



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 11:16 PM UTC

PDB ID : 9I1H / pdb_00009i1h
Title : Crystal structure of human CD73 (ecto-5'-nucleotidase) in complex with the AMPCP analog PSB-12730 in the closed state (crystal form IV)
Authors : Strater, N.; Moschuetz, S.; Idris, R.M.; Al-Hroub, H.; Schmies, C.C.; Muller, C.E.
Deposited on : 2025-01-16
Resolution : 2.35 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

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

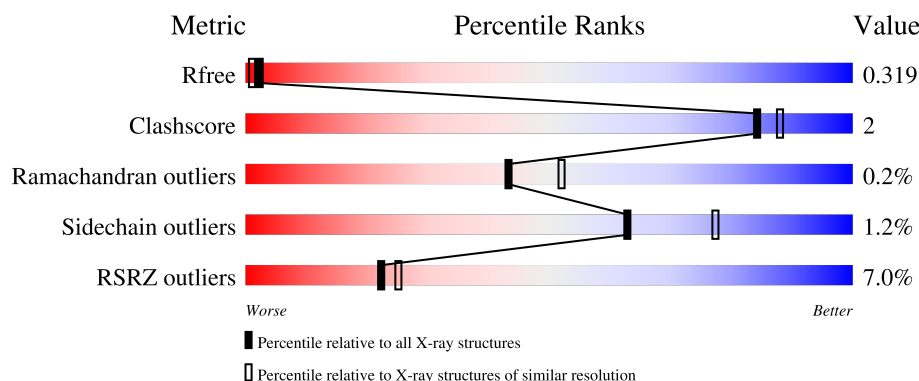
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

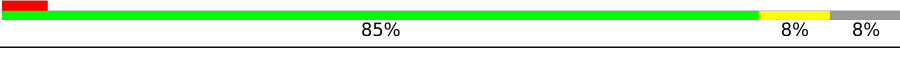
The reported resolution of this entry is 2.35 Å.

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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	567	 8% 86% 6% 8%
1	B	567	 5% 85% 8% 8%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 16517 atoms, of which 8186 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	524	Total	C	H	N	O	S	0	0	0
			8153	2599	4065	696	774	19			
1	B	524	Total	C	H	N	O	S	0	0	0
			8153	2599	4065	696	774	19			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	53	ASP	ASN	engineered mutation	UNP P21589
A	311	ASP	ASN	engineered mutation	UNP P21589
A	333	ASP	ASN	engineered mutation	UNP P21589
A	403	ASP	ASN	engineered mutation	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	53	ASP	ASN	engineered mutation	UNP P21589
B	311	ASP	ASN	engineered mutation	UNP P21589
B	333	ASP	ASN	engineered mutation	UNP P21589

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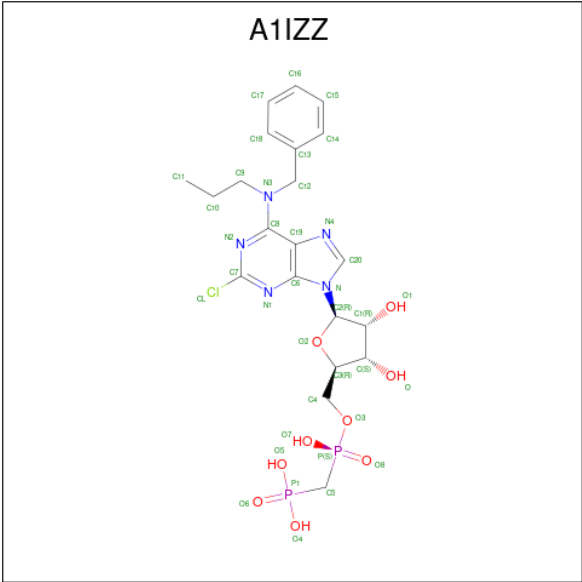
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Chain	Residue	Modelled	Actual	Comment	Reference
B	403	ASP	ASN	engineered mutation	UNP P21589
B	550	GLY	-	expression tag	UNP P21589
B	551	GLY	-	expression tag	UNP P21589
B	552	GLY	-	expression tag	UNP P21589
B	553	GLY	-	expression tag	UNP P21589
B	554	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	0	0
			2	2		
2	B	2	Total	Zn	0	0
			2	2		

