



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 01:50 PM UTC

PDB ID : 9HD5 / pdb_00009hd5
Title : Crystal structure of CD73 (ecto-5'-nucleotidase) in complex with the AOPCP derivative PSB19427 in the closed state
Authors : Strater, N.; Moschuetz, S.; Dobelmann, C.; Schmies, C.C.; Jacobson, K.A.; Muller, C.E.; Junker, A.
Deposited on : 2024-11-11
Resolution : 2.91 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

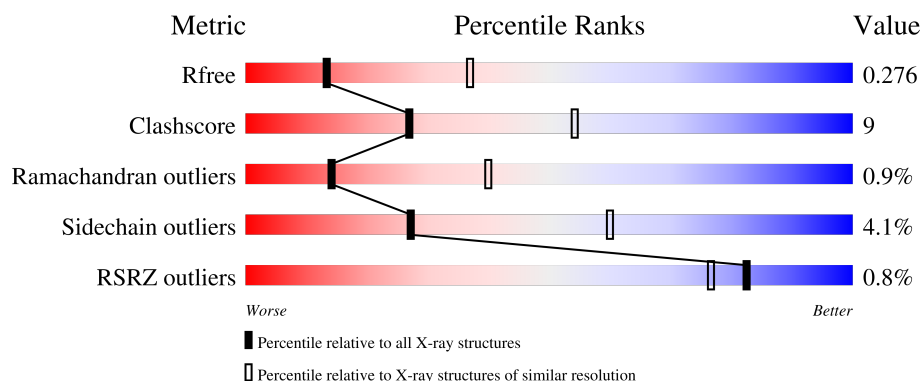
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.91 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}	180053	2995 (2.94-2.90)
Clashscore	190562	3213 (2.94-2.90)
Ramachandran outliers	187476	3128 (2.94-2.90)
Sidechain outliers	187428	3130 (2.94-2.90)
RSRZ outliers	180081	2995 (2.94-2.90)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 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	542	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: -10px; left: 0; width: 100%;"></div> <div style="position: absolute; top: 0; left: 0; width: 100%; height: 10px;"> <div style="width: 70%; height: 10px; background-color: green;"></div> <div style="width: 23%; height: 10px; background-color: yellow;"></div> <div style="width: 5%; height: 10px; background-color: grey;"></div> </div> </div> </div>
1	B	542	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: -10px; left: 0; width: 100%;"></div> <div style="position: absolute; top: 0; left: 0; width: 100%; height: 10px;"> <div style="width: 70%; height: 10px; background-color: green;"></div> <div style="width: 22%; height: 10px; background-color: yellow;"></div> <div style="width: 5%; height: 10px; background-color: grey;"></div> </div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8195 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 5'-nucleotidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	513	Total	C	N	O	S	0	0	0
			3987	2535	676	757	19			
1	B	513	Total	C	N	O	S	0	1	0
			3995	2540	679	757	19			

There are 46 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	26	MET	-	initiating methionine	UNP P21589
A	53	ASP	ASN	conflict	UNP P21589
A	311	ASP	ASN	conflict	UNP P21589
A	333	ASP	ASN	conflict	UNP P21589
A	403	ASP	ASN	conflict	UNP P21589
A	550	GLY	-	expression tag	UNP P21589
A	551	GLY	-	expression tag	UNP P21589
A	552	GLY	-	expression tag	UNP P21589
A	553	GLY	-	expression tag	UNP P21589
A	554	ALA	-	expression tag	UNP P21589
A	555	GLY	-	expression tag	UNP P21589
A	556	GLY	-	expression tag	UNP P21589
A	557	GLY	-	expression tag	UNP P21589
A	558	GLY	-	expression tag	UNP P21589
A	559	GLY	-	expression tag	UNP P21589
A	560	THR	-	expression tag	UNP P21589
A	561	LYS	-	expression tag	UNP P21589
A	562	HIS	-	expression tag	UNP P21589
A	563	HIS	-	expression tag	UNP P21589
A	564	HIS	-	expression tag	UNP P21589
A	565	HIS	-	expression tag	UNP P21589
A	566	HIS	-	expression tag	UNP P21589
A	567	HIS	-	expression tag	UNP P21589
B	26	MET	-	initiating methionine	UNP P21589
B	53	ASP	ASN	conflict	UNP P21589

