



# wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 10, 2023 – 11:28 PM EDT

PDB ID : 2PLV  
Title : STRUCTURAL FACTORS THAT CONTROL CONFORMATIONAL TRANSITIONS AND SEROTYPE SPECIFICITY IN TYPE 3 POLIOVIRUS  
Authors : Filman, D.J.; Hogle, J.M.  
Deposited on : 1989-10-17  
Resolution : 2.88 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](mailto: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>.

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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)  
Xtrriage (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) : 2.32.2

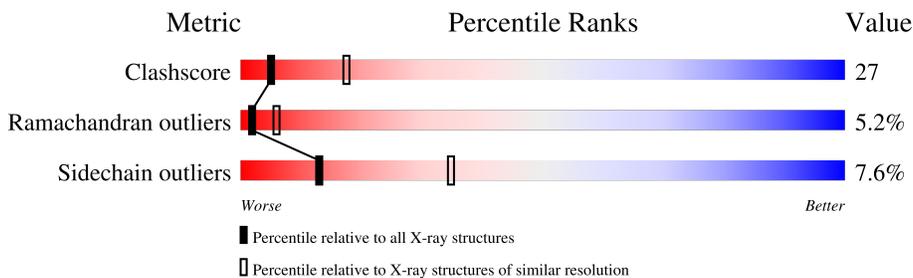
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.88 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	2947 (2.90-2.86)
Ramachandran outliers	138981	2868 (2.90-2.86)
Sidechain outliers	138945	2871 (2.90-2.86)

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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	1	302	53% (green), 33% (yellow), 8% (orange), 5% (red), 5% (grey)
2	2	272	54% (green), 35% (yellow), 8% (orange), 2% (red), 2% (grey)
3	3	238	47% (green), 42% (yellow), 7% (orange), 2% (red), 2% (grey)
4	4	68	37% (green), 38% (yellow), 16% (orange), 5% (red), 2% (grey)

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	SPH	1	0	X	-	X	-

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 7162 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 HUMAN POLIOVIRUS TYPE 1 (SUBUNIT VP1).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	1	288	2251	1431	383	432	5	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	8	SER	ARG	conflict	UNP P03300
1	9	SER	GLU	conflict	UNP P03300

- Molecule 2 is a protein called HUMAN POLIOVIRUS TYPE 1 (SUBUNIT VP2).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	2	268	2085	1317	358	396	14	0	0	0

- Molecule 3 is a protein called HUMAN POLIOVIRUS TYPE 1 (SUBUNIT VP3).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	3	235	1834	1169	299	349	17	0	0	0

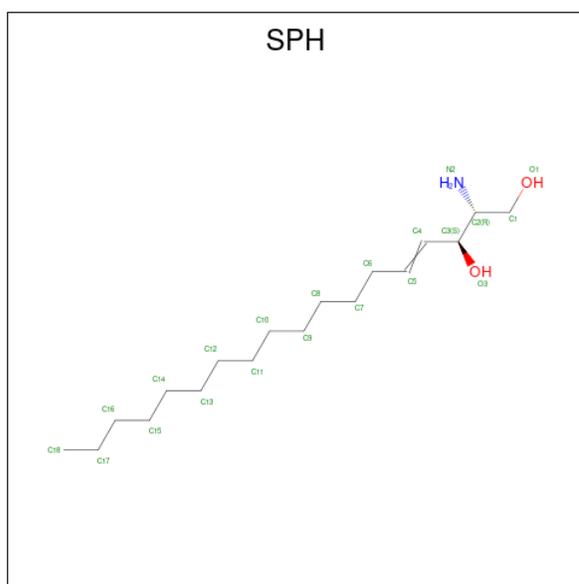
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
3	123	SER	PHE	conflict	UNP P03300

- Molecule 4 is a protein called HUMAN POLIOVIRUS TYPE 1 (SUBUNIT VP4).

