



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 8, 2023 – 01:21 AM EDT

PDB ID : 4QL1  
Title : Crystal structure of human WDR5 in complex with compound OICR-9429  
Authors : Dong, A.; Dombrovski, L.; Walker, J.R.; Getlik, M.; Kuznetsova, E.; Smil, D.; Barysytė, D.; Li, F.; Poda, G.; Senisterra, G.; Marcellus, R.; Al-Awar, R.; Bountra, C.; Arrowsmith, C.H.; Edwards, A.M.; Brown, P.J.; Schapira, M.; Vedadi, M.; Wu, H.; Structural Genomics Consortium (SGC)  
Deposited on : 2014-06-10  
Resolution : 1.50 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](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>.

---

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) : 1.13  
EDS : **FAILED**  
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) : 2.35.1

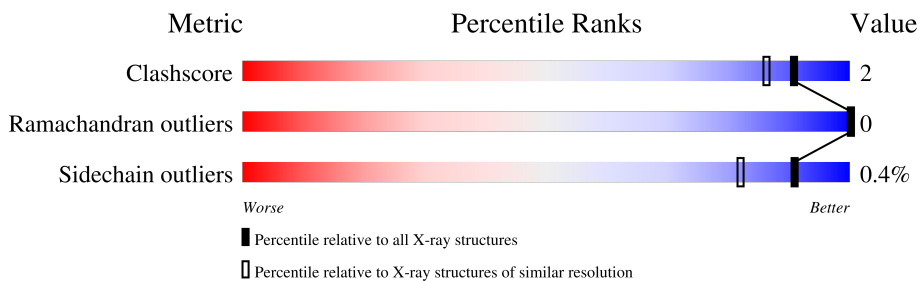
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.50 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	3144 (1.50-1.50)
Ramachandran outliers	138981	3066 (1.50-1.50)
Sidechain outliers	138945	3064 (1.50-1.50)

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 failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	312	95%
1	B	312	92%

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 5115 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.

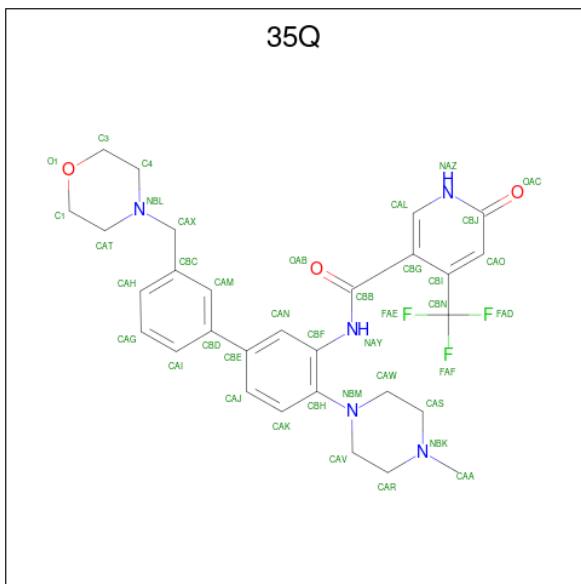
- Molecule 1 is a protein called WD repeat-containing protein 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	304	Total 2346	C 1501	N 387	O 448	S 10	0	6	0
1	B	302	Total 2353	C 1507	N 385	O 450	S 11	0	9	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	23	GLY	-	expression tag	UNP P61964
B	23	GLY	-	expression tag	UNP P61964

- Molecule 2 is N-(4-(4-methylpiperazin-1-yl)-3'-(morpholinomethyl)-[1,1'-biphenyl]-3-yl)-6-oxo-4-(trifluoromethyl)-1,6-dihydropyridine-3-carboxamide (three-letter code: 35Q) (formula: C<sub>29</sub>H<sub>32</sub>F<sub>3</sub>N<sub>5</sub>O<sub>3</sub>).

