



Full wwPDB X-ray Structure Validation Report ⓘ

May 27, 2020 – 11:34 pm BST

PDB ID : 3PW4
Title : Ternary complex of Aflatoxin B1 Adduct modified DNA (AFB1-N7-Gua) with DNA Polymerase IV and incoming dATP
Authors : Banerjee, S.
Deposited on : 2010-12-07
Resolution : 2.90 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 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	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

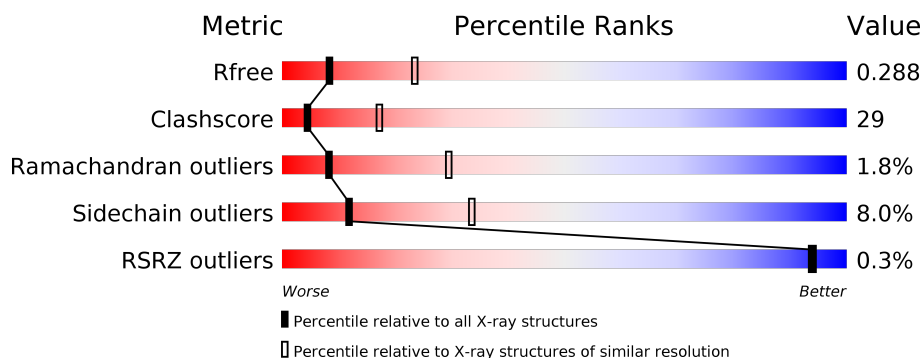
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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 on 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	347	
2	B	15	
3	C	13	

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
4	DTP	A	400	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 3449 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 DNA polymerase IV.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	342	Total	C	N	O	S	0	0	0
			2754	1766	475	506	7			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	HIS	-	expression tag	UNP Q97W02
A	-3	HIS	-	expression tag	UNP Q97W02
A	-2	HIS	-	expression tag	UNP Q97W02
A	-1	HIS	-	expression tag	UNP Q97W02
A	0	HIS	-	expression tag	UNP Q97W02
A	1	HIS	-	expression tag	UNP Q97W02

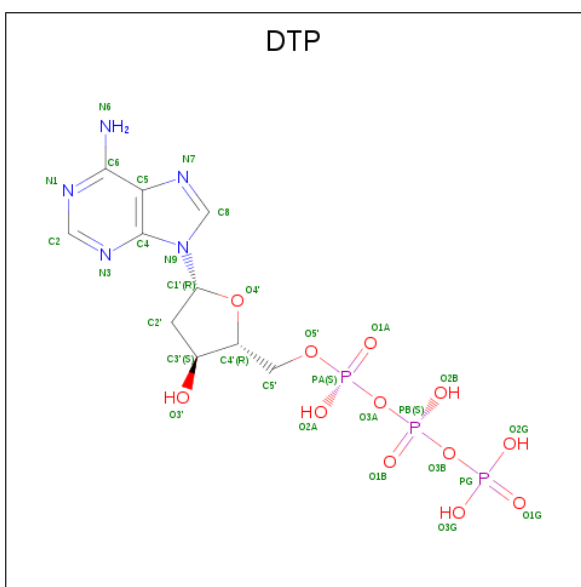
- Molecule 2 is a DNA chain called DNA (5'-D(*TP*TP*GP*AP*AP*TP*CP*CP*TP*TP*CP*CP*CP*CP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	15	Total	C	N	O	P	0	0	0
			294	143	46	91	14			

- Molecule 3 is a DNA chain called DNA (5'-D(*GP*GP*GP*GP*GP*AP*AP*GP*GP*AP*TP*TP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	13	Total	C	N	O	P	0	0	0
			273	129	57	75	12			

- Molecule 4 is 2'-DEOXYADENOSINE 5'-TRIPHOSPHATE (three-letter code: DTP) (formula: C₁₀H₁₆N₅O₁₂P₃).

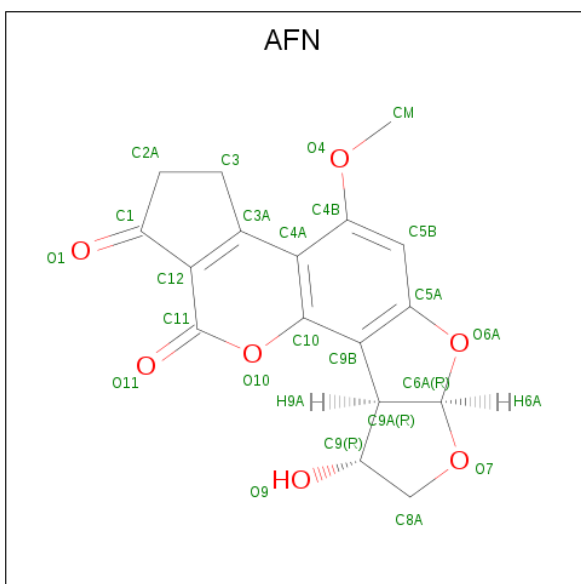


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			30	10	5	12	3		

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	3	Total	Ca	0	0
			3	3		

- Molecule 6 is 8,9-DIHYDRO-9-HYDROXY-AFLATOXIN B1 (three-letter code: AFN) (formula: C₁₇H₁₄O₇).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			24	17	7		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	50	Total	O	0	0
			50	50		
7	B	14	Total	O	0	0
			14	14		
7	C	7	Total	O	0	0
			7	7		

