

Full wwPDB X-ray Structure Validation Report (i)

Jan 2, 2024 – 12:20 PM JST

PDB ID	:	8184
Title	:	Crystal structure of Cph001-D189N in complex with CMN IIB
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Deposited on		
Resolution	:	2.20 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 (i) 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 (1)) were used in the production of this report:

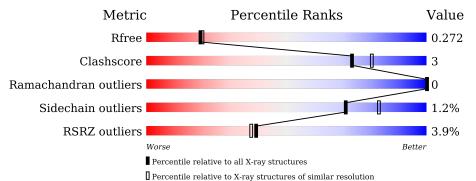
Xtriage (Phenix) EDS buster-report Percentile statistics	: : :	20191225.v01 (using entries in the PDB archive December 25th 2019)
-	:	
CCP4 Ideal geometry (proteins)		7.0.044 (Gargrove) Engh & Huber (2001)
Ideal geometry (DNA, RNA) Validation Pipeline (wwPDB-VP)		

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 2.20 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R _{free}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length		Quality of chain	
1	А	286	5%	90%	6% • •
1	В	286	2%	91%	9%
2	D	6	33%	50%	17%

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
2	KBE	D	1	-	-	-	Х



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 4471 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 Viomycin kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	В	285	Total 2127	C 1326		O 404	S 8	0	0	0
1	А	278	Total 2082	C 1299	N 382	O 392	S 9	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

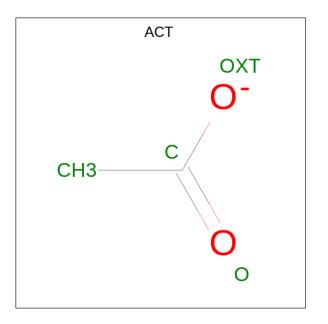
Chain	Residue	Modelled	Actual	Comment	Reference
В	189	ASN	ASP	engineered mutation	UNP D2B3F1
А	189	ASN	ASP	engineered mutation	UNP D2B3F1

• Molecule 2 is a protein called KBE-DPP-UAL-MYN-DPP-ALA.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace		
2	D	6	Total 46	C 25	N 14	0 7	0	0	0

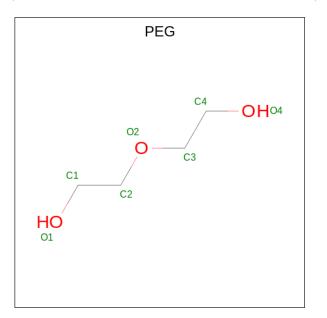
• Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0

• Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	В	1	Total 7	C 4	O 3	0	0



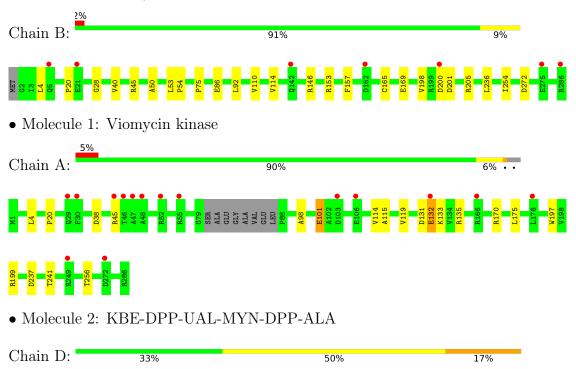
• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	В	113	Total O 113 113	0	0
5	А	85	Total O 85 85	0	0
5	D	3	Total O 3 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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). 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: Viomycin kinase