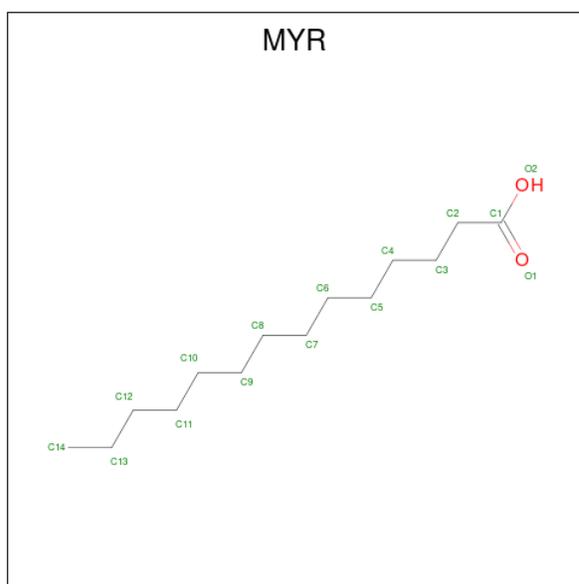
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	4	63	477	293	82	101	1	0	0	1

- Molecule 5 is SPHINGOSINE (three-letter code: SPH) (formula:  $C_{18}H_{37}NO_2$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
5	1	1	21	18	1	2	0	0

- Molecule 6 is MYRISTIC ACID (three-letter code: MYR) (formula:  $C_{14}H_{28}O_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
6	4	1	15	14	1	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	1	159	Total 159	O 159	0	0
7	2	149	Total 149	O 149	0	0
7	3	129	Total 129	O 129	0	0
7	4	42	Total 42	O 42	0	0

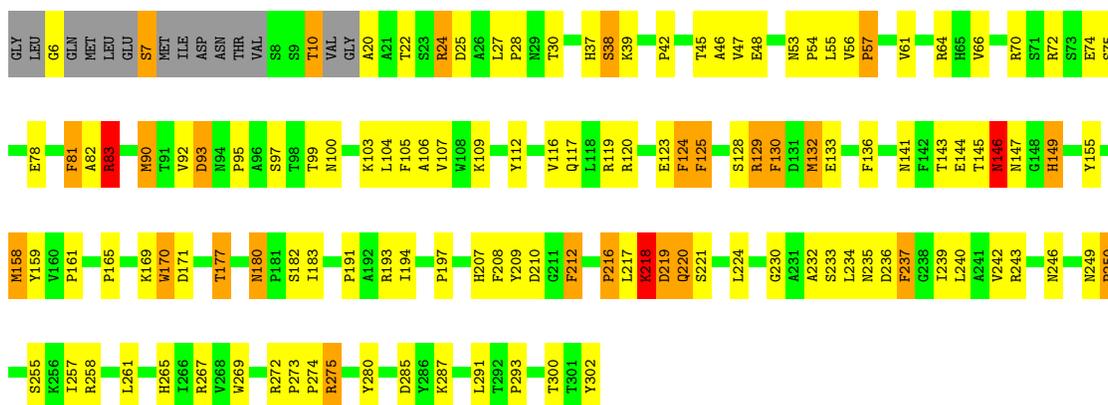
### 3 Residue-property plots

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.

Note EDS was not executed.

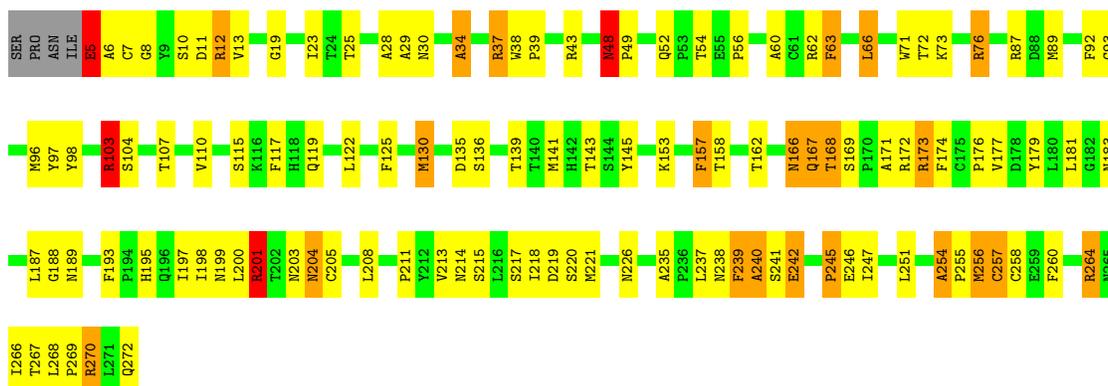
- Molecule 1: HUMAN POLIOVIRUS TYPE 1 (SUBUNIT VP1)