- Molecule 1: DNA polymerase IV

R329	R248	E171	M77	HIS
R330	R249	K172	R78	HIS
I331	V250	K173	K79	HIS
R332	T251	R174	E80	HIS
R333	V252	L175	V81	HIS
I334		I176		H1
G335	N255		R88	M2
V336	S256	L179	I89	I3
R337	R257	D180	M90	V4
	N258	I181		L5
			Y86	F6
K340	E261	I187	S97	I7
F341	I262	G188	E98	D8
I342	R263	N189	K99	F9
	T264	I190	I100	D10
	V265	T191	E101	Y11
			I102	F12
	I270	K194		Y13
	E271	L195	I105	I14
	E272	K196		Q15
	S273	R197	Y109	V16
	V274	K198	L110	E17
		G199	D111	
	I277	I200	I112	K25
	D278	N201	S113	G26
		K202	K27	K27
	R283	L203	K115	P28
A284	A284	V204	V116	V29
		D205	R117	
	V288		D118	C32
A289	A289	T209	Y119	V33
V290	V290	E210	R120	F34
		F211	E121	S35
	D293			G36
L294	L294	L214	L125	R37
D295	D295	K215		F38
I296	I296	G216	I129	E39
		T217	K130	D40
R299	R299	I218	N131	
			K132	A47
F303	F303	A221		I48
F304	F304	K222	K136	Y49
H305	H305	A223	E137	E50
			K138	A51
S308	S308	I227	I139	R52
K309	K309		T140	R52
F310	F310	R231	V141	K53
T311	T311	D232	T142	
A312	A312	E233	V143	V56
		Y234		
	E315		K149	T60
			V150	P61
L319	L319	I238	V150	I62
		R239		V63
		T240	P161	E64
I323	I323		M162	A65
L324	L324	R243	G163	K66
E325	E325	K244	I164	K67
E326	E326	S245		
R327	R327	I246	I167	L75
		C247		D76

T372	T373	G374	A375	A376	T377	C378	C379	T380	T381	C386
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G347	G354	T357
	G355	T358
	A356	C359

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	92.99 Å 102.58 Å 52.68 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.67 – 2.90 29.67 – 2.80	Depositor EDS
% Data completeness (in resolution range)	96.6 (29.67-2.90) 93.8 (29.67-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.61 (at 2.80 Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.232 , 0.294 0.223 , 0.288	Depositor DCC
R_{free} test set	1188 reflections (9.40%)	wwPDB-VP
Wilson B-factor (Å ²)	70.4	Xtriage
Anisotropy	0.253	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 40.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3449	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.33% 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: AFN, DTP, CA

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	0.40	0/2794	0.65	0/3751
2	B	1.20	3/326 (0.9%)	1.55	12/499 (2.4%)
3	C	0.70	0/308	0.86	0/476
All	All	0.56	3/3428 (0.1%)	0.82	12/4726 (0.3%)

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
2	B	1	0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	374	DG	N7-C5	10.58	1.45	1.39
2	B	374	DG	N9-C8	-6.73	1.33	1.37
2	B	374	DG	C5-C6	5.67	1.48	1.42

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	373	DT	O3'-P-O5'	-13.34	78.65	104.00
2	B	374	DG	C6-C5-N7	9.45	136.07	130.40
2	B	374	DG	N7-C8-N9	8.08	117.14	113.10
2	B	374	DG	C2-N3-C4	7.25	115.52	111.90
2	B	374	DG	C5-C6-N1	6.54	114.77	111.50
2	B	374	DG	C4-C5-N7	-6.38	108.25	110.80
2	B	374	DG	N1-C6-O6	-6.15	116.21	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	B	374	DG	C5-N7-C8	-6.09	101.25	104.30
2	B	374	DG	O4'-C4'-C3'	-5.97	102.11	104.50
2	B	374	DG	N9-C4-C5	5.64	107.66	105.40
2	B	374	DG	C4-C5-C6	-5.25	115.65	118.80
2	B	374	DG	N1-C2-N2	5.11	120.80	116.20

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	374	DG	C4'

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	2754	0	2896	160	0
2	B	294	0	172	25	0
3	C	273	0	147	5	0
4	A	30	0	11	9	0
5	A	3	0	0	0	0
6	B	24	0	13	3	0
7	A	50	0	0	11	4
7	B	14	0	0	5	0
7	C	7	0	0	1	0
All	All	3449	0	3239	189	4

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 29.

