EXPRESSION TAG	UNP Q9SEL7
B	334	GLU	-	EXPRESSION TAG	UNP Q9SEL7
B	335	HIS	-	EXPRESSION TAG	UNP Q9SEL7
B	336	HIS	-	EXPRESSION TAG	UNP Q9SEL7
B	337	HIS	-	EXPRESSION TAG	UNP Q9SEL7
B	338	HIS	-	EXPRESSION TAG	UNP Q9SEL7
B	339	HIS	-	EXPRESSION TAG	UNP Q9SEL7
B	340	HIS	-	EXPRESSION TAG	UNP Q9SEL7
C	50	MET	-	EXPRESSION TAG	UNP Q9SEL7
C	51	GLY	-	EXPRESSION TAG	UNP Q9SEL7
C	52	SER	-	EXPRESSION TAG	UNP Q9SEL7
C	53	SER	-	EXPRESSION TAG	UNP Q9SEL7
C	54	HIS	-	EXPRESSION TAG	UNP Q9SEL7
C	55	HIS	-	EXPRESSION TAG	UNP Q9SEL7
C	56	HIS	-	EXPRESSION TAG	UNP Q9SEL7
C	57	HIS	-	EXPRESSION TAG	UNP Q9SEL7
C	58	HIS	-	EXPRESSION TAG	UNP Q9SEL7
C	59	HIS	-	EXPRESSION TAG	UNP Q9SEL7
C	60	SER	-	EXPRESSION TAG	UNP Q9SEL7
C	61	SER	-	EXPRESSION TAG	UNP Q9SEL7
C	62	GLY	-	EXPRESSION TAG	UNP Q9SEL7
C	63	LEU	-	EXPRESSION TAG	UNP Q9SEL7
C	64	VAL	-	EXPRESSION TAG	UNP Q9SEL7
C	65	PRO	-	EXPRESSION TAG	UNP Q9SEL7
C	66	ARG	-	EXPRESSION TAG	UNP Q9SEL7
C	67	GLY	-	EXPRESSION TAG	UNP Q9SEL7
C	68	SER	-	EXPRESSION TAG	UNP Q9SEL7
C	69	HIS	-	EXPRESSION TAG	UNP Q9SEL7
C	70	MET	-	EXPRESSION TAG	UNP Q9SEL7
C	71	ALA	-	EXPRESSION TAG	UNP Q9SEL7
C	72	SER	-	EXPRESSION TAG	UNP Q9SEL7

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Chain	Residue	Modelled	Actual	Comment	Reference
C	266	ALA	SER	ENGINEERED MUTATION	UNP Q9SEL7
C	323	LEU	-	EXPRESSION TAG	UNP Q9SEL7
C	324	SER	-	EXPRESSION TAG	UNP Q9SEL7
C	325	SER	-	EXPRESSION TAG	UNP Q9SEL7
C	326	VAL	-	EXPRESSION TAG	UNP Q9SEL7
C	327	ASP	-	EXPRESSION TAG	UNP Q9SEL7
C	328	LYS	-	EXPRESSION TAG	UNP Q9SEL7
C	329	LEU	-	EXPRESSION TAG	UNP Q9SEL7
C	330	ALA	-	EXPRESSION TAG	UNP Q9SEL7
C	331	ALA	-	EXPRESSION TAG	UNP Q9SEL7
C	332	ALA	-	EXPRESSION TAG	UNP Q9SEL7
C	333	LEU	-	EXPRESSION TAG	UNP Q9SEL7
C	334	GLU	-	EXPRESSION TAG	UNP Q9SEL7
C	335	HIS	-	EXPRESSION TAG	UNP Q9SEL7
C	336	HIS	-	EXPRESSION TAG	UNP Q9SEL7
C	337	HIS	-	EXPRESSION TAG	UNP Q9SEL7
C	338	HIS	-	EXPRESSION TAG	UNP Q9SEL7
C	339	HIS	-	EXPRESSION TAG	UNP Q9SEL7
C	340	HIS	-	EXPRESSION TAG	UNP Q9SEL7

