



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 01:39 AM EDT

PDB ID : 1RND / pdb_00001rnd
Title : NEWLY OBSERVED BINDING MODE IN PANCREATIC RIBONUCLEASE
Authors : Aguilar, C.F.; Thomas, P.J.; Mills, A.; Moss, D.S.; Palmer, R.A.
Deposited on : 1991-10-21
Resolution : 1.50 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

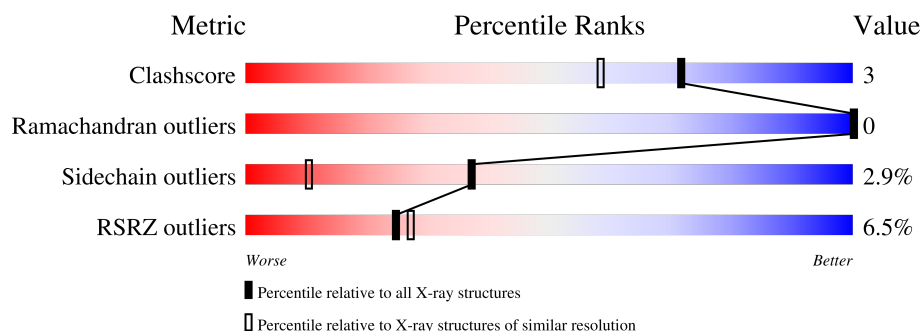
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.50 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	4235 (1.50-1.50)
Ramachandran outliers	187476	4153 (1.50-1.50)
Sidechain outliers	187428	4150 (1.50-1.50)
RSRZ outliers	180081	4039 (1.50-1.50)

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	124	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 1058 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 RIBONUCLEASE A.

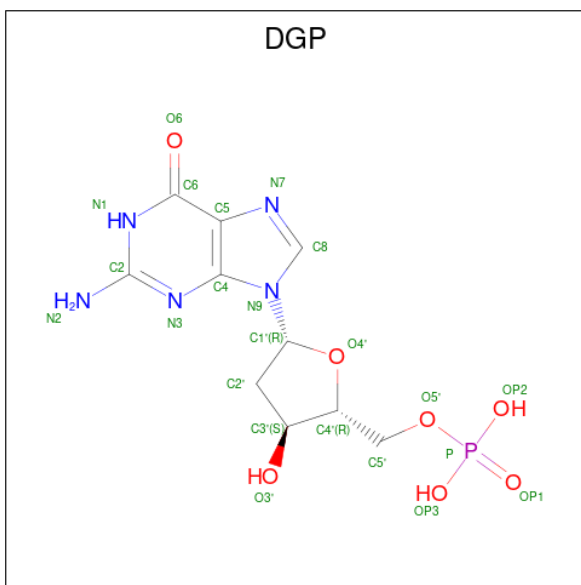
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	124	934	563	167	192	12	0	0	0

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	A	1	5	4	1	0	0

- Molecule 3 is 2'-DEOXYGUANOSINE-5'-MONOPHOSPHATE (CCD ID: DGP) (formula: C₁₀H₁₄N₅O₇P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

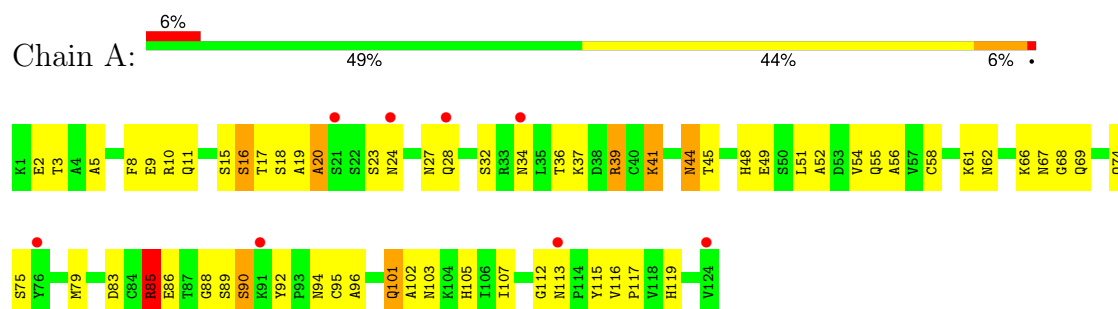
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	96	Total	O	0	0
			96	96		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: RIBONUCLEASE A



