



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 05:04 PM GMT

PDB ID : 4GZZ  
Title : Crystal structures of bacterial RNA Polymerase paused elongation complexes  
Authors : Weixlbaumer, A.; Leon, K.; Landick, R.; Darst, S.A.  
Deposited on : 2012-09-06  
Resolution : 4.29 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  
<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

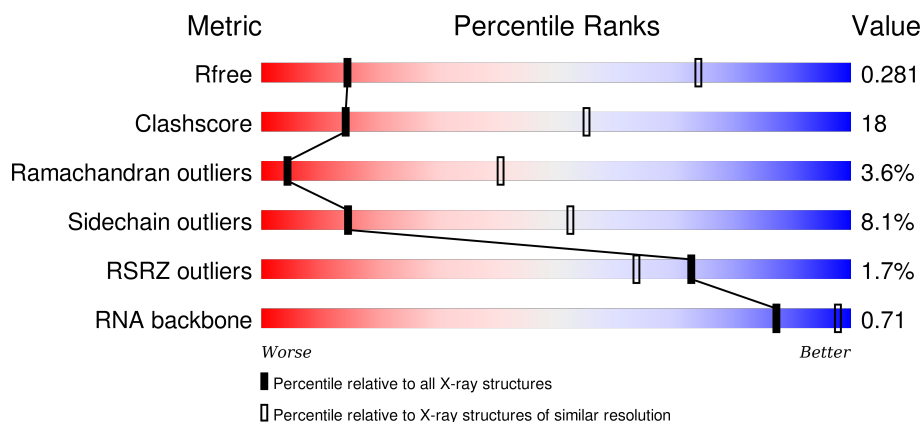
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 4.29 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	1059 (5.00-3.60)
Clashscore	102246	1166 (5.00-3.60)
Ramachandran outliers	100387	1106 (5.00-3.60)
Sidechain outliers	100360	1089 (5.00-3.60)
RSRZ outliers	91569	1062 (5.00-3.60)
RNA backbone	2183	1087 (5.60-2.80)

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	315	<div> <div style="width: 2%; background-color: red;"></div> <div style="width: 42%; background-color: green;"></div> <div style="width: 26%; background-color: yellow;"></div> <div style="width: 29%; background-color: grey;"></div> </div>
1	B	315	<div> <div style="width: 48%; background-color: green;"></div> <div style="width: 22%; background-color: yellow;"></div> <div style="width: 29%; background-color: grey;"></div> </div>
2	C	1119	<div> <div style="width: 2%; background-color: red;"></div> <div style="width: 54%; background-color: green;"></div> <div style="width: 38%; background-color: yellow;"></div> <div style="width: 5%; background-color: orange;"></div> <div style="width: 1%; background-color: grey;"></div> </div>
3	D	1534	<div> <div style="width: 2%; background-color: red;"></div> <div style="width: 50%; background-color: green;"></div> <div style="width: 34%; background-color: yellow;"></div> <div style="width: 5%; background-color: orange;"></div> <div style="width: 11%; background-color: grey;"></div> </div>

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Mol	Chain	Length	Quality of chain
4	E	99	
5	N	13	
6	R	16	
7	T	22	

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
8	ZN	D	1602	-	-	-	X

## 2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 24400 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-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	223	Total	C	N	O	S	0	0	0
			1759	1123	306	328	2			
1	B	223	Total	C	N	O	S	0	0	0
			1759	1123	306	328	2			

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	1083	Total	C	N	O	S	0	0	0
			8548	5412	1524	1588	24			

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	1358	Total	C	N	O	S	0	0	0
			10714	6780	1900	2001	33			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	1525	HIS	-	EXPRESSION TAG	UNP Q8RQE8
D	1526	HIS	-	EXPRESSION TAG	UNP Q8RQE8
D	1527	HIS	-	EXPRESSION TAG	UNP Q8RQE8
D	1528	HIS	-	EXPRESSION TAG	UNP Q8RQE8
D	1529	HIS	-	EXPRESSION TAG	UNP Q8RQE8
D	1530	HIS	-	EXPRESSION TAG	UNP Q8RQE8
D	1531	HIS	-	EXPRESSION TAG	UNP Q8RQE8
D	1532	HIS	-	EXPRESSION TAG	UNP Q8RQE8
D	1533	HIS	-	EXPRESSION TAG	UNP Q8RQE8
D	1534	HIS	-	EXPRESSION TAG	UNP Q8RQE8

- Molecule 4 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	93	Total	C	N	O	S	0	0	0
			754	481	131	138	4			

- Molecule 5 is a DNA chain called non-template DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	N	11	Total	C	N	O	P	0	0	0
			225	107	43	64	11			

- Molecule 6 is a RNA chain called RNA transcript.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	R	9	Total	C	N	O	P	0	0	0
			191	85	31	66	9			

- Molecule 7 is a DNA chain called template DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	T	22	Total	C	N	O	P	0	0	0
			447	213	81	131	22			

- Molecule 8 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	D	2	Total	Zn	0	0
			2	2		

