

wwPDB X-ray Structure Validation Summary Report (i)

Jul 7, 2021 - 10:14 am BST

PDB ID	:	70PJ
Title	:	Trypanosoma brucei PTR1 (TbPTR1) in complex with pyrimethamine
Authors	:	Tassone, G.; Landi, G.; Pozzi, C.; Mangani, S.
Deposited on		
$\operatorname{Resolution}$:	1.34 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

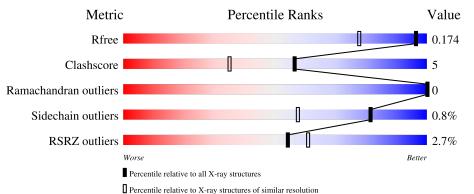
MolProbity	:	4.02b-467 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)		1.13
EDŚ	:	2.22
buster-report	:	1.1.7(2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.22

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 1.34 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	1385 (1.36-1.32)
Clashscore	141614	1417 (1.36-1.32)
Ramachandran outliers	138981	1397 (1.36-1.32)
Sidechain outliers	138945	1397 (1.36-1.32)
RSRZ outliers	127900	1369(1.36-1.32)

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% 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	А	288	76%	10%	13%
1	В	288	80%	6%	14%
1	С	288	4% 74% 11	.%	16%
1	D	288	^{2%} 80%	7%	14%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard



residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	GOL	С	303	-	-	Х	-



2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 8847 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.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	Λ	250	Total	С	Ν	Ο	\mathbf{S}	0	16	0
	A	250	1925	1232	329	353	11	0	16	0
1	В	248	Total	С	Ν	Ο	S	0	13	0
	ГБ	240	1909	1209	328	360	12	0		
1	С	243	Total	С	Ν	0	S	0	13	0
		240	1816	1155	306	345	10	0	10	
1	1 D	249	Total	С	Ν	Ο	S	0	13	0
			1890	1202	325	352	11	0	10	U

• Molecule 1 is a protein called Pteridine reductase.

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	-19	MET	-	initiating methionine	UNP 076290
A	-18	GLY	-	expression tag	UNP 076290
A	-17	SER	-	expression tag	UNP 076290
A	-16	SER	-	expression tag	UNP 076290
A	-15	HIS	-	expression tag	UNP 076290
A	-14	HIS	-	expression tag	UNP 076290
A	-13	HIS	-	expression tag	UNP 076290
A	-12	HIS	-	expression tag	UNP 076290
A	-11	HIS	-	expression tag	UNP 076290
A	-10	HIS	-	expression tag	UNP 076290
A	-9	SER	-	expression tag	UNP 076290
A	-8	SER	-	expression tag	UNP 076290
A	-7	GLY	-	expression tag	UNP 076290
A	-6	LEU	-	expression tag	UNP 076290
A	-5	VAL	-	expression tag	UNP 076290
A	-4	PRO	-	expression tag	UNP 076290
A	-3	ARG	-	expression tag	UNP 076290
А	-2	GLY	-	expression tag	UNP 076290
А	-1	SER	-	expression tag	UNP 076290
А	0	HIS	-	expression tag	UNP 076290
В	-19	MET	-	initiating methionine	UNP 076290

