



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:04 AM GMT

PDB ID : 1ZKP  
Title : 1.5A Resolution Crystal Structure of a Metallo Beta Lactamase Family Protein, the ELAC Homologue of Bacillus anthracis, a Putative Ribonuclease  
Authors : Brunzelle, J.S.; Minasov, G.; Shuvalova, L.; Collart, F.R.; Anderson, W.F.; Midwest Center for Structural Genomics (MCSG)  
Deposited on : 2005-05-03  
Resolution : 1.50 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

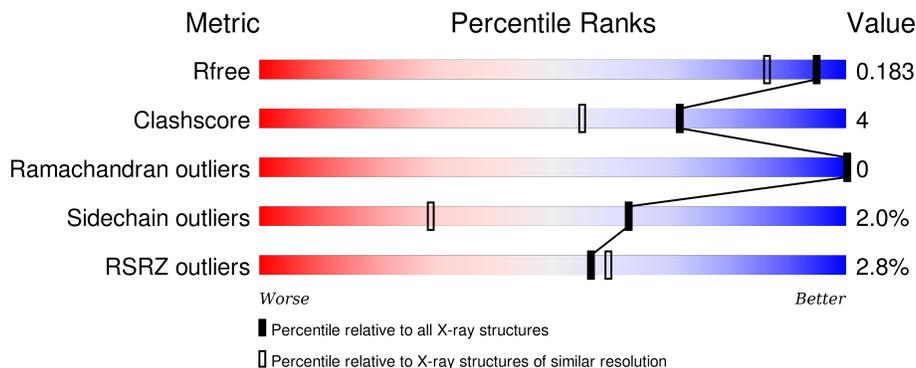
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.50 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	2072 (1.50-1.50)
Clashscore	102246	2274 (1.50-1.50)
Ramachandran outliers	100387	2218 (1.50-1.50)
Sidechain outliers	100360	2216 (1.50-1.50)
RSRZ outliers	91569	2075 (1.50-1.50)

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	268	85% 8% • 6%
1	B	268	86% 7% • 6%
1	C	268	83% 8% 9%
1	D	268	84% 9% • 6%

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 9487 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 hypothetical protein BA1088.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	N	O	S				Se
1	A	251	2003	1281	331	382	4	5	0	7	0
1	B	251	2030	1296	334	391	4	5	0	10	0
1	C	245	1964	1252	324	379	4	5	0	9	0
1	D	251	2023	1292	334	388	4	5	0	9	0

There are 116 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-23	MSE	-	CLONING ARTIFACT	UNP Q81U06
A	-22	HIS	-	EXPRESSION TAG	UNP Q81U06
A	-21	HIS	-	EXPRESSION TAG	UNP Q81U06
A	-20	HIS	-	EXPRESSION TAG	UNP Q81U06
A	-19	HIS	-	EXPRESSION TAG	UNP Q81U06
A	-18	HIS	-	EXPRESSION TAG	UNP Q81U06
A	-17	HIS	-	EXPRESSION TAG	UNP Q81U06
A	-16	SER	-	cloning artifact	UNP Q81U06
A	-15	SER	-	cloning artifact	UNP Q81U06
A	-14	GLY	-	cloning artifact	UNP Q81U06
A	-13	VAL	-	cloning artifact	UNP Q81U06
A	-12	ASP	-	cloning artifact	UNP Q81U06
A	-11	LEU	-	cloning artifact	UNP Q81U06
A	-10	GLY	-	cloning artifact	UNP Q81U06
A	-9	THR	-	cloning artifact	UNP Q81U06
A	-8	GLU	-	cloning artifact	UNP Q81U06
A	-7	ASN	-	cloning artifact	UNP Q81U06
A	-6	LEU	-	cloning artifact	UNP Q81U06
A	-5	TYR	-	cloning artifact	UNP Q81U06
A	-4	PHE	-	cloning artifact	UNP Q81U06
A	-3	GLN	-	cloning artifact	UNP Q81U06

