



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:00 AM GMT

PDB ID : 2P1J  
Title : Crystal structure of a polC-type DNA polymerase III exonuclease domain from *Thermotoga maritima*  
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Deposited on : 2007-03-05  
Resolution : 2.50 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

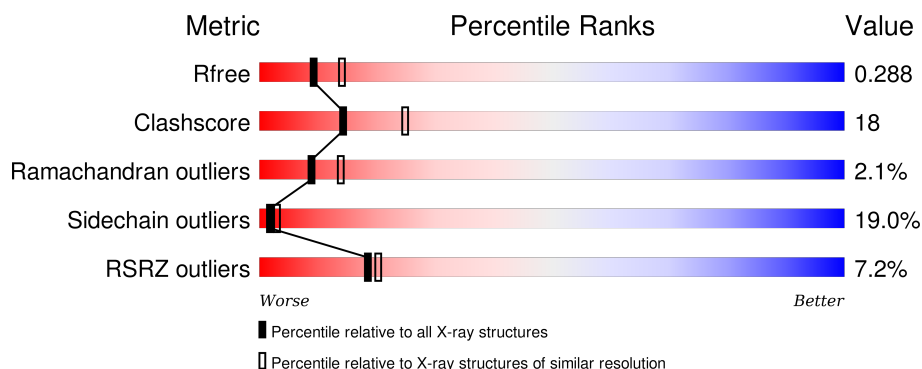
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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	186	
1	B	186	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2809 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 DNA polymerase III polC-type.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	164	Total	C	N	O	S	0	0	0
			1331	857	224	246	4			
1	B	171	Total	C	N	O	S	0	0	0
			1392	894	239	255	4			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	345	MET	-	CLONING ARTIFACT	UNP Q9ZHF6
A	346	SER	-	CLONING ARTIFACT	UNP Q9ZHF6
A	523	GLU	-	CLONING ARTIFACT	UNP Q9ZHF6
A	524	GLY	-	CLONING ARTIFACT	UNP Q9ZHF6
A	525	HIS	-	CLONING ARTIFACT	UNP Q9ZHF6
A	526	HIS	-	CLONING ARTIFACT	UNP Q9ZHF6
A	527	HIS	-	CLONING ARTIFACT	UNP Q9ZHF6
A	528	HIS	-	CLONING ARTIFACT	UNP Q9ZHF6
A	529	HIS	-	CLONING ARTIFACT	UNP Q9ZHF6
A	530	HIS	-	CLONING ARTIFACT	UNP Q9ZHF6
B	345	MET	-	CLONING ARTIFACT	UNP Q9ZHF6
B	346	SER	-	CLONING ARTIFACT	UNP Q9ZHF6
B	523	GLU	-	CLONING ARTIFACT	UNP Q9ZHF6
B	524	GLY	-	CLONING ARTIFACT	UNP Q9ZHF6
B	525	HIS	-	CLONING ARTIFACT	UNP Q9ZHF6
B	526	HIS	-	CLONING ARTIFACT	UNP Q9ZHF6
B	527	HIS	-	CLONING ARTIFACT	UNP Q9ZHF6
B	528	HIS	-	CLONING ARTIFACT	UNP Q9ZHF6
B	529	HIS	-	CLONING ARTIFACT	UNP Q9ZHF6
B	530	HIS	-	CLONING ARTIFACT	UNP Q9ZHF6

