



# wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 08:25 AM GMT

PDB ID : 1TT5  
Title : Structure of APPBP1-UBA3-Ubc12N26:a unique E1-E2 interaction required for optimal conjugation of the ubiquitin-like protein NEDD8  
Authors : Huang, D.T.; Miller, D.W.; Mathew, R.; Cassell, R.; Holton, J.M.; Roussel, M.F.; Schulman, B.A.  
Deposited on : 2004-06-21  
Resolution : 2.60 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

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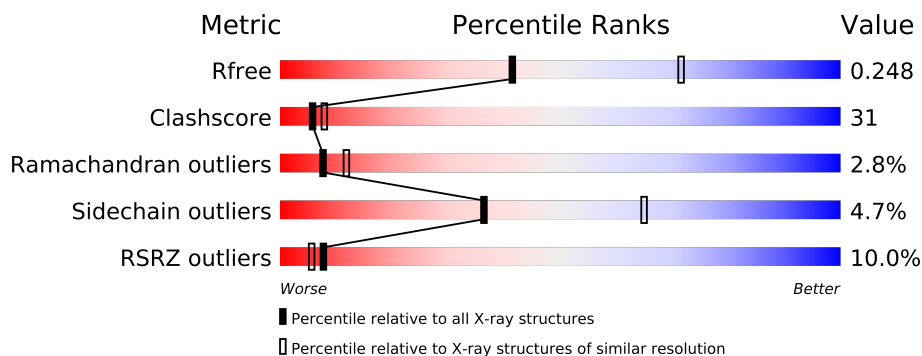
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.60 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))
$R_{free}$	66092	1718 (2.60-2.60)
Clashscore	79885	2154 (2.60-2.60)
Ramachandran outliers	78287	2113 (2.60-2.60)
Sidechain outliers	78261	2113 (2.60-2.60)
RSRZ outliers	66119	1718 (2.60-2.60)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	531	
1	C	531	
2	B	434	
2	D	434	
3	E	26	
3	F	26	

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 14637 atoms, of which 0 are hydrogen and 0 are deuterium.

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 amyloid protein-binding protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	522	Total	C	N	O	S	4	0	0
			4108	2600	701	792	15			
1	C	512	Total	C	N	O	S	4	0	0
			4020	2546	684	775	15			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	CLONING ARTIFACT	GB 4502169
A	0	SER	-	CLONING ARTIFACT	GB 4502169
A	?	-	ASN	DELETION	GB 4502169
A	?	-	GLU	DELETION	GB 4502169
A	?	-	ASN	DELETION	GB 4502169
A	?	-	GLY	DELETION	GB 4502169
A	?	-	ALA	DELETION	GB 4502169
C	-1	GLY	-	CLONING ARTIFACT	GB 4502169
C	0	SER	-	CLONING ARTIFACT	GB 4502169
C	?	-	ASN	DELETION	GB 4502169
C	?	-	GLU	DELETION	GB 4502169
C	?	-	ASN	DELETION	GB 4502169
C	?	-	GLY	DELETION	GB 4502169
C	?	-	ALA	DELETION	GB 4502169

- Molecule 2 is a protein called ubiquitin-activating enzyme E1C isoform 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	414	Total	C	N	O	S	0	0	0
			3152	2010	540	584	18			
2	D	395	Total	C	N	O	S	12	0	0
			2866	1806	503	540	17			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	9	MET	-	CLONING ARTIFACT	GB 38045942
B	10	LYS	-	CLONING ARTIFACT	GB 38045942
B	11	LEU	-	CLONING ARTIFACT	GB 38045942
D	9	MET	-	CLONING ARTIFACT	GB 38045942
D	10	LYS	-	CLONING ARTIFACT	GB 38045942
D	11	LEU	-	CLONING ARTIFACT	GB 38045942

- Molecule 3 is a protein called Ubiquitin-conjugatingenzyme E2 M.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	13	Total 108	C 72	N 19	O 16	S 1	2	0	0
3	F	10	Total 83	C 55	N 15	O 13		9	0	0

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Zn	0	0
			1	1		
4	D	1	Total	Zn	0	0
			1	1		