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	cloning artifact	UNP Q81U06
A	-1	ASN	-	cloning artifact	UNP Q81U06
A	0	ALA	-	cloning artifact	UNP Q81U06
A	1	MSE	MET	modified residue	UNP Q81U06
A	3	MSE	MET	modified residue	UNP Q81U06
A	141	MSE	MET	modified residue	UNP Q81U06
A	178	MSE	MET	modified residue	UNP Q81U06
A	190	MSE	MET	modified residue	UNP Q81U06
B	-23	MSE	-	cloning artifact	UNP Q81U06
B	-22	HIS	-	EXPRESSION TAG	UNP Q81U06
B	-21	HIS	-	EXPRESSION TAG	UNP Q81U06
B	-20	HIS	-	EXPRESSION TAG	UNP Q81U06
B	-19	HIS	-	EXPRESSION TAG	UNP Q81U06
B	-18	HIS	-	EXPRESSION TAG	UNP Q81U06
B	-17	HIS	-	EXPRESSION TAG	UNP Q81U06
B	-16	SER	-	cloning artifact	UNP Q81U06
B	-15	SER	-	cloning artifact	UNP Q81U06
B	-14	GLY	-	cloning artifact	UNP Q81U06
B	-13	VAL	-	cloning artifact	UNP Q81U06
B	-12	ASP	-	cloning artifact	UNP Q81U06
B	-11	LEU	-	cloning artifact	UNP Q81U06
B	-10	GLY	-	cloning artifact	UNP Q81U06
B	-9	THR	-	cloning artifact	UNP Q81U06
B	-8	GLU	-	cloning artifact	UNP Q81U06
B	-7	ASN	-	cloning artifact	UNP Q81U06
B	-6	LEU	-	cloning artifact	UNP Q81U06
B	-5	TYR	-	cloning artifact	UNP Q81U06
B	-4	PHE	-	cloning artifact	UNP Q81U06
B	-3	GLN	-	cloning artifact	UNP Q81U06
B	-2	SER	-	cloning artifact	UNP Q81U06
B	-1	ASN	-	cloning artifact	UNP Q81U06
B	0	ALA	-	cloning artifact	UNP Q81U06
B	1	MSE	MET	modified residue	UNP Q81U06
B	3	MSE	MET	modified residue	UNP Q81U06
B	141	MSE	MET	modified residue	UNP Q81U06
B	178	MSE	MET	modified residue	UNP Q81U06
B	190	MSE	MET	modified residue	UNP Q81U06
C	-23	MSE	-	cloning artifact	UNP Q81U06
C	-22	HIS	-	EXPRESSION TAG	UNP Q81U06
C	-21	HIS	-	EXPRESSION TAG	UNP Q81U06
C	-20	HIS	-	EXPRESSION TAG	UNP Q81U06
C	-19	HIS	-	EXPRESSION TAG	UNP Q81U06

