



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 13, 2023 – 04:04 PM EDT

PDB ID : 8H6T
Title : Complex structure of CDK2/Cyclin E1 and a potent, selective small molecule inhibitor
Authors : Ren, X.
Deposited on : 2022-10-18
Resolution : 3.00 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 : 1.8.5 (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

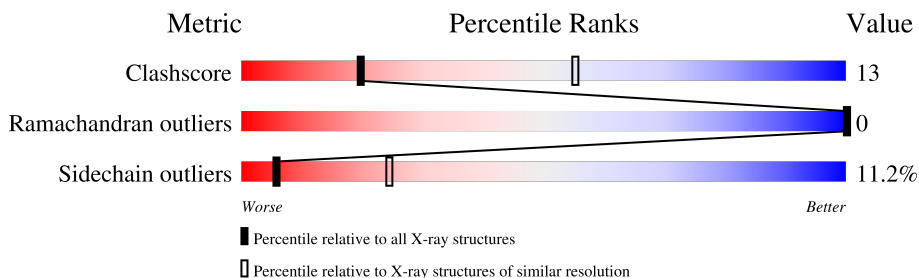
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)

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	A	298	
2	B	272	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4653 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 Cyclin-dependent kinase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	N	O	P				S
1	A	298	2400	1558	408	425	1	8	0	0	0

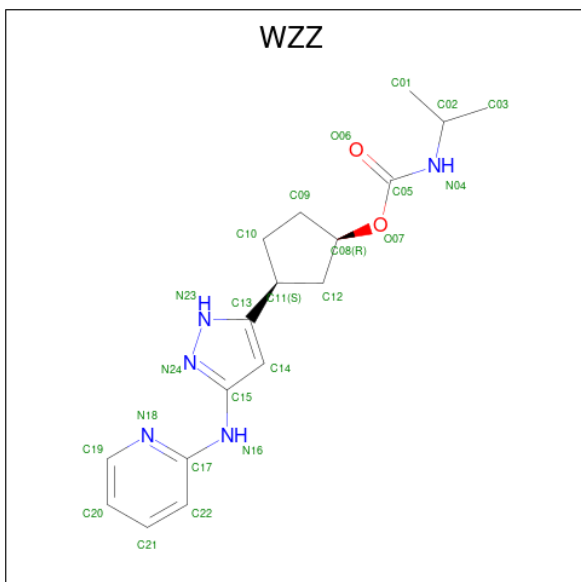
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	PRO	-	expression tag	UNP P24941

- Molecule 2 is a protein called G1/S-specific cyclin-E1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	272	2227	1449	361	400	17	0	0	0

- Molecule 3 is (1R,3S)-3-{3-[(pyridin-2-yl)amino]-1H-pyrazol-5-yl}cyclopentyl propan-2-ylcarbamate (three-letter code: WZZ) (formula: C₁₇H₂₃N₅O₂) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 4 is water.

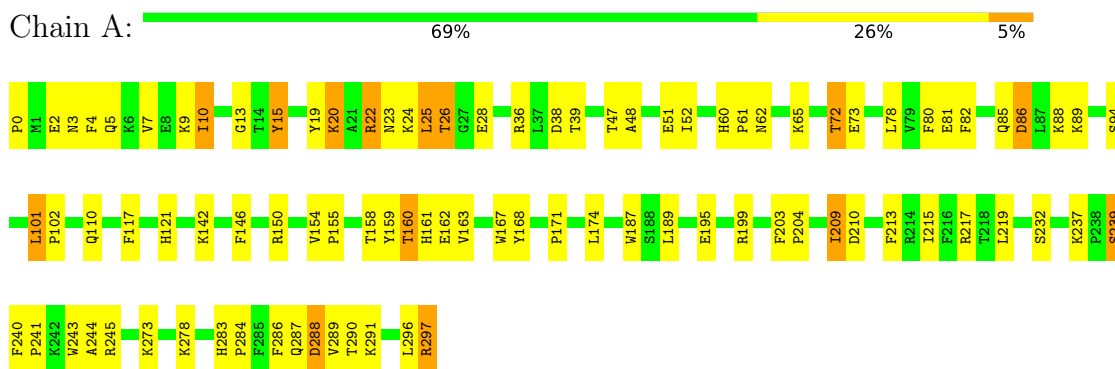
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	O	0	0
			2	2		