- Molecule 3 is [(2 {R},3 {S},4 {R},5 {R})-5-[2-chloranyl-6-[(phenylmethyl)-propyl-amin o]purin-9-yl]-3,4-bis(oxidanyl)oxolan-2-yl]methoxy-oxidanyl-phosphoryl]methylphospho nic acid (CCD ID: A1IZZ) (formula: C₂₁H₂₈ClN₅O₉P₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
3	A	1	Total	C	Cl	H	N	O	P	25	0
			66	21	1	28	5	9	2		
3	B	1	Total	C	Cl	H	N	O	P	25	0
			66	21	1	28	5	9	2		

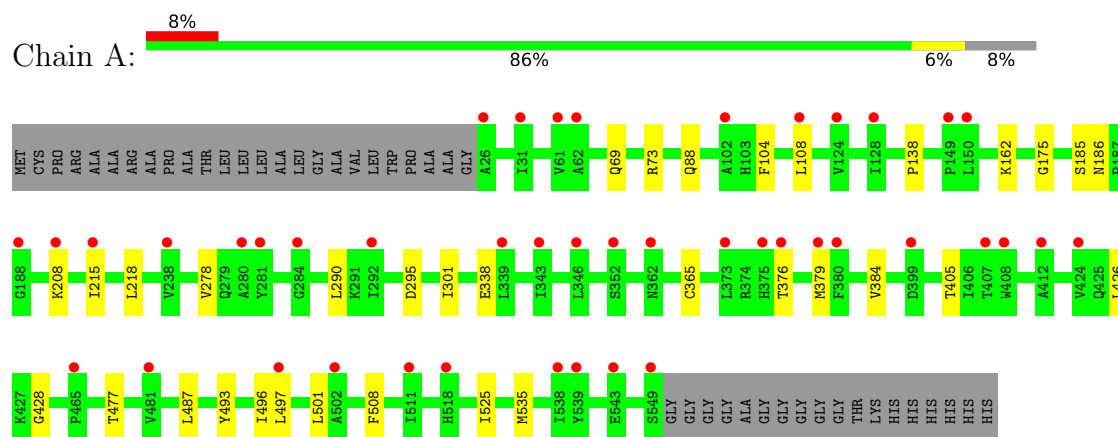
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	35	Total	O	0	0
			35	35		
4	B	40	Total	O	0	0
			40	40		

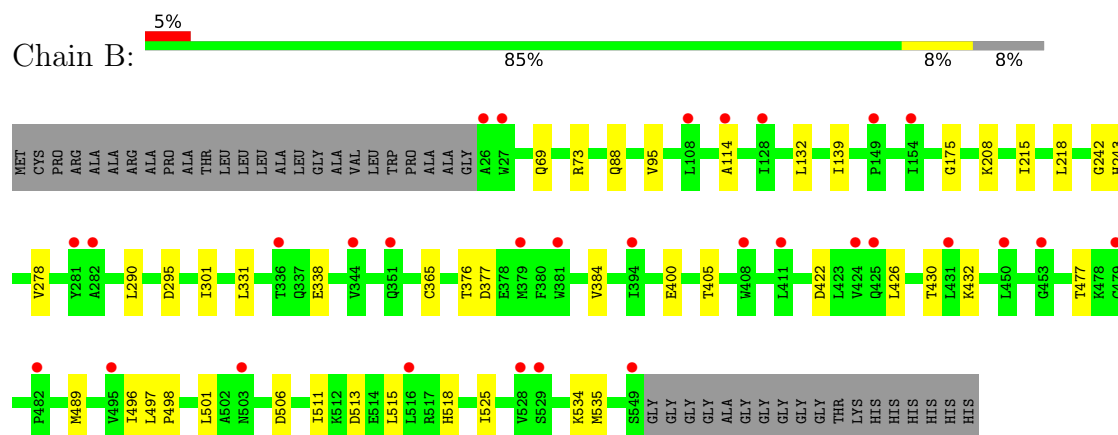
3 Residue-property plots [i](#)

