



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 04:58 AM UTC

PDB ID : 1DTP / pdb_00001dtp
Title : THE STRUCTURE OF THE ISOLATED CATALYTIC DOMAIN OF DIPHTHERIA TOXIN
Authors : Weiss, M.S.; Eisenberg, D.
Deposited on : 1994-09-08
Resolution : 2.50 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 Phenix2.0
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

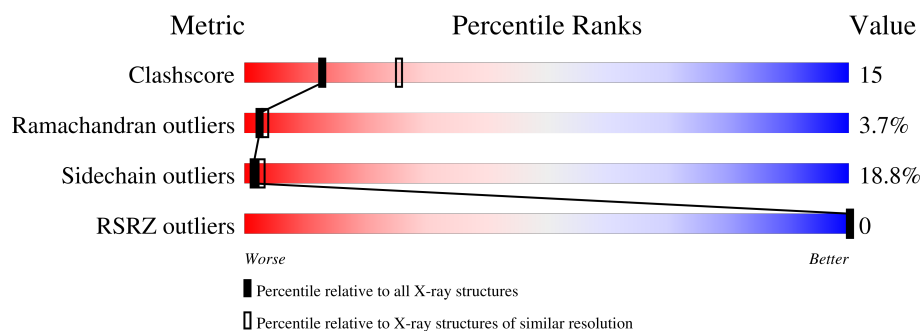
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	190	35% 42% 20% .

2 Entry composition [i](#)

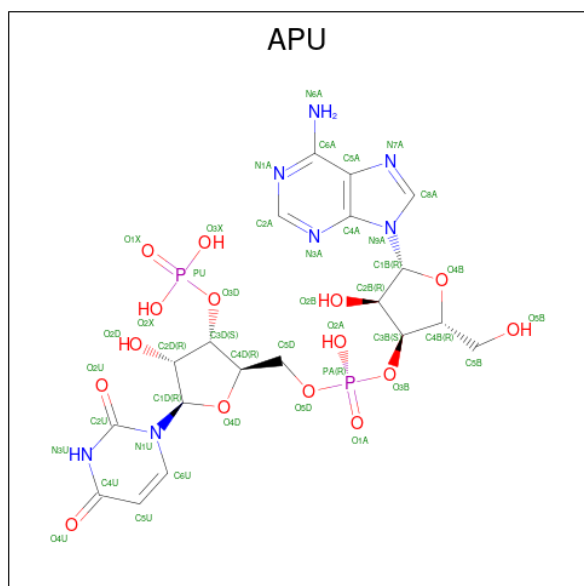
There are 3 unique types of molecules in this entry. The entry contains 1505 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 DIPHTHERIA TOXIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	190	Total	C	N	O	S	0	0	0
			1454	910	240	299	5			

- Molecule 2 is ADENYLYL-3'-5'-PHOSPHO-URIDINE-3'-MONOPHOSPHATE (CCD ID: APU) (formula: $C_{19}H_{25}N_7O_{15}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			43	19	7	15	2		

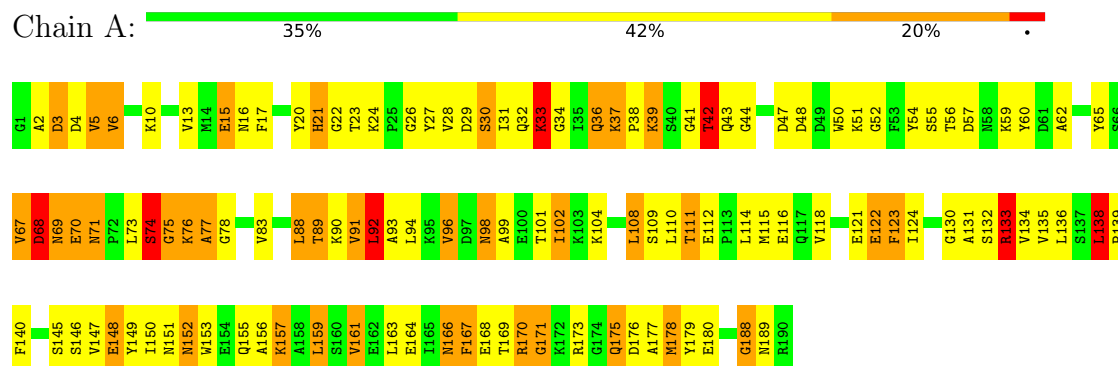
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	8	Total	O	0	0
			8	8		

