Full wwPDB X-ray Structure Validation Report (i)

Aug 16, 2023 – 12:45 AM EDT

PDB ID	:	1TBF
Title	:	Catalytic Domain Of Human Phosphodiesterase 5A in Complex with Sildenafil
Authors	:	Zhang, K.Y.J.; Card, G.L.; Suzuki, Y.; Artis, D.R.; Fong, D.; Gillette, S.; Hsieh, D.; Neiman, J.; West, B.L.; Zhang, C.; Milburn, M.V.; Kim, S.-H.; Schlessinger, J.; Bollag, G.
Deposited on	:	2004-05-20
Resolution	:	1.30 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 (i) 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 (i)) were used in the production of this report:

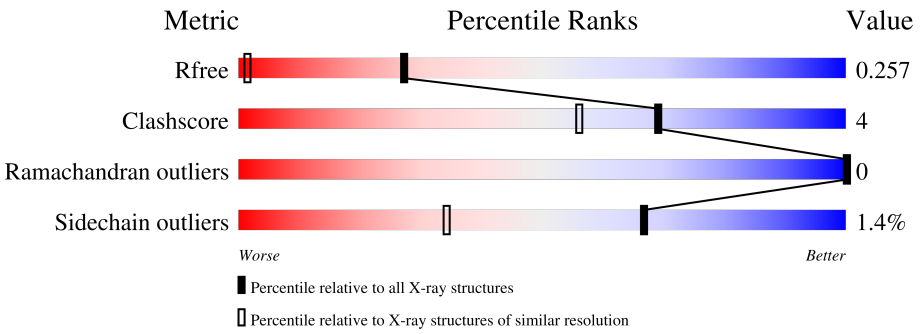
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.30 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	1058 (1.30-1.30)
Clashscore	141614	1101 (1.30-1.30)
Ramachandran outliers	138981	1058 (1.30-1.30)
Sidechain outliers	138945	1058 (1.30-1.30)

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	347	83% 10% • 6%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 3021 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 cGMP-specific 3',5'-cyclic phosphodiesterase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	326	2657	1689	455	493	20	0	7	0

There are 39 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	513	MET	-	expression tag	UNP O76074
A	514	GLY	-	expression tag	UNP O76074
A	515	SER	-	expression tag	UNP O76074
A	516	SER	-	expression tag	UNP O76074
A	517	HIS	-	expression tag	UNP O76074
A	518	HIS	-	expression tag	UNP O76074
A	519	HIS	-	expression tag	UNP O76074
A	520	HIS	-	expression tag	UNP O76074
A	521	HIS	-	expression tag	UNP O76074
A	522	HIS	-	expression tag	UNP O76074
A	523	SER	-	expression tag	UNP O76074
A	524	SER	-	expression tag	UNP O76074
A	525	GLY	-	expression tag	UNP O76074
A	526	LEU	-	expression tag	UNP O76074
A	527	VAL	-	expression tag	UNP O76074
A	528	PRO	-	expression tag	UNP O76074
A	529	ARG	-	expression tag	UNP O76074
A	530	GLY	-	expression tag	UNP O76074
A	531	SER	-	expression tag	UNP O76074
A	532	HIS	-	expression tag	UNP O76074
A	533	MET	-	expression tag	UNP O76074
A	658	PRO	ARG	engineered mutation	UNP O76074
A	661	SER	ASN	engineered mutation	UNP O76074
A	663	GLN	SER	engineered mutation	UNP O76074
A	664	PHE	TYR	engineered mutation	UNP O76074
A	665	LEU	ILE	engineered mutation	UNP O76074
A	666	ILE	GLN	engineered mutation	UNP O76074

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Chain	Residue	Modelled	Actual	Comment	Reference
A	667	ASN	ARG	engineered mutation	UNP O76074
A	668	THR	SER	engineered mutation	UNP O76074
A	669	ASN	GLU	engineered mutation	UNP O76074
A	670	SER	HIS	engineered mutation	UNP O76074
A	671	GLU	PRO	engineered mutation	UNP O76074
A	674	LEU	GLN	engineered mutation	UNP O76074
A	675	MET	LEU	engineered mutation	UNP O76074
A	676A	ASN	CYS	engineered mutation	UNP O76074
A	677	ASP	-	engineered mutation	UNP O76074
A	678	GLU	HIS	engineered mutation	UNP O76074
A	680	VAL	ILE	engineered mutation	UNP O76074
A	681	LEU	MET	engineered mutation	UNP O76074