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



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	95.17Å 233.61Å 54.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	88.13 – 2.35 88.13 – 2.35	Depositor EDS
% Data completeness (in resolution range)	92.2 (88.13-2.35) 92.2 (88.13-2.35)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	18.35 (at 2.34Å)	Xtriage
Refinement program	PHENIX (1.21.2_5419: ???)	Depositor
R, R_{free}	0.267 , 0.316 0.268 , 0.319	Depositor DCC
R_{free} test set	2379 reflections (4.64%)	wwPDB-VP
Wilson B-factor (Å ²)	47.7	Xtriage
Anisotropy	0.642	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 40.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	16517	wwPDB-VP
Average B, all atoms (Å ²)	74.0	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 89.54 % 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 3.2838e-08. 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: ZN, A1IZZ

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	0.13	0/4174	0.33	0/5653
1	B	0.14	0/4174	0.34	0/5653
All	All	0.14	0/8348	0.34	0/11306

There are no bond length outliers.

There are no bond angle outliers.

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	4088	4065	4064	15	0
1	B	4088	4065	4064	23	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	38	28	0	0	0
3	B	38	28	0	1	0
4	A	35	0	0	0	0
4	B	40	0	0	1	0
All	All	8331	8186	8128	37	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 2.

All (37) 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:513:ASP:OD2	4:B:701:HOH:O	2.13	0.67
1:B:498:PRO:HD2	1:B:501:LEU:HD12	1.78	0.66
1:B:295:ASP:HB3	1:B:301:ILE:HD11	1.81	0.61
1:B:376:THR:HG22	1:B:377:ASP:H	1.65	0.60
1:A:104:PHE:O	1:A:108:LEU:HD13	2.03	0.59
1:A:535:MET:HE1	1:B:535:MET:HE1	1.87	0.55
1:A:208:LYS:HE2	1:A:215:ILE:HD12	1.89	0.55
1:B:384:VAL:HG21	1:B:496:ILE:HG12	1.88	0.55
1:B:278:VAL:HG11	1:B:290:LEU:HD22	1.90	0.53
1:A:295:ASP:HB3	1:A:301:ILE:HD11	1.91	0.53
1:B:208:LYS:HE2	1:B:215:ILE:HD12	1.91	0.53
1:B:426:LEU:HD23	1:B:515:LEU:HA	1.93	0.51
1:B:338:GLU:HG3	1:B:405:THR:HG23	1.93	0.51
1:B:426:LEU:HD21	1:B:511:ILE:HG23	1.93	0.50
1:B:506:ASP:OD2	3:B:603:A1IZZ:O1	2.30	0.50
1:B:376:THR:HG22	1:B:377:ASP:N	2.26	0.50
1:B:95:VAL:HG21	1:B:331:LEU:HD23	1.95	0.48
1:A:428:GLY:O	1:A:487:LEU:HD21	2.14	0.48
1:A:69:GLN:O	1:A:73:ARG:HG3	2.14	0.47
1:B:69:GLN:O	1:B:73:ARG:HG3	2.15	0.47
1:A:175:GLY:HA2	1:A:218:LEU:O	2.15	0.46
1:A:278:VAL:HG11	1:A:290:LEU:HD22	1.98	0.46
1:B:432:LYS:HG2	1:B:489:MET:HE1	1.99	0.45
1:B:426:LEU:HD22	1:B:430:THR:HG21	1.99	0.44
1:A:384:VAL:HG21	1:A:496:ILE:HG12	2.00	0.44
1:B:132:LEU:HD23	1:B:139:ILE:HD13	2.00	0.44
1:A:426:LEU:N	1:A:493:TYR:O	2.39	0.43
1:B:175:GLY:HA2	1:B:218:LEU:O	2.18	0.43
1:B:114:ALA:HB2	1:B:218:LEU:HG	1.99	0.43
1:A:338:GLU:HG3	1:A:405:THR:HG23	2.00	0.43
1:A:426:LEU:O	1:A:493:TYR:N	2.35	0.43
1:A:138:PRO:HG2	1:A:162:LYS:HG2	2.00	0.42
1:A:501:LEU:HD22	1:A:508:PHE:CD2	2.54	0.42
1:B:242:GLY:O	1:B:243:HIS:HB3	2.20	0.41
1:A:185:SER:OG	1:A:186:ASN:N	2.51	0.41
1:B:400:GLU:OE1	1:B:400:GLU:N	2.52	0.40
1:B:422:ASP:OD2	1:B:518:HIS:NE2	2.54	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	522/567 (92%)	489 (94%)	32 (6%)	1 (0%)	43	52
1	B	522/567 (92%)	492 (94%)	29 (6%)	1 (0%)	43	52
All	All	1044/1134 (92%)	981 (94%)	61 (6%)	2 (0%)	43	52

