

# Full wwPDB X-ray Structure Validation Report (i)

Jun 15, 2020 – 10:26 pm BST

PDB ID : 1CYN

Title: CYCLOPHILIN B COMPLEXED WITH [D-(CHOLINYLESTER)SER8]-C

YCLOSPORIN

Authors: Mikol, V.; Kallen, J.; Walkinshaw, M.D.

Deposited on : 1995-05-22

Resolution : 1.85 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 following versions of software and data (see references (1)) 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

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)

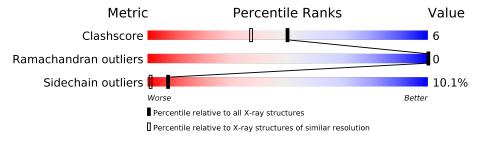
Validation Pipeline (wwPDB-VP) : 2.11

## 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.85 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	Similar resolution
	$(\#  ext{Entries})$	$(\#  ext{Entries},  ext{resolution range}( ext{Å}))$
Clashscore	141614	2625 (1.86-1.86)
Ramachandran outliers	138981	2592 (1.86-1.86)
Sidechain outliers	138945	2592 (1.86-1.86)

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 <=5%

Note EDS was not executed.

Mol	Chain	Length		Quality of chain					
1	A	178		81%	15%	•••			
2	С	11	27%	73%					



# 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 1710 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 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B.

$\mathbf{Mol}$	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	A	178	Total 1429	C 926	N 238	O 261	S 4	0	12	0

• Molecule 2 is a protein called CYCLOSPORIN A.

$\mathbf{Mol}$	Chain	Residues	Atoms	ZeroOcc	$\mathbf{AltConf}$	Trace
2	С	11	Total C N 85 62 11	 0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	${f Comment}$	Reference
С	1	DSN	DAL	ENGINEERED MUTATION	NOR NOR00033

• Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	188	Total O 188 188	0	0
3	С	8	Total O 8 8	0	0

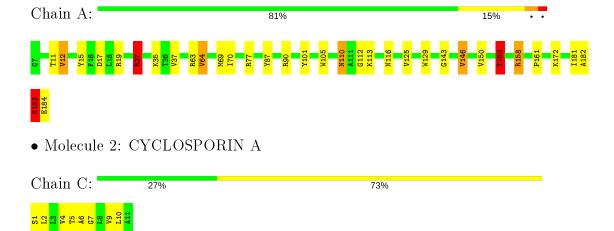


## 3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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.

Note EDS was not executed.

• Molecule 1: PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B





# 4 Data and refinement statistics (i)

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

Property	Value	Source	
Space group	P 21 21 21	Depositor	
Cell constants	37.46Å 46.94Å 115.44Å	Depositor	
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	8.00 - 1.85	Depositor	
% Data completeness	(Not available) (8.00-1.85)	Depositor	
(in resolution range)	, , , , , , , , , , , , , , , , , , , ,		
$R_{merge}$	(Not available)	Depositor	
$R_{sym}$	(Not available)	Depositor	
Refinement program	X-PLOR	Depositor	
$R, R_{free}$	0.160 , (Not available)	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	1710	wwPDB-VP	
Average B, all atoms (Å <sup>2</sup> )	17.0	wwPDB-VP	



# 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: ABA, MLE, DSN, MVA, BMT, SAR

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		
MIOI		RMSZ	# Z >5	RMSZ	# Z  > 5	
1	A	0.80	0/1507	1.46	$22/2023 \ (1.1\%)$	
2	С	0.59	0/10	1.60	0/11	
All	All	0.79	0/1517	1.46	$22/2034 \ (1.1\%)$	

There are no bond length outliers.