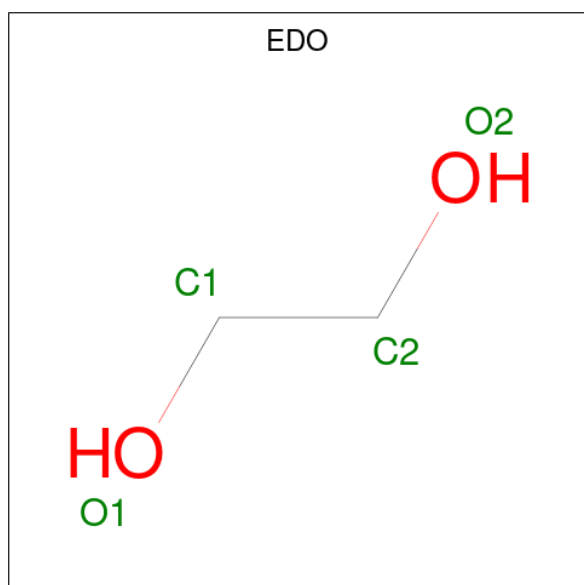


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	0	0
			36	26	3	5	2		
2	B	1	Total	C	F	N	O	0	0
			36	26	3	5	2		

- Molecule 3 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	X	0	0
			1	1		
3	B	1	Total	X	0	0
			1	1		

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	169	Total O 173 173	0	4
6	B	157	Total O 159 159	0	2

### 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: WD repeat-containing protein 5

Chain A:  95%



- Molecule 1: WD repeat-containing protein 5

Chain B:  92%



## 4 Data and refinement statistics [i](#)

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

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	46.84Å 56.63Å 64.69Å 71.45° 88.94° 65.43°	Depositor
Resolution (Å)	50.00 – 1.50	Depositor
% Data completeness (in resolution range)	94.5 (50.00-1.50)	Depositor
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	6.61 (at 1.50Å)	Xtrriage
Refinement program	REFMAC 5.8.0049	Depositor
R, $R_{free}$	0.195 , 0.227	Depositor
Wilson B-factor (Å <sup>2</sup> )	13.2	Xtrriage
Anisotropy	0.333	Xtrriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.118 for h,h-k,-l	Xtrriage
Total number of atoms	5115	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	15.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.67% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: UNX, EDO, 35Q, 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	A	0.48	0/2414	0.65	0/3282
1	B	0.47	0/2435	0.66	0/3309
All	All	0.47	0/4849	0.65	0/6591

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	A	2346	0	2280	4	0
1	B	2353	0	2308	12	0
2	A	36	0	24	0	0
2	B	36	0	24	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	B	4	0	6	0	0
5	B	6	0	8	3	0
6	A	173	0	0	0	0
6	B	159	0	0	1	0
All	All	5115	0	4650	16	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 2.

All (16) 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:207:LYS:CD	1:B:243:TYR:O	2.48	0.62
1:B:263:PHE:CE1	5:B:403:GOL:H31	2.35	0.62
1:B:263:PHE:HE1	5:B:403:GOL:H31	1.66	0.60
1:A:209:LEU:HD12	1:A:229:ILE:HD11	1.88	0.55
1:B:91[A]:SER:HB2	6:B:569:HOH:O	2.11	0.50
1:B:97[A]:SER:OG	1:B:139:PRO:O	2.27	0.50
1:B:140[A]:GLN:HE21	1:B:140[A]:GLN:H	1.58	0.50
1:A:63:SER:HB3	1:A:93:VAL:HG13	1.97	0.46
1:B:140[B]:GLN:HE21	1:B:140[B]:GLN:HA	1.80	0.46
1:B:41:LEU:HB2	1:B:327:ILE:HB	1.98	0.45
1:A:41:LEU:HB2	1:A:327:ILE:HB	1.99	0.45
1:B:263:PHE:CE1	5:B:403:GOL:C3	3.01	0.43
1:A:303:VAL:HB	1:A:321:LEU:HD12	2.00	0.42
1:B:218:SER:HB2	1:B:261:CYS:HA	2.02	0.41
1:B:35:TYR:CG	1:B:332:SER:HB2	2.56	0.41
1:B:220:VAL:HG23	1:B:229[B]:ILE:HG23	2.03	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	Percentiles	
1	A	308/312 (99%)	295 (96%)	13 (4%)	0	100	100
1	B	307/312 (98%)	297 (97%)	10 (3%)	0	100	100
All	All	615/624 (99%)	592 (96%)	23 (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	A	256/273 (94%)	256 (100%)	0	100	100
1	B	262/273 (96%)	259 (99%)	3 (1%)	73	53
All	All	518/546 (95%)	515 (99%)	3 (1%)	91	74

