



# Full wwPDB X-ray Structure Validation Report i

Jun 19, 2024 – 01:43 AM EDT

PDB ID : 4CJ9

Title : BurrH DNA-binding protein from Burkholderia rhizoxinica in its apo form

Authors : Stella, S.; Molina, R.; Lopez-Mendez, B.; Campos-Olivas, R.; Duchateau, P.; Montoya, G.

Deposited on : 2013-12-19

Resolution : 2.21 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 i symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-467

Mogul : 2022.3.0, CSD as543be (2022)

Xtriage (Phenix) : 1.20.1

EDS : 2.37.1

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) : 2.37.1

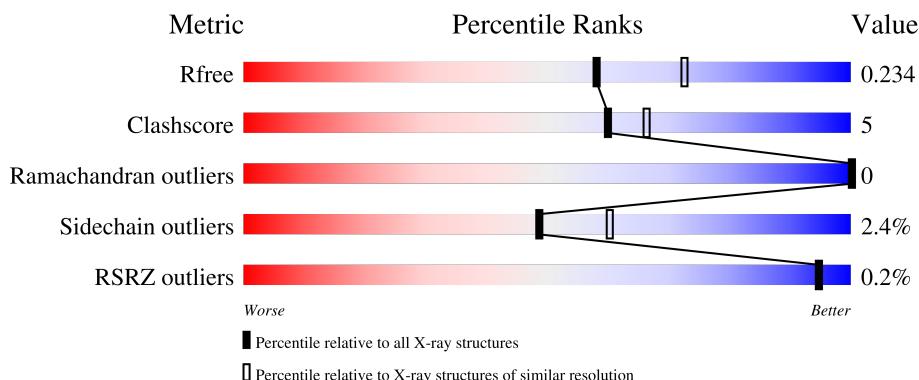
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## X-RAY DIFFRACTION

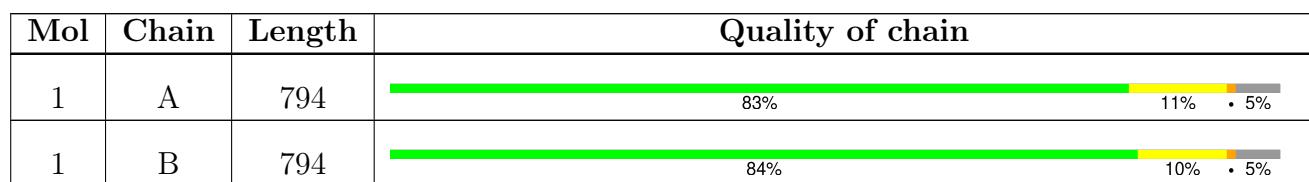
The reported resolution of this entry is 2.21 Å.

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	5912 (2.24-2.20)
Clashscore	141614	6646 (2.24-2.20)
Ramachandran outliers	138981	6543 (2.24-2.20)
Sidechain outliers	138945	6544 (2.24-2.20)
RSRZ outliers	127900	5797 (2.24-2.20)

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  $\geq 3$ , 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.



The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SE	A	1002	-	-	-	X

## 2 Entry composition [\(i\)](#)

There are 3 unique types of molecules in this entry. The entry contains 11880 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 BURRH.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	752	Total	C 5488	N 3410	O 1022	S 1041	Se 4	0	1	0
1	B	752	Total	C 5482	N 3407	O 1019	S 1041	Se 4	0	1	0

- Molecule 2 is SELENIUM ATOM (three-letter code: SE) (formula: Se).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Se 2 2	0	0