4 Data and refinement statistics (i)

Property	Value	Source	
Space group	P 21 21 21	Depositor	
Cell constants	82.75Å 85.15Å 86.81Å	Derection	
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	23.93 - 2.20	Depositor	
Resolution (A)	23.93 - 2.20	EDS	
% Data completeness	84.4 (23.93-2.20)	Depositor	
(in resolution range)	$84.5\ (23.93-2.20)$	EDS	
R _{merge}	0.07	Depositor	
R _{sym}	(Not available)	Depositor	
$\begin{array}{ c c c }\hline R_{sym} \\ \hline < I/\sigma(I) > 1 \\ \hline \end{array}$	5.04 (at 2.19Å)	Xtriage	
Refinement program	REFMAC 8.0.004	Depositor	
D D	0.212 , 0.267	Depositor	
R, R_{free}	0.217 , 0.272	DCC	
R_{free} test set	1265 reflections (4.68%)	wwPDB-VP	
Wilson B-factor $(Å^2)$	30.8	Xtriage	
Anisotropy	0.060	Xtriage	
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.37, 43.6	EDS	
L-test for twinning ²	$< L >=0.49, < L^2>=0.32$	Xtriage	
	0.018 for -h,l,k		
	0.013 for -l,-k,-h		
Estimated twinning fraction	0.019 for k,h,-l	Xtriage	
	0.000 for k,l,h		
	0.000 for l,h,k		
$\mathbf{F}_o, \mathbf{F}_c$ correlation	0.93	EDS	
Total number of atoms	4471	wwPDB-VP	
Average B, all atoms $(Å^2)$	38.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.34% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

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: ACT, PEG, KBE, MYN, UAL, DPP

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		
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.28	0/2115	0.53	0/2873	
1	В	0.29	0/2161	0.56	0/2939	
2	D	0.33	0/4	0.66	0/4	
All	All	0.29	0/4280	0.55	0/5816	

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	А	0	1
1	В	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	А	45	ARG	Sidechain
1	В	146	ARG	Sidechain

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



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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	А	2082	0	2095	13	0
1	В	2127	0	2133	14	0
2	D	46	0	39	2	0
3	В	8	0	6	0	0
4	В	7	0	10	0	0
5	А	85	0	0	0	0
5	В	113	0	0	0	0
5	D	3	0	0	1	0
All	All	4471	0	4283	28	0

the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

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 3.

All (28) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

A. 1		Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
2:D:1:KBE:HAA	2:D:6:ALA:HB1	1.67	0.77
1:A:132:GLU:HG3	1:A:133:LYS:N	2.07	0.68
1:A:101:GLU:OE1	1:A:199:ARG:NH2	2.37	0.58
1:A:4:LEU:HD13	1:A:20:PRO:O	2.05	0.56
1:B:201:ASP:N	1:B:201:ASP:OD1	2.39	0.56
1:A:98:ALA:HB3	1:A:199:ARG:NH1	2.23	0.54
1:B:50:ALA:HB1	1:B:86:GLU:HG2	1.91	0.51
1:B:153:ARG:O	1:B:157:PHE:HB2	2.10	0.50
1:B:236:LEU:HD21	1:B:254:ILE:HG21	1.94	0.50
1:A:98:ALA:HB3	1:A:199:ARG:HH11	1.78	0.49
1:B:4:LEU:HD13	1:B:20:PRO:O	2.12	0.48
1:A:131:ASP:O	1:A:135:ARG:HG3	2.12	0.48
1:B:201:ASP:CG	1:B:205:ARG:HH22	2.16	0.48
2:D:1:KBE:HG	5:D:102:HOH:O	2.13	0.47
1:B:45:ARG:HH12	1:B:272:ASP:HA	1.82	0.45
1:B:75:PRO:HA	1:B:92:LEU:HD23	1.98	0.44
1:B:198:VAL:HG23	1:B:205:ARG:HB3	2.00	0.44
1:A:175:LEU:HD23	1:A:256:THR:CG2	2.49	0.43
1:A:115:ALA:O	1:A:119:VAL:HG23	2.18	0.43
1:B:53:LEU:N	1:B:54:PRO:CD	2.82	0.42
1:A:132:GLU:HG3	1:A:133:LYS:H	1.84	0.42
1:A:237:ASP:O	1:A:241:THR:HG23	2.19	0.42
1:B:165:CYS:O	1:B:169:GLU:HG2	2.20	0.42
1:B:110:VAL:O	1:B:114:VAL:HG23	2.20	0.41

Continued on next page...



