



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:55 PM UTC

PDB ID : 3T60 / pdb_00003t60
Title : 5'-Diphenyl Nucleoside Inhibitors of Plasmodium falciparum dUTPase
Authors : Hampton, S.E.; Baragana, B.; Schipani, A.; Bosch-Navarrete, C.; Musso-Buendia, A.; Recio, E.; Kaiser, M.; Whittingham, J.L.; Roberts, S.M.; Shevtsov, M.; Brannigan, J.A.; Kahnberg, P.; Brun, R.; Wilson, K.S.; Gonzalez-Pacanowska, D.; Johansson, N.G.; Gilbert, I.H.
Deposited on : 2011-07-28
Resolution : 2.40 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](#) ①) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

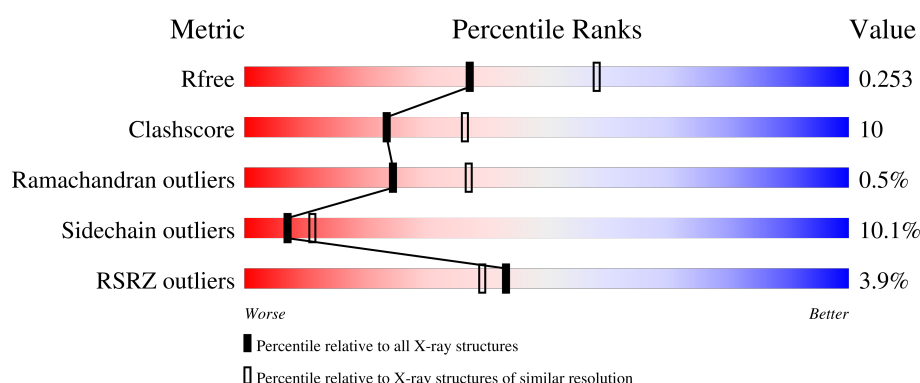
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	181	3% 51% 25% •• 21%
1	B	181	4% 46% 22% •• 28%
1	C	181	2% 55% 21% • 20%

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	DUA	B	182	X	-	-	-
2	DUA	C	182	X	-	-	-
3	GOL	A	183	-	-	X	-
3	GOL	B	183	-	-	X	-
3	GOL	C	183	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3545 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 Deoxyuridine 5'-triphosphate nucleotidohydrolase, putative.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	143	Total	C	N	O	S	118	0	0
			1128	722	184	219	3			
1	B	131	Total	C	N	O	S	87	1	0
			1049	678	170	198	3			
1	C	145	Total	C	N	O	S	62	0	0
			1149	737	187	222	3			

There are 24 discrepancies between the modelled and reference sequences:

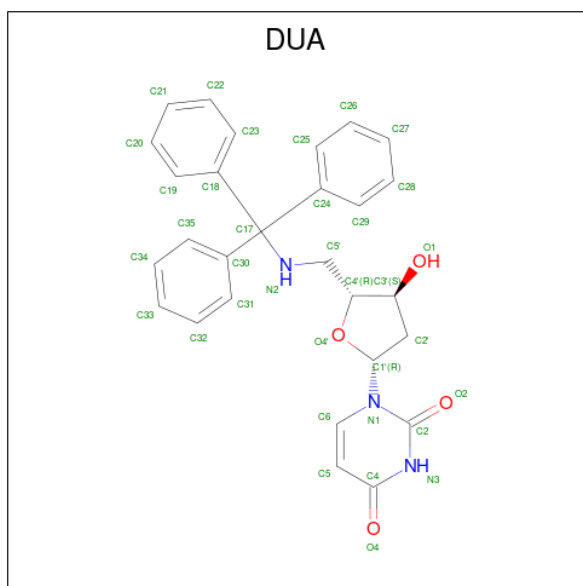
Chain	Residue	Modelled	Actual	Comment	Reference
A	174	LEU	-	expression tag	UNP Q8II92
A	175	GLU	-	expression tag	UNP Q8II92
A	176	HIS	-	expression tag	UNP Q8II92
A	177	HIS	-	expression tag	UNP Q8II92
A	178	HIS	-	expression tag	UNP Q8II92
A	179	HIS	-	expression tag	UNP Q8II92
A	180	HIS	-	expression tag	UNP Q8II92
A	181	HIS	-	expression tag	UNP Q8II92
B	174	LEU	-	expression tag	UNP Q8II92
B	175	GLU	-	expression tag	UNP Q8II92
B	176	HIS	-	expression tag	UNP Q8II92
B	177	HIS	-	expression tag	UNP Q8II92
B	178	HIS	-	expression tag	UNP Q8II92
B	179	HIS	-	expression tag	UNP Q8II92
B	180	HIS	-	expression tag	UNP Q8II92
B	181	HIS	-	expression tag	UNP Q8II92
C	174	LEU	-	expression tag	UNP Q8II92
C	175	GLU	-	expression tag	UNP Q8II92
C	176	HIS	-	expression tag	UNP Q8II92
C	177	HIS	-	expression tag	UNP Q8II92
C	178	HIS	-	expression tag	UNP Q8II92
C	179	HIS	-	expression tag	UNP Q8II92
C	180	HIS	-	expression tag	UNP Q8II92

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Chain	Residue	Modelled	Actual	Comment	Reference
C	181	HIS	-	expression tag	UNP Q8II92

- Molecule 2 is 2',5'-dideoxy-5'-(tritylamino)uridine (CCD ID: DUA) (formula: $C_{28}H_{27}N_3O_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			35	28	3	4		
2	B	1	Total	C	N	O	0	0
			35	28	3	4		
2	C	1	Total	C	N	O	0	0
			35	28	3	4		

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	38	Total	O	0	0
			38	38		
4	B	23	Total	O	0	0
			23	23		
4	C	35	Total	O	0	0
			35	35		

- Molecule 1: Deoxyuridine 5'-triphosphate nucleotidohydrolase, putative



4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	76.97 Å 76.97 Å 106.92 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.40 40.00 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.3 (40.00-2.40) 99.2 (40.00-2.40)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.10 (at 2.39 Å)	Xtriage
Refinement program	REFMAC 5.3.0037	Depositor
R, R_{free}	0.196 , 0.254 0.194 , 0.253	Depositor DCC
R_{free} test set	1244 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	42.5	Xtriage
Anisotropy	0.164	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 44.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.052 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3545	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.61% 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: DUA, 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	1.78	14/1144 (1.2%)	1.97	25/1538 (1.6%)
1	B	1.71	13/1070 (1.2%)	1.43	10/1440 (0.7%)
1	C	1.98	10/1166 (0.9%)	1.81	24/1567 (1.5%)
All	All	1.83	37/3380 (1.1%)	1.76	59/4545 (1.3%)