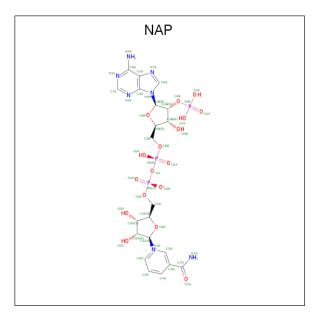


	Continued from previous page										
Chain	Residue	Modelled	Actual	Comment	Reference						
В	-18	GLY	-	expression tag	UNP 076290						
В	-17	SER	-	expression tag	UNP 076290						
В	-16	SER	-	expression tag	UNP 076290						
В	-15	HIS	-	expression tag	UNP 076290						
В	-14	HIS	-	expression tag	UNP 076290						
В	-13	HIS	-	expression tag	UNP 076290						
В	-12	HIS	-	expression tag	UNP 076290						
В	-11	HIS	-	expression tag	UNP 076290						
В	-10	HIS	-	expression tag	UNP 076290						
В	-9	SER	-	expression tag	UNP 076290						
В	-8	SER	-	expression tag	UNP 076290						
В	-7	GLY	-	expression tag	UNP 076290						
В	-6	LEU	-	expression tag	UNP 076290						
В	-5	VAL	-	expression tag	UNP 076290						
В	-4	PRO	-	expression tag	UNP 076290						
В	-3	ARG	-	expression tag	UNP 076290						
В	-2	GLY	-	expression tag	UNP 076290						
В	-1	SER	-	expression tag	UNP 076290						
В	0	HIS	-	expression tag	UNP 076290						
С	-19	MET	-	initiating methionine	UNP 076290						
С	-18	GLY	-	expression tag	UNP 076290						
С	-17	SER	-	expression tag	UNP 076290						
С	-16	SER	-	expression tag	UNP 076290						
С	-15	HIS	-	expression tag	UNP 076290						
С	-14	HIS	-	expression tag	UNP 076290						
С	-13	HIS	-	expression tag	UNP 076290						
С	-12	HIS	-	expression tag	UNP 076290						
С	-11	HIS	-	expression tag	UNP 076290						
С	-10	HIS	-	expression tag	UNP 076290						
С	-9	SER	-	expression tag	UNP 076290						
С	-8	SER	-	expression tag	UNP 076290						
С	-7	GLY	-	expression tag	UNP 076290						
С	-6	LEU		expression tag	UNP 076290						
С	-5	VAL	-	expression tag	UNP 076290						
С	-4	PRO	-	expression tag	UNP 076290						
С	-3	ARG	-	expression tag	UNP 076290						
С	-2	GLY	-	expression tag	UNP 076290						
С	-1	SER	-	expression tag	UNP 076290						
С	0	HIS		expression tag	UNP 076290						
D	-19	MET	-	initiating methionine	UNP 076290						
D	-18	GLY	-	expression tag	UNP 076290						
D	-17	SER		expression tag	UNP 076290						



Chain	Residue	Modelled	Actual Comment		Reference
D	-16	SER	-	expression tag	UNP 076290
D	-15	HIS	-	expression tag	UNP 076290
D	-14	HIS	-	expression tag	UNP 076290
D	-13	HIS	-	expression tag	UNP 076290
D	-12	HIS	_	expression tag	UNP 076290
D	-11	HIS	_	expression tag	UNP 076290
D	-10	HIS	_	expression tag	UNP 076290
D	-9	SER	-	expression tag	UNP 076290
D	-8	SER	_	expression tag	UNP 076290
D	-7	GLY	-	expression tag	UNP 076290
D	-6	LEU	_	expression tag	UNP 076290
D	-5	VAL	-	expression tag	UNP 076290
D	-4	PRO	_	expression tag	UNP 076290
D	-3	ARG	-	expression tag	UNP 076290
D	-2	GLY	_	expression tag	UNP 076290
D	-1	SER	_	expression tag	UNP 076290
D	0	HIS	-	expression tag	UNP 076290

• Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: $C_{21}H_{28}N_7O_{17}P_3$).

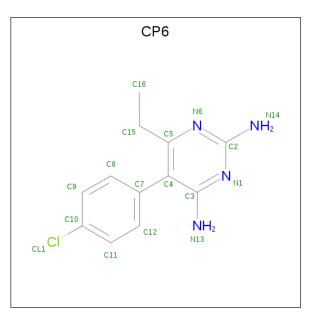


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
0	2 A	1	Total	С	Ν	Ο	Р	0	0	
		1	48	21	7	17	3	0	0	
0	р	1	Total	С	Ν	Ο	Р	0	0	
	2 B		48	21	7	17	3	U	0	



Mol	Chain	Residues		Ate	oms			ZeroOcc	AltConf
9	C	1 Tota		С	Ν	Ο	Р	0	0
	U	L	48	21	7	17	3	0	0
0	Л	1	Total	С	Ν	Ο	Р	0	0
	D	L	48	21	7	17	3	0	0

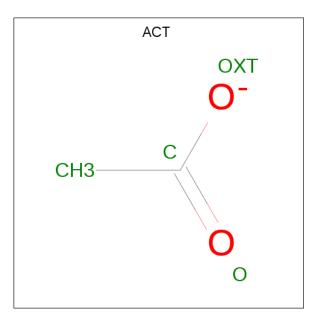
• Molecule 3 is 5-(4-CHLORO-PHENYL)-6-ETHYL-PYRIMIDINE-2,4-DIAMINE (three-letter code: CP6) (formula: C₁₂H₁₃ClN₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
3	Δ	1	Total	С	Cl	Ν	0	0	
0	Л	L	17	12	1	4	0	0	
3	В	1	Total	С	Cl	Ν	0	0	
0	D	L	17	12	1	4	0		
3	C	1	Total	С	Cl	Ν	0	0	
		T	17	12	1	4	0	0	
3	р	1	Total	С	Cl	Ν	0	0	
J	D	L	17	12	1	4	0	0	