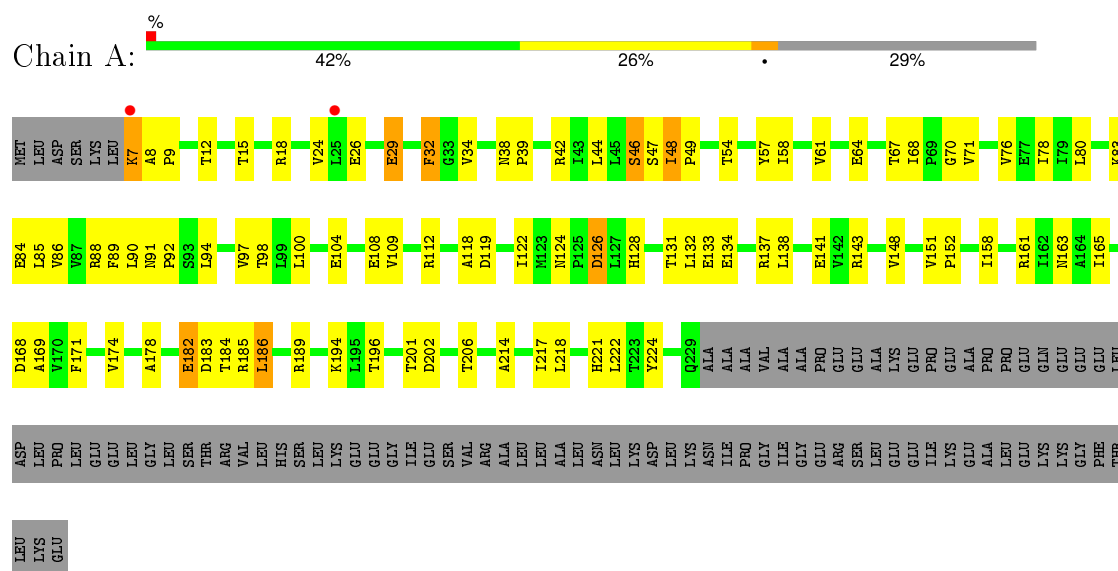
- Molecule 9 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	D	1	Total	Mg	0	0
			1	1		

### 3 Residue-property plots

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.

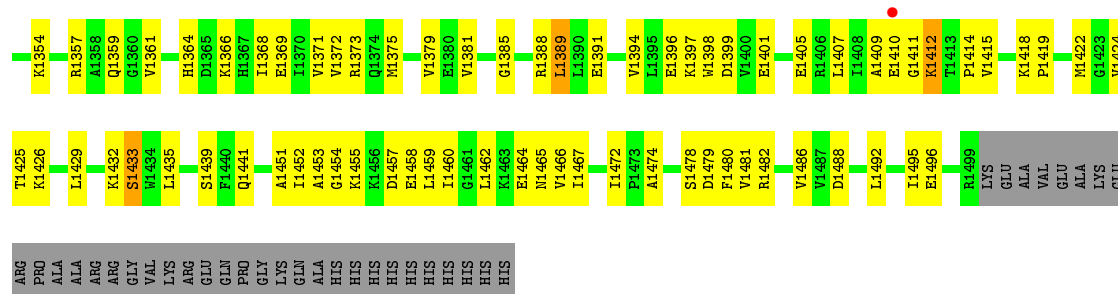
#### • Molecule 1: DNA-directed RNA polymerase subunit alpha



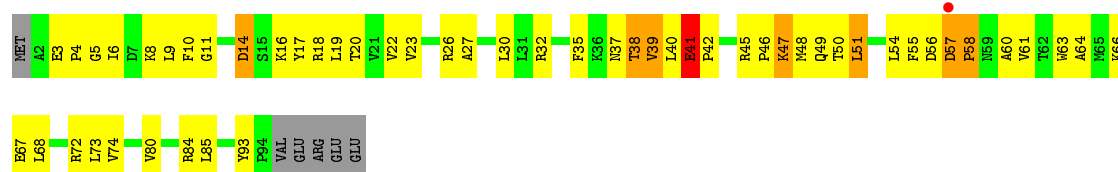








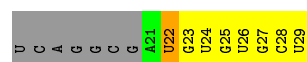
- Molecule 4: DNA-directed RNA polymerase subunit omega



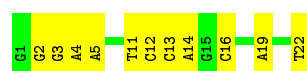
- Molecule 5: non-template DNA



- Molecule 6: RNA transcript



- Molecule 7: template DNA



## 4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	286.55Å 286.55Å 199.41Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	38.78 – 4.29 38.79 – 4.29	Depositor EDS
% Data completeness (in resolution range)	99.0 (38.78-4.29) 87.8 (38.79-4.29)	Depositor EDS
$R_{merge}$	0.44	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.90 (at 4.28Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, $R_{free}$	0.234 , 0.285 0.232 , 0.281	Depositor DCC
$R_{free}$ test set	1848 reflections (5.05%)	DCC
Wilson B-factor (Å <sup>2</sup> )	166.9	Xtriage
Anisotropy	0.112	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
Estimated twinning fraction	0.047 for h,-h-k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	0 of 41308 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	24400	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	121.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.16% 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: ZN, MG