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: DIPHTHERIA TOXIN



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	55.70Å 43.90Å 73.90Å 90.00° 101.50° 90.00°	Depositor
Resolution (Å)	10.00 – 2.50 10.00 – 2.51	Depositor EDS
% Data completeness (in resolution range)	(Not available) (10.00-2.50) 85.1 (10.00-2.51)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.197 , (Not available) 0.192 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	52.1	Xtriage
Anisotropy	0.137	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.13 , 75.0	EDS
L-test for twinning ¹	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	1505	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 10.03% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Theoretical 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: APU

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	1.45	9/1481 (0.6%)	2.54	118/1997 (5.9%)

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	A	0	1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	21	HIS	CD2-NE2	-6.93	1.30	1.37
1	A	170	ARG	CA-CB	6.86	1.63	1.53
1	A	17	PHE	CA-CB	-6.02	1.44	1.53
1	A	149	TYR	CA-CB	6.00	1.62	1.53
1	A	17	PHE	CA-C	-5.96	1.45	1.52
1	A	21	HIS	C-N	5.70	1.36	1.33
1	A	68	ASP	CA-CB	5.51	1.62	1.53
1	A	6	VAL	CA-CB	-5.40	1.47	1.54
1	A	131	ALA	CA-C	-5.36	1.46	1.52

