



wwPDB X-ray Structure Validation Summary Report ⓘ

May 17, 2020 – 11:39 am BST

PDB ID : 1ECF
Title : ESCHERICHIA COLI GLUTAMINE PHOSPHORIBOSYLPYROPHOSPHATE (PRPP) AMIDOTRANSFERASE
Authors : Krahn, J.M.
Deposited on : 1996-04-23
Resolution : 2.00 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

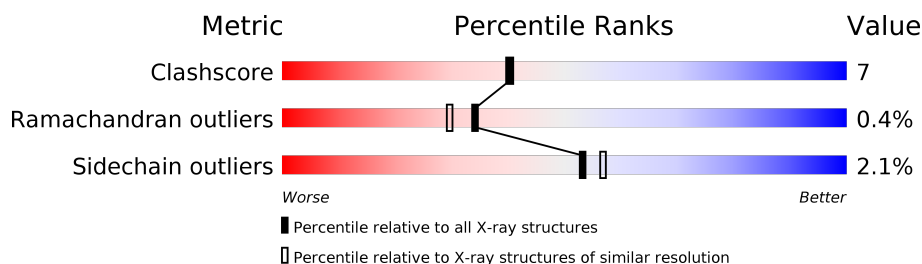
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)

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 ≥ 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	504	
1	B	504	

2 Entry composition [i](#)

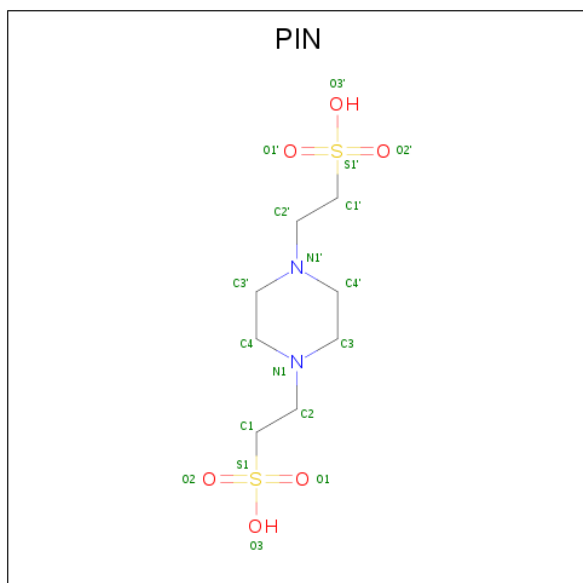
There are 3 unique types of molecules in this entry. The entry contains 9124 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 GLUTAMINE PHOSPHORIBOSYLPYROPHOSPHATE AMIDOTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	492	Total	C	N	O	S	0	18	0
			4008	2519	712	760	17			
1	B	500	Total	C	N	O	S	0	13	0
			4042	2537	723	764	18			

- Molecule 2 is PIPERAZINE-N,N'-BIS(2-ETHANESULFONIC ACID) (three-letter code: PIN) (formula: $C_8H_{18}N_2O_6S_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			18	8	2	6	2		
2	A	1	Total	C	N	O	S	0	0
			18	8	2	6	2		
2	A	1	Total	C	N	O	S	0	0
			7	2	1	3	1		

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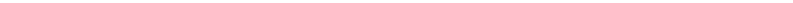
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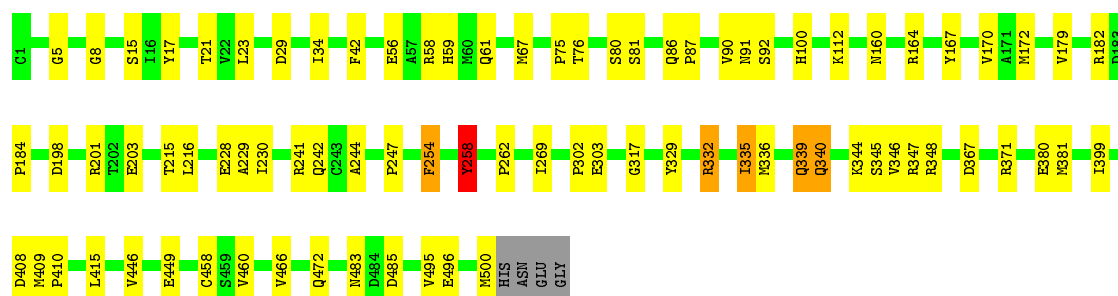
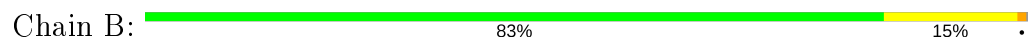
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	S	0	0
			18	8	2	6	2		
2	B	1	Total	C	N	O	S	0	0
			18	8	2	6	2		
2	B	1	Total	C	N	O	S	0	0
			9	4	1	3	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	514	Total	O	0	0
			514	514		
3	B	472	Total	O	0	0
			472	472		

Note EDS was not executed.

