



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 2, 2026 – 03:49 AM UTC

PDB ID : 1Q9Y / pdb_00001q9y
Title : CRYSTAL STRUCTURE OF ENTEROBACTERIA PHAGE RB69 GP43
DNA POLYMERASE COMPLEXED WITH 8-OXOGUANOSINE CON-
TAINING DNA
Authors : Freisinger, E.; Grollman, A.P.; Miller, H.; Kisker, C.
Deposited on : 2003-08-26
Resolution : 2.80 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

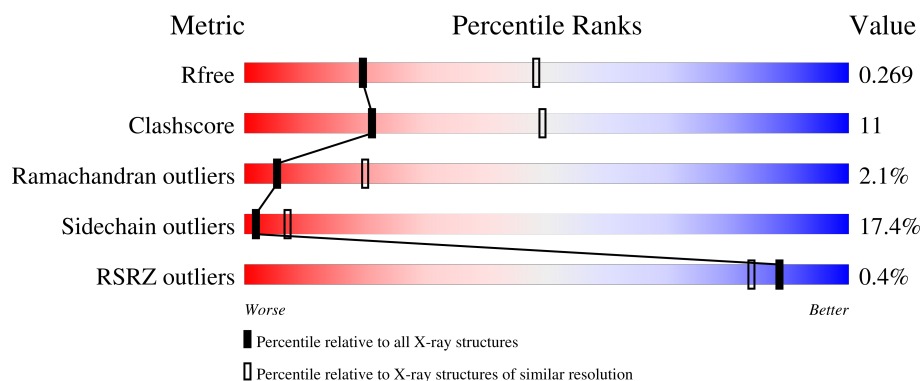
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	T	18	50% 39% 11%
2	P	14	29% 43% 29%
3	A	906	67% 25% 6%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8123 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 DNA chain called 5'-AC(8-OXOGUANOSINE)GGTAAGCAGTCCGCG-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	T	18	Total	C	N	O	P	0	0	0
			371	175	74	105	17			

- Molecule 2 is a DNA chain called 5'-GCGGACTGCTTAC(DIDEOXYCYTIDINE)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	14	Total	C	N	O	P	0	0	0
			281	135	51	82	13			

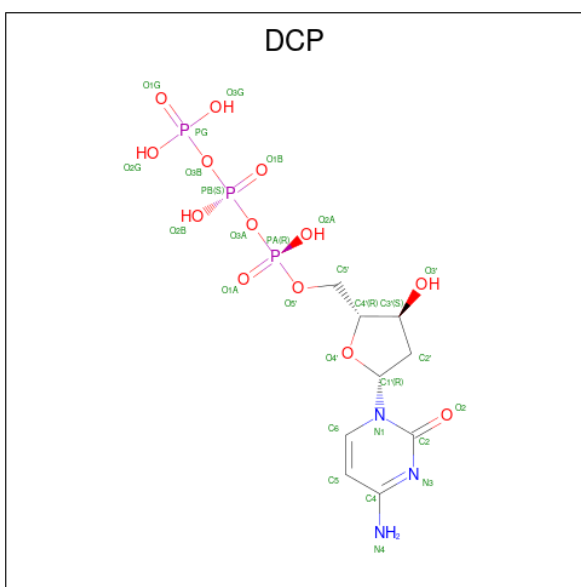
- Molecule 3 is a protein called DNA POLYMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	902	Total	C	N	O	S	0	0	0
			7356	4721	1227	1376	32			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	HIS	-	cloning artifact	UNP Q38087
A	2	GLY	-	cloning artifact	UNP Q38087
A	3	SER	-	cloning artifact	UNP Q38087
A	225	ALA	ASP	engineered mutation	UNP Q38087
A	330	ALA	ASP	engineered mutation	UNP Q38087

- Molecule 4 is 2'-DEOXYCYTIDINE-5'-TRIPHOSPHATE (CCD ID: DCP) (formula: C₉H₁₆N₃O₁₃P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	P	1	Total	C	N	O	P	0	0
			28	9	3	13	3		

- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

- Molecule 6 is water.