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	30.34Å 38.19Å 53.37Å 90.00° 105.90° 90.00°	Depositor
Resolution (Å)	(Not available) – 1.50 200.00 – 1.54	Depositor EDS
% Data completeness (in resolution range)	(Not available) ((Not available)-1.50) 93.3 (200.00-1.54)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.24 (at 1.54Å)	Xtriage
Refinement program	RESTRAIN	Depositor
R, R_{free}	0.190 , (Not available) 0.263 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	12.2	Xtriage
Anisotropy	0.166	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 17.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.042 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	1058	wwPDB-VP
Average B, all atoms (Å ²)	0.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.19% 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: DGP, SO4

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	1.87	17/950 (1.8%)	2.87	101/1287 (7.8%)

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 (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	105	HIS	ND1-CE1	10.56	1.43	1.32
1	A	48	HIS	ND1-CE1	8.17	1.40	1.32
1	A	101	GLN	CD-OE1	7.04	1.36	1.23
1	A	113	ASN	CG-OD1	6.95	1.36	1.23
1	A	112	GLY	N-CA	6.91	1.52	1.45
1	A	119	HIS	ND1-CE1	6.73	1.39	1.32
1	A	69	GLN	CD-OE1	6.59	1.36	1.23
1	A	36	THR	N-CA	6.28	1.53	1.46
1	A	28	GLN	CD-OE1	6.18	1.35	1.23
1	A	79	MET	C-N	-6.13	1.24	1.33
1	A	105	HIS	CE1-NE2	5.94	1.38	1.32
1	A	119	HIS	CE1-NE2	5.92	1.38	1.32
1	A	67	ASN	CG-OD1	5.70	1.34	1.23
1	A	94	ASN	CG-OD1	5.65	1.34	1.23
1	A	74	GLN	CD-OE1	5.48	1.33	1.23
1	A	34	ASN	CG-OD1	5.22	1.33	1.23
1	A	115	TYR	C-N	5.09	1.38	1.33

All (101) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	24	ASN	CA-CB-CG	-12.14	100.46	112.60
1	A	92	TYR	CA-C-O	-11.48	110.07	119.71
1	A	112	GLY	CA-C-N	10.92	136.29	122.64
1	A	112	GLY	C-N-CA	10.92	136.29	122.64
1	A	37	LYS	CA-C-O	-10.50	108.59	120.24
1	A	34	ASN	CA-CB-CG	-9.86	102.74	112.60
1	A	39	ARG	CD-NE-CZ	-9.43	111.20	124.40
1	A	17	THR	O-C-N	-9.04	112.24	123.27
1	A	39	ARG	NE-CZ-NH2	-8.57	111.49	119.20
1	A	113	ASN	N-CA-CB	8.35	126.81	110.61
1	A	48	HIS	CB-CG-CD2	-8.24	120.48	131.20
1	A	113	ASN	CB-CG-ND2	8.18	128.67	116.40
1	A	16	SER	CA-C-N	8.16	135.96	122.73
1	A	16	SER	C-N-CA	8.16	135.96	122.73
1	A	18	SER	CA-C-O	7.89	129.09	119.31
1	A	23	SER	CA-C-N	7.78	133.72	120.72
1	A	23	SER	C-N-CA	7.78	133.72	120.72
1	A	10	ARG	NE-CZ-NH2	7.69	126.12	119.20
1	A	102	ALA	O-C-N	-7.65	114.30	123.10
1	A	2	GLU	N-CA-CB	-7.55	98.43	109.83
1	A	68	GLY	CA-C-O	-7.53	111.21	119.27
1	A	5	ALA	CA-C-O	-7.46	112.51	120.42
1	A	66	LYS	CA-C-O	-7.29	112.82	120.55
1	A	16	SER	CB-CA-C	7.26	123.67	109.72
1	A	90	SER	O-C-N	7.25	132.09	122.96
1	A	55	GLN	CA-C-N	7.21	130.66	120.28
1	A	55	GLN	C-N-CA	7.21	130.66	120.28
1	A	24	ASN	CB-CG-OD1	-7.17	106.47	120.80
1	A	24	ASN	N-CA-C	7.16	121.28	112.54
1	A	102	ALA	CA-C-N	7.11	133.21	123.11
1	A	102	ALA	C-N-CA	7.11	133.21	123.11
1	A	18	SER	N-CA-CB	-7.08	98.87	110.40
1	A	95	CYS	N-CA-C	-7.07	99.81	110.28
1	A	116	VAL	N-CA-CB	-7.04	105.69	111.67
1	A	49	GLU	CA-C-O	6.97	129.28	121.40
1	A	15	SER	CA-CB-OG	-6.95	97.20	111.10
1	A	62	ASN	CB-CG-ND2	6.94	126.81	116.40
1	A	61	LYS	CA-C-O	-6.87	112.45	120.62
1	A	41	LYS	CA-C-O	6.84	126.18	119.75
1	A	105	HIS	CG-CD2-NE2	6.81	114.01	107.20
1	A	15	SER	N-CA-C	-6.75	105.01	113.18
1	A	107	ILE	CA-C-O	6.74	127.40	120.39

