



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 28, 2025 – 12:53 PM EDT

PDB ID : 2PGJ / pdb_00002pgj
Title : Catalysis associated conformational changes revealed by human cd38 complexed with a non-hydrolyzable substrate analog
Authors : Liu, Q.; Kriksunov, I.A.; Moreau, C.; Graeff, R.; Potter, B.V.L.; Lee, H.C.; Hao, Q.
Deposited on : 2007-04-09
Resolution : 1.71 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	:	4-5-2 with Phenix2.0rc1
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0rc1
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.006 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.43.1

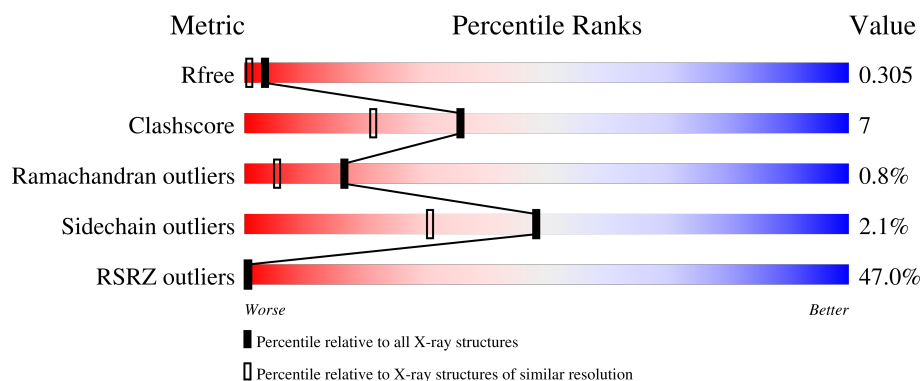
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.71 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}	164625	7106 (1.74-1.70)
Clashscore	180529	7746 (1.74-1.70)
Ramachandran outliers	177936	7654 (1.74-1.70)
Sidechain outliers	177891	7654 (1.74-1.70)
RSRZ outliers	164620	7104 (1.74-1.70)

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 $\leq 5\%$. 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	A	262	
1	B	262	

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	N1C	A	301	X	-	-	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4535 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.

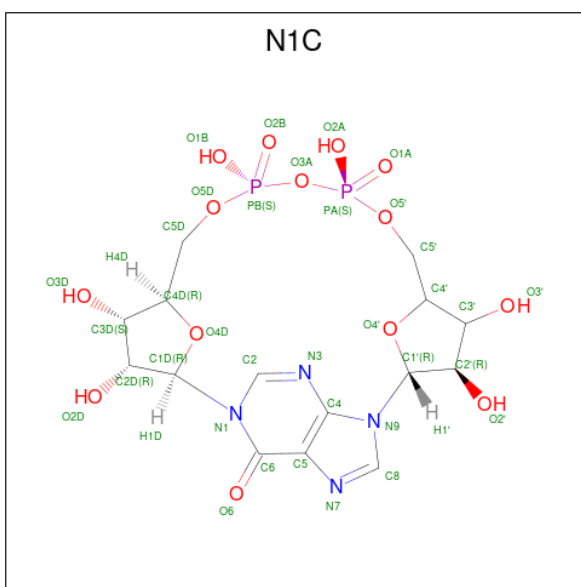
- Molecule 1 is a protein called ADP-ribosyl cyclase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	252	Total	C	N	O	S	0	0	0
			2050	1290	358	386	16			
1	B	252	Total	C	N	O	S	0	0	0
			2050	1290	358	386	16			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	39	LYS	-	cloning artifact	UNP P28907
A	40	ARG	-	cloning artifact	UNP P28907
A	41	GLU	-	cloning artifact	UNP P28907
A	42	ALA	-	cloning artifact	UNP P28907
A	43	GLU	-	cloning artifact	UNP P28907
A	44	ALA	-	cloning artifact	UNP P28907
A	49	THR	GLN	engineered mutation	UNP P28907
A	100	ASP	ASN	engineered mutation	UNP P28907
A	164	ASP	ASN	engineered mutation	UNP P28907
A	209	ASP	ASN	engineered mutation	UNP P28907
A	219	ASP	ASN	engineered mutation	UNP P28907
B	39	LYS	-	cloning artifact	UNP P28907
B	40	ARG	-	cloning artifact	UNP P28907
B	41	GLU	-	cloning artifact	UNP P28907
B	42	ALA	-	cloning artifact	UNP P28907
B	43	GLU	-	cloning artifact	UNP P28907
B	44	ALA	-	cloning artifact	UNP P28907
B	49	THR	GLN	engineered mutation	UNP P28907
B	100	ASP	ASN	engineered mutation	UNP P28907
B	164	ASP	ASN	engineered mutation	UNP P28907
B	209	ASP	ASN	engineered mutation	UNP P28907
B	219	ASP	ASN	engineered mutation	UNP P28907

