



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:47 PM GMT

PDB ID : 4MS0  
Title : Crystal structure of PDE10A2 with fragment ZT0443 (6-chloropyrimidine-2,4-diamine)  
Authors : Sridhar, V.; Badger, J.; Logan, C.; Chie-Leon, B.; Nienaber, V.  
Deposited on : 2013-09-18  
Resolution : 1.79 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

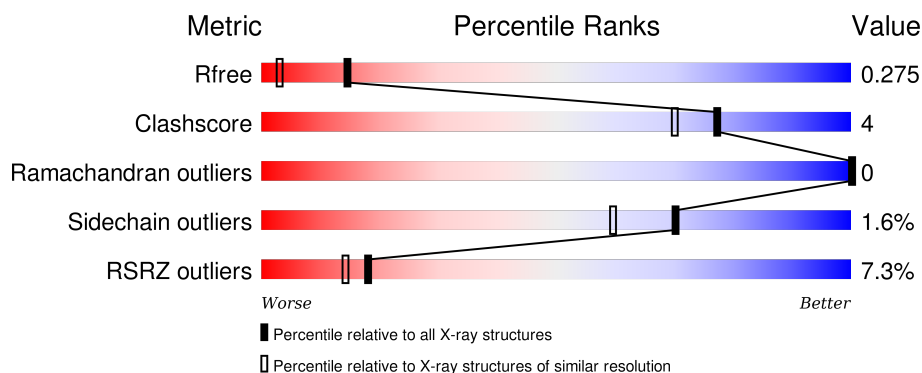
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.79 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	4533 (1.80-1.80)
Clashscore	102246	5383 (1.80-1.80)
Ramachandran outliers	100387	5320 (1.80-1.80)
Sidechain outliers	100360	5319 (1.80-1.80)
RSRZ outliers	91569	4547 (1.80-1.80)

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	345	<div> <div>5%</div> <div>87%</div> <div>8%</div> <div>.</div> </div>
1	B	345	<div> <div>9%</div> <div>86%</div> <div>7%</div> <div>6%</div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5489 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.

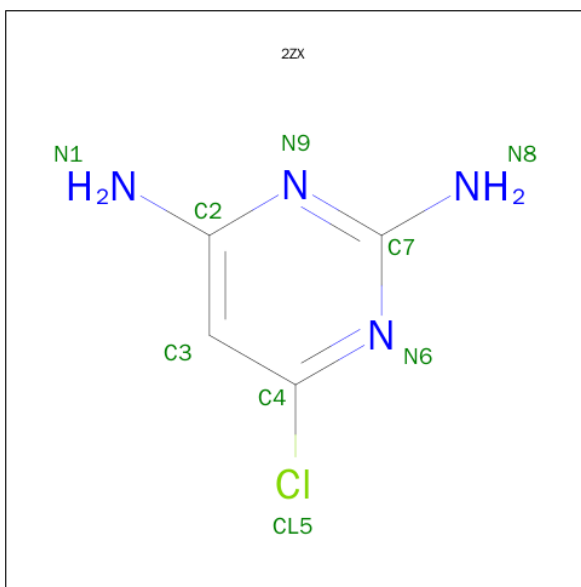
- Molecule 1 is a protein called cAMP and cAMP-inhibited cGMP 3',5'-cyclic phosphodiesterase 10A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	330	Total	C	N	O	S	0	4	0
			2625	1676	441	484	24			
1	B	324	Total	C	N	O	S	0	3	0
			2581	1651	436	469	25			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	445	GLY	-	EXPRESSION TAG	UNP Q9Y233
A	446	ALA	-	EXPRESSION TAG	UNP Q9Y233
A	447	GLY	-	EXPRESSION TAG	UNP Q9Y233
A	448	THR	-	EXPRESSION TAG	UNP Q9Y233
B	445	GLY	-	EXPRESSION TAG	UNP Q9Y233
B	446	ALA	-	EXPRESSION TAG	UNP Q9Y233
B	447	GLY	-	EXPRESSION TAG	UNP Q9Y233
B	448	THR	-	EXPRESSION TAG	UNP Q9Y233

- Molecule 2 is 6-CHLOROPYRIMIDINE-2,4-DIAMINE (three-letter code: 2ZX) (formula: C<sub>4</sub>H<sub>5</sub>ClN<sub>4</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	Cl	N	0	0
			9	4	1	4		

- Molecule 3 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

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

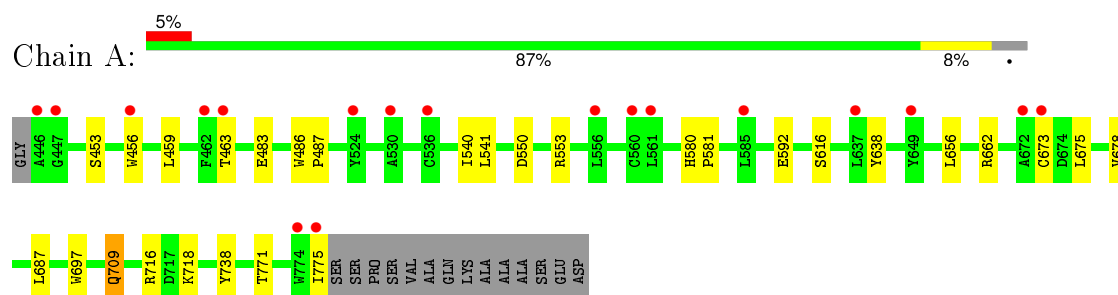
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	160	Total	O	0	0
			160	160		
4	B	110	Total	O	0	0
			110	110		