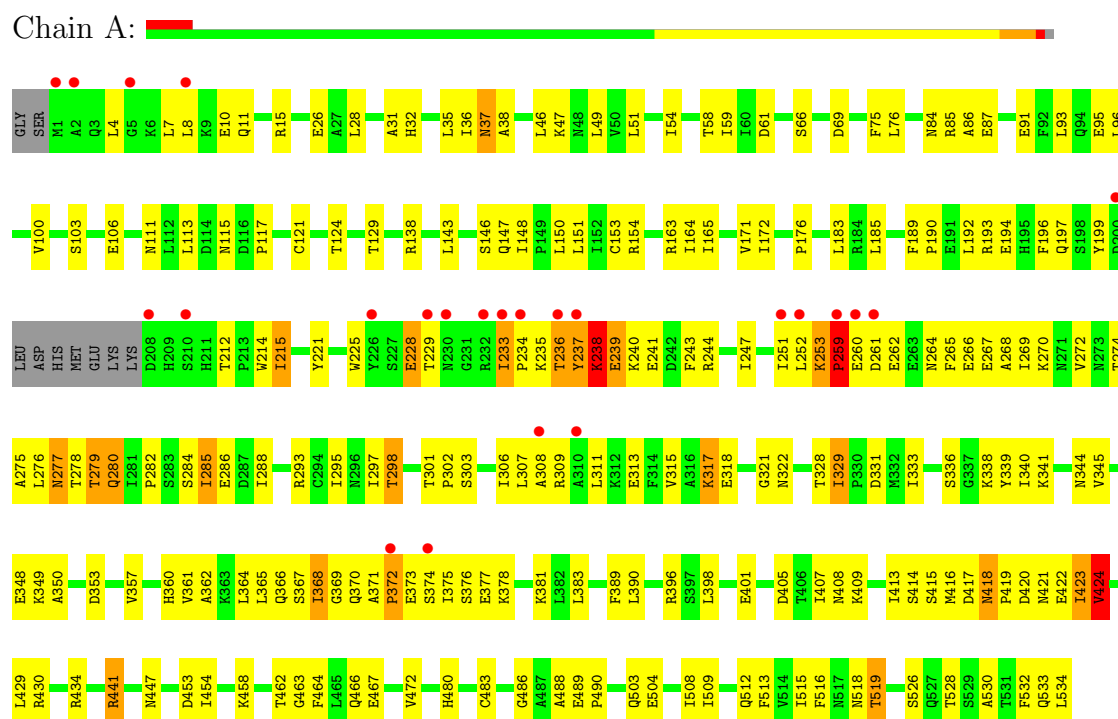
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	105	Total	O	0	0
			105	105		
5	B	114	Total	O	0	0
			114	114		
5	C	45	Total	O	0	0
			45	45		
5	D	29	Total	O	0	0
			29	29		
5	E	5	Total	O	0	0
			5	5		

### 3 Residue-property plots

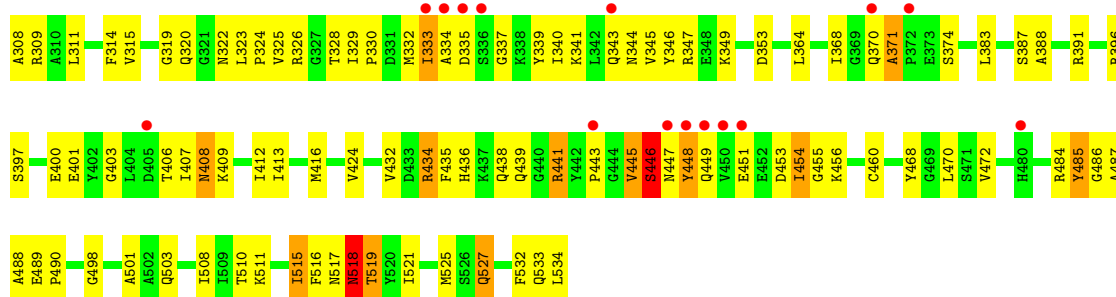
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: amyloid protein-binding protein 1



