



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:33 PM GMT

PDB ID : 1G7G  
Title : HUMAN PTP1B CATALYTIC DOMAIN COMPLEXES WITH PNU179326  
Authors : Bleasdale, J.E.; Ogg, D.; Larsen, S.D.  
Deposited on : 2000-11-10  
Resolution : 2.20 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

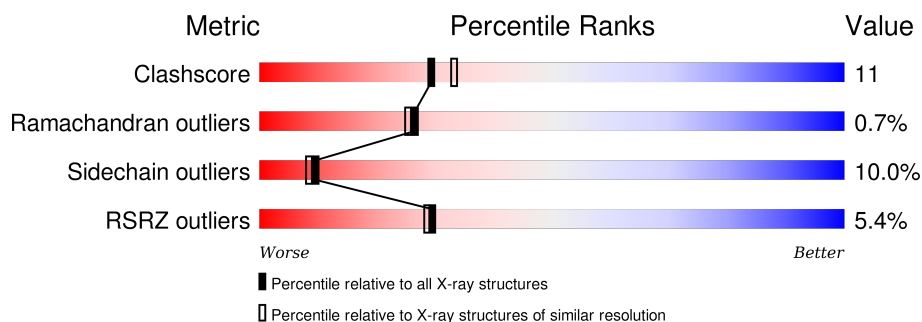
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*


The reported resolution of this entry is 2.20 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	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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	298	

## 2 Entry composition [i](#)

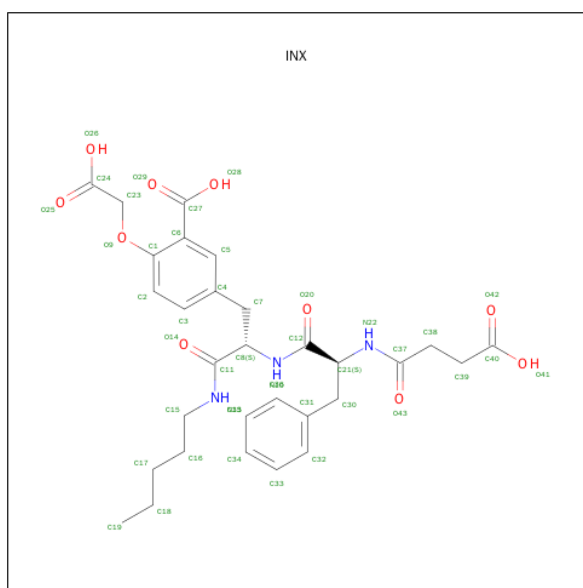
There are 3 unique types of molecules in this entry. The entry contains 2579 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 PROTEIN-TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	297	2427	1535	418	458	16	0	0	0

- Molecule 2 is 2-(CARBOXYMETHOXY)-5-[(2S)-2-[(2S)-2-[(3-CARBOXYPROPANOYL)AMINO]-3-PHENYLPROPANOYL}AMINO)-3-OXO-3-(PENTYLAMINO)PROPYL]BENZOIC ACID (three-letter code: INX) (formula: C<sub>30</sub>H<sub>37</sub>N<sub>3</sub>O<sub>10</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	43	30	3	10	0	0

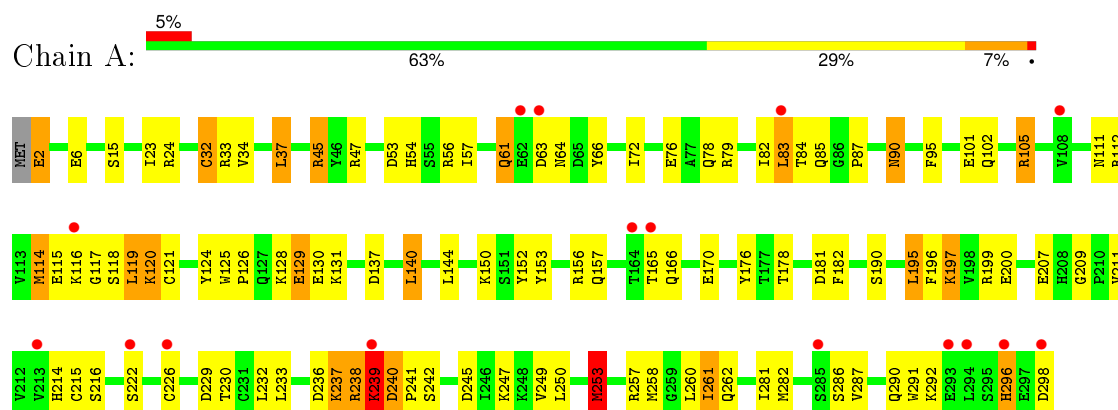
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	109	Total	O	0	0
			109	109		

