



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 20, 2020 – 07:51 PM BST

PDB ID : 4F5Y  
Title : Crystal structure of human STING CTD complex with C-di-GMP  
Authors : Gu, L.; Shang, G.; Zhu, D.; Li, N.; Zhang, J.; Zhu, C.; Lu, D.; Liu, C.; Yu, Q.; Zhao, Y.; Xu, S.  
Deposited on : 2012-05-13  
Resolution : 2.40 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](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 : 2.13.1  
buster-report : 1.1.7 (2018)  
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) : 2.13.1

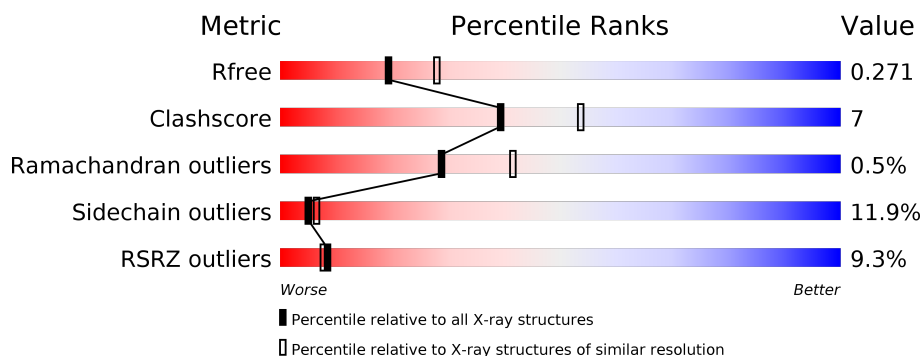
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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	239	<div> <div>8%</div> <div>66%</div> <div>13%</div> <div>•</div> <div>19%</div> </div>
1	B	239	<div> <div>8%</div> <div>58%</div> <div>19%</div> <div>•</div> <div>19%</div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3292 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 Transmembrane protein 173.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	193	Total	C	N	O	S	0	0	0
			1553	974	274	299	6			
1	B	193	Total	C	N	O	S	0	0	0
			1553	974	274	299	6			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	232	ARG	HIS	SEE REMARK 999	UNP Q86WV6
A	380	LEU	-	EXPRESSION TAG	UNP Q86WV6
A	381	GLU	-	EXPRESSION TAG	UNP Q86WV6
A	382	HIS	-	EXPRESSION TAG	UNP Q86WV6
A	383	HIS	-	EXPRESSION TAG	UNP Q86WV6
A	384	HIS	-	EXPRESSION TAG	UNP Q86WV6
A	385	HIS	-	EXPRESSION TAG	UNP Q86WV6
A	386	HIS	-	EXPRESSION TAG	UNP Q86WV6
A	387	HIS	-	EXPRESSION TAG	UNP Q86WV6
B	232	ARG	HIS	SEE REMARK 999	UNP Q86WV6
B	380	LEU	-	EXPRESSION TAG	UNP Q86WV6
B	381	GLU	-	EXPRESSION TAG	UNP Q86WV6
B	382	HIS	-	EXPRESSION TAG	UNP Q86WV6
B	383	HIS	-	EXPRESSION TAG	UNP Q86WV6
B	384	HIS	-	EXPRESSION TAG	UNP Q86WV6
B	385	HIS	-	EXPRESSION TAG	UNP Q86WV6
B	386	HIS	-	EXPRESSION TAG	UNP Q86WV6
B	387	HIS	-	EXPRESSION TAG	UNP Q86WV6