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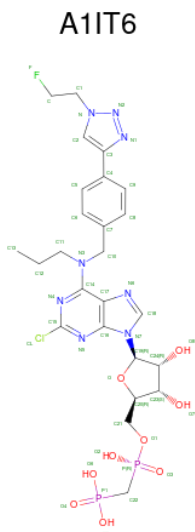
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Chain	Residue	Modelled	Actual	Comment	Reference
B	311	ASP	ASN	conflict	UNP P21589
B	333	ASP	ASN	conflict	UNP P21589
B	403	ASP	ASN	conflict	UNP P21589
B	550	GLY	-	expression tag	UNP P21589
B	551	GLY	-	expression tag	UNP P21589
B	552	GLY	-	expression tag	UNP P21589
B	553	GLY	-	expression tag	UNP P21589
B	554	ALA	-	expression tag	UNP P21589
B	555	GLY	-	expression tag	UNP P21589
B	556	GLY	-	expression tag	UNP P21589
B	557	GLY	-	expression tag	UNP P21589
B	558	GLY	-	expression tag	UNP P21589
B	559	GLY	-	expression tag	UNP P21589
B	560	THR	-	expression tag	UNP P21589
B	561	LYS	-	expression tag	UNP P21589
B	562	HIS	-	expression tag	UNP P21589
B	563	HIS	-	expression tag	UNP P21589
B	564	HIS	-	expression tag	UNP P21589
B	565	HIS	-	expression tag	UNP P21589
B	566	HIS	-	expression tag	UNP P21589
B	567	HIS	-	expression tag	UNP P21589

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 3 is [(2 {R},3 {S},4 {R},5 {R})-5-[2-chloranyl-6-[[4-[1-(2-fluoranylethyl)-1,2,3-triazol-4-yl]phenyl]methyl-propyl-amino]purin-9-yl]-3,4-bis(oxidanyl)oxolan-2-yl]methoxy-oxidanyl-phosphoryl]methylphosphonic acid (CCD ID: A1IT6) (formula: C₂₅H₃₂ClFN₈O₉P₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
3	A	1	Total 46	C 25	Cl 1	F 1	N 8	O 9	P 2	0	0
3	B	1	Total 46	C 25	Cl 1	F 1	N 8	O 9	P 2	0	0

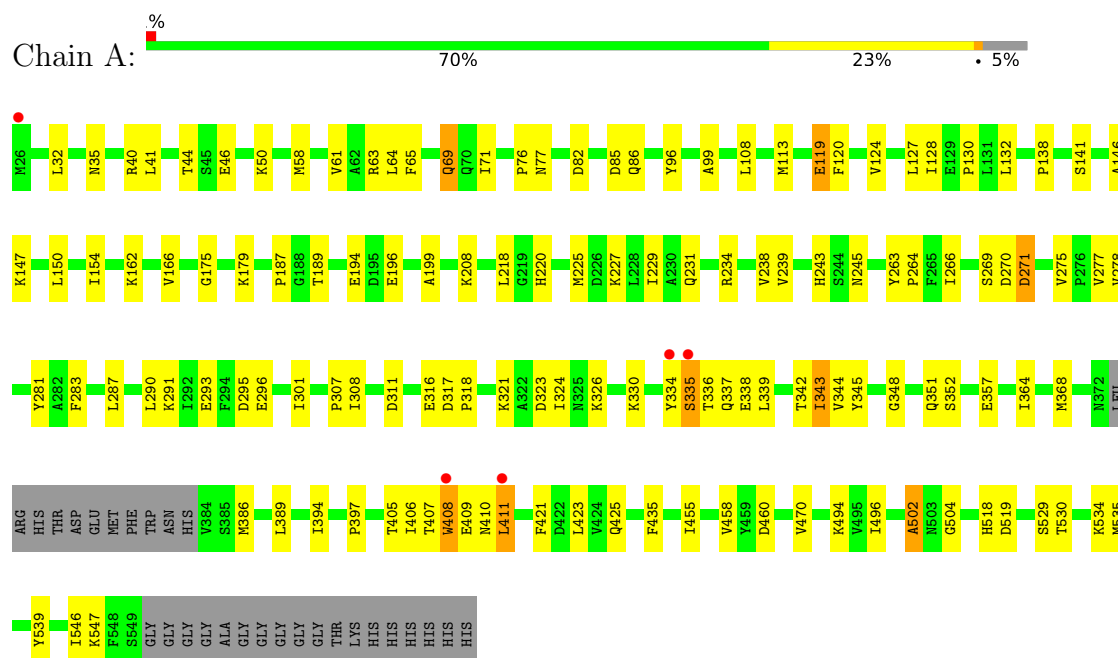
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	67	Total O 67 67	0	0
4	B	50	Total O 50 50	0	0