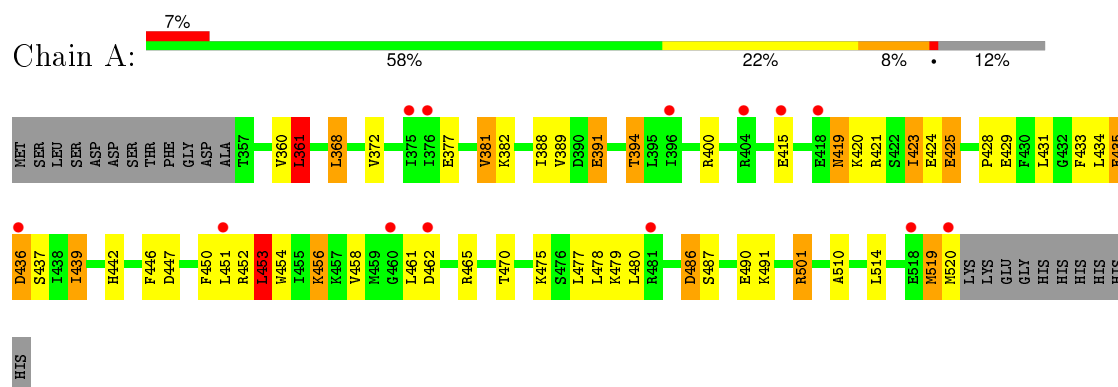
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	45	Total 45	O 45	0	0
2	B	41	Total 41	O 41	0	0

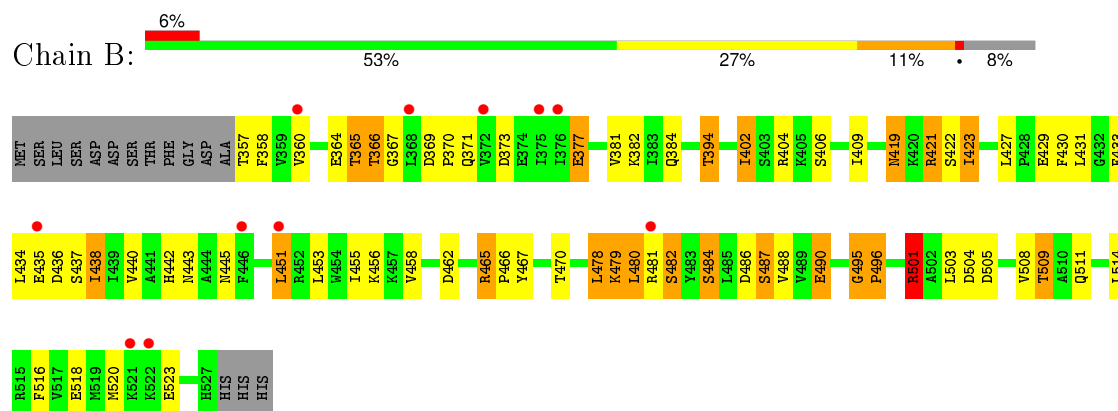
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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 ( $\text{RSRZ} > 2$ ). 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: DNA polymerase III polC-type



#### • Molecule 1: DNA polymerase III polC-type



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	55.70Å 124.94Å 143.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.50 19.99 – 2.50	Depositor EDS
% Data completeness (in resolution range)	96.0 (20.00-2.50) 96.0 (19.99-2.50)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	0.11	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.42 (at 2.50Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.229 , 0.298 0.224 , 0.288	Depositor DCC
$R_{free}$ test set	848 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	62.2	Xtriage
Anisotropy	0.036	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 55.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 16961 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	2809	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.99% 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

### 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	0.81	0/1356	0.96	2/1831 (0.1%)
1	B	0.89	1/1420 (0.1%)	0.95	2/1915 (0.1%)
All	All	0.85	1/2776 (0.0%)	0.95	4/3746 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	377	GLU	CG-CD	5.53	1.60	1.51

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	453	LEU	CA-CB-CG	8.93	135.83	115.30
1	A	361	LEU	CA-CB-CG	6.31	129.81	115.30
1	B	478	LEU	N-CA-C	5.72	126.44	111.00
1	B	501	ARG	CG-CD-NE	-5.16	100.97	111.80

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	436	ASP	Peptide
1	B	495	GLY	Peptide

## 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	1331	0	1351	47	0
1	B	1392	0	1407	57	0
2	A	45	0	0	3	0
2	B	41	0	0	10	0
All	All	2809	0	2758	99	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 18.