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	88	GLN
1	B	88	GLN

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	451/474 (95%)	445 (99%)	6 (1%)	61	76
1	B	451/474 (95%)	446 (99%)	5 (1%)	65	79
All	All	902/948 (95%)	891 (99%)	11 (1%)	63	77

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	365	CYS
1	A	376	THR
1	A	379	MET
1	A	477	THR

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Mol	Chain	Res	Type
1	A	497	LEU
1	A	525	ILE
1	B	365	CYS
1	B	477	THR
1	B	497	LEU
1	B	525	ILE
1	B	534	LYS

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

Mol	Chain	Res	Type
1	A	153	GLN
1	A	523	GLN
1	B	299	ASN
1	B	509	GLN

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 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	A1IZZ	A	603	2	38,41,41	0.20	0	54,61,61	0.70	2 (3%)
3	A1IZZ	B	603	2	38,41,41	0.20	0	54,61,61	0.65	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	A1IZZ	A	603	2	-	3/27/43/43	0/4/4/4
3	A1IZZ	B	603	2	-	4/27/43/43	0/4/4/4

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	603	A1IZZ	O8-P-C5	4.01	119.62	109.05
3	B	603	A1IZZ	O8-P-C5	3.56	118.43	109.05
3	B	603	A1IZZ	C7-N2-C8	2.33	117.57	110.98
3	A	603	A1IZZ	C7-N2-C8	2.32	117.54	110.98

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	603	A1IZZ	C4-O3-P-C5
3	B	603	A1IZZ	C4-O3-P-C5
3	B	603	A1IZZ	C13-C12-N3-C9
3	A	603	A1IZZ	C13-C12-N3-C9
3	A	603	A1IZZ	C13-C12-N3-C8
3	B	603	A1IZZ	C13-C12-N3-C8
3	B	603	A1IZZ	C4-O3-P-O8

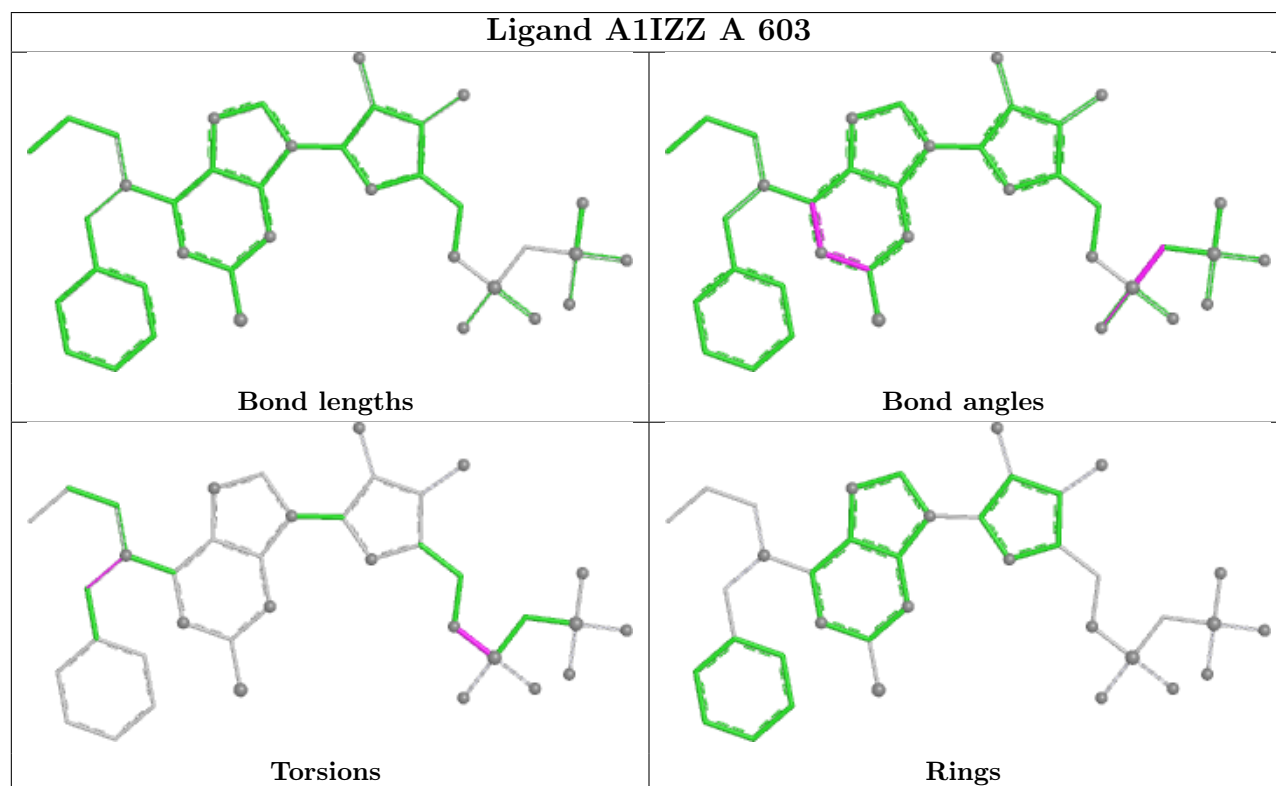
There are no ring outliers.