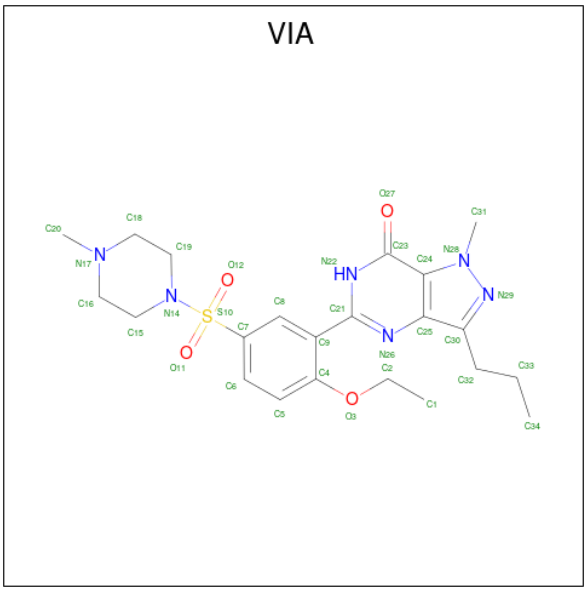
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

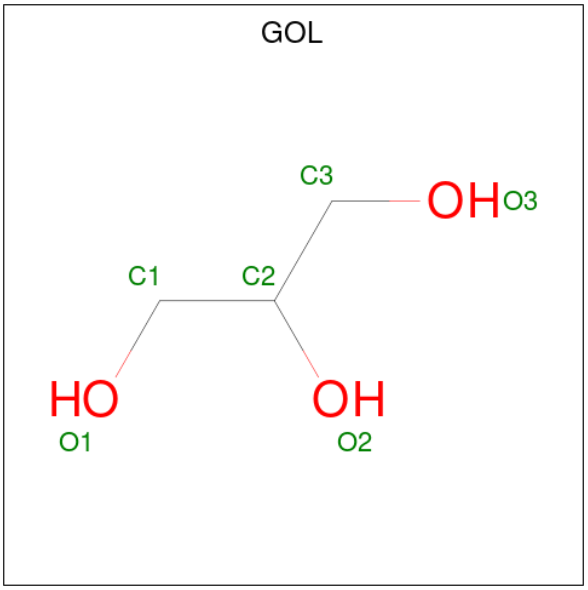
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
3	A	1	1	1	0	0

- Molecule 4 is 5-{2-ETHOXY-5-[(4-METHYLPIPERAZIN-1-YL)SULFONYL]PHENYL}-1-METHYL-3-PROPYL-1H,6H,7H-PYRAZOLO[4,3-D]PYRIMIDIN-7-ONE (three-letter code: VIA) (formula: $C_{22}H_{30}N_6O_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
4	A	1	33	22	6	4	1	0	0

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
5	A	1	6	3	3	0	0

- Molecule 6 is water.

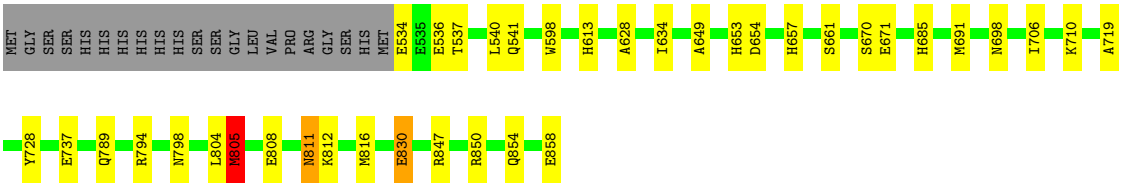
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	323	323	323	0	0

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. 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. 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: cGMP-specific 3',5'-cyclic phosphodiesterase

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	76.10Å 76.10Å 99.27Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	65.94 – 1.30 65.90 – 1.30	Depositor EDS
% Data completeness (in resolution range)	99.2 (65.94-1.30) 99.2 (65.90-1.30)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.64 (at 1.30Å)	Xtriage
Refinement program	REFMAC 5.1.25	Depositor
R, R_{free}	0.157 , 0.185 0.239 , 0.257	Depositor DCC
R_{free} test set	4086 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	16.6	Xtriage
Anisotropy	0.155	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.41 , 56.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.017 for -h,-k,l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	3021	wwPDB-VP
Average B, all atoms (Å^2)	13.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.83% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: MG, ZN, GOL, VIA