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	0.26	0/1791	0.47	0/2436
1	B	0.28	0/1791	0.47	0/2436
2	C	0.28	0/8711	0.51	0/11784
3	D	0.28	0/10897	0.50	1/14726 (0.0%)
4	E	0.29	0/768	0.55	0/1035
5	N	0.44	0/252	1.08	0/386
6	R	0.21	0/212	0.77	0/328
7	T	0.44	0/500	1.08	0/768
All	All	0.29	0/24922	0.53	1/33899 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	705	ALA	C-N-CD	5.17	139.25	128.40

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	1759	0	1805	65	0
1	B	1759	0	1805	50	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	8548	0	8650	371	0
3	D	10714	0	10936	408	1
4	E	754	0	769	40	0
5	N	225	0	124	3	0
6	R	191	0	95	10	0
7	T	447	0	248	10	0
8	D	2	0	0	0	0
9	D	1	0	0	0	0
All	All	24400	0	24432	882	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 18.

The worst 5 of 882 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)
2:C:428:ARG:HH12	3:D:1086:LEU:HD21	1.24	0.98
2:C:610:ARG:HH11	2:C:610:ARG:HG3	1.27	0.96
2:C:846:LYS:NZ	6:R:29:U:OP1	1.99	0.96
1:B:188:GLN:O	3:D:646:LYS:NZ	2.00	0.94
1:A:80:LEU:HD21	2:C:573:ARG:HH11	1.34	0.92

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)
1:B:143:ARG:NH1	3:D:1297:GLU:OE2[3_455]	2.18	0.02

## 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	221/315 (70%)	186 (84%)	29 (13%)	6 (3%)	6	47
1	B	221/315 (70%)	193 (87%)	25 (11%)	3 (1%)	14	59
2	C	1077/1119 (96%)	897 (83%)	144 (13%)	36 (3%)	5	43
3	D	1352/1534 (88%)	1097 (81%)	198 (15%)	57 (4%)	3	35
4	E	91/99 (92%)	73 (80%)	13 (14%)	5 (6%)	2	30
All	All	2962/3382 (88%)	2446 (83%)	409 (14%)	107 (4%)	4	40

5 of 107 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	118	ALA
1	A	184	THR
2	C	2	GLU
2	C	111	ASP
2	C	164	PRO

### 5.3.2 Protein sidechains ⓘ

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	196/273 (72%)	188 (96%)	8 (4%)	37	72
1	B	196/273 (72%)	189 (96%)	7 (4%)	42	76
2	C	912/941 (97%)	837 (92%)	75 (8%)	14	51
3	D	1147/1289 (89%)	1044 (91%)	103 (9%)	12	47
4	E	82/88 (93%)	70 (85%)	12 (15%)	4	26
All	All	2533/2864 (88%)	2328 (92%)	205 (8%)	15	52

5 of 205 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	D	58	CYS
3	D	178	LEU
3	D	1433	SER

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Mol	Chain	Res	Type
3	D	68	PHE
3	D	124	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	434	HIS
2	C	609	ASN
3	D	1031	ASN
2	C	431	HIS
3	D	462	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
6	R	8/16 (50%)	1 (12%)	0

All (1) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
6	R	22	U

There are no RNA pucker outliers to report.

## 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 3 ligands modelled in this entry, 3 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

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	223/315 (70%)	-0.11	2 (0%) 85 80	52, 116, 169, 205	0
1	B	223/315 (70%)	-0.12	1 (0%) 93 90	53, 107, 163, 198	0
2	C	1083/1119 (96%)	-0.13	12 (1%) 82 76	34, 108, 177, 264	0
3	D	1358/1534 (88%)	-0.01	35 (2%) 59 49	31, 110, 196, 250	0
4	E	93/99 (93%)	0.05	1 (1%) 82 76	65, 121, 179, 228	0
5	N	11/13 (84%)	0.35	1 (9%) 11 9	340, 362, 386, 405	0
6	R	9/16 (56%)	-0.21	0 100 100	201, 206, 235, 243	0
7	T	22/22 (100%)	-0.09	0 100 100	219, 336, 388, 406	0
All	All	3022/3433 (88%)	-0.07	52 (1%) 73 63	31, 111, 192, 406	0

The worst 5 of 52 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	D	368	VAL	6.0
3	D	1311	LEU	5.1
3	D	1279	GLY	4.8
3	D	1276	GLU	4.4
2	C	372	LEU	4.3

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

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

### 6.3 Carbohydrates ⓘ

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
8	ZN	D	1602	1/1	0.98	0.29	2.20	70,70,70,70	0
8	ZN	D	1601	1/1	0.92	0.12	-1.39	70,70,70,70	0
9	MG	D	1603	1/1	0.93	0.22	-	70,70,70,70	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.