All (22) bond angle outliers are listed below:

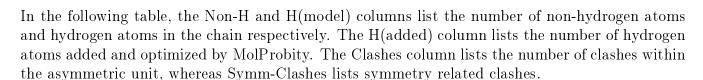
Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}(^{o})$
1	A	27	ARG	NE-CZ-NH1	12.54	126.57	120.30
1	A	19	ARG	NE-CZ-NH1	8.87	124.73	120.30
1	A	129	TRP	CD1-CG-CD2	8.05	112.74	106.30
1	A	158	ARG	NE-CZ-NH1	7.96	124.28	120.30
1	A	129	TRP	CE2-CD2-CG	-7.53	101.28	107.30
1	A	27	ARG	NE-CZ-NH2	-7.04	116.78	120.30
1	A	19	ARG	NE-CZ-NH2	-7.03	116.78	120.30
1	A	12	VAL	CB-CA-C	-6.91	98.28	111.40
1	A	105	TRP	CD1-CG-CD2	6.90	111.82	106.30
1	A	105	TRP	CE2-CD2-CG	-6.34	102.23	107.30
1	A	129	TRP	CG-CD2-CE3	5.69	139.02	133.90
1	A	129	TRP	CB-CG-CD1	-5.59	119.73	127.00
1	A	153[A]	THR	CB-CA-C	-5.59	96.50	111.60
1	A	153[B]	THR	CB-CA-C	-5.59	96.50	111.60
1	A	153[A]	THR	N-CA-CB	5.51	120.78	110.30
1	A	153[B]	THR	N-CA-CB	5.51	120.78	110.30
1	A	182	ALA	CA-C-N	-5.38	105.36	117.20
1	A	63	ARG	NE-CZ-NH1	5.37	122.98	120.30
1	A	101	TYR	CB-CG-CD2	-5.25	117.85	121.00
1	A	183	LYS	N-CA-C	5.23	125.11	111.00
1	A	129	TRP	CG-CD1-NE1	-5.06	105.04	110.10
1	A	87	TYR	CB-CG-CD2	-5.05	117.97	121.00



There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts (i)



Mol	Chain	Non-H	H(model)	$\mathbf{H}(\mathbf{added})$	Clashes	Symm-Clashes
1	A	1429	0	1451	14	0
2	С	85	0	106	4	0
3	A	188	0	0	4	0
3	С	8	0	0	0	0
All	All	1710	0	1557	18	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 6.

All (18) 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:A:143:GLY:HA2	3:A:2142:HOH:O	1.98	0.64
1:A:64[A]:VAL:HB	1:A:70:ILE:HG22	1.80	0.64
1:A:15:TYR:HB2	1:A:27:ARG:HD2	1.83	0.60
1:A:17:ASP:OD1	1:A:27:ARG:HD3	2.01	0.60
1:A:153[B]:THR:HG22	3:A:2152:HOH:O	2.01	0.60
1:A:153[B]:THR:HG23	3:A:2073:HOH:O	2.12	0.49
1:A:110:ASN:HD22	1:A:112:GLY:H	1.62	0.47
1:A:143:GLY:O	1:A:146[B]:VAL:HG22	2.17	0.45
1:A:64[A]:VAL:HG13	1:A:161:PRO:HG3	1.98	0.45
1:A:110:ASN:ND2	1:A:112:GLY:H	2.15	0.44
2:C:1:DSN:HA	2:C:2:MLE:HN1	1.81	0.42
2:C:9:VAL:HA	2:C:10:MLE:HN1	1.84	0.42
1:A:181:ILE:O	1:A:183:LYS:HD3	2.20	0.42
2:C:6:ABA:HA	2:C:7:SAR:HN1	1.83	0.41
1:A:90:ARG:HA	1:A:116:ASN:O	2.20	0.41
1:A:11:THR:HG21	1:A:35:LYS:HD3	2.03	0.41
2:C:4:MVA:HA	2:C:5:BMT:HN1	1.88	0.41
1:A:113:LYS:HG3	3:A:2095:HOH:O	2.21	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	Perce	$_{ m ntiles}$
1	A	188/178 (106%)	182 (97%)	6 (3%)	0	100	100
2	С	1/11 (9%)	1 (100%)	0	0	100	100
All	All	189/189 (100%)	183 (97%)	6 (3%)	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	159/147 (108%)	139 (87%)	20 (13%)		4	C		
2	С	1/1 (100%)	1 (100%)	0	1	00	1	.00	
All	All	160/148 (108%)	140 (88%)	20 (12%)		7	C	)	