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	101	GLN	O-C-N	-6.64	115.66	123.22
1	A	52	ALA	CA-C-N	6.58	130.30	120.31
1	A	52	ALA	C-N-CA	6.58	130.30	120.31
1	A	54	VAL	CA-C-O	-6.56	113.18	120.46
1	A	85	ARG	CD-NE-CZ	6.55	133.58	124.40
1	A	11	GLN	OE1-CD-NE2	-6.45	116.15	122.60
1	A	17	THR	CA-C-O	6.38	128.00	120.66
1	A	88	GLY	O-C-N	-6.37	115.53	122.54
1	A	105	HIS	CE1-NE2-CD2	-6.25	102.75	109.00
1	A	48	HIS	CB-CA-C	-6.24	103.20	111.74
1	A	103	ASN	CA-CB-CG	-6.20	106.40	112.60
1	A	45	THR	CA-C-N	6.18	131.86	122.65
1	A	45	THR	C-N-CA	6.18	131.86	122.65
1	A	24	ASN	CB-CG-ND2	6.15	125.63	116.40
1	A	5	ALA	O-C-N	6.15	129.16	122.15
1	A	85	ARG	NE-CZ-NH1	6.12	127.62	121.50
1	A	113	ASN	O-C-N	6.01	129.82	121.47
1	A	8	PHE	O-C-N	-5.98	115.91	122.07
1	A	19	ALA	O-C-N	-5.97	117.55	123.46
1	A	28	GLN	CA-C-O	-5.96	114.56	120.70
1	A	66	LYS	N-CA-C	-5.95	104.79	111.28
1	A	39	ARG	CG-CD-NE	-5.89	99.04	112.00
1	A	39	ARG	NH1-CZ-NH2	5.87	126.94	119.30
1	A	56	ALA	N-CA-CB	5.78	119.12	110.22
1	A	96	ALA	CA-C-O	-5.75	113.69	120.60
1	A	119	HIS	CA-C-N	5.72	130.03	122.42
1	A	119	HIS	C-N-CA	5.72	130.03	122.42
1	A	113	ASN	CA-C-O	-5.71	113.61	119.49
1	A	90	SER	CA-C-O	-5.71	113.96	120.58
1	A	10	ARG	CD-NE-CZ	5.70	132.38	124.40
1	A	15	SER	N-CA-CB	-5.67	100.88	110.41
1	A	36	THR	O-C-N	-5.64	115.37	122.19
1	A	116	VAL	CA-CB-CG2	5.63	119.97	110.40
1	A	48	HIS	CB-CG-ND1	5.59	131.09	122.70
1	A	95	CYS	CA-C-O	-5.56	114.93	121.16
1	A	18	SER	N-CA-C	5.49	119.70	112.89
1	A	28	GLN	N-CA-C	-5.49	105.22	111.14
1	A	75	SER	O-C-N	-5.45	116.24	122.89
1	A	44	ASN	CA-CB-CG	-5.45	107.15	112.60
1	A	32	SER	CA-C-O	-5.42	113.73	119.97
1	A	34	ASN	CB-CG-ND2	5.41	124.52	116.40
1	A	51	LEU	CB-CG-CD1	5.38	126.83	110.70

