



# wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 29, 2025 – 02:10 PM EDT

PDB ID : 1JQJ / pdb\_00001jqj  
Title : Mechanism of Processivity Clamp Opening by the Delta Subunit Wrench of the Clamp Loader Complex of E. coli DNA Polymerase III: Structure of the beta-delta complex  
Authors : Jeruzalmi, D.; Yurieva, O.; Zhao, Y.; Young, M.; Stewart, J.; Hingorani, M.; O'Donnell, M.; Kuriyan, J.  
Deposited on : 2001-08-07  
Resolution : 2.90 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0rc1
Xtriage (Phenix)	:	2.0rc1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.006 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.43.1

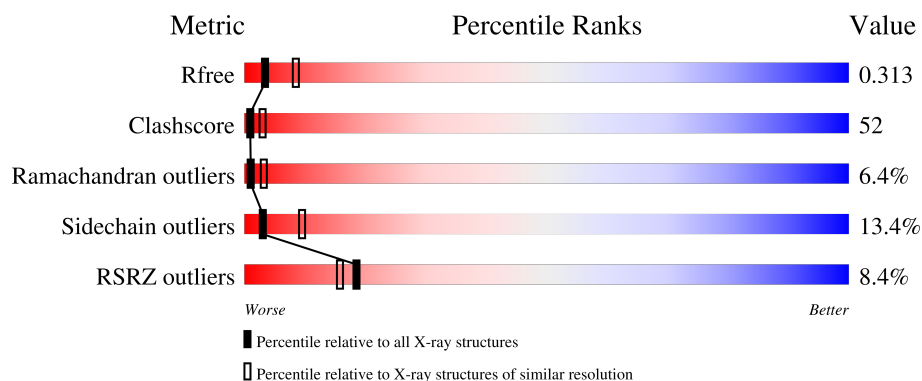
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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))
$R_{free}$	164625	2335 (2.90-2.90)
Clashscore	180529	2564 (2.90-2.90)
Ramachandran outliers	177936	2514 (2.90-2.90)
Sidechain outliers	177891	2516 (2.90-2.90)
RSRZ outliers	164620	2337 (2.90-2.90)

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.

Mol	Chain	Length	Quality of chain
1	A	366	<div> <div>8%</div> <div>31%</div> <div>54%</div> <div>12%</div> <div>.</div> </div>
1	B	366	<div> <div>11%</div> <div>33%</div> <div>53%</div> <div>13%</div> <div>.</div> </div>
2	C	343	<div> <div>6%</div> <div>27%</div> <div>50%</div> <div>15%</div> <div>.</div> </div>
2	D	343	<div> <div>8%</div> <div>30%</div> <div>51%</div> <div>12%</div> <div>5%</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 10860 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, beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	366	Total	C	N	O	S	0	0	0
			2837	1780	498	540	19			
1	B	366	Total	C	N	O	S	0	0	0
			2837	1780	498	540	19			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	272	ALA	ILE	engineered mutation	UNP P0A988
A	273	ALA	LEU	engineered mutation	UNP P0A988
B	272	ALA	ILE	engineered mutation	UNP P0A988
B	273	ALA	LEU	engineered mutation	UNP P0A988