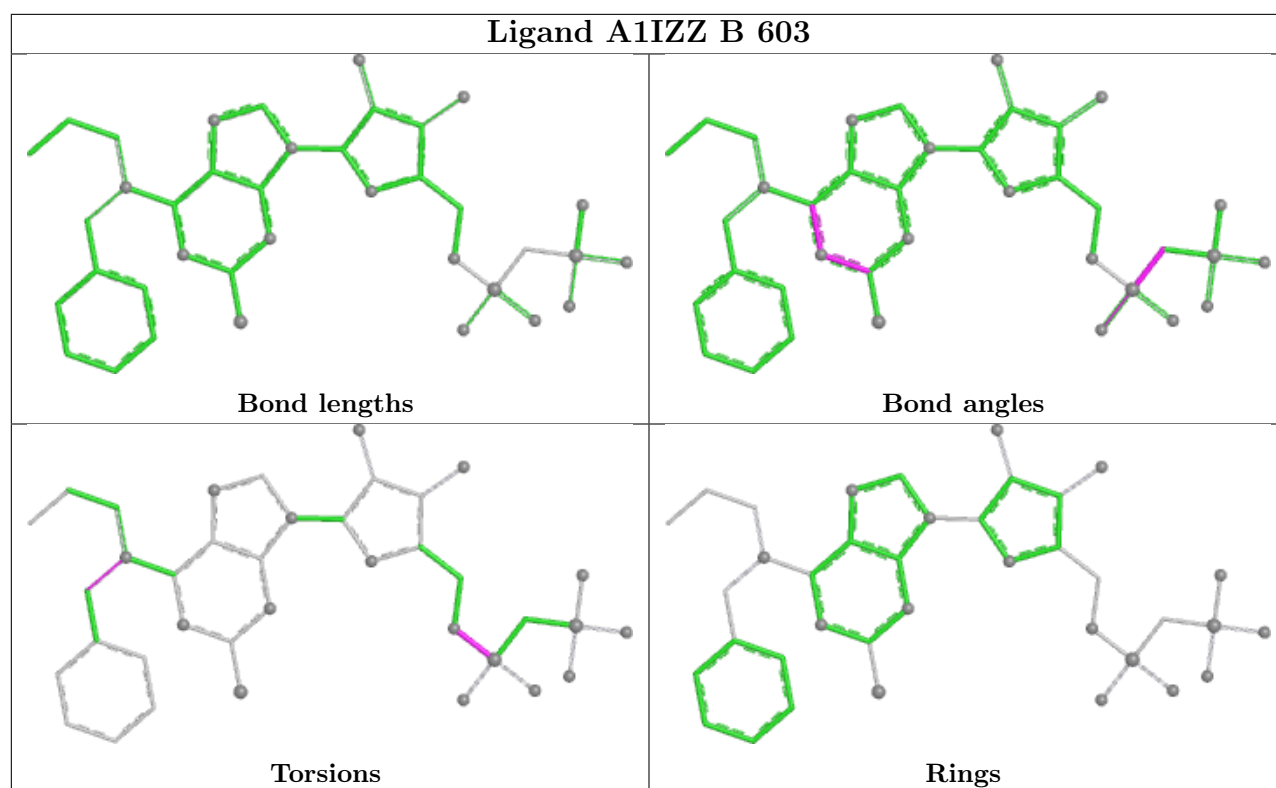
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	603	A1IZZ	1	0

