



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 17, 2026 – 11:45 PM UTC

PDB ID : 5SDX / pdb\_00005sdx  
Title : CRYSTAL STRUCTURE OF HUMAN PHOSPHODIESTERASE 10 IN COMPLEX WITH c1(cccc(n1)CCc2nc(en2C)c3ccccc3)N4CCOCC4, micromolar IC<sub>50</sub>=3.142777  
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Deposited on : 2022-01-21  
Resolution : 2.19 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.

The types of validation reports are described at

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

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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)  
Xtrriage (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

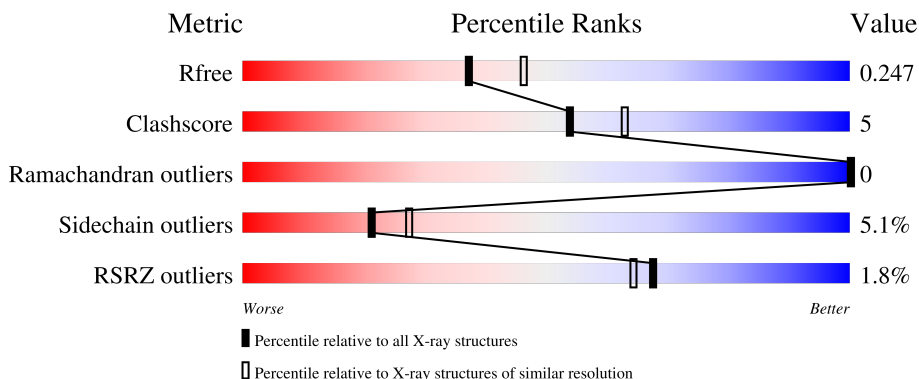
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*


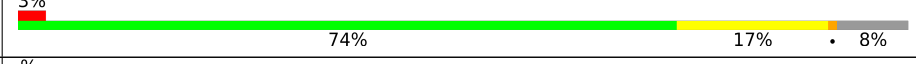


The reported resolution of this entry is 2.19 Å.

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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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  $\geq 3$ , 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	343	 75% 14% • 9%
1	B	343	 74% 17% • 8%
1	C	343	 77% 12% • 9%
1	D	343	 76% 13% • 10%

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10669 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
			Total	C	N	O	S			
1	A	313	2549	1629	435	461	24	0	1	0
1	B	315	2559	1635	437	463	24	0	1	0
1	C	313	2549	1629	435	461	24	0	1	0
1	D	310	2519	1612	429	454	24	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	447	GLY	-	expression tag	UNP Q9Y233
A	448	SER	-	expression tag	UNP Q9Y233
B	447	GLY	-	expression tag	UNP Q9Y233
B	448	SER	-	expression tag	UNP Q9Y233
C	447	GLY	-	expression tag	UNP Q9Y233
C	448	SER	-	expression tag	UNP Q9Y233
D	447	GLY	-	expression tag	UNP Q9Y233
D	448	SER	-	expression tag	UNP Q9Y233

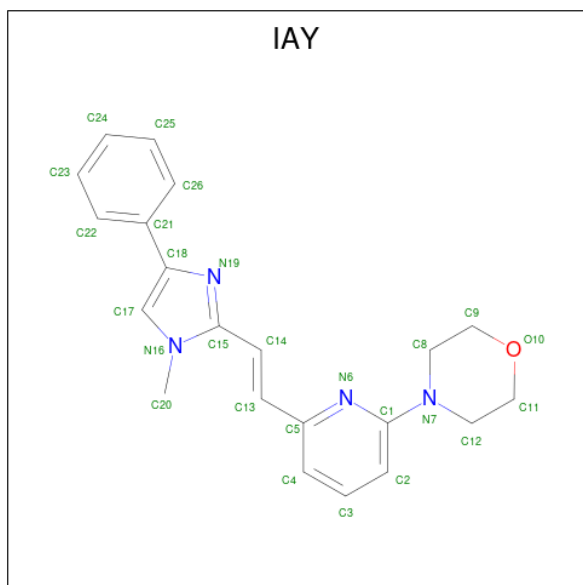
- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 4 is 4-{6-[(E)-2-(1-methyl-4-phenyl-1H-imidazol-2-yl)ethen-1-yl]pyridin-2-yl}morpholine (CCD ID: IAY) (formula: C<sub>21</sub>H<sub>22</sub>N<sub>4</sub>O) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N O 26 21 4 1	0	0
4	B	1	Total C N O 26 21 4 1	0	0
4	C	1	Total C N O 26 21 4 1	0	0
4	D	1	Total C N O 26 21 4 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	105	Total 105	O 105	0	0
5	B	108	Total 108	O 108	0	0
5	C	108	Total 108	O 108	0	0
5	D	60	Total 60	O 60	0	0