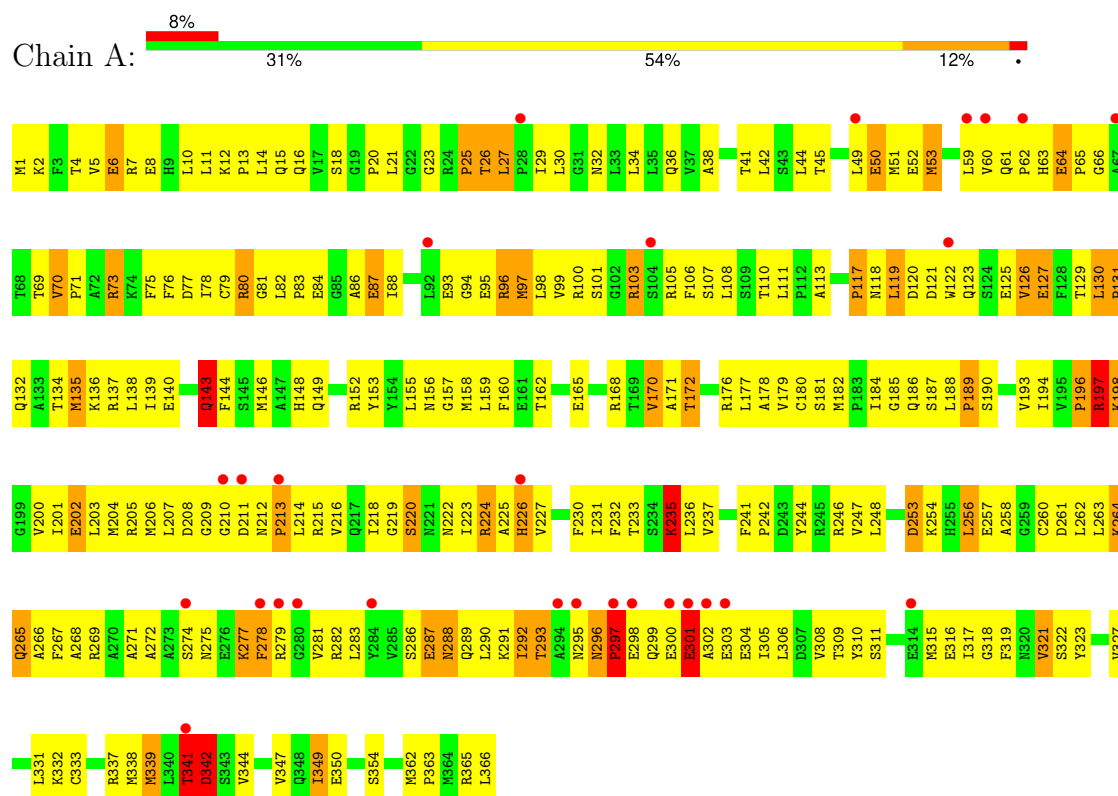
- Molecule 2 is a protein called DNA polymerase III, delta subunit.

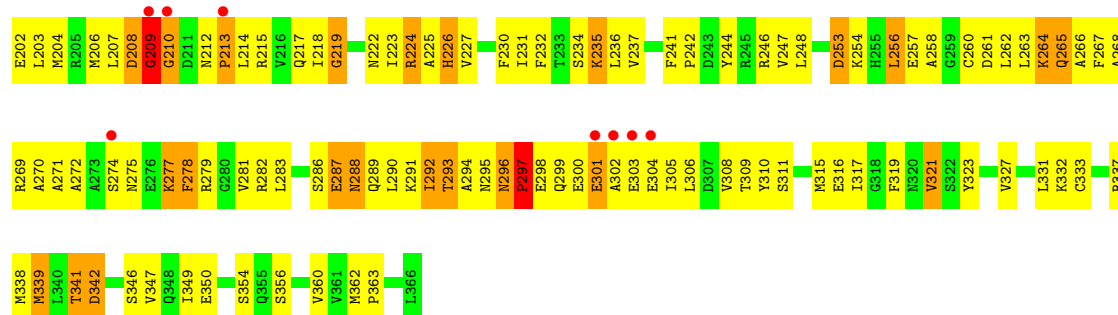
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	328	Total	C	N	O	S	0	0	0
			2606	1650	474	472	10			
2	D	325	Total	C	N	O	S	0	0	0
			2580	1632	469	469	10			