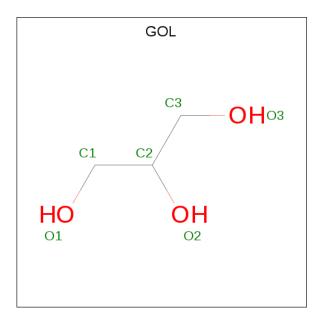
• Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 4 2 2 \end{array}$	0	0
4	А	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 4 2 2 \end{array}$	0	0
4	А	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 4 2 2 \end{array}$	0	0
4	В	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 4 2 2 \end{array}$	0	0

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





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

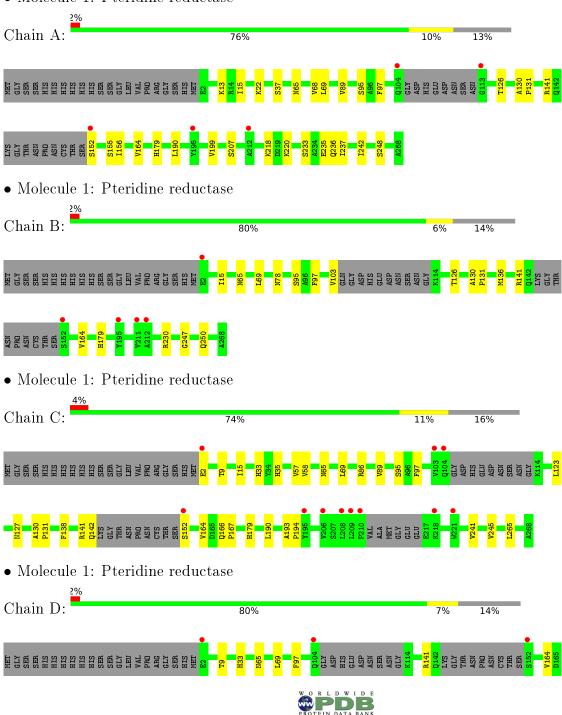
• Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	263	Total O 265 265	0	2
6	В	293	Total O 293 293	0	0
6	С	219	Total O 219 219	0	0
6	D	248	Total O 248 248	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 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: Pteridine reductase





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	74.90Å 91.03 Å 82.80 Å	Depositor
a, b, c, α , β , γ	90.00° 115.63° 90.00°	Depositor
Resolution (Å)	18.07 - 1.34	Depositor
Resolution (A)	18.07 - 1.34	EDS
% Data completeness	$93.8\ (18.07-1.34)$	Depositor
(in resolution range)	$93.8\ (18.07 - 1.34)$	EDS
R _{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.20 ({\rm at} 1.34{ m \AA})$	Xtriage
Refinement program	REFMAC $5.8.0258$	Depositor
R, R_{free}	0.130 , 0.174	Depositor
n, n <i>free</i>	0.131 , 0.174	DCC
R_{free} test set	10516 reflections (5.01%)	wwPDB-VP
Wilson B-factor $(Å^2)$	12.3	Xtriage
Anisotropy	0.620	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.36 , 53.4	EDS
L-test for twinning ²	$< L > = 0.49, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.015 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	8847	wwPDB-VP
Average B, all atoms $(Å^2)$	19.0	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 26.17 % 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 2.7683e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

²Theoretical 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.



¹Intensities estimated from amplitudes.

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: ACT, NAP, CP6, GOL

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	А	0.75	0/2006	0.95	0/2727	
1	В	0.72	0/1981	0.95	0/2689	
1	С	0.72	0/1887	0.91	0/2571	
1	D	0.70	0/1959	0.94	0/2664	
All	All	0.72	0/7833	0.94	0/10651	

There are no bond length outliers.

There are no bond angle outliers.