- Chain A:  82% 15% ..



4 Data and refinement statistics

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

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	116.90 Å 157.50 Å 106.30 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.00	Depositor
% Data completeness (in resolution range)	98.2 (30.00-2.00)	Depositor
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.175 , 0.230	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	9124	wwPDB-VP
Average B, all atoms (Å ²)	27.0	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: PIN

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	0.71	3/4079 (0.1%)	0.86	5/5523 (0.1%)
1	B	0.64	2/4112 (0.0%)	0.80	0/5565
All	All	0.68	5/8191 (0.1%)	0.83	5/11088 (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	B	0	1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	234	GLU	C-N	13.74	1.65	1.34
1	A	234	GLU	CA-C	-7.10	1.34	1.52
1	B	496	GLU	CD-OE2	6.75	1.33	1.25
1	A	234	GLU	C-O	-6.12	1.11	1.23
1	B	458	CYS	CB-SG	-5.45	1.73	1.81

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	234	GLU	CA-C-O	18.07	158.06	120.10
1	A	234	GLU	O-C-N	-16.33	96.57	122.70
1	A	168	ALA	N-CA-C	-5.79	95.37	111.00
1	A	343	ARG	N-CA-C	5.48	125.80	111.00
1	A	234	GLU	CA-C-N	-5.39	105.35	117.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	258	TYR	Sidechain

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	4008	0	3952	54	0
1	B	4042	0	4003	70	0
2	A	43	0	36	5	0
2	B	45	0	36	2	0
3	A	514	0	0	11	0
3	B	472	0	0	18	0
All	All	9124	0	8027	117	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.

The worst 5 of 117 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:91[A]:ASN:ND2	3:B:508:HOH:O	1.57	1.28
1:B:91[A]:ASN:CG	3:B:508:HOH:O	1.84	1.02
1:A:56:GLU:H	1:A:59:HIS:HD2	1.15	0.93
1:A:291[B]:GLU:HB2	3:A:979:HOH:O	1.73	0.89
1:A:10:MET:SD	1:B:340:GLN:HB3	2.13	0.88

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	508/504 (101%)	493 (97%)	14 (3%)	1 (0%)	47	44
1	B	511/504 (101%)	492 (96%)	16 (3%)	3 (1%)	25	19
All	All	1019/1008 (101%)	985 (97%)	30 (3%)	4 (0%)	34	30

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	343	ARG
1	B	340	GLN
1	B	258	TYR
1	B	339	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	427/422 (101%)	415 (97%)	12 (3%)	43	44
1	B	432/422 (102%)	425 (98%)	7 (2%)	62	67
All	All	859/844 (102%)	840 (98%)	19 (2%)	53	55

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	304[A]	THR
1	A	348	ARG

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Mol	Chain	Res	Type
1	B	254	PHE
1	A	303	GLU
1	B	332	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	437	GLN
1	B	59	HIS
1	B	242	GLN
1	A	322	GLN
1	B	160	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

6 ligands 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	$\# Z > 2$
2	PIN	A	506	-	18,18,18	1.52	3 (16%)	22,26,26	0.61	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PIN	B	507	1	8,8,18	1.56	2 (25%)	10,11,26	0.61	0
2	PIN	B	506	-	18,18,18	1.14	3 (16%)	22,26,26	0.61	0
2	PIN	A	505	-	18,18,18	1.04	3 (16%)	22,26,26	0.58	0
2	PIN	A	507	1	6,6,18	1.93	1 (16%)	6,8,26	0.47	0
2	PIN	B	505	-	18,18,18	0.87	1 (5%)	22,26,26	0.59	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
2	PIN	A	506	-	-	3/12/22/22	0/1/1/1
2	PIN	B	507	1	-	3/6/6/22	-
2	PIN	B	506	-	-	1/12/22/22	0/1/1/1
2	PIN	A	505	-	-	4/12/22/22	0/1/1/1
2	PIN	A	507	1	-	1/4/4/22	-
2	PIN	B	505	-	-	4/12/22/22	0/1/1/1

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	507	PIN	C1-S1	4.40	1.83	1.77
2	A	506	PIN	C1'-S1'	4.06	1.83	1.77
2	A	506	PIN	C1-S1	3.64	1.82	1.77
2	B	507	PIN	C1-S1	3.41	1.82	1.77
2	B	506	PIN	C1'-S1'	2.79	1.81	1.77

There are no bond angle outliers.