### 3 Residue-property plots

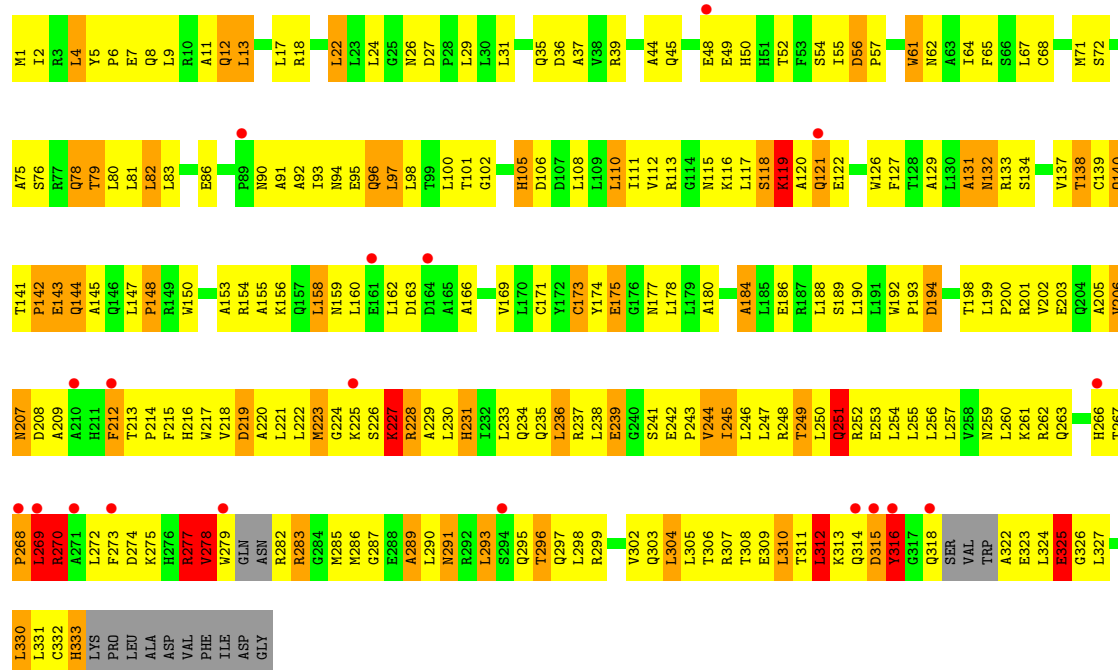
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: DNA polymerase III, beta chain

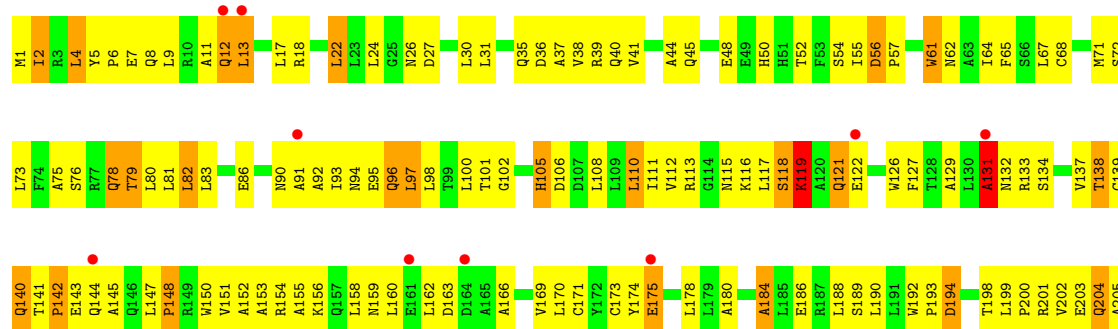


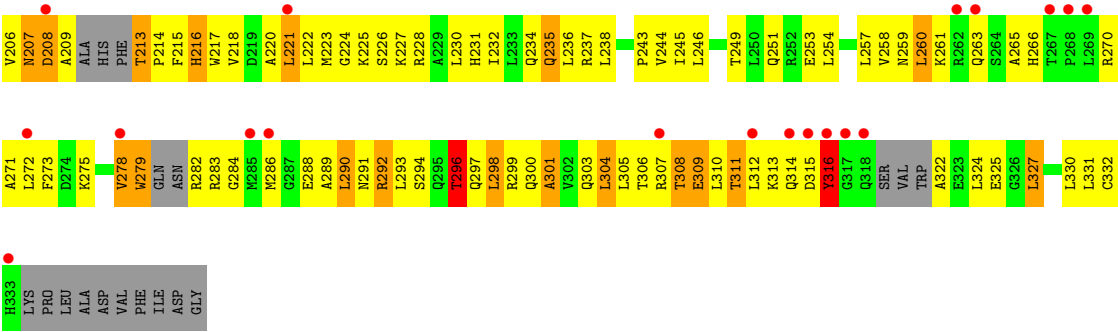


• Molecule 2: DNA polymerase III, delta subunit



• Molecule 2: DNA polymerase III, delta subunit





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	198.84Å 99.29Å 113.02Å 90.00° 119.17° 90.00°	Depositor
Resolution (Å)	500.00 – 2.90 98.69 – 2.90	Depositor EDS
% Data completeness (in resolution range)	(Not available) (500.00-2.90) 96.5 (98.69-2.90)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.11	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.86 (at 2.88Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.266 , 0.308 0.276 , 0.313	Depositor DCC
$R_{free}$ test set	2129 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	58.3	Xtriage
Anisotropy	0.414	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 59.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	10860	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.71% 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, 0.333 respectively for untwinned datasets, and 0.375, 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	0.59	1/2886 (0.0%)	1.07	17/3907 (0.4%)
1	B	0.54	1/2886 (0.0%)	1.05	15/3907 (0.4%)
2	C	0.90	3/2649 (0.1%)	1.41	28/3594 (0.8%)
2	D	0.45	0/2620	1.06	17/3553 (0.5%)
All	All	0.64	5/11041 (0.0%)	1.15	77/14961 (0.5%)