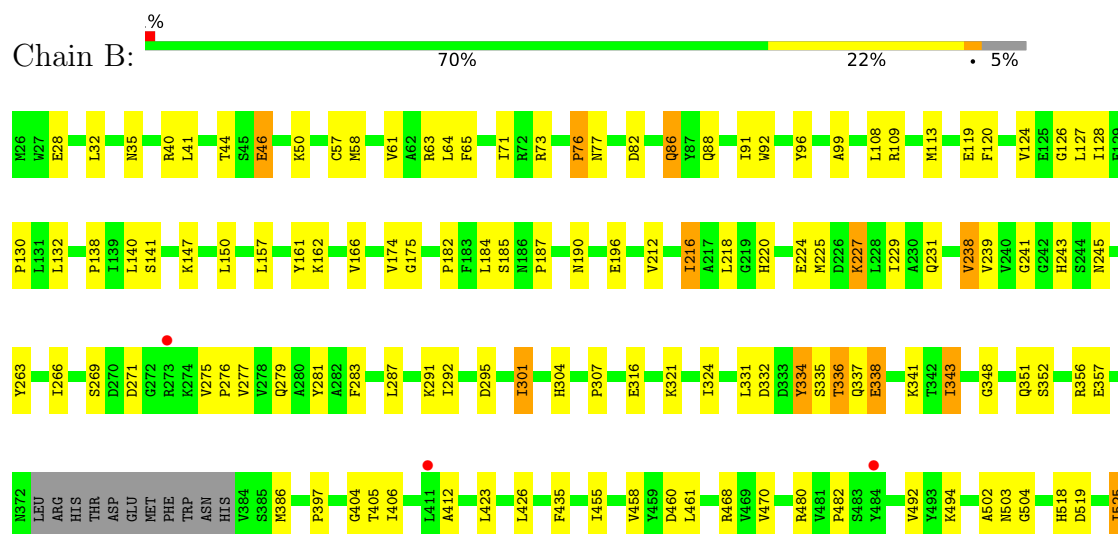
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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: 5'-nucleotidase



• Molecule 1: 5'-nucleotidase



S529	I546	F548	S549	GLY	GLY	GLY	GLY	ALA	GLY	GLY	GLY	GLY	GLY	THR	LYS	HIS	HIS	HIS	HIS	HIS
I530	K547	S548																		
Y531																				
I532																				
Y539																				

4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	92.64Å 233.37Å 54.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.37 – 2.91 49.37 – 2.91	Depositor EDS
% Data completeness (in resolution range)	63.9 (49.37-2.91) 63.8 (49.37-2.91)	Depositor EDS
R_{merge}	0.95	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.92 (at 2.91Å)	Xtriage
Refinement program	BUSTER 2.10.3 (18-SEP-2020)	Depositor
R, R_{free}	0.190 , 0.273 0.208 , 0.276	Depositor DCC
R_{free} test set	978 reflections (3.68%)	wwPDB-VP
Wilson B-factor (Å ²)	43.5	Xtriage
Anisotropy	0.506	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 68.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	8195	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 35.54 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.7415e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical 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: A1IT6, ZN

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	0.75	0/4067	1.18	16/5505 (0.3%)
1	B	0.74	0/4078	1.17	17/5519 (0.3%)
All	All	0.74	0/8145	1.17	33/11024 (0.3%)

There are no bond length outliers.

