



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:06 AM GMT

PDB ID : 3O3V  
Title : Crystal structure of ClbP peptidase domain  
Authors : Dubois, D.; Cougnoux, A.; Delmas, J.; Bonnet, R.  
Deposited on : 2010-07-26  
Resolution : 2.40 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  
<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

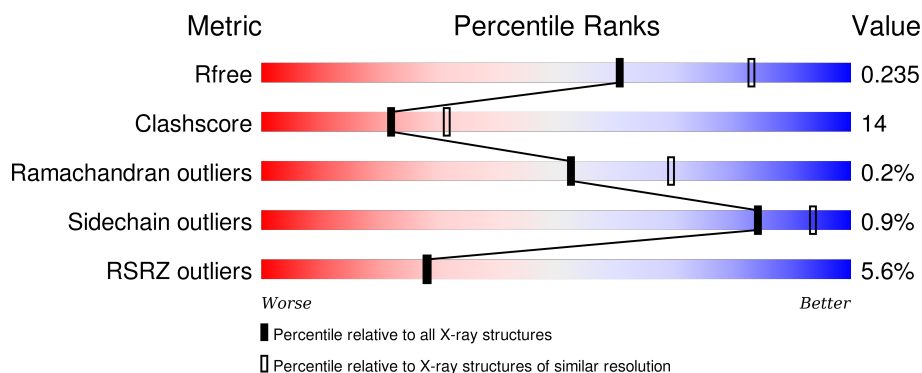
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	335	<div> <div>6%</div> <div>75%</div> <div>25%</div> </div>
1	B	335	<div> <div>6%</div> <div>75%</div> <div>24%</div> </div>
1	C	335	<div> <div>5%</div> <div>75%</div> <div>25%</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7968 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 beta-lactamase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	335	Total	C	N	O	S	0	0	0
			2571	1634	450	477	10			
1	B	335	Total	C	N	O	S	0	0	0
			2571	1634	450	477	10			
1	C	335	Total	C	N	O	S	0	1	0
			2577	1638	451	478	10			

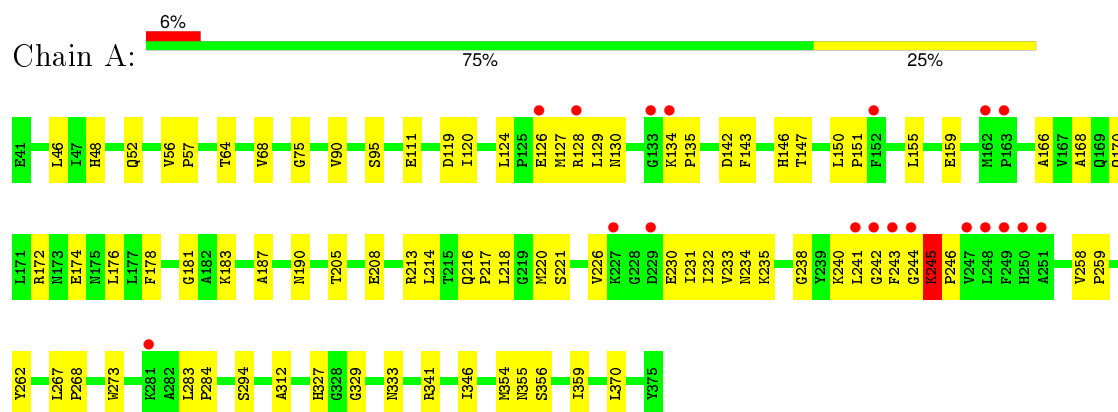
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	81	Total	O	0	0
			81	81		
2	B	82	Total	O	0	0
			82	82		
2	C	86	Total	O	0	0
			86	86		