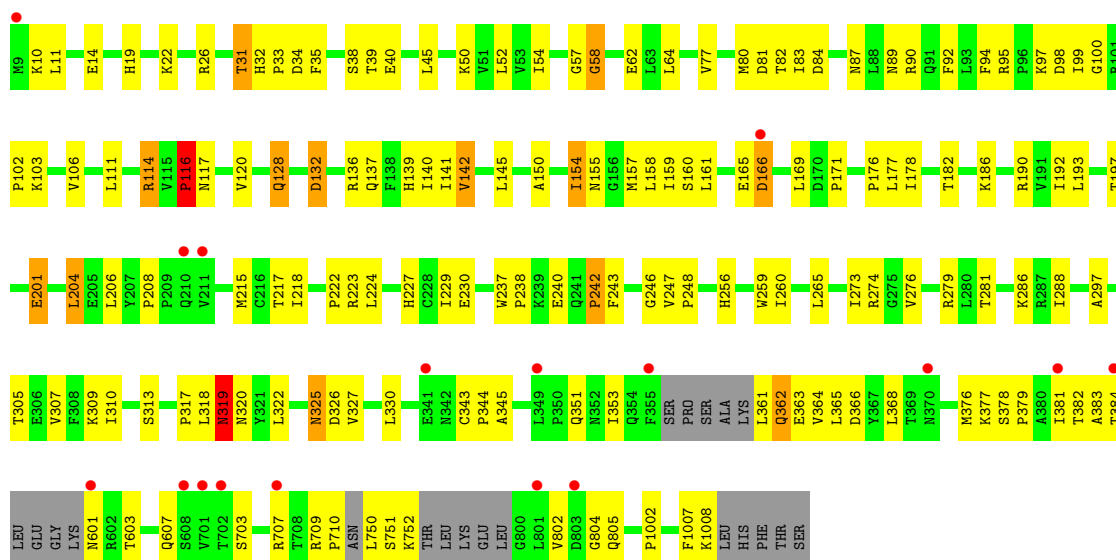
- Molecule 1: amyloid protein-binding protein 1

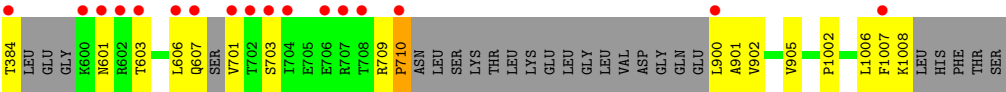




• Molecule 2: ubiquitin-activating enzyme E1C isoform 1

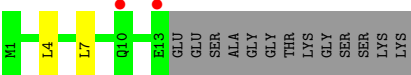
Chain B:





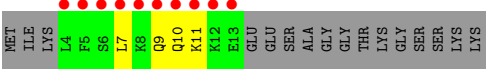
• Molecule 3: Ubiquitin-conjugatingenzyme E2 M

Chain E: 



• Molecule 3: Ubiquitin-conjugatingenzyme E2 M

Chain F: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	92.41Å 122.77Å 195.91Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	18.00 – 2.60 18.10 – 2.61	Depositor EDS
% Data completeness (in resolution range)	(Not available) (18.00-2.60) 98.9 (18.10-2.61)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.68 (at 2.63Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.237 , 0.279 0.249 , 0.248	Depositor DCC
$R_{free}$ test set	3377 reflections (5.02%)	DCC
Wilson B-factor (Å <sup>2</sup> )	55.4	Xtriage
Anisotropy	0.374	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 40.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 67222 reflections (0.001%)	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	14637	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.29% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.



## 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	0.44	1/4187 (0.0%)	0.69	9/5664 (0.2%)
1	C	0.34	0/4099	0.59	0/5547
2	B	0.42	0/3219	0.69	3/4380 (0.1%)
2	D	0.41	0/2923	0.74	4/3962 (0.1%)
3	E	0.37	0/108	0.50	0/139
3	F	0.63	0/83	0.83	0/107
All	All	0.40	1/14619 (0.0%)	0.67	16/19799 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	237	TYR	CB-CG	-5.14	1.44	1.51