All (118) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	68	ASP	CA-CB-CG	20.19	132.79	112.60
1	A	99	ALA	N-CA-C	12.00	124.36	111.28
1	A	65	TYR	N-CA-C	-11.48	98.71	113.17
1	A	189	ASN	N-CA-C	-10.56	97.94	112.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	176	ASP	CA-CB-CG	10.28	122.88	112.60
1	A	42	THR	N-CA-C	10.22	122.11	110.97
1	A	176	ASP	N-CA-C	-9.84	95.79	111.04
1	A	36	GLN	O-C-N	-9.29	114.27	123.46
1	A	152	ASN	CB-CG-ND2	9.19	130.18	116.40
1	A	92	LEU	N-CA-C	-9.03	93.80	108.52
1	A	33	LYS	N-CA-C	-8.52	102.08	111.36
1	A	152	ASN	CA-C-O	-8.38	112.65	121.87
1	A	138	LEU	O-C-N	-8.33	116.38	121.71
1	A	13	VAL	CG1-CB-CG2	-8.22	92.72	110.80
1	A	152	ASN	OD1-CG-ND2	-8.03	114.57	122.60
1	A	13	VAL	N-CA-C	-8.02	96.50	108.85
1	A	52	GLY	O-C-N	-7.72	114.75	123.62
1	A	48	ASP	CA-CB-CG	7.68	120.28	112.60
1	A	21	HIS	CA-C-N	7.65	129.10	122.29
1	A	21	HIS	C-N-CA	7.65	129.10	122.29
1	A	32	GLN	OE1-CD-NE2	-7.61	114.99	122.60
1	A	159	LEU	CD1-CG-CD2	-7.39	94.55	110.80
1	A	69	ASN	OD1-CG-ND2	-7.35	115.25	122.60
1	A	17	PHE	O-C-N	7.35	132.06	123.02
1	A	56	THR	O-C-N	-7.30	114.70	123.10
1	A	91	VAL	N-CA-C	-7.24	94.28	109.34
1	A	108	LEU	N-CA-C	-7.12	98.60	109.85
1	A	140	PHE	N-CA-C	7.00	118.70	111.14
1	A	13	VAL	CA-CB-CG1	7.00	122.30	110.40
1	A	102	ILE	N-CA-C	-6.89	103.95	110.42
1	A	57	ASP	CA-CB-CG	6.87	119.47	112.60
1	A	157	LYS	O-C-N	6.85	129.12	122.07
1	A	130	GLY	N-CA-C	-6.84	104.80	115.67
1	A	33	LYS	CA-C-O	-6.76	113.25	120.42
1	A	3	ASP	N-CA-C	6.75	121.12	112.34
1	A	37	LYS	N-CA-C	6.70	120.03	110.24
1	A	159	LEU	N-CA-C	-6.68	99.78	110.14
1	A	2	ALA	CA-C-O	6.60	127.56	119.97
1	A	92	LEU	CD1-CG-CD2	-6.49	96.52	110.80
1	A	71	ASN	N-CA-C	6.46	124.10	109.81
1	A	29	ASP	N-CA-CB	-6.44	100.31	110.22
1	A	10	LYS	CA-CB-CG	6.43	126.95	114.10
1	A	109	SER	CA-C-O	6.39	128.21	120.92
1	A	114	LEU	O-C-N	-6.35	115.39	122.12
1	A	161	VAL	CA-C-O	-6.35	113.96	120.25
1	A	149	TYR	O-C-N	-6.30	115.96	123.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	133	ARG	CA-C-N	6.29	131.75	123.06
1	A	133	ARG	C-N-CA	6.29	131.75	123.06
1	A	30	SER	CA-CB-OG	6.29	123.67	111.10
1	A	67	VAL	N-CA-CB	-6.21	104.58	112.60
1	A	130	GLY	CA-C-N	-6.17	112.94	122.87
1	A	130	GLY	C-N-CA	-6.17	112.94	122.87
1	A	98	ASN	CA-C-O	6.17	127.20	119.98
1	A	155	GLN	OE1-CD-NE2	-6.13	116.47	122.60
1	A	65	TYR	CA-C-O	-6.10	112.22	119.35
1	A	132	SER	N-CA-C	-6.09	104.64	111.28
1	A	140	PHE	CA-CB-CG	-6.08	107.72	113.80