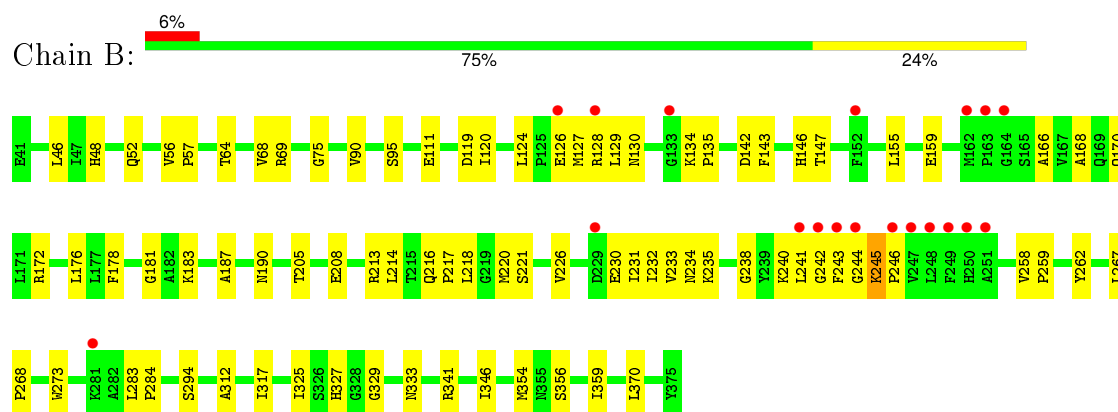
### 3 Residue-property plots [i](#)

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.

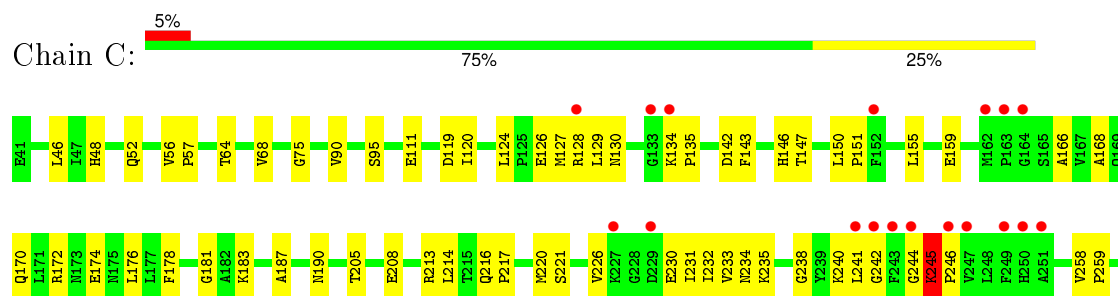
- Molecule 1: beta-lactamase



- Molecule 1: beta-lactamase



- Molecule 1: beta-lactamase



Y262	
T266	
L267	
P268	
W273	
L283	
P284	
S294	
A312	
I317	
I325	
S326	
H327	
G328	
G329	
N333	
R344	
I346	
N354	
N355	
S356	
I359	
L360	
Q361	
L370	
T375	

## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	103.94Å 149.93Å 87.33Å 90.00° 123.90° 90.00°	Depositor
Resolution (Å)	19.94 – 2.40 19.94 – 2.40	Depositor EDS
% Data completeness (in resolution range)	92.1 (19.94-2.40) 91.0 (19.94-2.40)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.43 (at 2.41Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, $R_{free}$	0.204 , 0.241 0.201 , 0.235	Depositor DCC
$R_{free}$ test set	1993 reflections (5.27%)	DCC
Wilson B-factor (Å <sup>2</sup> )	20.1	Xtriage
Anisotropy	0.035	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.41 , 23.4	EDS
Estimated twinning fraction	0.013 for -h,h+2*1,1/2*h+1/2*k 0.018 for -h,-h-2*1,1/2*h-1/2*k 0.014 for -1/2*h+1/2*k-l,3/2*h+1/2*k+l,1/2*h-1/2*k 0.014 for 1/2*h-1/2*k+l,-1/2*h+1/2*k+l,-h 0.011 for -1/2*h-1/2*k-l,-3/2*h+1/2*k-l,1/2*h+1/2*k 0.012 for 1/2*h+1/2*k+l,1/2*h+1/2*k-l,-h-1/2*k 0.467 for 1/2*h+1/2*k+l,3/2*h-1/2*k+l,-l 0.467 for 1/2*h-1/2*k+l,-3/2*h-1/2*k-l,-l 0.014 for -1/2*h-1/2*k-l,-1/2*h-1/2*k+l,-1/2*h+1/2*k 0.014 for -1/2*h+1/2*k-l,1/2*h-1/2*k-l,-1/2*h-1/2*k 0.020 for h,-k,-h-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 39789 reflections (0.003%)	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	7968	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	22.0	wwPDB-VP