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)	
1:A:114:VAL:HG13	1:A:197:TRP:CH2	2.55	0.41	
1:A:175:LEU:HD23	1:A:256:THR:HG22	2.01	0.41	
1:B:205:ARG:NH1	1:A:38:ASP:OD1	2.53	0.41	
1:B:28:GLY:O	1:B:45:ARG:NH1	2.52	0.40	

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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	Perce	ntiles
1	А	274/286~(96%)	265~(97%)	9~(3%)	0	100	100
1	В	283/286~(99%)	279~(99%)	4 (1%)	0	100	100
All	All	557/572~(97%)	544 (98%)	13~(2%)	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 side chain 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	А	211/216~(98%)	208~(99%)	3~(1%)	67 80		
1	В	215/216~(100%)	213~(99%)	2(1%)	78 88		
All	All	426/432~(99%)	421~(99%)	5 (1%)	71 83		



All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	40	VAL
1	В	200	ASP
1	А	101	GLU
1	А	132	GLU
1	А	170	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	В	29	GLN
1	В	32	GLN
1	В	167	GLN
1	А	29	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)

5 non-standard protein/DNA/RNA residues 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).

Mal	Mol Type Chain Res		Res	Link	Bond lengths		Bond angles			
Mol Type Chain	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2		
2	MYN	D	4	2	7,11,12	0.61	0	6,14,16	1.84	2 (33%)
2	UAL	D	3	2	7,8,9	1.76	1 (14%)	5,9,11	1.24	1 (20%)
2	DPP	D	2	2	3,5,6	0.99	0	1,5,7	0.10	0
2	DPP	D	5	2	$3,\!5,\!6$	0.62	0	$1,\!5,\!7$	0.20	0
2	KBE	D	1	2	8,8,9	0.82	0	7,8,10	1.47	1 (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



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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MYN	D	4	2	-	0/1/16/18	0/1/1/1
2	UAL	D	3	2	-	2/3/7/9	-
2	DPP	D	2	2	-	0/2/4/6	-
2	DPP	D	5	2	-	0/2/4/6	-
2	KBE	D	1	2	-	4/7/7/8	-

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
2	D	3	UAL	C-CA	-4.43	1.37	1.45

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
2	D	1	KBE	O-C-CA	-3.60	114.93	125.43
2	D	4	MYN	O-C-CA	-2.85	117.32	124.78
2	D	3	UAL	O-C-CA	-2.64	122.03	125.39
2	D	4	MYN	CA-CB-N1	-2.34	107.62	111.41

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	1	KBE	C-CA-CB-N
2	D	1	KBE	N-CB-CG-CD
2	D	1	KBE	CA-CB-CG-CD
2	D	3	UAL	O2-C1-N1-CB
2	D	3	UAL	N2-C1-N1-CB
2	D	1	KBE	CG-CD-CE-NZ

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1	KBE	2	0



5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

3 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	Turne	Chain	Res	Link	B	Bond lengths			Bond angles		
IVIOI	Type	Unam	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2	
4	PEG	В	302	-	$6,\!6,\!6$	0.17	0	$5,\!5,\!5$	0.21	0	
3	ACT	В	301	-	3,3,3	0.89	0	$3,\!3,\!3$	0.85	0	
3	ACT	В	303	-	3,3,3	1.04	0	$3,\!3,\!3$	0.93	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
4	PEG	В	302	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

