



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 1, 2022 – 02:42 pm GMT

PDB ID : 8BB4
Title : Structure of human WDR5 and pVHL:ElonginC:ElonginB bound to PROTAC with C3 linker
Authors : Kraemer, A.; Doelle, A.; Knapp, S.; Structural Genomics Consortium (SGC)
Deposited on : 2022-10-12
Resolution : 2.80 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 ⓘ 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	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.31.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

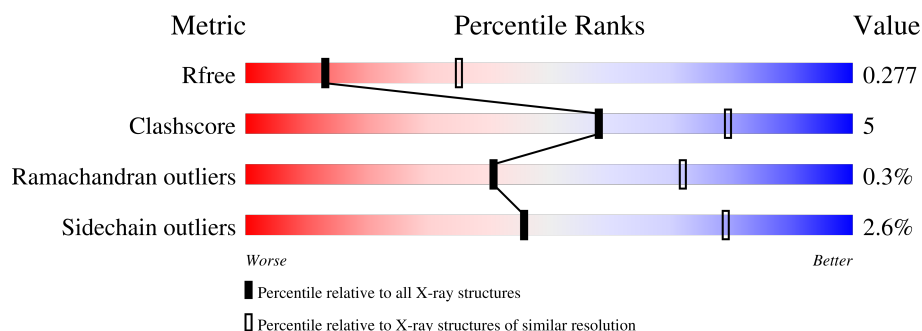
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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))
R_{free}	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	I	104	
2	O	98	
3	P	162	
4	Q	321	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 5077 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 Elongin-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	I	104	Total	C	N	O	S	0	0	0
			809	513	134	158	4			

- Molecule 2 is a protein called Elongin-C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	O	88	Total	C	N	O	S	0	0	0
			696	448	112	130	6			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	15	LYS	-	expression tag	UNP Q15369

- Molecule 3 is a protein called von Hippel-Lindau disease tumor suppressor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	P	147	Total	C	N	O	S	0	0	0
			1186	754	216	214	2			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	52	GLY	-	expression tag	UNP P40337
P	53	SER	-	expression tag	UNP P40337

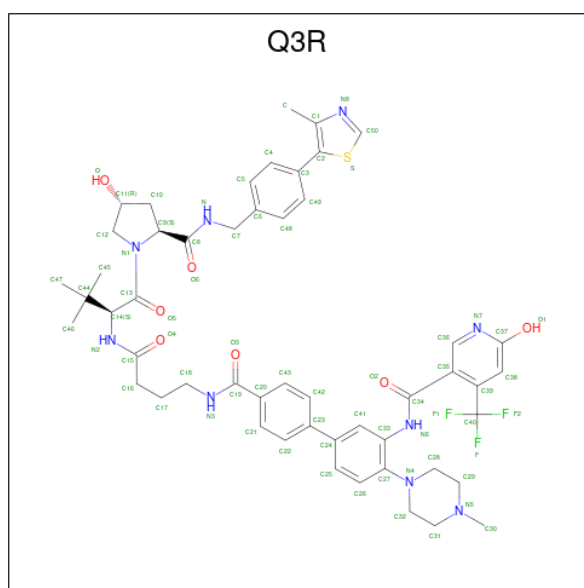
- Molecule 4 is a protein called WD repeat-containing protein 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	Q	297	Total	C	N	O	S	0	0	0
			2257	1439	372	436	10			

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	14	MET	-	initiating methionine	UNP P61964
Q	15	GLY	-	expression tag	UNP P61964
Q	16	SER	-	expression tag	UNP P61964
Q	17	SER	-	expression tag	UNP P61964
Q	18	HIS	-	expression tag	UNP P61964
Q	19	HIS	-	expression tag	UNP P61964
Q	20	HIS	-	expression tag	UNP P61964
Q	21	HIS	-	expression tag	UNP P61964
Q	22	HIS	-	expression tag	UNP P61964
Q	23	HIS	-	expression tag	UNP P61964
Q	24	SER	-	expression tag	UNP P61964
Q	25	SER	-	expression tag	UNP P61964
Q	26	GLY	-	expression tag	UNP P61964
Q	27	LEU	-	expression tag	UNP P61964
Q	28	VAL	-	expression tag	UNP P61964
Q	29	PRO	-	expression tag	UNP P61964
Q	30	ARG	-	expression tag	UNP P61964
Q	31	GLY	-	expression tag	UNP P61964
Q	32	SER	-	expression tag	UNP P61964

