



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 11:31 PM UTC

PDB ID : 1BYG / pdb_00001byg
Title : KINASE DOMAIN OF HUMAN C-TERMINAL SRC KINASE (CSK) IN
COMPLEX WITH INHIBITOR STAUROSPORINE
Authors : Antson, A.A.; Lamers, M.B.A.C.; Scott, R.K.; Williams, D.H.; Hubbard, R.E.
Deposited on : 1998-10-14
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

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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

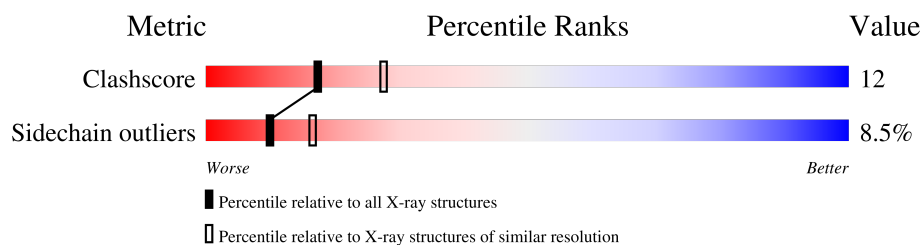
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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))
Clashscore	190562	5391 (2.40-2.40)
Sidechain outliers	187428	5321 (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 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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	278	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2140 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.

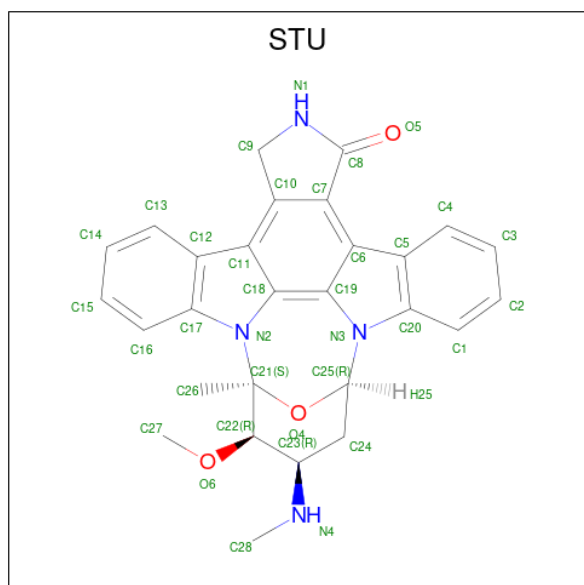
- Molecule 1 is a protein called PROTEIN (C-TERMINAL SRC KINASE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	246	1953	1254	333	353	13	48	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	174	GLY	GLU	conflict	UNP P41240
A	176	SER	THR	conflict	UNP P41240

- Molecule 2 is STAUROSPORINE (CCD ID: STU) (formula: $C_{28}H_{26}N_4O_3$).



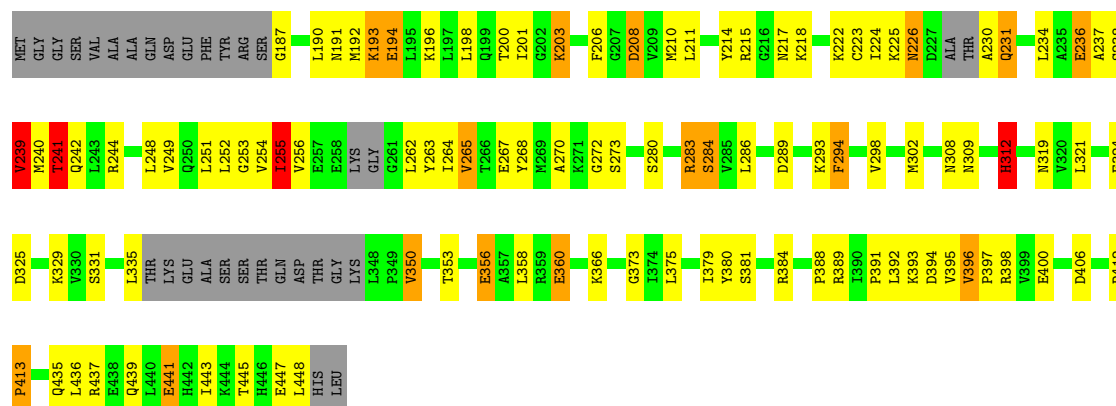
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	35	28	4	3	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	152	Total 152	O 152	0	0

Note EDS was not executed.