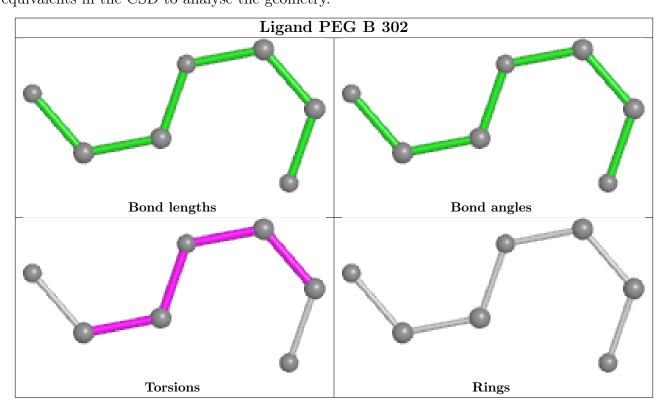
Mol	Chain	Res	Type	Atoms
4	В	302	PEG	O2-C3-C4-O4
4	В	302	PEG	O1-C1-C2-O2
4	В	302	PEG	C1-C2-O2-C3
4	В	302	PEG	C4-C3-O2-C2

There are no ring outliers.

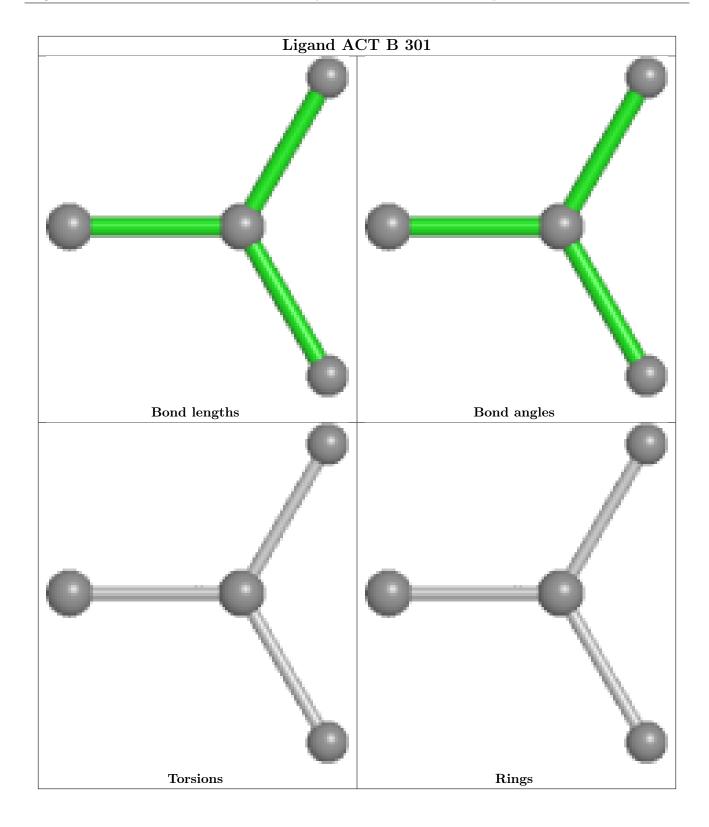
No monomer is involved in short contacts.