- Molecule 5 is {N}-[5-[4-[[(2 {S})-3,3-dimethyl-1-[(2 {S},4 {R})-2-[[4-(4-methyl-1,3-t hiazol-5-yl)phenyl]methylcarbamoyl]-4-oxidanyl-pyrrolidin-1-yl]-1-oxidanylidene-butan-2-yl]amino]-4-oxidanylidene-butyl]carbamoyl]phenyl]-2-(4-methylpiperazin-1-yl)phenyl]-6-oxidanyl-4-(trifluoromethyl)pyridine-3-carboxamide (three-letter code: Q3R) (formula: C₅₁H₅₈F₃N₉O₇S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
5	P	1	Total	C	F	N	O	S	0	0
			71	51	3	9	7	1		


- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	I	7	Total	O	0	0
			7	7		
6	O	10	Total	O	0	0
			10	10		
6	P	18	Total	O	0	0
			18	18		
6	Q	23	Total	O	0	0
			23	23		

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.

- Molecule 1: Elongin-B

Chain I:  89% 11%




- Molecule 2: Elongin-C

Chain O:  81% 8% 10%




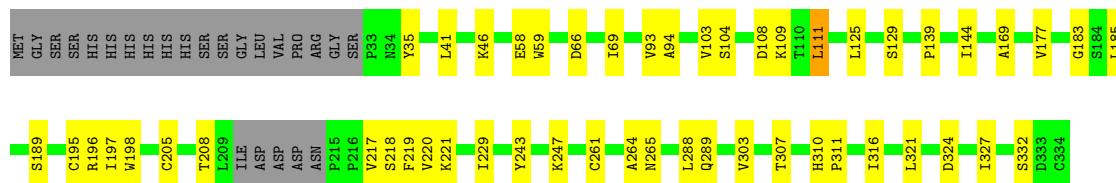
- Molecule 3: von Hippel-Lindau disease tumor suppressor

Chain P:  78% 12% 9%



- Molecule 4: WD repeat-containing protein 5

Chain Q:  77% 16% 7%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	46.79Å 184.51Å 47.95Å 90.00° 102.78° 90.00°	Depositor
Resolution (Å)	92.25 – 2.80 92.25 – 2.80	Depositor EDS
% Data completeness (in resolution range)	100.0 (92.25-2.80) 100.0 (92.25-2.80)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.47 (at 2.82Å)	Xtriage
Refinement program	REFMAC 5.8.0352	Depositor
R, R_{free}	0.203 , 0.279 0.208 , 0.277	Depositor DCC
R_{free} test set	888 reflections (4.56%)	wwPDB-VP
Wilson B-factor (Å ²)	39.5	Xtriage
Anisotropy	0.863	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.036 for l,-k,h	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	5077	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.24% 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: Q3R

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	I	0.32	0/825	0.63	0/1117
2	O	0.37	0/710	0.66	0/957
3	P	0.35	0/1216	0.69	0/1662
4	Q	0.34	0/2312	0.66	0/3144
All	All	0.34	0/5063	0.66	0/6880

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	I	809	0	800	5	0
2	O	696	0	693	5	0
3	P	1186	0	1173	9	0
4	Q	2257	0	2177	29	0
5	P	71	0	0	1	0
6	I	7	0	0	0	0
6	O	10	0	0	1	0
6	P	18	0	0	0	0
6	Q	23	0	0	1	0
All	All	5077	0	4843	47	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.