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-18	HIS	-	EXPRESSION TAG	UNP Q81U06
C	-17	HIS	-	EXPRESSION TAG	UNP Q81U06
C	-16	SER	-	cloning artifact	UNP Q81U06
C	-15	SER	-	cloning artifact	UNP Q81U06
C	-14	GLY	-	cloning artifact	UNP Q81U06
C	-13	VAL	-	cloning artifact	UNP Q81U06
C	-12	ASP	-	cloning artifact	UNP Q81U06
C	-11	LEU	-	cloning artifact	UNP Q81U06
C	-10	GLY	-	cloning artifact	UNP Q81U06
C	-9	THR	-	cloning artifact	UNP Q81U06
C	-8	GLU	-	cloning artifact	UNP Q81U06
C	-7	ASN	-	cloning artifact	UNP Q81U06
C	-6	LEU	-	cloning artifact	UNP Q81U06
C	-5	TYR	-	cloning artifact	UNP Q81U06
C	-4	PHE	-	cloning artifact	UNP Q81U06
C	-3	GLN	-	cloning artifact	UNP Q81U06
C	-2	SER	-	cloning artifact	UNP Q81U06
C	-1	ASN	-	cloning artifact	UNP Q81U06
C	0	ALA	-	cloning artifact	UNP Q81U06
C	1	MSE	MET	modified residue	UNP Q81U06
C	3	MSE	MET	modified residue	UNP Q81U06
C	141	MSE	MET	modified residue	UNP Q81U06
C	178	MSE	MET	modified residue	UNP Q81U06
C	190	MSE	MET	modified residue	UNP Q81U06
D	-23	MSE	-	cloning artifact	UNP Q81U06
D	-22	HIS	-	EXPRESSION TAG	UNP Q81U06
D	-21	HIS	-	EXPRESSION TAG	UNP Q81U06
D	-20	HIS	-	EXPRESSION TAG	UNP Q81U06
D	-19	HIS	-	EXPRESSION TAG	UNP Q81U06
D	-18	HIS	-	EXPRESSION TAG	UNP Q81U06
D	-17	HIS	-	EXPRESSION TAG	UNP Q81U06
D	-16	SER	-	cloning artifact	UNP Q81U06
D	-15	SER	-	cloning artifact	UNP Q81U06
D	-14	GLY	-	cloning artifact	UNP Q81U06
D	-13	VAL	-	cloning artifact	UNP Q81U06
D	-12	ASP	-	cloning artifact	UNP Q81U06
D	-11	LEU	-	cloning artifact	UNP Q81U06
D	-10	GLY	-	cloning artifact	UNP Q81U06
D	-9	THR	-	cloning artifact	UNP Q81U06
D	-8	GLU	-	cloning artifact	UNP Q81U06
D	-7	ASN	-	cloning artifact	UNP Q81U06
D	-6	LEU	-	cloning artifact	UNP Q81U06

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-5	TYR	-	cloning artifact	UNP Q81U06
D	-4	PHE	-	cloning artifact	UNP Q81U06
D	-3	GLN	-	cloning artifact	UNP Q81U06
D	-2	SER	-	cloning artifact	UNP Q81U06
D	-1	ASN	-	cloning artifact	UNP Q81U06
D	0	ALA	-	cloning artifact	UNP Q81U06
D	1	MSE	MET	modified residue	UNP Q81U06
D	3	MSE	MET	modified residue	UNP Q81U06
D	141	MSE	MET	modified residue	UNP Q81U06
D	178	MSE	MET	modified residue	UNP Q81U06
D	190	MSE	MET	modified residue	UNP Q81U06

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	2	Total Zn 2 2	0	0
2	A	2	Total Zn 2 2	0	0
2	D	2	Total Zn 2 2	0	0
2	C	2	Total Zn 2 2	0	0

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Cl 1 1	0	0

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	2	Total Na 2 2	0	0
4	A	1	Total Na 1 1	0	0
4	C	1	Total Na 1 1	0	0

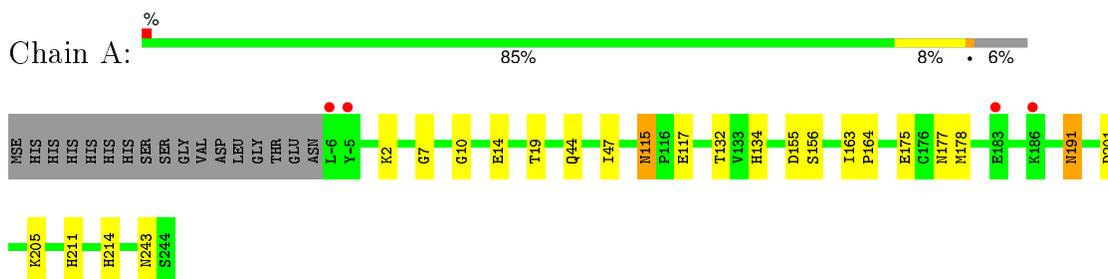
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	353	Total 371	O 371	0	35
5	B	377	Total 406	O 406	0	34
5	C	331	Total 348	O 348	0	23
5	D	314	Total 329	O 329	0	33