### 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 ( $RSRZ > 2$ ). 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: PROTEIN-TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	52.92Å 82.44Å 88.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.20 31.42 – 2.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.20) 72.1 (31.42-2.00)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.17 (at 2.01Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.193 , 0.262 0.192 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	22.0	Xtriage
Anisotropy	1.003	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 59.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 19269 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	2579	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.15% 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 ⓘ

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

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	0.96	3/2482 (0.1%)	1.70	43/3344 (1.3%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	101	GLU	CB-CG	5.22	1.62	1.52
1	A	129	GLU	CB-CG	-5.14	1.42	1.52
1	A	53	ASP	CA-CB	5.03	1.65	1.53

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	239	LYS	C-N-CA	13.10	154.45	121.70
1	A	24	ARG	NE-CZ-NH1	-10.99	114.80	120.30
1	A	129	GLU	CA-CB-CG	10.24	135.94	113.40
1	A	79	ARG	NE-CZ-NH2	-10.22	115.19	120.30
1	A	32	CYS	CA-CB-SG	9.97	131.94	114.00
1	A	112	ARG	CD-NE-CZ	9.84	137.37	123.60
1	A	240	ASP	N-CA-CB	9.79	128.21	110.60
1	A	257	ARG	NE-CZ-NH1	-9.15	115.72	120.30
1	A	156	ARG	NE-CZ-NH2	9.13	124.86	120.30
1	A	238	ARG	CD-NE-CZ	9.10	136.33	123.60
1	A	79	ARG	NE-CZ-NH1	8.39	124.49	120.30
1	A	61	GLN	CA-CB-CG	7.91	130.80	113.40
1	A	296	HIS	CA-CB-CG	7.78	126.83	113.60
1	A	83	LEU	CA-CB-CG	7.76	133.15	115.30
1	A	56	ARG	NE-CZ-NH2	-7.65	116.47	120.30
1	A	199	ARG	NE-CZ-NH2	7.49	124.04	120.30
1	A	66	TYR	CB-CG-CD2	7.32	125.39	121.00
1	A	140	LEU	CA-CB-CG	6.90	131.17	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	253	MET	CG-SD-CE	-6.84	89.25	100.20
1	A	66	TYR	CB-CG-CD1	-6.63	117.02	121.00
1	A	245	ASP	CB-CG-OD1	6.61	124.25	118.30
1	A	33	ARG	CD-NE-CZ	6.59	132.83	123.60
1	A	199	ARG	CD-NE-CZ	6.32	132.45	123.60
1	A	129	GLU	CB-CG-CD	6.21	130.96	114.20
1	A	79	ARG	CD-NE-CZ	6.16	132.22	123.60
1	A	229	ASP	CB-CG-OD2	-6.15	112.77	118.30
1	A	226	CYS	CA-CB-SG	-6.08	103.06	114.00
1	A	45	ARG	NE-CZ-NH2	6.00	123.30	120.30
1	A	112	ARG	NE-CZ-NH1	5.88	123.24	120.30
1	A	56	ARG	NE-CZ-NH1	5.71	123.15	120.30
1	A	176	TYR	CB-CG-CD2	-5.64	117.61	121.00
1	A	32	CYS	O-C-N	-5.64	113.68	122.70
1	A	233	LEU	CA-CB-CG	5.53	128.01	115.30
1	A	105	ARG	NE-CZ-NH1	-5.49	117.56	120.30
1	A	6	GLU	CG-CD-OE1	5.48	129.26	118.30
1	A	61	GLN	CB-CG-CD	5.48	125.85	111.60
1	A	121	CYS	N-CA-CB	-5.36	100.95	110.60
1	A	195	LEU	CB-CG-CD2	5.34	120.08	111.00
1	A	257	ARG	NE-CZ-NH2	5.28	122.94	120.30
1	A	230	THR	CA-CB-CG2	-5.18	105.14	112.40
1	A	24	ARG	NE-CZ-NH2	5.07	122.83	120.30
1	A	137	ASP	CB-CG-OD1	5.05	122.85	118.30
1	A	124	TYR	CB-CG-CD1	-5.03	117.98	121.00

There are no chirality outliers.