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	1.08	7/2743 (0.3%)	1.03	4/3703 (0.1%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	830	GLU	CD-OE2	-6.99	1.18	1.25
1	A	670[A]	SER	CB-OG	-6.59	1.33	1.42
1	A	670[B]	SER	CB-OG	-6.59	1.33	1.42
1	A	798	ASN	CB-CG	-6.30	1.36	1.51
1	A	728	TYR	CE1-CZ	-5.88	1.30	1.38
1	A	830	GLU	CD-OE1	-5.22	1.20	1.25
1	A	808	GLU	CD-OE1	5.20	1.31	1.25

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	805[A]	MET	CA-CB-CG	8.65	128.01	113.30
1	A	805[B]	MET	CA-CB-CG	8.65	128.01	113.30
1	A	850	ARG	NE-CZ-NH2	6.67	123.63	120.30
1	A	794	ARG	CB-CA-C	5.64	121.68	110.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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	2657	0	2665	20	2
2	A	1	0	0	0	0
3	A	1	0	0	0	0
4	A	33	0	30	0	0
5	A	6	0	8	0	0
6	A	323	0	0	5	3
All	All	3021	0	2703	20	3

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (20) 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:671:GLU:OE1	6:A:1122:HOH:O	1.91	0.86
1:A:830:GLU:OE1	6:A:900:HOH:O	2.05	0.75
1:A:534:GLU:OE2	1:A:536:GLU:OE2	2.09	0.68
1:A:537:THR:HG22	1:A:541:GLN:OE1	1.95	0.66
1:A:598:TRP:HA	1:A:698:ASN:HD22	1.69	0.57
1:A:811:ASN:ND2	6:A:913:HOH:O	2.39	0.56
1:A:654:ASP:HA	1:A:685:HIS:CD2	2.47	0.49
1:A:804:LEU:HG	1:A:805[A]:MET:SD	2.55	0.46
1:A:613:HIS:HB2	1:A:657:HIS:CD2	2.50	0.46
1:A:613:HIS:CB	1:A:657:HIS:CD2	2.99	0.46
1:A:540:LEU:HD22	6:A:1082:HOH:O	2.14	0.46
1:A:706:ILE:HG22	1:A:710:LYS:HE3	2.00	0.44
1:A:540:LEU:HD23	1:A:540:LEU:C	2.39	0.43
1:A:854:GLN:O	1:A:858:GLU:HG3	2.18	0.43
1:A:812:LYS:O	1:A:816[B]:MET:HG3	2.19	0.42
1:A:719:ALA:HA	6:A:1143:HOH:O	2.19	0.41
1:A:811:ASN:HD22	1:A:811:ASN:H	1.67	0.41
1:A:628:ALA:HB1	1:A:634[A]:ILE:HD12	2.03	0.41
1:A:649:ALA:O	1:A:653:HIS:HB3	2.22	0.40
1:A:661:SER:H	1:A:789:GLN:NE2	2.19	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:847[A]:ARG:NH2	6:A:908:HOH:O[2_655]	1.13	1.07
6:A:908:HOH:O	6:A:984:HOH:O[3_664]	2.00	0.20
1:A:847[A]:ARG:CZ	6:A:908:HOH:O[2_655]	2.01	0.19

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	331/347 (95%)	329 (99%)	2 (1%)	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	298/309 (96%)	292 (98%)	6 (2%)	55 17

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	691[A]	MET
1	A	691[B]	MET
1	A	737	GLU
1	A	805[A]	MET
1	A	805[B]	MET
1	A	811	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	587	ASN
1	A	657	HIS
1	A	676(A)	ASN
1	A	698	ASN
1	A	742	ASN
1	A	789	GLN
1	A	811	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 2 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	$\#\|Z\| > 2$
4	VIA	A	501	-	31,36,36	2.04	9 (29%)	34,53,53	2.97	16 (47%)
5	GOL	A	502	-	5,5,5	0.42	0	5,5,5	0.52	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
4	VIA	A	501	-	-	4/18/32/32	0/4/4/4
5	GOL	A	502	-	-	0/4/4/4	-