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	B	1	3
1	C	0	1
All	All	1	4

All (37) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	80	ASN	C-N	-27.98	0.99	1.33
1	C	166	GLY	CA-C	-24.19	1.08	1.52
1	A	80	ASN	C-N	-23.77	1.00	1.33
1	B	133	ASN	CA-CB	-20.36	1.19	1.53
1	C	59	LYS	CA-CB	-17.64	1.24	1.53
1	C	26	ASP	CA-C	17.32	1.89	1.52
1	A	166	GLY	CA-C	13.77	1.76	1.52
1	B	10	ASP	CA-CB	-12.88	1.32	1.53
1	A	58	TYR	C-N	12.68	1.50	1.33
1	C	60	SER	CA-CB	-12.44	1.33	1.53
1	C	17	LYS	C-N	11.45	1.49	1.33
1	B	35	LYS	CA-CB	-11.38	1.27	1.53
1	B	127	GLU	CD-OE2	10.94	1.46	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	13	ARG	CA-CB	-10.28	1.36	1.53
1	B	135	LYS	CD-CE	9.78	1.81	1.52
1	B	127	GLU	CD-OE1	-9.72	1.06	1.25
1	B	14	GLU	CA-CB	-9.46	1.37	1.53
1	C	159	SER	CB-OG	-9.14	1.23	1.42
1	A	109	ASP	CB-CG	8.89	1.74	1.52
1	B	59	LYS	CA-CB	-8.42	1.39	1.53
1	A	18	ASN	CA-CB	-8.33	1.36	1.53
1	A	166	GLY	N-CA	7.26	1.57	1.45
1	A	131	LYS	CG-CD	6.91	1.73	1.52
1	C	102	ALA	CA-CB	-6.45	1.43	1.53
1	B	11	GLU	CB-CG	-6.44	1.33	1.52
1	A	14	GLU	CB-CG	-6.33	1.33	1.52
1	B	47	VAL	CA-CB	-5.94	1.47	1.54
1	A	140	VAL	C-O	-5.87	1.18	1.23
1	A	102	ALA	C-O	5.81	1.30	1.24
1	A	125	ASP	CB-CG	5.69	1.66	1.52
1	A	96	LYS	CD-CE	5.69	1.69	1.52
1	A	161	GLY	C-O	-5.64	1.17	1.23
1	C	4	LYS	CD-CE	-5.46	1.36	1.52
1	B	96	LYS	CB-CG	-5.41	1.36	1.52
1	C	61	ASN	CA-CB	5.34	1.61	1.53
1	A	159	SER	C-O	-5.29	1.18	1.24
1	B	152	VAL	CA-C	5.05	1.63	1.52

All (59) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	80	ASN	CA-C-N	25.26	157.46	123.11
1	A	80	ASN	C-N-CA	25.26	157.46	123.11
1	A	62	TYR	N-CA-C	21.97	139.58	111.24
1	C	17	LYS	O-C-N	-19.63	93.34	122.39
1	C	80	ASN	CA-C-N	18.63	148.82	123.11
1	C	80	ASN	C-N-CA	18.63	148.82	123.11
1	A	63	TYR	N-CA-CB	17.31	139.93	110.50
1	C	61	ASN	CA-CB-CG	-16.10	96.50	112.60
1	A	125	ASP	CA-CB-CG	-15.52	97.08	112.60
1	B	133	ASN	CA-CB-CG	13.61	126.21	112.60
1	A	80	ASN	O-C-N	-11.85	104.04	123.00
1	B	133	ASN	CB-CA-C	11.06	132.43	110.42
1	C	80	ASN	O-C-N	-10.90	105.56	123.00
1	C	42	LYS	CD-CE-NZ	9.52	142.35	111.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	96	LYS	CG-CD-CE	-8.78	91.10	111.30
1	C	26	ASP	CA-C-O	8.19	134.72	120.80
1	A	166	GLY	CA-C-O	-7.81	104.40	120.80
1	C	60	SER	N-CA-CB	7.54	122.45	110.85
1	C	34	VAL	N-CA-CB	-7.44	103.48	112.33
1	B	127	GLU	CG-CD-OE2	-7.12	102.02	118.40
1	B	135	LYS	CG-CD-CE	-7.11	94.95	111.30
1	A	34	VAL	CB-CA-C	7.03	118.54	110.88
1	A	10	ASP	N-CA-CB	6.98	120.49	110.16
1	A	34	VAL	N-CA-CB	-6.94	102.77	112.35
1	A	63	TYR	N-CA-C	-6.73	92.16	111.00
1	A	35	LYS	CA-CB-CG	-6.71	100.69	114.10
1	B	26	ASP	CB-CA-C	-6.66	97.45	110.10
1	C	131	LYS	CB-CG-CD	6.65	126.60	111.30
1	A	152	VAL	CB-CA-C	6.57	122.47	110.71
1	A	10	ASP	CA-CB-CG	6.53	119.13	112.60
1	C	96	LYS	CG-CD-CE	-6.39	96.60	111.30
1	C	59	LYS	N-CA-CB	6.29	118.96	109.34
1	A	145	GLU	CA-C-N	6.12	126.06	119.76
1	A	145	GLU	C-N-CA	6.12	126.06	119.76
1	B	10	ASP	N-CA-CB	6.10	119.15	110.13
1	C	112	TYR	N-CA-C	-6.01	99.49	109.46
1	C	110	ALA	CA-C-N	-5.84	109.96	121.41
1	C	110	ALA	C-N-CA	-5.84	109.96	121.41
1	C	40	LYS	CG-CD-CE	-5.82	97.92	111.30
1	B	59	LYS	CB-CA-C	5.75	118.96	109.70
1	A	14	GLU	CA-CB-CG	5.67	125.44	114.10
1	B	13	ARG	CA-CB-CG	5.67	125.44	114.10
1	C	60	SER	CB-CA-C	5.56	119.72	109.71
1	B	30	ASP	N-CA-C	5.55	118.06	110.24
1	B	13	ARG	N-CA-CB	5.49	119.76	110.49
1	A	58	TYR	O-C-N	5.42	129.50	122.89
1	A	59	LYS	N-CA-C	-5.40	102.62	110.24
1	A	111	GLY	N-CA-C	5.38	120.37	114.40
1	C	109	ASP	CA-C-N	5.35	128.84	120.82
1	C	109	ASP	C-N-CA	5.35	128.84	120.82
1	C	59	LYS	CB-CA-C	5.34	117.14	109.71
1	A	108	ILE	CB-CA-C	5.26	118.68	111.31
1	C	152	VAL	N-CA-CB	-5.23	102.68	112.36
1	A	18	ASN	N-CA-CB	-5.21	101.65	110.50
1	C	166	GLY	N-CA-C	5.19	128.35	113.30
1	C	34	VAL	CB-CA-C	5.18	116.21	110.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	97	THR	N-CA-C	5.14	116.04	110.13
1	A	86	PHE	N-CA-C	5.11	115.79	108.74
1	C	113	ARG	CD-NE-CZ	-5.06	117.32	124.40