Chain 1: 



- Molecule 2: HUMAN POLIOVIRUS TYPE 1 (SUBUNIT VP2)

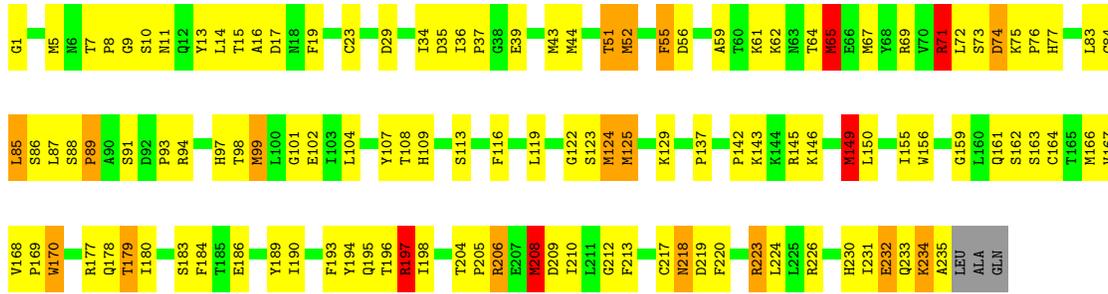
Chain 2: 



- Molecule 3: HUMAN POLIOVIRUS TYPE 1 (SUBUNIT VP3)

Chain 3: 





• Molecule 4: HUMAN POLIOVIRUS TYPE 1 (SUBUNIT VP4)



## 4 Data and refinement statistics

Xtrriage (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, $\alpha$ , $\beta$ , $\gamma$	322.94Å 358.04Å 380.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.88	Depositor
% Data completeness (in resolution range)	72.6 ((Not available)-2.88)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	REAL-SPACE REFINEMENT	Depositor
R, $R_{free}$	0.200 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	7162	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	21.0	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: SPH, MYR

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	1	1.94	3/2313 (0.1%)	2.09	34/3160 (1.1%)
2	2	1.95	8/2142 (0.4%)	2.10	38/2928 (1.3%)
3	3	1.92	6/1881 (0.3%)	2.07	33/2562 (1.3%)
4	4	1.95	5/484 (1.0%)	2.11	11/653 (1.7%)
All	All	1.94	22/6820 (0.3%)	2.09	116/9303 (1.2%)

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	6	GLY	N-CA	10.41	1.61	1.46
3	3	1	GLY	N-CA	9.08	1.59	1.46
1	1	20	ALA	N-CA	7.87	1.62	1.46
4	4	23	SER	N-CA	7.71	1.61	1.46
4	4	14	GLU	CD-OE2	6.58	1.32	1.25

The worst 5 of 116 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	3	197	ARG	NE-CZ-NH2	7.72	124.16	120.30
2	2	264	ARG	NE-CZ-NH2	7.67	124.14	120.30
1	1	267	ARG	NE-CZ-NH2	7.65	124.12	120.30
3	3	223	ARG	NE-CZ-NH2	7.57	124.08	120.30
3	3	69	ARG	NE-CZ-NH2	7.55	124.08	120.30

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	1	2251	0	2197	125	0
2	2	2085	0	2000	106	0
3	3	1834	0	1816	120	0
4	4	477	0	457	41	0
5	1	21	0	36	26	0
6	4	15	0	27	1	0
7	1	159	0	0	7	0
7	2	149	0	0	4	0
7	3	129	0	0	12	0
7	4	42	0	0	6	0
All	All	7162	0	6533	359	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 27.