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	501	VIA	O11-S10	-5.90	1.37	1.43
4	A	501	VIA	C23-N22	4.14	1.40	1.33
4	A	501	VIA	C15-N14	-3.57	1.44	1.47
4	A	501	VIA	O12-S10	-3.08	1.40	1.43
4	A	501	VIA	C19-N14	-3.02	1.44	1.47
4	A	501	VIA	C4-C9	-2.48	1.35	1.42
4	A	501	VIA	C8-C7	2.41	1.41	1.36
4	A	501	VIA	C21-N22	2.29	1.39	1.35
4	A	501	VIA	C7-S10	-2.25	1.73	1.76

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	501	VIA	C24-C23-N22	-8.50	111.81	123.43
4	A	501	VIA	C30-N29-N28	7.44	110.90	104.48
4	A	501	VIA	C18-C19-N14	6.35	113.77	108.91
4	A	501	VIA	C19-N14-S10	3.98	124.28	117.05
4	A	501	VIA	C16-C15-N14	3.83	111.84	108.91
4	A	501	VIA	C6-C7-C8	-3.63	116.60	121.05
4	A	501	VIA	O11-S10-C7	3.53	112.51	108.05
4	A	501	VIA	C15-N14-S10	3.03	122.56	117.05
4	A	501	VIA	C16-N17-C18	3.03	113.76	109.52
4	A	501	VIA	C20-N17-C18	2.78	114.82	110.66
4	A	501	VIA	C25-N26-C21	-2.29	112.21	116.75
4	A	501	VIA	C5-C6-C7	2.24	121.77	119.45
4	A	501	VIA	O12-S10-O11	-2.21	115.94	119.52
4	A	501	VIA	C19-C18-N17	2.04	113.11	110.80
4	A	501	VIA	O12-S10-N14	2.04	108.55	106.69
4	A	501	VIA	C6-C7-S10	2.03	121.89	119.76

There are no chirality outliers.

All (4) torsion outliers are listed below:

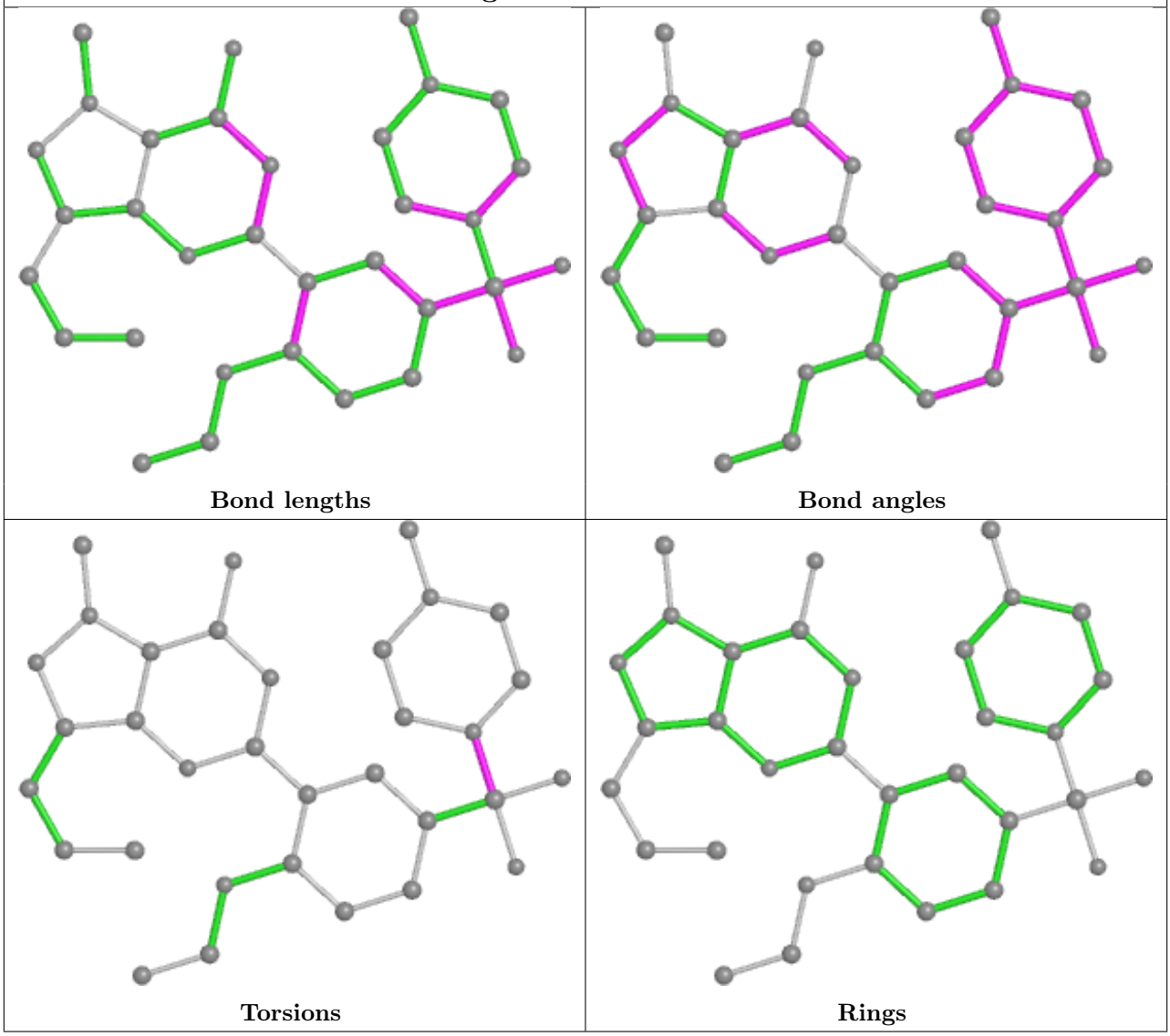
Mol	Chain	Res	Type	Atoms
4	A	501	VIA	C19-N14-S10-O12
4	A	501	VIA	C15-N14-S10-O12
4	A	501	VIA	C19-N14-S10-C7
4	A	501	VIA	C15-N14-S10-C7