<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.

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.37% of the height of the origin peak. No significant pseudotranslation is detected.*

## 5 Model quality

### 5.1 Standard geometry

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	0.29	0/2625	0.47	0/3570
1	B	0.28	0/2625	0.47	0/3570
1	C	0.28	0/2634	0.47	0/3583
All	All	0.28	0/7884	0.47	0/10723

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

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	2571	0	2569	73	0
1	B	2571	0	2569	75	0
1	C	2577	0	2577	73	0
2	A	81	0	0	1	0
2	B	82	0	0	1	0
2	C	86	0	0	0	0
All	All	7968	0	7715	215	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 14.

All (215) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:245:LYS:HB2	1:A:354:MET:HE2	1.22	1.14
1:C:244:GLY:O	1:C:246:PRO:HD3	1.48	1.14
1:C:245:LYS:HB2	1:C:354:MET:HE2	1.24	1.11
1:A:244:GLY:O	1:A:246:PRO:HD3	1.48	1.11
1:B:244:GLY:O	1:B:246:PRO:HD3	1.48	1.11
1:B:245:LYS:HB2	1:B:354:MET:HE2	1.22	1.09
1:B:240:LYS:O	1:B:246:PRO:HD2	1.56	1.06
1:C:240:LYS:O	1:C:246:PRO:HD2	1.56	1.04
1:A:240:LYS:O	1:A:246:PRO:HD2	1.56	1.04
1:A:231:ILE:HG12	1:B:221:SER:HA	1.49	0.95
1:B:231:ILE:HG12	1:C:221:SER:HA	1.48	0.94
1:A:221:SER:HA	1:C:231:ILE:HG12	1.57	0.87
1:B:245:LYS:HB2	1:B:354:MET:CE	2.05	0.86
1:C:245:LYS:HB2	1:C:354:MET:CE	2.07	0.84
1:A:245:LYS:CB	1:A:354:MET:HE2	2.07	0.83
1:C:57:PRO:HD3	1:C:354:MET:HE3	1.62	0.82
1:B:155:LEU:O	1:B:159:GLU:HG2	1.82	0.79
1:B:245:LYS:CB	1:B:354:MET:HE2	2.09	0.78
1:C:220:MET:HE1	1:C:273:TRP:HE3	1.47	0.78
1:A:245:LYS:HB2	1:A:354:MET:CE	2.09	0.77
1:C:155:LEU:O	1:C:159:GLU:HG2	1.84	0.76
1:B:57:PRO:HD3	1:B:354:MET:HE3	1.66	0.76
1:A:155:LEU:O	1:A:159:GLU:HG2	1.85	0.76
1:A:245:LYS:O	1:A:245:LYS:HG2	1.86	0.75
1:C:245:LYS:O	1:C:245:LYS:HG2	1.85	0.75
1:C:245:LYS:CB	1:C:354:MET:HE2	2.12	0.74
1:B:245:LYS:HG2	1:B:245:LYS:O	1.87	0.74
1:A:57:PRO:HD3	1:A:354:MET:HE3	1.69	0.73
1:B:220:MET:HE1	1:B:273:TRP:HE3	1.55	0.71