3 Residue-property plots

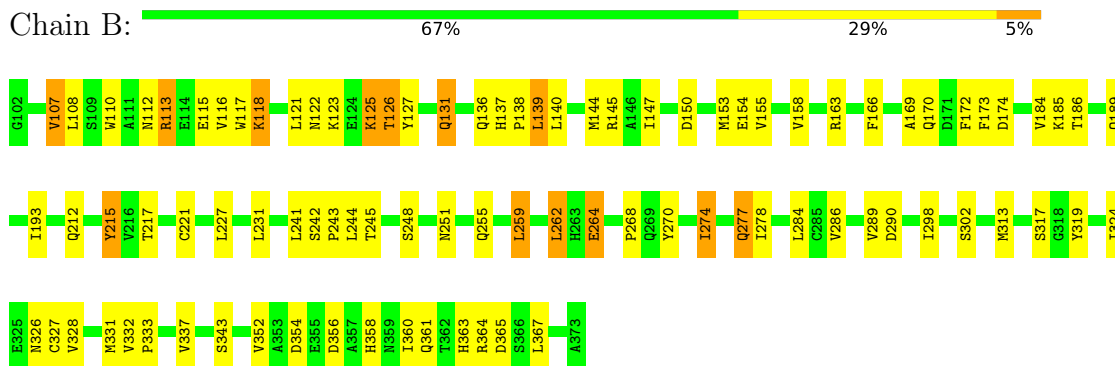
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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 failed to run properly.

- Molecule 1: Cyclin-dependent kinase 2



- Molecule 2: G1/S-specific cyclin-E1



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	101.97Å 101.97Å 151.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.32 – 3.00	Depositor
% Data completeness (in resolution range)	98.1 (45.32-3.00)	Depositor
R_{merge}	0.02	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.16 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.249 , 0.358	Depositor
Wilson B-factor (Å ²)	80.3	Xtriage
Anisotropy	0.154	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.37$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4653	wwPDB-VP
Average B, all atoms (Å ²)	93.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.01% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: WZZ, TPO

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	0.75	0/2451	0.96	0/3325
2	B	0.75	0/2283	0.91	0/3099
All	All	0.75	0/4734	0.94	0/6424

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

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	2400	0	2444	51	0
2	B	2227	0	2227	70	0
3	A	24	0	0	0	0
4	A	2	0	0	0	0
All	All	4653	0	4671	118	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 13.

