



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 28, 2026 – 02:17 AM UTC

PDB ID : 1QJX / pdb_00001qjx
Title : HUMAN RHINOVIRUS 16 COAT PROTEIN IN COMPLEX WITH ANTIVIRAL COMPOUND WIN68934
Authors : Hadfield, A.T.; Diana, G.D.; Rossmann, M.G.
Deposited on : 1999-07-06
Resolution : 2.80 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 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) : 2.0
EDS : **FAILED**
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

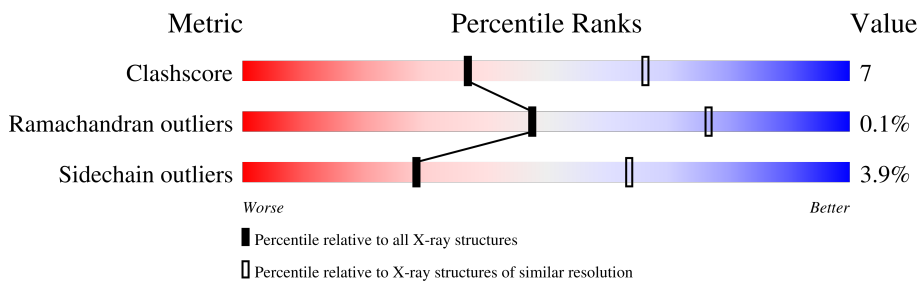
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)

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 failed to run properly.

Mol	Chain	Length	Quality of chain
1	1	285	
2	2	261	
3	3	238	
4	4	68	

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 6646 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 VP1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1	285	Total	C	N	O	S	0	0	0
			2288	1442	397	438	11			

- Molecule 2 is a protein called PROTEIN VP2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	2	252	Total	C	N	O	S	0	0	0
			1978	1252	343	373	10			

- Molecule 3 is a protein called PROTEIN VP3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	3	238	Total	C	N	O	S	0	0	0
			1846	1186	298	347	15			

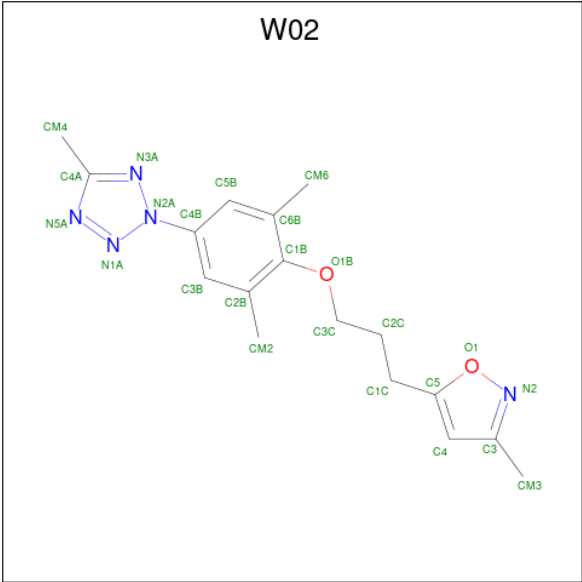
- Molecule 4 is a protein called PROTEIN VP4.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	4	29	Total	C	N	O	0	0	0
			224	138	41	45			

- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn).

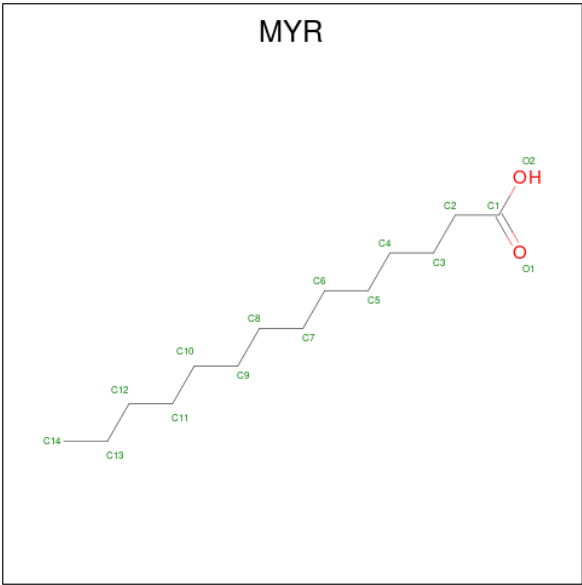
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	1	1	Total	Zn	0	0
			1	1		