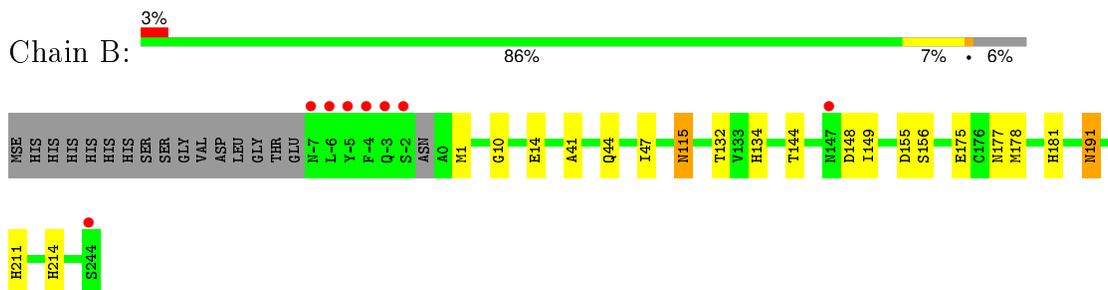
### 3 Residue-property plots [\(i\)](#)

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.

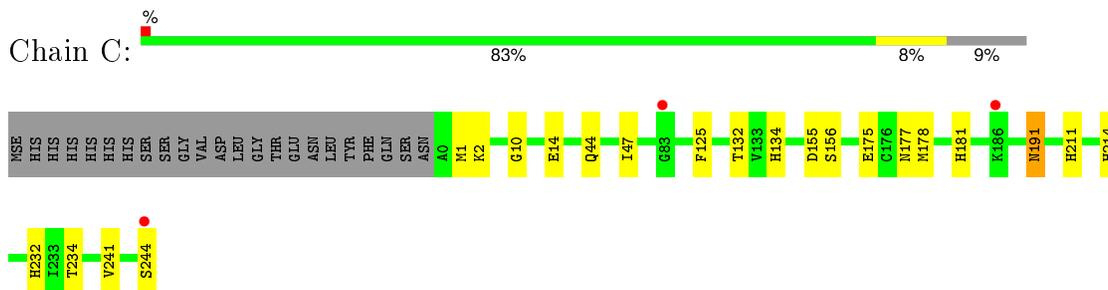
- Molecule 1: hypothetical protein BA1088



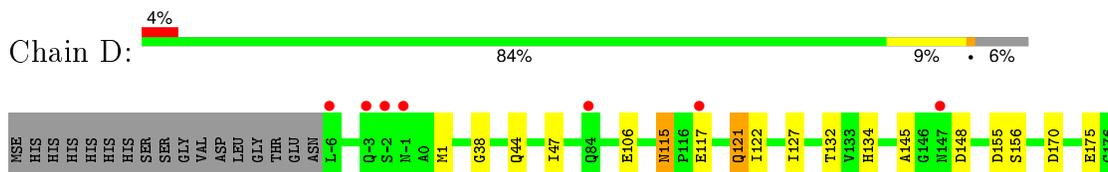
- Molecule 1: hypothetical protein BA1088



- Molecule 1: hypothetical protein BA1088



- Molecule 1: hypothetical protein BA1088





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	73.38Å 91.19Å 78.47Å 90.00° 115.31° 90.00°	Depositor
Resolution (Å)	25.00 – 1.50 24.32 – 1.50	Depositor EDS
% Data completeness (in resolution range)	95.8 (25.00-1.50) 95.7 (24.32-1.50)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.30 (at 1.50Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.147 , 0.180 0.152 , 0.183	Depositor DCC
$R_{free}$ test set	7103 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	11.3	Xtriage
Anisotropy	0.225	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 51.8	EDS
Estimated twinning fraction	0.021 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	0 of 142135 reflections	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	9487	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.56% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NA, ZN, CL