The worst 5 of 359 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)
2:2:5:GLU:CG	2:2:7:CYS:HB3	1.58	1.32
3:3:124:MET:HG3	7:3:320:HOH:O	1.32	1.23
1:1:132:MET:CE	5:1:0:SPH:H81	1.69	1.23
1:1:177:THR:HG21	1:1:182:SER:OG	1.40	1.21
3:3:124:MET:CG	7:3:320:HOH:O	1.83	1.17

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	Percentiles	
1	1	284/302 (94%)	225 (79%)	43 (15%)	16 (6%)	2	5
2	2	266/272 (98%)	222 (84%)	36 (14%)	8 (3%)	4	15
3	3	233/238 (98%)	180 (77%)	38 (16%)	15 (6%)	1	3
4	4	59/68 (87%)	47 (80%)	7 (12%)	5 (8%)	1	2
All	All	842/880 (96%)	674 (80%)	124 (15%)	44 (5%)	2	6

5 of 44 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1	82	ALA
1	1	145	THR
1	1	219	ASP
2	2	200	LEU
2	2	257	CYS

### 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	1	249/261 (95%)	232 (93%)	17 (7%)	16	40
2	2	228/232 (98%)	208 (91%)	20 (9%)	10	28
3	3	210/212 (99%)	199 (95%)	11 (5%)	23	53
4	4	54/57 (95%)	46 (85%)	8 (15%)	3	8
All	All	741/762 (97%)	685 (92%)	56 (8%)	13	35

5 of 56 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	2	167	GLN
4	4	64	THR
2	2	264	ARG
4	4	61	LEU

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Mol	Chain	Res	Type
4	4	7	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
3	3	233	GLN
4	4	13	HIS
4	4	39	ASN
4	4	31	ASN
3	3	218	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](#)

2 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
6	MYR	4	1	4	14,14,15	0.51	0	13,13,15	1.14	1 (7%)
5	SPH	1	0	-	19,20,20	1.38	2 (10%)	18,21,21	1.65	2 (11%)

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
6	MYR	4	1	4	-	7/11/12/13	-
5	SPH	1	0	-	2/2/2/4	12/21/21/21	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	1	0	SPH	C4-C5	5.13	1.53	1.31
5	1	0	SPH	C3-C4	2.01	1.53	1.50

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	1	0	SPH	C3-C4-C5	-5.51	112.51	124.79
5	1	0	SPH	C6-C5-C4	-2.69	113.37	125.39
6	4	1	MYR	O1-C1-C2	-2.27	112.00	126.89

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	1	0	SPH	C2
5	1	0	SPH	C3

5 of 19 torsion outliers are listed below:

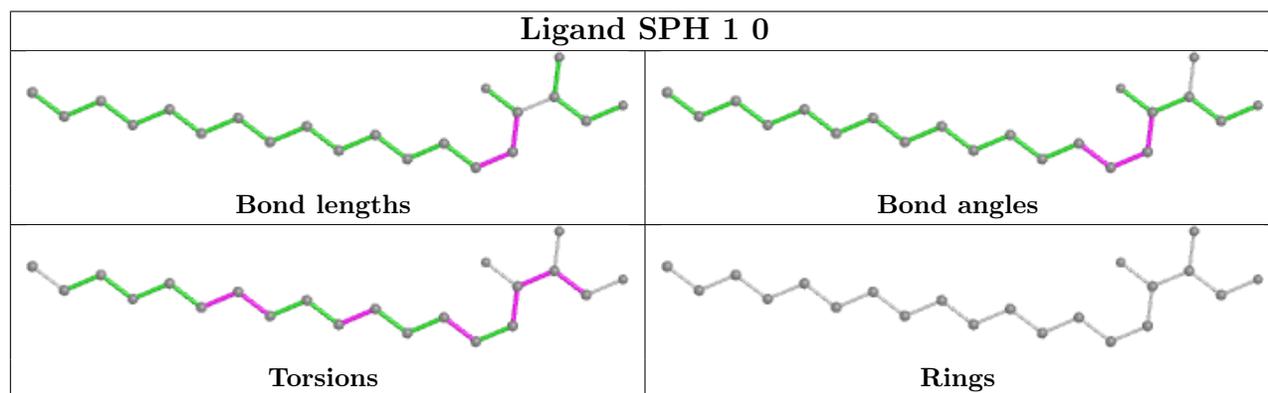
Mol	Chain	Res	Type	Atoms
5	1	0	SPH	O1-C1-C2-N2
5	1	0	SPH	O1-C1-C2-C3
5	1	0	SPH	C1-C2-C3-O3
5	1	0	SPH	C1-C2-C3-C4
5	1	0	SPH	N2-C2-C3-C4

There are no ring outliers.

2 monomers are involved in 27 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	4	1	MYR	1	0
5	1	0	SPH	26	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 [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.