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

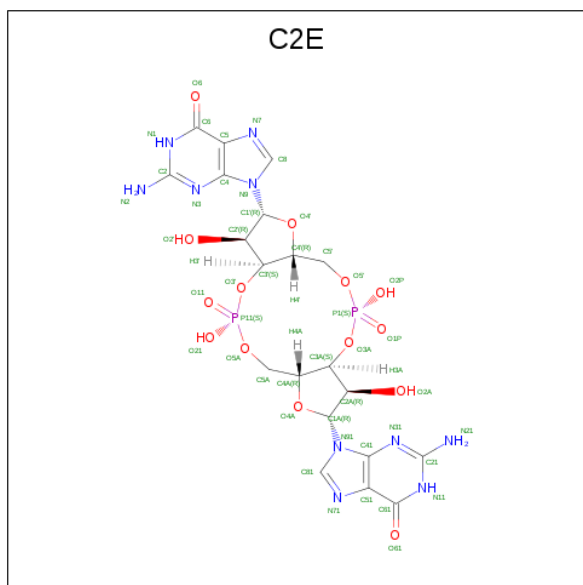
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Ca	0	0
			1	1		

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

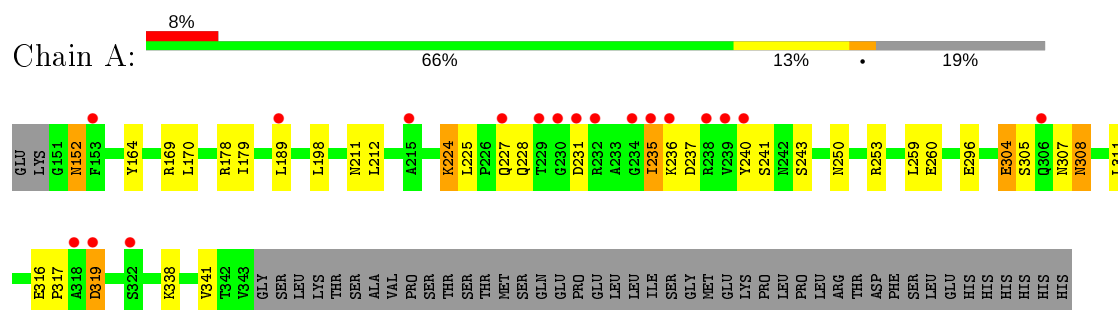
- Molecule 3 is 9,9'-[(2R,3R,3aS,5S,7aR,9R,10R,10aS,12S,14aR)-3,5,10,12-tetrahydroxy-5,12-dioxidoctahydro-2H,7H-difuro[3,2-d:3',2'-j][1,3,7,9,2,8]tetraoxadiphosphacyclododecine-2,9-diyl]bis(2-amino-1,9-dihydro-6H-purin-6-one) (three-letter code: C2E) (formula: C<sub>20</sub>H<sub>24</sub>N<sub>10</sub>O<sub>14</sub>P<sub>2</sub>).



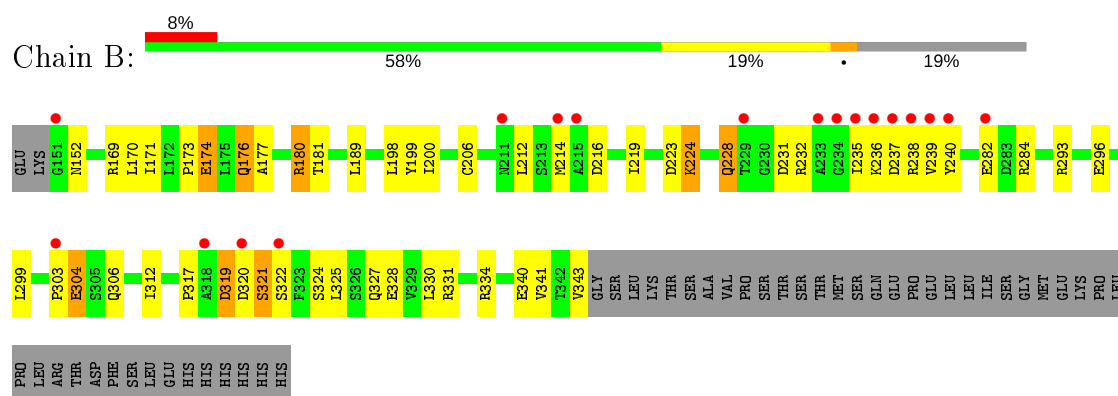
### 3 Residue-property plots [i](#)