1:A:220:MET:HE1	1:A:273:TRP:HE3	1.57	0.70
1:B:134:LYS:HB3	1:B:135:PRO:HD2	1.76	0.67
1:A:126:GLU:H	1:A:126:GLU:CD	2.01	0.64
1:C:46:LEU:HD23	1:C:46:LEU:C	2.19	0.63
1:C:126:GLU:CD	1:C:126:GLU:H	2.01	0.63
1:B:126:GLU:CD	1:B:126:GLU:H	2.00	0.62
1:A:245:LYS:O	1:A:245:LYS:CG	2.49	0.61
1:B:46:LEU:HD23	1:B:46:LEU:C	2.20	0.61
1:C:134:LYS:HB3	1:C:135:PRO:HD2	1.81	0.60
1:B:245:LYS:CG	1:B:245:LYS:O	2.49	0.60
1:A:46:LEU:C	1:A:46:LEU:HD23	2.21	0.60
1:C:245:LYS:O	1:C:245:LYS:CG	2.48	0.60
1:A:233:VAL:O	1:A:234:ASN:HB2	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:231:ILE:HG12	1:B:221:SER:CA	2.28	0.60
1:C:220:MET:HE1	1:C:273:TRP:CE3	2.34	0.59
1:C:233:VAL:O	1:C:234:ASN:HB2	2.03	0.59
1:B:233:VAL:O	1:B:234:ASN:HB2	2.01	0.59
1:C:216[B]:GLN:HB3	1:C:217:PRO:HD3	1.85	0.58
1:A:356:SER:HB3	1:A:359:ILE:HG12	1.84	0.58
1:B:240:LYS:O	1:B:246:PRO:CD	2.44	0.58
1:A:240:LYS:O	1:A:246:PRO:CD	2.45	0.58
1:C:356:SER:HB3	1:C:359:ILE:HG12	1.86	0.57
1:C:240:LYS:O	1:C:246:PRO:CD	2.44	0.57
1:B:356:SER:HB3	1:B:359:ILE:HG12	1.85	0.57
1:B:244:GLY:O	1:B:246:PRO:CD	2.40	0.56
1:B:245:LYS:CB	1:B:354:MET:CE	2.76	0.56
1:B:231:ILE:HG12	1:C:221:SER:CA	2.30	0.56
1:A:126:GLU:O	1:A:172:ARG:NH2	2.39	0.55
1:B:126:GLU:O	1:B:172:ARG:NH2	2.40	0.55
1:B:283:LEU:HB3	1:B:284:PRO:HD2	1.89	0.55
1:C:126:GLU:HG2	1:C:168:ALA:CB	2.37	0.55
1:C:283:LEU:HB3	1:C:284:PRO:HD2	1.89	0.54
1:B:130:ASN:HA	1:B:135:PRO:HA	1.88	0.54
1:C:126:GLU:O	1:C:172:ARG:NH2	2.39	0.54
1:C:245:LYS:CB	1:C:354:MET:CE	2.79	0.54
1:C:95:SER:HB2	1:C:329:GLY:HA2	1.89	0.54
1:B:267:LEU:HB3	1:B:268:PRO:HD3	1.90	0.54
1:C:244:GLY:O	1:C:246:PRO:CD	2.39	0.54
1:A:126:GLU:HG2	1:A:168:ALA:CB	2.37	0.53
1:A:95:SER:HB2	1:A:329:GLY:HA2	1.90	0.53
1:B:95:SER:HB2	1:B:329:GLY:HA2	1.90	0.53
1:A:283:LEU:HB3	1:A:284:PRO:HD2	1.90	0.53
1:B:126:GLU:HG2	1:B:168:ALA:CB	2.37	0.53
1:C:226:VAL:CG1	1:C:232:ILE:HD11	2.39	0.53
1:A:238:GLY:HA3	1:A:333:ASN:HB2	1.91	0.53
1:B:69:ARG:NH1	2:B:431:HOH:O	2.24	0.52
1:A:245:LYS:CB	1:A:354:MET:CE	2.80	0.52