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	B	133	ASN	CA

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	127	GLU	Sidechain
1	B	26	ASP	Peptide,Mainchain
1	C	17	LYS	Mainchain

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	1128	0	1144	21	0
1	B	1049	0	1082	24	0
1	C	1149	0	1166	18	2
2	A	35	0	26	3	0
2	B	35	0	26	0	0
2	C	35	0	26	2	0
3	A	6	0	8	6	0
3	B	6	0	8	4	0
3	C	6	0	8	5	0
4	A	38	0	0	0	0
4	B	23	0	0	0	0
4	C	35	0	0	2	2
All	All	3545	0	3494	65	2

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 10.

All (65) 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:C:92:SER:HB2	3:C:183:GOL:H32	1.51	0.92
1:B:88:LEU:HD11	1:B:137:VAL:HG13	1.57	0.86
1:B:31:LEU:HD21	1:B:139:LEU:HD22	1.65	0.78
1:B:8:LEU:HD21	1:B:52:LYS:HE3	1.67	0.77
1:B:143:THR:OG1	1:B:145:GLU:HG2	1.89	0.73
1:B:12:VAL:HA	1:B:15:MET:HE3	1.70	0.73
1:C:15:MET:HE2	1:C:132:LYS:HE3	1.71	0.72
1:B:92:SER:HB2	3:B:183:GOL:H32	1.70	0.72
1:B:88:LEU:HD11	1:B:137:VAL:CG1	2.22	0.69
1:C:92:SER:H	3:C:183:GOL:H11	1.58	0.69
1:B:1:MET:N	1:B:145:GLU:OE1	2.22	0.68
2:A:182:DUA:H5'	2:A:182:DUA:H31	1.75	0.68
1:B:12:VAL:HG22	1:B:34:VAL:HG22	1.75	0.68
1:A:92:SER:H	3:A:183:GOL:H11	1.59	0.67
1:B:92:SER:OG	3:B:183:GOL:H11	1.98	0.64
1:B:92:SER:H	3:B:183:GOL:C1	2.13	0.61
1:C:92:SER:HB2	3:C:183:GOL:C3	2.26	0.60
1:B:92:SER:H	3:B:183:GOL:H11	1.68	0.59
1:C:31:LEU:HD21	1:C:139:LEU:HD22	1.84	0.58
1:B:12:VAL:HA	1:B:15:MET:CE	2.35	0.56
1:B:88:LEU:CD1	1:B:137:VAL:HG13	2.34	0.56
2:A:182:DUA:H31	2:A:182:DUA:C5'	2.35	0.56
1:B:1:MET:SD	1:B:55:ALA:HB1	2.46	0.55
1:C:92:SER:CB	3:C:183:GOL:H32	2.31	0.55
1:B:40:LYS:O	1:B:43:SER:OG	2.25	0.54
1:C:13:ARG:NH1	4:C:191:HOH:O	2.41	0.54
1:B:33:ILE:O	1:B:132:LYS:HA	2.08	0.53
1:A:92:SER:H	3:A:183:GOL:H32	1.73	0.53
1:A:88:LEU:HD11	1:A:137:VAL:HG13	1.89	0.53
1:A:92:SER:HB2	3:A:183:GOL:H32	1.92	0.52
1:A:92:SER:N	3:A:183:GOL:H32	2.26	0.51
1:C:138:GLN:HE22	3:C:183:GOL:H12	1.75	0.51
1:B:15:MET:SD	1:B:132:LYS:HE2	2.50	0.51
1:A:152:VAL:HG13	1:A:154:GLU:O	2.11	0.51
2:A:182:DUA:C25	1:B:92:SER:HB3	2.42	0.50
1:B:33:ILE:CG2	1:B:130:ILE:HD12	2.44	0.48
1:C:107:LEU:HD13	1:C:142:PHE:HZ	1.79	0.47
1:A:92:SER:HB2	3:A:183:GOL:C3	2.45	0.47
1:A:31:LEU:HD21	1:A:139:LEU:HD22	1.97	0.47
1:C:15:MET:HE2	1:C:132:LYS:CE	2.41	0.46
1:C:160:ARG:NH2	4:C:184:HOH:O	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:44:THR:HB	1:A:121:ASP:OD2	2.16	0.46
1:A:27:SER:HB2	1:A:144:GLY:O	2.16	0.46
2:C:182:DUA:H31	2:C:182:DUA:H5'	1.98	0.45
1:C:3:LEU:O	1:C:149:PHE:HA	2.16	0.45
1:C:49:LEU:HD12	1:C:116:ILE:HG22	1.99	0.45
1:A:82:VAL:HG12	1:A:83:ASN:O	2.17	0.44
1:A:6:VAL:HG23	1:A:155:LEU:CD2	2.47	0.44
1:A:88:LEU:HD11	1:A:137:VAL:CG1	2.47	0.44
1:C:90:PRO:HG3	1:C:101:LEU:HB2	1.99	0.44
1:A:89:PHE:CD1	1:A:140:VAL:HG13	2.52	0.43
1:C:4:LYS:HB2	1:C:54:ILE:HG22	1.99	0.43
1:C:98:PRO:HD2	1:C:128:TYR:CE1	2.53	0.43
1:A:12:VAL:HA	1:A:15:MET:HE3	2.01	0.43
1:B:52:LYS:HD3	1:B:113:ARG:O	2.18	0.43
1:A:92:SER:CB	3:A:183:GOL:H32	2.49	0.42
1:A:92:SER:HB3	2:C:182:DUA:C25	2.50	0.42
1:A:52:LYS:HB3	1:A:155:LEU:HD11	2.02	0.42
1:B:12:VAL:HG22	1:B:34:VAL:CG2	2.46	0.42
1:A:95:SER:O	1:C:44:THR:HG21	2.20	0.41
1:A:88:LEU:HD12	1:A:139:LEU:CD1	2.49	0.41
1:C:54:ILE:HB	1:C:155:LEU:HD22	2.02	0.41
1:B:43:SER:O	1:B:121:ASP:HA	2.21	0.41
1:B:83:ASN:ND2	1:B:110:ALA:O	2.52	0.41
1:A:3:LEU:O	1:A:149:PHE:HA	2.20	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:131:LYS:NZ	4:C:218:HOH:O[4_564]	1.02	1.18
1:C:131:LYS:CE	4:C:218:HOH:O[4_564]	1.97	0.23