All (189) 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:374:DG:H2''	2:B:375:DA:H5'	1.34	1.10
1:A:115:LYS:H	1:A:115:LYS:HD2	1.15	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:290:VAL:HB	1:A:333:ARG:HB2	1.38	1.03
1:A:258:ASN:HD22	1:A:261:GLU:HB2	1.24	1.00
1:A:138:LYS:HE2	7:A:2050:HOH:O	1.64	0.97
1:A:233:GLU:HG2	7:A:2051:HOH:O	1.63	0.96
2:B:376:DA:H2	7:B:2063:HOH:O	1.48	0.95
1:A:98:GLU:H	1:A:98:GLU:CD	1.68	0.92
2:B:376:DA:C2	7:B:2063:HOH:O	2.21	0.91
1:A:115:LYS:N	1:A:115:LYS:HD2	1.87	0.86
4:A:400:DTP:H8	4:A:400:DTP:H5'1	1.60	0.83
7:A:2016:HOH:O	2:B:372:DT:H5''	1.77	0.83
2:B:376:DA:N7	7:B:2037:HOH:O	2.13	0.82
1:A:96:TYR:HD2	1:A:125:LEU:HD11	1.46	0.79
1:A:289:ALA:HB1	1:A:331:ILE:HD12	1.63	0.78
2:B:374:DG:C2'	2:B:375:DA:H5'	2.14	0.76
1:A:130:LYS:HZ1	1:A:162:ASN:HD22	1.35	0.75
1:A:15:GLN:OE1	1:A:140:THR:HG22	1.87	0.75
1:A:80:GLU:CD	1:A:80:GLU:H	1.88	0.75
1:A:88:ARG:HD2	1:A:137:GLU:OE2	1.85	0.75
1:A:149:LYS:HE3	7:A:2026:HOH:O	1.85	0.74
1:A:258:ASN:ND2	1:A:261:GLU:HB2	2.03	0.74
1:A:37:ARG:HG2	1:A:37:ARG:HH11	1.51	0.74
2:B:380:DT:H2''	2:B:381:DT:OP2	1.88	0.74
2:B:376:DA:H2''	2:B:377:DT:OP2	1.89	0.73
1:A:243:ARG:HD3	1:A:246:ILE:HD11	1.70	0.72
4:A:400:DTP:PB	7:A:2067:HOH:O	2.48	0.71
1:A:227:ILE:O	1:A:231:ARG:HG2	1.91	0.69
1:A:115:LYS:H	1:A:115:LYS:CD	1.99	0.69
1:A:257:ARG:HB2	7:A:2027:HOH:O	1.92	0.69
1:A:211:PHE:CE2	1:A:215:LYS:HE3	2.28	0.68
1:A:96:TYR:CD2	1:A:125:LEU:HD11	2.29	0.67
1:A:257:ARG:HH21	1:A:328:GLU:HA	1.61	0.66
1:A:211:PHE:HE2	1:A:215:LYS:HE3	1.60	0.66
1:A:200:ILE:HD12	1:A:200:ILE:N	2.10	0.66
1:A:209:ILE:O	1:A:209:ILE:HD12	1.97	0.65
1:A:296:ILE:N	1:A:296:ILE:HD12	2.12	0.65
1:A:52:ARG:NH1	4:A:400:DTP:O3G	2.31	0.64
1:A:174:ARG:HH11	1:A:174:ARG:HG2	1.64	0.63
6:B:387:AFN:H32	7:C:2069:HOH:O	1.98	0.63
1:A:337:ARG:HH22	2:B:375:DA:H2''	1.63	0.63
1:A:249:ILE:HD11	1:A:288:VAL:HG21	1.79	0.63
1:A:130:LYS:NZ	1:A:162:ASN:ND2	2.47	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:37:ARG:HG2	1:A:37:ARG:NH1	2.13	0.62
1:A:12:PHE:O	1:A:16:VAL:HG23	1.99	0.62
1:A:200:ILE:H	1:A:200:ILE:HD12	1.64	0.62
1:A:187:ILE:HG23	1:A:191:THR:HG22	1.79	0.62
1:A:130:LYS:HZ1	1:A:162:ASN:ND2	1.97	0.62
1:A:61:PRO:HG2	1:A:64:GLU:HG2	1.81	0.62
2:B:375:DA:H61	3:C:358:DT:H3	1.48	0.61
2:B:379:DC:H3'	7:B:2015:HOH:O	2.01	0.61
1:A:337:ARG:NH2	2:B:375:DA:H2''	2.16	0.60
1:A:162:ASN:C	1:A:162:ASN:HD22	2.03	0.60
3:C:358:DT:H2''	3:C:359:DC:C6	2.37	0.59
1:A:249:ILE:HG22	1:A:250:VAL:N	2.16	0.58
1:A:130:LYS:NZ	1:A:162:ASN:HD22	2.02	0.58
1:A:130:LYS:HE3	1:A:141:VAL:O	2.03	0.57
1:A:27:LYS:HG2	1:A:28:PRO:HD2	1.86	0.57
1:A:194:LYS:HD3	1:A:217:MET:HE2	1.86	0.57
1:A:61:PRO:HB3	2:B:372:DT:H5'	1.86	0.57
1:A:39:GLU:O	1:A:40:ASP:HB2	2.03	0.57
1:A:248:ARG:NH1	1:A:249:ILE:O	2.37	0.57
1:A:174:ARG:NH1	1:A:174:ARG:HG2	2.19	0.56
1:A:337:ARG:HH22	2:B:375:DA:C2'	2.18	0.56
1:A:197:LYS:O	1:A:197:LYS:HD3	2.06	0.56
1:A:98:GLU:CD	1:A:98:GLU:N	2.46	0.56
1:A:138:LYS:CE	7:A:2062:HOH:O	2.53	0.55
1:A:175:LEU:O	1:A:179:LEU:HB3	2.07	0.55
1:A:198:LEU:HB3	1:A:200:ILE:HD13	1.88	0.55
1:A:337:ARG:NH2	2:B:375:DA:C2'	2.69	0.55
4:A:400:DTP:O1B	7:A:2067:HOH:O	2.18	0.55
1:A:290:VAL:CB	1:A:333:ARG:HB2	2.23	0.54
1:A:109:TYR:C	1:A:110:LEU:HD12	2.28	0.54
1:A:9:PHE:CD1	1:A:9:PHE:N	2.74	0.54
1:A:28:PRO:HB2	1:A:51:ALA:HB2	1.90	0.54
1:A:221:ALA:HB3	2:B:379:DC:OP1	2.08	0.53
4:A:400:DTP:C8	4:A:400:DTP:H5'1	2.35	0.53
1:A:63:VAL:O	1:A:67:LYS:HG3	2.08	0.53
1:A:29:VAL:HG23	1:A:48:ASN:ND2	2.24	0.53
1:A:303:PHE:HZ	1:A:315:GLU:HG2	1.73	0.53
1:A:270:ILE:HG12	1:A:336:VAL:HG11	1.91	0.53
1:A:111:ASP:OD1	1:A:113:SER:HB2	2.09	0.52
1:A:167:ILE:HG23	1:A:171:GLU:HB3	1.90	0.52
1:A:194:LYS:HD3	1:A:217:MET:CE	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:379:DC:H2"	2:B:380:DT:OP2	2.09	0.52
1:A:245:SER:O	1:A:246:ILE:HD13	2.10	0.52
1:A:101:GLU:O	1:A:102:ILE:HB	2.10	0.51
6:B:387:AFN:HM3	7:B:2071:HOH:O	2.11	0.51
1:A:190:ILE:HB	3:C:358:DT:OP2	2.10	0.51
1:A:102:ILE:HG22	1:A:102:ILE:O	2.08	0.51
1:A:249:ILE:CG2	1:A:250:VAL:N	2.74	0.51
1:A:319:LEU:O	1:A:323:ILE:HG13	2.10	0.51
1:A:209:ILE:HD11	1:A:214:LEU:HG	1.94	0.50
