



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 01:57 pm GMT

PDB ID : 2F6J  
Title : Crystal structure of PHD finger-linker-bromodomain fragment of human BPTF in the H3(1-15)K4me3 bound state  
Authors : Li, H.; Patel, D.J.  
Deposited on : 2005-11-29  
Resolution : 2.00 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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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) : recalc28949

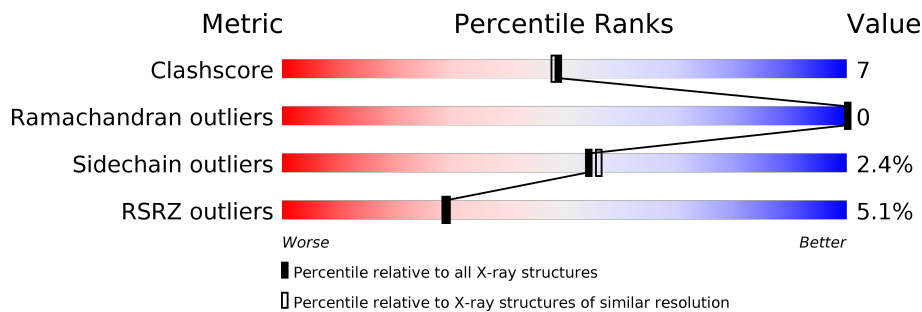
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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))
Clashscore	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)
RSRZ outliers	101464	6696 (2.00-2.00)

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	174	
1	B	174	
1	C	174	
2	P	15	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4643 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 bromodomain PHD finger transcription factor.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	168	Total	C	N	O	S	Se	0	0	0
			1386	885	222	265	9	5			
1	B	167	Total	C	N	O	S	Se	0	0	0
			1378	881	221	262	9	5			
1	C	166	Total	C	N	O	S	Se	0	0	0
			1371	877	220	260	9	5			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	CLONING ARTIFACT	UNP Q7Z7D6
A	2	PRO	-	CLONING ARTIFACT	UNP Q7Z7D6
A	3	LEU	-	CLONING ARTIFACT	UNP Q7Z7D6
A	4	GLY	-	CLONING ARTIFACT	UNP Q7Z7D6
A	5	SER	-	CLONING ARTIFACT	UNP Q7Z7D6
A	63	MSE	MET	MODIFIED RESIDUE	UNP Q7Z7D6
A	89	MSE	MET	MODIFIED RESIDUE	UNP Q7Z7D6
A	113	MSE	MET	MODIFIED RESIDUE	UNP Q7Z7D6
A	118	MSE	MET	MODIFIED RESIDUE	UNP Q7Z7D6
A	137	MSE	MET	MODIFIED RESIDUE	UNP Q7Z7D6
B	1	GLY	-	CLONING ARTIFACT	UNP Q7Z7D6
B	2	PRO	-	CLONING ARTIFACT	UNP Q7Z7D6
B	3	LEU	-	CLONING ARTIFACT	UNP Q7Z7D6
B	4	GLY	-	CLONING ARTIFACT	UNP Q7Z7D6
B	5	SER	-	CLONING ARTIFACT	UNP Q7Z7D6
B	63	MSE	MET	MODIFIED RESIDUE	UNP Q7Z7D6
B	89	MSE	MET	MODIFIED RESIDUE	UNP Q7Z7D6
B	113	MSE	MET	MODIFIED RESIDUE	UNP Q7Z7D6
B	118	MSE	MET	MODIFIED RESIDUE	UNP Q7Z7D6
B	137	MSE	MET	MODIFIED RESIDUE	UNP Q7Z7D6
C	1	GLY	-	CLONING ARTIFACT	UNP Q7Z7D6
C	2	PRO	-	CLONING ARTIFACT	UNP Q7Z7D6
C	3	LEU	-	CLONING ARTIFACT	UNP Q7Z7D6

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Chain	Residue	Modelled	Actual	Comment	Reference
C	4	GLY	-	CLONING ARTIFACT	UNP Q7Z7D6
C	5	SER	-	CLONING ARTIFACT	UNP Q7Z7D6
C	63	MSE	MET	MODIFIED RESIDUE	UNP Q7Z7D6
C	89	MSE	MET	MODIFIED RESIDUE	UNP Q7Z7D6
C	113	MSE	MET	MODIFIED RESIDUE	UNP Q7Z7D6
C	118	MSE	MET	MODIFIED RESIDUE	UNP Q7Z7D6
C	137	MSE	MET	MODIFIED RESIDUE	UNP Q7Z7D6

- Molecule 2 is a protein called histone H3, N-terminal.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	P	6	Total	C	N	O	0	0	0
			51	31	11	9			

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	Zn	0	0
			2	2		
3	A	2	Total	Zn	0	0
			2	2		
3	C	2	Total	Zn	0	0
			2	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	184	Total	O	0	0
			184	184		
4	B	144	Total	O	0	0
			144	144		
4	C	114	Total	O	0	0
			114	114		
4	P	9	Total	O	0	0
			9	9		