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	A	137/181 (76%)	132 (96%)	4 (3%)	1 (1%)	18	28
1	B	126/181 (70%)	123 (98%)	2 (2%)	1 (1%)	16	25
1	C	139/181 (77%)	134 (96%)	5 (4%)	0	100	100
All	All	402/543 (74%)	389 (97%)	11 (3%)	2 (0%)	24	37

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	104	SER
1	B	133	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	A	127/164 (77%)	117 (92%)	10 (8%)	11	19
1	B	120/164 (73%)	102 (85%)	18 (15%)	3	3
1	C	129/164 (79%)	119 (92%)	10 (8%)	11	20
All	All	376/492 (76%)	338 (90%)	38 (10%)	7	11

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	17	LYS
1	A	34	VAL
1	A	44	THR
1	A	137	VAL
1	A	139	LEU
1	A	140	VAL
1	A	152	VAL

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Mol	Chain	Res	Type
1	A	157	GLU
1	A	160	ARG
1	B	17	LYS
1	B	26	ASP
1	B	29	LEU
1	B	34	VAL
1	B	36	ASP
1	B	57	GLN
1	B	80	ASN
1	B	81	ILE
1	B	84	THR
1	B	117	ILE
1	B	126	GLN
1	B	133	ASN
1	B	137	VAL
1	B	139	LEU
1	B	140	VAL
1	B	145	GLU
1	B	147	LEU
1	B	152	VAL
1	C	34	VAL
1	C	54	ILE
1	C	82	VAL
1	C	109	ASP
1	C	124	SER
1	C	126	GLN
1	C	137	VAL
1	C	139	LEU
1	C	140	VAL
1	C	152	VAL

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

Mol	Chain	Res	Type
1	A	57	GLN
1	B	57	GLN
1	B	126	GLN
1	C	138	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](#)

6 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	DUA	B	182	-	39,39,39	1.39	5 (12%)	53,55,55	3.10	16 (30%)
2	DUA	A	182	-	39,39,39	1.67	7 (17%)	53,55,55	3.03	26 (49%)
3	GOL	B	183	-	5,5,5	0.90	0	5,5,5	0.47	0
3	GOL	A	183	-	5,5,5	0.80	0	5,5,5	2.01	1 (20%)
3	GOL	C	183	-	5,5,5	0.85	0	5,5,5	1.28	1 (20%)
2	DUA	C	182	-	39,39,39	1.63	10 (25%)	53,55,55	3.56	26 (49%)

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	DUA	B	182	-	1/1/4/5	2/28/40/40	0/5/5/5
2	DUA	A	182	-	-	2/28/40/40	0/5/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	B	183	-	-	4/4/4/4	-
3	GOL	A	183	-	-	4/4/4/4	-
3	GOL	C	183	-	-	3/4/4/4	-
2	DUA	C	182	-	1/1/4/5	2/28/40/40	0/5/5/5

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	182	DUA	C17-N2	-4.87	1.44	1.48
2	A	182	DUA	C17-C24	-4.47	1.48	1.54
2	C	182	DUA	C2-N3	-3.49	1.31	1.38
2	C	182	DUA	C17-C24	-3.37	1.49	1.54
2	B	182	DUA	C17-C18	3.30	1.59	1.54
2	C	182	DUA	C17-C18	3.21	1.59	1.54
2	B	182	DUA	C17-C30	-3.08	1.50	1.54
2	C	182	DUA	C5-C4	-2.67	1.37	1.43
2	A	182	DUA	C4-N3	-2.59	1.34	1.38
2	C	182	DUA	C19-C18	2.57	1.43	1.39
2	C	182	DUA	C22-C23	2.51	1.43	1.38
2	C	182	DUA	C20-C19	2.46	1.43	1.38
2	A	182	DUA	C20-C19	2.40	1.43	1.38
2	B	182	DUA	C5'-N2	2.35	1.50	1.46
2	B	182	DUA	C5-C4	-2.28	1.38	1.43
2	C	182	DUA	C28-C29	2.16	1.42	1.38
2	B	182	DUA	C35-C30	2.11	1.42	1.39
2	A	182	DUA	C17-C18	2.09	1.57	1.54
2	C	182	DUA	C1'-N1	-2.04	1.42	1.48
2	A	182	DUA	C6-C5	2.03	1.39	1.35
2	A	182	DUA	C2-N3	-2.03	1.34	1.38
2	C	182	DUA	C5'-N2	2.01	1.49	1.46