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

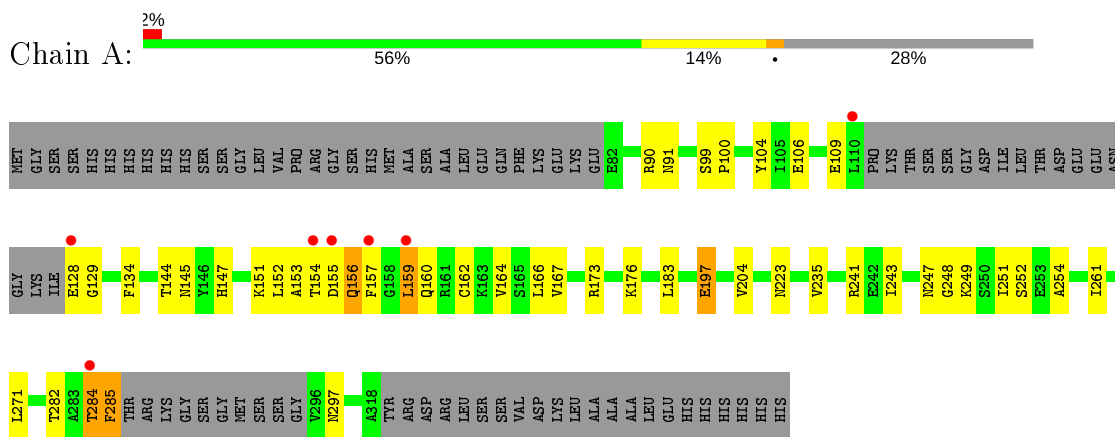
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	37	Total O 37 37	0	0
3	B	45	Total O 45 45	0	0
3	C	49	Total O 49 49	0	0

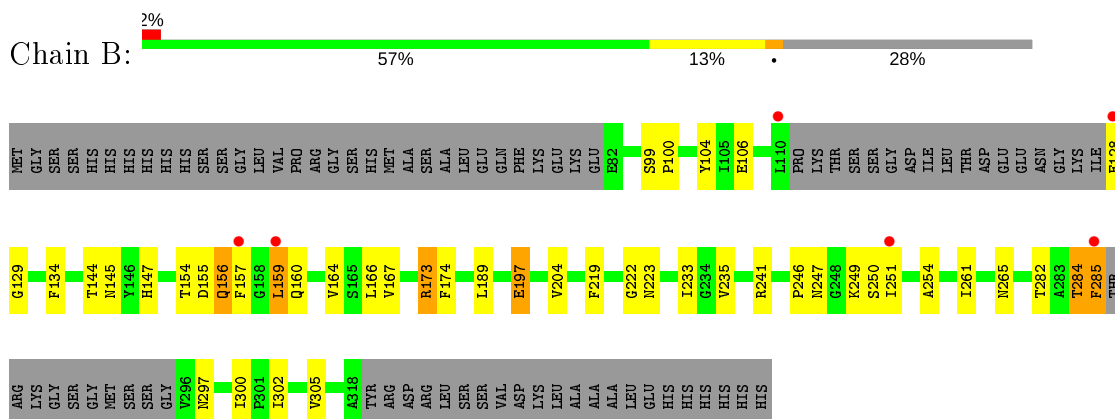
### 3 Residue-property plots [i](#)

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

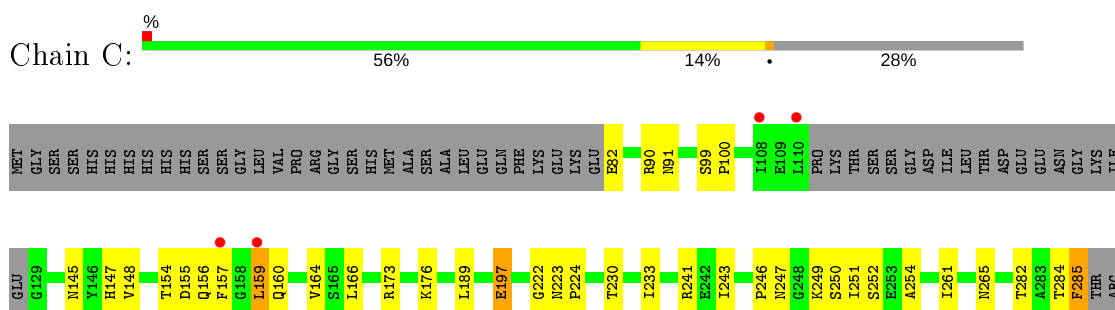
- Molecule 1: Protease Do-like 5, chloroplastic



- Molecule 1: Protease Do-like 5, chloroplastic



- Molecule 1: Protease Do-like 5, chloroplastic



LYS	GLY	SER	GLY	MET	SER	SER	GLY	V286	N297	I300	F301	I302	V305	V309	P310	A318	TYR	ARG	ASP	ARG	LEU	SER	SER	VAL	ASP	LYS	LEU	ALA	ALA	ALA	LEU	GLU	HIS	HIS	HIS	HIS	HIS	HIS
-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