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 then 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 VIA A 501



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)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

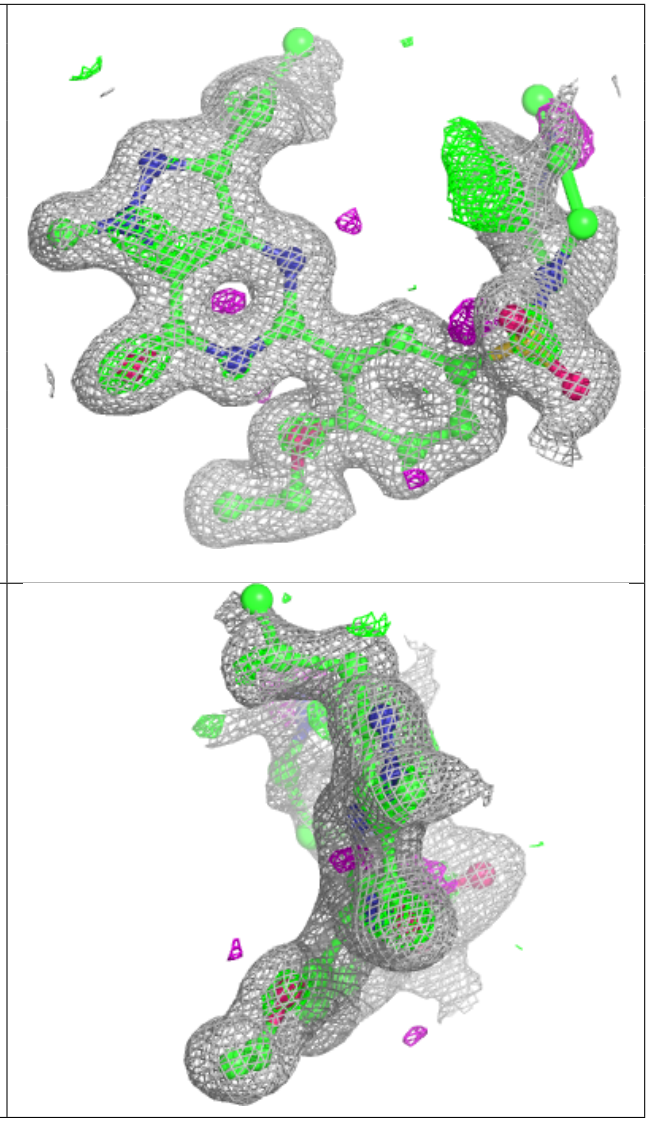
6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

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 VIA A 501:

$2mF_o$-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)

Unable to reproduce the depositors R factor - this section is therefore empty.