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: Transmembrane protein 173



- Molecule 1: Transmembrane protein 173



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	73.14Å 81.44Å 91.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.84 – 2.40 46.75 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.7 (39.84-2.40) 99.8 (46.75-2.40)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.04 (at 2.39Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.2_869)	Depositor
R, $R_{free}$	0.211 , 0.275 0.207 , 0.271	Depositor DCC
$R_{free}$ test set	1129 reflections (5.14%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	39.0	Xtriage
Anisotropy	0.515	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 47.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	3292	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	47.0	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 33.73 % 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 7.6309e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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, C2E

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	0.44	0/1582	0.63	2/2144 (0.1%)
1	B	0.43	0/1582	0.58	0/2144
All	All	0.44	0/3164	0.60	2/4288 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	319	ASP	N-CA-C	-5.54	96.05	111.00
1	A	259	LEU	CA-CB-CG	5.29	127.48	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	228	GLN	Peptide

### 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	1553	0	1517	16	0
1	B	1553	0	1517	31	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	46	0	22	0	0
4	A	71	0	0	4	0
4	B	67	0	0	2	0
All	All	3292	0	3056	46	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 7.

All (46) 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:238:ARG:HG3	1:B:239:VAL:H	1.25	1.01
1:B:237:ASP:HB3	1:B:240:TYR:CE1	2.13	0.82
1:B:237:ASP:CB	1:B:240:TYR:CE1	2.65	0.80
1:A:224:LYS:NZ	1:A:243:SER:OG	2.22	0.72
1:B:237:ASP:HB3	1:B:240:TYR:HE1	1.55	0.71
1:B:173:PRO:HG2	1:B:236:LYS:HE2	1.73	0.70
1:B:238:ARG:HG3	1:B:239:VAL:N	2.05	0.67
1:A:178:ARG:NH1	1:A:240:TYR:OH	2.28	0.67
1:B:293:ARG:NH2	4:B:629:HOH:O	2.28	0.66
1:A:178:ARG:HE	1:A:227:GLN:HA	1.59	0.66
1:B:324:SER:HB3	1:B:327:GLN:HB2	1.77	0.66
1:B:237:ASP:HB2	1:B:240:TYR:CE1	2.35	0.61
1:A:296:GLU:HG3	1:A:311:LEU:HD12	1.83	0.61
1:B:235:ILE:HG22	1:B:236:LYS:HG3	1.83	0.60
1:A:305:SER:HA	1:A:308:ASN:HB2	1.83	0.59
1:A:169:ARG:HD2	4:A:547:HOH:O	2.05	0.57
1:B:284:ARG:HD2	4:B:636:HOH:O	2.05	0.56
1:A:198:LEU:HD11	1:A:260:GLU:HG2	1.87	0.55
1:B:224:LYS:HZ2	1:B:224:LYS:HA	1.71	0.54
1:B:176:GLN:OE1	1:B:180:ARG:NH1	2.41	0.54
1:B:299:LEU:O	1:B:306:GLN:HB2	2.08	0.54
1:B:174:GLU:HG2	1:B:228:GLN:HG3	1.89	0.53
1:B:199:TYR:HD2	1:B:312:ILE:HD11	1.75	0.51
1:B:216:ASP:HB3	1:B:219:ILE:HG13	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:237:ASP:HB2	1:B:240:TYR:CD1	2.46	0.50
1:B:177:ALA:O	1:B:181:THR:HG23	2.12	0.49
1:A:305:SER:OG	4:A:565:HOH:O	2.20	0.48
1:A:338:LYS:NZ	4:A:566:HOH:O	2.48	0.47
1:B:319:ASP:N	1:B:319:ASP:OD1	2.36	0.47
1:A:253:ARG:HD2	4:A:543:HOH:O	2.16	0.46
1:B:206:CYS:HB2	1:B:284:ARG:HD3	1.98	0.45
1:B:317:PRO:HB2	1:B:321:SER:HB3	1.98	0.45
1:A:317:PRO:O	1:A:319:ASP:O	2.34	0.45
1:B:328:GLU:OE1	1:B:331:ARG:NH2	2.43	0.45
1:B:237:ASP:CB	1:B:240:TYR:CD1	3.00	0.44
1:B:321:SER:OG	1:B:322:SER:N	2.49	0.43
1:A:235:ILE:H	1:A:235:ILE:HD13	1.84	0.43
1:B:238:ARG:O	1:B:239:VAL:HG23	2.18	0.43
1:A:179:ILE:HA	1:A:225:LEU:HD11	1.99	0.43
1:B:199:TYR:CD2	1:B:312:ILE:HD11	2.54	0.42
1:B:304:GLU:HG3	1:B:304:GLU:O	2.15	0.42
1:A:164:TYR:O	1:A:169:ARG:HB2	2.21	0.41
1:A:316:GLU:HA	1:A:317:PRO:HD3	1.95	0.41
1:A:152:ASN:CG	1:B:152:ASN:HB2	2.42	0.40
1:B:330:LEU:O	1:B:334:ARG:HG3	2.21	0.40
1:B:198:LEU:HG	1:B:200:ILE:HD11	2.04	0.40