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	61	LYS	CB-CG-CD	5.35	123.61	111.30
1	A	20	ALA	O-C-N	5.35	129.42	122.89
1	A	27	ASN	CB-CG-ND2	5.34	124.41	116.40
1	A	101	GLN	OE1-CD-NE2	5.34	127.94	122.60
1	A	27	ASN	CA-C-O	-5.33	114.90	120.55
1	A	107	ILE	O-C-N	-5.31	117.57	123.20
1	A	3	THR	N-CA-CB	5.25	117.76	110.04
1	A	24	ASN	OD1-CG-ND2	5.24	127.84	122.60
1	A	9	GLU	N-CA-CB	5.22	117.58	110.01
1	A	58	CYS	CA-C-O	5.22	125.68	119.10
1	A	34	ASN	O-C-N	-5.20	113.66	122.03
1	A	83	ASP	N-CA-CB	-5.20	101.59	110.16
1	A	10	ARG	NE-CZ-NH1	-5.18	116.32	121.50
1	A	61	LYS	CA-CB-CG	-5.18	103.75	114.10
1	A	11	GLN	CG-CD-NE2	5.15	124.13	116.40
1	A	117	PRO	O-C-N	-5.14	117.34	123.10
1	A	23	SER	CA-C-O	-5.08	113.34	119.49

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	85	ARG	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	934	0	858	5	0
2	A	5	0	0	0	0
3	A	23	0	11	1	0
4	A	96	0	0	1	0
All	All	1058	0	869	6	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 3.

All (6) 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)
3:A:126:DGP:H2''	4:A:216:HOH:O	1.99	0.62
1:A:41:LYS:NZ	1:A:44:ASN:HD22	2.07	0.53
1:A:86:GLU:HG2	1:A:90:SER:CB	2.43	0.48
1:A:39:ARG:HH11	1:A:39:ARG:HD2	1.53	0.44
1:A:20:ALA:H	1:A:101:GLN:NE2	2.17	0.42
1:A:41:LYS:HZ1	1:A:44:ASN:HD22	1.67	0.41

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	122/124 (98%)	115 (94%)	7 (6%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent 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	104/109 (95%)	101 (97%)	3 (3%)	37	10

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	SER
1	A	85	ARG
1	A	89	SER

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	11	GLN
1	A	34	ASN
1	A	44	ASN
1	A	101	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](#)

2 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	$\# Z > 2$
3	DGP	A	126	-	25,25,25	1.10	3 (12%)	37,38,38	2.52	11 (29%)
2	SO4	A	125	-	4,4,4	0.68	0	6,6,6	0.89	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	DGP	A	126	-	-	3/10/22/22	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	126	DGP	C5-N7	-2.20	1.34	1.39
3	A	126	DGP	C6-N1	2.14	1.42	1.38
3	A	126	DGP	P-OP3	2.09	1.62	1.54

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	126	DGP	O5'-C5'-C4'	8.98	139.56	108.99
3	A	126	DGP	OP2-P-OP1	7.95	141.81	110.83
3	A	126	DGP	O4'-C1'-N9	3.66	114.36	107.86
3	A	126	DGP	OP2-P-O5'	-3.64	97.17	106.67
3	A	126	DGP	O3'-C3'-C2'	-3.24	99.63	110.88
3	A	126	DGP	C5'-C4'-C3'	2.40	128.08	114.64
3	A	126	DGP	C2-N1-C6	-2.33	120.88	125.11
3	A	126	DGP	C2'-C3'-C4'	2.22	107.30	102.80
3	A	126	DGP	OP3-P-OP1	-2.20	102.27	110.83
3	A	126	DGP	OP3-P-O5'	-2.18	100.98	106.67
3	A	126	DGP	O4'-C1'-C2'	2.01	110.00	106.25

There are no chirality outliers.