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	A	0	1
1	B	0	1
2	C	0	2
All	All	0	4

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	269	LEU	C-N	-28.53	0.93	1.33
2	C	278	VAL	N-CA	22.34	1.74	1.46
2	C	270	ARG	CB-CG	-9.06	1.25	1.52
1	A	125	GLU	C-N	-6.31	1.30	1.33
1	B	209	GLY	CA-C	-5.51	1.44	1.51

The worst 5 of 77 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	269	LEU	O-C-N	-27.04	89.37	122.89
2	C	269	LEU	CA-C-N	26.77	172.67	121.54
2	C	269	LEU	C-N-CA	26.77	172.67	121.54
2	C	278	VAL	N-CA-C	18.21	147.22	109.34

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Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	B	341	THR	CA-C-N	14.95	146.06	122.59

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	341	THR	Peptide
1	B	209	GLY	Mainchain
2	C	269	LEU	Peptide
2	C	277	ARG	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	2837	0	2849	289	1
1	B	2837	0	2849	272	0
2	C	2606	0	2662	283	2
2	D	2580	0	2641	300	1
All	All	10860	0	11001	1126	2

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 52.

The worst 5 of 1126 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance ( $\text{\AA}$ )	Clash overlap ( $\text{\AA}$ )
2:C:278:VAL:N	2:C:278:VAL:CA	1.74	1.51
2:D:304:LEU:HA	2:D:307:ARG:HD2	1.15	1.11
1:B:136:LYS:HG3	1:B:204:MET:HE1	1.39	1.05
2:D:304:LEU:CA	2:D:307:ARG:HD2	1.85	1.04
1:A:1:MET:HB3	1:A:66:GLY:HA3	1.39	1.04

All (2) 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:C:315:ASP:OD2	2:D:315:ASP:OD2[2_647]	1.79	0.41
1:A:279:ARG:NH1	2:C:132:ASN:OD1[2_656]	1.81	0.39

## 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	364/366 (100%)	281 (77%)	62 (17%)	21 (6%)	1	4
1	B	364/366 (100%)	284 (78%)	59 (16%)	21 (6%)	1	4
2	C	322/343 (94%)	234 (73%)	62 (19%)	26 (8%)	1	2
2	D	317/343 (92%)	229 (72%)	69 (22%)	19 (6%)	1	4
All	All	1367/1418 (96%)	1028 (75%)	252 (18%)	87 (6%)	1	3

5 of 87 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	6	GLU
1	A	26	THR
1	A	119	LEU
1	B	6	GLU
1	B	26	THR

### 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	311/311 (100%)	270 (87%)	41 (13%)	3	10
1	B	311/311 (100%)	274 (88%)	37 (12%)	4	13
2	C	278/291 (96%)	234 (84%)	44 (16%)	2	6
2	D	276/291 (95%)	240 (87%)	36 (13%)	3	11
All	All	1176/1204 (98%)	1018 (87%)	158 (13%)	3	9

5 of 158 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	304	LEU
2	D	190	LEU
2	C	325	GLU
2	D	97	LEU
2	D	292	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	266	HIS
2	D	94	ASN
2	C	303	GLN
2	D	69	GLN
2	D	105	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 oligosaccharides 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	269:LEU	C	270:ARG	N	0.93

## 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	366/366 (100%)	0.44	28 (7%) 21 18	26, 72, 106, 122	0
1	B	366/366 (100%)	0.66	42 (11%) 11 9	30, 81, 135, 149	0
2	C	328/343 (95%)	0.26	19 (5%) 30 26	21, 60, 132, 168	0
2	D	325/343 (94%)	0.56	28 (8%) 18 15	22, 82, 142, 160	0
All	All	1385/1418 (97%)	0.49	117 (8%) 18 16	21, 73, 132, 168	0

The worst 5 of 117 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	131	ALA	5.9
2	D	318	GLN	4.7
1	A	303	GLU	4.7
2	C	225	LYS	4.6
1	B	94	GLY	4.6

### 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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.