- Molecule 1: bromodomain PHD finger transcription factor



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	38.58Å 84.99Å 109.39Å 90.00° 99.23° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.00 19.95 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.6 ((Not available)-2.00) 97.5 (19.95-2.00)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.14 (at 1.99Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.198 , 0.227 (Not available) , (Not available)	Depositor DCC
$R_{free}$ test set	NotAvailable	DCC
Wilson B-factor (Å <sup>2</sup> )	25.2	Xtriage
Anisotropy	0.167	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 56.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.033 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4643	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.42% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, M3L

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	0.34	0/1417	0.54	0/1910
1	B	0.32	0/1409	0.51	0/1899
1	C	0.30	0/1402	0.48	0/1889
2	P	0.42	0/38	0.61	0/50
All	All	0.32	0/4266	0.51	0/5748

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	1386	0	1320	17	0
1	B	1378	0	1316	22	0
1	C	1371	0	1309	18	0
2	P	51	0	60	1	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
4	A	184	0	0	1	0
4	B	144	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	114	0	0	0	0
4	P	9	0	0	0	0
All	All	4643	0	4005	56	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 7.

All (56) 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:137:MSE:HE2	1:B:141:PHE:CZ	2.18	0.79
1:A:84:LEU:HD13	1:A:161:LEU:HD22	1.72	0.70
1:B:80:VAL:O	1:B:84:LEU:HD23	1.91	0.69
1:C:90:ALA:HA	1:C:161:LEU:HD11	1.75	0.69
1:B:74:TYR:CE2	1:B:125:ARG:HD3	2.34	0.62
1:B:150:SER:HA	1:B:155:TYR:CD2	2.36	0.60
1:A:59:THR:O	1:A:63:MSE:HB2	2.02	0.59
1:C:74:TYR:CE2	1:C:125:ARG:HD3	2.38	0.59
1:B:65:VAL:HB	1:B:131:THR:HG23	1.86	0.57
1:B:65:VAL:O	1:B:131:THR:HG23	2.05	0.56
1:A:17:TYR:CE2	1:A:19:GLU:HG3	2.40	0.56
1:A:172:PHE:HD2	1:A:173:LYS:HG3	1.70	0.55
1:A:74:TYR:CE2	1:A:125:ARG:HD3	2.42	0.55
1:A:149:PRO:HG2	1:A:152:SER:HB2	1.87	0.55
1:B:137:MSE:HE3	1:B:140:ILE:HB	1.88	0.54
1:C:149:PRO:HG2	1:C:152:SER:HB2	1.90	0.54
1:A:172:PHE:CD2	1:A:173:LYS:HG3	2.43	0.53
1:B:91:TRP:CD2	1:B:92:PRO:HD3	2.44	0.53
1:A:7:THR:HG22	1:A:7:THR:O	2.11	0.51
1:C:40:ILE:HD12	1:C:51:TYR:CE1	2.47	0.50
1:C:91:TRP:CG	1:C:92:PRO:HD3	2.47	0.50
1:A:78:LYS:O	1:A:82:ARG:HG3	2.11	0.49
1:C:65:VAL:HA	1:C:130:LEU:HB3	1.94	0.49
1:B:91:TRP:CG	1:B:92:PRO:HD3	2.48	0.48
1:A:65:VAL:HA	1:A:130:LEU:HB3	1.96	0.47
1:C:22:PHE:CD2	1:C:42:GLN:HG2	2.49	0.47
1:A:150:SER:HA	1:A:155:TYR:CD2	2.50	0.47
1:B:150:SER:HA	1:B:155:TYR:CG	2.49	0.46
1:C:92:PRO:HG2	1:C:93:PHE:CE2	2.51	0.46
1:B:65:VAL:HB	1:B:131:THR:CG2	2.45	0.46
1:C:113:MSE:HE1	1:C:117:THR:CG2	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:166:VAL:O	1:C:170:LYS:HD3	2.16	0.46
1:B:59:THR:O	1:B:63:MSE:HG2	2.17	0.45
1:B:83:SER:OG	1:B:168:LYS:HE2	2.17	0.45
1:B:139:LYS:HB2	1:B:139:LYS:NZ	2.33	0.44
1:C:59:THR:O	1:C:63:MSE:HG2	2.17	0.44
1:C:91:TRP:CD2	1:C:92:PRO:HD3	2.53	0.44
2:P:3:THR:OG1	2:P:5:GLN:NE2	2.39	0.44
1:A:110:LYS:HE2	4:A:1129:HOH:O	2.18	0.44
1:B:19:GLU:OE2	1:C:41:LEU:HA	2.18	0.43
1:B:19:GLU:O	1:C:42:GLN:NE2	2.51	0.43
1:B:64:THR:HB	1:B:173:LYS:HG3	2.00	0.43
1:C:60:GLU:HA	1:C:63:MSE:HG2	2.00	0.43
1:C:45:ALA:O	1:C:48:ILE:HG12	2.18	0.43
1:C:91:TRP:CD1	1:C:92:PRO:HD3	2.54	0.43
1:A:91:TRP:CG	1:A:92:PRO:HD3	2.55	0.42
1:B:111:GLU:O	1:B:139:LYS:HD3	2.20	0.42
1:B:98:ASP:HB3	1:B:101:ASP:OD2	2.20	0.41
1:A:145:ARG:HG2	1:A:155:TYR:CZ	2.55	0.41
1:B:96:PRO:HG3	1:B:114:ASP:OD1	2.20	0.41
1:A:161:LEU:HA	1:A:161:LEU:HD23	1.85	0.41
1:A:28:ARG:HD3	1:A:28:ARG:HA	1.80	0.41
1:B:81:LEU:O	1:B:85:GLN:HG3	2.21	0.41
1:B:20:SER:HA	4:B:1103:HOH:O	2.20	0.41
1:C:150:SER:HA	1:C:155:TYR:CD2	2.56	0.41
1:A:72:LYS:HA	1:A:72:LYS:HD3	1.92	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	166/174 (95%)	163 (98%)	3 (2%)	0	<a href="#">100</a> <a href="#">100</a>

