



# wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 1S18  
Title : Structure and protein design of human apyrase  
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Deposited on : 2004-01-05  
Resolution : 1.70 Å(reported)

This is a wwPDB X-ray Structure 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

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

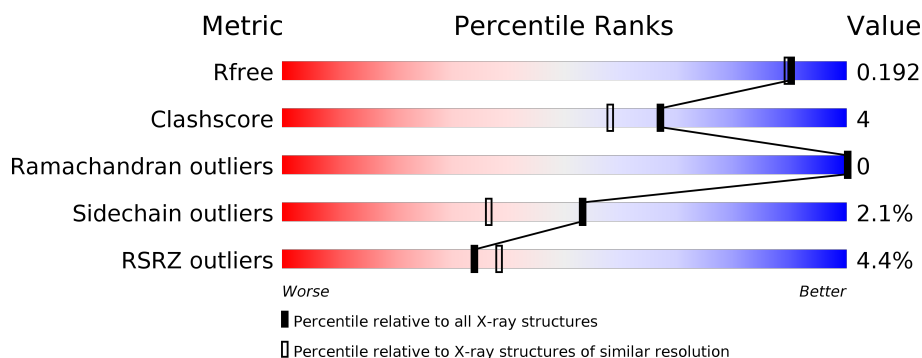
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.70 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))
$R_{free}$	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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 respectively. 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	331	<div> <div>5%</div> <div> <div></div> <div>87%</div> <div>8%</div> <div>• •</div> </div> </div>
1	B	331	<div> <div>4%</div> <div> <div></div> <div>87%</div> <div>8%</div> <div>5%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	ACT	B	3003	-	-	X	-

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 5597 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 apyrase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	317	Total	C	N	O	S	0	0	0
			2510	1599	421	487	3			
1	B	315	Total	C	N	O	S	0	0	0
			2488	1584	417	484	3			

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

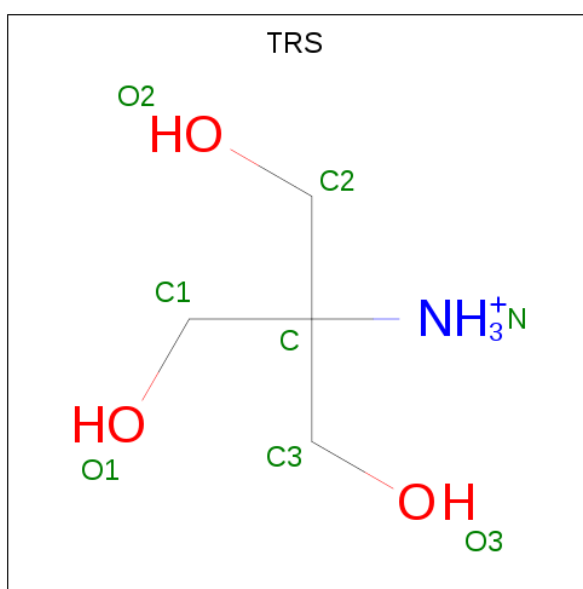
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Ca	0	0
			1	1		
2	A	1	Total	Ca	0	0
			1	1		

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0

- Molecule 4 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: C<sub>4</sub>H<sub>12</sub>NO<sub>3</sub>).



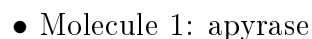
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N O 8 4 1 3	0	0
4	A	1	Total C N O 8 4 1 3	0	0
4	A	1	Total C N O 8 4 1 3	0	0
4	B	1	Total C N O 8 4 1 3	0	0
4	B	1	Total C N O 8 4 1 3	0	0
4	B	1	Total C N O 8 4 1 3	0	0
4	B	1	Total C N O 8 4 1 3	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	277	Total 277	O 277	0	0
5	B	248	Total 248	O 248	0	0



- Molecule 1: apyrase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	43.16Å 52.50Å 77.92Å 99.44° 106.58° 99.89°	Depositor
Resolution (Å)	72.55 – 1.70 37.64 – 1.70	Depositor EDS
% Data completeness (in resolution range)	95.1 (72.55-1.70) 95.1 (37.64-1.70)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.13 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, $R_{free}$	0.157 , 0.191 0.158 , 0.192	Depositor DCC
$R_{free}$ test set	3323 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	14.8	Xtriage
Anisotropy	0.111	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 50.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	5597	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.27% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, TRS, ACT

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	0.76	0/2574	0.88	8/3496 (0.2%)
1	B	0.74	0/2550	0.88	3/3462 (0.1%)
All	All	0.75	0/5124	0.88	11/6958 (0.2%)

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	259	ASP	CB-CG-OD2	6.63	124.27	118.30
1	A	310	ASP	CB-CG-OD2	6.29	123.96	118.30
1	A	259	ASP	CB-CG-OD2	6.03	123.72	118.30
1	A	242	ASP	CB-CG-OD2	5.97	123.67	118.30
1	A	296	ASP	CB-CG-OD2	5.65	123.38	118.30

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	2510	0	2418	16	0
1	B	2488	0	2402	18	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	4	0	3	0	0
3	B	12	0	9	3	0
4	A	24	0	36	3	0
4	B	32	0	48	2	0
5	A	277	0	0	11	0
5	B	248	0	0	2	0
All	All	5597	0	4916	39	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.

