



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:34 PM UTC

PDB ID : 8ZAC / pdb_00008zac
Title : Crystal structure of BcABA3 from Botrytis cinerea
Authors : Li, S.Y.; Li, H.; Yang, Y.; Huang, J.-W.; Chen, C.-C.; Guo, R.-T.
Deposited on : 2024-04-25
Resolution : 2.45 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

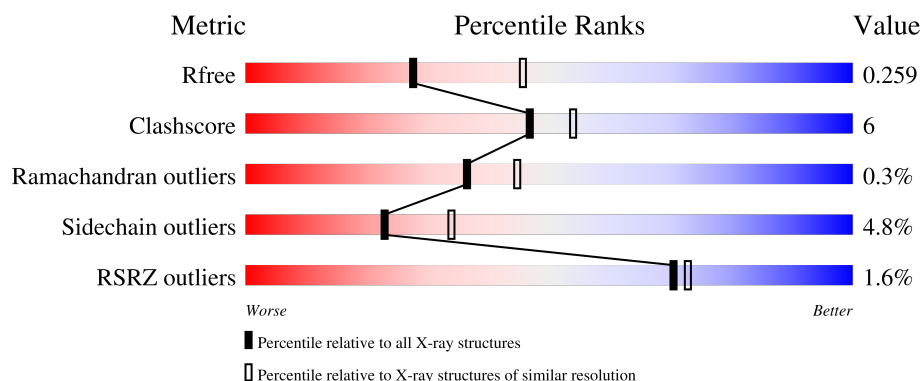
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1190 (2.46-2.46)
Clashscore	190562	1229 (2.46-2.46)
Ramachandran outliers	187476	1218 (2.46-2.46)
Sidechain outliers	187428	1218 (2.46-2.46)
RSRZ outliers	180081	1190 (2.46-2.46)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 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	463	61%14%25%
1	B	463	2% 63%13%22%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6005 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 Alpha-ionylideneethane synthase aba3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	349	Total	C	N	O	S	0	0	0
			2850	1820	487	522	21			
1	B	359	Total	C	N	O	S	0	1	0
			2944	1878	507	537	22			

There are 46 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-22	HIS	-	expression tag	UNP A0A384JQC9
A	-21	HIS	-	expression tag	UNP A0A384JQC9
A	-20	HIS	-	expression tag	UNP A0A384JQC9
A	-19	HIS	-	expression tag	UNP A0A384JQC9
A	-18	HIS	-	expression tag	UNP A0A384JQC9
A	-17	HIS	-	expression tag	UNP A0A384JQC9
A	-16	GLU	-	expression tag	UNP A0A384JQC9
A	-15	ASN	-	expression tag	UNP A0A384JQC9
A	-14	LEU	-	expression tag	UNP A0A384JQC9
A	-13	TYR	-	expression tag	UNP A0A384JQC9
A	-12	PHE	-	expression tag	UNP A0A384JQC9
A	-11	GLN	-	expression tag	UNP A0A384JQC9
A	-10	GLY	-	expression tag	UNP A0A384JQC9
A	-9	ALA	-	expression tag	UNP A0A384JQC9
A	-8	GLY	-	expression tag	UNP A0A384JQC9
A	-7	ALA	-	expression tag	UNP A0A384JQC9
A	-6	GLY	-	expression tag	UNP A0A384JQC9
A	-5	ALA	-	expression tag	UNP A0A384JQC9
A	-4	GLY	-	expression tag	UNP A0A384JQC9
A	-3	ALA	-	expression tag	UNP A0A384JQC9
A	-2	GLY	-	expression tag	UNP A0A384JQC9
A	-1	ALA	-	expression tag	UNP A0A384JQC9
A	0	GLY	-	expression tag	UNP A0A384JQC9
B	-22	HIS	-	expression tag	UNP A0A384JQC9
B	-21	HIS	-	expression tag	UNP A0A384JQC9