- Molecule 6 is 2,6-DIMETHYL-1-(3-[3-METHYL-5-ISOXAZOLYL]-PROPANYL)-4-[4-METHYL-2H-TETRAZOL-2-YL]-PHENOL (CCD ID: W02) (formula: C₁₇H₂₁N₅O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	1	1	Total	C	N	O	0	0
			24	17	5	2		

- Molecule 7 is MYRISTIC ACID (CCD ID: MYR) (formula: C₁₄H₂₈O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	4	1	Total	C	O	0	0
			15	14	1		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	1	89	Total 89	O 89	0	0
8	2	97	Total 97	O 97	0	0
8	3	81	Total 81	O 81	0	0
8	4	3	Total 3	O 3	0	0

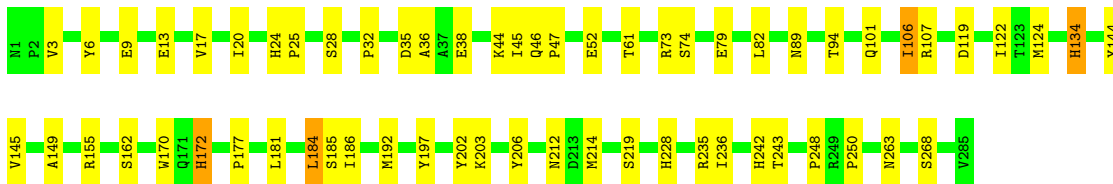
3 Residue-property plots [i](#)

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. 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 failed to run properly.

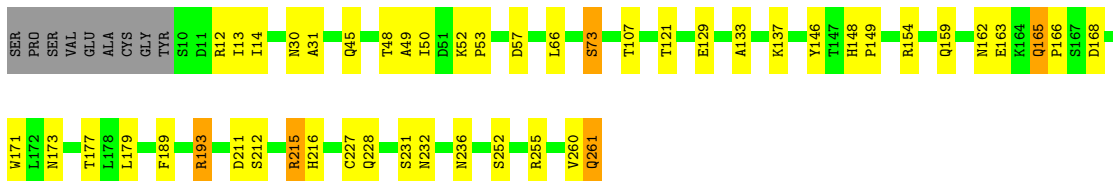
• Molecule 1: PROTEIN VP1

Chain 1:  79% 20% .



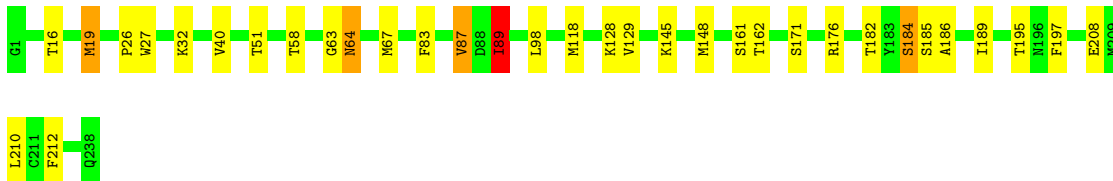
• Molecule 2: PROTEIN VP2

Chain 2:  78% 16% . .



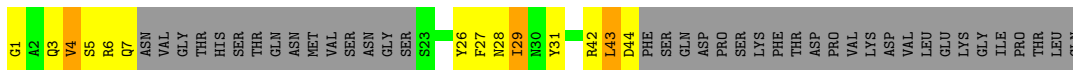
• Molecule 3: PROTEIN VP3

Chain 3:  86% 12% .