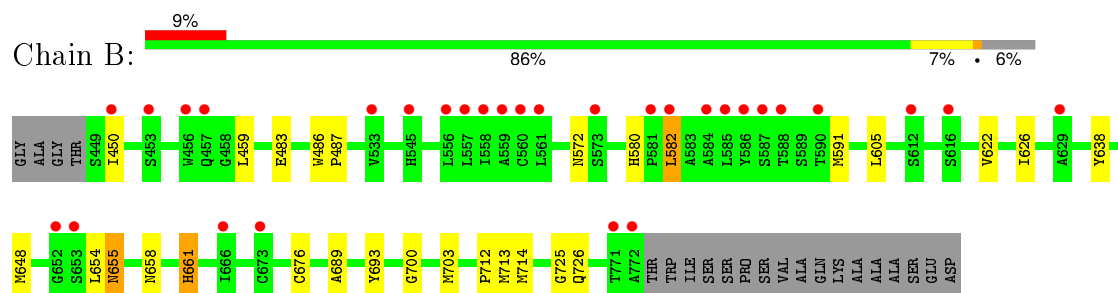
### 3 Residue-property plots

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 ( $\text{RSRZ} > 2$ ). 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: cAMP and cAMP-inhibited cGMP 3',5'-cyclic phosphodiesterase 10A



- Molecule 1: cAMP and cAMP-inhibited cGMP 3',5'-cyclic phosphodiesterase 10A



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	51.30 Å 82.38 Å 155.61 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	31.46 – 1.79 31.46 – 1.79	Depositor EDS
% Data completeness (in resolution range)	(Not available) (31.46-1.79) 97.0 (31.46-1.79)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.93 (at 1.79 Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, $R_{free}$	0.252 , 0.296 0.235 , 0.275	Depositor DCC
$R_{free}$ test set	3097 reflections (5.34%)	DCC
Wilson B-factor (Å <sup>2</sup> )	29.2	Xtriage
Anisotropy	0.851	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 39.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 61080 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5489	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 4.91% 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: NI, 2ZX

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	0.67	1/2711 (0.0%)	0.65	0/3684
1	B	0.63	1/2660 (0.0%)	0.63	0/3610
All	All	0.65	2/5371 (0.0%)	0.64	0/7294

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	738	TYR	CD1-CE1	5.79	1.48	1.39
1	B	676	CYS	CB-SG	-5.20	1.73	1.81

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	2625	0	2521	15	0
1	B	2581	0	2485	24	0
2	A	9	0	5	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
4	A	160	0	0	2	0
4	B	110	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5489	0	5011	38	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 4.

All (38) 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:655:ASN:H	1:B:661:HIS:HD2	1.11	0.95
1:A:718:LYS:HE2	4:A:1139:HOH:O	1.83	0.78
1:B:655:ASN:H	1:B:661:HIS:CD2	2.02	0.76
1:B:572:ASN:HD21	1:B:591:MET:H	1.42	0.66
1:B:450:ILE:HG22	1:B:605:LEU:HD13	1.80	0.64
1:A:675:LEU:O	1:A:678:VAL:HG22	1.96	0.64
1:B:580:HIS:HD2	1:B:582:LEU:H	1.46	0.62
1:B:580:HIS:CD2	1:B:582:LEU:H	2.20	0.59
1:B:483:GLU:HA	1:B:486:TRP:CE2	2.38	0.59
1:A:687:LEU:HD21	1:A:775:ILE:HA	1.87	0.57
1:B:580:HIS:HD2	1:B:582:LEU:HB2	1.71	0.54
1:B:655:ASN:N	1:B:661:HIS:HD2	1.92	0.54
1:A:483:GLU:HA	1:A:486:TRP:CE2	2.43	0.54
1:A:771:THR:HA	1:B:713:MET:HB3	1.89	0.54
1:B:572:ASN:ND2	1:B:591:MET:H	2.08	0.52
1:B:700:GLY:HA2	1:B:703[B]:MET:CE	2.40	0.51
1:B:622:VAL:O	1:B:626:ILE:HG13	2.10	0.51
1:A:541:LEU:HD22	1:A:553:ARG:HG2	1.92	0.50
1:B:648:MET:HE2	1:B:654:LEU:HD12	1.94	0.48
1:A:453:SER:HA	1:A:456:TRP:NE1	2.30	0.46
1:B:658:ASN:HD22	1:B:661:HIS:CE1	2.34	0.46
1:B:700:GLY:HA3	1:B:714:MET:O	2.16	0.46
1:B:700:GLY:HA2	1:B:703[B]:MET:HE2	1.99	0.45
1:A:540:ILE:HD12	1:A:673:CYS:SG	2.56	0.45
1:B:580:HIS:CD2	1:B:582:LEU:HB2	2.52	0.45
1:A:709:GLN:NE2	4:A:1136:HOH:O	2.49	0.44
1:B:648:MET:HE2	1:B:654:LEU:CD1	2.48	0.43
1:B:459:LEU:HD13	1:B:487:PRO:HB2	2.00	0.43
1:A:550[A]:ASP:OD1	1:A:553:ARG:NH2	2.47	0.42
1:A:459:LEU:HD13	1:A:487:PRO:HB2	2.01	0.42
1:B:693:TYR:OH	1:B:725:GLY:HA3	2.20	0.42
1:B:648:MET:CE	1:B:654:LEU:HD12	2.50	0.42
1:A:592:GLU:CD	1:A:592:GLU:H	2.23	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:656:LEU:O	1:A:662:ARG:HG3	2.21	0.41
1:A:580:HIS:CG	1:A:581:PRO:HD2	2.56	0.41
1:A:697:TRP:HB3	1:A:716:ARG:HB3	2.03	0.41
1:B:689:ALA:O	1:B:726:GLN:NE2	2.53	0.40
1:B:700:GLY:HA2	1:B:703[B]:MET:HE3	2.04	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	332/345 (96%)	327 (98%)	5 (2%)	0	100	100
1	B	325/345 (94%)	316 (97%)	9 (3%)	0	100	100
All	All	657/690 (95%)	643 (98%)	14 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	285/306 (93%)	281 (99%)	4 (1%)	74	65
1	B	277/306 (90%)	272 (98%)	5 (2%)	66	54
All	All	562/612 (92%)	553 (98%)	9 (2%)	70	59