- Molecule 2 is N1-CYCLIC INOSINE 5'-DIPHOSPHORIBOSE (CCD ID: N1C) (formula: $C_{15}H_{20}N_4O_{14}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 35	C 15	N 4	O 14	P 2	0	0

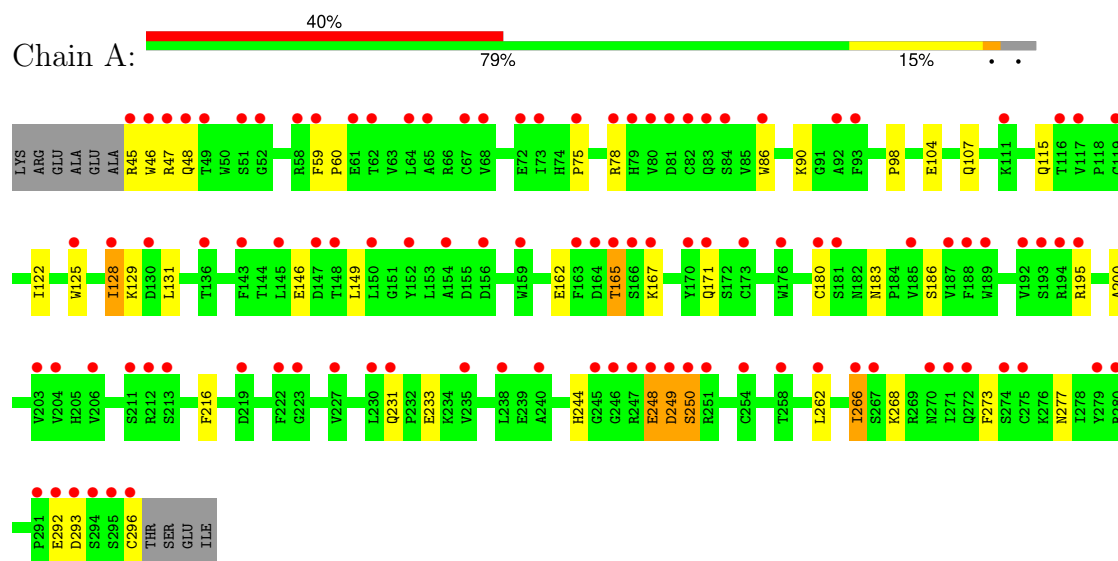
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	210	Total O 210 210	0	0
3	B	190	Total O 190 190	0	0