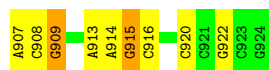
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	T	5	Total O 5 5	0	0
6	P	2	Total O 2 2	0	0
6	A	77	Total O 77 77	0	0

3 Residue-property plots

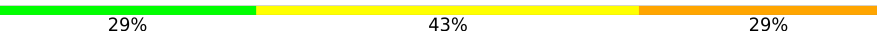
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

- Molecule 1: 5'-AC(8-OXOGUANOSINE)GGTAAGCAGTCCGCG-3'

Chain T: 



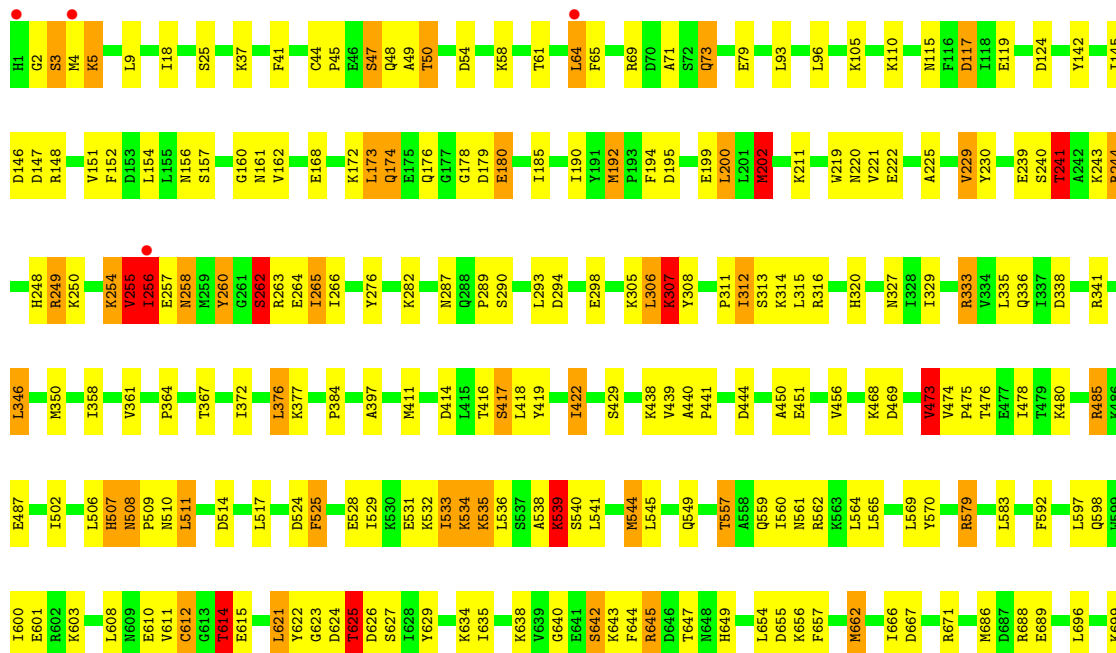
- Molecule 2: 5'-GCGGACTGCTTAC(DIDEOXYCYTIDINE)-3'

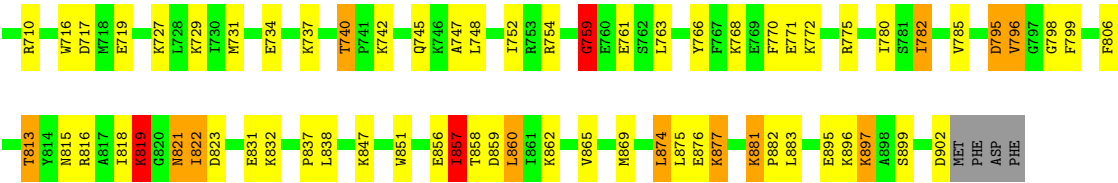
Chain P: 



- Molecule 3: DNA POLYMERASE

Chain A: 





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	80.82Å 118.56Å 127.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.06 – 2.80 46.06 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.5 (46.06-2.80) 90.8 (46.06-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.51 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.204 , 0.271 0.203 , 0.269	Depositor DCC
R_{free} test set	1579 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	47.4	Xtriage
Anisotropy	0.079	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 33.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	8123	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.38% 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: 8OG, DCP, CA, DOC

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	T	0.66	0/390	1.58	4/598 (0.7%)
2	P	0.69	0/294	1.70	8/452 (1.8%)
3	A	0.94	3/7536 (0.0%)	1.14	17/10184 (0.2%)
All	All	0.92	3/8220 (0.0%)	1.20	29/11234 (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
3	A	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	202	MET	SD-CE	8.92	2.01	1.79
3	A	192	MET	SD-CE	6.07	1.94	1.79
3	A	256	ILE	CA-CB	5.80	1.62	1.54