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	229	ILE	N-CA-C	-8.57	102.47	110.53
1	A	227	LYS	N-CA-C	7.90	119.89	111.28
1	A	502	ALA	N-CA-C	-6.93	103.81	111.36
1	B	227	LYS	N-CA-C	6.91	118.81	111.28
1	A	271	ASP	CA-CB-CG	6.71	119.31	112.60

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	3987	0	3978	77	0
1	B	3995	0	3991	74	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	46	0	0	0	0
3	B	46	0	0	0	0
4	A	67	0	0	1	0
4	B	50	0	0	2	0
All	All	8195	0	7969	147	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 9.

The worst 5 of 147 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:295:ASP:HB3	1:A:301:ILE:HD11	1.19	1.17
1:A:124:VAL:HG22	1:A:128:ILE:HD11	1.46	0.96
1:B:502:ALA:HB1	1:B:518:HIS:CD2	2.16	0.81
1:A:502:ALA:HB1	1:A:518:HIS:CD2	2.16	0.80
1:A:124:VAL:HG22	1:A:128:ILE:CD1	2.12	0.80

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	509/542 (94%)	472 (93%)	33 (6%)	4 (1%)	16	43
1	B	510/542 (94%)	474 (93%)	31 (6%)	5 (1%)	12	37
All	All	1019/1084 (94%)	946 (93%)	64 (6%)	9 (1%)	14	40

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	335	SER
1	B	88	GLN
1	B	127	LEU
1	B	141	SER
1	A	141	SER

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	441/460 (96%)	425 (96%)	16 (4%)	31	63
1	B	442/460 (96%)	422 (96%)	20 (4%)	24	56
All	All	883/920 (96%)	847 (96%)	36 (4%)	27	60

5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	352	SER
1	B	530	THR
1	B	356	ARG
1	B	503	ASN
1	A	343	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	526	ASN
1	B	304	HIS
1	B	523	GLN
1	B	370	ASN
1	A	437	HIS

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 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	$\# Z > 2$
3	A1IT6	B	603	2	47,50,50	0.59	3 (6%)	66,74,74	0.57	2 (3%)
3	A1IT6	A	603	2	47,50,50	0.60	3 (6%)	66,74,74	0.58	2 (3%)

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
3	A1IT6	B	603	2	-	3/34/50/50	0/5/5/5
3	A1IT6	A	603	2	-	3/34/50/50	0/5/5/5

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	603	A1IT6	C-C1	2.58	1.58	1.48
3	B	603	A1IT6	C-C1	2.42	1.58	1.48
3	B	603	A1IT6	P-O2	-2.09	1.51	1.56
3	B	603	A1IT6	P-O3	2.06	1.56	1.51
3	A	603	A1IT6	P-O3	2.03	1.56	1.51

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	603	A1IT6	O2-P-C22	2.76	118.14	106.73
3	A	603	A1IT6	O2-P-C22	2.66	117.75	106.73
3	A	603	A1IT6	C15-N4-C14	2.41	117.79	110.98
3	B	603	A1IT6	C15-N4-C14	2.38	117.71	110.98