There are no planarity outliers.

## 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	2427	0	2380	55	0
2	A	43	0	34	2	0
3	A	109	0	0	2	0
All	All	2579	0	2414	55	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 11.

All (55) 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:A:90:ASN:H	1:A:90:ASN:HD22	1.10	0.96
1:A:236:ASP:HB2	1:A:281:ILE:HD12	1.50	0.94
1:A:45:ARG:H	1:A:85:GLN:HE22	1.12	0.94
1:A:2:GLU:HG2	1:A:242:SER:HB2	1.58	0.86
1:A:57:ILE:HD11	1:A:82:ILE:HG12	1.57	0.85
1:A:90:ASN:H	1:A:90:ASN:ND2	1.79	0.81
1:A:240:ASP:N	1:A:241:PRO:HD3	2.01	0.76
1:A:130:GLU:HG2	1:A:131:LYS:HE2	1.70	0.74
1:A:45:ARG:H	1:A:85:GLN:NE2	1.87	0.72
1:A:54:HIS:ND1	3:A:798:HOH:O	2.23	0.71
1:A:90:ASN:N	1:A:90:ASN:HD22	1.88	0.67
1:A:197:LYS:HZ3	1:A:197:LYS:HB2	1.60	0.66
1:A:286:SER:O	1:A:290:GLN:HG3	1.99	0.62
1:A:157:GLN:NE2	1:A:170:GLU:OE1	2.33	0.62
1:A:34:VAL:HA	1:A:37:LEU:HD22	1.81	0.60
1:A:150:LYS:HG3	1:A:153:TYR:CZ	2.38	0.58
1:A:57:ILE:CD1	1:A:82:ILE:HG12	2.33	0.58
1:A:197:LYS:HB2	1:A:197:LYS:NZ	2.18	0.58
1:A:197:LYS:HZ3	1:A:197:LYS:CB	2.13	0.56
1:A:240:ASP:N	1:A:241:PRO:CD	2.69	0.56
1:A:115:GLU:O	1:A:116:LYS:HB2	2.06	0.56
1:A:128:LYS:HD3	1:A:131:LYS:HE3	1.88	0.55
1:A:196:PHE:O	1:A:200:GLU:HG3	2.07	0.55
1:A:90:ASN:N	1:A:90:ASN:ND2	2.50	0.55
1:A:87:PRO:HG3	1:A:95:PHE:CD2	2.44	0.53
1:A:102:GLN:O	1:A:209:GLY:HA3	2.10	0.52
1:A:239:LYS:HA	1:A:239:LYS:HE2	1.93	0.51
1:A:152:TYR:HB2	1:A:178:THR:OG1	2.11	0.50
1:A:165:THR:O	1:A:166:GLN:HB2	2.12	0.50
1:A:120:LYS:HB3	1:A:216:SER:HB2	1.94	0.50
1:A:253:MET:HB2	1:A:260:LEU:HD12	1.94	0.49
1:A:61:GLN:HG3	1:A:63:ASP:HB3	1.95	0.49
1:A:84:THR:O	1:A:214:HIS:HB2	2.13	0.49
1:A:83:LEU:HD13	1:A:222:SER:HB3	1.94	0.49
1:A:250:LEU:HD22	1:A:261:ILE:HD12	1.95	0.48
1:A:47:ARG:NE	2:A:600:INX:O41	2.47	0.47
1:A:125:TRP:HB2	1:A:126:PRO:HD2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:111:ASN:HD22	1:A:215:CYS:HA	1.79	0.47
1:A:126:PRO:HG2	1:A:144:LEU:HB2	1.97	0.46
1:A:116:LYS:O	1:A:118:SER:N	2.49	0.45
1:A:23:ILE:HD11	1:A:247:LYS:HG2	1.99	0.45
1:A:181:ASP:O	1:A:182:PHE:HB2	2.17	0.44
1:A:61:GLN:HG3	1:A:64:ASN:H	1.83	0.43
1:A:111:ASN:ND2	1:A:215:CYS:HA	2.34	0.43
1:A:262:GLN:HG3	2:A:600:INX:HC2	2.00	0.43
1:A:287:VAL:HG22	1:A:291:TRP:CE2	2.54	0.42
1:A:119:LEU:HD22	1:A:119:LEU:HA	1.79	0.42
1:A:114:MET:HG2	1:A:119:LEU:CD2	2.50	0.42
1:A:76:GLU:O	1:A:237:LYS:HE2	2.19	0.42
1:A:249:VAL:O	1:A:253:MET:HG3	2.20	0.42
1:A:211:VAL:HG12	3:A:731:HOH:O	2.19	0.41
1:A:247:LYS:HB2	1:A:247:LYS:HZ3	1.85	0.41
1:A:239:LYS:HE2	1:A:239:LYS:CA	2.50	0.41
1:A:260:LEU:O	1:A:261:ILE:HB	2.20	0.41
1:A:111:ASN:HD21	1:A:214:HIS:CE1	2.38	0.40