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-20	HIS	-	expression tag	UNP A0A384JQC9
B	-19	HIS	-	expression tag	UNP A0A384JQC9
B	-18	HIS	-	expression tag	UNP A0A384JQC9
B	-17	HIS	-	expression tag	UNP A0A384JQC9
B	-16	GLU	-	expression tag	UNP A0A384JQC9
B	-15	ASN	-	expression tag	UNP A0A384JQC9
B	-14	LEU	-	expression tag	UNP A0A384JQC9
B	-13	TYR	-	expression tag	UNP A0A384JQC9
B	-12	PHE	-	expression tag	UNP A0A384JQC9
B	-11	GLN	-	expression tag	UNP A0A384JQC9
B	-10	GLY	-	expression tag	UNP A0A384JQC9
B	-9	ALA	-	expression tag	UNP A0A384JQC9
B	-8	GLY	-	expression tag	UNP A0A384JQC9
B	-7	ALA	-	expression tag	UNP A0A384JQC9
B	-6	GLY	-	expression tag	UNP A0A384JQC9
B	-5	ALA	-	expression tag	UNP A0A384JQC9
B	-4	GLY	-	expression tag	UNP A0A384JQC9
B	-3	ALA	-	expression tag	UNP A0A384JQC9
B	-2	GLY	-	expression tag	UNP A0A384JQC9
B	-1	ALA	-	expression tag	UNP A0A384JQC9
B	0	GLY	-	expression tag	UNP A0A384JQC9

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

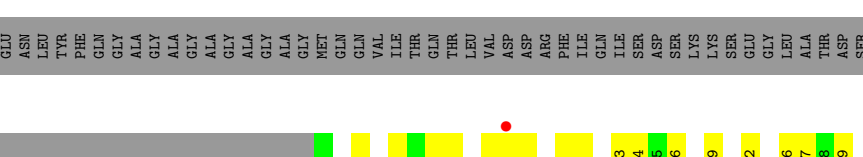
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Zn 1 1	0	0
2	B	1	Total Zn 1 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	95	Total O 95 95	0	0
3	B	114	Total O 114 114	0	0

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

- Chain A: 



Position	Frequency (bits)	Amino Acid
1	0.05	HIS
2	0.04	PRO
3	0.03	ILE
4	0.02	ASP
5	0.03	LYS
6	0.04	ASP
7	0.03	PRO
8	0.02	ILE
9	0.03	LEU
10	0.02	TYR
11	0.03	PHE
12	0.04	ALA
13	0.03	GLN
14	0.02	GLY
15	0.03	ALA
16	0.04	GLY
17	0.03	ALA
18	0.02	GLY
19	0.03	ALA
20	0.04	GLY
21	0.03	ALA
22	0.02	PRO
23	0.03	ILE
24	0.04	VAL
25	0.03	LYS
26	0.05	GLN
27	0.04	VAL
28	0.03	ILE
29	0.02	THR
30	0.03	GLN
31	0.02	THR
32	0.03	LEU
33	0.04	VAL
34	0.03	ASP
35	0.02	ARG
36	0.03	PHE
37	0.02	ILE
38	0.03	GLN
39	0.02	ILE
40	0.03	SER
41	0.04	ASP
42	0.03	SER
43	0.02	LYS
44	0.03	LYS
45	0.02	SER
46	0.03	GLY
47	0.02	GLY
48	0.03	LEU
49	0.04	ALA
50	0.03	THR
51	0.02	ASP
52	0.03	SER
53	0.02	THR
54	0.03	LYS
55	0.02	ARG
56	0.03	GLN
57	0.02	SER
58	0.03	GLN
59	0.02	THR
60	0.03	VAL

- [illegible]

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	81.20Å 166.89Å 57.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.47 – 2.45 24.47 – 2.45	Depositor EDS
% Data completeness (in resolution range)	98.7 (24.47-2.45) 99.0 (24.47-2.45)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.05 (at 2.44Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.184 , 0.254 (Not available) , 0.259	Depositor DCC
R_{free} test set	1449 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	48.0	Xtriage
Anisotropy	0.654	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 41.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6005	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.89% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.09	4/2920 (0.1%)	1.49	5/3947 (0.1%)
1	B	1.07	2/3018 (0.1%)	1.53	5/4076 (0.1%)
All	All	1.08	6/5938 (0.1%)	1.51	10/8023 (0.1%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	241	LEU	C-O	6.55	1.31	1.24
1	A	122	ILE	C-O	5.92	1.31	1.24
1	A	117	ILE	C-O	5.42	1.30	1.24
1	B	272	TYR	C-O	5.42	1.30	1.24
1	A	167	PHE	C-O	5.32	1.30	1.24
1	A	112	ALA	C-O	5.23	1.30	1.24

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	284	ALA	CA-C-N	6.38	129.70	120.38
1	A	284	ALA	C-N-CA	6.38	129.70	120.38
1	A	77	GLN	CA-C-N	5.98	128.57	120.38
1	A	77	GLN	C-N-CA	5.98	128.57	120.38
1	B	180	ASP	CA-C-N	5.94	126.60	120.60
1	B	180	ASP	C-N-CA	5.94	126.60	120.60
1	A	72	ILE	N-CA-C	-5.22	107.89	112.90
1	B	311	ARG	CA-C-N	5.04	127.03	120.28
1	B	311	ARG	C-N-CA	5.04	127.03	120.28
1	B	283	ASP	CA-CB-CG	5.00	117.60	112.60

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	2850	0	2748	37	0
1	B	2944	0	2860	33	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	95	0	0	1	0
3	B	114	0	0	4	0
All	All	6005	0	5608	65	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 6.