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.





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

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, 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	524/567 (92%)	0.91	43 (8%)	17 20	56, 72, 104, 161	0
1	B	524/567 (92%)	0.77	30 (5%)	29 34	45, 68, 101, 172	0
All	All	1048/1134 (92%)	0.84	73 (6%)	22 25	45, 71, 104, 172	0

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	102	ALA	4.3
1	A	61	VAL	4.2
1	A	339	LEU	3.8
1	B	394	ILE	3.7
1	A	497	LEU	3.7
1	A	424	VAL	3.6
1	A	150	LEU	3.6
1	B	431	LEU	3.6
1	B	516	LEU	3.6
1	A	124	VAL	3.6
1	B	424	VAL	3.5
1	A	511	ILE	3.5
1	B	381	TRP	3.3
1	A	379	MET	3.3
1	A	518	HIS	3.3
1	A	380	PHE	3.3
1	B	26	ALA	3.2
1	A	128	ILE	3.2
1	A	343	ILE	3.2
1	B	154	ILE	3.2
1	A	26	ALA	3.1
1	A	373	LEU	3.1
1	B	549	SER	3.1
1	B	408	TRP	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	408	TRP	3.0
1	B	114	ALA	2.9
1	A	549	SER	2.9
1	A	399	ASP	2.9
1	B	425	GLN	2.8
1	B	379	MET	2.8
1	A	31	ILE	2.8
1	A	412	ALA	2.8
1	A	375	HIS	2.7
1	A	502	ALA	2.6
1	A	352	SER	2.6
1	B	336	THR	2.5
1	A	539	TYR	2.5
1	B	495	VAL	2.5
1	A	538	ILE	2.5
1	B	453	GLY	2.5
1	B	281	TYR	2.4
1	A	543	GLU	2.4
1	B	411	LEU	2.4
1	B	149	PRO	2.4
1	A	376	THR	2.4
1	A	238	VAL	2.4
1	B	503	ASN	2.4
1	B	344	VAL	2.4
1	B	482	PRO	2.3
1	A	108	LEU	2.3
1	A	188	GLY	2.3
1	A	215	ILE	2.3
1	A	292	ILE	2.2
1	A	346	LEU	2.2
1	B	351	GLN	2.2
1	B	282	ALA	2.2
1	B	27	TRP	2.2
1	A	465	PRO	2.2
1	A	62	ALA	2.2
1	B	479	CYS	2.2
1	A	280	ALA	2.2
1	B	529	SER	2.2
1	B	128	ILE	2.1
1	A	481	VAL	2.1
1	B	528	VAL	2.1
1	B	108	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	149	PRO	2.1
1	A	284	GLY	2.1
1	A	208	LYS	2.1
1	A	281	TYR	2.1
1	A	407	THR	2.0
1	A	362	ASN	2.0
1	B	450	LEU	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