All (70) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	182	DUA	C30-C17-N2	11.82	125.54	108.64
2	C	182	DUA	C30-C17-N2	11.24	124.72	108.64
2	A	182	DUA	C18-C17-N2	-8.11	97.03	108.64
2	B	182	DUA	C2'-C1'-N1	7.98	133.76	113.81
2	C	182	DUA	C18-C17-N2	-7.82	97.46	108.64
2	C	182	DUA	O4'-C1'-N1	7.48	121.14	107.86
2	B	182	DUA	C3'-C2'-C1'	-6.63	86.37	102.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	182	DUA	C18-C17-N2	-6.59	99.21	108.64
2	C	182	DUA	C2'-C1'-N1	6.57	130.23	113.81
2	A	182	DUA	C30-C17-N2	6.16	117.45	108.64
2	C	182	DUA	C20-C19-C18	6.12	126.97	120.75
2	A	182	DUA	O4'-C1'-N1	6.07	118.64	107.86
2	C	182	DUA	C3'-C2'-C1'	-5.87	88.24	102.60
2	C	182	DUA	C5-C4-N3	5.73	122.82	114.80
2	A	182	DUA	C4-N3-C2	-5.70	119.54	126.61
2	C	182	DUA	C4-N3-C2	-5.70	119.54	126.61
2	C	182	DUA	O4-C4-C5	-5.67	115.39	125.16
2	A	182	DUA	C3'-C2'-C1'	-5.56	88.99	102.60
2	A	182	DUA	C24-C17-N2	5.30	116.21	108.64
2	C	182	DUA	C23-C18-C19	-4.99	110.59	118.03
2	B	182	DUA	O4'-C1'-N1	4.94	116.63	107.86
2	A	182	DUA	C5-C4-N3	4.86	121.61	114.80
2	C	182	DUA	C30-C17-C18	-4.86	94.40	110.23
2	B	182	DUA	C4-N3-C2	-4.68	120.80	126.61
2	A	182	DUA	N3-C2-N1	4.60	120.88	114.89
2	B	182	DUA	C30-C17-C18	-4.45	95.71	110.23
2	A	182	DUA	C2'-C1'-N1	4.42	124.87	113.81
2	B	182	DUA	C22-C23-C18	4.21	125.03	120.75
2	B	182	DUA	C5-C4-N3	4.12	120.57	114.80
2	A	182	DUA	C34-C35-C30	4.11	124.93	120.75
2	C	182	DUA	C1'-N1-C6	-4.07	113.52	121.53
2	C	182	DUA	C26-C25-C24	4.02	124.84	120.75
2	B	182	DUA	O4-C4-C5	-4.01	118.24	125.16
2	A	182	DUA	C22-C23-C18	3.99	124.81	120.75
3	A	183	GOL	O2-C2-C1	-3.85	93.24	109.18
2	B	182	DUA	C4'-O4'-C1'	-3.79	100.50	109.51
2	A	182	DUA	O2-C2-N1	-3.71	117.96	122.80
2	A	182	DUA	C25-C24-C17	3.57	128.07	120.84
2	A	182	DUA	O4-C4-C5	-3.55	119.03	125.16
2	C	182	DUA	C33-C34-C35	-3.50	115.92	120.24
2	A	182	DUA	C2'-C3'-C4'	3.45	109.79	102.80
2	A	182	DUA	C29-C24-C17	-3.38	113.98	120.84
2	C	182	DUA	O2-C2-N1	-3.29	118.51	122.80
2	C	182	DUA	C22-C21-C20	-3.24	115.43	119.87
2	A	182	DUA	C35-C30-C17	3.23	127.38	120.84
2	C	182	DUA	C21-C22-C23	3.15	124.12	120.24
2	B	182	DUA	O2-C2-N1	-3.11	118.74	122.80
2	A	182	DUA	C23-C18-C19	-3.02	113.53	118.03
2	A	182	DUA	O4'-C1'-C2'	3.02	111.88	106.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	182	DUA	C30-C17-C18	-2.98	100.52	110.23
2	C	182	DUA	C6-N1-C2	2.78	124.38	121.00
2	C	182	DUA	C34-C35-C30	2.74	123.53	120.75
2	A	182	DUA	C22-C21-C20	-2.65	116.25	119.87
2	C	182	DUA	C23-C18-C17	2.62	126.14	120.84
2	A	182	DUA	C35-C30-C31	-2.56	114.22	118.03
2	B	182	DUA	C2'-C3'-C4'	2.49	107.85	102.80
2	B	182	DUA	C1'-N1-C6	-2.46	116.70	121.53
2	A	182	DUA	C1'-N1-C6	-2.44	116.74	121.53
2	B	182	DUA	C23-C18-C19	-2.41	114.43	118.03
2	A	182	DUA	C5-C6-N1	-2.30	118.09	121.84
2	C	182	DUA	C5-C6-N1	-2.29	118.11	121.84
2	C	182	DUA	C27-C28-C29	2.29	123.06	120.24
2	C	182	DUA	C30-C17-C24	2.29	117.68	110.23
2	B	182	DUA	N3-C2-N1	2.28	117.85	114.89
2	C	182	DUA	C22-C23-C18	2.26	123.06	120.75
3	C	183	GOL	O2-C2-C1	-2.21	100.03	109.18
2	C	182	DUA	C34-C33-C32	2.18	122.85	119.87
2	A	182	DUA	C1'-N1-C2	2.18	121.91	117.66
2	A	182	DUA	C23-C18-C17	2.17	125.23	120.84
2	C	182	DUA	C4'-O4'-C1'	-2.03	104.68	109.51

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	182	DUA	C1'
2	C	182	DUA	C1'

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	182	DUA	O4'-C1'-N1-C2
3	A	183	GOL	C1-C2-C3-O3
3	B	183	GOL	C1-C2-C3-O3
3	C	183	GOL	C1-C2-C3-O3
3	A	183	GOL	O2-C2-C3-O3
2	B	182	DUA	O4'-C1'-N1-C6
3	A	183	GOL	O1-C1-C2-C3
3	B	183	GOL	O1-C1-C2-C3
3	A	183	GOL	O1-C1-C2-O2
3	B	183	GOL	O2-C2-C3-O3
3	C	183	GOL	O2-C2-C3-O3