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	А	1925	0	2018	20	0
1	В	1909	0	1970	13	0
1	С	1816	0	1833	34	0
1	D	1890	0	1943	13	0
2	А	48	0	25	1	0
2	В	48	0	25	2	0
2	С	48	0	25	6	0
2	D	48	0	25	0	0
3	A	17	0	13	2	0



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	В	17	0	13	2	0
3	С	17	0	13	5	0
3	D	17	0	13	1	0
4	А	12	0	9	1	0
4	В	4	0	3	0	0
5	С	6	0	8	5	0
6	А	265	0	0	3	0
6	В	293	0	0	1	0
6	С	219	0	0	2	0
6	D	248	0	0	2	0
All	All	8847	0	7936	79	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 79 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic}\\ {\rm distance}~({\rm \AA}) \end{array}$	Clash overlap (Å)
1:C:58:VAL:H	5:C:303:GOL:H11	1.49	0.78
1:C:58:VAL:HG22	5:C:303:GOL:H12	1.67	0.76
1:C:2:GLU:HG2	1:C:86:ARG:HH11	1.52	0.73
1:C:97:PHE:CZ	3:C:302:CP6:H12	2.26	0.71
1:D:164:VAL:HG22	1:D:179:HIS:CE1	2.27	0.70

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	Perce	entiles
1	А	262/288~(91%)	251 (96%)	11 (4%)	0	100	100
1	В	257/288~(89%)	249 (97%)	8 (3%)	0	100	100



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	С	250/288~(87%)	241 (96%)	9~(4%)	0	100	100
1	D	257/288~(89%)	247 (96%)	10 (4%)	0	100	100
All	All	1026/1152~(89%)	988 (96%)	38 (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	А	211/231~(91%)	209~(99%)	2(1%)	78 52		
1	В	210/231~(91%)	210~(100%)	0	100 100		
1	С	195/231~(84%)	193~(99%)	2(1%)	76 47		
1	D	204/231~(88%)	202~(99%)	2(1%)	76 47		
All	All	820/924~(89%)	814 (99%)	6 (1%)	81 62		

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	\mathbf{Res}	Type
1	С	166	GLN
1	D	166	GLN
1	D	230	ARG
1	А	220	LYS
1	А	152	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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)

13 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	Tune	Chain	Res	Link	B	ond leng	gths	B	ond ang	gles
	Type	Ullalli	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
4	ACT	А	303	-	$1,\!3,\!3$	<mark>4.76</mark>	1 (100%)	0,3,3	0.00	-
5	GOL	С	303	-	$5,\!5,\!5$	0.57	0	5, 5, 5	0.71	0
2	NAP	А	301	-	45,52,52	1.35	5 (11%)	56,80,80	1.62	8 (14%)
3	CP6	В	302	-	18,18,18	1.25	3 (16%)	25,25,25	2.62	8 (32%)
3	CP6	С	302	-	18,18,18	2.04	3 (16%)	25,25,25	3.06	11 (44%)
3	CP6	D	302	-	18,18,18	1.25	3 (16%)	25,25,25	2.63	8 (32%)
3	CP6	А	302	-	18, 18, 18	1.26	3 (16%)	25,25,25	2.62	8 (32%)
4	ACT	А	305	-	$1,\!3,\!3$	2.53	1 (100%)	0,3,3	0.00	-
2	NAP	D	301	-	45,52,52	1.37	4 (8%)	56,80,80	1.31	5 (8%)
2	NAP	В	301	-	45,52,52	1.37	<mark>6 (13%)</mark>	56,80,80	1.93	12 (21%)
4	ACT	В	303	-	$1,\!3,\!3$	<mark>5.12</mark>	1 (100%)	0,3,3	0.00	-
4	ACT	А	304	-	$1,\!3,\!3$	4.99	1 (100%)	0,3,3	0.00	-
2	NAP	С	301	-	45,52,52	1.44	10 (22%)	56,80,80	1.80	13 (23%)

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
5	GOL	С	303	-	-	0/4/4/4	-
2	NAP	А	301	-	-	0/31/67/67	0/5/5/5
3	CP6	В	302	-	-	0/6/6/6	0/2/2/2
3	CP6	С	302	-	-	0/6/6/6	0/2/2/2
3	CP6	D	302	-	-	0/6/6/6	0/2/2/2
3	CP6	А	302	-	-	0/6/6/6	0/2/2/2
2	NAP	D	301	-	-	0/31/67/67	0/5/5/5
2	NAP	В	301	-	-	0/31/67/67	0/5/5/5
2	NAP	С	301	_	-	0/31/67/67	0/5/5/5