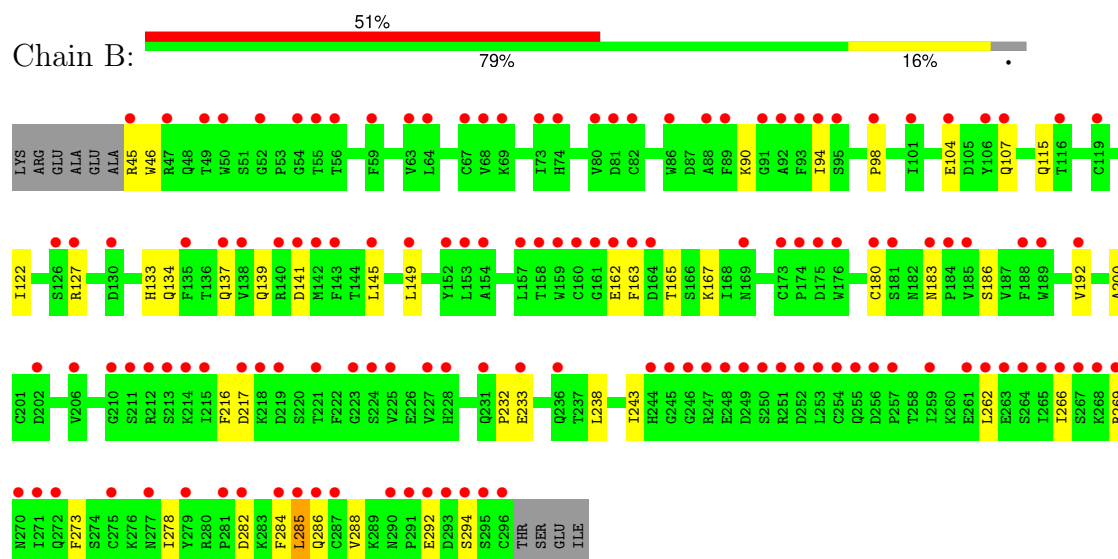
3 Residue-property plots

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 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: ADP-ribosyl cyclase 1



• Molecule 1: ADP-ribosyl cyclase 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	41.89Å 53.20Å 65.64Å 105.34° 91.96° 94.94°	Depositor
Resolution (Å)	28.41 – 1.71 28.41 – 1.71	Depositor EDS
% Data completeness (in resolution range)	100.0 (28.41-1.71) 92.3 (28.41-1.71)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.21 (at 1.71Å)	Xtriage
Refinement program	REFMAC 5.3.0021	Depositor
R, R_{free}	0.191 , 0.224 0.280 , 0.305	Depositor DCC
R_{free} test set	2759 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	18.5	Xtriage
Anisotropy	0.400	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 52.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	4535	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.51% 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: N1C

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	0.54	0/2101	0.78	1/2846 (0.0%)
1	B	0.53	0/2101	0.77	0/2846
All	All	0.53	0/4202	0.77	1/5692 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	250	SER	N-CA-C	5.59	116.74	108.86

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	2050	0	1976	33	0
1	B	2050	0	1976	26	0
2	A	35	0	15	3	0
3	A	210	0	0	4	0
3	B	190	0	0	1	0
All	All	4535	0	3967	58	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.