All (65) 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:308:MET:HE3	1:B:322:ILE:HD13	1.63	0.79
1:A:186:ARG:HD3	1:A:357:TYR:CZ	2.27	0.70
1:B:116:ILE:HG23	1:B:164:TYR:CE1	2.29	0.68
1:B:346:ALA:HB1	1:B:351:VAL:HG21	1.76	0.67
1:B:412:LEU:O	1:B:416:LYS:HG2	1.95	0.67
1:A:357:TYR:CZ	1:A:361:ILE:HD11	2.30	0.66
1:A:106:ASN:ND2	1:A:109:ARG:HD2	2.12	0.65
1:A:155:PRO:HD3	1:A:222:ASP:O	1.97	0.65
1:A:79:ILE:HD11	1:A:139:LEU:HA	1.79	0.63
1:B:180:ASP:HB2	1:B:351:VAL:HG11	1.83	0.60
1:A:164:TYR:CE2	1:A:168:LEU:HD11	2.37	0.60
1:A:103:ASN:HB2	1:B:103:ASN:OD1	2.04	0.57
1:A:265:GLU:HB3	3:A:630:HOH:O	2.04	0.57
1:A:269:ILE:HD12	1:B:320:LEU:HG	1.87	0.56
1:A:357:TYR:CZ	1:A:361:ILE:CD1	2.90	0.55
1:A:64:ASP:OD1	1:A:311:ARG:HD2	2.06	0.55
1:A:357:TYR:CE1	1:A:361:ILE:HD11	2.42	0.54
1:B:286:TRP:CE3	1:B:292:LEU:HB3	2.43	0.54
1:A:116:ILE:HG23	1:A:164:TYR:CE1	2.42	0.53
1:A:70:PRO:HA	1:A:73:ALA:HB2	1.93	0.51
1:A:319:ASN:HA	1:B:269:ILE:HD12	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:188:VAL:O	1:B:191:LEU:HB2	2.12	0.50
1:A:152:GLU:HA	1:A:157:HIS:ND1	2.27	0.49
1:B:251:ARG:NH1	1:B:265:GLU:OE1	2.45	0.49
1:B:163:GLU:OE1	1:B:200:ARG:NH2	2.38	0.49
1:A:148:ALA:HA	1:A:157:HIS:CE1	2.49	0.48
1:B:81:LEU:HD21	1:B:129:MET:HE1	1.94	0.48
1:A:126:ARG:CB	1:A:129:MET:HE3	2.43	0.48
1:B:297:ASN:O	1:B:298:PHE:C	2.57	0.48
1:A:119:MET:HG2	1:A:139:LEU:HD12	1.96	0.47
1:A:103:ASN:HD22	1:A:104:TYR:N	2.12	0.47
1:A:136:ASN:HD21	1:A:144:ASP:H	1.63	0.47
1:A:186:ARG:CD	1:A:357:TYR:CZ	2.96	0.46
1:A:210:PHE:O	1:A:213:ALA:HB3	2.13	0.46
1:B:202:ARG:HH12	1:B:206:ALA:HB2	1.80	0.46
1:A:103:ASN:HD22	1:A:104:TYR:H	1.62	0.46
1:B:142:ASP:HB3	1:B:145:ALA:HB3	1.98	0.45
1:B:355:GLN:HE21	1:B:355:GLN:HA	1.81	0.45
1:B:165:LYS:NZ	3:B:609:HOH:O	2.48	0.45
1:B:403:GLY:N	3:B:612:HOH:O	2.49	0.44
1:B:150:LEU:HD23	1:B:151:PHE:CE2	2.53	0.44
1:B:164:TYR:HB2	1:B:210:PHE:CE2	2.53	0.44
1:A:174:LYS:NZ	1:A:255:GLU:OE2	2.40	0.43
1:A:260:PHE:CE1	1:A:268:ARG:HA	2.52	0.43
1:B:346:ALA:HB1	1:B:351:VAL:CG2	2.45	0.43
1:B:339:LYS:HD2	1:B:339:LYS:C	2.44	0.43
1:A:186:ARG:HD3	1:A:357:TYR:CE1	2.54	0.43
1:A:164:TYR:HB2	1:A:210:PHE:CE2	2.54	0.42
1:B:169:LEU:HD13	1:B:183:LEU:HD21	2.02	0.42
1:B:202:ARG:NH1	1:B:206:ALA:HB2	2.34	0.42
1:B:126:ARG:HB3	1:B:129:MET:HE3	2.01	0.42
1:B:102:PRO:HD2	3:B:660:HOH:O	2.20	0.42
1:A:254:GLY:HA2	1:A:400:GLN:O	2.19	0.42
1:A:182:GLU:OE2	1:A:186:ARG:HD2	2.19	0.42
1:A:209:ARG:HH12	1:A:228:GLU:CD	2.28	0.41
1:B:173:ASP:OD2	1:B:183:LEU:HD23	2.20	0.41
1:A:179:ARG:NE	1:A:393:TYR:O	2.50	0.41
1:B:156:GLY:O	1:B:157:HIS:C	2.62	0.41
1:B:188:VAL:HG11	1:B:390:ARG:HD3	2.02	0.41
1:B:138:LEU:HD12	1:B:143:LEU:HD22	2.01	0.41
1:A:280:TRP:CH2	1:B:95:GLU:HA	2.56	0.41
1:A:234:LEU:HD12	1:A:234:LEU:HA	1.91	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:195:PRO:HB2	1:A:417:TYR:CD2	2.55	0.40
1:A:136:ASN:O	1:A:136:ASN:CG	2.63	0.40
1:B:415:ARG:NH1	3:B:610:HOH:O	2.51	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	345/463 (74%)	319 (92%)	24 (7%)	2 (1%)	21	27
1	B	354/463 (76%)	335 (95%)	19 (5%)	0	100	100
All	All	699/926 (76%)	654 (94%)	43 (6%)	2 (0%)	36	45