All (3) torsion outliers are listed below:

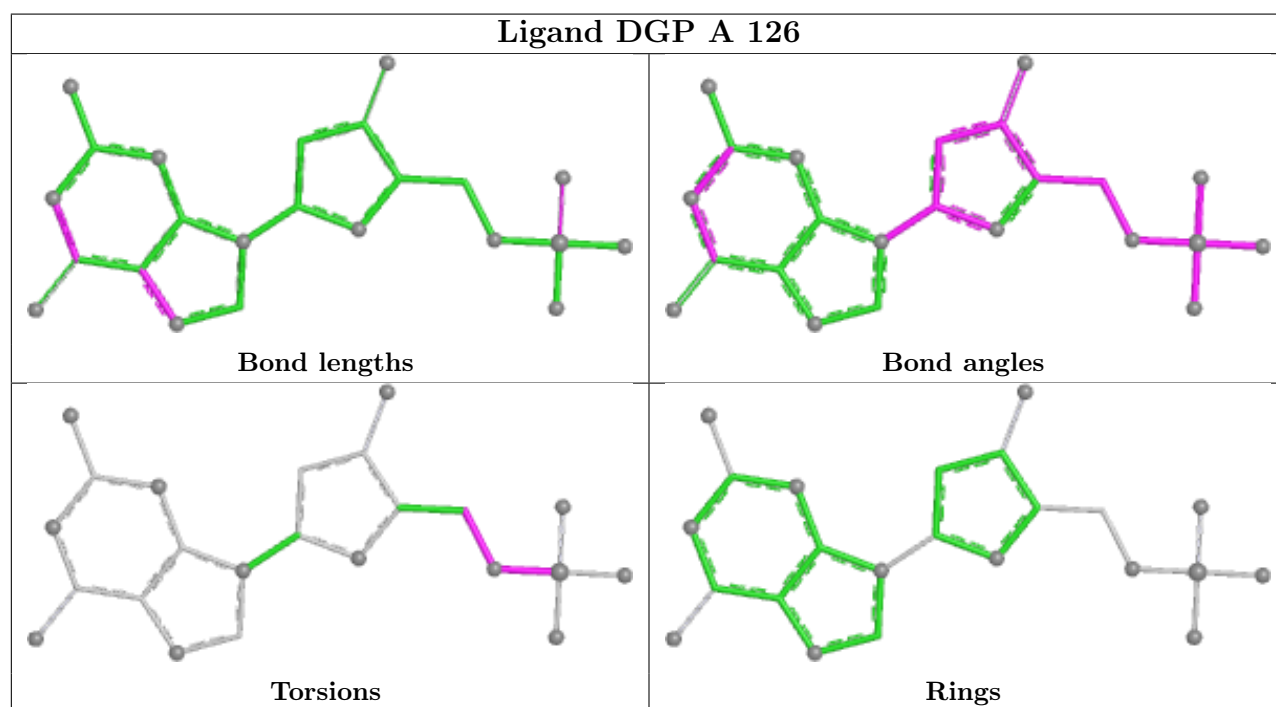
Mol	Chain	Res	Type	Atoms
3	A	126	DGP	C5'-O5'-P-OP2
3	A	126	DGP	C5'-O5'-P-OP3
3	A	126	DGP	C4'-C5'-O5'-P

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	126	DGP	1	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	124/124 (100%)	0.60	8 (6%)	25 27	0, 0, 0, 1	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	113	ASN	4.2
1	A	76	TYR	3.1
1	A	124	VAL	2.6
1	A	91	LYS	2.5
1	A	24	ASN	2.4
1	A	28	GLN	2.1
1	A	21	SER	2.1
1	A	34	ASN	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](#)

