



# wwPDB X-ray Structure Validation Summary Report i

Nov 25, 2014 – 05:29 PM EST

PDB ID : 4PM0  
Title : PDE7A catalytic domain in complex with 2-(Cyclopentylamino)thieno[3,2-d]pyrimidin-4(3H)-onederivative  
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Deposited on : 2014-05-20  
Resolution : 2.10 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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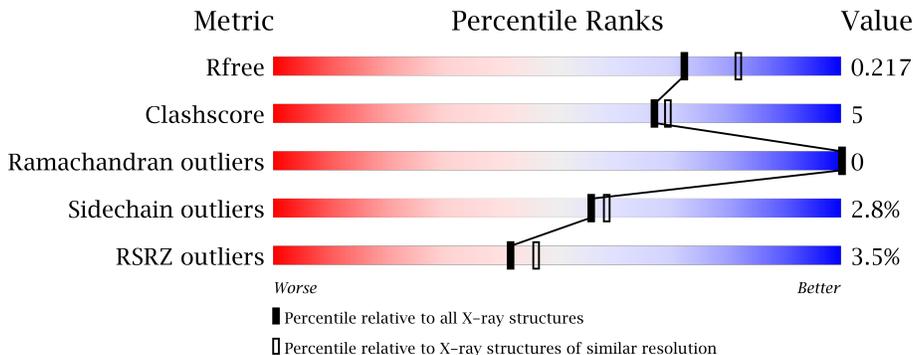
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.16 November 2013  
Xtrriage (Phenix) : dev-1439  
EDS : stable24195  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.1.3  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable24195

# 1 Overall quality at a glance

The reported resolution of this entry is 2.10 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	3012 (2.10-2.10)
Clashscore	79885	3649 (2.10-2.10)
Ramachandran outliers	78287	3610 (2.10-2.10)
Sidechain outliers	78261	3611 (2.10-2.10)
RSRZ outliers	66119	3013 (2.10-2.10)

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	389	

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 2855 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 High affinity cAMP-specific 3',5'-cyclic phosphodiesterase 7A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	318	2595	1653	459	467	16	0	0	0

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	94	GLY	-	expression tag	UNP Q13946
A	95	SER	-	expression tag	UNP Q13946
A	96	GLY	-	expression tag	UNP Q13946
A	97	MET	-	expression tag	UNP Q13946
A	98	LYS	-	expression tag	UNP Q13946
A	99	GLU	-	expression tag	UNP Q13946
A	100	THR	-	expression tag	UNP Q13946
A	101	ALA	-	expression tag	UNP Q13946
A	102	ALA	-	expression tag	UNP Q13946
A	103	ALA	-	expression tag	UNP Q13946
A	104	LYS	-	expression tag	UNP Q13946
A	105	PRO	-	expression tag	UNP Q13946
A	106	GLU	-	expression tag	UNP Q13946
A	107	ARG	-	expression tag	UNP Q13946
A	108	GLN	-	expression tag	UNP Q13946
A	109	HIS	-	expression tag	UNP Q13946
A	110	MET	-	expression tag	UNP Q13946
A	111	ASP	-	expression tag	UNP Q13946
A	112	SER	-	expression tag	UNP Q13946
A	113	PRO	-	expression tag	UNP Q13946
A	114	ASP	-	expression tag	UNP Q13946
A	115	LEU	-	expression tag	UNP Q13946
A	116	GLY	-	expression tag	UNP Q13946
A	117	THR	-	expression tag	UNP Q13946
A	118	ASP	-	expression tag	UNP Q13946
A	119	ASP	-	expression tag	UNP Q13946
A	120	ASP	-	expression tag	UNP Q13946

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Chain	Residue	Modelled	Actual	Comment	Reference
A	121	ASP	-	expression tag	UNP Q13946
A	122	LYS	-	expression tag	UNP Q13946
A	123	ALA	-	expression tag	UNP Q13946
A	124	MET	-	expression tag	UNP Q13946
A	125	ALA	-	expression tag	UNP Q13946
A	126	ASP	-	expression tag	UNP Q13946
A	127	ILE	-	expression tag	UNP Q13946
A	128	GLY	-	expression tag	UNP Q13946
A	129	SER	-	expression tag	UNP Q13946

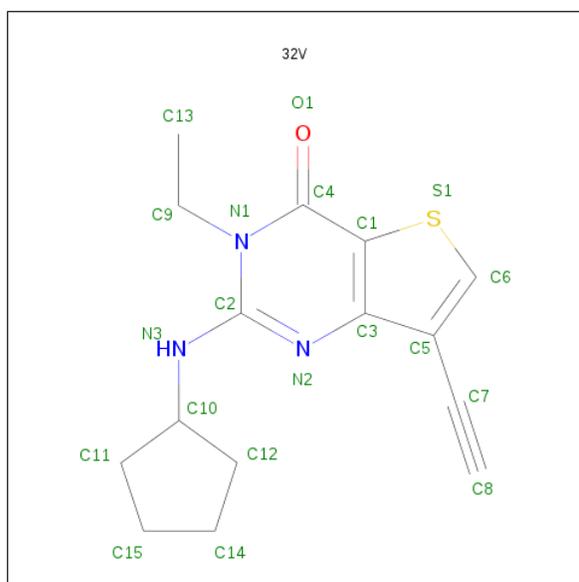
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Zn 1 1	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Mg 1 1	0	0

- Molecule 4 is 2-(cyclopentylamino)-3-ethyl-7-ethynylthieno[3,2-d]pyrimidin-4(3H)-one (three-letter code: 32V) (formula: C<sub>15</sub>H<sub>17</sub>N<sub>3</sub>OS).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
4	A	1	20	15	3	1	1	0	0

- Molecule 5 is water.