- Chain A: 50% 31% 6% 12%



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	44.49Å 120.58Å 48.29Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.40	Depositor
% Data completeness (in resolution range)	93.6 (20.00-2.40)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.199 , 0.287	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2140	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: STU

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	1.32	13/1992 (0.7%)	2.14	65/2687 (2.4%)

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	1	1

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	239	VAL	CA-CB	-23.31	1.24	1.54
1	A	240	MET	CG-SD	-17.55	1.36	1.80
1	A	293	LYS	CG-CD	16.95	2.03	1.52
1	A	255	ILE	CB-CG1	-16.88	1.19	1.53
1	A	284	SER	CB-OG	-12.13	1.17	1.42
1	A	448	LEU	CA-CB	9.82	1.73	1.53
1	A	187	GLY	CA-C	-9.72	1.34	1.52
1	A	196	LYS	CE-NZ	-8.67	1.23	1.49
1	A	236	GLU	CG-CD	-6.80	1.35	1.52
1	A	393	LYS	CB-CG	5.85	1.70	1.52
1	A	193	LYS	CG-CD	5.51	1.69	1.52
1	A	206	PHE	CB-CG	5.39	1.63	1.50
1	A	196	LYS	CD-CE	-5.03	1.37	1.52

All (65) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	448	LEU	CB-CA-C	-24.56	63.44	110.10
1	A	206	PHE	CA-CB-CG	-17.70	96.10	113.80
1	A	283	ARG	CB-CG-CD	17.66	151.91	111.30
1	A	187	GLY	CA-C-O	-17.20	84.68	120.80
1	A	384	ARG	NE-CZ-NH2	10.86	128.98	119.20
1	A	255	ILE	CB-CG1-CD1	-9.55	93.75	113.80
1	A	395	VAL	CA-C-N	8.27	128.37	120.43
1	A	395	VAL	C-N-CA	8.27	128.37	120.43
1	A	217	ASN	N-CA-C	8.24	123.28	109.76
1	A	196	LYS	CD-CE-NZ	8.24	138.26	111.90
1	A	201	ILE	CA-C-O	8.06	125.75	119.46
1	A	445	THR	CA-C-O	-7.89	112.05	120.42
1	A	267	GLU	CA-C-O	7.82	129.84	121.55
1	A	267	GLU	CA-CB-CG	7.43	128.97	114.10
1	A	255	ILE	CA-CB-CG1	7.26	122.73	110.40
1	A	284	SER	CA-CB-OG	7.09	125.29	111.10
1	A	329	LYS	CA-C-O	-6.82	113.69	121.40
1	A	293	LYS	CB-CG-CD	-6.75	95.77	111.30
1	A	280	SER	CB-CA-C	-6.58	100.75	110.95