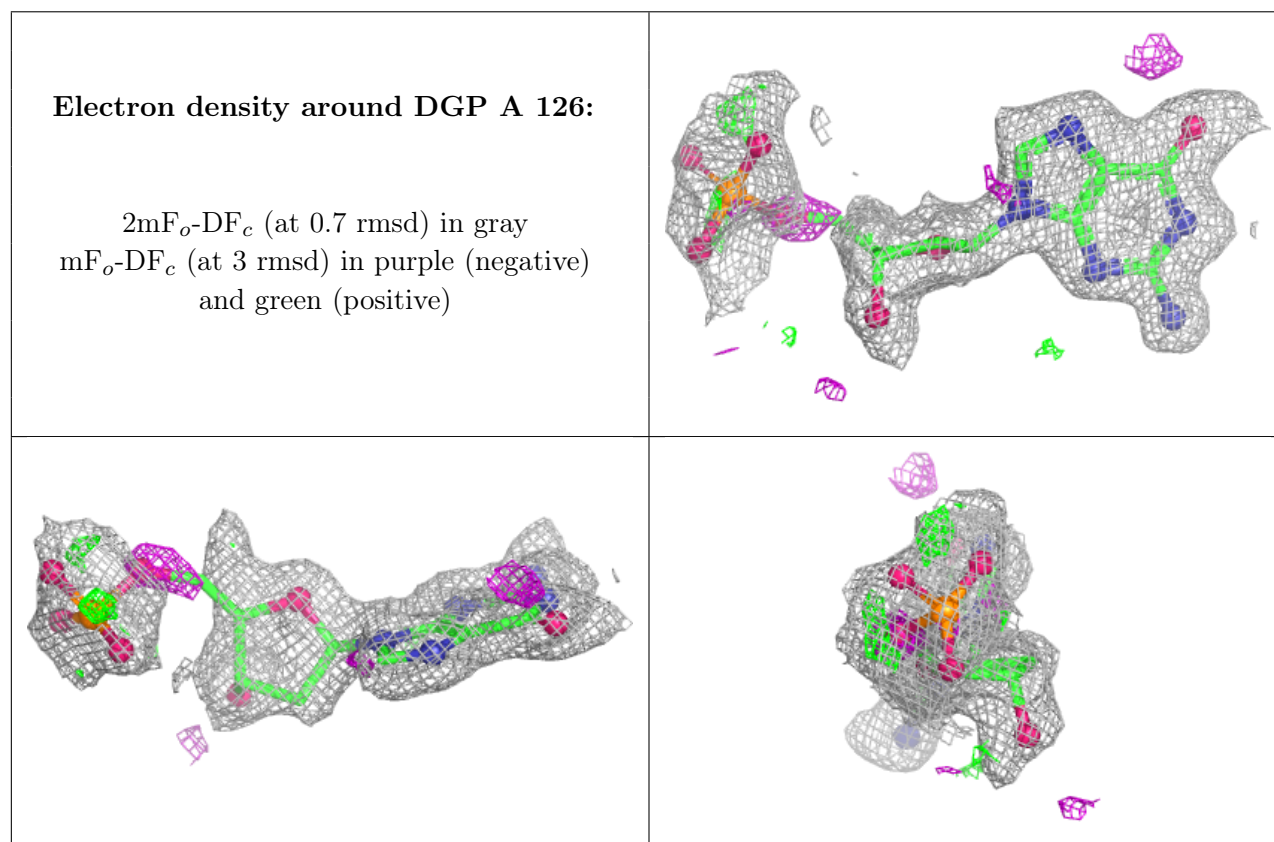
There are no oligosaccharides in this entry.

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	DGP	A	126	23/23	0.80	0.09	0,0,0,0	12
2	SO4	A	125	5/5	0.97	0.07	0,0,0,0	5

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers [i](#)

There are no such residues in this entry.