1:C:238:GLY:HA3	1:C:333:ASN:HB2	1.90	0.52
1:C:130:ASN:HA	1:C:135:PRO:HA	1.90	0.52
1:A:226:VAL:HG12	1:A:232:ILE:HD11	1.92	0.52
1:C:267:LEU:HB3	1:C:268:PRO:HD3	1.91	0.52
1:A:226:VAL:CG1	1:A:232:ILE:HD11	2.40	0.52
1:A:267:LEU:HB3	1:A:268:PRO:HD3	1.91	0.51
1:C:226:VAL:HG12	1:C:232:ILE:HD11	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:221:SER:CA	1:C:231:ILE:HG12	2.36	0.51
1:A:90:VAL:HB	1:A:235:LYS:HA	1.93	0.51
1:A:178:PHE:CD1	1:A:183:LYS:HE2	2.46	0.51
1:B:124:LEU:HD23	1:B:168:ALA:HB2	1.92	0.50
1:B:226:VAL:CG1	1:B:232:ILE:HD11	2.40	0.50
1:C:124:LEU:HD23	1:C:168:ALA:HB2	1.93	0.50
1:A:127:MET:HB2	1:A:168:ALA:HB1	1.93	0.50
1:B:127:MET:HB2	1:B:168:ALA:HB1	1.91	0.50
1:B:238:GLY:HA3	1:B:333:ASN:HB2	1.92	0.50
1:C:127:MET:HB2	1:C:168:ALA:HB1	1.93	0.50
1:A:205:THR:OG1	1:A:208:GLU:HG3	2.11	0.50
1:B:143:PHE:HD1	1:B:190:ASN:HD22	1.60	0.50
1:B:205:THR:OG1	1:B:208:GLU:HG3	2.12	0.50
1:A:124:LEU:HD23	1:A:168:ALA:HB2	1.93	0.50
1:B:226:VAL:HG12	1:B:232:ILE:HD11	1.93	0.50
1:A:244:GLY:O	1:A:246:PRO:CD	2.40	0.49
1:B:90:VAL:HB	1:B:235:LYS:HA	1.94	0.49
1:B:129:LEU:HB3	1:B:176:LEU:HD11	1.95	0.49
1:C:129:LEU:HB3	1:C:176:LEU:HD11	1.94	0.49
1:B:95:SER:HB3	1:B:327:HIS:CE1	2.47	0.49
1:B:220:MET:HE1	1:B:273:TRP:CE3	2.42	0.49
1:A:258:VAL:HA	1:A:262:TYR:HB2	1.95	0.49
1:C:143:PHE:HD1	1:C:190:ASN:HD22	1.60	0.49
1:B:166:ALA:O	1:B:170:GLN:HB2	2.13	0.49
1:C:90:VAL:HB	1:C:235:LYS:HA	1.94	0.49
1:A:218:LEU:HD13	1:A:220:MET:HE1	1.95	0.48
1:B:147:THR:HB	1:B:181:GLY:HA2	1.94	0.48
1:B:258:VAL:HA	1:B:262:TYR:HB2	1.94	0.48
1:C:178:PHE:CD1	1:C:183:LYS:HE2	2.48	0.48
1:A:95:SER:HB3	1:A:327:HIS:CE1	2.47	0.48
1:B:294:SER:O	1:B:312:ALA:HB1	2.14	0.48
1:A:147:THR:HB	1:A:181:GLY:HA2	1.96	0.48
1:C:258:VAL:HA	1:C:262:TYR:HB2	1.96	0.48
1:C:146:HIS:HD2	1:C:187:ALA:H	1.61	0.48
1:C:126:GLU:HG2	1:C:168:ALA:HB1	1.96	0.48
1:A:166:ALA:O	1:A:170:GLN:HB2	2.14	0.48
1:A:111:GLU:OE2	1:A:213:ARG:NH2	2.39	0.48
1:A:57:PRO:HD3	1:A:354:MET:CE	2.43	0.47
1:C:95:SER:HB3	1:C:327:HIS:CE1	2.48	0.47