All (99) 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:B:480:LEU:HD22	1:B:482:SER:O	1.40	1.21
1:A:423:ILE:H	1:A:423:ILE:CD1	1.46	1.21
1:B:366:THR:CG2	1:B:373:ASP:HB2	1.75	1.16
1:A:423:ILE:H	1:A:423:ILE:HD13	0.93	1.08
1:A:423:ILE:N	1:A:423:ILE:HD13	1.72	1.03
1:B:366:THR:HG22	1:B:373:ASP:HB2	1.03	1.02
1:B:366:THR:HG22	1:B:373:ASP:CB	1.92	0.99
1:A:434:LEU:O	1:A:435:GLU:HB2	1.65	0.97
1:A:419:ASN:HD21	1:A:420:LYS:HE3	1.30	0.95
1:B:480:LEU:CD2	1:B:482:SER:O	2.14	0.94
1:B:364:GLU:HB2	1:B:377:GLU:HB3	1.49	0.91
1:B:481:ARG:HB3	2:B:66:HOH:O	1.71	0.89
1:A:368:LEU:HD22	2:A:65:HOH:O	1.75	0.84
1:A:423:ILE:N	1:A:423:ILE:CD1	2.30	0.83
1:A:435:GLU:HA	1:A:465:ARG:NH2	1.93	0.83
1:A:475:LYS:HE3	2:A:31:HOH:O	1.81	0.80
1:A:361:LEU:HD13	1:A:439:ILE:HD12	1.66	0.77
1:B:465:ARG:HH11	1:B:465:ARG:HB2	1.49	0.77
1:B:505:ASP:O	1:B:509:THR:HG23	1.88	0.72
1:A:361:LEU:CD1	1:A:439:ILE:HD12	2.20	0.71
1:A:419:ASN:ND2	1:A:420:LYS:HE3	2.04	0.71
1:B:435:GLU:HB2	2:B:63:HOH:O	1.89	0.70
1:B:495:GLY:HA3	2:B:45:HOH:O	1.91	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:478:LEU:O	1:B:479:LYS:HB2	1.92	0.69
1:B:394:THR:HG21	1:B:421:ARG:NH1	2.07	0.69
1:A:434:LEU:O	1:A:435:GLU:CB	2.39	0.68
1:B:523:GLU:HA	2:B:78:HOH:O	1.93	0.67
1:A:519:MET:CB	1:A:520:MET:HA	2.24	0.66
1:A:519:MET:HB3	1:A:520:MET:HA	1.78	0.64
1:A:419:ASN:H	1:A:419:ASN:HD22	1.46	0.63
1:B:409:ILE:HD13	2:B:64:HOH:O	1.98	0.63
1:B:402:ILE:HD11	1:B:406:SER:HB3	1.81	0.62
1:B:486:ASP:O	1:B:490:GLU:HG3	1.98	0.62
1:A:501:ARG:HD3	2:B:16:HOH:O	1.99	0.62
1:B:427:LEU:O	1:B:431:LEU:HD23	2.01	0.60
1:A:478:LEU:O	1:A:479:LYS:HB3	2.01	0.60
1:A:486:ASP:O	1:A:490:GLU:HG3	2.02	0.59
1:B:357:THR:N	2:B:81:HOH:O	2.36	0.58
1:A:394:THR:HG21	1:A:421:ARG:NH1	2.19	0.57
1:A:391:GLU:CG	1:B:503:LEU:HD11	2.35	0.56
1:A:442:HIS:HD2	1:A:470:THR:OG1	1.87	0.56
1:A:361:LEU:HD11	1:A:439:ILE:CD1	2.36	0.56
1:B:365:THR:HG23	1:B:367:GLY:H	1.70	0.56
1:A:435:GLU:O	1:A:436:ASP:CB	2.54	0.55
1:B:508:VAL:HA	1:B:511:GLN:HE21	1.71	0.55
1:B:394:THR:HG21	1:B:421:ARG:HH12	1.72	0.55
1:B:402:ILE:CD1	1:B:406:SER:HB3	2.36	0.55
1:B:360:VAL:HB	1:B:381:VAL:HG22	1.89	0.54
1:A:435:GLU:HA	1:A:465:ARG:HH21	1.73	0.53
1:A:477:LEU:O	1:A:478:LEU:HD23	2.08	0.53
1:A:361:LEU:CD1	1:A:439:ILE:CD1	2.86	0.53