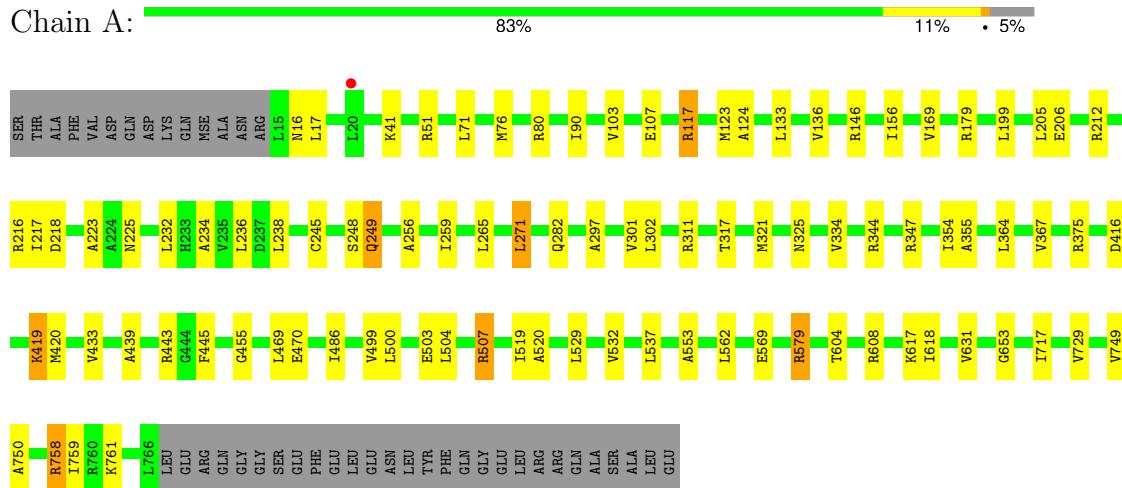
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	475	Total O 475 475	0	0
3	B	433	Total O 433 433	0	0

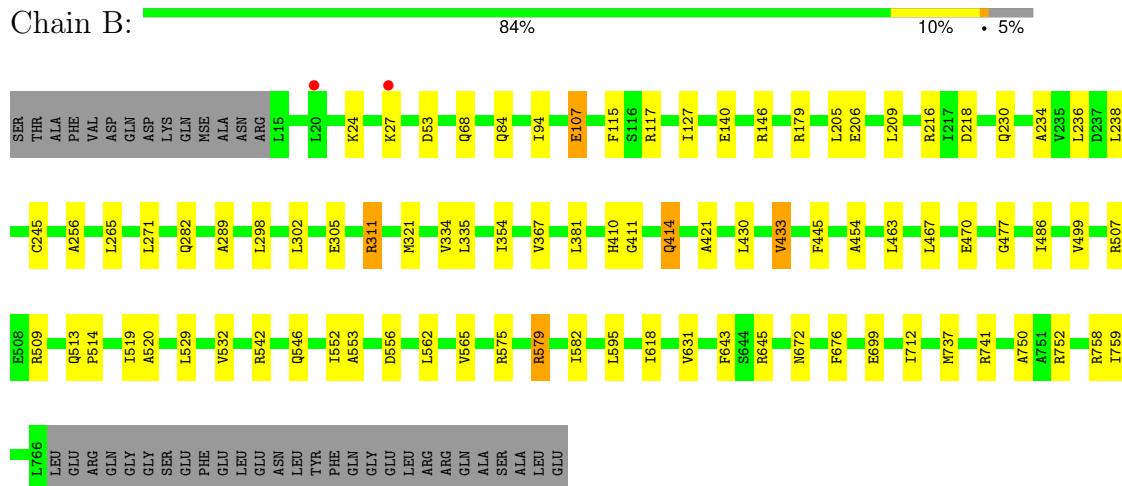
### 3 Residue-property plots [\(i\)](#)

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.