1:A:222:LYS:HB3	1:A:222:LYS:HZ2	1.76	0.50
1:A:172:VAL:O	1:A:176:ILE:HG12	2.11	0.50
1:A:181:ILE:HD13	1:A:195:LEU:HD13	1.93	0.50
1:A:138:LYS:HE2	7:A:2062:HOH:O	2.11	0.50
1:A:171:GLU:OE1	1:A:171:GLU:HA	2.10	0.49
1:A:222:LYS:HB3	1:A:222:LYS:NZ	2.27	0.49
1:A:246:ILE:HG22	1:A:247:GLY:N	2.28	0.49
1:A:50:GLU:HA	1:A:53:LYS:HE2	1.94	0.49
1:A:125:LEU:O	1:A:129:ILE:HG13	2.12	0.48
1:A:299:ARG:NE	1:A:326:GLU:OE1	2.45	0.48
1:A:100:ILE:HG12	1:A:101:GLU:N	2.28	0.48
1:A:303:PHE:CZ	1:A:315:GLU:HG2	2.49	0.48
1:A:11:TYR:HD1	1:A:14:ALA:HB3	1.79	0.48
1:A:293:ASP:OD2	1:A:329:ARG:CD	2.62	0.48
1:A:17:GLU:OE2	1:A:78:ARG:HD3	2.13	0.47
1:A:37:ARG:NH2	1:A:255:ASN:OD1	2.36	0.47
1:A:332:ARG:NH2	2:B:373:DT:OP1	2.47	0.47
1:A:9:PHE:HA	1:A:141:VAL:HG12	1.95	0.47
1:A:231:ARG:HB2	1:A:231:ARG:HH11	1.80	0.47
1:A:111:ASP:C	1:A:113:SER:H	2.17	0.47
1:A:187:ILE:HG23	1:A:191:THR:CG2	2.45	0.47
1:A:162:ASN:O	1:A:162:ASN:ND2	2.48	0.46
1:A:10:ASP:O	1:A:11:TYR:C	2.54	0.46
1:A:140:THR:OG1	1:A:162:ASN:HB2	2.16	0.46
1:A:56:VAL:HA	1:A:60:ILE:HD11	1.97	0.46
1:A:138:LYS:HE3	7:A:2062:HOH:O	2.13	0.46
1:A:37:ARG:NH1	1:A:332:ARG:NH2	2.64	0.46
1:A:283:LYS:HG2	1:A:305:HIS:O	2.15	0.46
1:A:47:ALA:O	1:A:52:ARG:NH2	2.38	0.46
3:C:355:DG:H2"	3:C:356:DA:OP2	2.16	0.46
1:A:217:MET:O	1:A:217:MET:HE2	2.16	0.46
1:A:209:ILE:HD12	1:A:209:ILE:C	2.36	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:252:MET:CE	1:A:331:ILE:HG22	2.47	0.45
1:A:52:ARG:CZ	4:A:400:DTP:O3G	2.65	0.45
1:A:248:ARG:NE	1:A:272:GLU:OE1	2.48	0.45
1:A:296:ILE:CD1	1:A:296:ILE:N	2.79	0.45
1:A:257:ARG:HH21	1:A:328:GLU:CA	2.27	0.45
1:A:25:LYS:HB2	1:A:25:LYS:NZ	2.32	0.45
1:A:201:ASN:O	1:A:202:LYS:HD3	2.17	0.45
1:A:238:ILE:HD12	1:A:238:ILE:N	2.31	0.45
1:A:263:LYS:N	1:A:264:PRO:HD2	2.31	0.45
1:A:252:MET:HA	1:A:265:TYR:CE1	2.52	0.45
1:A:288:VAL:O	1:A:334:ILE:HD12	2.16	0.45
3:C:354:DG:H2''	3:C:355:DG:OP2	2.17	0.45
2:B:379:DC:H1'	2:B:380:DT:H5'	1.99	0.44
4:A:400:DTP:O2B	4:A:400:DTP:O2G	2.36	0.44
1:A:270:ILE:HA	1:A:336:VAL:HG21	1.98	0.44
1:A:117:ARG:HG2	1:A:121:GLU:OE1	2.17	0.44
1:A:143:VAL:HB	1:A:164:ILE:HD13	1.99	0.44
1:A:204:VAL:HG13	1:A:205:ASP:N	2.33	0.43
1:A:56:VAL:HA	1:A:60:ILE:CD1	2.48	0.43
1:A:293:ASP:OD2	1:A:329:ARG:HD3	2.19	0.43
1:A:175:LEU:HD22	1:A:179:LEU:HB2	2.01	0.43
1:A:284:ALA:HB2	1:A:340:LYS:HD2	1.99	0.43
1:A:162:ASN:C	1:A:162:ASN:ND2	2.71	0.43
4:A:400:DTP:O3B	7:A:2067:HOH:O	2.22	0.43
1:A:118:ASP:OD2	1:A:120:ARG:HB2	2.19	0.43
1:A:35:SER:O	1:A:37:ARG:N	2.52	0.43
1:A:257:ARG:HG2	1:A:324:LEU:HD22	2.00	0.42
2:B:375:DA:C4	2:B:376:DA:C8	3.07	0.42
1:A:130:LYS:HB3	1:A:130:LYS:HE2	1.82	0.42
1:A:248:ARG:HD3	2:B:375:DA:OP1	2.19	0.42
4:A:400:DTP:N3	6:B:387:AFN:HM2	2.34	0.42
2:B:376:DA:N3	2:B:377:DT:O4'	2.52	0.42
1:A:150:VAL:HG23	1:A:234:TYR:CE2	2.54	0.42
1:A:198:LEU:HB3	1:A:200:ILE:CD1	2.48	0.42
1:A:293:ASP:OD2	1:A:329:ARG:HD2	2.19	0.42
2:B:377:DT:H2''	2:B:378:DC:OP2	2.18	0.42
1:A:223:ALA:O	1:A:227:ILE:HG13	2.20	0.42
1:A:75:LEU:HA	1:A:76:PRO:HD3	1.92	0.42
1:A:6:PHE:CE2	1:A:8:ASP:HB2	2.54	0.42
1:A:11:TYR:CD1	1:A:11:TYR:O	2.73	0.42
1:A:80:GLU:CD	1:A:80:GLU:N	2.65	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:195:LEU:HD21	1:A:218:ILE:HD13	2.01	0.42
1:A:333:ARG:HH11	1:A:333:ARG:HG2	1.85	0.42
1:A:188:GLY:O	1:A:190:ILE:N	2.53	0.42
1:A:309:LYS:O	1:A:312:ALA:HB3	2.19	0.41
1:A:101:GLU:HB2	1:A:238:ILE:HG23	2.02	0.41
1:A:200:ILE:HA	1:A:205:ASP:HB2	2.03	0.41
1:A:40:ASP:OD2	1:A:66:LYS:HD2	2.20	0.41
1:A:238:ILE:O	1:A:238:ILE:HG22	2.19	0.41
1:A:116:VAL:HG13	1:A:121:GLU:HB2	2.02	0.41
1:A:258:ASN:ND2	1:A:261:GLU:N	2.67	0.41
1:A:295:ASP:HB3	1:A:329:ARG:NH1	2.35	0.41
1:A:274:TYR:O	1:A:277:LEU:HB2	2.21	0.41
1:A:105:ILE:HG12	1:A:105:ILE:O	2.20	0.41
1:A:132:LYS:HE3	1:A:136:LYS:NZ	2.36	0.41
1:A:161:PRO:O	1:A:162:ASN:C	2.58	0.41
1:A:277:LEU:O	1:A:278:ASP:HB3	2.20	0.41
2:B:378:DC:H2''	2:B:379:DC:O5'	2.20	0.41
1:A:187:ILE:HD13	1:A:222:LYS:HZ1	1.86	0.41
1:A:39:GLU:HA	1:A:39:GLU:OE1	2.19	0.41
1:A:78:ARG:HB3	1:A:81:VAL:HG23	2.03	0.41
2:B:372:DT:H2''	2:B:373:DT:OP2	2.19	0.41
1:A:252:MET:HG2	1:A:265:TYR:CG	2.56	0.41
1:A:214:LEU:HD23	1:A:214:LEU:HA	1.86	0.40