ALA  
SER  
GLU  
ASP

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

Chain D: %

GLY SER SER ILE CYS THR SER GLU TRP GLN GLY L459 M460 Q461 F462 Y492 M493 R496 S497 T500 E504 S514 V515 K516 H535 Y538 Q542 D550 R553 R568 L575 Q576 K577 H594 H595 I602 L603 Q604 L605 E606 G607 H608 S617

Q621 V622 L623 F639 Q644 Y649 Q650 T651 Q659 S660 D663 L675 C676 S677 V678 A689 I692 Y693 D701 E702 M703 Q709 R716 K719 V722 P723 Q724 G725 L727 T742 P746 I766 R767 G768 GLU GLU THR ALA THR TRP ILE SER

PRO  
SER  
VAL  
ALA  
GLN  
LYS  
ALA  
ALA  
SER  
GLU  
ASP

## 4 Data and refinement statistics i

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	135.38Å 135.38Å 235.36Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	43.68 – 2.19 43.68 – 2.19	Depositor EDS
% Data completeness (in resolution range)	96.3 (43.68-2.19) 96.3 (43.68-2.19)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.37 (at 2.20Å)	Xtrriage
Refinement program	REFMAC 5.8.0258	Depositor
R, $R_{free}$	0.187 , 0.242 0.194 , 0.247	Depositor DCC
$R_{free}$ test set	4122 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	36.9	Xtrriage
Anisotropy	0.005	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 30.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.027 for h,-h-k,-l	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	10669	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	47.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.52% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: IAY, ZN, CME, 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	1.19	4/2603 (0.2%)	1.47	15/3521 (0.4%)
1	B	1.16	1/2613 (0.0%)	1.51	13/3535 (0.4%)
1	C	1.17	5/2603 (0.2%)	1.49	11/3521 (0.3%)
1	D	1.18	2/2570 (0.1%)	1.54	12/3478 (0.3%)
All	All	1.17	12/10389 (0.1%)	1.50	51/14055 (0.4%)

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	595	HIS	C-O	6.43	1.31	1.24
1	A	481	PRO	C-O	-6.30	1.16	1.24
1	C	465	PRO	C-O	-5.97	1.16	1.24
1	C	710	PRO	C-O	-5.80	1.17	1.23
1	C	755	CYS	C-O	5.72	1.30	1.24

The worst 5 of 51 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	735	ILE	CA-C-O	8.18	124.17	118.69
1	B	554	LYS	CA-C-N	7.12	127.89	119.98
1	B	554	LYS	C-N-CA	7.12	127.89	119.98
1	D	746	PRO	N-CA-C	6.72	118.90	110.70
1	A	719	LYS	CB-CA-C	-6.69	99.31	110.68

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	2549	0	2524	28	0
1	B	2559	0	2528	21	0
1	C	2549	0	2524	22	0
1	D	2519	0	2496	30	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	26	0	0	1	0
4	B	26	0	0	0	0
4	C	26	0	0	3	0
4	D	26	0	0	5	0
5	A	105	0	0	2	0
5	B	108	0	0	2	0
5	C	108	0	0	1	0
5	D	60	0	0	2	0
All	All	10669	0	10072	100	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 5.

The worst 5 of 100 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:469:CYS:SG	5:A:993:HOH:O	2.27	0.92
1:D:677:SER:OG	4:D:803:IAY:O10	2.10	0.70
1:A:461:GLN:NE2	1:A:461:GLN:HA	2.09	0.68
1:D:644:GLN:HE21	1:D:644:GLN:HA	1.59	0.67
1:C:677:SER:OG	4:C:803:IAY:O10	2.14	0.66

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	311/343 (91%)	301 (97%)	10 (3%)	0	100	100
1	B	313/343 (91%)	301 (96%)	12 (4%)	0	100	100
1	C	311/343 (91%)	300 (96%)	11 (4%)	0	100	100
1	D	307/343 (90%)	295 (96%)	12 (4%)	0	100	100
All	All	1242/1372 (90%)	1197 (96%)	45 (4%)	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	282/305 (92%)	269 (95%)	13 (5%)	24	32
1	B	282/305 (92%)	267 (95%)	15 (5%)	20	26
1	C	282/305 (92%)	266 (94%)	16 (6%)	18	23
1	D	279/305 (92%)	266 (95%)	13 (5%)	23	31
All	All	1125/1220 (92%)	1068 (95%)	57 (5%)	21	27