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

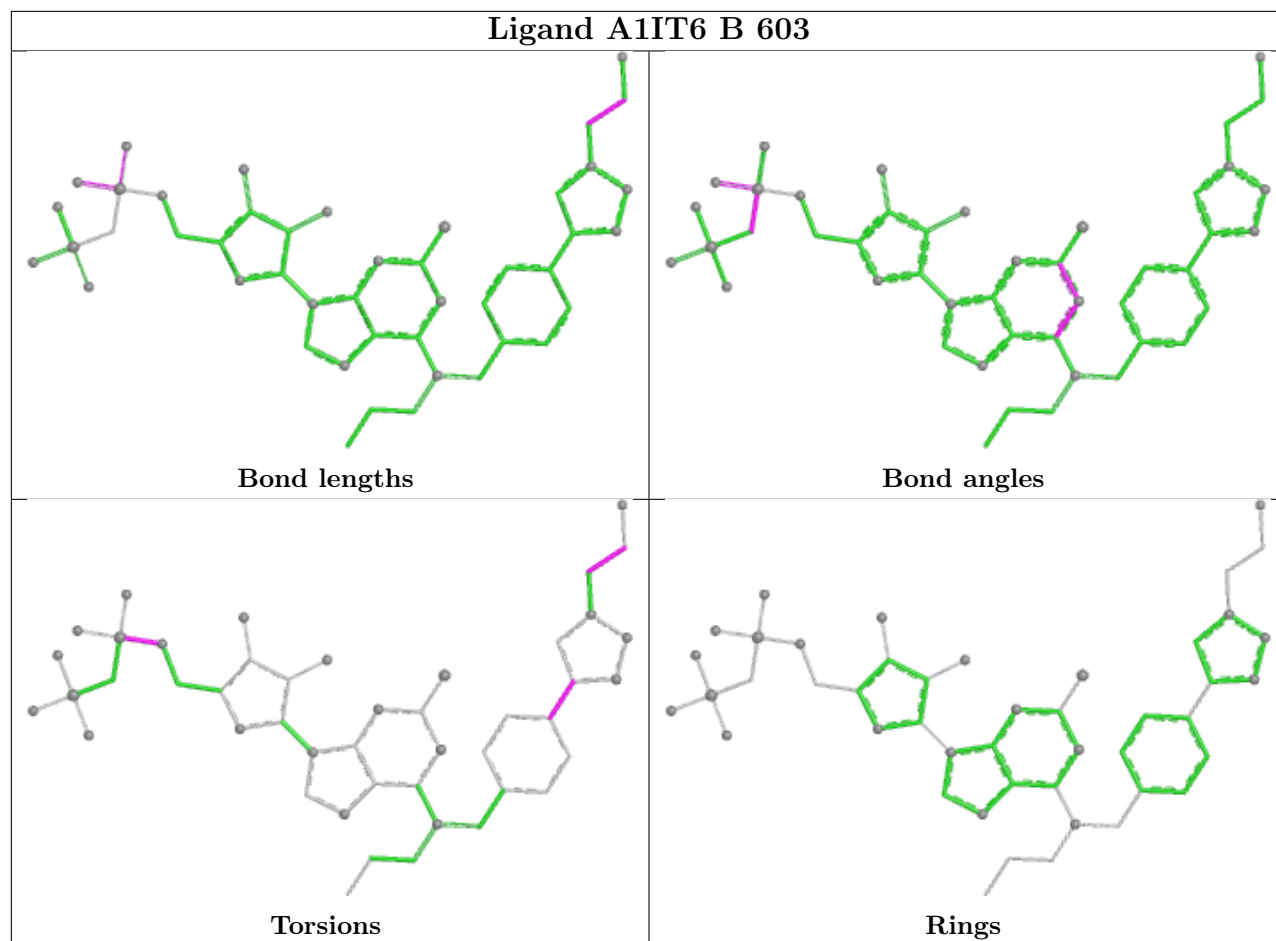
Mol	Chain	Res	Type	Atoms
3	A	603	A1IT6	C21-O1-P-C22
3	A	603	A1IT6	F-C-C1-N
3	B	603	A1IT6	C21-O1-P-C22
3	B	603	A1IT6	F-C-C1-N
3	B	603	A1IT6	C2-C3-C4-C9