1	A	16	ASN	N-CA-C	6.04	119.58	111.24
1	A	151	ASN	O-C-N	-6.01	116.00	123.04
1	A	99	ALA	O-C-N	-5.99	115.77	122.12
1	A	135	VAL	N-CA-C	-5.96	99.77	108.11
1	A	176	ASP	CA-C-O	-5.94	114.65	120.89
1	A	104	LYS	CA-C-O	-5.91	114.23	120.55
1	A	170	ARG	CB-CG-CD	5.89	124.84	111.30
1	A	188	GLY	CA-C-O	5.88	130.81	120.57
1	A	133	ARG	CA-C-O	-5.87	115.17	121.45
1	A	60	TYR	N-CA-C	-5.85	104.60	110.97
1	A	55	SER	CA-C-O	-5.84	114.92	121.40
1	A	151	ASN	CA-C-O	-5.82	114.06	120.69
1	A	89	THR	N-CA-CB	-5.75	100.82	110.83
1	A	43	GLN	N-CA-C	5.73	119.47	111.90
1	A	96	VAL	N-CA-CB	-5.73	104.89	112.34
1	A	133	ARG	O-C-N	5.72	129.68	123.10
1	A	56	THR	N-CA-C	5.72	117.48	108.96
1	A	50	TRP	N-CA-C	5.71	119.23	112.72
1	A	75	GLY	O-C-N	-5.71	115.28	122.70
1	A	70	GLU	CA-C-N	5.70	135.72	121.80
1	A	70	GLU	C-N-CA	5.70	135.72	121.80
1	A	153	TRP	N-CA-C	5.65	118.37	111.82
1	A	70	GLU	O-C-N	5.61	130.05	122.59
1	A	26	GLY	O-C-N	5.58	129.95	122.70
1	A	10	LYS	CB-CG-CD	5.57	124.12	111.30
1	A	69	ASN	CB-CG-ND2	5.54	124.72	116.40
1	A	74	SER	N-CA-C	-5.53	100.79	109.25
1	A	101	THR	N-CA-C	-5.52	105.42	111.82
1	A	21	HIS	CB-CG-CD2	-5.50	124.04	131.20
1	A	131	ALA	N-CA-C	-5.50	101.20	109.95
1	A	140	PHE	O-C-N	5.48	128.01	122.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	178	MET	CA-C-O	5.43	126.28	120.20
1	A	34	GLY	CA-C-O	-5.38	116.27	121.86
1	A	47	ASP	CA-CB-CG	5.36	117.96	112.60
1	A	123	PHE	N-CA-C	-5.36	104.33	112.04
1	A	15	GLU	O-C-N	-5.32	116.48	123.02
1	A	42	THR	CA-CB-OG1	-5.31	101.64	109.60
1	A	16	ASN	N-CA-CB	-5.31	103.27	111.65
1	A	152	ASN	CA-CB-CG	5.31	117.91	112.60
1	A	99	ALA	CA-C-O	-5.27	114.96	120.55
1	A	69	ASN	CA-C-O	5.23	127.99	120.51
1	A	178	MET	O-C-N	-5.23	116.24	122.20
1	A	179	TYR	CA-CB-CG	-5.19	104.56	113.90
1	A	16	ASN	CA-CB-CG	-5.18	107.42	112.60
1	A	188	GLY	O-C-N	5.15	129.40	122.70
1	A	28	VAL	CG1-CB-CG2	-5.13	99.50	110.80
1	A	122	GLU	O-C-N	-5.13	115.72	122.39
1	A	164	GLU	CA-C-O	-5.13	115.41	120.70
1	A	118	VAL	CG1-CB-CG2	-5.13	99.51	110.80
1	A	90	LYS	CA-CB-CG	5.13	124.36	114.10
1	A	175	GLN	CA-C-O	5.12	125.89	120.10
1	A	166	ASN	N-CA-C	5.11	115.76	107.23
1	A	54	TYR	O-C-N	5.11	129.04	123.27
1	A	175	GLN	N-CA-C	5.10	117.58	111.71
1	A	39	LYS	N-CA-C	-5.10	105.36	112.45
1	A	20	TYR	N-CA-C	5.09	117.78	109.59
1	A	167	PHE	CA-CB-CG	5.06	118.86	113.80
1	A	77	ALA	O-C-N	-5.06	115.86	122.59
1	A	88	LEU	N-CA-CB	-5.05	102.64	110.87
1	A	146	SER	CA-C-O	-5.04	115.33	121.28
1	A	148	GLU	O-C-N	-5.01	116.71	123.23