All (58) 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:115:GLN:HE22	1:B:149:LEU:H	1.20	0.88
1:A:115:GLN:HE22	1:A:149:LEU:H	1.23	0.86
1:B:165:THR:HG23	1:B:167:LYS:H	1.46	0.80
1:A:268:LYS:HD3	1:B:163:PHE:CE1	2.17	0.79
1:A:165:THR:HG23	1:A:167:LYS:H	1.47	0.78
1:A:268:LYS:HD3	1:B:163:PHE:HE1	1.49	0.77
2:A:301:N1C:O6	2:A:301:N1C:H2D	1.94	0.67
1:B:162:GLU:HB2	1:B:165:THR:HG22	1.79	0.64
1:A:180:CYS:HB2	3:A:432:HOH:O	2.00	0.61
1:A:183:ASN:ND2	1:A:186:SER:H	2.00	0.60
1:A:162:GLU:HB2	1:A:165:THR:HG22	1.84	0.59
1:A:266:ILE:HD11	1:A:273:PHE:HB2	1.86	0.57
1:A:75:PRO:O	1:A:78:ARG:HB2	2.03	0.57
1:B:266:ILE:HD11	1:B:273:PHE:HB2	1.86	0.57
1:B:127:ARG:HH12	1:B:217:ASP:HB3	1.68	0.57
1:A:104:GLU:HA	1:A:107:GLN:HG2	1.87	0.57
1:B:104:GLU:HA	1:B:107:GLN:HG2	1.86	0.56
1:B:133:HIS:O	1:B:137:GLN:HG3	2.06	0.56
1:A:231:GLN:HG3	3:A:510:HOH:O	2.05	0.56
1:A:115:GLN:NE2	1:A:149:LEU:H	2.01	0.56
1:A:146:GLU:OE2	2:A:301:N1C:O6	2.24	0.55
1:B:238:LEU:HB3	1:B:266:ILE:HD13	1.89	0.54
1:B:139:GLN:C	1:B:141:ASP:H	2.13	0.54
1:A:183:ASN:HD21	1:A:186:SER:H	1.54	0.54
1:B:115:GLN:NE2	1:B:149:LEU:H	1.98	0.53
1:B:284:PHE:O	1:B:288:VAL:HG23	2.08	0.53
1:A:293:ASP:HB3	1:A:296:CYS:SG	2.50	0.52
1:A:195:ARG:HG3	3:A:326:HOH:O	2.11	0.50
1:B:183:ASN:ND2	1:B:186:SER:H	2.10	0.49
1:A:216:PHE:CE1	1:A:262:LEU:HD13	2.48	0.49
1:B:145:LEU:HD21	1:B:192:VAL:HG23	1.95	0.49
1:A:48:GLN:NE2	1:A:171:GLN:HB3	2.28	0.48
1:B:45:ARG:HG2	1:B:46:TRP:H	1.79	0.48
1:B:134:GLN:HB3	1:B:285:LEU:HD11	1.96	0.47
1:A:86:TRP:CE2	1:A:90:LYS:HG3	2.49	0.47
1:B:233:GLU:H	1:B:233:GLU:CD	2.22	0.47
1:A:233:GLU:H	1:A:233:GLU:CD	2.22	0.47
1:B:139:GLN:C	1:B:141:ASP:N	2.74	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:90:LYS:HG3	1:B:94:ILE:HG13	1.96	0.45
1:A:125:TRP:CH2	1:A:129:LYS:HB3	2.51	0.45
1:A:125:TRP:CZ3	1:A:129:LYS:HB3	2.52	0.44
1:A:125:TRP:O	2:A:301:N1C:H5D1	2.16	0.44
1:A:59:PHE:HB3	1:A:60:PRO:HD3	2.00	0.44
1:B:122:ILE:HD12	1:B:200:ALA:HA	1.99	0.44
1:A:78:ARG:NH1	3:A:382:HOH:O	2.51	0.43
1:B:216:PHE:CE1	1:B:262:LEU:HD13	2.53	0.43
1:B:232:PRO:HG3	1:B:269:ARG:O	2.18	0.43
1:B:180:CYS:HB2	3:B:324:HOH:O	2.18	0.43
1:A:46:TRP:HE1	1:A:47:ARG:NH1	2.17	0.42
1:A:162:GLU:OE2	1:A:165:THR:HG21	2.19	0.42
1:A:98:PRO:O	1:A:183:ASN:HA	2.20	0.42
1:A:248:GLU:O	1:A:249:ASP:CB	2.67	0.42
1:B:98:PRO:O	1:B:183:ASN:HA	2.18	0.42
1:B:243:ILE:CD1	1:B:278:ILE:HD12	2.50	0.42
1:A:244:HIS:HD2	1:A:250:SER:HB3	1.85	0.41
1:A:122:ILE:HD12	1:A:200:ALA:HA	2.03	0.41
1:A:248:GLU:O	1:A:249:ASP:HB2	2.20	0.41
1:A:244:HIS:HE1	1:A:277:ASN:OD1	2.04	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	250/262 (95%)	239 (96%)	8 (3%)	3 (1%)	11	2
1	B	250/262 (95%)	237 (95%)	12 (5%)	1 (0%)	30	17
All	All	500/524 (95%)	476 (95%)	20 (4%)	4 (1%)	16	5

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	249	ASP
1	A	248	GLU
1	B	292	GLU
1	A	128	ILE

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	A	233/241 (97%)	227 (97%)	6 (3%)	41	22
1	B	233/241 (97%)	229 (98%)	4 (2%)	56	40
All	All	466/482 (97%)	456 (98%)	10 (2%)	48	31

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	ARG
1	A	128	ILE
1	A	131	LEU
1	A	165	THR
1	A	266	ILE
1	A	292	GLU
1	B	282	ASP
1	B	285	LEU
1	B	286	GLN
1	B	294	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	48	GLN
1	A	74	HIS
1	A	83	GLN
1	A	115	GLN
1	A	134	GLN

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Mol	Chain	Res	Type
1	A	139	GLN
1	A	183	ASN
1	A	229	ASN
1	A	244	HIS
1	A	290	ASN
1	B	83	GLN
1	B	115	GLN
1	B	134	GLN
1	B	137	GLN
1	B	171	GLN
1	B	183	ASN
1	B	229	ASN
1	B	244	HIS
1	B	286	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](#)

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
2	N1C	A	301	-	35,39,39	1.97	5 (14%)	41,62,62	2.09	13 (31%)

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
2	N1C	A	301	-	3/3/10/10	8/22/58/58	0/3/5/5