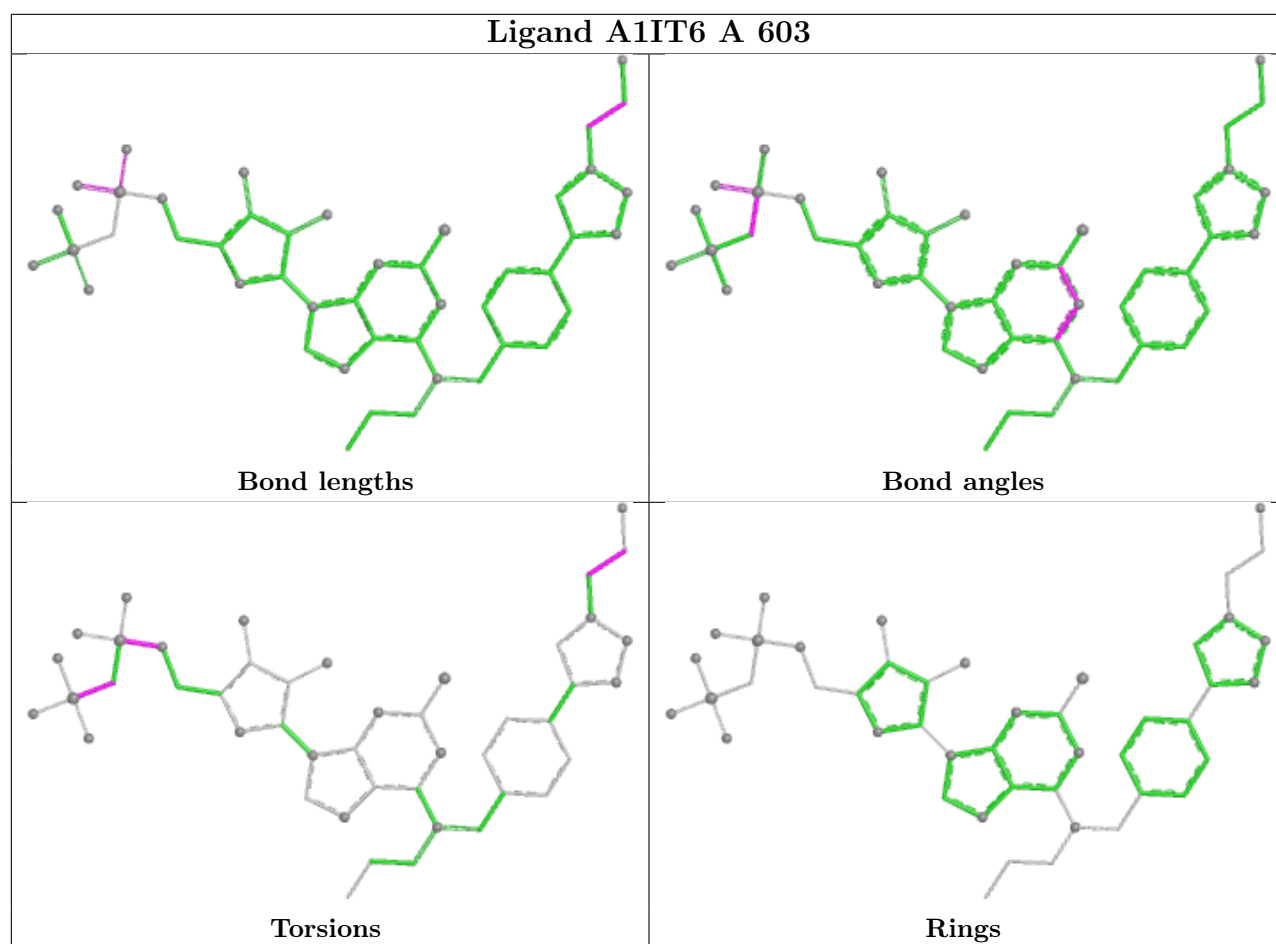
There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand A1IT6 B 603





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, 95th 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 ²)	Q<0.9
1	A	513/542 (94%)	-0.07	5 (0%)	79 72	23, 54, 78, 99	0
1	B	513/542 (94%)	0.07	3 (0%)	85 81	25, 60, 88, 97	1 (0%)
All	All	1026/1084 (94%)	-0.00	8 (0%)	82 76	23, 57, 86, 99	1 (0%)