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

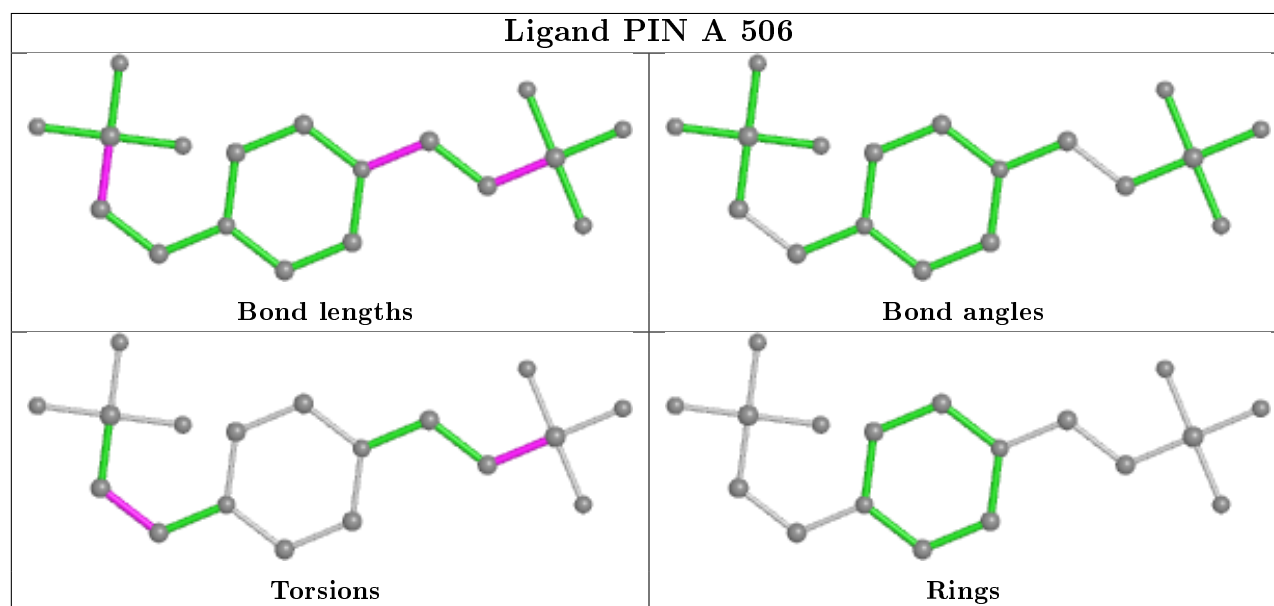
Mol	Chain	Res	Type	Atoms
2	B	507	PIN	C2-C1-S1-O2
2	B	507	PIN	C2-C1-S1-O3
2	A	505	PIN	C2-C1-S1-O1
2	A	505	PIN	S1'-C1'-C2'-N1'
2	A	507	PIN	S1-C1-C2-N1