1	A	210	MET	N-CA-C	6.52	120.03	109.40
1	A	187	GLY	N-CA-C	-6.48	94.51	113.30
1	A	283	ARG	CG-CD-NE	-6.35	98.04	112.00
1	A	208	ASP	CA-C-O	6.31	129.19	121.87
1	A	236	GLU	CB-CG-CD	6.29	123.30	112.60
1	A	289	ASP	CA-CB-CG	-6.25	106.35	112.60
1	A	312	HIS	CA-CB-CG	-6.12	107.68	113.80
1	A	241	THR	N-CA-CB	6.07	119.72	110.44
1	A	439	GLN	OE1-CD-NE2	-6.00	116.60	122.60
1	A	441	GLU	N-CA-CB	5.99	118.93	110.12
1	A	265	VAL	N-CA-C	5.95	116.67	107.99
1	A	329	LYS	O-C-N	5.92	130.34	123.17
1	A	380	TYR	CA-C-O	5.92	126.75	119.05
1	A	445	THR	N-CA-CB	5.87	118.84	110.16
1	A	192	MET	CA-C-O	5.79	126.89	120.63
1	A	406	ASP	CA-CB-CG	-5.79	106.81	112.60
1	A	255	ILE	CG1-CB-CG2	5.78	128.03	110.70
1	A	389	ARG	N-CA-CB	5.74	119.48	110.46
1	A	208	ASP	O-C-N	-5.74	116.25	122.79
1	A	356	GLU	CB-CG-CD	5.71	122.31	112.60
1	A	286	LEU	N-CA-C	5.68	117.99	107.99
1	A	280	SER	O-C-N	5.68	128.16	122.03
1	A	389	ARG	CA-CB-CG	5.68	125.45	114.10
1	A	294	PHE	CA-C-O	5.67	126.56	120.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	379	ILE	N-CA-CB	5.50	116.98	110.55
1	A	241	THR	CA-CB-OG1	5.49	117.84	109.60
1	A	196	LYS	CG-CD-CE	5.48	123.91	111.30
1	A	366	LYS	CA-C-O	-5.48	114.75	120.55
1	A	384	ARG	NE-CZ-NH1	-5.46	116.04	121.50
1	A	272	GLY	CA-C-O	5.46	128.50	122.01
1	A	331	SER	N-CA-C	5.45	118.94	110.17
1	A	436	LEU	N-CA-CB	5.39	118.04	110.12
1	A	381	SER	O-C-N	-5.33	115.79	122.35
1	A	350	VAL	N-CA-C	5.32	120.41	109.34
1	A	319	ASN	CA-CB-CG	-5.28	107.32	112.60
1	A	441	GLU	CB-CG-CD	5.28	121.57	112.60
1	A	396	VAL	N-CA-CB	5.27	114.05	110.52
1	A	283	ARG	CA-C-N	5.21	127.52	120.38
1	A	283	ARG	C-N-CA	5.21	127.52	120.38
1	A	435	GLN	OE1-CD-NE2	5.21	127.81	122.60
1	A	373	GLY	CA-C-O	-5.17	115.42	120.75
1	A	319	ASN	OD1-CG-ND2	5.10	127.70	122.60
1	A	381	SER	CA-C-O	5.08	125.82	119.78
1	A	231	GLN	N-CA-C	-5.06	105.95	111.82
1	A	198	LEU	O-C-N	5.04	129.10	122.30
1	A	325	ASP	CA-CB-CG	-5.00	107.60	112.60