1:A:130:ASN:HA	1:A:135:PRO:HA	1.96	0.47
1:A:129:LEU:HB3	1:A:176:LEU:HD11	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:126:GLU:HG2	1:A:168:ALA:HB1	1.95	0.47
1:A:119:ASP:OD1	1:A:120:ILE:N	2.48	0.47
1:C:119:ASP:OD1	1:C:120:ILE:N	2.48	0.47
1:C:341:ARG:HB3	1:C:346:ILE:HB	1.97	0.47
1:A:341:ARG:HB3	1:A:346:ILE:HB	1.97	0.47
1:A:57:PRO:O	1:A:75:GLY:HA3	2.15	0.47
1:C:111:GLU:OE2	1:C:213:ARG:NH2	2.38	0.47
1:A:294:SER:O	1:A:312:ALA:HB1	2.15	0.47
1:C:147:THR:HB	1:C:181:GLY:HA2	1.96	0.47
1:A:56:VAL:HG12	1:A:354:MET:HB3	1.97	0.46
1:C:166:ALA:O	1:C:170:GLN:HB2	2.14	0.46
1:B:341:ARG:HB3	1:B:346:ILE:HB	1.97	0.46
1:A:220:MET:HE1	1:A:273:TRP:CE3	2.45	0.46
1:B:119:ASP:OD1	1:B:120:ILE:N	2.48	0.46
1:B:57:PRO:O	1:B:75:GLY:HA3	2.15	0.46
1:A:242:GLY:HA2	1:A:243:PHE:HA	1.77	0.46
1:C:57:PRO:O	1:C:75:GLY:HA3	2.17	0.45
1:B:126:GLU:HG2	1:B:168:ALA:HB1	1.97	0.45
1:C:146:HIS:CD2	1:C:187:ALA:H	2.33	0.45
1:A:220:MET:HE2	1:A:273:TRP:CA	2.47	0.45
1:C:294:SER:O	1:C:312:ALA:HB1	2.16	0.45
1:B:178:PHE:CD1	1:B:183:LYS:HE2	2.50	0.45
1:C:205:THR:OG1	1:C:208:GLU:HG3	2.16	0.45
1:A:333:ASN:OD1	1:A:333:ASN:N	2.49	0.45
1:A:355:ASN:HB3	2:A:436:HOH:O	2.16	0.45
1:B:218:LEU:HD13	1:B:220:MET:HE1	1.99	0.45
1:B:57:PRO:HD3	1:B:354:MET:CE	2.43	0.45
1:C:220:MET:HE2	1:C:273:TRP:CA	2.47	0.45
1:B:241:LEU:HD12	1:B:242:GLY:H	1.81	0.45
1:A:143:PHE:HD1	1:A:190:ASN:HD22	1.65	0.44
1:A:146:HIS:CD2	1:A:187:ALA:H	2.35	0.44
1:A:230:GLU:O	1:A:230:GLU:HG2	2.17	0.44
1:B:220:MET:HE2	1:B:273:TRP:CA	2.48	0.44
1:A:146:HIS:HD2	1:A:187:ALA:H	1.66	0.44
1:C:56:VAL:HG12	1:C:354:MET:HB3	1.98	0.44
1:C:142:ASP:HA	1:C:147:THR:OG1	2.18	0.44
1:C:333:ASN:OD1	1:C:333:ASN:N	2.50	0.44
1:A:142:ASP:HA	1:A:147:THR:OG1	2.17	0.44
1:B:56:VAL:HG12	1:B:354:MET:HB3	2.00	0.43
1:B:48:HIS:O	1:B:52:GLN:HG2	2.19	0.43
1:B:128:ARG:HG2	1:B:172:ARG:NH2	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:46:LEU:C	1:C:46:LEU:CD2	2.86	0.43
1:B:230:GLU:O	1:B:230:GLU:HG2	2.18	0.43
1:B:146:HIS:CD2	1:B:187:ALA:H	2.36	0.43