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	27	TYR	Sidechain

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	1454	0	1392	44	0
2	A	43	0	22	3	0
3	A	8	0	0	0	0
All	All	1505	0	1414	44	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 15.

All (44) 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:A:115:MET:HE2	1:A:150:ILE:HG22	1.66	0.78
1:A:124:ILE:HG13	1:A:133:ARG:HA	1.77	0.67
1:A:89:THR:HG23	1:A:133:ARG:HG2	1.80	0.63
1:A:31:ILE:HA	2:A:200:APU:N6A	2.13	0.63
1:A:31:ILE:HG13	2:A:200:APU:N6A	2.14	0.62
1:A:76:LYS:O	1:A:175:GLN:HG3	1.99	0.62
1:A:78:GLY:HA2	1:A:168:GLU:HB2	1.82	0.62
1:A:83:VAL:HG12	1:A:161:VAL:HG22	1.83	0.60
1:A:94:LEU:HD11	1:A:136:LEU:HD13	1.83	0.59
1:A:152:ASN:O	1:A:156:ALA:HB2	2.05	0.57
1:A:83:VAL:HB	1:A:159:LEU:HD22	1.89	0.55
1:A:67:VAL:HG21	1:A:178:MET:SD	2.48	0.54
1:A:74:SER:HB2	1:A:76:LYS:HG2	1.90	0.54
1:A:31:ILE:HG13	2:A:200:APU:C6A	2.38	0.53
1:A:177:ALA:O	1:A:180:GLU:HB3	2.08	0.53
1:A:166:ASN:OD1	1:A:168:GLU:HB3	2.09	0.52
1:A:37:LYS:HG2	1:A:38:PRO:O	2.10	0.52
1:A:67:VAL:CG2	1:A:178:MET:SD	2.98	0.52
1:A:94:LEU:HD12	1:A:138:LEU:HD21	1.92	0.52
1:A:139:PRO:HA	1:A:147:VAL:HA	1.92	0.51
1:A:76:LYS:HA	1:A:171:GLY:O	2.10	0.51
1:A:77:ALA:HB3	1:A:167:PHE:HB2	1.93	0.51
1:A:96:VAL:O	1:A:102:ILE:HD11	2.11	0.50
1:A:108:LEU:HD11	1:A:123:PHE:CD2	2.46	0.50
1:A:96:VAL:HG12	1:A:102:ILE:HG13	1.94	0.50
1:A:30:SER:O	1:A:33:LYS:HB2	2.14	0.48
1:A:170:ARG:HD3	1:A:173:ARG:HH11	1.77	0.48
1:A:36:GLN:HA	1:A:157:LYS:HD2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:67:VAL:HG12	1:A:68:ASP:HB3	1.97	0.47
1:A:108:LEU:HD11	1:A:123:PHE:HD2	1.81	0.46
1:A:42:THR:HG23	1:A:44:GLY:H	1.80	0.46
1:A:6:VAL:HG13	1:A:93:ALA:O	2.16	0.45
1:A:75:GLY:HA2	1:A:175:GLN:NE2	2.31	0.45
1:A:36:GLN:HA	1:A:157:LYS:CD	2.47	0.45
1:A:42:THR:O	1:A:51:LYS:HE3	2.17	0.45
1:A:170:ARG:HB3	1:A:173:ARG:HB3	1.99	0.44
1:A:36:GLN:HA	1:A:157:LYS:CE	2.47	0.44
1:A:5:VAL:HG12	1:A:6:VAL:HG23	1.99	0.43
1:A:92:LEU:HD12	1:A:134:VAL:HG11	1.98	0.43
1:A:94:LEU:HB2	1:A:138:LEU:HD23	2.01	0.42
1:A:59:LYS:O	1:A:62:ALA:HB3	2.19	0.42
1:A:136:LEU:HA	1:A:136:LEU:HD23	1.83	0.41
1:A:21:HIS:CD2	1:A:22:GLY:O	2.74	0.41
1:A:33:LYS:HA	1:A:33:LYS:NZ	2.36	0.41

There are no symmetry-related clashes.

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	188/190 (99%)	151 (80%)	30 (16%)	7 (4%)	2 3

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	41	GLY
1	A	171	GLY
1	A	188	GLY
1	A	69	ASN
1	A	71	ASN

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Mol	Chain	Res	Type
1	A	111	THR
1	A	70	GLU

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	154/156 (99%)	125 (81%)	29 (19%)	1 3

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ASP
1	A	4	ASP
1	A	5	VAL
1	A	15	GLU
1	A	23	THR
1	A	24	LYS
1	A	33	LYS
1	A	39	LYS
1	A	42	THR
1	A	68	ASP
1	A	73	LEU
1	A	74	SER
1	A	76	LYS
1	A	88	LEU
1	A	91	VAL
1	A	92	LEU
1	A	98	ASN
1	A	110	LEU
1	A	111	THR
1	A	112	GLU
1	A	116	GLU
1	A	121	GLU
1	A	122	GLU
1	A	133	ARG