All (4) 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)
7:A:2047:HOH:O	7:A:2047:HOH:O[2_525]	1.99	0.21
7:A:2046:HOH:O	7:A:2046:HOH:O[2_525]	2.11	0.09
7:A:2051:HOH:O	7:A:2059:HOH:O[4_528]	2.16	0.04
7:A:2053:HOH:O	7:A:2060:HOH:O[4_528]	2.18	0.02

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	340/347 (98%)	302 (89%)	32 (9%)	6 (2%)	8	29

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	11	TYR
1	A	36	GLY
1	A	189	ASN
1	A	205	ASP
1	A	115	LYS
1	A	102	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	301/306 (98%)	277 (92%)	24 (8%)	12	33

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	HIS
1	A	5	LEU
1	A	9	PHE
1	A	25	LYS
1	A	27	LYS
1	A	32	CYS
1	A	33	VAL
1	A	37	ARG
1	A	40	ASP
1	A	50	GLU
1	A	80	GLU
1	A	90	MET
1	A	98	GLU

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Mol	Chain	Res	Type
1	A	132	LYS
1	A	162	ASN
1	A	197	LYS
1	A	198	LEU
1	A	222	LYS
1	A	231	ARG
1	A	233	GLU
1	A	240	THR
1	A	243	ARG
1	A	308	SER
1	A	311	THR

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

Mol	Chain	Res	Type
1	A	1	HIS
1	A	84	GLN
1	A	162	ASN
1	A	258	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 3 are monoatomic - leaving 2 for Mogul analysis.

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
6	AFN	B	387	2	24,28,28	2.38	9 (37%)	32,44,44	2.53	11 (34%)
4	DTP	A	400	5	26,32,32	2.76	5 (19%)	30,50,50	2.45	10 (33%)

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
6	AFN	B	387	2	-	0/2/32/32	0/5/5/5
4	DTP	A	400	5	-	7/18/34/34	0/3/3/3

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	400	DTP	O3'-C3'	-10.41	1.21	1.43
4	A	400	DTP	O5'-C5'	-7.04	1.17	1.44
6	B	387	AFN	C8A-C9	6.41	1.62	1.51
6	B	387	AFN	O7-C6A	3.77	1.49	1.41
6	B	387	AFN	C4B-C4A	3.72	1.50	1.42
6	B	387	AFN	O10-C10	3.14	1.41	1.36
4	A	400	DTP	C8-N7	-3.13	1.29	1.34
6	B	387	AFN	O6A-C5A	3.00	1.42	1.37
6	B	387	AFN	C5B-C4B	2.98	1.46	1.37
4	A	400	DTP	C5'-C4'	-2.96	1.42	1.51
6	B	387	AFN	C3-C2A	-2.68	1.50	1.54
6	B	387	AFN	C5B-C5A	2.58	1.43	1.38
6	B	387	AFN	O6A-C6A	2.32	1.48	1.44
4	A	400	DTP	C2'-C1'	2.05	1.58	1.52