All (47) 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)
4:Q:195:CYS:SG	4:Q:220:VAL:HG21	2.31	0.71
5:P:301:Q3R:C32	5:P:301:Q3R:N6	2.60	0.63
4:Q:310:HIS:CG	4:Q:311:PRO:HD2	2.39	0.57
3:P:63:LEU:HD23	3:P:198:LEU:HD22	1.86	0.56
2:O:74:CYS:O	2:O:78:THR:HG22	2.08	0.54
4:Q:103:VAL:HG21	4:Q:144:ILE:HG21	1.92	0.51
4:Q:94:ALA:HB3	4:Q:103:VAL:CG1	2.41	0.51
4:Q:185:LEU:HD13	4:Q:197:ILE:HG21	1.92	0.51
4:Q:265:ASN:HD21	4:Q:307:THR:C	2.14	0.51
4:Q:35:TYR:CG	4:Q:332:SER:HB2	2.47	0.49
4:Q:58:GLU:HB3	4:Q:59:TRP:CD1	2.47	0.49
3:P:65:SER:OG	3:P:89:LEU:O	2.26	0.49
4:Q:189:SER:HB2	4:Q:217:VAL:CG1	2.43	0.49
3:P:85:LEU:HB2	3:P:122:ALA:HB2	1.94	0.49
4:Q:219:PHE:CE2	4:Q:264:ALA:HB3	2.47	0.49
4:Q:69:ILE:HD11	4:Q:104:SER:HB3	1.95	0.48
4:Q:303:VAL:HB	4:Q:321:LEU:HD12	1.96	0.47
4:Q:229:ILE:HD12	4:Q:243:TYR:HB3	1.97	0.46
4:Q:108:ASP:O	4:Q:109:LYS:HB2	2.16	0.45
1:I:99:LEU:HD13	2:O:98:GLU:HA	1.98	0.45
4:Q:218:SER:HB2	4:Q:261:CYS:HA	1.99	0.45
3:P:162:CYS:O	3:P:166:VAL:HG23	2.17	0.44
3:P:112:TYR:HB2	3:P:115:HIS:CD2	2.53	0.44
4:Q:109:LYS:HD3	4:Q:129:SER:C	2.37	0.44
4:Q:189:SER:HB2	4:Q:217:VAL:HG12	2.00	0.44
1:I:6:MET:HA	1:I:14:ILE:O	2.18	0.44
3:P:84:VAL:HG21	3:P:151:ILE:HG21	1.99	0.44
4:Q:289:GLN:NE2	6:Q:402:HOH:O	2.51	0.44
4:Q:198:TRP:CZ3	4:Q:205:CYS:HB2	2.54	0.43
4:Q:288:LEU:C	4:Q:288:LEU:HD23	2.39	0.43
4:Q:35:TYR:CE1	4:Q:316:ILE:HG13	2.54	0.42
2:O:104:LEU:HB2	3:P:162:CYS:HB3	2.01	0.42
4:Q:111:LEU:HB2	4:Q:125:LEU:HB2	2.01	0.42
4:Q:197:ILE:HD11	4:Q:229:ILE:CD1	2.49	0.42
4:Q:169:ALA:O	4:Q:196:ARG:NH1	2.53	0.42
4:Q:46:LYS:HB2	4:Q:66:ASP:HB3	2.02	0.42
4:Q:185:LEU:HD13	4:Q:197:ILE:CG2	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:P:78:ASN:ND2	3:P:103:PRO:HA	2.36	0.41
4:Q:139:PRO:HD2	4:Q:183:GLY:HA3	2.03	0.41
1:I:24:VAL:HB	1:I:53:ASP:HA	2.02	0.41
3:P:180:ILE:HD12	3:P:184:LEU:CB	2.51	0.41
2:O:72:LYS:HE2	6:O:210:HOH:O	2.21	0.40
2:O:77:PHE:O	2:O:81:VAL:HG23	2.22	0.40
4:Q:41:LEU:HB2	4:Q:327:ILE:HB	2.03	0.40
4:Q:177:VAL:O	4:Q:177:VAL:HG23	2.21	0.40
1:I:25:PHE:HB2	1:I:53:ASP:HB3	2.02	0.40
1:I:28:LYS:HG3	1:I:44:LEU:HD12	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	I	102/104 (98%)	96 (94%)	5 (5%)	1 (1%)	15	44
2	O	84/98 (86%)	78 (93%)	6 (7%)	0	100	100
3	P	145/162 (90%)	136 (94%)	8 (6%)	1 (1%)	22	53
4	Q	293/321 (91%)	265 (90%)	28 (10%)	0	100	100
All	All	624/685 (91%)	575 (92%)	47 (8%)	2 (0%)	41	72