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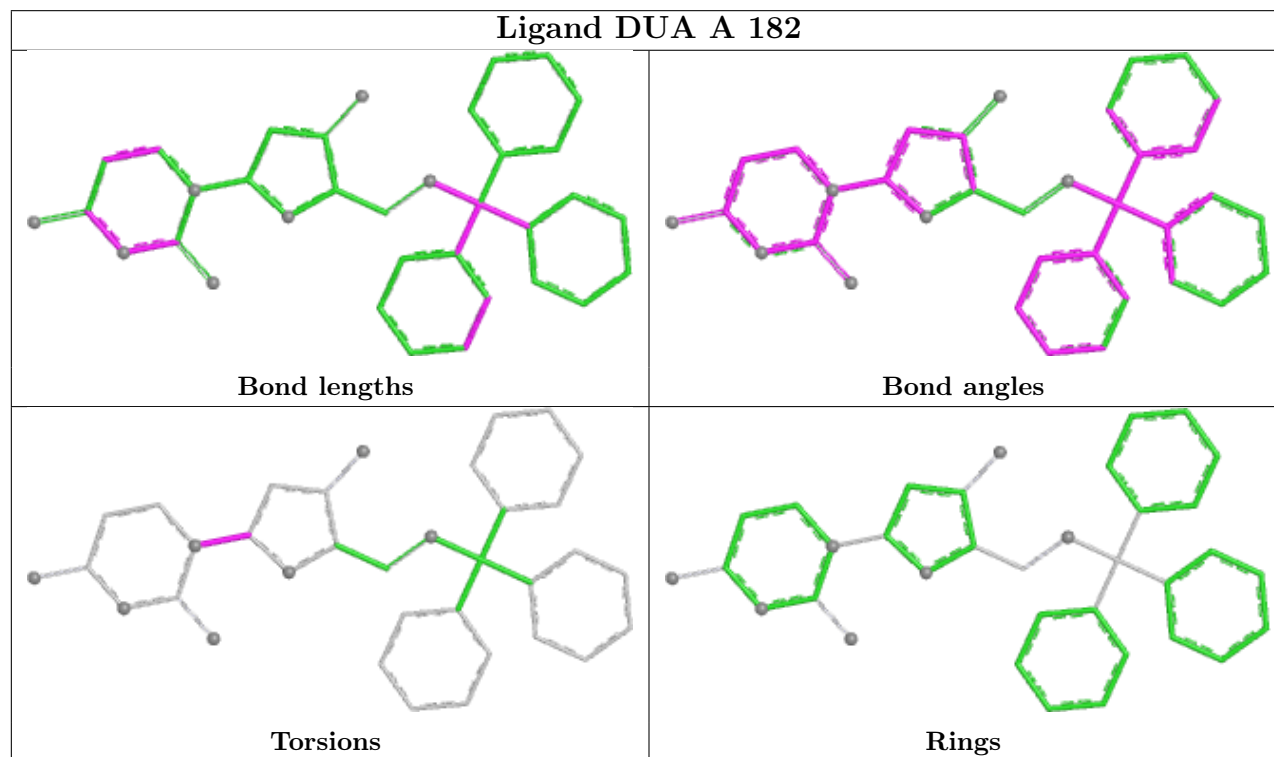
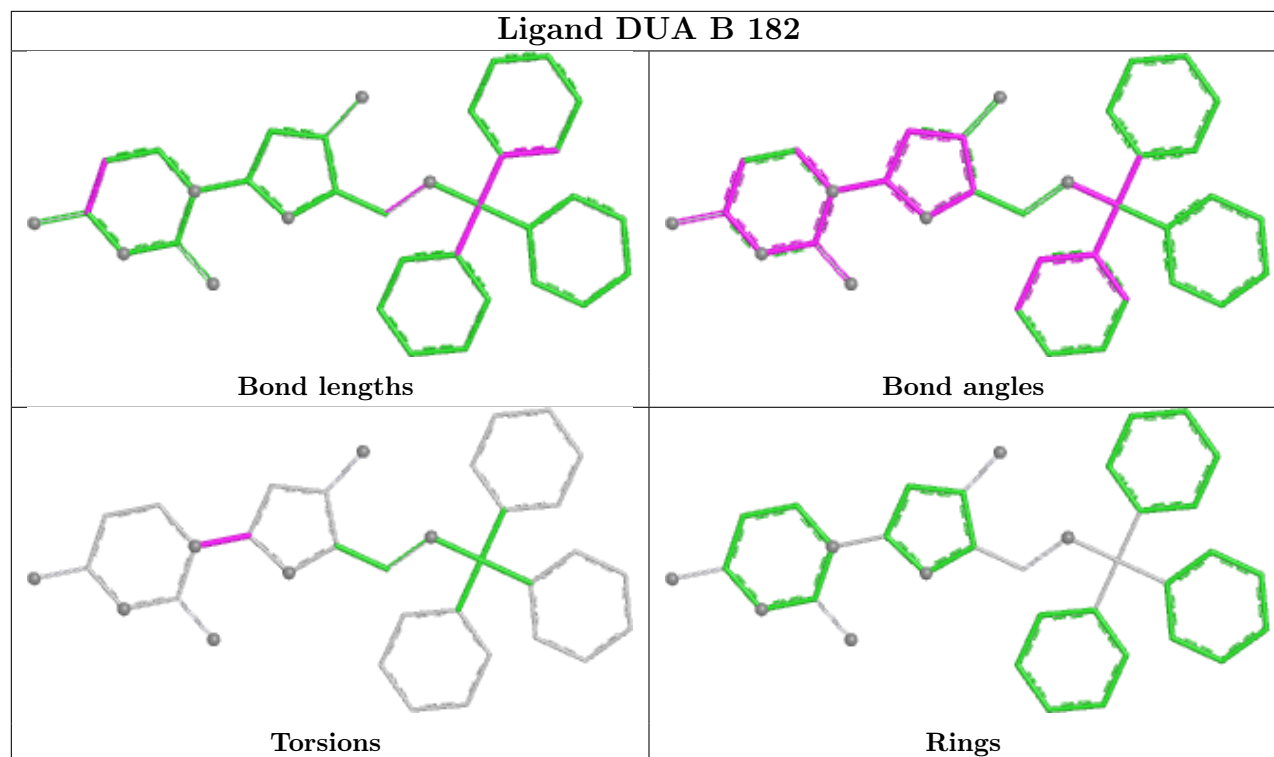
Mol	Chain	Res	Type	Atoms
2	C	182	DUA	O4'-C1'-N1-C2
2	A	182	DUA	O4'-C1'-N1-C2
3	B	183	GOL	O1-C1-C2-O2
2	C	182	DUA	O4'-C1'-N1-C6
2	A	182	DUA	O4'-C1'-N1-C6
3	C	183	GOL	O1-C1-C2-O2