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	191/239 (80%)	179 (94%)	11 (6%)	1 (0%)	29	41
1	B	191/239 (80%)	178 (93%)	12 (6%)	1 (0%)	29	41
All	All	382/478 (80%)	357 (94%)	23 (6%)	2 (0%)	29	41

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	304	GLU
1	B	303	PRO

### 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	168/211 (80%)	152 (90%)	16 (10%)	8	12
1	B	168/211 (80%)	144 (86%)	24 (14%)	3	4
All	All	336/422 (80%)	296 (88%)	40 (12%)	5	6

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	152	ASN
1	A	170	LEU
1	A	189	LEU
1	A	211	ASN
1	A	212	LEU
1	A	224	LYS
1	A	231	ASP
1	A	235	ILE
1	A	236	LYS
1	A	237	ASP
1	A	241	SER
1	A	250	ASN
1	A	304	GLU
1	A	307	ASN
1	A	308	ASN
1	A	341	VAL
1	B	169	ARG
1	B	170	LEU
1	B	171	ILE
1	B	174	GLU
1	B	176	GLN

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Mol	Chain	Res	Type
1	B	180	ARG
1	B	189	LEU
1	B	212	LEU
1	B	214	MET
1	B	223	ASP
1	B	224	LYS
1	B	228	GLN
1	B	231	ASP
1	B	232	ARG
1	B	282	GLU
1	B	296	GLU
1	B	304	GLU
1	B	319	ASP
1	B	320	ASP
1	B	321	SER
1	B	325	LEU
1	B	340	GLU
1	B	341	VAL
1	B	343	VAL

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

Mol	Chain	Res	Type
1	B	157	HIS

### 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 monosaccharides 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
3	C2E	A	402	-	44,52,52	2.71	15 (34%)	54,82,82	2.03	14 (25%)

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	C2E	A	402	-	-	0/22/62/62	0/6/7/7

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	402	C2E	O61-C61	7.00	1.42	1.24
3	A	402	C2E	C21-N11	6.17	1.46	1.35
3	A	402	C2E	C2-N2	5.62	1.45	1.33
3	A	402	C2E	C21-N21	5.47	1.44	1.33
3	A	402	C2E	O6-C6	5.31	1.37	1.24
3	A	402	C2E	C6-N1	5.27	1.42	1.33
3	A	402	C2E	C2A-C1A	-3.82	1.48	1.53
3	A	402	C2E	C2-N1	3.39	1.41	1.35
3	A	402	C2E	C4-N3	3.33	1.40	1.35
3	A	402	C2E	C61-C51	3.32	1.47	1.41
3	A	402	C2E	C61-N11	3.22	1.38	1.33
3	A	402	C2E	C2'-C3'	-2.74	1.46	1.52
3	A	402	C2E	O4A-C4A	-2.69	1.39	1.45
3	A	402	C2E	C41-N31	2.65	1.39	1.35
3	A	402	C2E	O3A-C3A	-2.28	1.35	1.44