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	295/298 (99%)	280 (95%)	13 (4%)	2 (1%)	26	25

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	261	ILE
1	A	117	GLY

### 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	270/271 (100%)	243 (90%)	27 (10%)	<b>9</b> <b>8</b>

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	GLU
1	A	15	SER
1	A	32	CYS
1	A	37	LEU
1	A	72	ILE
1	A	78	GLN
1	A	90	ASN
1	A	105	ARG
1	A	114	MET
1	A	119	LEU
1	A	120	LYS
1	A	129	GLU
1	A	140	LEU
1	A	190	SER
1	A	195	LEU
1	A	197	LYS
1	A	207	GLU
1	A	232	LEU
1	A	237	LYS
1	A	238	ARG
1	A	239	LYS
1	A	253	MET
1	A	258	MET
1	A	282	MET
1	A	292	LYS
1	A	296	HIS
1	A	298	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	85	GLN
1	A	90	ASN
1	A	111	ASN
1	A	123	GLN

### 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 ⓘ

1 ligand 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	INX	A	600	-	35,44,44	1.59	6 (17%)	46,57,57	2.02	11 (23%)

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	INX	A	600	-	-	0/36/44/44	0/2/2/2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	600	INX	C35-C34	2.00	1.43	1.38
2	A	600	INX	C33-C32	2.33	1.43	1.38
2	A	600	INX	C3-C4	2.46	1.44	1.38
2	A	600	INX	C35-C36	2.99	1.45	1.38
2	A	600	INX	C32-C31	3.00	1.45	1.38
2	A	600	INX	C6-C1	4.18	1.47	1.40

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	600	INX	O9-C1-C2	-3.84	115.98	124.01
2	A	600	INX	C8-C11-N13	-3.08	110.67	116.72
2	A	600	INX	C31-C30-C21	-2.78	105.31	113.41
2	A	600	INX	C35-C36-C31	-2.36	116.90	120.65
2	A	600	INX	C8-N10-C12	-2.34	116.37	121.62
2	A	600	INX	C38-C37-N22	2.40	119.74	115.83
2	A	600	INX	O14-C11-N13	3.01	129.12	123.08
2	A	600	INX	C36-C31-C32	3.43	123.63	118.13
2	A	600	INX	C15-N13-C11	3.51	129.47	122.53
2	A	600	INX	C23-O9-C1	5.66	129.03	117.82
2	A	600	INX	O9-C1-C6	6.03	124.99	115.96

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	600	INX	2	0

## 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 [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	297/298 (99%)	0.09	16 (5%)	29 29	23, 34, 60, 91	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	239	LYS	4.3
1	A	296	HIS	3.8
1	A	62	GLU	3.8
1	A	298	ASP	2.8
1	A	226	CYS	2.6
1	A	165	THR	2.6
1	A	213	VAL	2.5
1	A	116	LYS	2.5
1	A	63	ASP	2.5
1	A	83	LEU	2.3
1	A	293	GLU	2.3
1	A	108	VAL	2.3
1	A	222	SER	2.3
1	A	294	LEU	2.2
1	A	285	SER	2.1
1	A	164	THR	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](#)

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( $\text{\AA}^2$ )	Q<0.9
2	INX	A	600	43/43	0.93	0.13	0.14	30,40,62,73	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.