All (118) 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:B:277:GLN:HG2	2:B:343:SER:HB3	1.64	0.80
2:B:284:LEU:O	2:B:286:VAL:N	2.23	0.72
2:B:150:ASP:OD1	2:B:363:HIS:NE2	2.24	0.71
2:B:302:SER:OG	2:B:327:CYS:SG	2.44	0.70
2:B:298:ILE:HG23	2:B:327:CYS:SG	2.34	0.68
2:B:217:THR:HG21	2:B:221:CYS:HB2	1.77	0.67
2:B:332:VAL:HB	2:B:333:PRO:HD3	1.79	0.65
2:B:163:ARG:NH1	2:B:358:HIS:O	2.29	0.65
2:B:166:PHE:O	2:B:169:ALA:HB3	1.97	0.64
2:B:245:THR:OG1	2:B:248:SER:HB3	1.98	0.64
2:B:298:ILE:CG2	2:B:327:CYS:SG	2.85	0.64
2:B:163:ARG:O	2:B:166:PHE:HB3	1.98	0.63
1:A:117:PHE:CE1	1:A:121:HIS:CE1	2.88	0.62
1:A:62:ASN:ND2	1:A:110:GLN:HB3	2.14	0.62
1:A:9:LYS:HA	1:A:19:TYR:HA	1.84	0.60
2:B:328:VAL:O	2:B:332:VAL:HG23	2.01	0.59
2:B:139:LEU:HD23	2:B:139:LEU:H	1.67	0.59
2:B:324:ILE:O	2:B:326:ASN:N	2.35	0.59
1:A:171:PRO:HD3	1:A:187:TRP:CZ2	2.39	0.58
1:A:286:PHE:O	1:A:290:THR:N	2.35	0.57
2:B:107:VAL:HA	2:B:113:ARG:HG2	1.87	0.56
1:A:168:TYR:OH	1:A:195:GLU:OE1	2.23	0.55
1:A:20:LYS:HD3	1:A:82:PHE:CE2	2.41	0.55
2:B:172:PHE:HE1	2:B:241:LEU:HA	1.72	0.55
1:A:101:LEU:N	1:A:102:PRO:HD2	2.23	0.54
2:B:277:GLN:CG	2:B:343:SER:HB3	2.36	0.54
2:B:108:LEU:HG	2:B:113:ARG:HB3	1.90	0.54
2:B:215:TYR:C	2:B:215:TYR:CD1	2.82	0.53
1:A:167:TRP:CD2	1:A:204:PRO:HA	2.44	0.53
1:A:278:LYS:NZ	2:B:112:ASN:HB2	2.24	0.53
2:B:145:ARG:HD3	2:B:289:VAL:HG22	1.89	0.53
1:A:3:ASN:ND2	1:A:25:LEU:HD22	2.24	0.53
2:B:242:SER:N	2:B:243:PRO:CD	2.73	0.52
2:B:364:ARG:CZ	2:B:365:ASP:H	2.23	0.52
2:B:137:HIS:O	2:B:139:LEU:N	2.42	0.52
1:A:203:PHE:CE1	1:A:215:ILE:HA	2.45	0.52
1:A:48:ALA:O	1:A:52:ILE:HG13	2.09	0.51
2:B:354:ASP:C	2:B:356:ASP:H	2.13	0.51
2:B:333:PRO:O	2:B:337:VAL:HG23	2.10	0.51
2:B:125:LYS:O	2:B:127:TYR:N	2.43	0.51
1:A:4:PHE:HA	1:A:22:ARG:O	2.11	0.51
1:A:10:ILE:CD1	1:A:20:LYS:N	2.74	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:13:GLY:N	1:A:15:TYR:CE1	2.79	0.50
2:B:127:TYR:CD1	2:B:243:PRO:HB3	2.46	0.50
2:B:324:ILE:HG13	2:B:328:VAL:CG1	2.42	0.50
2:B:298:ILE:HD12	2:B:319:TYR:CE2	2.47	0.50
1:A:283:HIS:CG	1:A:284:PRO:HD2	2.47	0.49
2:B:242:SER:N	2:B:243:PRO:HD3	2.27	0.49
2:B:123:LYS:HG2	2:B:244:LEU:HG	1.95	0.49
1:A:51:GLU:HG3	1:A:146:PHE:HB2	1.94	0.49
2:B:251:ASN:ND2	2:B:270:TYR:OH	2.46	0.49
2:B:170:GLN:O	2:B:173:PHE:HB3	2.13	0.48
2:B:324:ILE:HG13	2:B:328:VAL:HG11	1.95	0.48
1:A:159:TYR:O	1:A:160:TPO:C	2.61	0.48
1:A:86:ASP:C	1:A:86:ASP:OD1	2.52	0.48
1:A:155:PRO:HG3	2:B:255:GLN:CB	2.43	0.48
2:B:131:GLN:NE2	2:B:290:ASP:OD1	2.47	0.48
1:A:60:HIS:CG	1:A:61:PRO:HD2	2.49	0.47
2:B:153:MET:HG2	2:B:166:PHE:CE1	2.49	0.47
2:B:332:VAL:HB	2:B:333:PRO:CD	2.43	0.47
1:A:155:PRO:HG3	2:B:255:GLN:HB3	1.95	0.47