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	463	THR
1	A	616	SER
1	A	638	TYR
1	A	709	GLN
1	B	582	LEU
1	B	638	TYR
1	B	655	ASN
1	B	661	HIS
1	B	712	PRO

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	476	HIS
1	A	709	GLN
1	A	724	GLN
1	A	743	GLN
1	B	476	HIS
1	B	572	ASN
1	B	580	HIS
1	B	655	ASN
1	B	658	ASN
1	B	661	HIS

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 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

Of 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 for Mogul analysis.

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	2ZX	A	900	-	9,9,9	0.88	0	11,12,12	2.33	4 (36%)

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	2ZX	A	900	-	-	0/0/0/0	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	900	2ZX	C3-C4-N6	-3.25	121.72	125.62
2	A	900	2ZX	N6-C7-N9	-3.07	120.50	125.53
2	A	900	2ZX	C4-C3-C2	2.51	117.19	115.39
2	A	900	2ZX	C4-N6-C7	4.71	119.52	114.61

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	330/345 (95%)	0.38	18 (5%) 29 23	23, 35, 54, 63	0
1	B	324/345 (93%)	0.63	30 (9%) 11 8	25, 38, 59, 67	0
All	All	654/690 (94%)	0.51	48 (7%) 18 14	23, 37, 57, 67	0

All (48) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	446	ALA	7.7
1	B	585	LEU	6.9
1	B	584	ALA	5.4
1	B	456	TRP	5.1
1	B	450	ILE	3.9
1	B	558	ILE	3.3
1	B	653	SER	3.2
1	B	586	TYR	3.2
1	B	673	CYS	3.1
1	B	559	ALA	3.1
1	B	533	VAL	3.0
1	A	673	CYS	3.0
1	A	447	GLY	2.9
1	B	560	CYS	2.9
1	B	573	SER	2.8
1	A	649	TYR	2.8
1	A	456	TRP	2.8
1	A	462	PHE	2.8
1	B	772	ALA	2.8
1	B	771	THR	2.8
1	B	453	SER	2.7
1	B	612	SER	2.7
1	B	545	HIS	2.6
1	A	774	TRP	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	652	GLY	2.6
1	B	588	THR	2.5
1	A	560	CYS	2.5
1	A	672	ALA	2.5
1	B	581	PRO	2.5
1	B	629	ALA	2.5
1	B	556	LEU	2.4
1	B	561	LEU	2.3
1	A	775	ILE	2.3
1	A	536	CYS	2.3
1	B	582	LEU	2.2
1	B	587	SER	2.2
1	A	463	THR	2.2
1	A	637	LEU	2.2
1	B	457	GLN	2.1
1	A	585	LEU	2.1
1	B	666	ILE	2.1
1	B	616	SER	2.1
1	A	524	TYR	2.1
1	A	556	LEU	2.1
1	B	557	LEU	2.1
1	A	530	ALA	2.1
1	A	561	LEU	2.1
1	B	590	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	2ZX	A	900	9/9	0.92	0.11	-0.35	37,42,43,45	0
3	NI	B	902	1/1	0.98	0.06	-1.68	52,52,52,52	0
3	NI	B	901	1/1	0.99	0.02	-2.27	41,41,41,41	0
3	NI	A	902	1/1	0.99	0.03	-3.35	44,44,44,44	0
3	NI	A	901	1/1	0.99	0.05	-8.59	27,27,27,27	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.