1:B:126:GLU:HG2	1:B:168:ALA:HB3	2.00	0.43
1:B:127:MET:HB2	1:B:168:ALA:CB	2.48	0.43
1:B:146:HIS:HD2	1:B:187:ALA:H	1.66	0.43
1:A:127:MET:HB2	1:A:168:ALA:CB	2.48	0.43
1:A:128:ARG:HG2	1:A:172:ARG:NH2	2.33	0.43
1:C:266:THR:HB	1:C:268:PRO:HD2	2.01	0.43
1:A:241:LEU:HD12	1:A:242:GLY:H	1.83	0.43
1:C:128:ARG:HG2	1:C:172:ARG:NH2	2.34	0.43
1:A:150:LEU:HA	1:A:151:PRO:HD3	1.89	0.43
1:A:126:GLU:HG2	1:A:168:ALA:HB3	2.01	0.42
1:C:214:LEU:C	1:C:217:PRO:HD2	2.40	0.42
1:C:241:LEU:HD12	1:C:242:GLY:H	1.83	0.42
1:A:64:THR:HA	1:A:68:VAL:O	2.19	0.42
1:B:64:THR:HA	1:B:68:VAL:O	2.19	0.42
1:C:127:MET:HB2	1:C:168:ALA:CB	2.49	0.42
1:B:176:LEU:CD1	1:B:176:LEU:N	2.82	0.42
1:C:230:GLU:O	1:C:230:GLU:HG2	2.19	0.42
1:C:126:GLU:HG2	1:C:168:ALA:HB3	2.00	0.42
1:B:214:LEU:C	1:B:217:PRO:HD2	2.40	0.42
1:C:151:PRO:HG2	1:C:174:GLU:OE2	2.19	0.42
1:A:176:LEU:CD1	1:A:176:LEU:N	2.83	0.42
1:C:48:HIS:O	1:C:52:GLN:HG2	2.20	0.42
1:A:46:LEU:C	1:A:46:LEU:CD2	2.88	0.42
1:B:333:ASN:N	1:B:333:ASN:OD1	2.51	0.42
1:B:142:ASP:HA	1:B:147:THR:OG1	2.20	0.42
1:C:150:LEU:HA	1:C:151:PRO:HD3	1.89	0.41
1:C:64:THR:HA	1:C:68:VAL:O	2.19	0.41
1:B:111:GLU:OE2	1:B:213:ARG:NH2	2.40	0.41
1:B:183:LYS:HE3	1:B:183:LYS:HB2	1.62	0.41
1:A:214:LEU:C	1:A:217:PRO:HD2	2.41	0.41
1:B:126:GLU:N	1:B:126:GLU:OE1	2.54	0.41
1:C:258:VAL:N	1:C:259:PRO:CD	2.83	0.41
1:C:176:LEU:CD1	1:C:176:LEU:N	2.84	0.41
1:A:258:VAL:N	1:A:259:PRO:CD	2.82	0.41
1:B:317:ILE:HD13	1:B:325:ILE:HG23	2.03	0.41
1:B:258:VAL:N	1:B:259:PRO:CD	2.84	0.41
1:C:317:ILE:HD13	1:C:325:ILE:HG23	2.02	0.41
1:B:240:LYS:HB2	1:B:240:LYS:HE3	1.93	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:PRO:HG2	1:A:174:GLU:OE2	2.21	0.41
1:A:48:HIS:O	1:A:52:GLN:HG2	2.21	0.41
1:A:242:GLY:HA2	1:A:243:PHE:C	2.41	0.41
1:A:216:GLN:HB2	1:A:217:PRO:HD3	2.03	0.41
1:C:361:GLN:HG3	1:C:361:GLN:O	2.21	0.40
1:B:134:LYS:HB2	1:B:134:LYS:HE2	1.79	0.40
1:B:216:GLN:HB2	1:B:217:PRO:HD3	2.03	0.40
1:C:238:GLY:CA	1:C:333:ASN:HB2	2.52	0.40
1:B:242:GLY:HA2	1:B:243:PHE:HA	1.78	0.40