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Mol	Chain	Res	Type
1	A	138	LEU
1	A	145	SER
1	A	148	GLU
1	A	163	LEU
1	A	169	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	98	ASN
1	A	151	ASN
1	A	155	GLN
1	A	175	GLN
1	A	184	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	APU	A	200	-	47,47,47	1.18	3 (6%)	70,72,72	1.52	12 (17%)

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	APU	A	200	-	-	2/26/58/58	0/5/5/5

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	200	APU	PU-O1X	2.52	1.58	1.50
2	A	200	APU	PU-O3D	2.39	1.63	1.59
2	A	200	APU	PA-O5D	-2.17	1.50	1.59

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	200	APU	O4B-C1B-N9A	4.44	116.63	108.09
2	A	200	APU	O4B-C4B-C5B	-3.55	101.71	109.22
2	A	200	APU	C1D-N1U-C2U	-3.53	111.26	117.59
2	A	200	APU	O3X-PU-O2X	3.32	120.26	107.80
2	A	200	APU	O4D-C1D-C2D	2.90	112.82	106.62
2	A	200	APU	O2B-C2B-C1B	2.38	118.29	110.10
2	A	200	APU	C4A-N9A-C1B	2.35	132.13	126.63
2	A	200	APU	O2X-PU-O1X	-2.24	102.12	110.83
2	A	200	APU	O3B-C3B-C2B	-2.22	103.71	111.68
2	A	200	APU	O3B-C3B-C4B	2.12	117.49	110.03
2	A	200	APU	C4A-N9A-C8A	-2.08	103.56	105.74
2	A	200	APU	C4D-O4D-C1D	-2.04	104.95	109.47

There are no chirality outliers.

All (2) torsion outliers are listed below:

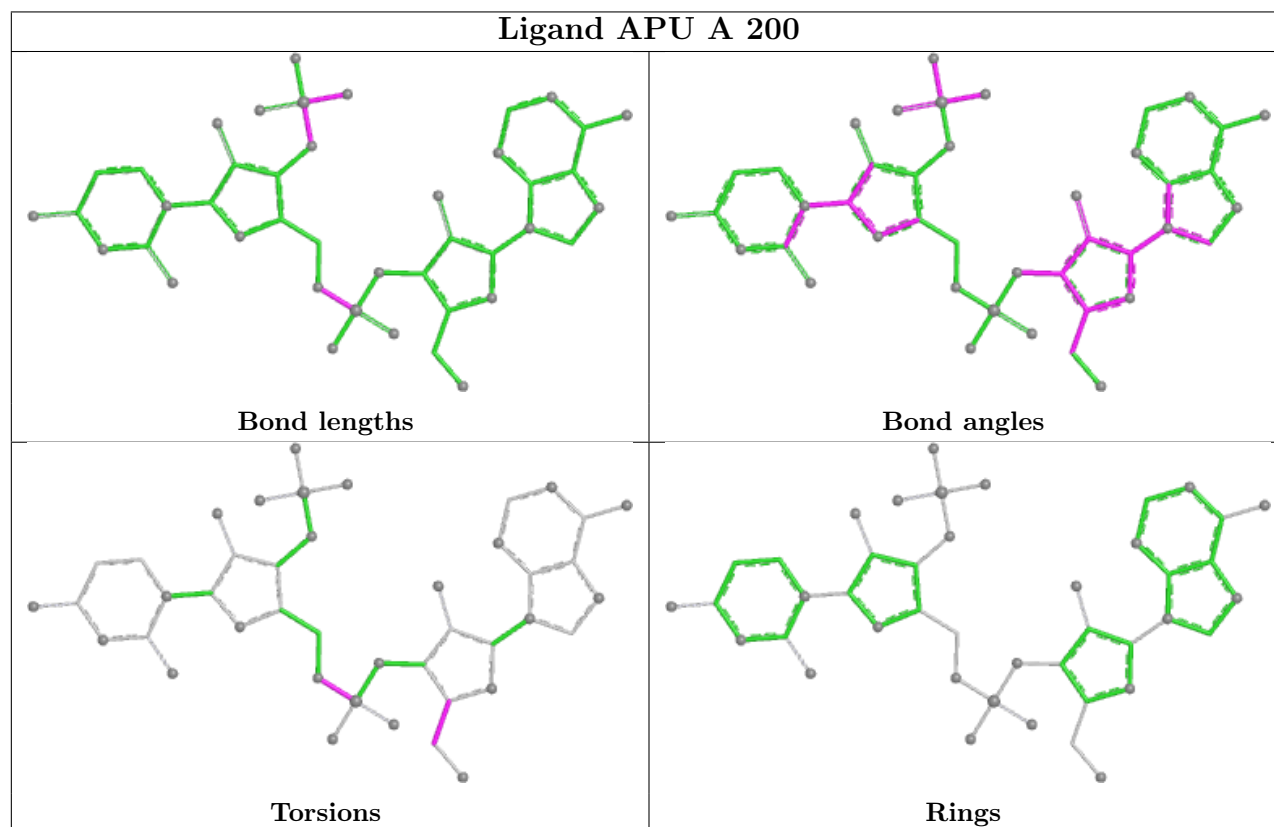
Mol	Chain	Res	Type	Atoms
2	A	200	APU	C5D-O5D-PA-O1A
2	A	200	APU	O4B-C4B-C5B-O5B