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	255	VAL	N-CA-C	8.25	118.83	110.82
2	P	933	DC	C4'-C3'-O3'	-7.24	99.14	110.00
3	A	473	VAL	CB-CA-C	-6.98	102.95	111.88
3	A	601	GLU	N-CA-C	-6.65	103.96	111.14
1	T	916	DC	P-O3'-C3'	6.58	130.08	120.20
2	P	925	DG	P-O3'-C3'	6.47	129.91	120.20
2	P	932	DG	P-O5'-C5'	6.43	129.64	120.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	73	GLN	N-CA-C	-6.20	104.97	112.54
2	P	928	DG	C4'-C3'-O3'	6.20	119.30	110.00
1	T	920	DC	P-O5'-C5'	6.09	129.14	120.00
3	A	151	VAL	N-CA-C	6.00	116.76	107.99
1	T	915	DG	O5'-C5'-C4'	-5.97	101.84	110.80
3	A	315	LEU	N-CA-C	5.95	117.44	111.07
3	A	759	GLY	N-CA-C	5.63	126.52	113.18
3	A	740	THR	CB-CA-C	5.59	116.42	108.76
3	A	562	ARG	N-CA-C	-5.55	105.63	112.90
3	A	857	ILE	CB-CA-C	-5.51	104.14	111.13
1	T	922	DG	O3'-P-O5'	-5.44	95.84	104.00
3	A	307	LYS	N-CA-C	5.36	117.44	110.53
2	P	936	DA	C5'-C4'-O4'	5.33	117.40	109.40
2	P	931	DT	O4'-C1'-N1	5.29	116.33	108.40
3	A	3	SER	N-CA-C	5.23	115.45	108.23
3	A	145	ILE	N-CA-CB	5.19	116.52	110.65
3	A	241	THR	OG1-CB-CG2	-5.18	98.95	109.30
3	A	603	LYS	N-CA-C	-5.12	105.34	111.03
2	P	933	DC	P-O5'-C5'	5.11	127.67	120.00
2	P	928	DG	O4'-C1'-N9	5.10	116.05	108.40
3	A	93	LEU	N-CA-C	5.07	116.81	111.28
3	A	47	SER	N-CA-C	5.06	117.91	111.69

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	A	3	SER	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	T	371	0	202	5	0
2	P	281	0	159	7	0
3	A	7356	0	7251	164	0
4	P	28	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	3	0	0	0	0
6	A	77	0	0	10	0
6	P	2	0	0	0	0
6	T	5	0	0	0	0
All	All	8123	0	7624	172	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 11.