1:A:215:ILE:HG23	1:A:219:LEU:HD12	1.96	0.47
2:B:112:ASN:HB3	2:B:115:GLU:HB2	1.97	0.47
2:B:215:TYR:C	2:B:215:TYR:HD1	2.17	0.47
2:B:364:ARG:O	2:B:365:ASP:C	2.54	0.47
1:A:213:PHE:O	1:A:217:ARG:HG3	2.15	0.46
2:B:150:ASP:OD1	2:B:363:HIS:CD2	2.68	0.46
2:B:262:LEU:O	2:B:264:GLU:N	2.46	0.46
1:A:3:ASN:HD21	1:A:25:LEU:HD22	1.81	0.46
2:B:166:PHE:CG	2:B:361:GLN:NE2	2.84	0.46
1:A:241:PRO:HB2	1:A:243:TRP:CZ3	2.51	0.46
2:B:173:PHE:HD2	2:B:174:ASP:OD1	1.99	0.46
2:B:172:PHE:CE1	2:B:241:LEU:HA	2.50	0.46
1:A:171:PRO:HD3	1:A:187:TRP:CE2	2.51	0.46
1:A:78:LEU:HB3	1:A:80:PHE:CE1	2.51	0.46
2:B:144:MET:HA	2:B:147:ILE:HD12	1.97	0.46
1:A:5:GLN:HB2	1:A:24:LYS:HE3	1.98	0.45
1:A:161:HIS:CG	1:A:162:GLU:N	2.83	0.45
1:A:23:ASN:HB3	1:A:28:GLU:HB2	1.98	0.45
1:A:26:THR:CG2	1:A:28:GLU:HG3	2.47	0.45
2:B:118:LYS:CD	2:B:122:ASN:HD21	2.30	0.45
2:B:189:GLN:O	2:B:193:ILE:HG22	2.16	0.45
2:B:117:TRP:O	2:B:121:LEU:HG	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:284:PRO:O	1:A:287:GLN:HB2	2.17	0.45
2:B:137:HIS:CB	2:B:140:LEU:HD12	2.46	0.45
2:B:184:VAL:HG22	2:B:186:THR:H	1.82	0.45
1:A:296:LEU:HD12	1:A:297:ARG:H	1.82	0.44
1:A:82:PHE:CD1	1:A:82:PHE:C	2.90	0.44
1:A:209:ILE:HD13	1:A:209:ILE:HA	1.87	0.44
1:A:239:SER:O	1:A:240:PHE:C	2.55	0.44
2:B:136:GLN:C	2:B:138:PRO:HD3	2.39	0.44
2:B:274:ILE:HD11	2:B:278:ILE:HD11	2.00	0.43
1:A:85:GLN:HG3	1:A:89:LYS:HE2	2.00	0.43
2:B:327:CYS:O	2:B:331:MET:HB2	2.18	0.43
2:B:352:VAL:HG21	2:B:360:ILE:HG13	2.00	0.43
1:A:0:PRO:HG2	1:A:72:THR:HG21	2.00	0.43
1:A:154:VAL:HB	1:A:155:PRO:HD3	2.01	0.43
2:B:108:LEU:HD12	2:B:116:VAL:HG21	2.00	0.43
2:B:154:GLU:O	2:B:158:VAL:HG23	2.18	0.43
2:B:255:GLN:OE1	2:B:268:PRO:HA	2.19	0.43
1:A:26:THR:HG21	1:A:28:GLU:HG3	2.00	0.42
1:A:61:PRO:O	1:A:142:LYS:HE2	2.18	0.42
2:B:259:LEU:H	2:B:259:LEU:HD22	1.83	0.42
2:B:125:LYS:O	2:B:126:THR:C	2.57	0.42
1:A:189:LEU:HD23	1:A:189:LEU:HA	1.86	0.42
1:A:237:LYS:HD2	1:A:237:LYS:HA	1.80	0.42
2:B:169:ALA:O	2:B:170:GLN:C	2.57	0.42
2:B:365:ASP:C	2:B:367:LEU:H	2.22	0.42
1:A:288:ASP:OD1	1:A:288:ASP:N	2.53	0.41
2:B:118:LYS:HD3	2:B:122:ASN:HD21	1.85	0.41
1:A:171:PRO:HA	1:A:174:LEU:HD12	2.02	0.41
2:B:212:GLN:O	2:B:215:TYR:HB3	2.21	0.41
1:A:244:ALA:C	1:A:245:ARG:O	2.59	0.41
2:B:259:LEU:H	2:B:259:LEU:HD13	1.85	0.41
1:A:209:ILE:HG22	1:A:210:ASP:N	2.36	0.41
1:A:10:ILE:HD13	1:A:20:LYS:N	2.34	0.40
2:B:313:MET:SD	2:B:317:SER:OG	2.77	0.40
1:A:101:LEU:N	1:A:102:PRO:CD	2.84	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	42/298 (14%)	37 (88%)	5 (12%)	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	262/262 (100%)	230 (88%)	32 (12%)	5	21
2	B	185/246 (75%)	167 (90%)	18 (10%)	8	31
All	All	447/508 (88%)	397 (89%)	50 (11%)	6	24