- Molecule 1: BURRH



- Molecule 1: BURRH



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	73.31Å 73.31Å 268.34Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	63.49 – 2.21 89.45 – 2.21	Depositor EDS
% Data completeness (in resolution range)	99.4 (63.49-2.21) 99.4 (89.45-2.21)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) >$ <sup>1</sup>	4.18 (at 2.22Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
$R$ , $R_{free}$	0.180 , 0.229 0.185 , 0.234	Depositor DCC
$R_{free}$ test set	1994 reflections (2.48%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	39.0	Xtriage
Anisotropy	0.416	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 30.1	EDS
L-test for twinning <sup>2</sup>	$<  L  > = 0.43$ , $< L^2 > = 0.25$	Xtriage
Estimated twinning fraction	0.104 for -h,-k,l 0.077 for h,-h-k,-l 0.063 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	11880	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.92% 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  $< |L| >$ ,  $< L^2 >$  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: SE

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	0.22	0/5537	0.39	0/7446
1	B	0.22	0/5531	0.39	0/7439
All	All	0.22	0/11068	0.39	0/14885

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	5488	0	5615	54	0
1	B	5482	0	5604	47	0
2	A	2	0	0	0	1
3	A	475	0	0	10	0
3	B	433	0	0	9	1
All	All	11880	0	11219	101	1

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 5.