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	0.47	0/2056	0.60	0/2793
1	B	0.49	0/2081	0.62	0/2821
1	C	0.49	0/2014	0.62	0/2733
1	D	0.45	0/2076	0.59	0/2822
All	All	0.47	0/8227	0.61	0/11169

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	2003	0	1908	17	0
1	B	2030	0	1931	13	0
1	C	1964	0	1870	17	0
1	D	2023	0	1921	20	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
3	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	1	0	0	0	0
4	B	2	0	0	0	0
4	C	1	0	0	0	0
5	A	371	0	0	1	0
5	B	406	0	0	1	0
5	C	348	0	0	2	0
5	D	329	0	0	8	0
All	All	9487	0	7630	67	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 4.

All (67) 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:14[A]:GLU:OE2	1:C:214:HIS:HD2	1.66	0.79
1:B:14[A]:GLU:OE1	1:B:214:HIS:HD2	1.73	0.72
1:A:14[A]:GLU:OE2	1:A:214:HIS:HD2	1.77	0.67
1:C:2:LYS:HE3	1:C:241:VAL:HG11	1.77	0.66
1:B:1:MSE:HE3	1:B:148:ASP:HB2	1.76	0.66
1:C:2:LYS:HE3	1:C:241:VAL:CG1	2.26	0.66
1:A:10:GLY:O	1:A:214:HIS:HE1	1.79	0.65
1:C:10:GLY:O	1:C:214:HIS:HE1	1.78	0.65
1:A:163:ILE:HB	1:A:164:PRO:HD3	1.80	0.64
1:B:10:GLY:O	1:B:214:HIS:HE1	1.80	0.64
1:D:38:GLY:HA3	5:D:539:HOH:O	1.98	0.64
1:D:115:ASN:HD22	1:D:115:ASN:C	2.04	0.61
1:D:226:LYS:HD3	5:D:322:HOH:O	2.00	0.60
1:C:181:HIS:HD2	5:C:309:HOH:O	1.83	0.60
1:D:191:ASN:C	1:D:191:ASN:HD22	2.05	0.59
1:A:2:LYS:NZ	1:A:243:ASN:HD21	2.03	0.57
1:B:191:ASN:C	1:B:191:ASN:HD22	2.08	0.56
1:D:191:ASN:ND2	1:D:194:GLU:H	2.03	0.56
1:C:191:ASN:C	1:C:191:ASN:HD22	2.09	0.54
1:D:1:MSE:HE2	1:D:145:ALA:HB3	1.88	0.54
1:A:191:ASN:HD22	1:A:191:ASN:C	2.10	0.54
1:D:115:ASN:ND2	1:D:117:GLU:H	2.07	0.53
1:A:115:ASN:C	1:A:115:ASN:HD22	2.11	0.53
1:C:1:MSE:HE2	1:C:125:PHE:CE1	2.44	0.52
1:D:237:HIS:HD2	5:D:312[A]:HOH:O	1.92	0.52
1:D:115:ASN:HD22	1:D:117:GLU:H	1.56	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:41:ALA:HB2	5:D:539:HOH:O	2.09	0.52
1:B:177:ASN:ND2	1:B:211:HIS:HD1	2.08	0.51
1:D:170:ASP:OD1	1:D:205:LYS:HE3	2.10	0.51
1:C:232:HIS:HD2	5:C:578[B]:HOH:O	1.95	0.50
1:A:132:THR:HB	1:A:156:SER:HB2	1.94	0.49