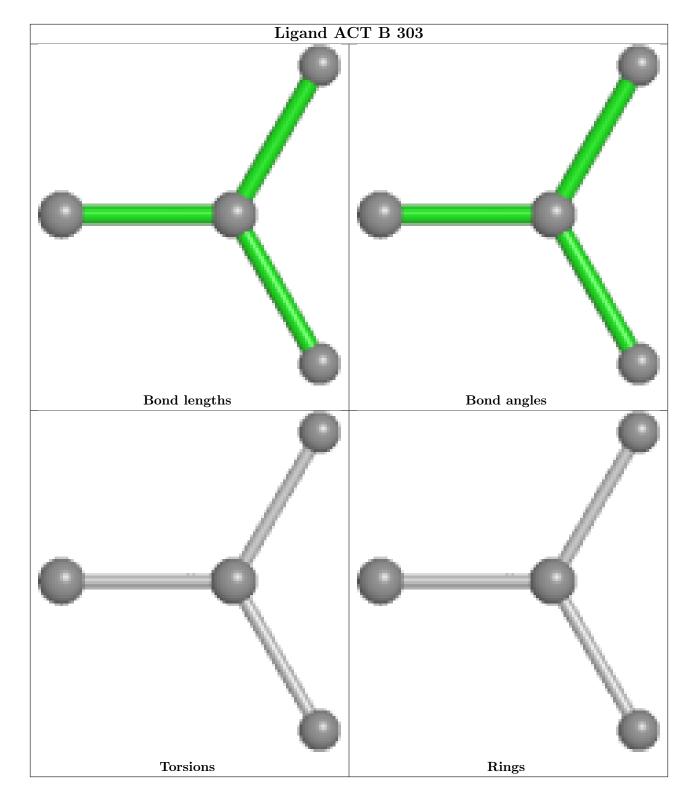


The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ $>$	#RSRZ>2	$OWAB(A^2)$	$\mathbf{Q}{<}0.9$
1	А	278/286~(97%)	0.14	15 (5%) 25 24	22, 38, 65, 86	0
1	В	285/286~(99%)	-0.07	7 (2%) 57 55	18, 33, 57, 84	0
2	D	1/6~(16%)	-0.47	0 100 100	33, 33, 33, 33	0
All	All	564/578~(97%)	0.03	22 (3%) 39 37	18, 35, 63, 86	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	30	PHE	5.7
1	В	21	GLU	4.8
1	В	286	ARG	4.7
1	А	29	GLN	4.6
1	А	178	LEU	3.7
1	В	200	ASP	3.5
1	А	272	ASP	3.3
1	А	103	ASP	3.3
1	В	275	GLU	3.1
1	А	132	GLU	3.0
1	А	166	ARG	3.0
1	А	48	ALA	2.9
1	А	55	ARG	2.6
1	А	249	ARG	2.5
1	А	45	ARG	2.4
1	А	52	ARG	2.3
1	В	142	GLN	2.2
1	В	5	GLN	2.2
1	А	106	GLU	2.1
1	В	162	ASP	2.1
1	А	46	THR	2.0
1	А	47	ALA	2.0



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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} extsf{-}\mathbf{B} extsf{-}\mathbf{factors}(\mathbf{A}^2)$	Q<0.9
2	KBE	D	1	9/10	0.69	0.47	54,69,73,74	0
2	UAL	D	3	9/10	0.91	0.13	27,31,32,34	0
2	MYN	D	4	11/12	0.93	0.11	27,28,29,30	0
2	DPP	D	2	6/7	0.94	0.10	28,33,36,41	0
2	DPP	D	5	6/7	0.97	0.16	30,31,31,31	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

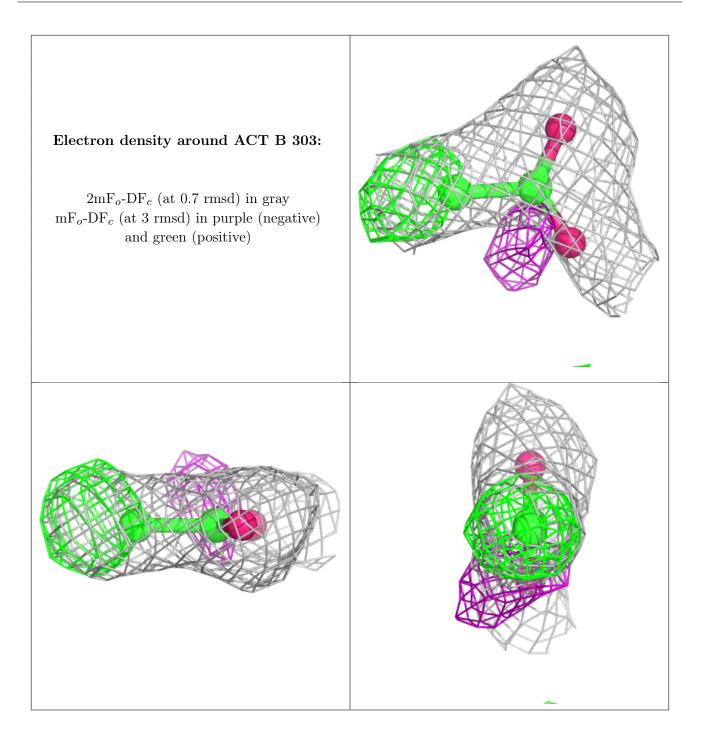
6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