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	41	LEU
1	B	140[A]	GLN
1	B	140[B]	GLN

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](#)

Of 6 ligands modelled in this entry, 2 are unknown - leaving 4 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
4	EDO	B	402	-	3,3,3	0.50	0	2,2,2	0.30	0
5	GOL	B	403	-	5,5,5	0.13	0	5,5,5	0.67	0
2	35Q	A	401	-	39,39,44	1.67	8 (20%)	54,56,63	1.43	6 (11%)
2	35Q	B	401	-	39,39,44	1.63	8 (20%)	54,56,63	1.49	8 (14%)

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
4	EDO	B	402	-	-	1/1/1/1	-
5	GOL	B	403	-	-	2/4/4/4	-
2	35Q	A	401	-	-	4/24/35/44	0/4/4/5
2	35Q	B	401	-	-	4/24/35/44	0/4/4/5

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	35Q	CAX-CBC	-5.66	1.39	1.51
2	B	401	35Q	CAX-CBC	-4.80	1.41	1.51
2	A	401	35Q	CBN-CBI	-4.15	1.40	1.49
2	B	401	35Q	CBN-CBI	-3.94	1.41	1.49
2	B	401	35Q	CAL-CBG	2.97	1.40	1.36
2	B	401	35Q	CBG-CBB	-2.69	1.41	1.49
2	A	401	35Q	CBD-CBE	-2.66	1.42	1.49
2	B	401	35Q	CBF-NAY	-2.57	1.36	1.41
2	B	401	35Q	FAF-CBN	-2.51	1.21	1.32
2	A	401	35Q	CAL-CBG	2.51	1.40	1.36
2	B	401	35Q	CBH-NBM	-2.45	1.36	1.41
2	A	401	35Q	CBH-NBM	-2.44	1.36	1.41
2	A	401	35Q	CBF-NAY	-2.21	1.37	1.41
2	B	401	35Q	CAO-CBI	2.21	1.40	1.35
2	A	401	35Q	CBJ-NAZ	2.17	1.40	1.37
2	A	401	35Q	CBG-CBB	-2.15	1.43	1.49

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	35Q	CAL-NAZ-CBJ	-5.23	119.99	124.12
2	A	401	35Q	CAL-NAZ-CBJ	-4.97	120.20	124.12
2	A	401	35Q	CAV-CAR-NBK	4.32	115.68	110.80
2	A	401	35Q	CAS-CAW-NBM	3.60	117.70	110.70
2	B	401	35Q	CAW-CAS-NBK	-3.30	107.07	110.80
2	B	401	35Q	CAK-CBH-NBM	-3.27	117.09	122.30
2	B	401	35Q	CAS-CAW-NBM	2.54	115.64	110.70
2	A	401	35Q	CAK-CBH-NBM	-2.54	118.25	122.30
2	A	401	35Q	OAC-CBJ-CAO	-2.38	122.13	125.47
2	B	401	35Q	CAO-CBJ-NAZ	2.30	119.09	116.00
2	A	401	35Q	CAV-NBM-CBH	2.28	121.68	116.27
2	B	401	35Q	OAC-CBJ-CAO	-2.20	122.38	125.47
2	B	401	35Q	CBE-CAN-CBF	2.12	123.27	120.18
2	B	401	35Q	CAV-NBM-CBH	2.12	121.29	116.27

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	35Q	OAB-CBB-CBG-CBI
2	B	401	35Q	OAB-CBB-CBG-CBI
2	A	401	35Q	NAY-CBB-CBG-CBI
2	B	401	35Q	NAY-CBB-CBG-CBI
4	B	402	EDO	O1-C1-C2-O2
2	A	401	35Q	OAB-CBB-CBG-CAL
2	B	401	35Q	OAB-CBB-CBG-CAL
2	A	401	35Q	NAY-CBB-CBG-CAL
2	B	401	35Q	NAY-CBB-CBG-CAL
5	B	403	GOL	O2-C2-C3-O3
5	B	403	GOL	C1-C2-C3-O3