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	301	N1C	C3'-C4'	-8.15	1.32	1.53
2	A	301	N1C	C2-N3	5.03	1.34	1.28
2	A	301	N1C	O3'-C3'	-3.82	1.33	1.43
2	A	301	N1C	C6-N1	2.47	1.42	1.38
2	A	301	N1C	O4'-C1'	2.20	1.43	1.40

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	N1C	O3'-C3'-C4'	4.90	125.17	111.08
2	A	301	N1C	O4'-C4'-C5'	4.37	123.35	109.33
2	A	301	N1C	C2'-C3'-C4'	4.28	110.89	102.61
2	A	301	N1C	O3'-C3'-C2'	3.77	123.91	111.82
2	A	301	N1C	C4'-O4'-C1'	-3.72	106.51	109.92
2	A	301	N1C	O4'-C1'-N9	-3.25	104.43	108.75
2	A	301	N1C	C3D-C2D-C1D	3.06	107.26	101.46
2	A	301	N1C	O4'-C4'-C3'	2.95	111.00	105.15
2	A	301	N1C	C5'-C4'-C3'	2.90	125.65	115.21
2	A	301	N1C	O6-C6-C5	-2.85	119.50	124.18
2	A	301	N1C	C5-C6-N1	2.74	117.84	113.96
2	A	301	N1C	C8-N7-C5	2.54	106.87	102.55
2	A	301	N1C	O6-C6-N1	2.37	122.64	120.71

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	301	N1C	C3'
2	A	301	N1C	N1

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Mol	Chain	Res	Type	Atom
2	A	301	N1C	C4'

All (8) torsion outliers are listed below:

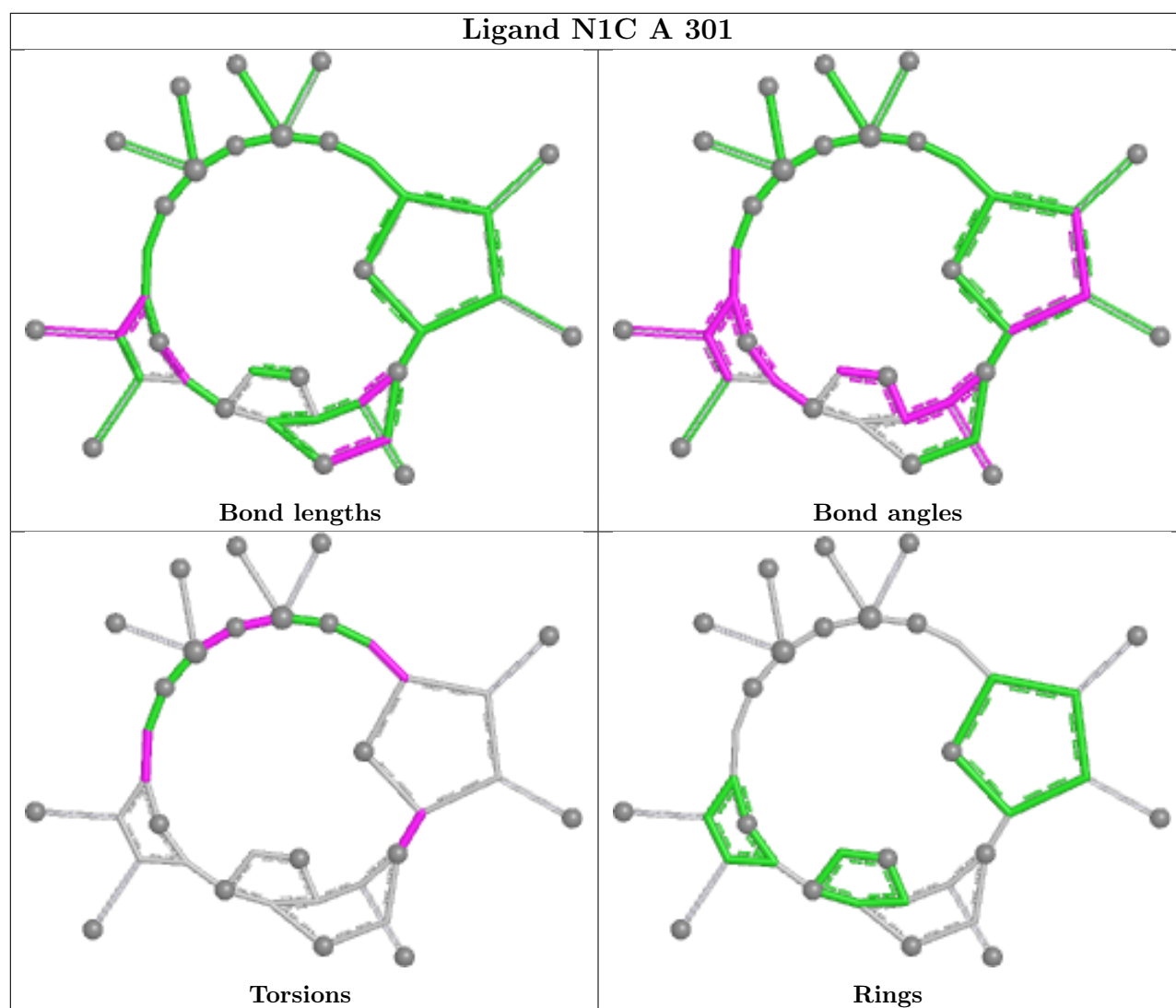
Mol	Chain	Res	Type	Atoms
2	A	301	N1C	O4'-C4'-C5'-O5'
2	A	301	N1C	C2D-C1D-N1-C6
2	A	301	N1C	PA-O3A-PB-O2B
2	A	301	N1C	PB-O3A-PA-O5'
2	A	301	N1C	C2D-C1D-N1-C2
2	A	301	N1C	C3'-C4'-C5'-O5'
2	A	301	N1C	PA-O3A-PB-O1B
2	A	301	N1C	C3D-C4D-C5D-O5D