1:B:366:THR:HG21	1:B:373:ASP:HB2	1.83	0.52
1:B:421:ARG:HD3	2:B:17:HOH:O	2.10	0.52
1:A:453:LEU:HD12	1:A:454:TRP:CD1	2.45	0.52
1:A:419:ASN:N	1:A:419:ASN:HD22	2.07	0.51
1:A:382:LYS:NZ	1:A:433:PHE:O	2.31	0.51
1:B:504:ASP:O	1:B:508:VAL:HG13	2.12	0.50
1:A:368:LEU:HD12	1:A:446:PHE:CE1	2.47	0.49
1:B:402:ILE:HG12	1:B:406:SER:CB	2.43	0.49
1:B:516:PHE:O	1:B:520:MET:HG3	2.12	0.49
1:A:510:ALA:HB2	1:B:381:VAL:HG21	1.94	0.49
1:B:480:LEU:HD21	1:B:487:SER:HB3	1.94	0.48
1:B:421:ARG:NH2	1:B:429:GLU:OE1	2.47	0.47
1:B:364:GLU:HB2	1:B:377:GLU:CB	2.34	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:423:ILE:HG12	2:B:18:HOH:O	2.14	0.47
1:B:508:VAL:HA	1:B:511:GLN:NE2	2.30	0.46
1:A:377:GLU:OE2	1:B:501:ARG:HB2	2.16	0.46
1:A:421:ARG:HH22	1:A:429:GLU:CD	2.19	0.46
1:B:360:VAL:HA	1:B:440:VAL:O	2.14	0.46
1:A:382:LYS:HG2	1:A:389:VAL:CG2	2.45	0.46
1:B:442:HIS:O	1:B:443:ASN:HB3	2.16	0.45
1:B:419:ASN:CG	1:B:419:ASN:O	2.55	0.45
1:B:480:LEU:HD21	1:B:487:SER:CB	2.46	0.45
1:B:431:LEU:N	1:B:431:LEU:CD2	2.79	0.45
1:B:451:LEU:O	1:B:455:ILE:HG13	2.17	0.45
1:A:456:LYS:HE2	1:A:462:ASP:OD1	2.18	0.44
1:A:425:GLU:O	1:A:428:PRO:HD2	2.17	0.44
1:A:480:LEU:HD21	1:A:491:LYS:HD3	1.99	0.44
1:B:358:PHE:CD2	1:B:438:ILE:HB	2.53	0.44
1:A:388:ILE:HD13	2:A:32:HOH:O	2.17	0.44
1:A:361:LEU:HD11	1:A:439:ILE:HD13	1.99	0.44
1:B:437:SER:O	1:B:465:ARG:HD3	2.18	0.44
1:A:391:GLU:HG2	1:B:503:LEU:HD11	1.99	0.44
1:B:369:ASP:HA	1:B:370:PRO:HD3	1.89	0.44
1:B:431:LEU:HD11	1:B:455:ILE:HD13	2.01	0.43
1:A:446:PHE:HD2	1:A:447:ASP:OD1	2.01	0.43
1:A:435:GLU:O	1:A:436:ASP:HB2	2.18	0.42
1:B:467:TYR:C	1:B:467:TYR:CD2	2.93	0.42
1:A:442:HIS:CD2	1:A:470:THR:OG1	2.70	0.42
1:B:431:LEU:N	1:B:431:LEU:HD22	2.33	0.42
1:B:365:THR:CG2	1:B:367:GLY:O	2.68	0.41
1:A:391:GLU:HG3	1:B:503:LEU:HD11	2.02	0.41
1:B:402:ILE:HG12	1:B:406:SER:HB2	2.02	0.41
1:A:381:VAL:CG2	1:A:388:ILE:HG13	2.50	0.41
1:B:430:PHE:O	1:B:433:PHE:HB3	2.20	0.41
1:A:452:ARG:HH11	1:A:452:ARG:HD3	1.76	0.41
1:B:465:ARG:HG3	1:B:466:PRO:HD2	2.03	0.40
1:B:358:PHE:N	1:B:358:PHE:CD1	2.89	0.40
1:B:382:LYS:HE3	2:B:68:HOH:O	2.21	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	162/186 (87%)	149 (92%)	10 (6%)	3 (2%)	10	16
1	B	169/186 (91%)	150 (89%)	15 (9%)	4 (2%)	7	11
All	All	331/372 (89%)	299 (90%)	25 (8%)	7 (2%)	9	14