• Molecule 4: PROTEIN VP4

Chain 4:  22% 16% . 57%



4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants a, b, c, α , β , γ	362.60Å 347.10Å 334.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.80	Depositor
% Data completeness (in resolution range)	48.0 (30.00-2.80)	Depositor
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.34 (at 2.58Å)	Xtriage
Refinement program	X-PLOR 3.1, X-PLOR 3.85	Depositor
R, R_{free}	0.231 , 0.235	Depositor
Wilson B-factor (Å ²)	20.6	Xtriage
Anisotropy	0.348	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.034 for -h,l,k	Xtriage
Total number of atoms	6646	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.42% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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.

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: ZN, W02, 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	0.50	1/2350 (0.0%)	0.90	8/3204 (0.2%)
2	2	0.51	0/2030	0.94	3/2770 (0.1%)
3	3	0.48	0/1898	0.93	7/2596 (0.3%)
4	4	0.92	0/226	1.27	4/301 (1.3%)
All	All	0.52	1/6504 (0.0%)	0.94	22/8871 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	134	HIS	CD2-NE2	5.82	1.44	1.37

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	184	LEU	N-CA-C	7.79	122.78	113.28
2	2	50	ILE	N-CA-C	6.81	119.57	112.83
3	3	89	ILE	N-CA-C	6.79	118.36	110.62
1	1	192	MET	N-CA-C	-6.58	105.06	113.23
1	1	185	SER	N-CA-C	6.27	118.65	110.43

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	2288	0	2201	35	0
2	2	1978	0	1920	32	0
3	3	1846	0	1826	19	0
4	4	224	0	208	12	0
5	1	1	0	0	0	0
6	1	24	0	21	1	0
7	4	15	0	27	0	0
8	1	89	0	0	1	0
8	2	97	0	0	3	0
8	3	81	0	0	0	0
8	4	3	0	0	0	0
All	All	6646	0	6203	89	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 89 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)
2:2:12:ARG:HH11	2:2:12:ARG:HG3	1.34	0.89
2:2:173:ASN:HD21	2:2:179:LEU:HA	1.45	0.81
2:2:73:SER:HB2	2:2:228:GLN:HE21	1.50	0.76
2:2:260:VAL:O	2:2:261:GLN:HB2	1.83	0.76
8:2:2082:HOH:O	3:3:208:GLU:HG3	1.86	0.76

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	283/285 (99%)	273 (96%)	10 (4%)	0	100	100
2	2	250/261 (96%)	236 (94%)	13 (5%)	1 (0%)	30	60

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	3	236/238 (99%)	226 (96%)	10 (4%)	0	100	100
4	4	25/68 (37%)	25 (100%)	0	0	100	100
All	All	794/852 (93%)	760 (96%)	33 (4%)	1 (0%)	48	77

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	2	73	SER

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	1	256/256 (100%)	247 (96%)	9 (4%)	32	67
2	2	221/228 (97%)	212 (96%)	9 (4%)	27	62
3	3	210/210 (100%)	202 (96%)	8 (4%)	29	64
4	4	23/59 (39%)	21 (91%)	2 (9%)	9	30
All	All	710/753 (94%)	682 (96%)	28 (4%)	28	64

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	2	215	ARG
4	4	6	ARG
2	2	261	GLN
3	3	182	THR
2	2	252	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
2	2	232	ASN

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Mol	Chain	Res	Type
3	3	124	ASN
4	4	28	ASN
3	3	230	HIS
3	3	59	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

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	W02	1	7002	-	25,26,26	1.31	1 (4%)	29,36,36	1.45	6 (20%)
7	MYR	4	4000	4	13,14,15	0.85	0	12,13,15	0.71	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
6	W02	1	7002	-	-	1/11/11/11	0/3/3/3
7	MYR	4	4000	4	-	5/12/12/13	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	1	7002	W02	C4B-N2A	4.33	1.49	1.43

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	1	7002	W02	C3B-C2B-C1B	2.80	121.99	117.94
6	1	7002	W02	C5B-C6B-C1B	2.60	121.70	117.94
6	1	7002	W02	C4B-N2A-N3A	2.49	124.73	122.18
6	1	7002	W02	C4B-C3B-C2B	-2.46	119.11	121.55
6	1	7002	W02	C6B-C1B-C2B	-2.27	117.31	122.07