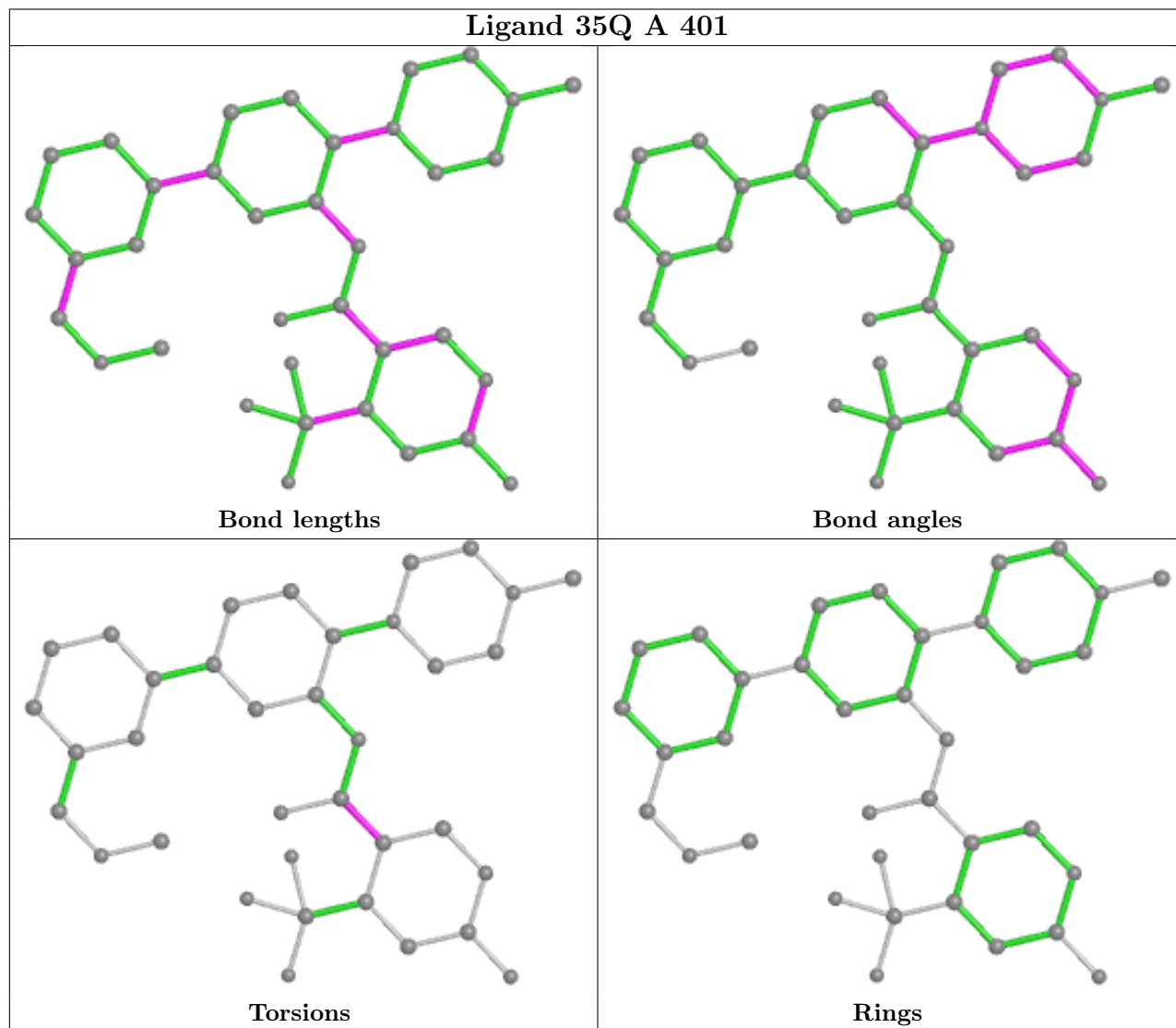
There are no ring outliers.