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	N1C	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

6.1 Protein, DNA and RNA chains

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, 95th 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(Å ²)	Q<0.9
1	A	252/262 (96%)	2.11	104 (41%) 1 1	23, 29, 36, 43	0
1	B	252/262 (96%)	2.26	133 (52%) 0 0	23, 29, 35, 40	0
All	All	504/524 (96%)	2.19	237 (47%) 0 0	23, 29, 36, 43	0

All (237) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	246	GLY	10.6
1	A	249	ASP	8.5
1	B	246	GLY	7.8
1	B	213	SER	7.3
1	B	249	ASP	6.8
1	B	245	GLY	6.5
1	B	287	CYS	6.3
1	B	291	PRO	6.1
1	B	248	GLU	6.1
1	B	295	SER	5.9
1	B	296	CYS	5.9
1	A	296	CYS	5.6
1	A	47	ARG	5.5
1	B	254	CYS	5.4
1	A	294	SER	5.3
1	B	290	ASN	5.3
1	A	143	PHE	5.3
1	A	295	SER	5.2
1	A	248	GLU	5.2
1	A	46	TRP	5.1
1	A	79	HIS	5.1
1	A	165	THR	4.8
1	A	82	CYS	4.7
1	A	176	TRP	4.7

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Mol	Chain	Res	Type	RSRZ
1	A	164	ASP	4.7
1	B	219	ASP	4.6
1	B	294	SER	4.5
1	A	213	SER	4.4
1	B	247	ARG	4.4
1	B	141	ASP	4.3
1	B	159	TRP	4.3
1	A	292	GLU	4.3
1	A	80	VAL	4.2
1	A	81	ASP	4.2
1	B	270	ASN	4.2
1	A	180	CYS	4.2
1	B	292	GLU	4.1
1	B	73	ILE	4.1
1	A	266	ILE	4.0
1	B	212	ARG	3.9
1	A	187	VAL	3.9
1	A	227	VAL	3.9
1	A	293	ASP	3.8
1	B	176	TRP	3.8
1	A	194	ARG	3.7
1	A	111	LYS	3.7
1	B	80	VAL	3.7
1	B	180	CYS	3.7
1	B	286	GLN	3.7
1	B	267	SER	3.7
1	A	247	ARG	3.7
1	B	82	CYS	3.6
1	B	275	CYS	3.6
1	A	245	GLY	3.6
1	B	143	PHE	3.6
1	B	293	ASP	3.6
1	B	157	LEU	3.5
1	B	55	THR	3.5
1	B	54	GLY	3.5
1	A	189	TRP	3.5
1	A	68	VAL	3.5
1	B	227	VAL	3.5
1	B	215	ILE	3.5
1	B	253	LEU	3.5
1	B	255	GLN	3.4
1	A	250	SER	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	282	ASP	3.4
1	B	224	SER	3.4
1	B	138	VAL	3.4
1	A	73	ILE	3.4
1	B	164	ASP	3.4
1	A	204	VAL	3.3
1	A	58	ARG	3.3
1	B	160	CYS	3.3
1	B	153	LEU	3.3
1	A	254	CYS	3.3
1	B	130	ASP	3.2
1	B	252	ASP	3.2
1	B	185	VAL	3.2
1	B	63	VAL	3.2
1	A	230	LEU	3.2
1	B	50	TRP	3.2
1	B	211	SER	3.2
1	B	279	TYR	3.2
1	B	116	THR	3.2
1	A	212	ARG	3.1
1	B	266	ILE	3.1
1	A	48	GLN	3.1
1	A	235	VAL	3.1
1	B	91	GLY	3.1
1	A	51	SER	3.1
1	B	45	ARG	3.1
1	A	61	GLU	3.1
1	A	45	ARG	3.1
1	A	222	PHE	3.1
1	A	223	GLY	3.0
1	A	84	SER	3.0
1	A	203	VAL	3.0
1	A	270	ASN	3.0
1	B	277	ASN	3.0
1	B	244	HIS	3.0
1	A	192	VAL	3.0
1	B	217	ASP	3.0
1	A	181	SER	3.0