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	165/174 (95%)	164 (99%)	1 (1%)	0	100	100
1	C	164/174 (94%)	161 (98%)	3 (2%)	0	100	100
2	P	3/15 (20%)	3 (100%)	0	0	100	100
All	All	498/537 (93%)	491 (99%)	7 (1%)	0	100	100

There are no Ramachandran outliers to report.

### 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	154/152 (101%)	148 (96%)	6 (4%)	37	34
1	B	153/152 (101%)	151 (99%)	2 (1%)	73	78
1	C	152/152 (100%)	149 (98%)	3 (2%)	60	64
2	P	4/9 (44%)	4 (100%)	0	100	100
All	All	463/465 (100%)	452 (98%)	11 (2%)	54	56

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	ARG
1	A	79	ARG
1	A	81	LEU
1	A	89	MSE
1	A	120	GLU
1	A	168	LYS
1	B	89	MSE
1	B	130	LEU
1	C	89	MSE
1	C	113	MSE
1	C	170	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	GLN
1	A	167	GLN
1	B	42	GLN
1	B	100	ASN
1	B	167	GLN
1	C	55	GLN
1	C	167	GLN
2	P	5	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	M3L	P	4	2	11,11,12	0.85	1 (9%)	11,14,16	0.97	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	M3L	P	4	2	-	0/8/10/12	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	P	4	M3L	CA-C	2.51	1.53	1.50

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.

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 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 [i](#)

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	163/174 (93%)	-0.09	3 (1%) 69 68	15, 24, 42, 50	0
1	B	162/174 (93%)	0.04	6 (3%) 42 43	18, 27, 52, 67	0
1	C	161/174 (92%)	0.49	15 (9%) 9 9	23, 34, 67, 75	0
2	P	5/15 (33%)	0.80	1 (20%) 1 1	27, 30, 50, 57	0
All	All	491/537 (91%)	0.15	25 (5%) 29 29	15, 29, 56, 75	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	7	THR	5.8
1	B	47	LEU	5.7
1	C	47	LEU	5.3
1	C	43	SER	5.3
1	C	103	PRO	5.2
1	C	100	ASN	5.0
1	C	41	LEU	4.8
1	B	7	THR	4.8
1	B	43	SER	4.6
1	C	101	ASP	4.4
1	C	46	GLU	4.3
1	C	49	ASP	4.1
1	B	46	GLU	3.6
2	P	6	THR	3.6
1	C	171	GLY	3.6
1	C	48	ILE	3.4
1	C	102	ALA	3.3
1	B	49	ASP	3.3
1	C	150	SER	3.0
1	C	12	ILE	2.8
1	B	100	ASN	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	47	LEU	2.8
1	C	42	GLN	2.7
1	A	6	ASP	2.1
1	C	151	ASP	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [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
2	M3L	P	4	12/13	0.94	0.12	-	30,31,33,35	0

## 6.3 Carbohydrates [i](#)

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
3	ZN	C	1005	1/1	0.99	0.03	-1.60	37,37,37,37	0
3	ZN	A	1002	1/1	1.00	0.07	-1.86	21,21,21,21	0
3	ZN	B	1004	1/1	1.00	0.05	-1.93	25,25,25,25	0
3	ZN	A	1001	1/1	1.00	0.04	-2.20	24,24,24,24	0
3	ZN	C	1006	1/1	0.98	0.05	-2.81	30,30,30,30	0
3	ZN	B	1003	1/1	1.00	0.04	-2.81	27,27,27,27	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.