The worst 5 of 41 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	С	302	CP6	C3-N1	5.22	1.42	1.35
4	В	303	ACT	CH3-C	5.12	1.55	1.48
2	D	301	NAP	C4N-C3N	5.06	1.48	1.39
4	А	304	ACT	CH3-C	4.99	1.55	1.48
4	А	303	ACT	CH3-C	4.76	1.54	1.48

The worst 5 of 73 bond angle outliers are listed below:

Mol	Chain	Res	Type	Type Atoms		$Observed(^{o})$	$Ideal(^{o})$
3	С	302	CP6	C2-N6-C5	9.58	124.22	116.24
3	D	302	CP6	C4-C3-N1	-7.24	118.45	122.52
3	А	302	CP6	C4-C3-N1	-7.13	118.51	122.52
3	В	302	CP6	C4-C3-N1	-7.12	118.52	122.52
3	В	302	CP6	C2-N6-C5	6.69	121.82	116.24

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 21 short contacts:

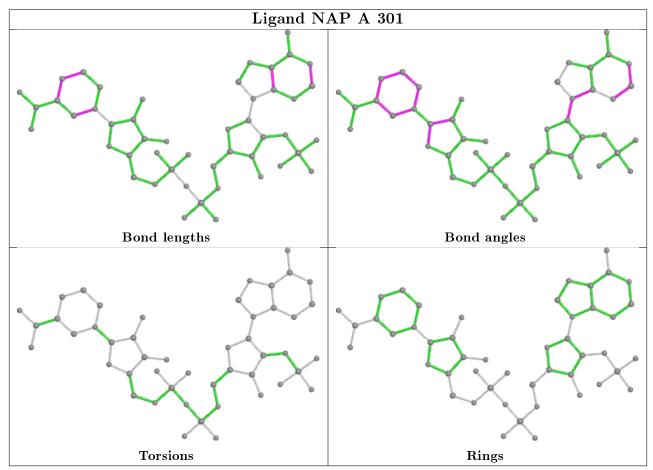
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	С	303	GOL	5	0
2	А	301	NAP	1	0
3	В	302	CP6	2	0
3	С	302	CP6	5	0
3	D	302	CP6	1	0
3	А	302	CP6	2	0
4	А	305	ACT	1	0



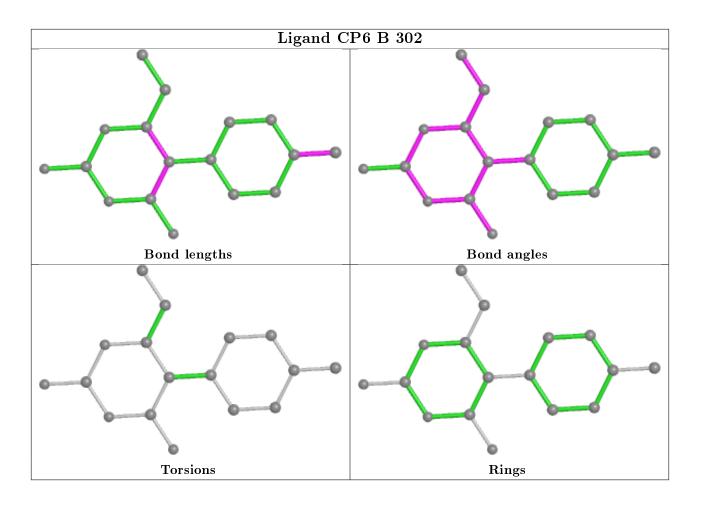
\mathbf{N}	ſol	Chain	Res	Type	Clashes	Symm-Clashes
	2	В	301	NAP	2	0
	2	С	301	NAP	6	0

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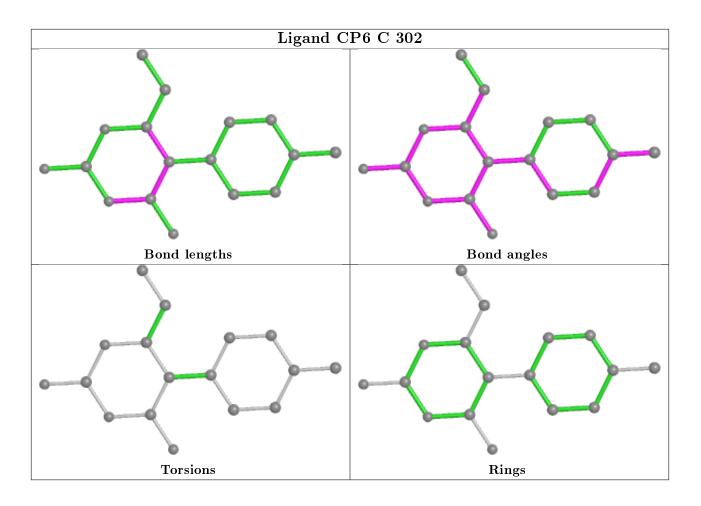
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.