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	402	C2E	C2-N3-C4	5.91	122.11	115.36
3	A	402	C2E	N3-C2-N1	-5.42	119.99	127.22
3	A	402	C2E	N31-C21-N11	-5.15	120.35	127.22
3	A	402	C2E	C21-N31-C41	4.20	120.15	115.36
3	A	402	C2E	C61-C51-C41	-3.81	117.16	120.80
3	A	402	C2E	C6-C5-C4	-3.78	117.19	120.80
3	A	402	C2E	C61-N11-C21	2.99	120.69	115.93
3	A	402	C2E	N21-C21-N11	2.99	121.90	117.25
3	A	402	C2E	C4-C5-N7	-2.95	106.33	109.40
3	A	402	C2E	C51-C61-N11	-2.85	119.53	123.43
3	A	402	C2E	C6-N1-C2	2.66	120.16	115.93
3	A	402	C2E	C41-C51-N71	-2.43	106.86	109.40
3	A	402	C2E	C2A-C3A-C4A	-2.10	99.50	103.22
3	A	402	C2E	C1'-N9-C4	-2.07	123.00	126.64

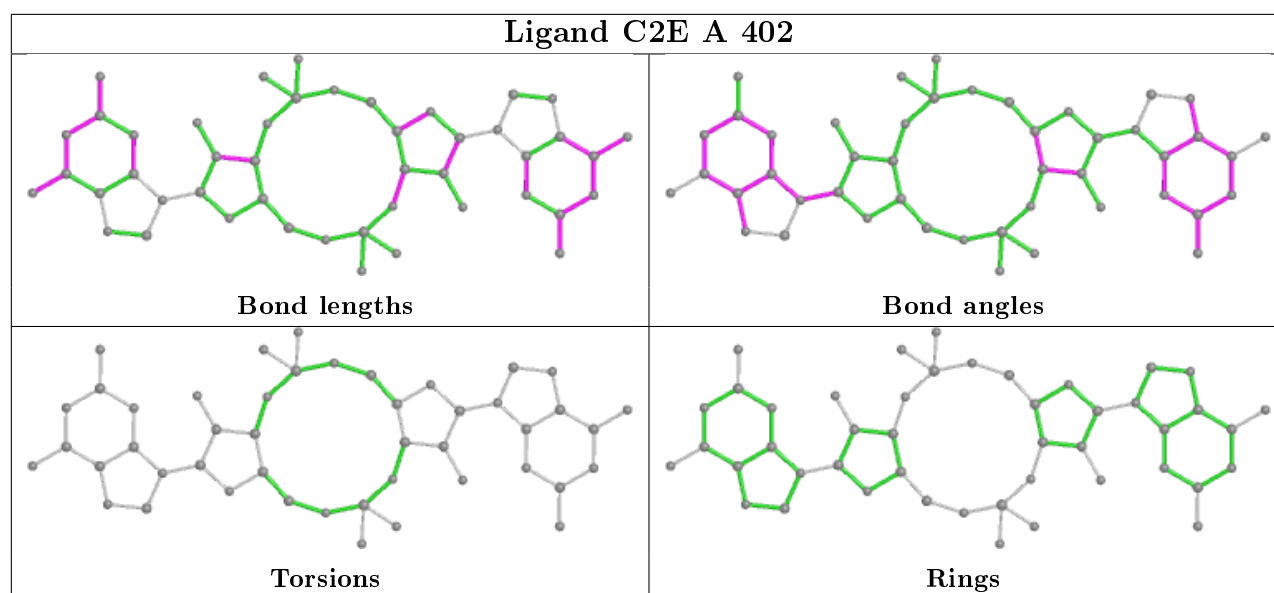
There are no chirality outliers.

There are no torsion outliers.

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.