## 4 Data and refinement statistics i

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	109.09Å 125.95Å 83.33Å 90.00° 102.91° 90.00°	Depositor
Resolution (Å)	49.88 – 2.61 49.88 – 2.61	Depositor EDS
% Data completeness (in resolution range)	98.7 (49.88-2.61) 98.6 (49.88-2.61)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.29 (at 2.61Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, $R_{free}$	0.182 , 0.232 0.177 , 0.228	Depositor DCC
$R_{free}$ test set	1674 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	39.3	Xtrriage
Anisotropy	0.397	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 36.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.448 for $-1/2^*h+1/2^*k-l, 1/2^*h-1/2^*k-l, -1/2^*h-1/2^*k$ 0.457 for $-1/2^*h-1/2^*k-l, -1/2^*h-1/2^*k+l, -1/2^*h+1/2^*k$	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4946	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.95% 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: CA

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.39	0/1641	0.54	0/2229
1	B	0.38	0/1630	0.54	0/2215
1	C	0.38	0/1632	0.54	0/2217
All	All	0.39	0/4903	0.54	0/6661

There are no bond length outliers.

There are no bond angle outliers.

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	1609	0	1589	33	0
1	B	1601	0	1576	32	0
1	C	1600	0	1583	37	0
2	A	3	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
3	A	37	0	0	0	0
3	B	45	0	0	0	0
3	C	49	0	0	1	0
All	All	4946	0	4748	100	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 10.