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	255	ILE	CB

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	312	HIS	Mainchain

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	1953	0	1970	47	0
2	A	35	0	26	2	0
3	A	152	0	0	3	0
All	All	2140	0	1996	48	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 12.

All (48) 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:224:ILE:HD12	1:A:262:LEU:HB2	1.51	0.91
1:A:211:LEU:HD21	1:A:218:LYS:HE2	1.52	0.89
1:A:194:GLU:OE2	1:A:215:ARG:HD2	1.86	0.74
1:A:203:LYS:HB3	1:A:208:ASP:OD1	1.92	0.69
1:A:255:ILE:HB	1:A:263:TYR:HB2	1.79	0.64
1:A:396:VAL:O	1:A:400:GLU:HG3	1.97	0.64
1:A:249:VAL:HB	3:A:110:HOH:O	2.00	0.61
1:A:190:LEU:HG	1:A:253:GLY:HA3	1.83	0.61
1:A:234:LEU:HD21	1:A:256:VAL:HG23	1.82	0.59
1:A:190:LEU:HD13	1:A:214:TYR:CZ	2.41	0.56
1:A:237:ALA:O	1:A:241:THR:N	2.34	0.56
1:A:203:LYS:HA	1:A:208:ASP:HA	1.87	0.56
1:A:252:LEU:HB2	1:A:265:VAL:HG12	1.88	0.55
1:A:223:CYS:SG	1:A:263:TYR:HE1	2.30	0.55
1:A:256:VAL:HA	1:A:262:LEU:HD23	1.88	0.55
2:A:501:STU:H261	2:A:501:STU:H16	1.88	0.55
1:A:218:LYS:HE3	3:A:60:HOH:O	2.07	0.53
1:A:356:GLU:O	1:A:360:GLU:HB2	2.08	0.53
1:A:230:ALA:O	1:A:234:LEU:HB2	2.09	0.52
1:A:194:GLU:OE2	1:A:215:ARG:NH1	2.42	0.52
1:A:394:ASP:O	1:A:398:ARG:HG3	2.11	0.51
1:A:211:LEU:HD13	1:A:268:TYR:CE1	2.46	0.51
1:A:353:THR:HB	1:A:358:LEU:HD21	1.94	0.50
1:A:443:ILE:HA	1:A:447:GLU:OE1	2.11	0.50
1:A:242:GLN:HA	1:A:244:ARG:NH2	2.26	0.49
1:A:234:LEU:HD22	1:A:262:LEU:HD21	1.93	0.48
1:A:190:LEU:HD13	1:A:214:TYR:CE1	2.49	0.48
1:A:239:VAL:O	1:A:242:GLN:HB3	2.14	0.48
1:A:302:MET:HE1	1:A:312:HIS:HB2	1.94	0.48
1:A:251:LEU:HD11	1:A:253:GLY:O	2.14	0.47
1:A:253:GLY:O	1:A:254:VAL:HG23	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:191:ASN:OD1	1:A:193:LYS:HG3	2.14	0.47
1:A:396:VAL:HB	1:A:397:PRO:HD3	1.97	0.46
1:A:437:ARG:O	1:A:441:GLU:HG2	2.15	0.46
1:A:298:VAL:HG11	1:A:375:LEU:CD2	2.46	0.45
1:A:222:LYS:HB3	1:A:264:ILE:HB	1.98	0.45
1:A:214:TYR:O	1:A:215:ARG:C	2.59	0.44
1:A:394:ASP:OD2	1:A:398:ARG:NH2	2.48	0.44
1:A:391:PRO:O	1:A:392:LEU:C	2.61	0.44
1:A:321:LEU:HD21	2:A:501:STU:H271	2.00	0.43
1:A:308:ASN:O	1:A:309:ASN:HB2	2.19	0.42
1:A:255:ILE:CB	1:A:263:TYR:HB2	2.49	0.42
1:A:388:PRO:HD2	3:A:1:HOH:O	2.19	0.42
1:A:412:PRO:O	1:A:413:PRO:C	2.60	0.42
1:A:270:ALA:HB3	1:A:324:GLU:HB2	2.01	0.41
1:A:226:ASN:ND2	1:A:226:ASN:H	2.18	0.41
1:A:225:LYS:HE3	1:A:225:LYS:HB2	1.95	0.41
1:A:294:PHE:O	1:A:298:VAL:HG23	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

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	211/235 (90%)	193 (92%)	18 (8%)	10	16

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	194	GLU
1	A	200	THR
1	A	203	LYS
1	A	226	ASN
1	A	231	GLN
1	A	236	GLU
1	A	238	SER
1	A	239	VAL
1	A	241	THR
1	A	248	LEU
1	A	255	ILE
1	A	273	SER
1	A	283	ARG
1	A	284	SER
1	A	335	LEU
1	A	350	VAL
1	A	360	GLU
1	A	413	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	226	ASN
1	A	231	GLN
1	A	446	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 oligosaccharides in this entry.

5.6 Ligand geometry

1 ligand is 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
2	STU	A	501	-	39,42,42	1.25	4 (10%)	50,68,68	1.68	8 (16%)

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
2	STU	A	501	-	-	0/4/42/42	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	STU	C5-C6	-2.51	1.40	1.46
2	A	501	STU	C26-C21	2.39	1.54	1.51
2	A	501	STU	C9-N1	-2.36	1.43	1.45
2	A	501	STU	C18-N2	-2.08	1.37	1.40

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	STU	C3-C4-C5	-4.35	113.02	120.23
2	A	501	STU	C24-C23-C22	-3.78	102.29	109.53
2	A	501	STU	C3-C2-C1	3.70	124.80	120.24
2	A	501	STU	C2-C1-C20	-3.59	111.04	118.28
2	A	501	STU	C1-C20-C5	3.58	125.79	121.59
2	A	501	STU	C9-C10-C7	-3.58	108.57	109.88
2	A	501	STU	C2-C3-C4	3.01	123.96	120.24
2	A	501	STU	C1-C20-N3	-2.67	125.18	129.73

There are no chirality outliers.