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	I	82	ASP
3	P	174	ASN

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	I	89/92 (97%)	87 (98%)	2 (2%)	52	83
2	O	78/86 (91%)	75 (96%)	3 (4%)	33	67
3	P	133/148 (90%)	130 (98%)	3 (2%)	50	82
4	Q	248/280 (89%)	242 (98%)	6 (2%)	49	81
All	All	548/606 (90%)	534 (97%)	14 (3%)	46	79

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	40	ASP
1	I	68	ARG
2	O	78	THR
2	O	82	ARG
2	O	89	GLU
3	P	66	VAL
3	P	152	THR
3	P	194	VAL
4	Q	93	VAL
4	Q	111	LEU
4	Q	208	THR
4	Q	221	LYS
4	Q	247	LYS
4	Q	324	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
3	P	73	GLN
3	P	132	GLN
3	P	193	ASN
4	Q	128	HIS
4	Q	225	ASN

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Mol	Chain	Res	Type
4	Q	265	ASN
4	Q	289	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

1 ligand is 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	$\# Z > 2$
5	Q3R	P	301	-	72,77,77	0.32	0	97,112,112	0.62	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
5	Q3R	P	301	-	-	6/64/86/86	0/7/7/7

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

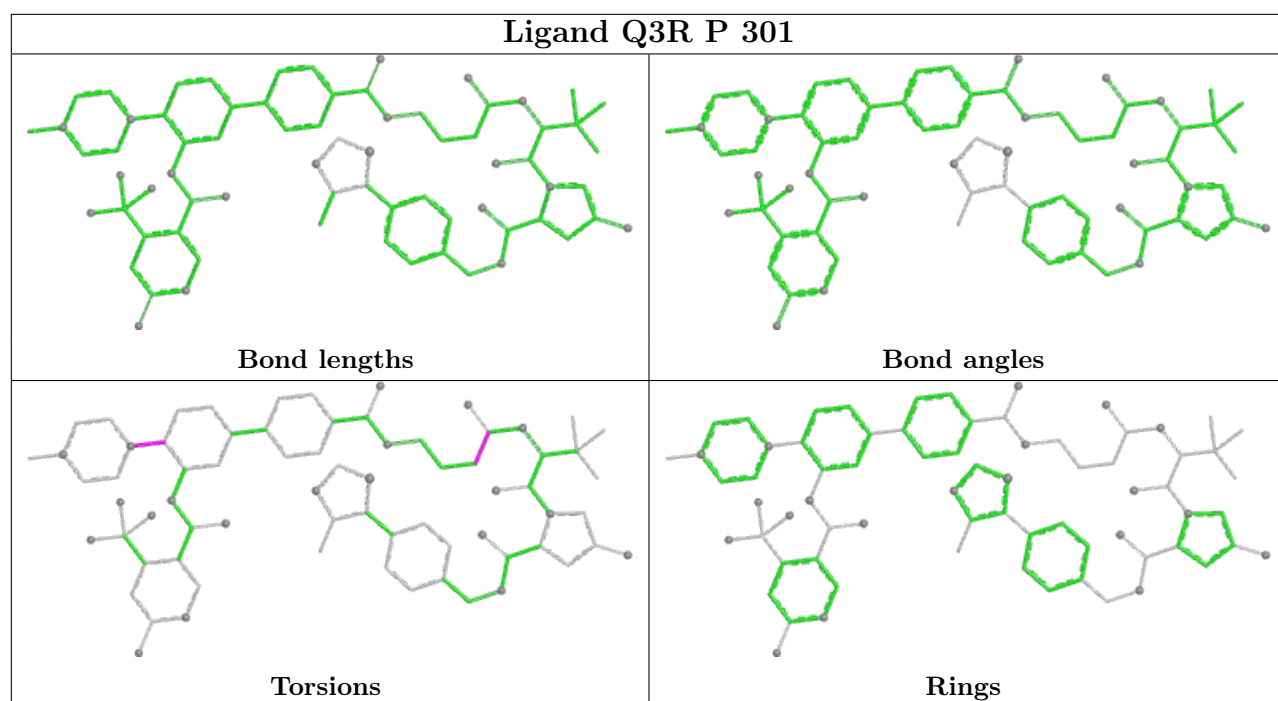
Mol	Chain	Res	Type	Atoms
5	P	301	Q3R	C33-C27-N4-C32
5	P	301	Q3R	C26-C27-N4-C28
5	P	301	Q3R	O4-C15-C16-C17
5	P	301	Q3R	N2-C15-C16-C17
5	P	301	Q3R	C26-C27-N4-C32
5	P	301	Q3R	C33-C27-N4-C28