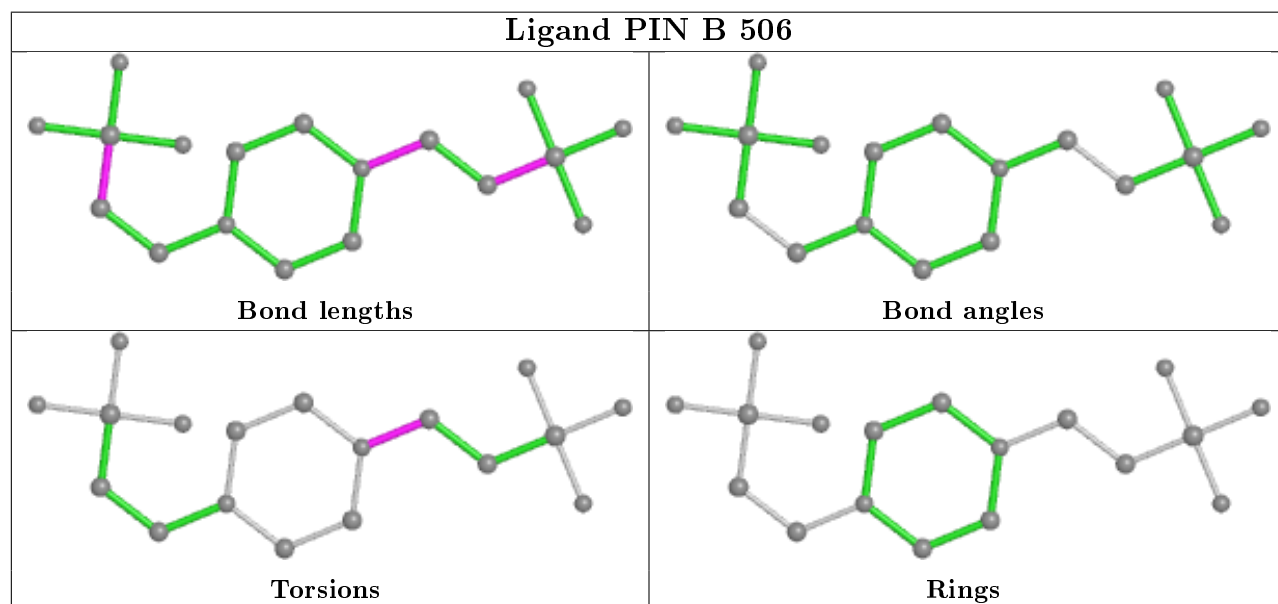
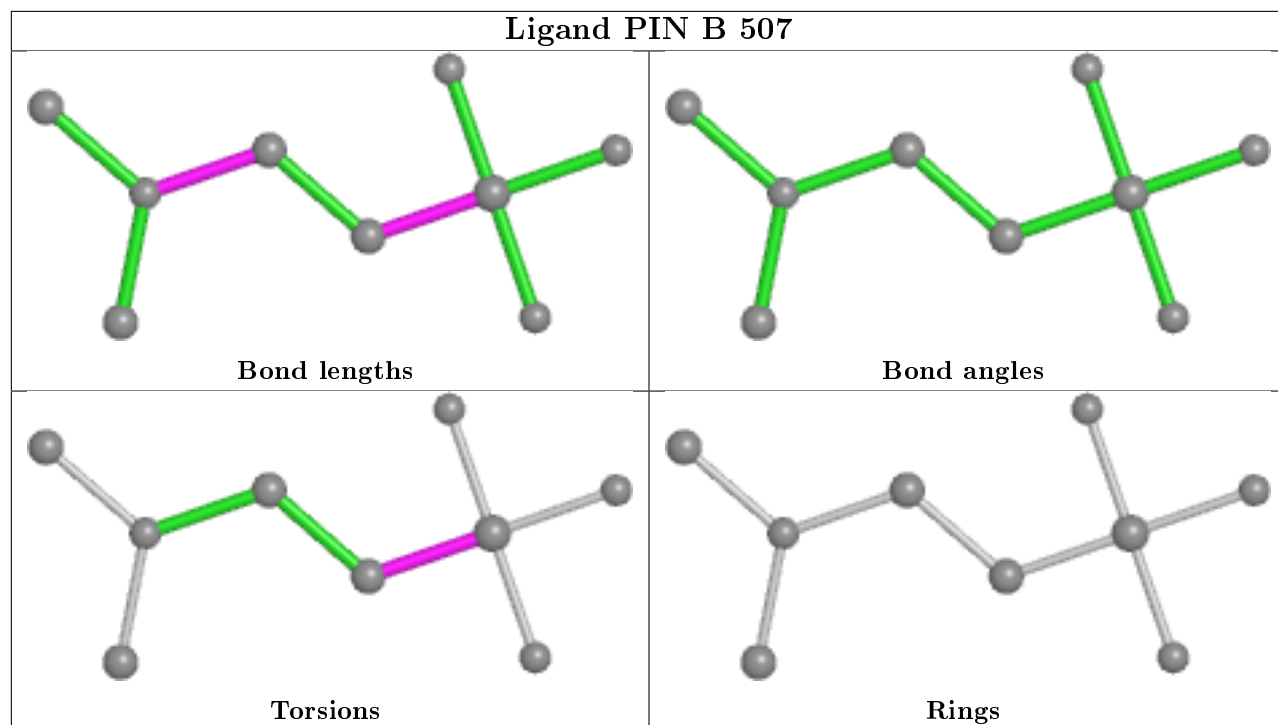
There are no ring outliers.