All (100) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:197:GLU:HG2	1:C:197:GLU:O	1.61	0.97
1:B:197:GLU:HG2	1:B:197:GLU:O	1.68	0.91
1:A:197:GLU:HG2	1:A:197:GLU:O	1.70	0.87
1:A:249:LYS:HA	1:A:285:PHE:HE1	1.48	0.78
1:C:249:LYS:HA	1:C:285:PHE:HE1	1.50	0.77
1:C:251:ILE:HB	1:C:254:ALA:HB2	1.67	0.77
1:B:251:ILE:HB	1:B:254:ALA:HB2	1.70	0.74
1:C:82:GLU:OE2	3:C:541:HOH:O	2.05	0.73
1:B:249:LYS:HA	1:B:285:PHE:HE1	1.54	0.73
1:A:90[B]:ARG:HG3	1:A:91:ASN:N	2.02	0.72
1:A:251:ILE:HB	1:A:254:ALA:HB2	1.70	0.71
1:A:249:LYS:HA	1:A:285:PHE:CE1	2.26	0.71
1:A:147[B]:HIS:ND1	1:A:284:THR:HB	2.06	0.70
1:C:147[B]:HIS:ND1	1:C:284:THR:HB	2.07	0.70
1:A:128:GLU:HG2	1:A:129:GLY:H	1.57	0.70
1:B:145:ASN:HD21	1:B:282:THR:HA	1.62	0.65
1:C:90[B]:ARG:HG3	1:C:91:ASN:N	2.11	0.65
1:B:249:LYS:HA	1:B:285:PHE:CE1	2.31	0.65
1:C:249:LYS:HA	1:C:285:PHE:CE1	2.32	0.63
1:C:249:LYS:HG3	1:C:285:PHE:HD1	1.63	0.62
1:A:159:LEU:HD12	1:A:160:GLN:H	1.65	0.62
1:A:147[B]:HIS:CE1	1:A:284:THR:HB	2.34	0.62
1:C:154:THR:HG23	1:C:155:ASP:N	2.16	0.61
1:B:147[B]:HIS:ND1	1:B:284:THR:HB	2.15	0.60
1:A:197:GLU:CG	1:A:197:GLU:O	2.48	0.59
1:C:147[B]:HIS:CE1	1:C:284:THR:HB	2.39	0.58
1:C:164:VAL:HG12	1:C:166:LEU:HD22	1.85	0.57
1:B:154:THR:HG23	1:B:155:ASP:N	2.19	0.57
1:A:104:TYR:CE2	1:A:106:GLU:HG3	2.40	0.57
1:B:154:THR:CG2	1:B:155:ASP:N	2.67	0.57
1:A:99:SER:N	1:A:100:PRO:CD	2.70	0.56
1:A:154:THR:HG23	1:A:155:ASP:N	2.21	0.55
1:C:155:ASP:O	1:C:157:PHE:N	2.39	0.55
1:B:147[B]:HIS:CE1	1:B:284:THR:HB	2.41	0.55
1:C:222:GLY:HA3	1:C:265:ASN:CB	2.36	0.55
1:A:109:GLU:HG3	1:A:159:LEU:HD13	1.88	0.54
1:C:166:LEU:N	1:C:166:LEU:HD23	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:154:THR:CG2	1:C:155:ASP:N	2.70	0.53
1:C:251:ILE:HD11	1:C:285:PHE:CE2	2.42	0.53
1:C:197:GLU:CG	1:C:197:GLU:O	2.47	0.53
1:B:235:VAL:HG11	1:C:233:ILE:HD12	1.91	0.53
1:C:159:LEU:HD12	1:C:160:GLN:H	1.74	0.53
1:C:249:LYS:HG3	1:C:285:PHE:CD1	2.44	0.52
1:A:144:THR:OG1	1:A:145:ASN:N	2.41	0.52
1:A:166:LEU:N	1:A:166:LEU:HD23	2.25	0.52
1:A:153:ALA:HB1	1:A:183:LEU:HD11	1.93	0.51
1:C:145:ASN:HD21	1:C:282:THR:HA	1.75	0.51
1:A:145:ASN:HD21	1:A:282:THR:HA	1.75	0.51
1:A:154:THR:CG2	1:A:155:ASP:N	2.75	0.49
1:B:144:THR:OG1	1:B:145:ASN:N	2.44	0.49
1:A:155:ASP:O	1:A:157:PHE:N	2.46	0.49
1:B:164:VAL:HG12	1:B:166:LEU:HD22	1.94	0.48
1:B:251:ILE:HD11	1:B:285:PHE:CE2	2.47	0.48
1:B:99:SER:N	1:B:100:PRO:CD	2.76	0.48
1:B:159:LEU:HD12	1:B:160:GLN:H	1.78	0.48
1:A:164:VAL:HG12	1:A:166:LEU:HD22	1.95	0.48
1:B:128:GLU:HG2	1:B:129:GLY:H	1.79	0.48
1:B:261:ILE:HB	1:B:297:ASN:HB3	1.95	0.48
1:C:99:SER:N	1:C:100:PRO:CD	2.77	0.48
1:C:154:THR:CG2	1:C:155:ASP:H	2.27	0.47
1:B:222:GLY:HA3	1:B:265:ASN:CB	2.44	0.47
1:C:145:ASN:HB2	1:C:148:VAL:HG23	1.96	0.47
1:C:261:ILE:HB	1:C:297:ASN:HB3	1.97	0.47
1:A:261:ILE:HB	1:A:297:ASN:HB3	1.97	0.47
1:A:243:ILE:HG12	1:A:252:SER:HA	1.96	0.46
1:B:189:LEU:HD11	1:B:305:VAL:HG22	1.96	0.46
1:B:166:LEU:HD23	1:B:166:LEU:N	2.30	0.46
1:A:128:GLU:HG2	1:A:129:GLY:N	2.27	0.46
1:A:152:LEU:HD22	1:A:162:CYS:HB2	1.97	0.46
1:C:147[B]:HIS:CG	1:C:284:THR:HB	2.51	0.46
1:A:235:VAL:HG11	1:B:233:ILE:HD12	1.98	0.46
1:A:159:LEU:HD12	1:A:160:GLN:N	2.31	0.45
1:A:249:LYS:HE3	1:A:284:THR:O	2.16	0.45
1:C:222:GLY:HA3	1:C:265:ASN:HB3	1.98	0.45
1:B:104:TYR:CE2	1:B:106:GLU:HG3	2.52	0.45
1:B:246:PRO:HB3	1:B:250:SER:O	2.16	0.44
1:B:302:ILE:HD12	1:B:302:ILE:HA	1.84	0.44
1:B:154:THR:CG2	1:B:155:ASP:H	2.30	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:282:THR:HG21	1:B:300:ILE:HD11	2.00	0.43
1:A:128:GLU:CG	1:A:129:GLY:H	2.27	0.43
1:B:155:ASP:O	1:B:157:PHE:N	2.51	0.43
1:C:282:THR:HG21	1:C:300:ILE:HD11	2.00	0.43
1:C:302:ILE:HA	1:C:302:ILE:HD12	1.85	0.43
1:B:134:PHE:CD1	1:B:204:VAL:HG11	2.54	0.42
1:C:224:PRO:HG3	1:C:230:THR:HG21	2.02	0.42
1:C:284:THR:HG22	1:C:285:PHE:CE2	2.54	0.42
1:C:176:LYS:HA	1:C:176:LYS:HD3	1.93	0.42
1:A:151:LYS:O	1:A:155:ASP:HB3	2.20	0.42
1:B:222:GLY:HA3	1:B:265:ASN:HB3	2.02	0.41
1:C:189:LEU:HD11	1:C:305:VAL:HG22	2.02	0.41
1:B:284:THR:HG22	1:B:285:PHE:CE2	2.56	0.41
1:A:176:LYS:HA	1:A:176:LYS:HD3	1.91	0.41
1:B:219:PHE:N	1:B:219:PHE:CD2	2.89	0.41
1:C:243:ILE:HG12	1:C:252:SER:HA	2.02	0.41
1:C:309:VAL:N	1:C:310:PRO:CD	2.84	0.41
1:A:134:PHE:CD1	1:A:204:VAL:HG11	2.56	0.40
1:C:246:PRO:HB3	1:C:250:SER:O	2.21	0.40
1:B:173:ARG:HD3	1:B:174:PHE:H	1.86	0.40
1:C:145:ASN:OD1	1:C:282:THR:HG22	2.22	0.40
1:A:251:ILE:HD11	1:A:285:PHE:CE2	2.56	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	207/291 (71%)	189 (91%)	15 (7%)	3 (1%)	11	22
1	B	206/291 (71%)	190 (92%)	14 (7%)	2 (1%)	15	32
1	C	206/291 (71%)	194 (94%)	10 (5%)	2 (1%)	15	32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	619/873 (71%)	573 (93%)	39 (6%)	7 (1%)	14	30