## 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, 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	193/239 (80%)	0.66	18 (9%) 8 8	25, 41, 97, 115	0
1	B	193/239 (80%)	0.74	18 (9%) 8 8	27, 41, 97, 120	0
All	All	386/478 (80%)	0.70	36 (9%) 8 8	25, 41, 97, 120	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	235	ILE	12.3
1	B	236	LYS	11.6
1	A	235	ILE	10.3
1	B	237	ASP	7.3
1	B	234	GLY	6.7
1	A	318	ALA	6.1
1	A	239	VAL	5.5
1	B	214	MET	5.5
1	B	233	ALA	4.6
1	B	151	GLY	4.3
1	B	239	VAL	4.2
1	B	215	ALA	4.2
1	B	322	SER	4.1
1	A	231	ASP	4.0
1	A	234	GLY	3.7
1	A	236	LYS	3.7
1	A	306	GLN	3.7
1	B	240	TYR	3.5
1	A	232	ARG	3.4
1	B	229	THR	3.4
1	A	240	TYR	3.2
1	A	230	GLY	3.1
1	A	238	ARG	3.1
1	B	318	ALA	2.9

*Continued on next page...*

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Mol	Chain	Res	Type	RSRZ
1	A	215	ALA	2.9
1	B	320	ASP	2.9
1	A	153	PHE	2.8
1	A	322	SER	2.7
1	A	229	THR	2.6
1	B	238	ARG	2.6
1	A	227	GLN	2.6
1	B	303	PRO	2.5
1	A	319	ASP	2.5
1	A	189	LEU	2.4
1	B	211	ASN	2.1
1	B	282	GLU	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 monosaccharides 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.

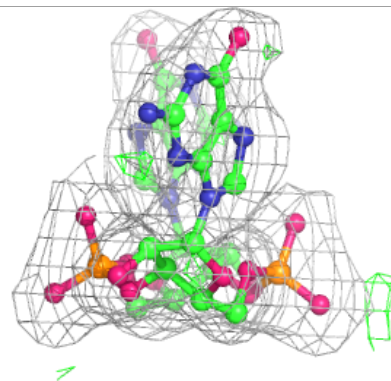
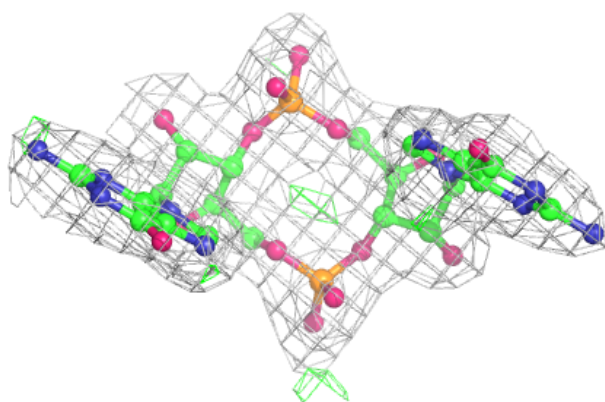
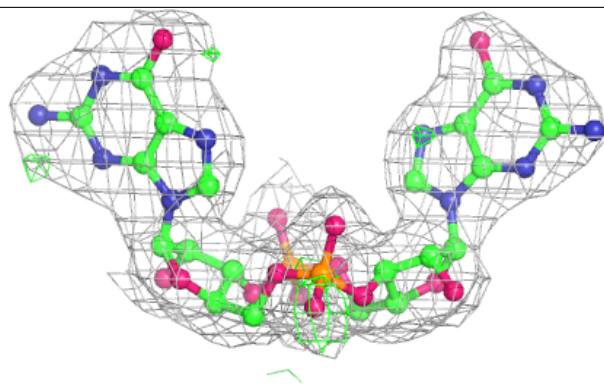
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	CA	A	401	1/1	0.91	0.15	57,57,57,57	0
2	CA	B	500	1/1	0.92	0.21	61,61,61,61	0
3	C2E	A	402	46/46	0.98	0.14	26,36,46,58	0

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 C2E A 402:**

$2mF_o-DF_c$  (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.