5 of 57 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	463	THR
1	D	722	VAL
1	C	605	LEU

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Mol	Chain	Res	Type
1	D	709	GLN
1	D	621	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	542	GLN
1	D	724	GLN
1	C	621	GLN
1	D	621	GLN
1	C	604	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](#)

4 non-standard protein/DNA/RNA residues are modelled in this entry.

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	$\# Z  > 2$
1	CME	B	509	1	8,9,10	0.45	0	6,9,11	0.88	0
1	CME	A	509	1	8,9,10	0.62	0	6,9,11	1.09	0
1	CME	C	509	1	8,9,10	0.55	0	6,9,11	1.08	0
1	CME	D	509	1	8,9,10	0.57	0	6,9,11	0.75	0

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
1	CME	B	509	1	-	1/5/8/10	-
1	CME	A	509	1	-	2/5/8/10	-
1	CME	C	509	1	-	2/5/8/10	-
1	CME	D	509	1	-	1/5/8/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	509	CME	SD-CE-CZ-OH
1	B	509	CME	SD-CE-CZ-OH
1	C	509	CME	CE-SD-SG-CB
1	C	509	CME	CZ-CE-SD-SG
1	A	509	CME	CZ-CE-SD-SG

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 8 are monoatomic - leaving 4 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	IAY	C	803	-	29,29,29	1.96	6 (20%)	38,39,39	2.76	20 (52%)
4	IAY	A	803	-	29,29,29	2.07	7 (24%)	38,39,39	2.81	14 (36%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	IAY	D	803	-	29,29,29	2.06	8 (27%)	38,39,39	2.58	13 (34%)
4	IAY	B	803	-	29,29,29	1.75	6 (20%)	38,39,39	2.62	16 (42%)

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	IAY	C	803	-	-	5/13/21/21	0/4/4/4
4	IAY	A	803	-	-	7/13/21/21	0/4/4/4
4	IAY	D	803	-	-	5/13/21/21	0/4/4/4
4	IAY	B	803	-	-	6/13/21/21	0/4/4/4

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	803	IAY	C14-C13	6.36	1.49	1.33
4	D	803	IAY	C14-C13	5.73	1.47	1.33
4	A	803	IAY	C14-C13	5.48	1.47	1.33
4	B	803	IAY	C14-C13	5.42	1.46	1.33
4	C	803	IAY	C17-C18	4.27	1.44	1.37

The worst 5 of 63 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	803	IAY	C14-C15-N19	-7.63	115.95	125.03
4	A	803	IAY	C14-C15-N16	7.63	132.98	122.69
4	B	803	IAY	C20-N16-C15	7.54	134.67	127.84
4	D	803	IAY	C14-C15-N16	7.15	132.33	122.69
4	C	803	IAY	C5-N6-C1	-6.81	110.64	118.15

There are no chirality outliers.

5 of 23 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	803	IAY	C14-C13-C5-C4
4	A	803	IAY	C14-C13-C5-N6
4	A	803	IAY	C13-C14-C15-N16
4	A	803	IAY	C13-C14-C15-N19