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	387	AFN	O1-C1-C2A	-6.56	119.73	125.72
6	B	387	AFN	CM-O4-C4B	6.33	126.61	117.75
4	A	400	DTP	O2A-PA-O5'	5.36	132.65	107.75
4	A	400	DTP	C2'-C1'-N9	-5.20	102.27	114.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	387	AFN	O1-C1-C12	5.14	132.43	127.19
4	A	400	DTP	O4'-C4'-C5'	-4.88	93.31	109.37
4	A	400	DTP	O5'-PA-O1A	-4.88	90.00	109.07
6	B	387	AFN	O7-C8A-C9	-4.79	96.71	105.99
4	A	400	DTP	O5'-C5'-C4'	4.24	123.58	108.99
6	B	387	AFN	C5A-C9B-C10	3.21	123.35	120.05
4	A	400	DTP	O4'-C4'-C3'	3.08	112.86	105.67
6	B	387	AFN	C3-C3A-C12	-2.94	108.84	111.38
6	B	387	AFN	C11-O10-C10	2.85	124.58	119.19
4	A	400	DTP	PA-O3A-PB	-2.83	123.11	132.83
6	B	387	AFN	C5B-C5A-C9B	-2.78	120.70	124.07
6	B	387	AFN	O4-C4B-C4A	2.51	119.58	115.89
4	A	400	DTP	O2A-PA-O1A	-2.44	100.18	112.24
6	B	387	AFN	C2A-C3-C3A	2.39	105.83	104.47
4	A	400	DTP	O2G-PG-O3B	2.37	112.59	104.64
6	B	387	AFN	O6A-C5A-C5B	2.37	126.66	123.36
4	A	400	DTP	C4-C5-N7	2.16	111.65	109.40

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	400	DTP	PB-O3B-PG-O2G
4	A	400	DTP	C5'-O5'-PA-O2A
4	A	400	DTP	PB-O3A-PA-O5'
4	A	400	DTP	PG-O3B-PB-O2B
4	A	400	DTP	C5'-O5'-PA-O1A
4	A	400	DTP	O4'-C4'-C5'-O5'
4	A	400	DTP	PB-O3B-PG-O3G

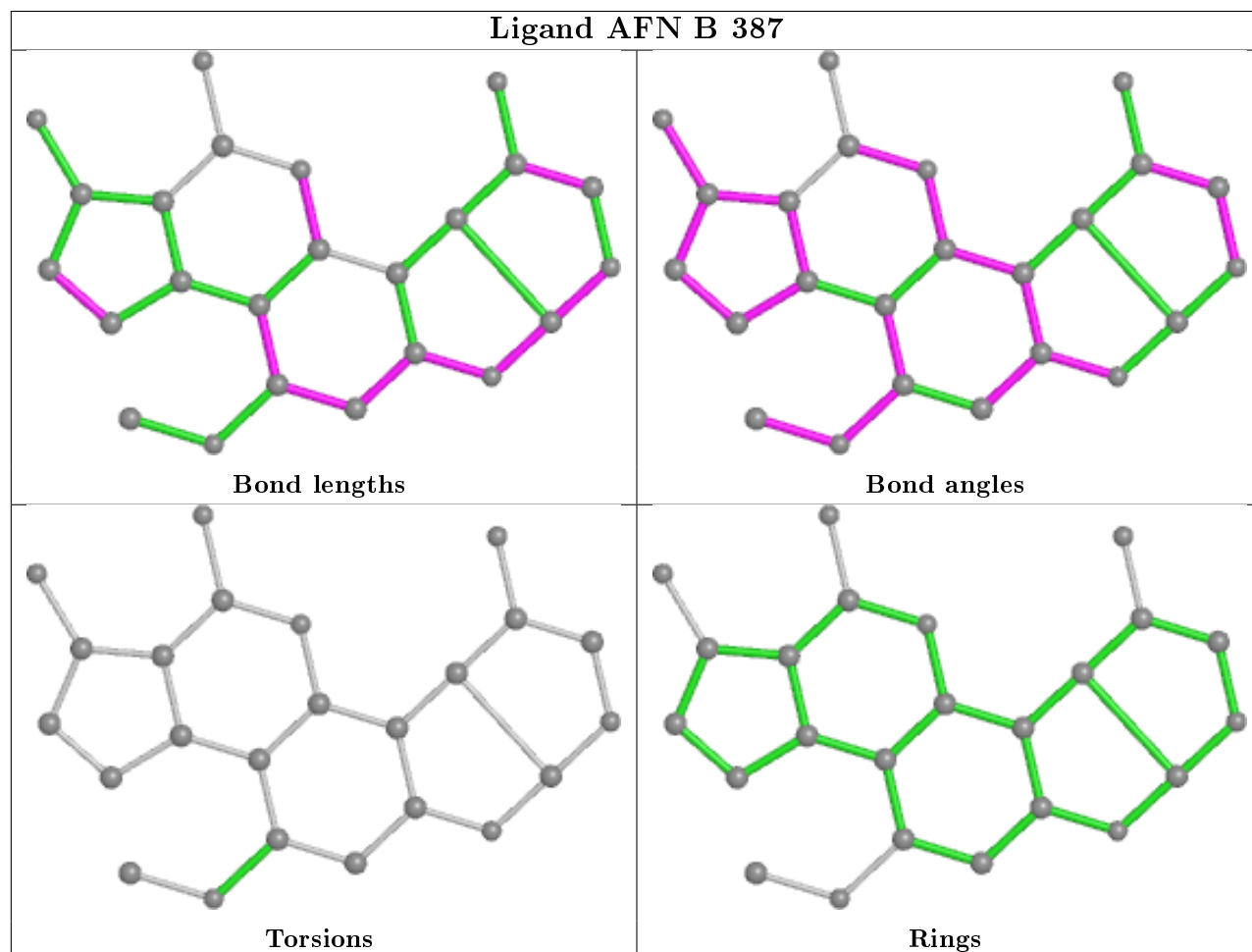
There are no ring outliers.