All (101) 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:107:GLU:OE1	1:A:117:ARG:NH2	2.17	0.78
1:A:569:GLU:OE1	1:A:579:ARG:NH2	2.25	0.68
1:B:311:ARG:NH2	1:B:335:LEU:O	2.27	0.67
1:B:245:CYS:O	1:B:282:GLN:NE2	2.27	0.66
1:B:414:GLN:NE2	3:B:2265:HOH:O	2.29	0.65
1:B:216:ARG:NH1	3:B:2120:HOH:O	2.30	0.64
1:A:617:LYS:NZ	3:A:2389:HOH:O	2.30	0.63
1:A:604:THR:HG22	1:A:608:ARG:HE	1.62	0.63
1:A:212:ARG:O	1:A:249:GLN:NE2	2.31	0.61
1:A:617:LYS:HD3	1:A:653:GLY:HA3	1.81	0.61
1:A:17:LEU:HD23	1:A:51:ARG:HH21	1.67	0.59
1:A:325:ASN:ND2	3:A:2200:HOH:O	2.35	0.59
1:B:179[B]:ARG:NH1	1:B:206:GLU:OE1	2.36	0.59
1:B:752:ARG:HD2	1:B:758:ARG:HG3	1.85	0.58
1:A:317:THR:HG22	1:A:321:MSE:HE2	1.87	0.57
1:A:334:VAL:HG23	1:A:364:LEU:HD11	1.86	0.57
1:B:507:ARG:NH2	1:B:513:GLN:OE1	2.37	0.57
1:B:519:ILE:HD13	1:B:532:VAL:HG21	1.85	0.57
1:B:477:GLY:O	1:B:513:GLN:NE2	2.39	0.56
1:B:206:GLU:OE2	1:B:216:ARG:NH2	2.39	0.55
1:B:53:ASP:OD2	1:B:84:GLN:NE2	2.39	0.55
1:B:618:ILE:HD13	1:B:631:VAL:HG21	1.89	0.54
1:B:24:LYS:HA	1:B:27:LYS:HD2	1.89	0.54
1:A:90:ILE:HD13	1:A:103:VAL:HG21	1.88	0.54
1:B:107:GLU:HG2	1:B:117:ARG:HH22	1.73	0.54
1:B:542:ARG:HB3	1:B:579:ARG:HH21	1.73	0.54
1:A:419:LYS:HD2	1:A:455:GLY:HA3	1.90	0.53
1:B:354:ILE:HD13	1:B:367:VAL:HG21	1.89	0.53
1:A:146:ARG:NH1	3:A:2075:HOH:O	2.42	0.53
1:A:245:CYS:O	1:A:282:GLN:NE2	2.30	0.52
1:A:80:ARG:NH1	1:A:107:GLU:OE2	2.42	0.52
1:A:271:LEU:HG	1:A:302:LEU:HD22	1.92	0.52
1:A:344:ARG:NH1	3:A:2211:HOH:O	2.29	0.52
1:A:375:ARG:NH1	3:A:2210:HOH:O	2.42	0.52
1:B:643:PHE:O	3:B:2381:HOH:O	2.19	0.52
1:A:618:ILE:HD13	1:A:631:VAL:HG21	1.91	0.52
1:A:761:LYS:NZ	3:A:2471:HOH:O	2.39	0.52
1:B:146:ARG:NH1	3:B:2091:HOH:O	2.43	0.51
1:A:117:ARG:NH1	3:A:2055:HOH:O	2.32	0.51
1:A:217:ILE:HD12	1:A:217:ILE:H	1.75	0.51
1:A:749:VAL:HG13	1:A:758:ARG:HB3	1.93	0.50
1:B:271:LEU:HG	1:B:302:LEU:HD22	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:16:ASN:O	1:A:51:ARG:NH2	2.44	0.50
1:B:410:HIS:N	1:B:411:GLY:HA2	2.26	0.49
1:B:520:ALA:HB2	1:B:529:LEU:HD11	1.93	0.49
1:A:41:LYS:HG2	1:A:71:LEU:HD11	1.94	0.49
1:A:750:ALA:HB2	1:A:759:ILE:HD11	1.93	0.49
1:B:321:MSE:SE	1:B:334:VAL:HG21	2.63	0.48
1:A:146:ARG:NH2	3:A:2077:HOH:O	2.46	0.48
1:A:469:LEU:HD22	1:A:500:LEU:HD22	1.96	0.48
1:A:216:ARG:NH2	3:A:2095:HOH:O	2.43	0.48
1:B:205:LEU:HG	1:B:236:LEU:HD12	1.96	0.47
1:A:218:ASP:OD2	3:A:2126:HOH:O	2.20	0.46
1:B:94:ILE:HG23	1:B:127:ILE:HG23	1.96	0.46
1:B:509:ARG:O	1:B:546:GLN:NE2	2.34	0.46
1:B:737:MSE:O	3:B:2419:HOH:O	2.21	0.45
1:B:68:GLN:NE2	3:B:2027:HOH:O	2.39	0.45
1:B:699:GLU:OE1	3:B:2404:HOH:O	2.21	0.45
1:B:750:ALA:HB2	1:B:759:ILE:HD11	1.99	0.45
1:B:552:ILE:HD13	1:B:565:VAL:HG21	1.99	0.44
1:A:354:ILE:HD13	1:A:367:VAL:HG21	1.99	0.44
1:A:553:ALA:HB2	1:A:562:LEU:HD11	2.00	0.44
1:B:234:ALA:O	1:B:238:LEU:HB2	2.18	0.44
1:B:712:ILE:H	1:B:712:ILE:HD12	1.83	0.44
1:A:124:ALA:HB2	1:A:133:LEU:HD11	1.98	0.44
1:A:297:ALA:O	1:A:301:VAL:HG23	2.18	0.44
1:B:741:ARG:NH1	3:B:2420:HOH:O	2.50	0.44
1:A:439:ALA:O	1:A:443:ARG:HG2	2.18	0.43
1:A:486:ILE:HD13	1:A:499:VAL:HG21	2.00	0.43
1:B:486:ILE:HD13	1:B:499:VAL:HG21	2.00	0.43
1:B:430:LEU:O	1:B:433:VAL:HG12	2.19	0.42
1:B:421:ALA:HB2	1:B:430:LEU:HD11	2.01	0.42
1:A:225:ASN:HB3	1:A:259:ILE:HG22	2.01	0.42
1:A:355:ALA:HB2	1:A:364:LEU:HD11	2.01	0.42
1:A:234:ALA:O	1:A:238:LEU:HB2	2.20	0.42
1:A:416:ASP:O	1:A:420:MSE:HG2	2.19	0.42
1:A:445:PHE:CZ	1:A:470:GLU:HG3	2.54	0.42
1:B:256:ALA:HB2	1:B:265:LEU:HD11	2.02	0.42
1:A:205:LEU:HG	1:A:236:LEU:HD12	2.01	0.42
1:A:179[B]:ARG:HD3	1:A:206:GLU:OE1	2.19	0.42
1:B:115:PHE:HE2	1:B:140:GLU:HG3	1.85	0.42
1:B:513:GLN:HB3	1:B:514:PRO:HD3	2.01	0.42
1:B:582:ILE:HG23	1:B:595:LEU:HD11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:223:ALA:HB2	1:A:232:LEU:HD11	2.01	0.41
1:A:519:ILE:HD13	1:A:532:VAL:HG21	2.01	0.41
1:B:553:ALA:HB2	1:B:562:LEU:HD11	2.02	0.41
1:A:717:ILE:HD13	1:A:729:VAL:HG21	2.01	0.41
1:B:645:ARG:HA	1:B:645:ARG:HD2	1.77	0.41
1:B:672:ASN:HA	1:B:676:PHE:O	2.21	0.41
1:A:256:ALA:HB2	1:A:265:LEU:HD11	2.02	0.41
1:A:520:ALA:HB2	1:A:529:LEU:HD11	2.03	0.41
1:B:218:ASP:OD1	3:B:2123:HOH:O	2.22	0.41
1:B:445:PHE:CZ	1:B:470:GLU:HG3	2.56	0.41
1:B:454:ALA:HB2	1:B:463:LEU:HD11	2.03	0.40
1:A:156:ILE:HD13	1:A:169:VAL:HG21	2.02	0.40
1:B:289:ALA:HB2	1:B:298:LEU:HD11	2.02	0.40
1:A:445:PHE:CE2	1:A:470:GLU:HG3	2.57	0.40
1:A:123:MSE:SE	1:A:136:VAL:HG21	2.71	0.40
1:A:199:LEU:HD23	1:A:199:LEU:HA	1.97	0.40
1:A:503:GLU:HG2	1:A:507:ARG:HD2	2.02	0.40
1:A:579:ARG:HA	1:A:579:ARG:HD2	1.78	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1001:SE:SE	3:B:2065:HOH:O[3_554]	1.75	0.45