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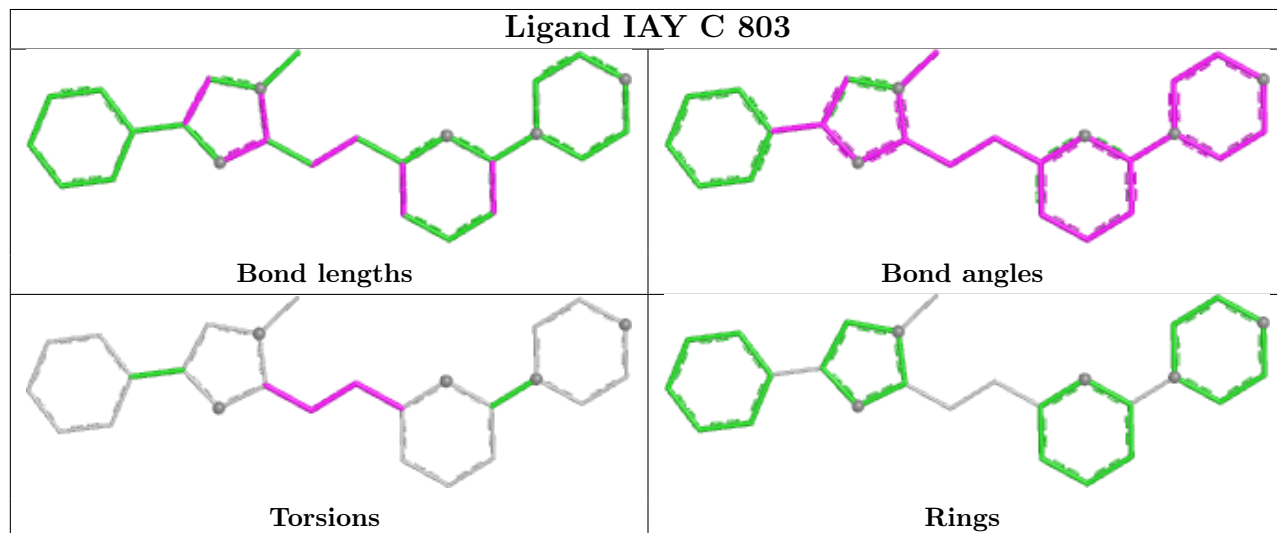
Mol	Chain	Res	Type	Atoms
4	B	803	IAY	C14-C13-C5-C4

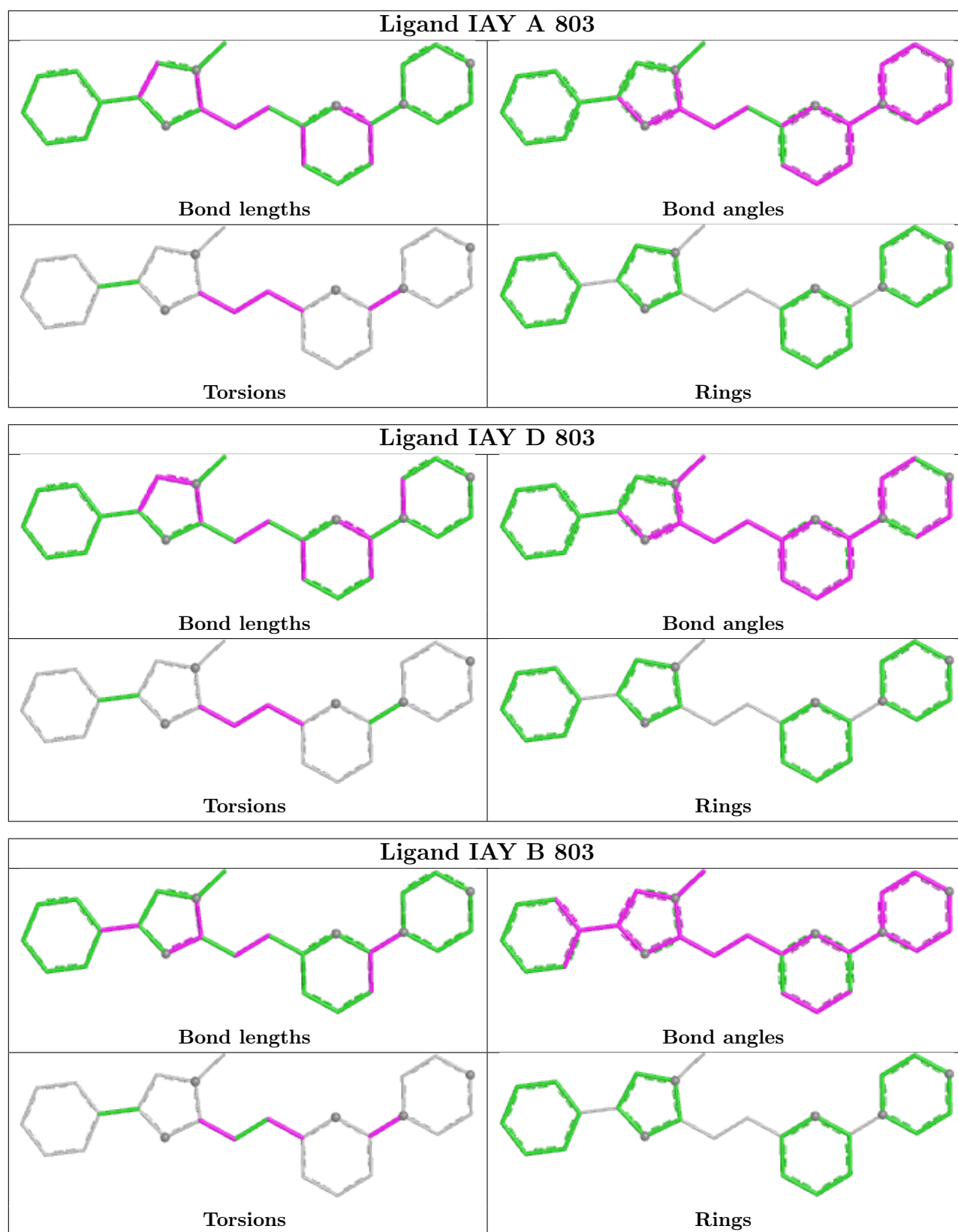
There are no ring outliers.