The worst 5 of 39 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:71:ASP:HB2	1:B:312:ARG:HH22	1.02	1.15
5:A:3259:HOH:O	1:B:80:ASP:HB2	1.66	0.96
1:B:71:ASP:HB2	1:B:312:ARG:NH2	1.88	0.88
1:B:263:SER:HA	4:B:2006:TRS:H31	1.70	0.74
1:A:145:GLU:HG3	1:A:159:LEU:HD13	1.69	0.73

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	315/331 (95%)	312 (99%)	3 (1%)	0	100	100
1	B	313/331 (95%)	310 (99%)	3 (1%)	0	100	100
All	All	628/662 (95%)	622 (99%)	6 (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	267/277 (96%)	262 (98%)	5 (2%)	57	41
1	B	265/277 (96%)	259 (98%)	6 (2%)	50	33
All	All	532/554 (96%)	521 (98%)	11 (2%)	53	36

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	236	ARG
1	B	44	ASP
1	B	184	LYS
1	A	179	LYS
1	B	179	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	195	ASN

### 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

Of 13 ligands modelled in this entry, 2 are monoatomic - leaving 11 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	TRS	B	2004	-	7,7,7	0.58	0	9,9,9	0.42	0
4	TRS	B	2003	-	7,7,7	1.13	1 (14%)	9,9,9	1.04	0
4	TRS	A	2005	-	7,7,7	0.51	0	9,9,9	0.64	0
4	TRS	B	2007	-	7,7,7	0.34	0	9,9,9	0.51	0
4	TRS	A	2001	-	7,7,7	0.90	0	9,9,9	1.13	0
3	ACT	B	3004	-	1,3,3	1.10	0	0,3,3	0.00	-
3	ACT	B	3003	-	1,3,3	1.55	0	0,3,3	0.00	-
3	ACT	A	3001	-	1,3,3	1.09	0	0,3,3	0.00	-
4	TRS	A	2002	-	7,7,7	0.38	0	9,9,9	0.49	0
4	TRS	B	2006	-	7,7,7	0.53	0	9,9,9	0.87	0
3	ACT	B	3002	-	1,3,3	1.31	0	0,3,3	0.00	-

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	TRS	B	2004	-	-	5/9/9/9	-
4	TRS	B	2003	-	-	3/9/9/9	-
4	TRS	A	2005	-	-	3/9/9/9	-
4	TRS	B	2007	-	-	6/9/9/9	-
4	TRS	A	2002	-	-	4/9/9/9	-
4	TRS	B	2006	-	-	6/9/9/9	-
4	TRS	A	2001	-	-	3/9/9/9	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	2003	TRS	O2-C2	2.37	1.50	1.42

There are no bond angle outliers.

There are no chirality outliers.

5 of 30 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	2003	TRS	C3-C-C2-O2
4	A	2005	TRS	N-C-C1-O1
4	A	2001	TRS	C3-C-C2-O2
4	A	2002	TRS	C3-C-C2-O2
4	B	2006	TRS	C2-C-C1-O1

There are no ring outliers.

6 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	2005	TRS	1	0
4	B	2007	TRS	1	0
4	A	2001	TRS	2	0
3	B	3004	ACT	1	0
3	B	3003	ACT	2	0
4	B	2006	TRS	1	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	317/331 (95%)	-0.13	15 (4%) 31 35	8, 16, 34, 48	0
1	B	315/331 (95%)	-0.21	13 (4%) 37 41	8, 16, 32, 39	0
All	All	632/662 (95%)	-0.17	28 (4%) 34 38	8, 16, 32, 48	0

The worst 5 of 28 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	170	VAL	5.9
1	A	169	ASP	5.0
1	A	167	THR	5.0
1	A	166	THR	4.6
1	A	165	THR	4.5

### 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. 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	B-factors( $\text{\AA}^2$ )	Q<0.9
4	TRS	B	2006	8/8	0.69	0.26	36,42,43,44	0
3	ACT	B	3003	4/4	0.75	0.23	39,40,40,41	0
4	TRS	B	2007	8/8	0.75	0.29	46,47,48,49	0
3	ACT	B	3002	4/4	0.82	0.14	47,47,47,48	0
4	TRS	B	2004	8/8	0.82	0.18	38,43,44,44	0
4	TRS	A	2005	8/8	0.83	0.20	22,27,30,32	0
4	TRS	B	2003	8/8	0.84	0.16	16,27,28,31	0
4	TRS	A	2001	8/8	0.86	0.19	17,27,30,33	0
3	ACT	B	3004	4/4	0.86	0.15	47,47,47,48	0
3	ACT	A	3001	4/4	0.87	0.11	49,49,49,49	0
4	TRS	A	2002	8/8	0.89	0.14	39,44,45,46	0
2	CA	B	1002	1/1	0.99	0.18	3,3,3,3	0
2	CA	A	1001	1/1	1.00	0.10	8,8,8,8	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.