1:A:115:ASN:ND2	1:A:117:GLU:H	2.10	0.49
1:C:134:HIS:CE1	1:C:155:ASP:HB3	2.47	0.49
1:C:132:THR:HB	1:C:156:SER:HB2	1.95	0.49
1:A:163:ILE:HD12	1:A:201:ASP:HB2	1.94	0.49
1:C:44:GLN:HA	1:C:47:ILE:O	2.12	0.49
1:D:44:GLN:HA	1:D:47:ILE:O	2.13	0.48
1:B:44:GLN:HA	1:B:47:ILE:O	2.13	0.48
1:C:14[A]:GLU:OE2	1:C:214:HIS:CD2	2.56	0.48
1:B:144[A]:THR:HG22	1:B:149:ILE:HG12	1.95	0.48
1:B:177:ASN:HD22	1:B:211:HIS:HD1	1.62	0.47
1:B:115:ASN:C	1:B:115:ASN:HD22	2.17	0.47
1:D:132:THR:HB	1:D:156:SER:HB2	1.97	0.47
1:C:177:ASN:ND2	1:C:211:HIS:HD1	2.13	0.46
1:D:134:HIS:CE1	1:D:155:ASP:HB3	2.51	0.46
1:B:134:HIS:CE1	1:B:155:ASP:HB3	2.50	0.45
1:A:205:LYS:HE3	5:A:464:HOH:O	2.17	0.45
1:A:44:GLN:HA	1:A:47:ILE:O	2.16	0.45
1:A:177:ASN:ND2	1:A:211:HIS:HD1	2.14	0.45
1:C:1:MSE:HE2	1:C:125:PHE:HE1	1.83	0.44
1:C:2:LYS:HE3	1:C:241:VAL:HG13	1.98	0.43
1:A:177:ASN:HD22	1:A:211:HIS:HD1	1.65	0.43
1:C:132:THR:HB	1:C:156:SER:CB	2.49	0.42
1:A:132:THR:HB	1:A:156:SER:CB	2.49	0.42
1:D:1:MSE:HE3	1:D:148:ASP:HB2	2.00	0.42
1:D:122:ILE:HD12	1:D:127:ILE:HD12	2.01	0.42
1:A:7:GLY:HA3	1:A:19:THR:O	2.19	0.42
1:D:226:LYS:HE2	5:D:334:HOH:O	2.19	0.41
1:A:2:LYS:HZ3	1:A:243:ASN:HD21	1.67	0.41
1:D:177:ASN:ND2	1:D:211:HIS:HD1	2.18	0.41
1:D:121[A]:GLN:HB3	1:D:121[A]:GLN:HE21	1.66	0.41
1:D:106[B]:GLU:HG2	5:D:373:HOH:O	2.21	0.41
1:C:234:THR:HG23	5:D:323:HOH:O	2.19	0.41
1:B:181:HIS:HD2	5:B:284:HOH:O	2.02	0.41
1:B:132:THR:HB	1:B:156:SER:HB2	2.01	0.41
1:D:237:HIS:CD2	5:D:312[A]:HOH:O	2.72	0.40
1:A:134:HIS:CE1	1:A:155:ASP:HB3	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	256/268 (96%)	248 (97%)	8 (3%)	0	100	100
1	B	257/268 (96%)	249 (97%)	8 (3%)	0	100	100
1	C	252/268 (94%)	243 (96%)	9 (4%)	0	100	100
1	D	258/268 (96%)	250 (97%)	8 (3%)	0	100	100
All	All	1023/1072 (95%)	990 (97%)	33 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	217/219 (99%)	213 (98%)	4 (2%)	66	35
1	B	220/219 (100%)	216 (98%)	4 (2%)	66	35
1	C	213/219 (97%)	209 (98%)	4 (2%)	65	31
1	D	219/219 (100%)	213 (97%)	6 (3%)	52	18
All	All	869/876 (99%)	851 (98%)	18 (2%)	63	27