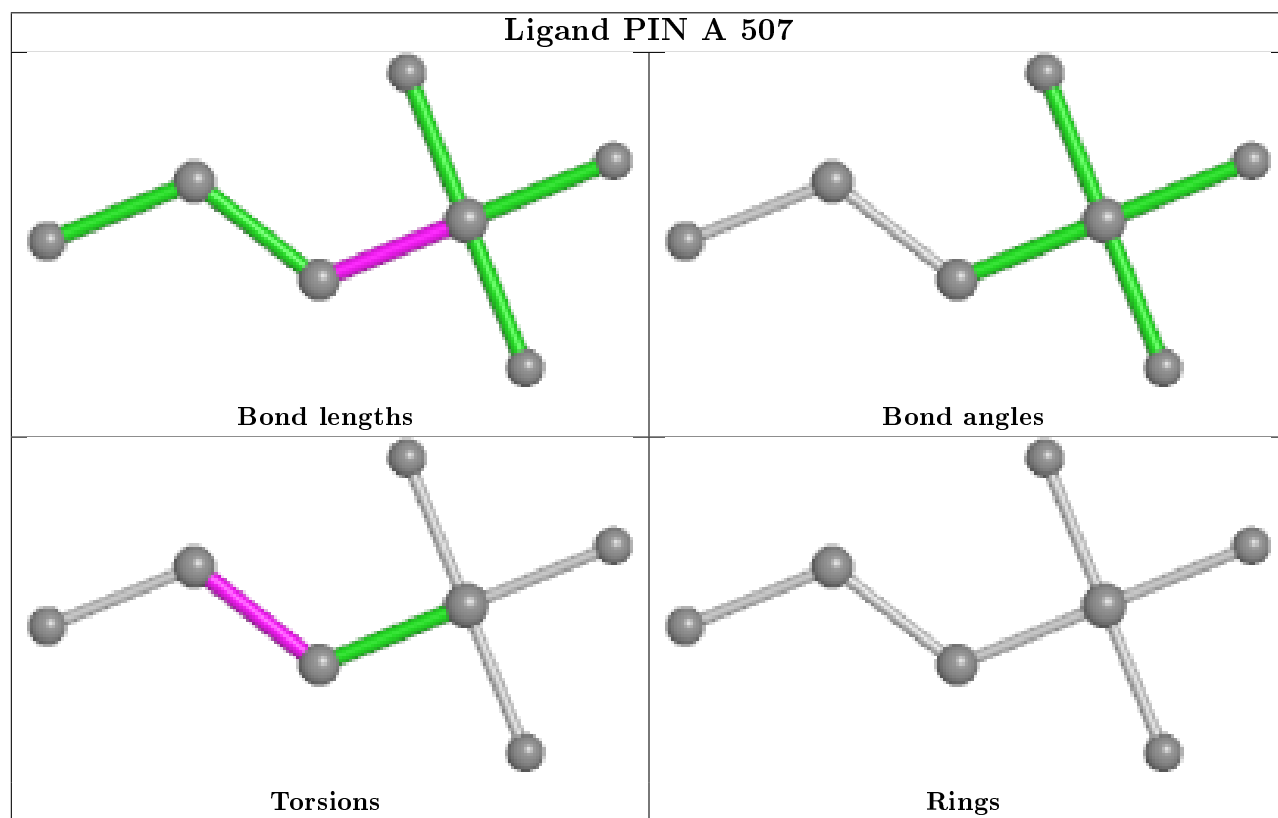
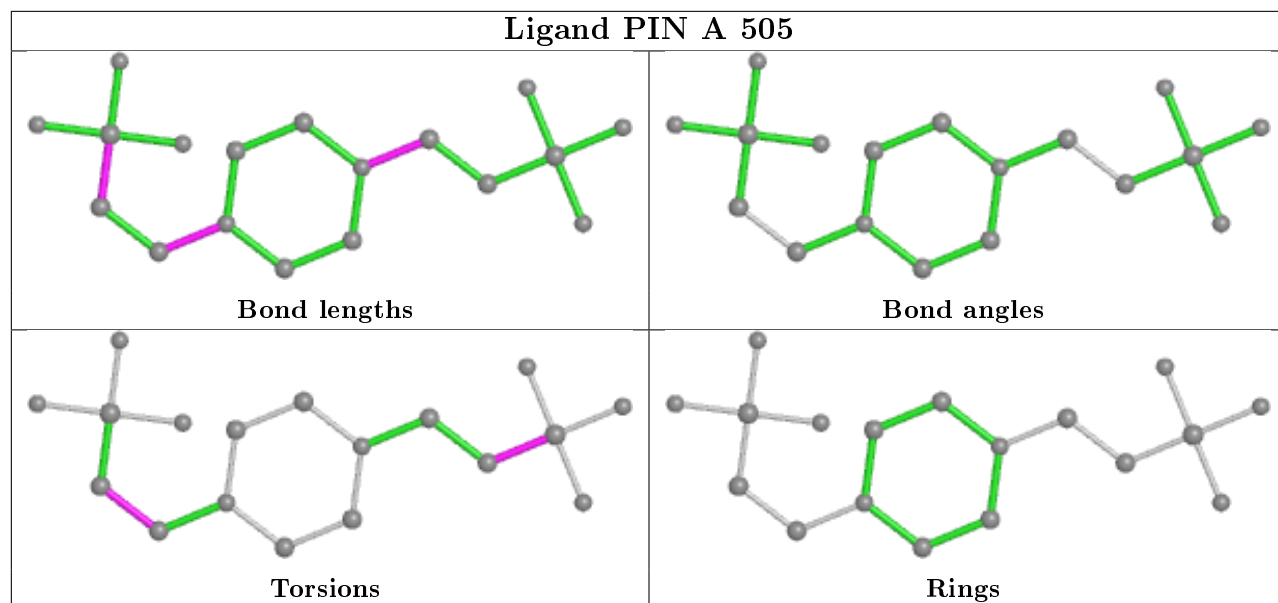
4 monomers are involved in 7 short contacts:

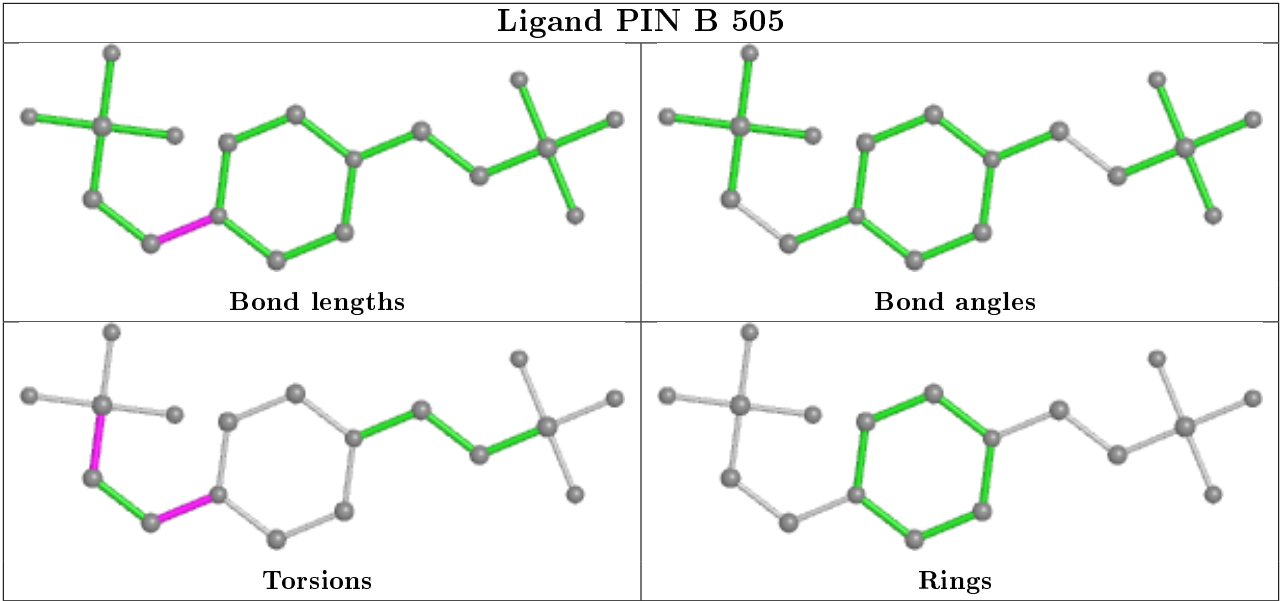
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	507	PIN	1	0
2	A	505	PIN	1	0
2	A	507	PIN	4	0
2	B	505	PIN	1	0

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	234:GLU	C	235[A]:GLU	N	1.65
1	A	234:GLU	C	235[B]:GLU	N	1.64

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.