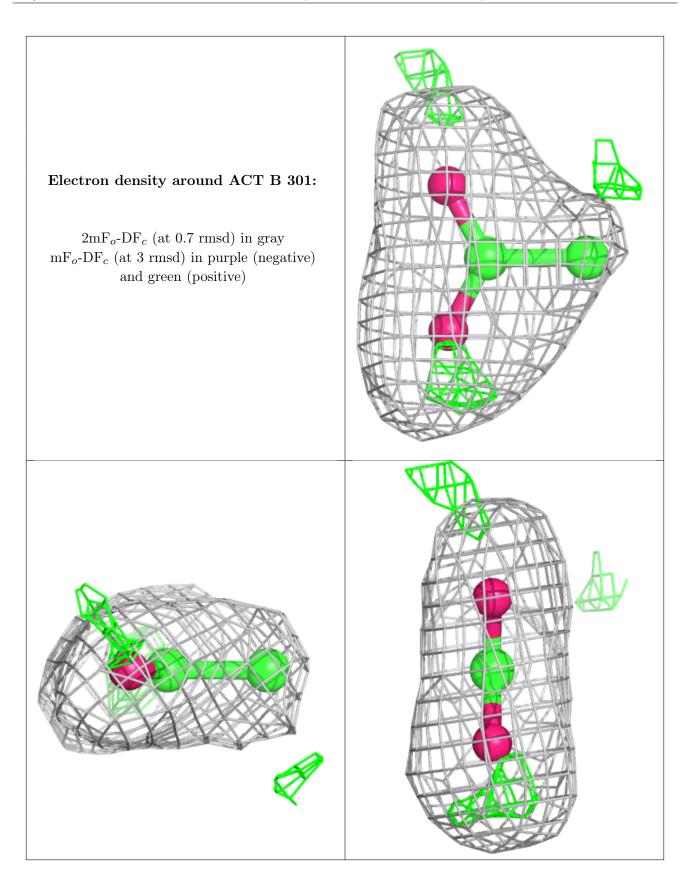
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q < 0.9
3	ACT	В	303	4/4	0.42	0.35	40,40,43,45	0
3	ACT	В	301	4/4	0.85	0.27	47,50,51,52	0
4	PEG	В	302	7/7	0.85	0.29	44,45,47,48	0

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.



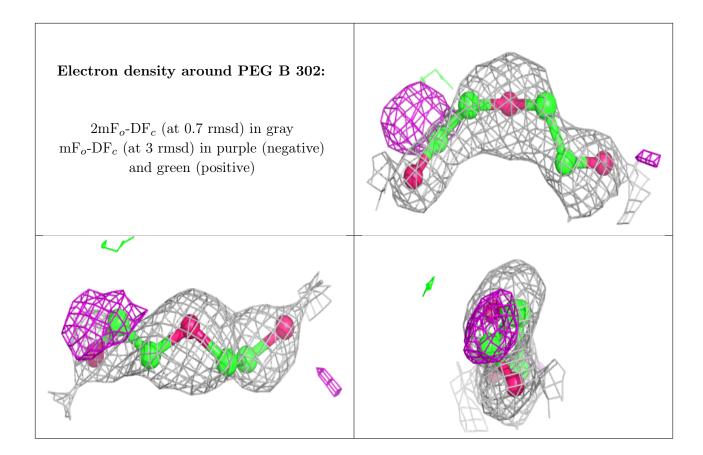












6.5 Other polymers (i)

There are no such residues in this entry.