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	200	APU	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	190/190 (100%)	-0.71	0 100 100	16, 38, 52, 63	0

There are no RSRZ outliers to report.

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](#)

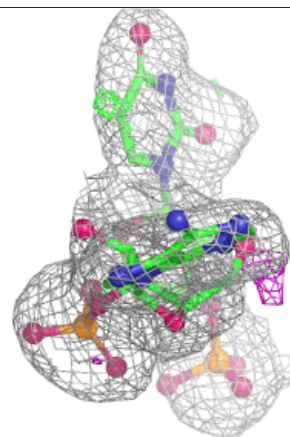
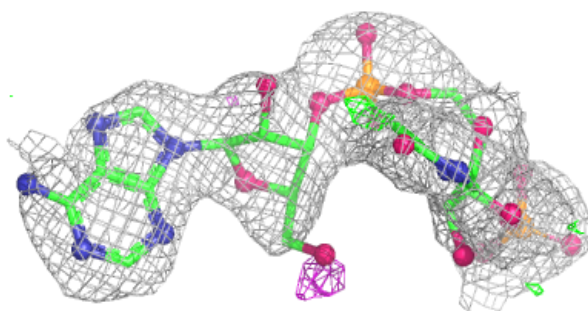
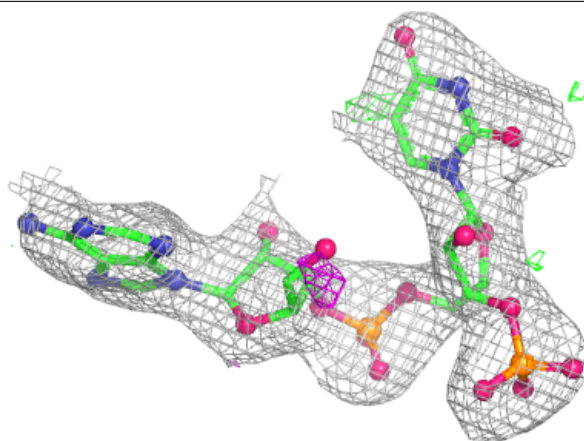
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	APU	A	200	43/43	0.95	0.06	29,38,47,51	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 APU A 200:

$2mF_o-DF_c$ (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.