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	A	333/335 (99%)	322 (97%)	10 (3%)	1 (0%)	46	63
1	B	333/335 (99%)	322 (97%)	11 (3%)	0	100	100
1	C	334/335 (100%)	323 (97%)	10 (3%)	1 (0%)	46	63
All	All	1000/1005 (100%)	967 (97%)	31 (3%)	2 (0%)	52	69

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	245	LYS
1	A	245	LYS

### 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	272/276 (99%)	269 (99%)	3 (1%)	80	92
1	B	272/276 (99%)	270 (99%)	2 (1%)	88	95
1	C	273/276 (99%)	271 (99%)	2 (1%)	88	95
All	All	817/828 (99%)	810 (99%)	7 (1%)	84	93

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	134	LYS
1	A	245	LYS
1	A	370	LEU
1	B	245	LYS
1	B	370	LEU
1	C	245	LYS
1	C	370	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	130	ASN
1	A	146	HIS
1	A	160	ASN
1	A	190	ASN
1	A	368	ASN
1	B	130	ASN
1	B	146	HIS
1	B	160	ASN
1	B	190	ASN
1	B	368	ASN
1	C	130	ASN
1	C	146	HIS
1	C	160	ASN
1	C	190	ASN
1	C	368	ASN

### 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](#)

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	A	335/335 (100%)	0.19	19 (5%)	27 27	7, 19, 47, 50	0
1	B	335/335 (100%)	0.15	19 (5%)	27 27	7, 19, 47, 50	0
1	C	335/335 (100%)	0.19	18 (5%)	29 30	7, 19, 47, 50	0
All	All	1005/1005 (100%)	0.17	56 (5%)	28 28	7, 19, 47, 50	0

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	249	PHE	12.0
1	A	249	PHE	9.9
1	B	249	PHE	8.4
1	B	242	GLY	7.9
1	C	162	MET	7.1
1	A	163	PRO	7.0
1	A	251	ALA	6.9
1	B	250	HIS	6.7
1	A	133	GLY	6.6
1	C	242	GLY	6.6
1	B	162	MET	6.2
1	C	163	PRO	6.2
1	A	242	GLY	5.8
1	C	251	ALA	5.7
1	A	250	HIS	5.6
1	C	250	HIS	5.6
1	A	244	GLY	5.0
1	B	133	GLY	4.6
1	A	162	MET	4.5
1	B	241	LEU	4.3
1	B	244	GLY	4.2
1	C	229	ASP	4.0
1	B	281	LYS	4.0

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Mol	Chain	Res	Type	RSRZ
1	B	243	PHE	3.9
1	C	164	GLY	3.8
1	C	243	PHE	3.6
1	C	244	GLY	3.5
1	B	251	ALA	3.3
1	C	133	GLY	3.3
1	B	163	PRO	3.2
1	A	128	ARG	2.9
1	A	241	LEU	2.9
1	A	134	LYS	2.7
1	A	243	PHE	2.7
1	C	152	PHE	2.7
1	B	164	GLY	2.7
1	B	229	ASP	2.6
1	A	229	ASP	2.6
1	C	128	ARG	2.6
1	B	128	ARG	2.5
1	C	247	VAL	2.5
1	B	247	VAL	2.5
1	C	134	LYS	2.4
1	C	241	LEU	2.4
1	B	126	GLU	2.4
1	A	281	LYS	2.4
1	B	246	PRO	2.4
1	B	152	PHE	2.3
1	A	227	LYS	2.3
1	C	246	PRO	2.3
1	A	247	VAL	2.2
1	A	248	LEU	2.2
1	B	248	LEU	2.1
1	A	152	PHE	2.0
1	A	126	GLU	2.0
1	C	227	LYS	2.0

## 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 [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.