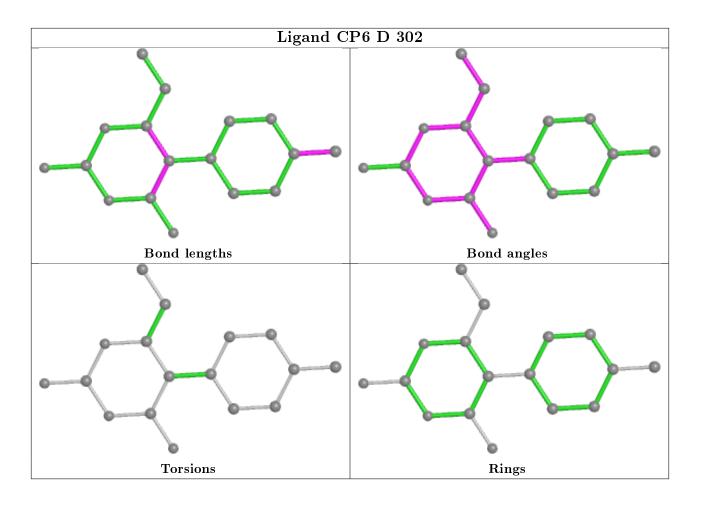




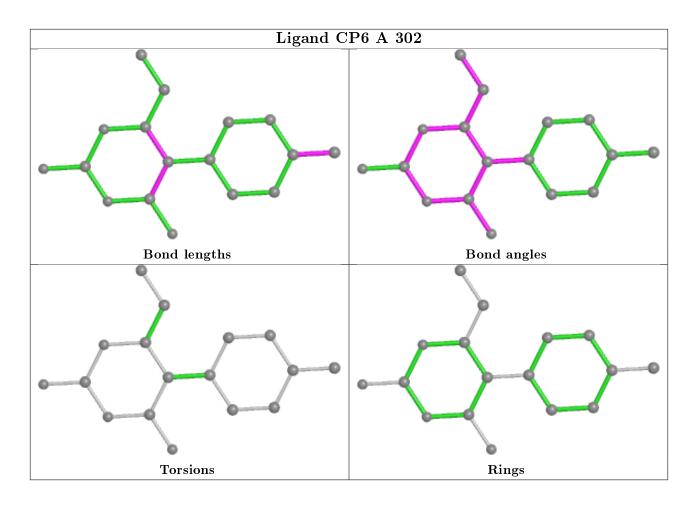






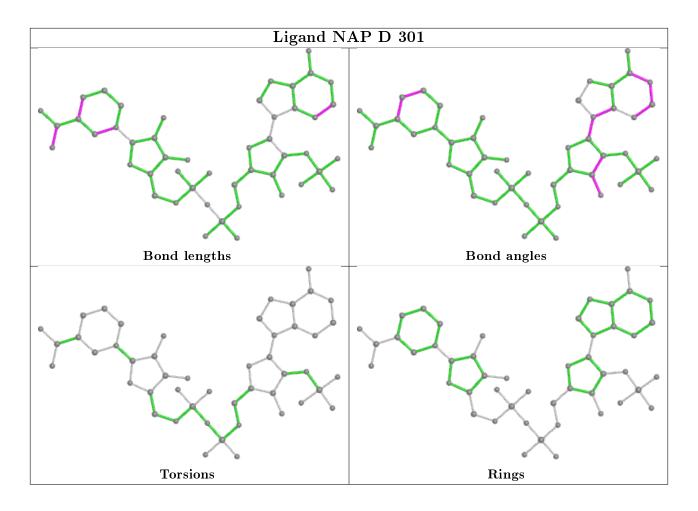




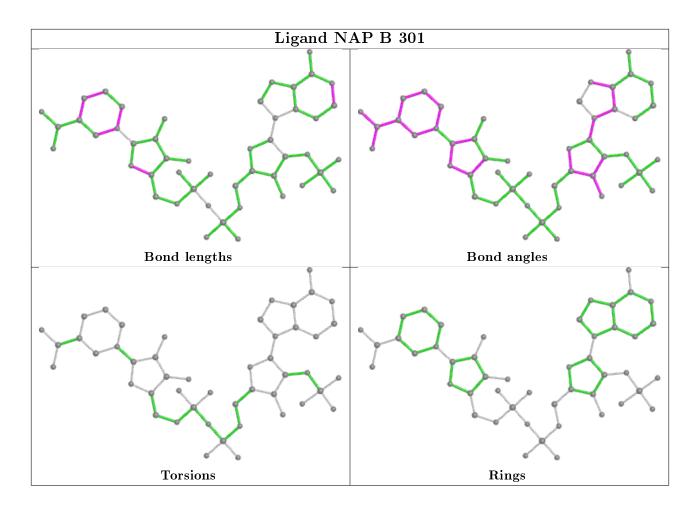




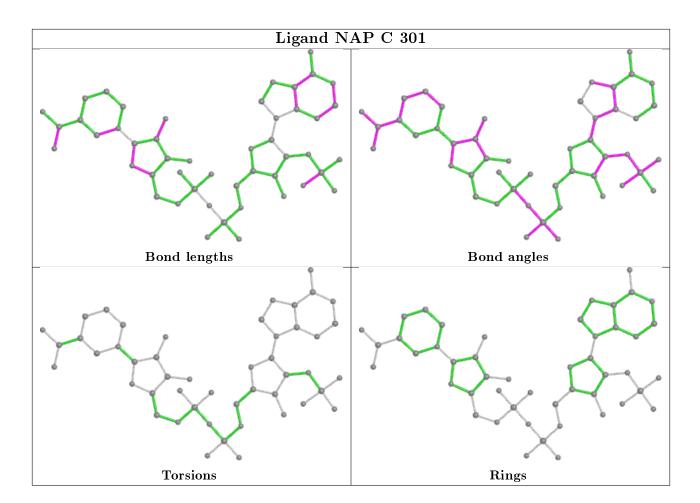












5.7 Other polymers (i)

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^{th} 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 $>$	$\# RSRZ {>}2$		$\mathbf{OWAB}(\mathrm{\AA}^2)$	Q<0.9	
1	А	250/288~(86%)	-0.18	5 (2%)	65	70	10, 14, 30, 55	6 (2%)
1	В	248/288~(86%)	-0.21	5 (2%)	65	70	9, 13, 25, 56	2(0%)
1	С	243/288~(84%)	-0.04	11 (4%)	33	39	9,16,30,64	16 (6%)
1	D	249/288~(86%)	-0.16	6 (2%)	59	65	9,15,33,52	3 (1%)
All	All	990/1152~(85%)	-0.15	27 (2%)	54	61	9,15,30,64	27 (2%)

The worst 5 of 27 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	211	VAL	5.6
1	С	209	LEU	5.2
1	С	208	LEU	5.0
1	В	212	ALA	4.8
1	А	113	GLY	4.6