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	435	GLU
1	B	496	PRO
1	B	484	SER
1	A	436	ASP
1	B	421	ARG
1	B	456	LYS
1	A	372	VAL

### 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	147/166 (89%)	121 (82%)	26 (18%)	2	4
1	B	153/166 (92%)	122 (80%)	31 (20%)	1	2
All	All	300/332 (90%)	243 (81%)	57 (19%)	2	3

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	360	VAL
1	A	361	LEU
1	A	368	LEU
1	A	381	VAL
1	A	391	GLU
1	A	394	THR
1	A	400	ARG
1	A	415	GLU
1	A	419	ASN
1	A	423	ILE
1	A	424	GLU
1	A	425	GLU
1	A	431	LEU
1	A	437	SER
1	A	439	ILE
1	A	450	PHE
1	A	451	LEU
1	A	453	LEU
1	A	456	LYS
1	A	458	VAL
1	A	461	LEU
1	A	486	ASP
1	A	487	SER
1	A	501	ARG
1	A	514	LEU
1	A	519	MET
1	B	365	THR
1	B	366	THR
1	B	371	GLN
1	B	384	GLN
1	B	394	THR
1	B	402	ILE
1	B	404	ARG
1	B	419	ASN
1	B	422	SER
1	B	423	ILE
1	B	434	LEU
1	B	438	ILE
1	B	445	ASN
1	B	451	LEU
1	B	453	LEU
1	B	458	VAL
1	B	462	ASP

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Mol	Chain	Res	Type
1	B	465	ARG
1	B	470	THR
1	B	479	LYS
1	B	480	LEU
1	B	482	SER
1	B	484	SER
1	B	487	SER
1	B	488	VAL
1	B	490	GLU
1	B	496	PRO
1	B	501	ARG
1	B	509	THR
1	B	514	LEU
1	B	518	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	419	ASN
1	A	442	HIS
1	A	511	GLN
1	B	445	ASN
1	B	511	GLN
1	B	526	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

There are no ligands in this entry.

## 5.7 Other polymers

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	164/186 (88%)	0.47	13 (7%) 15 17	45, 64, 82, 92	2 (1%)
1	B	171/186 (91%)	0.54	11 (6%) 23 25	48, 64, 79, 85	1 (0%)
All	All	335/372 (90%)	0.50	24 (7%) 18 20	45, 64, 81, 92	3 (0%)

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	520	MET	5.5
1	B	435	GLU	4.3
1	B	372	VAL	4.2
1	A	375	ILE	4.1
1	B	368	LEU	3.8
1	A	436	ASP	3.5
1	B	521	LYS	3.5
1	A	376	ILE	2.9
1	B	375	ILE	2.7
1	B	376	ILE	2.7
1	A	460	GLY	2.7
1	A	418	GLU	2.6
1	A	451	LEU	2.5
1	A	462	ASP	2.5
1	B	446	PHE	2.4
1	A	396	ILE	2.3
1	A	415	GLU	2.3
1	B	522	LYS	2.3
1	B	451	LEU	2.2
1	A	518	GLU	2.2
1	A	481	ARG	2.2
1	B	481	ARG	2.1
1	B	360	VAL	2.1
1	A	404	ARG	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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.