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	408	TRP	4.5
1	A	26	MET	2.6
1	A	334	TYR	2.4
1	A	411	LEU	2.4
1	B	484	TYR	2.3

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

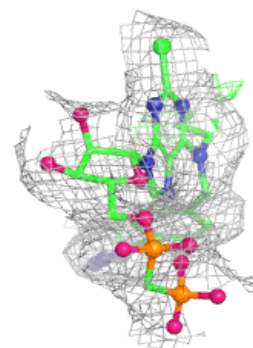
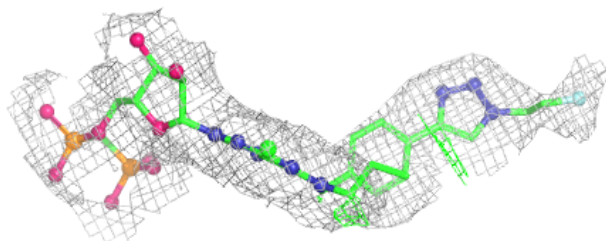
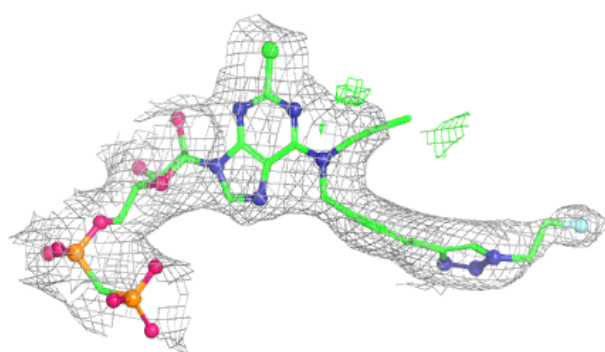
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	A1IT6	A	603	46/46	0.93	0.09	48,54,65,67	0
3	A1IT6	B	603	46/46	0.93	0.08	52,64,72,72	0
2	ZN	B	601	1/1	0.97	0.04	73,73,73,73	0
2	ZN	B	602	1/1	0.99	0.03	60,60,60,60	0
2	ZN	A	601	1/1	1.00	0.03	62,62,62,62	0
2	ZN	A	602	1/1	1.00	0.03	52,52,52,52	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

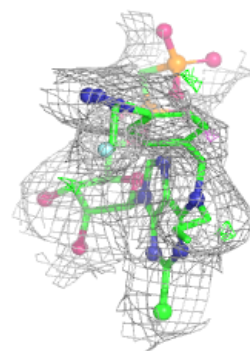
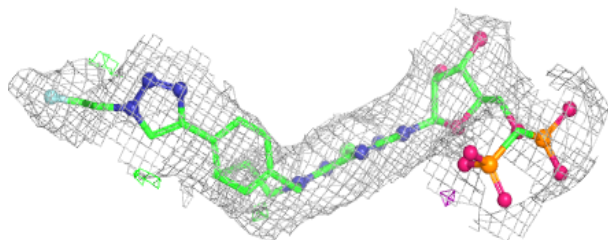
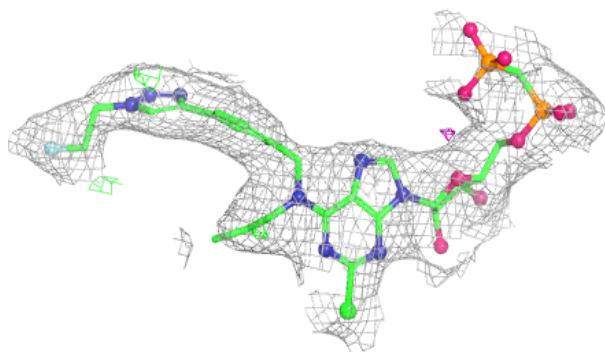
Electron density around A1IT6 A 603:

2mF_o-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around A1IT6 B 603:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.