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^{th} 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	$\mathbf{B} ext{-factors}(\mathbf{A}^2)$	$Q{<}0.9$
3	CP6	С	302	17/17	0.80	0.18	$20,\!25,\!34,\!34$	17
2	NAP	С	301	48/48	0.88	0.15	$15,\!22,\!26,\!32$	48
4	ACT	А	303	4/4	0.89	0.18	$44,\!50,\!51,\!53$	0
4	ACT	А	305	4/4	0.92	0.19	$25,\!36,\!47,\!49$	0
4	ACT	В	303	4/4	0.92	0.24	$26,\!36,\!39,\!44$	0
5	GOL	С	303	6/6	0.93	0.11	$20,\!33,\!39,\!39$	0
3	CP6	А	302	17/17	0.96	0.07	$12,\!14,\!19,\!20$	0
3	CP6	D	302	17/17	0.96	0.09	$13,\!15,\!22,\!23$	0
3	CP6	В	302	17/17	0.96	0.09	$12,\!15,\!22,\!23$	0
4	ACT	А	304	4/4	0.98	0.07	$18,\!20,\!22,\!23$	0
2	NAP	D	301	48/48	0.98	0.05	$11,\!14,\!16,\!18$	0
2	NAP	В	301	48/48	0.98	0.06	$10,\!13,\!15,\!17$	0
2	NAP	А	301	48/48	0.98	0.06	$9,\!12,\!16,\!18$	0

6.5 Other polymers (i)

There are no such residues in this entry.