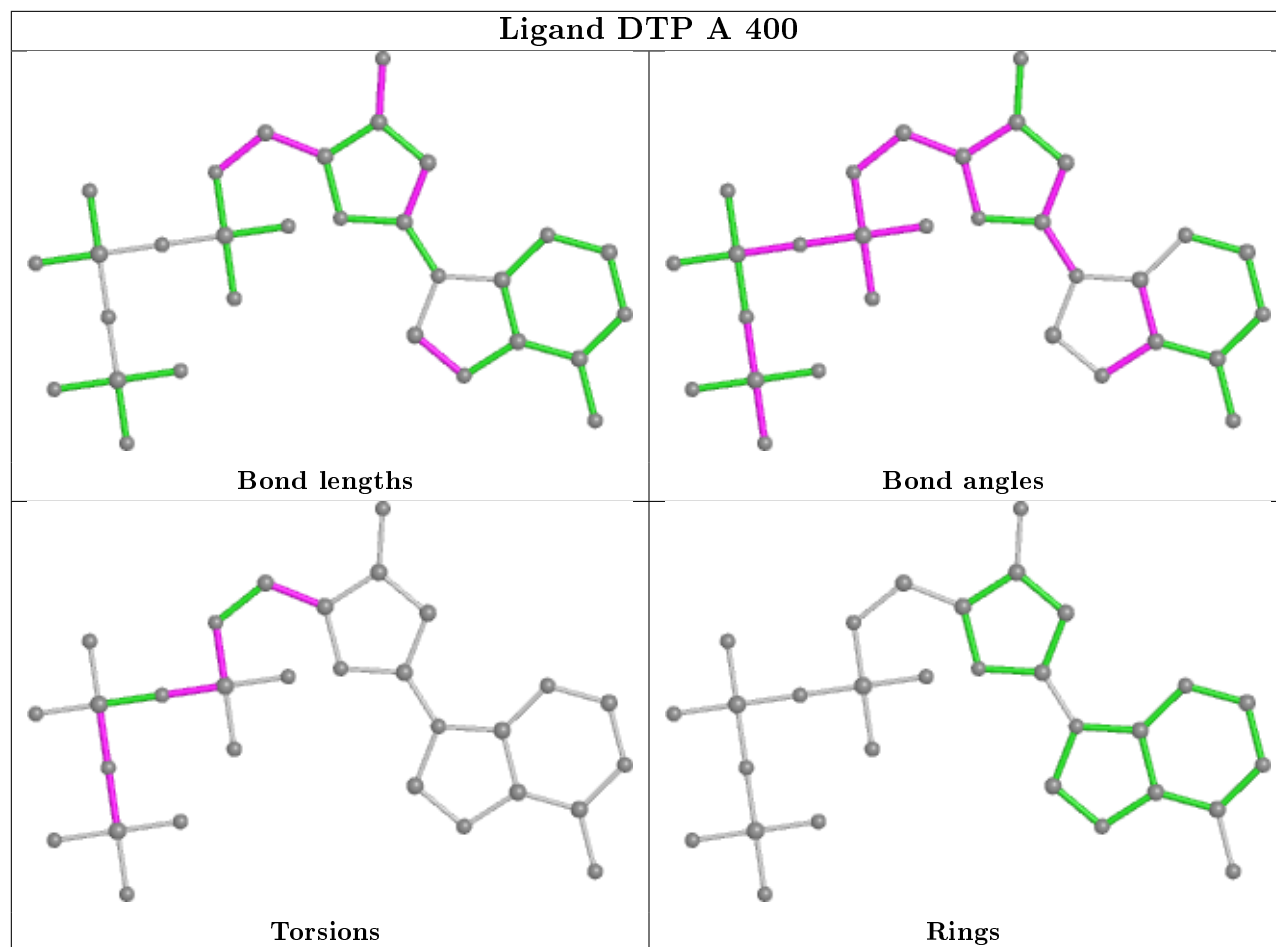
2 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	387	AFN	3	0
4	A	400	DTP	9	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier.

Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	342/347 (98%)	-0.17	1 (0%) 94 94	36, 60, 85, 103	0
2	B	15/15 (100%)	0.10	0 100 100	72, 81, 109, 134	0
3	C	13/13 (100%)	-0.37	0 100 100	56, 68, 88, 99	0
All	All	370/375 (98%)	-0.17	1 (0%) 94 94	36, 63, 87, 134	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	3	ILE	2.5

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 carbohydrates 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(Å ²)	Q<0.9
5	CA	A	1003	1/1	0.70	0.10	75,75,75,75	0
6	AFN	B	387	24/24	0.74	0.30	104,106,109,110	0