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	134	ALA
1	A	370	PRO

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	295/389 (76%)	285 (97%)	10 (3%)	32	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	308/389 (79%)	289 (94%)	19 (6%)	16	23
All	All	603/778 (78%)	574 (95%)	29 (5%)	23	34

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	78	SER
1	A	84	GLU
1	A	85	LEU
1	A	146	THR
1	A	169	LEU
1	A	177	GLU
1	A	234	LEU
1	A	352	LEU
1	A	365	GLU
1	A	381	ASP
1	B	60	LYS
1	B	77	GLN
1	B	110	TYR
1	B	152	GLU
1	B	158	LYS
1	B	169	LEU
1	B	216	LEU
1	B	228	GLU
1	B	256	THR
1	B	322	ILE
1	B	326	GLU
1	B	329	LYS
1	B	330	VAL
1	B	339	LYS
1	B	342	ASN
1	B	351	VAL
1	B	374	GLU
1	B	408	SER
1	B	413	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	74	ASN
1	A	77	GLN

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Mol	Chain	Res	Type
1	A	103	ASN
1	A	136	ASN
1	A	137	ASN
1	A	219	ASN
1	A	399	HIS
1	B	62	HIS
1	B	136	ASN
1	B	157	HIS
1	B	193	GLN
1	B	219	ASN
1	B	347	ASN
1	B	355	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 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, 95th 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 ²)	Q<0.9
1	A	349/463 (75%)	0.09	4 (1%) 78 79	34, 58, 95, 124	0
1	B	359/463 (77%)	0.04	7 (1%) 66 67	31, 58, 94, 149	1 (0%)
All	All	708/926 (76%)	0.06	11 (1%) 70 73	31, 58, 95, 149	1 (0%)

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	351	VAL	4.5
1	B	327	THR	3.7
1	B	436	PHE	3.0
1	A	352	LEU	2.7
1	B	352	LEU	2.6
1	B	330	VAL	2.5
1	A	78	SER	2.4
1	A	173	ASP	2.3
1	B	404	VAL	2.2
1	A	183	LEU	2.1
1	B	435	HIS	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th 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($\text{\AA}^2$)	Q<0.9
2	ZN	A	500	1/1	0.99	0.04	74,74,74,74	0
2	ZN	B	500	1/1	0.99	0.03	73,73,73,73	0

6.5 Other polymers [i](#)

There are no such residues in this entry.