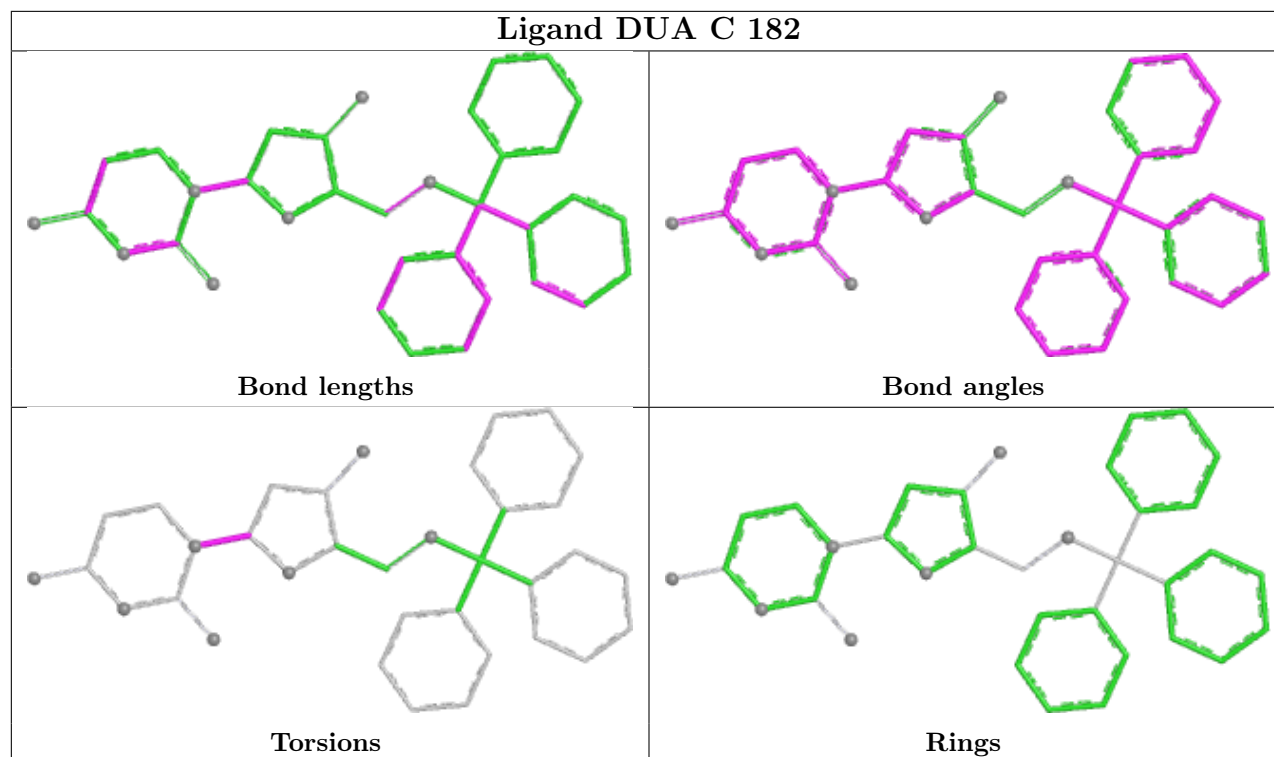
There are no ring outliers.

5 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	182	DUA	3	0
3	B	183	GOL	4	0
3	A	183	GOL	6	0
3	C	183	GOL	5	0
2	C	182	DUA	2	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1
1	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	80:ASN	C	81:ILE	N	1.00
1	C	80:ASN	C	81:ILE	N	0.99

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, 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	137/181 (75%)	-0.13	6 (4%)	39 34	15, 30, 44, 57	18 (13%)
1	B	130/181 (71%)	0.50	7 (5%)	31 28	12, 41, 61, 66	22 (16%)
1	C	143/181 (79%)	-0.11	3 (2%)	63 59	10, 31, 46, 68	15 (10%)
All	All	410/543 (75%)	0.08	16 (3%)	43 39	10, 33, 55, 68	55 (13%)

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	152	VAL	8.7
1	B	18	ASN	7.9
1	A	166	GLY	5.5
1	B	81	ILE	3.5
1	C	60	SER	3.2
1	B	65	LYS	3.1
1	C	166	GLY	3.1
1	A	111	GLY	3.0
1	A	125	ASP	2.8
1	B	82	VAL	2.5
1	A	18	ASN	2.5
1	B	60	SER	2.4
1	B	17	LYS	2.4
1	A	81	ILE	2.3
1	C	26	ASP	2.2
1	A	17	LYS	2.1

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

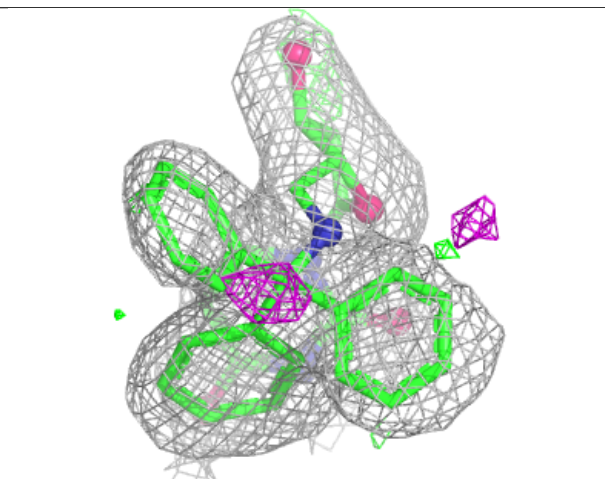
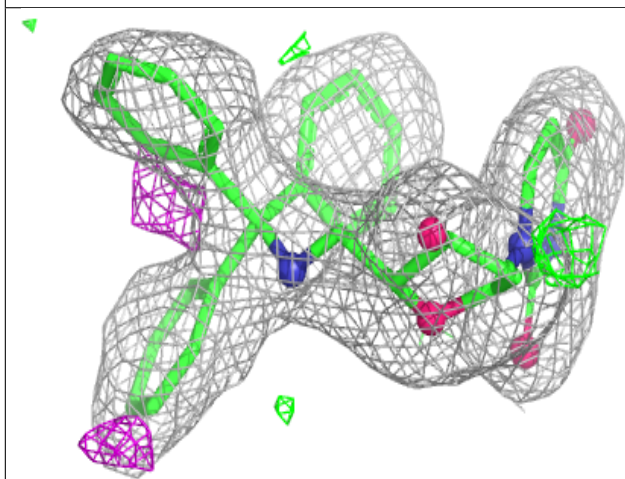
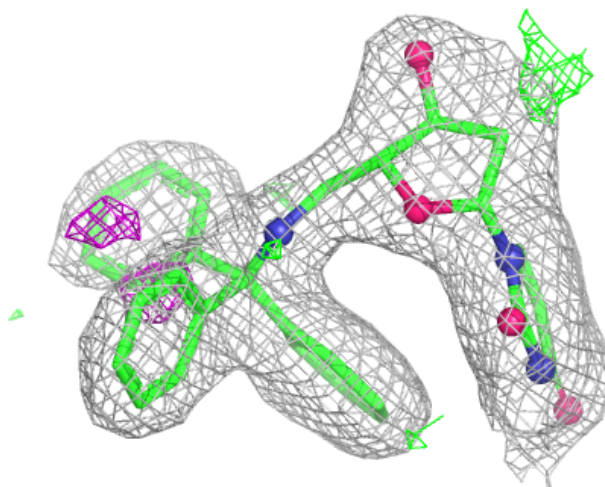
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	GOL	B	183	6/6	0.86	0.20	57,58,60,62	0
2	DUA	A	182	35/35	0.92	0.10	33,39,48,50	0
3	GOL	C	183	6/6	0.92	0.16	44,48,50,54	0
2	DUA	C	182	35/35	0.95	0.07	25,31,36,37	0
3	GOL	A	183	6/6	0.95	0.10	44,46,48,51	0
2	DUA	B	182	35/35	0.96	0.07	25,38,43,46	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.