## 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	751/794 (95%)	750 (100%)	1 (0%)	0	100 100
1	B	751/794 (95%)	748 (100%)	3 (0%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1502/1588 (95%)	1498 (100%)	4 (0%)	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	542/565 (96%)	528 (97%)	14 (3%)	46   57
1	B	541/565 (96%)	529 (98%)	12 (2%)	52   64
All	All	1083/1130 (96%)	1057 (98%)	26 (2%)	49   60

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	76	MSE
1	A	117	ARG
1	A	248	SER
1	A	249	GLN
1	A	271	LEU
1	A	311	ARG
1	A	347	ARG
1	A	419	LYS
1	A	433	VAL
1	A	504	LEU
1	A	507	ARG
1	A	537	LEU
1	A	579	ARG
1	A	758	ARG
1	B	107	GLU
1	B	209	LEU
1	B	230	GLN
1	B	305	GLU
1	B	311	ARG
1	B	381	LEU

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Mol	Chain	Res	Type
1	B	414	GLN
1	B	433	VAL
1	B	467	LEU
1	B	556	ASP
1	B	575	ARG
1	B	579	ARG

Sometimes 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 monosaccharides 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

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	741/794 (93%)	-0.59	1 (0%)	95	95	28, 46, 71, 105	0
1	B	741/794 (93%)	-0.58	2 (0%)	94	93	25, 48, 76, 119	0
All	All	1482/1588 (93%)	-0.58	3 (0%)	95	95	25, 47, 74, 119	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	20	LEU	3.1
1	B	20	LEU	2.6
1	B	27	LYS	2.3

### 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 monosaccharides 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	SE	A	1002	1/1	0.39	0.71	137,137,137,137	1
2	SE	A	1001	1/1	0.93	0.12	93,93,93,93	1

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

There are no such residues in this entry.