3 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	803	IAY	3	0
4	A	803	IAY	1	0
4	D	803	IAY	5	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 [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	312/343 (90%)	-0.01	4 (1%) 75 73	22, 42, 72, 100	1 (0%)
1	B	314/343 (91%)	0.06	10 (3%) 50 47	22, 41, 73, 102	1 (0%)
1	C	312/343 (90%)	-0.10	4 (1%) 75 73	26, 42, 67, 106	1 (0%)
1	D	309/343 (90%)	0.27	5 (1%) 70 67	36, 52, 76, 102	0
All	All	1247/1372 (90%)	0.06	23 (1%) 67 64	22, 45, 73, 106	3 (0%)

The worst 5 of 23 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	459	LEU	5.3
1	B	458	GLY	4.2
1	B	459	LEU	4.1
1	A	459	LEU	4.0
1	C	459	LEU	3.9

### 6.2 Non-standard residues in protein, DNA, RNA chains [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(Å <sup>2</sup> )	Q<0.9
1	CME	D	509	10/11	0.86	0.14	53,59,99,107	0
1	CME	B	509	10/11	0.88	0.18	42,52,91,106	0
1	CME	C	509	10/11	0.91	0.12	47,53,78,81	0
1	CME	A	509	10/11	0.94	0.10	46,56,81,85	0

### 6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 6.4 Ligands [i](#)

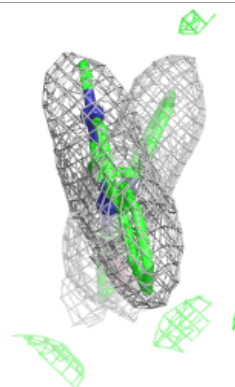
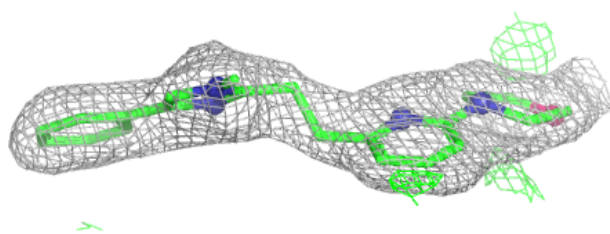
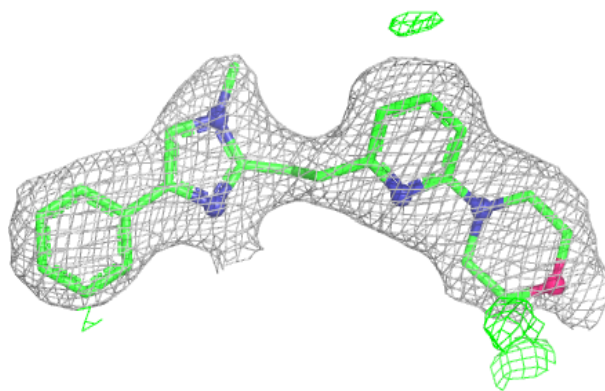
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	IAY	C	803	26/26	0.90	0.11	48,58,69,82	0
4	IAY	D	803	26/26	0.91	0.12	56,64,74,88	0
4	IAY	A	803	26/26	0.92	0.11	39,46,61,67	0
4	IAY	B	803	26/26	0.94	0.11	39,47,72,88	0
3	MG	C	802	1/1	0.98	0.02	29,29,29,29	0
3	MG	B	802	1/1	0.99	0.02	25,25,25,25	0
3	MG	D	802	1/1	0.99	0.04	44,44,44,44	0
2	ZN	C	801	1/1	1.00	0.01	37,37,37,37	0
2	ZN	D	801	1/1	1.00	0.01	45,45,45,45	0
3	MG	A	802	1/1	1.00	0.02	30,30,30,30	0
2	ZN	A	801	1/1	1.00	0.01	36,36,36,36	0
2	ZN	B	801	1/1	1.00	0.01	35,35,35,35	0