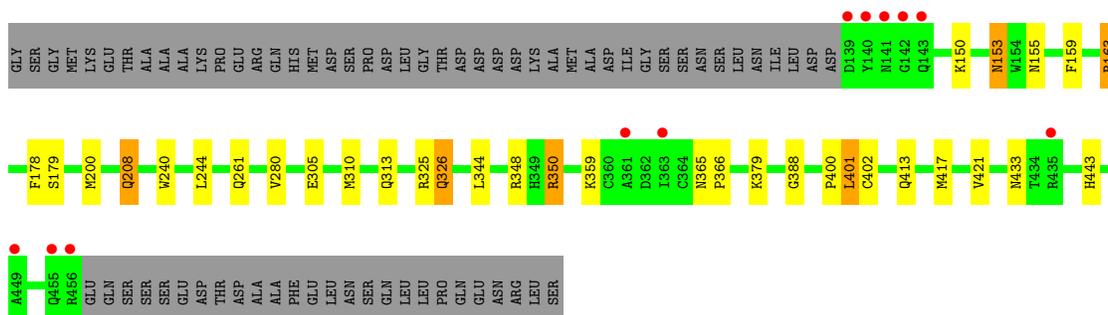
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	238	Total	O	0	0
			238	238		

### 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: High affinity cAMP-specific 3',5'-cyclic phosphodiesterase 7A

Chain A:



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	116.19Å 116.19Å 64.46Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.75 – 2.10 29.75 – 2.10	Depositor EDS
% Data completeness (in resolution range)	92.8 (29.75-2.10) 92.8 (29.75-2.10)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.60 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.172 , 0.218 0.172 , 0.217	Depositor DCC
$R_{free}$ test set	1417 reflections (5.45%)	DCC
Wilson B-factor (Å <sup>2</sup> )	30.1	Xtriage
Anisotropy	0.007	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 36.4	EDS
Estimated twinning fraction	0.030 for -h,-k,l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 27399 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	2855	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.06% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 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, 32V, 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	1.09	1/2662 (0.0%)	0.90	6/3607 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	178	PHE	CE2-CZ	5.22	1.47	1.37

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	350	ARG	NE-CZ-NH1	6.50	123.55	120.30
1	A	163	ARG	NE-CZ-NH2	-6.49	117.06	120.30
1	A	163	ARG	NE-CZ-NH1	6.18	123.39	120.30
1	A	200	MET	CG-SD-CE	6.07	109.91	100.20
1	A	325	ARG	NE-CZ-NH1	5.54	123.07	120.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 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	2595	0	2538	26	0
2	A	1	0	0	0	0
3	A	1	0	0	0	0
4	A	20	0	0	0	0
5	A	238	0	0	7	0
All	All	2855	0	2538	26	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 5.

The worst 5 of 26 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:163:ARG:NH2	5:A:726:HOH:O	2.16	0.76
1:A:417:MET:HE1	5:A:837:HOH:O	1.87	0.74
1:A:240:TRP:HE1	1:A:313:GLN:HE22	1.34	0.72
1:A:155:ASN:ND2	5:A:747:HOH:O	2.10	0.72
1:A:208:GLN:NE2	5:A:753:HOH:O	2.00	0.72

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	316/389 (81%)	310 (98%)	6 (2%)	0	<b>100</b> <b>100</b>

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	285/345 (83%)	277 (97%)	8 (3%)	56 59

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	305	GLU
1	A	433	ASN
1	A	348	ARG
1	A	208	GLN
1	A	326	GLN

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

Mol	Chain	Res	Type
1	A	261	GLN
1	A	308	GLN
1	A	386	HIS
1	A	208	GLN
1	A	326	GLN

### 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 3 ligands modelled in this entry, 2 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
4	32V	A	503	-	22,22,22	3.22	8 (36%)	25,31,31	1.89	5 (20%)

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
4	32V	A	503	-	-	0/6/15/15	0/3/3/3

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	503	32V	C5-C7	8.13	1.51	1.44
4	A	503	32V	C2-N3	7.53	1.43	1.34
4	A	503	32V	C6-C5	5.21	1.40	1.37
4	A	503	32V	O1-C4	4.91	1.36	1.24
4	A	503	32V	C2-N2	4.35	1.40	1.34

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	503	32V	C2-N3-C10	-5.27	117.14	123.25
4	A	503	32V	C6-C5-C3	5.23	112.29	107.76
4	A	503	32V	C1-C3-N2	-3.22	120.25	123.22
4	A	503	32V	C5-C3-N2	-2.40	125.82	129.92
4	A	503	32V	C9-N1-C4	2.08	121.72	119.26

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(Å <sup>2</sup> )	Q<0.9
1	A	318/389 (81%)	-0.20	11 (3%) 42 46	17, 29, 50, 93	0

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	140	TYR	4.1
1	A	139	ASP	3.7
1	A	142	GLY	3.6
1	A	456	ARG	3.1
1	A	141	ASN	2.8

### 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	32V	A	503	20/20	0.16	0.48	20,24,32,41	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	MG	A	502	1/1	0.09	-0.85	20,20,20,20	0
2	ZN	A	501	1/1	0.07	-2.63	27,27,27,27	0

## 6.5 Other polymers

There are no such residues in this entry.