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	156	GLN
1	A	247	ASN
1	C	156	GLN
1	B	156	GLN
1	B	247	ASN
1	C	247	ASN
1	A	248	GLY

### 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	177/243 (73%)	167 (94%)	10 (6%)	21	42
1	B	176/243 (72%)	167 (95%)	9 (5%)	24	46
1	C	176/243 (72%)	170 (97%)	6 (3%)	37	63
All	All	529/729 (73%)	504 (95%)	25 (5%)	25	50

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

Mol	Chain	Res	Type
1	A	156	GLN
1	A	159	LEU
1	A	167	VAL
1	A	173	ARG
1	A	197	GLU
1	A	223	ASN
1	A	241	ARG
1	A	271	LEU
1	A	284	THR

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Mol	Chain	Res	Type
1	A	285	PHE
1	B	156	GLN
1	B	159	LEU
1	B	167	VAL
1	B	173	ARG
1	B	197	GLU
1	B	223	ASN
1	B	241	ARG
1	B	284	THR
1	B	285	PHE
1	C	159	LEU
1	C	173	ARG
1	C	197	GLU
1	C	223	ASN
1	C	241	ARG
1	C	285	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 carbohydrates in this entry.

### 5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 5 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	210/291 (72%)	0.07	7 (3%) 46 39	18, 43, 109, 158	1 (0%)
1	B	210/291 (72%)	0.10	6 (2%) 51 45	18, 42, 112, 150	2 (0%)
1	C	209/291 (71%)	0.07	4 (1%) 66 62	17, 43, 103, 147	1 (0%)
All	All	629/873 (72%)	0.08	17 (2%) 54 48	17, 43, 109, 158	4 (0%)

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	159	LEU	4.0
1	B	285	PHE	3.6
1	A	159	LEU	3.6
1	A	157	PHE	3.2
1	A	110	LEU	3.0
1	B	128	GLU	2.9
1	B	251	ILE	2.8
1	A	155	ASP	2.8
1	C	159	LEU	2.7
1	A	128	GLU	2.7
1	C	110	LEU	2.6
1	C	108	ILE	2.6
1	C	157	PHE	2.3
1	A	154	THR	2.2
1	A	284	THR	2.2
1	B	157	PHE	2.2
1	B	110	LEU	2.1

### 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. 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	CA	A	402	1/1	0.96	0.11	64,64,64,64	0
2	CA	A	403	1/1	0.96	0.18	88,88,88,88	0
2	CA	C	401	1/1	0.98	0.20	33,33,33,33	0
2	CA	B	401	1/1	0.99	0.20	36,36,36,36	0
2	CA	A	401	1/1	0.99	0.21	33,33,33,33	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.