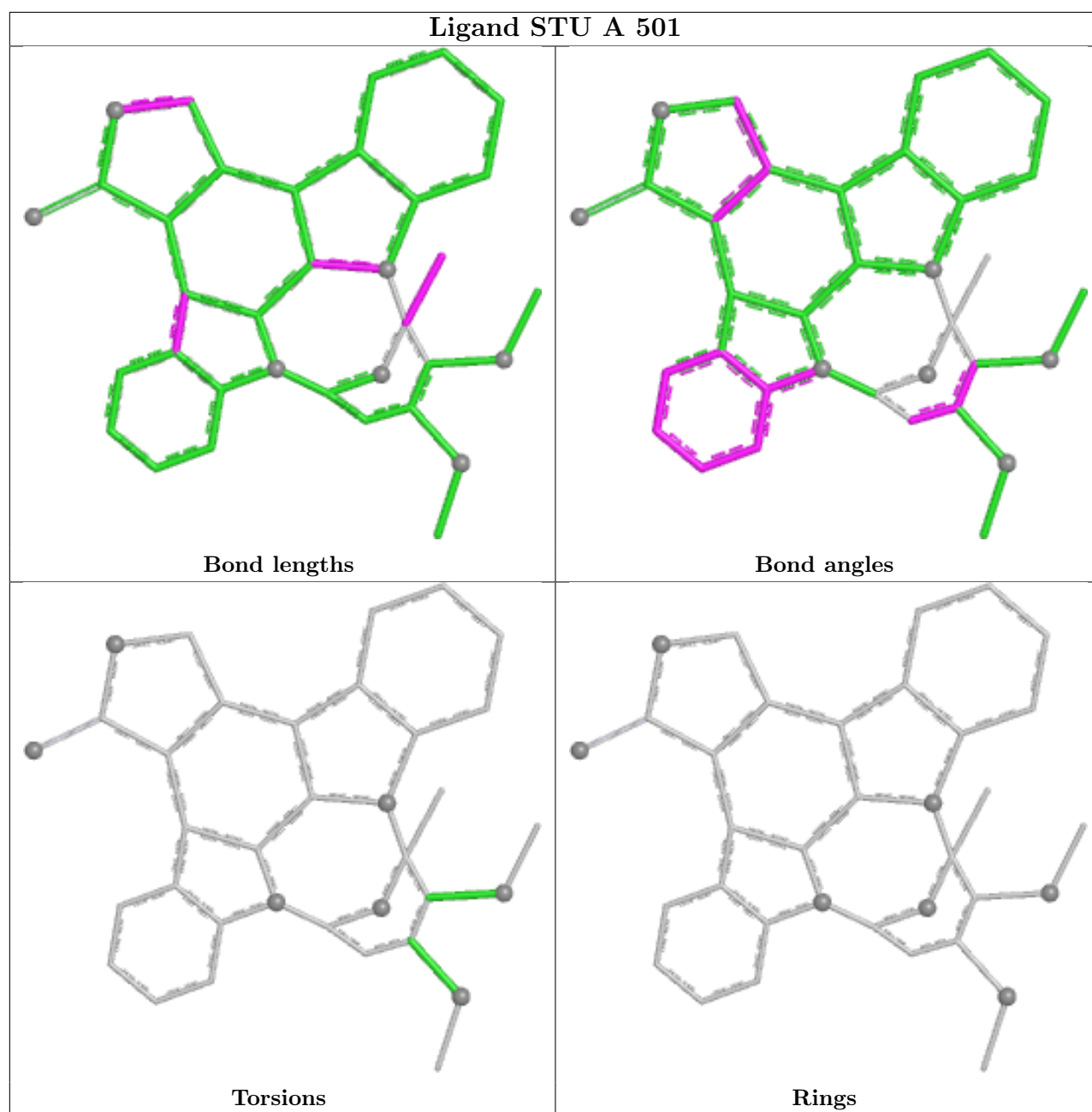
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	STU	2	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

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.