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	P	301	Q3R	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](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

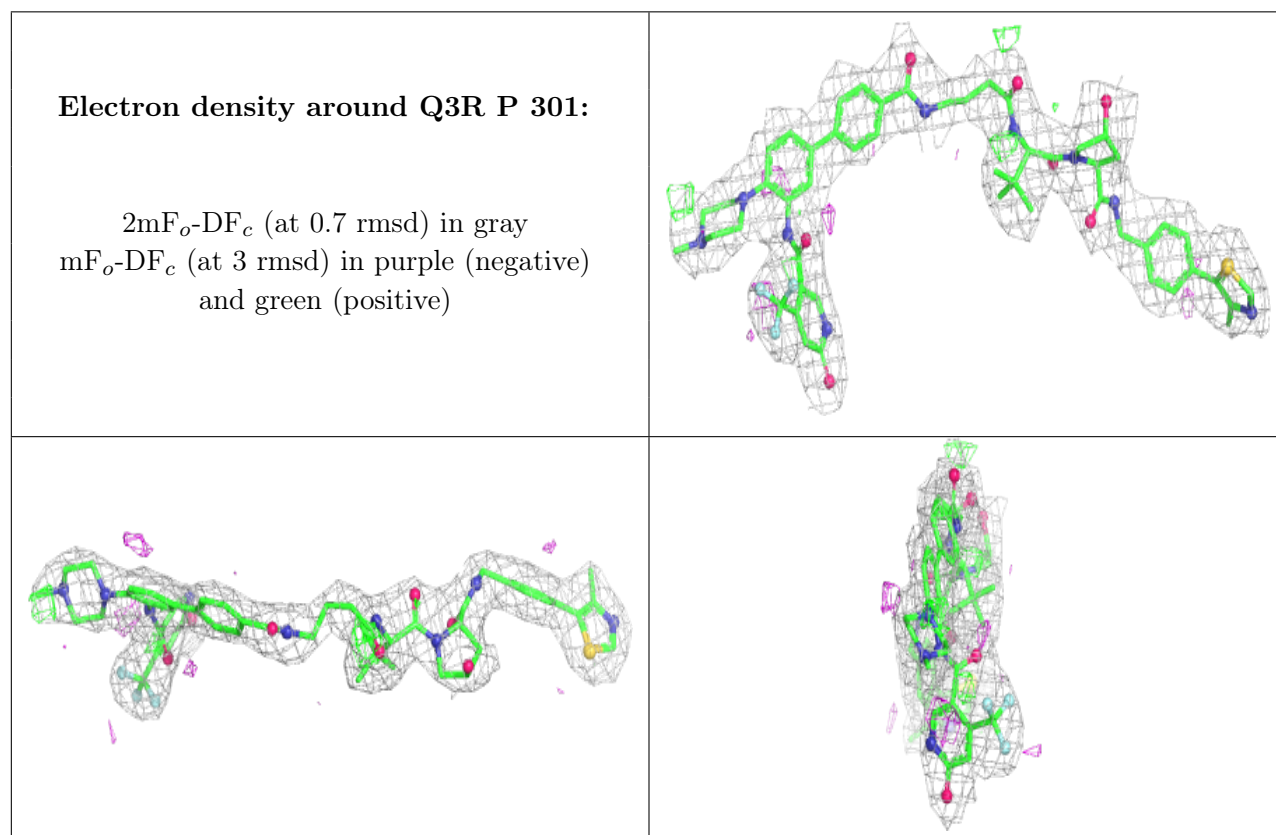
6.3 Carbohydrates [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.