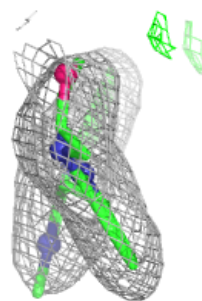
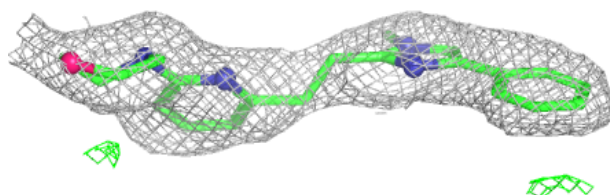
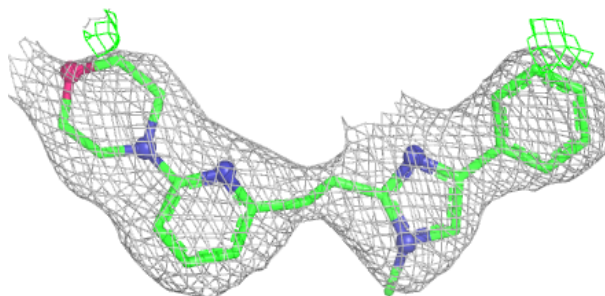
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around IAY C 803:**

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

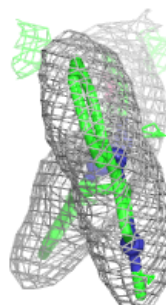
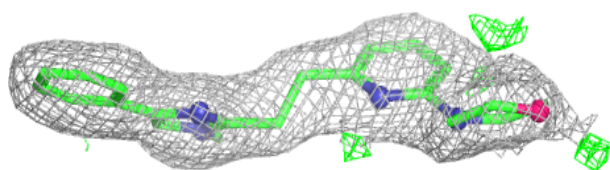
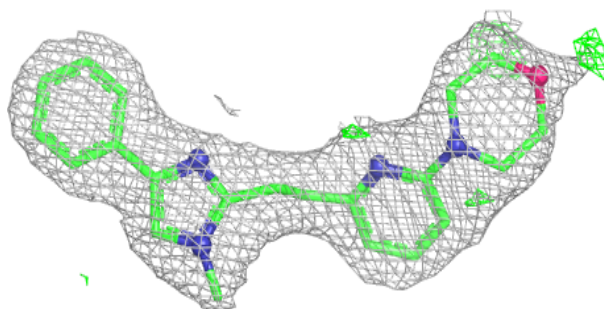
**Electron density around IAY D 803:**

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

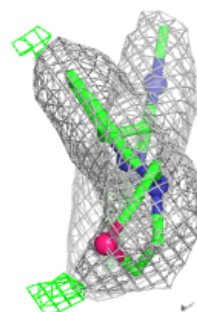
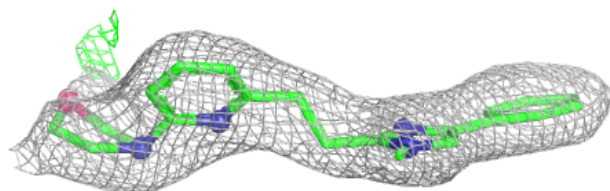
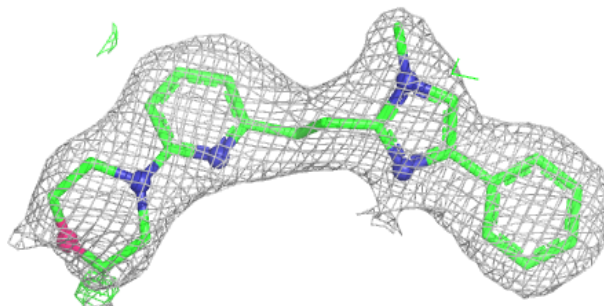


**Electron density around IAY A 803:**

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

**Electron density around IAY B 803:**

$2mF_o-DF_c$  (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.