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	4	4000	MYR	C9-C10-C11-C12
7	4	4000	MYR	C4-C5-C6-C7
6	1	7002	W02	C1C-C2C-C3C-O1B
7	4	4000	MYR	C11-C12-C13-C14
7	4	4000	MYR	C6-C7-C8-C9

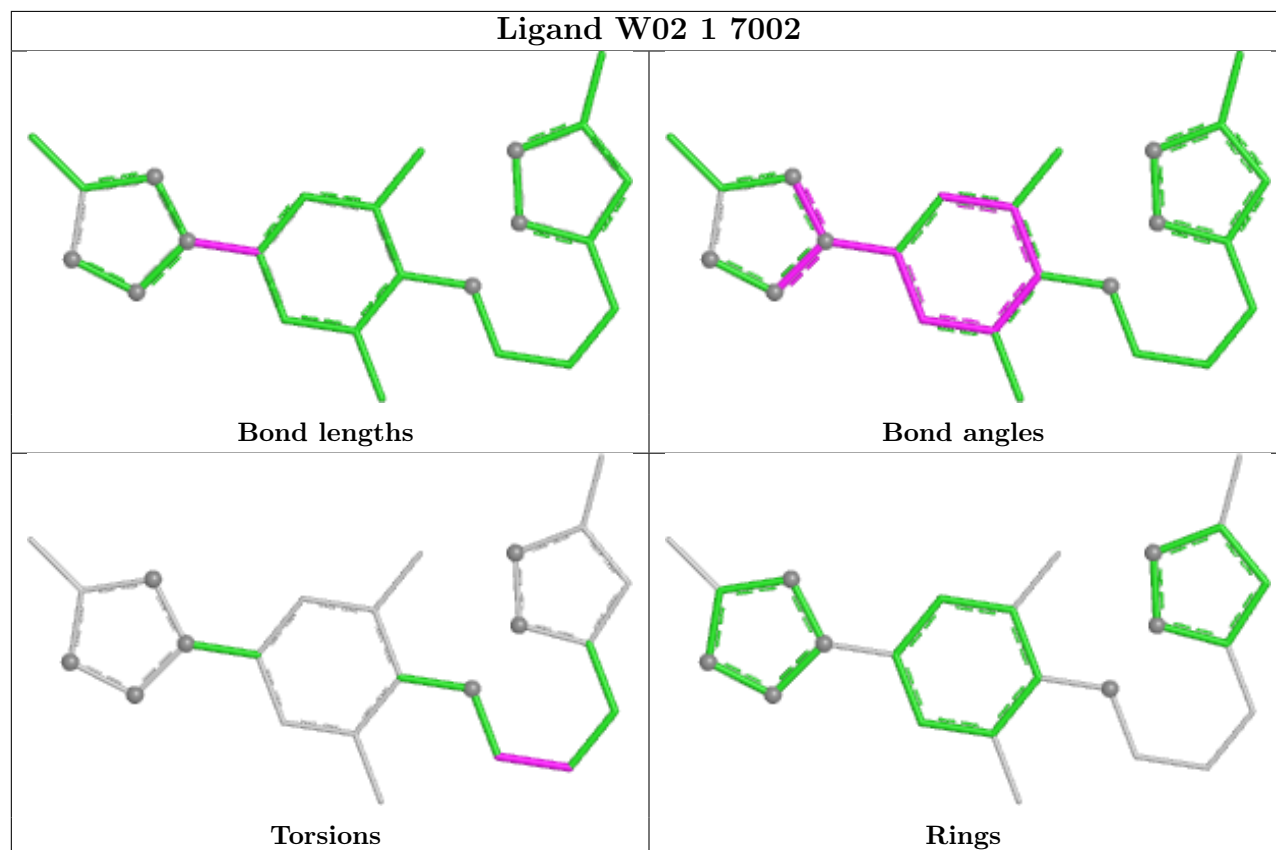
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	1	7002	W02	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 [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 failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS failed to run properly - this section is therefore empty.

6.4 Ligands [i](#)

EDS failed to run properly - this section is therefore empty.

6.5 Other polymers [i](#)

EDS failed to run properly - this section is therefore empty.