1	B	228	HIS	3.0
1	A	154	ALA	3.0
1	A	219	ASP	2.9
1	B	264	SER	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	163	PHE	2.9
1	B	174	PRO	2.9
1	A	279	TYR	2.9
1	B	154	ALA	2.9
1	B	250	SER	2.8
1	B	259	ILE	2.8
1	B	265	ILE	2.8
1	B	127	ARG	2.8
1	B	268	LYS	2.8
1	B	184	PRO	2.8
1	B	231	GLN	2.8
1	A	271	ILE	2.7
1	A	170	TYR	2.7
1	B	263	GLU	2.7
1	B	94	ILE	2.7
1	A	86	TRP	2.7
1	A	280	ARG	2.7
1	B	269	ARG	2.7
1	A	195	ARG	2.7
1	B	89	PHE	2.7
1	A	262	LEU	2.6
1	A	130	ASP	2.6
1	B	281	PRO	2.6
1	B	210	GLY	2.6
1	B	214	LYS	2.6
1	A	148	THR	2.6
1	A	272	GLN	2.6
1	B	223	GLY	2.6
1	A	193	SER	2.6
1	B	68	VAL	2.6
1	B	225	VAL	2.6
1	B	140	ARG	2.6
1	A	64	LEU	2.5
1	A	238	LEU	2.5
1	B	261	GLU	2.5
1	B	173	CYS	2.5
1	B	107	GLN	2.5
1	B	137	GLN	2.5
1	B	206	VAL	2.5
1	A	163	PHE	2.5
1	B	64	LEU	2.5
1	B	262	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	62	THR	2.5
1	A	206	VAL	2.5
1	A	152	TYR	2.5
1	A	65	ALA	2.5
1	A	93	PHE	2.5
1	B	95	SER	2.5
1	B	161	GLY	2.5
1	A	92	ALA	2.5
1	A	75	PRO	2.4
1	B	256	ASP	2.4
1	A	274	SER	2.4
1	A	119	CYS	2.4
1	A	173	CYS	2.4
1	B	93	PHE	2.4
1	A	52	GLY	2.4
1	B	81	ASP	2.4
1	B	284	PHE	2.4
1	A	171	GLN	2.4
1	B	181	SER	2.4
1	B	233	GLU	2.4
1	A	145	LEU	2.4
1	B	56	THR	2.3
1	A	251	ARG	2.3
1	B	162	GLU	2.3
1	B	88	ALA	2.3
1	A	117	VAL	2.3
1	A	159	TRP	2.3
1	B	86	TRP	2.3
1	B	142	MET	2.3
1	A	136	THR	2.3
1	A	166	SER	2.3
1	A	116	THR	2.3
1	B	271	ILE	2.3
1	A	156	ASP	2.3
1	A	240	ALA	2.3
1	B	104	GLU	2.3
1	B	158	THR	2.3
1	A	125	TRP	2.2
1	A	72	GLU	2.2
1	B	49	THR	2.2
1	A	211	SER	2.2
1	B	192	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	67	CYS	2.2
1	A	78	ARG	2.2
1	A	275	CYS	2.2
1	B	251	ARG	2.2
1	A	128	ILE	2.2
1	B	74	HIS	2.2
1	B	188	PHE	2.2
1	B	98	PRO	2.2
1	B	257	PRO	2.2
1	A	59	PHE	2.2
1	A	258	THR	2.2
1	A	291	PRO	2.2
1	B	52	GLY	2.2
1	B	202	ASP	2.1
1	A	49	THR	2.1
1	A	188	PHE	2.1
1	B	59	PHE	2.1
1	B	221	THR	2.1
1	A	150	LEU	2.1
1	B	285	LEU	2.1
1	B	47	ARG	2.1
1	B	67	CYS	2.1
1	A	83	GLN	2.1
1	A	231	GLN	2.1
1	A	185	VAL	2.1
1	B	106	TYR	2.1
1	B	152	TYR	2.1
1	B	92	ALA	2.1
1	B	135	PHE	2.1
1	B	236	GLN	2.1
1	A	267	SER	2.1
1	B	175	ASP	2.1
1	B	145	LEU	2.1
1	B	149	LEU	2.1
1	B	69	LYS	2.0
1	B	101	ILE	2.0
1	B	272	GLN	2.0
1	B	119	CYS	2.0
1	B	189	TRP	2.0
1	A	167	LYS	2.0
1	B	218	LYS	2.0
1	A	147	ASP	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	126	SER	2.0
1	B	169	ASN	2.0
1	B	183	ASN	2.0