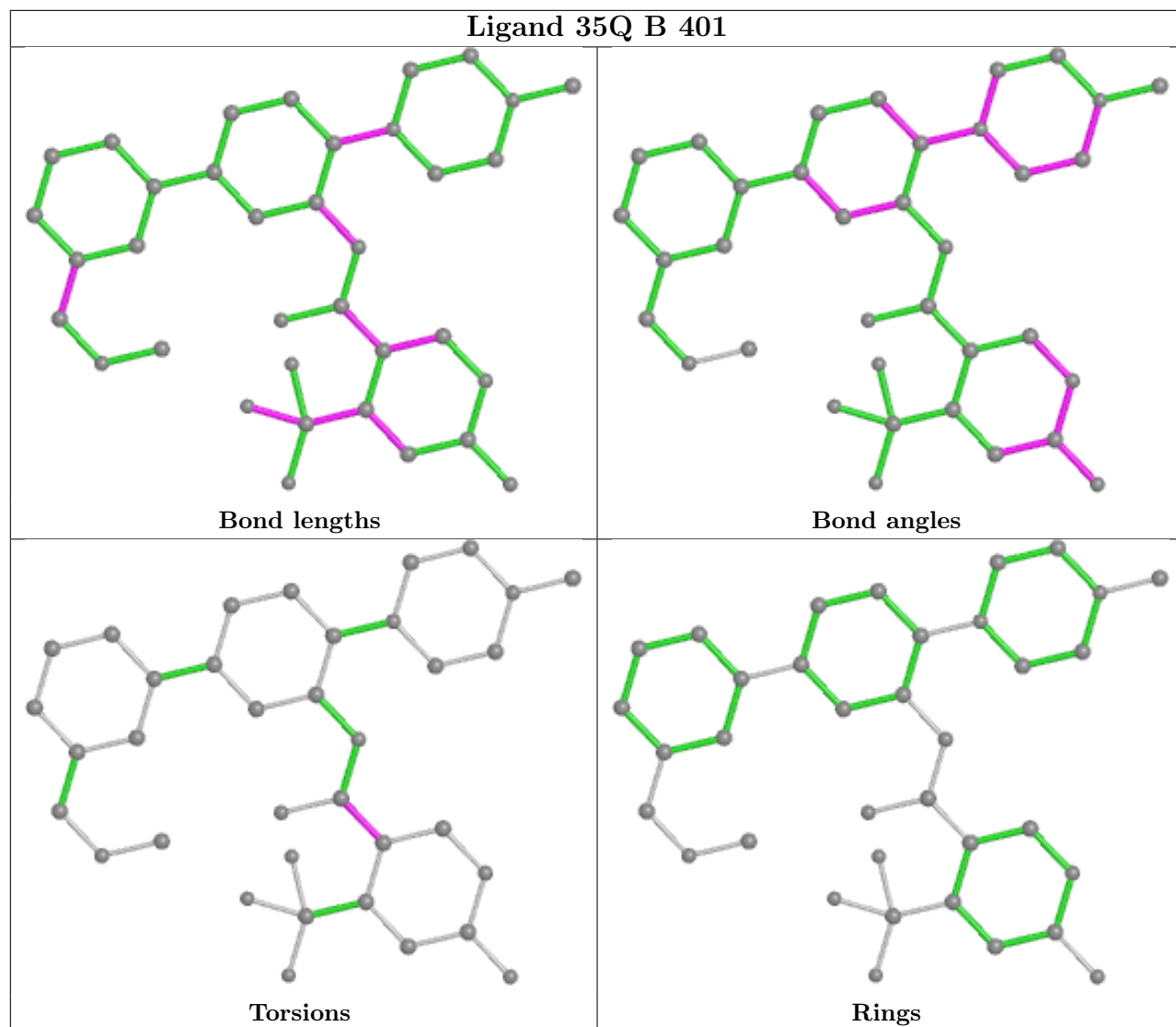
1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	403	GOL	3	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.