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	253	ASP	CB-CG-OD2	-11.96	107.54	118.30
1	A	233	ILE	N-CA-C	8.36	133.57	111.00
1	A	279	THR	N-CA-C	-7.06	91.94	111.00
2	D	710	PRO	N-CA-CB	6.54	111.15	103.30
1	A	239	GLU	N-CA-C	-6.06	94.63	111.00

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens

added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4108	0	4038	288	0
1	C	4020	0	3937	264	0
2	B	3152	0	2998	165	0
2	D	2866	0	2608	212	0
3	E	108	0	128	3	0
3	F	83	0	92	6	0
4	B	1	0	0	0	0
4	D	1	0	0	0	0
5	A	105	0	0	12	0
5	B	114	0	0	9	0
5	C	45	0	0	4	0
5	D	29	0	0	3	0
5	E	5	0	0	0	0
All	All	14637	0	13801	882	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 31.

The worst 5 of 882 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:518:ASN:ND2	1:A:534:LEU:H	1.07	1.41
1:A:518:ASN:ND2	1:A:534:LEU:N	1.76	1.31
1:A:225:TRP:NE1	1:A:233:ILE:HD11	1.58	1.19
1:A:282:PRO:HB2	1:A:285:ILE:HD13	1.19	1.18
1:A:235:LYS:HB2	1:A:239:GLU:HG3	1.22	1.17

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

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	518/531 (98%)	477 (92%)	30 (6%)	11 (2%)	11	19
1	C	508/531 (96%)	435 (86%)	56 (11%)	17 (3%)	6	9
2	B	404/434 (93%)	362 (90%)	33 (8%)	9 (2%)	10	18
2	D	385/434 (89%)	330 (86%)	41 (11%)	14 (4%)	5	7
3	E	11/26 (42%)	11 (100%)	0	0	100	100
3	F	8/26 (31%)	7 (88%)	1 (12%)	0	100	100
All	All	1834/1982 (92%)	1622 (88%)	161 (9%)	51 (3%)	8	12

5 of 51 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	236	THR
2	B	384	THR
1	C	38	ALA
1	C	227	SER
1	C	228	GLU

### 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	445/462 (96%)	427 (96%)	18 (4%)	42	73
1	C	435/462 (94%)	415 (95%)	20 (5%)	37	66
2	B	325/383 (85%)	308 (95%)	17 (5%)	32	59
2	D	278/383 (73%)	263 (95%)	15 (5%)	31	57
3	E	12/22 (54%)	12 (100%)	0	100	100
3	F	9/22 (41%)	9 (100%)	0	100	100
All	All	1504/1734 (87%)	1434 (95%)	70 (5%)	36	65

5 of 70 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	201	GLU
1	C	103	SER

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*Continued from previous page...*

Mol	Chain	Res	Type
2	D	260	ILE
2	B	204	LEU
1	C	69	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 62 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	351	GLN
1	C	147	GLN
2	D	256	HIS
1	C	111	ASN
1	C	195	HIS

### 5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

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.

## 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(Å²)	Q<0.9
1	A	521/531 (98%)	-0.01	24 (4%)	31	27	25, 52, 111, 130	0
1	C	511/531 (96%)	0.33	44 (8%)	11	8	38, 74, 122, 143	0
2	B	414/434 (95%)	-0.10	17 (4%)	35	32	25, 44, 107, 125	0
2	D	392/434 (90%)	0.83	89 (22%)	1	1	34, 82, 141, 160	0
3	E	13/26 (50%)	0.67	2 (15%)	3	2	58, 69, 83, 88	1 (7%)
3	F	10/26 (38%)	4.16	10 (100%)	0	0	105, 108, 110, 112	3 (30%)
All	All	1861/1982 (93%)	0.27	186 (9%)	8	5	25, 61, 126, 160	4 (0%)

The worst 5 of 186 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	33	PRO	10.3
2	D	259	TRP	8.1
2	D	219	ALA	7.7
1	A	236	THR	7.3
2	D	606	LEU	7.2

### 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

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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	ZN	B	1014	1/1	0.08	-1.56	49,49,49,49	0
4	ZN	D	1014	1/1	0.10	-3.05	62,62,62,62	0

## 6.5 Other polymers

There are no such residues in this entry.