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

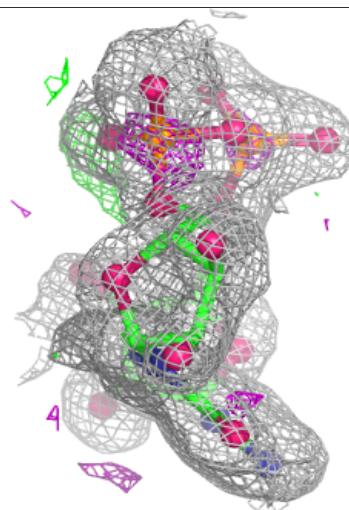
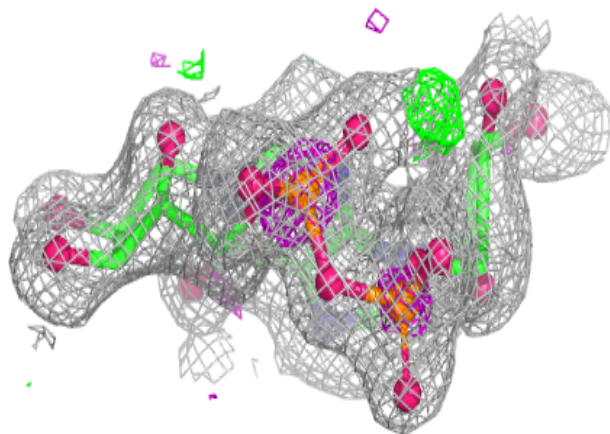
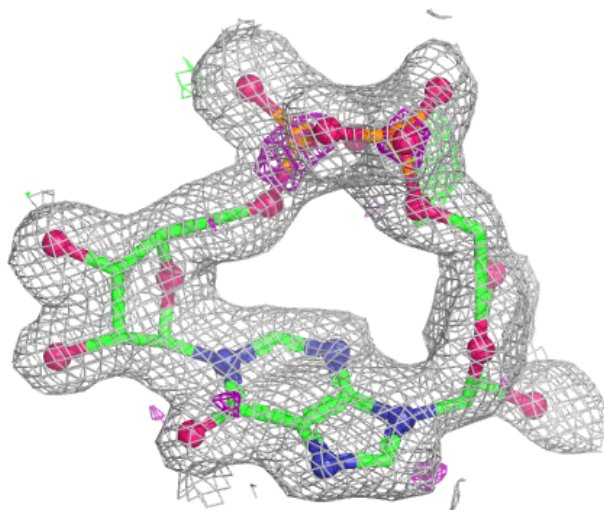
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	N1C	A	301	35/35	0.88	0.11	25,33,38,40	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.

Electron density around N1C A 301:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.