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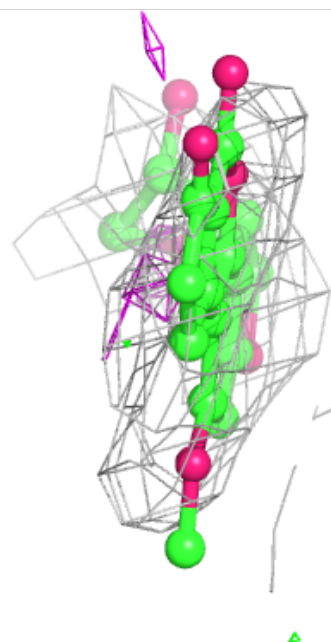
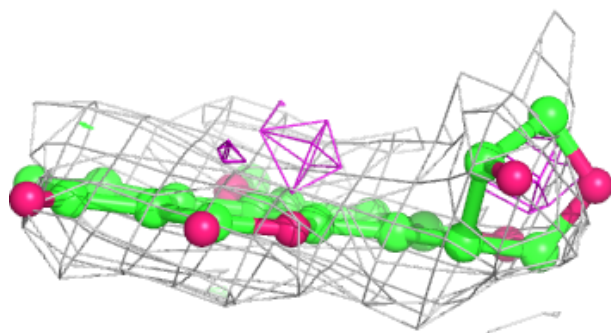
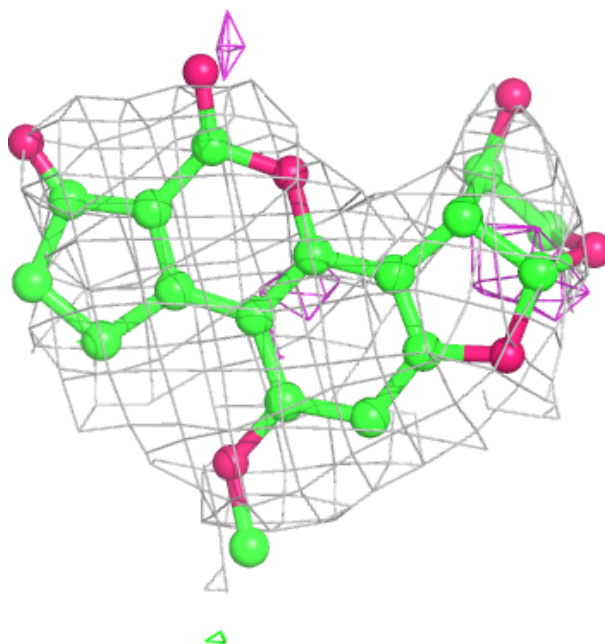
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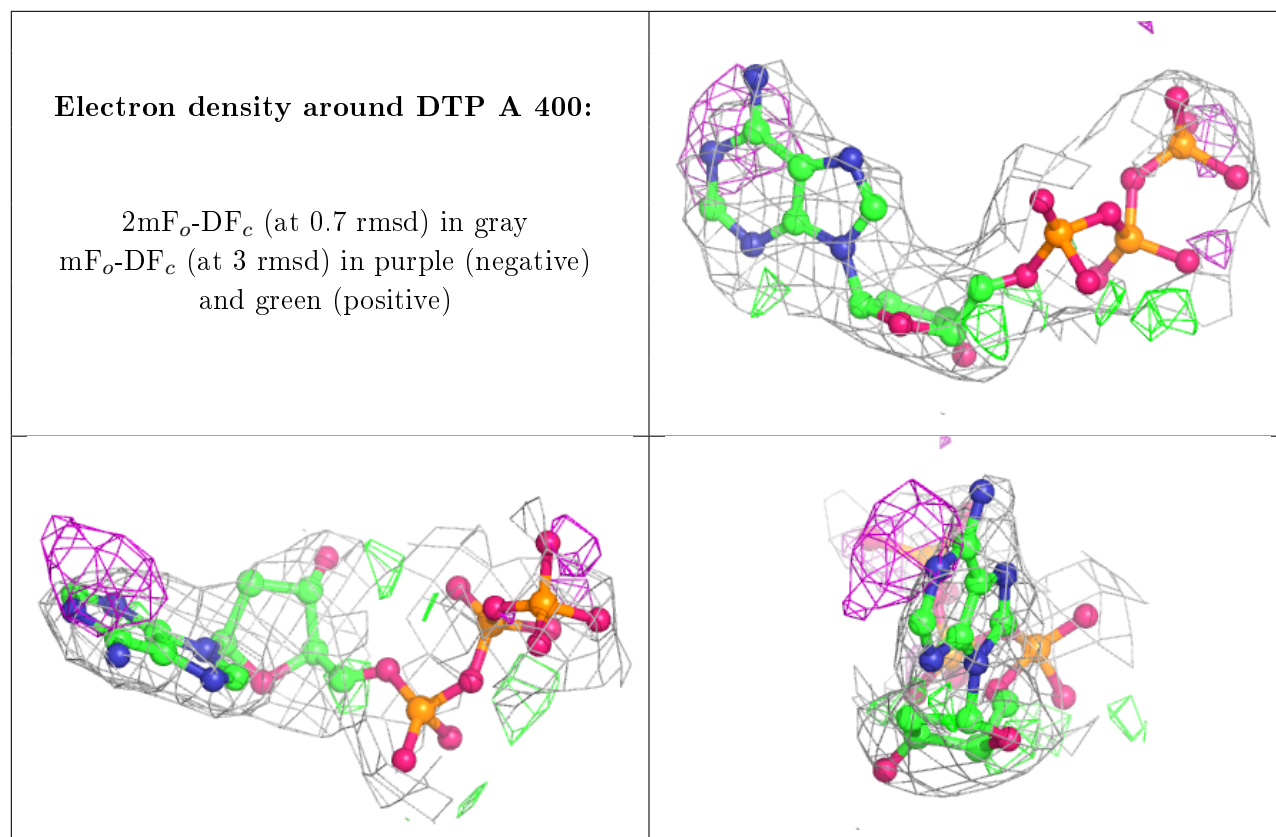
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	CA	A	1002	1/1	0.85	0.24	56,56,56,56	0
4	DTP	A	400	30/30	0.87	0.25	55,66,85,86	0
5	CA	A	1001	1/1	0.88	0.32	75,75,75,75	0

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 AFN B 387:

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.