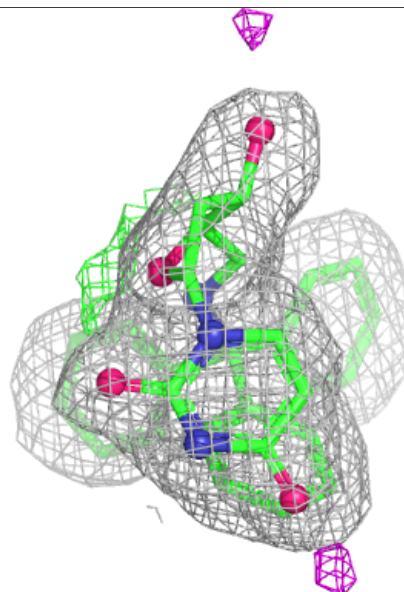
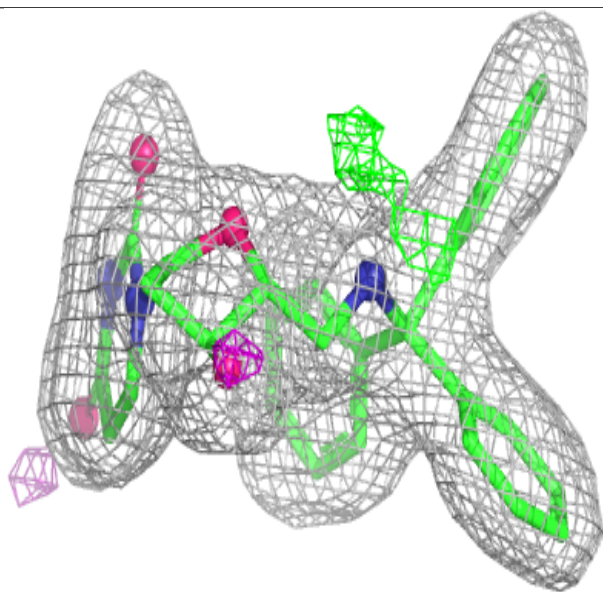
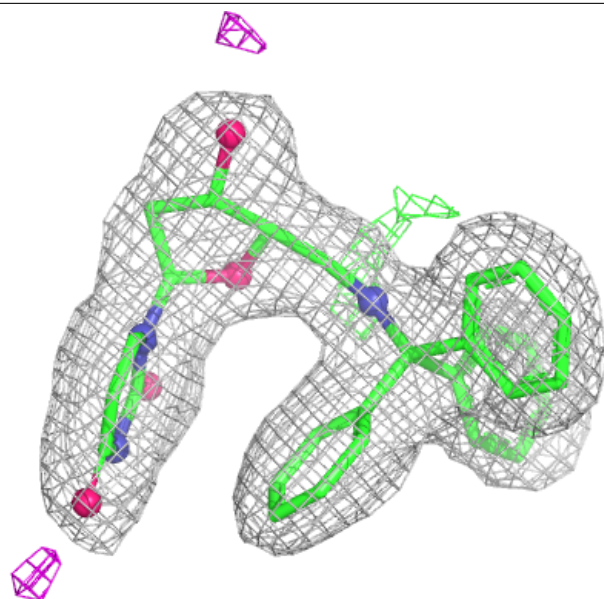
Electron density around DUA A 182:

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



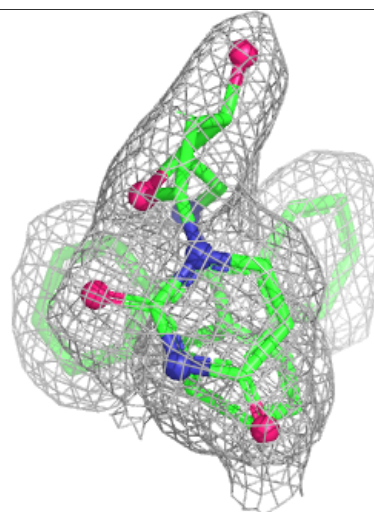
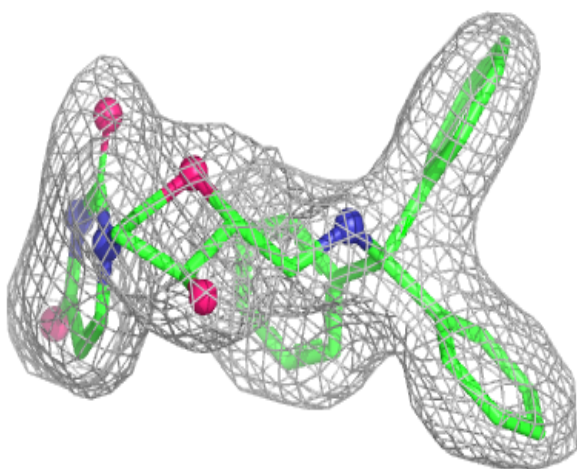
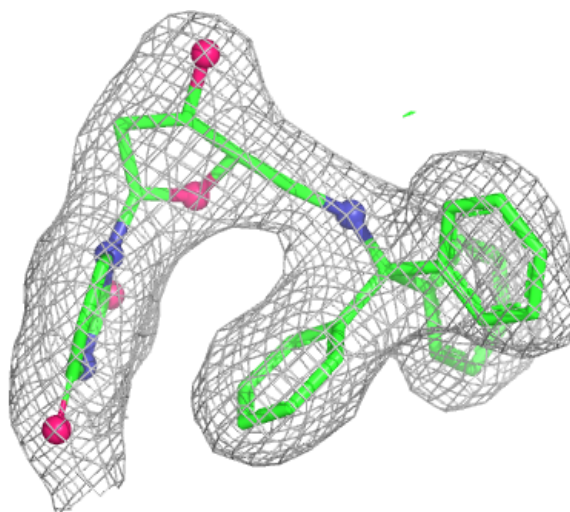
Electron density around DUA C 182:

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



Electron density around DUA B 182:

$2mF_o-DF_c$ (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.