All (20) residues with a non-rotameric sidechain are listed below:

$\mathbf{Mol}$	Chain	$\operatorname{Res}$	$\mathbf{Type}$	
1	A	12	VAL	
1	A	27	ARG	
1	A	37	VAL	
1	A	64[A]	VAL	
1	A	64[B]	VAL	

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Mol	Chain	Res	Type
1	A	69	MET
1	A	77	ARG
1	A	110	ASN
1	A	125[A]	VAL
1	A	125[B]	VAL
1	A	146[A]	VAL
1	A	146[B]	VAL
1	A	150[A]	VAL
1	A	150[B]	VAL
1	A	153[A]	THR
1	A	153[B]	THR
1	A	158	ARG
1	A	172	LYS
1	A	183	LYS
1	A	184	GLU

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

Mol	Chain	Res	Type
1	A	110	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)

9 non-standard protein/DNA/RNA residues 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	Mol Type Chain Res		Type	Dog	Pog	${ m Res}$	Dog	Dog	Dog	Dog	Dog	Dog	Des	Dog	Link	$\mathbf{B}\mathbf{c}$	ond leng	${ m ths}$	${f B}$	ond ang	gles
MIOI	туре	Chain	nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z >2											
2	MLE	С	10	2	7,8,9	0.93	0	6,9,11	0.92	0											
2	ABA	С	6	2	4,5,6	0.76	0	1,5,7	0.51	0											



Mol	Trino	Chain	Res	Link	Bo	ond leng	ths	Е	ond ang	gles
10101	Type	Chain	nes	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z >2
2	MVA	С	4	2	6,7,8	0.97	0	7,8,10	1.72	2 (28%)
2	MLE	С	3	2	7,8,9	0.96	1 (14%)	6,9,11	1.04	1 (16%)
2	SAR	С	7	2	4,4,5	0.76	0	1,3,5	2.40	1 (100%)
2	MLE	С	2	2	7,8,9	0.78	0	6,9,11	0.65	0
2	BMT	С	5	2	11,12,13	0.96	0	12,14,16	0.82	0
2	MLE	С	8	2	7,8,9	0.71	0	6,9,11	1.58	1 (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	MLE	С	10	2	-	0/5/8/10	-
2	ABA	С	6	2	-	1/3/4/6	-
2	MVA	С	4	2	-	1/6/8/10	-
2	MLE	С	3	2	-	0/5/8/10	-
2	SAR	С	7	2	-	1/1/2/3	-
2	MLE	С	2	2	-	0/5/8/10	-
2	BMT	С	5	2	-	1/13/16/18	-
2	MLE	С	8	2	-	1/5/8/10	-

#### All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	${f Observed(\AA)}$	$\operatorname{Ideal}( ext{\AA})$
2	С	3	MLE	CN-N	2.00	1.52	1.46

#### All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\mathbf{Observed}(^o)$	$\mathbf{Ideal}(^{o})$
2	С	4	MVA	CB-CA-C	-2.98	109.31	113.04
2	С	8	MLE	CG-CB-CA	2.81	122.36	115.34
2	С	7	SAR	O-C-CA	-2.40	118.49	125.42
2	С	4	MVA	CG1-CB-CA	-2.26	107.75	111.21
2	С	3	MLE	O-C-CA	-2.05	119.42	124.78

There are no chirality outliers.

All (5) torsion outliers are listed below:



Mol	Chain	Res	Type	Atoms
2	С	6	ABA	O-C-CA-CB
2	С	8	MLE	O-C-CA-CB
2	С	5	BMT	CB-CA-N-CN
2	С	4	MVA	CB-CA-N-CN
2	С	7	SAR	C-CA-N-CN

There are no ring outliers.

6 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	С	10	MLE	1	0
2	С	6	ABA	1	0
2	С	4	MVA	1	0
2	С	7	SAR	1	0
2	С	2	MLE	1	0
2	С	5	BMT	1	0

### 5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

### 5.6 Ligand geometry (i)

There are no ligands in this entry.

### 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)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

### 6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