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	GLU
1	A	7	VAL
1	A	10	ILE
1	A	15	TYR
1	A	20	LYS
1	A	22	ARG
1	A	25	LEU
1	A	26	THR
1	A	36	ARG
1	A	38	ASP
1	A	39	THR

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Mol	Chain	Res	Type
1	A	47	THR
1	A	65	LYS
1	A	72	THR
1	A	73	GLU
1	A	81	GLU
1	A	86	ASP
1	A	88	LYS
1	A	94	SER
1	A	101	LEU
1	A	150	ARG
1	A	158	THR
1	A	163	VAL
1	A	199	ARG
1	A	209	ILE
1	A	232	SER
1	A	239	SER
1	A	273	LYS
1	A	288	ASP
1	A	289	VAL
1	A	291	LYS
1	A	297	ARG
2	B	107	VAL
2	B	110	TRP
2	B	113	ARG
2	B	118	LYS
2	B	125	LYS
2	B	126	THR
2	B	131	GLN
2	B	139	LEU
2	B	155	VAL
2	B	185	LYS
2	B	215	TYR
2	B	227	LEU
2	B	231	LEU
2	B	259	LEU
2	B	262	LEU
2	B	264	GLU
2	B	274	ILE
2	B	277	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	265	GLN
2	B	122	ASN
2	B	131	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](#)

1 non-standard protein/DNA/RNA residue 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
1	TPO	A	160	1	8,10,11	1.17	1 (12%)	10,14,16	0.91	1 (10%)

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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	TPO	A	160	1	-	3/9/11/13	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	160	TPO	P-OG1	2.96	1.64	1.59

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	160	TPO	O-C-CA	-2.27	118.82	124.78

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	160	TPO	CB-OG1-P-O3P
1	A	160	TPO	CB-OG1-P-O2P
1	A	160	TPO	O-C-CA-CB

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	160	TPO	1	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

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
3	WZZ	A	301	-	25,26,26	2.70	8 (32%)	30,35,35	2.21	15 (50%)