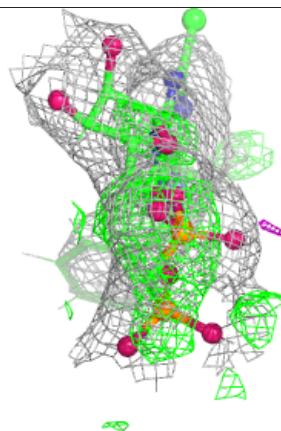
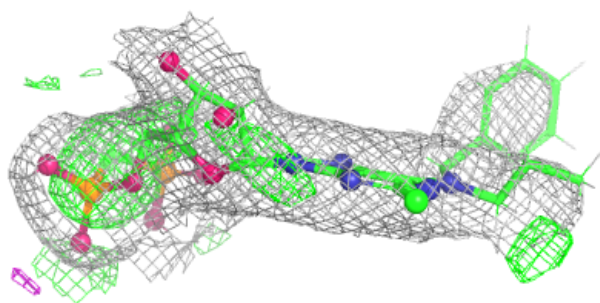
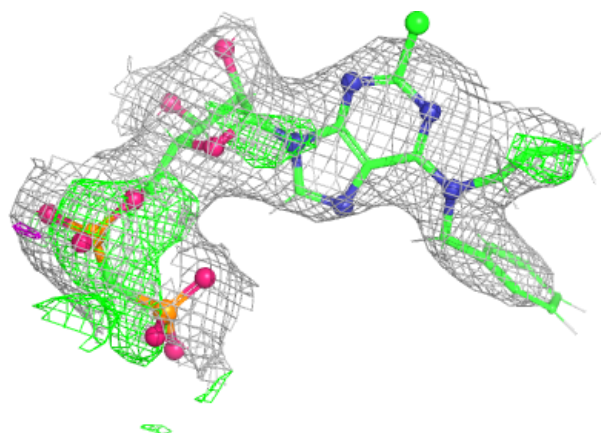
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	A1IZZ	A	603	38/38	0.92	0.16	39,54,71,95	66
3	A1IZZ	B	603	38/38	0.93	0.12	39,56,70,98	66
2	ZN	A	601	1/1	0.95	0.05	54,54,54,54	0
2	ZN	B	601	1/1	0.95	0.09	54,54,54,54	0
2	ZN	B	602	1/1	0.97	0.08	54,54,54,54	0
2	ZN	A	602	1/1	0.98	0.06	54,54,54,54	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.

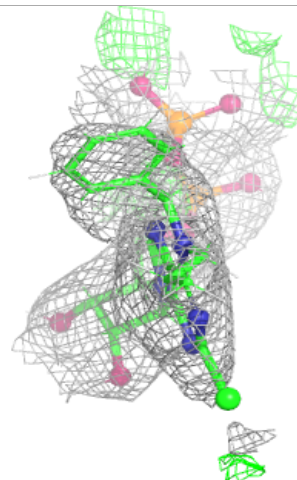
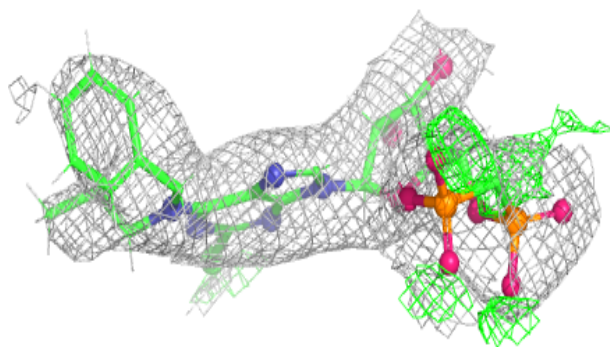
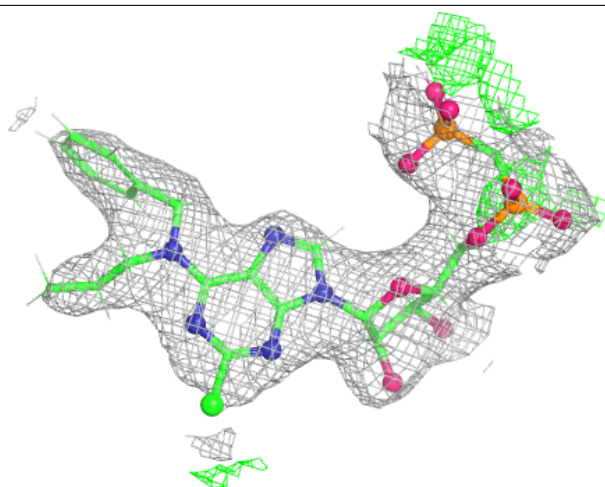
Electron density around A1IZZ A 603:

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



Electron density around A1IZZ 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.