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	115	ASN
1	A	175	GLU
1	A	178	MSE
1	A	191	ASN
1	B	115	ASN
1	B	175	GLU
1	B	178	MSE
1	B	191	ASN
1	C	175	GLU
1	C	178	MSE
1	C	191	ASN
1	C	244	SER
1	D	115	ASN
1	D	121[A]	GLN
1	D	121[B]	GLN
1	D	175	GLU
1	D	178	MSE
1	D	191	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	-1	ASN
1	A	98	ASN
1	A	115	ASN
1	A	121	GLN
1	A	177	ASN
1	A	191	ASN
1	A	214	HIS
1	A	243	ASN
1	B	26	HIS
1	B	98	ASN
1	B	115	ASN
1	B	177	ASN
1	B	181	HIS
1	B	191	ASN
1	B	214	HIS
1	B	237	HIS
1	C	84	GLN
1	C	98	ASN
1	C	177	ASN
1	C	181	HIS
1	C	191	ASN

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Mol	Chain	Res	Type
1	C	214	HIS
1	C	232	HIS
1	D	98	ASN
1	D	115	ASN
1	D	177	ASN
1	D	191	ASN
1	D	237	HIS

### 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 13 ligands modelled in this entry, 13 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

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	246/268 (91%)	-0.07	4 (1%) 74 78	10, 16, 26, 41	0
1	B	246/268 (91%)	-0.08	8 (3%) 50 52	10, 14, 26, 40	0
1	C	240/268 (89%)	-0.12	3 (1%) 79 82	9, 14, 27, 37	0
1	D	246/268 (91%)	0.12	12 (4%) 33 34	10, 17, 31, 42	0
All	All	978/1072 (91%)	-0.04	27 (2%) 56 59	9, 15, 29, 42	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	-6	LEU	9.8
1	B	-4	PHE	7.1
1	A	-6	LEU	5.7
1	B	-6	LEU	4.1
1	B	-2	SER	4.1
1	A	-5	TYR	3.6
1	B	244	SER	3.6
1	B	-7	ASN	3.5
1	A	186	LYS	3.4
1	D	186	LYS	3.3
1	D	185	ALA	3.1
1	D	-3	GLN	3.1
1	C	244	SER	3.1
1	D	-2	SER	2.8
1	D	184	ALA	2.6
1	D	84	GLN	2.5
1	B	-5	TYR	2.5
1	C	186	LYS	2.5
1	A	183	GLU	2.2
1	C	83	GLY	2.2
1	D	181	HIS	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	147	ASN	2.2
1	D	183	GLU	2.2
1	B	147	ASN	2.1
1	D	-1	ASN	2.1
1	B	-3	GLN	2.0
1	D	117	GLU	2.0

## 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	ZN	C	246	1/1	1.00	0.04	-2.23	11,11,11,11	0
2	ZN	C	245	1/1	1.00	0.03	-2.99	12,12,12,12	0
2	ZN	D	246	1/1	1.00	0.04	-3.24	13,13,13,13	0
2	ZN	B	246	1/1	1.00	0.05	-3.41	12,12,12,12	0
2	ZN	A	245	1/1	1.00	0.04	-3.67	13,13,13,13	0
2	ZN	A	246	1/1	1.00	0.04	-3.85	12,12,12,12	0
2	ZN	D	245	1/1	1.00	0.03	-4.20	14,14,14,14	0
2	ZN	B	245	1/1	1.00	0.03	-6.58	13,13,13,13	0
4	NA	C	247	1/1	0.98	0.09	-	21,21,21,21	0
4	NA	B	249	1/1	0.99	0.17	-	22,22,22,22	0
3	CL	B	247	1/1	0.99	0.03	-	18,18,18,18	0
4	NA	B	248	1/1	0.97	0.09	-	25,25,25,25	0
4	NA	A	247	1/1	0.99	0.21	-	26,26,26,26	0

## 6.5 Other polymers

There are no such residues in this entry.