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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	WZZ	A	301	-	-	4/14/25/25	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	301	WZZ	C12-C08	6.98	1.68	1.52
3	A	301	WZZ	C12-C11	-6.48	1.30	1.54
3	A	301	WZZ	C17-N16	4.13	1.45	1.38
3	A	301	WZZ	C15-N16	3.91	1.45	1.38
3	A	301	WZZ	C05-N04	3.85	1.44	1.34
3	A	301	WZZ	C09-C08	-3.53	1.33	1.52
3	A	301	WZZ	C13-C11	3.39	1.58	1.50
3	A	301	WZZ	O07-C05	2.30	1.39	1.35

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	301	WZZ	O07-C05-N04	6.33	118.53	110.32
3	A	301	WZZ	C11-C13-N23	3.63	125.58	120.23
3	A	301	WZZ	C14-C13-N23	-3.12	106.10	110.28
3	A	301	WZZ	O07-C05-O06	-2.95	120.09	124.53
3	A	301	WZZ	C13-C14-C15	2.44	108.23	106.07
3	A	301	WZZ	C12-C11-C10	2.42	104.65	100.78
3	A	301	WZZ	C10-C11-C13	-2.38	109.92	114.28
3	A	301	WZZ	C11-C12-C08	2.38	108.40	103.31
3	A	301	WZZ	C14-C15-N24	-2.30	107.18	110.47
3	A	301	WZZ	C12-C11-C13	-2.19	111.10	114.50
3	A	301	WZZ	C03-C02-N04	-2.17	105.42	109.79
3	A	301	WZZ	C19-N18-C17	2.16	120.28	117.22
3	A	301	WZZ	O06-C05-N04	-2.13	121.36	124.85
3	A	301	WZZ	C20-C21-C22	-2.11	116.98	120.19
3	A	301	WZZ	C01-C02-N04	2.03	113.87	109.79

There are no chirality outliers.

All (4) torsion outliers are listed below:

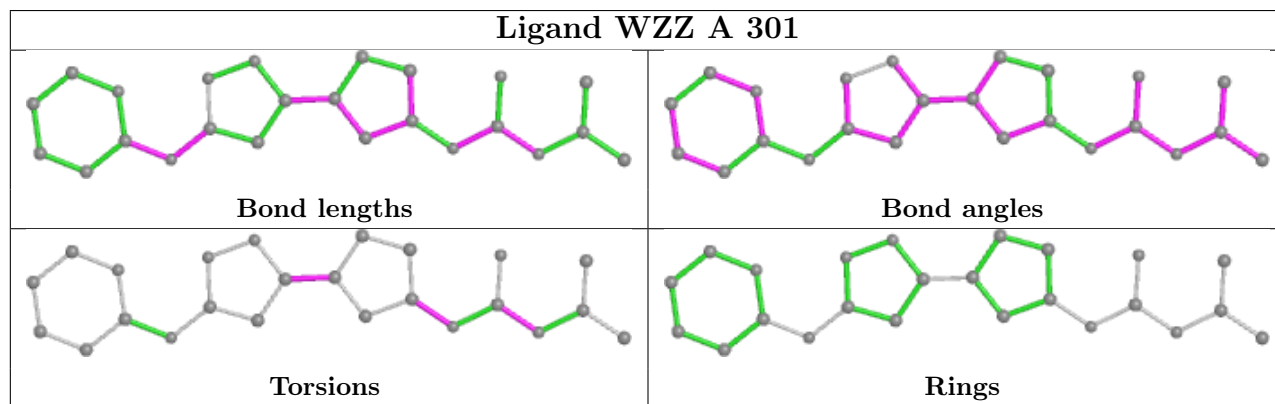
Mol	Chain	Res	Type	Atoms
3	A	301	WZZ	C09-C08-O07-C05
3	A	301	WZZ	O07-C05-N04-C02
3	A	301	WZZ	O06-C05-N04-C02
3	A	301	WZZ	C10-C11-C13-N23

There are no ring outliers.

No monomer is involved in short contacts.

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

6.1 Protein, DNA and RNA chains

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

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

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

6.4 Ligands

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

6.5 Other polymers

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