All (172) 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:202:MET:CE	3:A:202:MET:SD	2.01	1.48
3:A:174:GLN:HE21	3:A:174:GLN:HA	1.30	0.97
3:A:897:LYS:HA	3:A:897:LYS:NZ	1.91	0.86
3:A:508:ASN:O	3:A:508:ASN:CG	2.19	0.85
3:A:173:LEU:HD22	3:A:173:LEU:H	1.47	0.79
3:A:644:PHE:HA	3:A:649:HIS:HD2	1.47	0.78
3:A:5:LYS:HB3	3:A:5:LYS:NZ	1.99	0.78
3:A:2:GLY:HA2	6:A:997:HOH:O	1.83	0.77
3:A:49:ALA:O	3:A:50:THR:HG23	1.85	0.77
3:A:119:GLU:HG2	3:A:327:ASN:ND2	1.99	0.77
3:A:256:ILE:O	3:A:263:ARG:O	2.05	0.75
3:A:897:LYS:HA	3:A:897:LYS:HZ3	1.50	0.74
3:A:174:GLN:HE21	3:A:174:GLN:CA	2.01	0.72
2:P:928:DG:H4'	2:P:929:DA:OP1	1.89	0.72
3:A:44:CYS:HB2	3:A:45:PRO:HD2	1.71	0.71
3:A:667:ASP:O	3:A:671:ARG:HG3	1.90	0.71
3:A:644:PHE:HB2	6:A:952:HOH:O	1.93	0.69
3:A:174:GLN:NE2	3:A:178:GLY:O	2.26	0.68
3:A:64:LEU:HB3	6:A:973:HOH:O	1.92	0.68
3:A:119:GLU:HG2	3:A:327:ASN:HD22	1.58	0.68
3:A:644:PHE:HA	3:A:649:HIS:CD2	2.29	0.68
3:A:795:ASP:O	3:A:799:PHE:O	2.13	0.66
3:A:174:GLN:HA	3:A:174:GLN:NE2	2.09	0.65
3:A:49:ALA:O	3:A:50:THR:CG2	2.45	0.64
3:A:257:GLU:O	3:A:258:ASN:O	2.16	0.64
3:A:545:LEU:O	3:A:549:GLN:HG3	1.98	0.63
3:A:256:ILE:HA	6:A:990:HOH:O	1.98	0.63
3:A:857:ILE:HD12	3:A:862:LYS:HA	1.80	0.63
1:T:907:DA:H2''	1:T:908:DC:O5'	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:688:ARG:NH2	3:A:717:ASP:OD1	2.33	0.61
3:A:508:ASN:ND2	3:A:534:LYS:O	2.33	0.61
3:A:305:LYS:O	3:A:306:LEU:CB	2.48	0.61
3:A:5:LYS:HB3	3:A:5:LYS:HZ3	1.63	0.61
3:A:508:ASN:ND2	3:A:510:ASN:HD21	1.99	0.61
3:A:782:ILE:HD11	3:A:869:MET:CE	2.31	0.60
3:A:173:LEU:H	3:A:173:LEU:CD2	2.13	0.60
3:A:257:GLU:HG3	3:A:262:SER:HA	1.84	0.59
3:A:782:ILE:HD11	3:A:869:MET:HE1	1.83	0.59
3:A:329:ILE:HG22	3:A:333:ARG:HD3	1.85	0.59
3:A:418:LEU:HD22	3:A:626:ASP:HB3	1.85	0.58
3:A:737:LYS:O	3:A:745:GLN:NE2	2.36	0.57
3:A:747:ALA:HB2	3:A:770:PHE:CE2	2.39	0.57
2:P:925:DG:H1'	2:P:926:DC:H5'	1.86	0.57
3:A:225:ALA:O	3:A:229:VAL:HG13	2.04	0.57
3:A:748:LEU:O	3:A:752:ILE:HG13	2.05	0.57
3:A:644:PHE:HD2	3:A:649:HIS:CD2	2.22	0.56
3:A:289:PRO:HB3	3:A:785:VAL:HG21	1.86	0.56
3:A:782:ILE:O	3:A:874:LEU:HD11	2.06	0.55
3:A:49:ALA:C	3:A:50:THR:HG23	2.31	0.55
3:A:230:TYR:CD2	3:A:266:ILE:HD13	2.42	0.55
3:A:647:THR:HG21	3:A:716:TRP:CH2	2.42	0.55
3:A:174:GLN:HE22	3:A:179:ASP:HA	1.71	0.55
3:A:162:VAL:HG21	3:A:320:HIS:CD2	2.42	0.54
3:A:666:ILE:HG21	3:A:686:MET:HB3	1.88	0.54
3:A:508:ASN:N	3:A:509:PRO:CD	2.71	0.53
3:A:422:ILE:HD13	3:A:592:PHE:HD1	1.73	0.53
3:A:333:ARG:HA	3:A:336:GLN:HE21	1.73	0.53
3:A:422:ILE:HD13	3:A:592:PHE:CD1	2.43	0.53
3:A:821:ASN:OD1	3:A:823:ASP:HB3	2.10	0.53
3:A:856:GLU:OE1	3:A:862:LYS:NZ	2.20	0.53
3:A:444:ASP:HB3	3:A:450:ALA:HB2	1.92	0.52
3:A:614:THR:HG23	3:A:615:GLU:N	2.24	0.52
3:A:816:ARG:O	3:A:819:LYS:HB2	2.09	0.52
3:A:510:ASN:HB2	3:A:535:LYS:O	2.10	0.51
3:A:173:LEU:HD23	3:A:176:GLN:CB	2.40	0.51
3:A:858:THR:HG21	3:A:860:LEU:HD12	1.93	0.51
3:A:173:LEU:HD23	3:A:176:GLN:HB2	1.92	0.51
3:A:146:ASP:OD2	3:A:211:LYS:NZ	2.38	0.50
2:P:938:DOC:H3'2	3:A:625:THR:HG23	1.94	0.50
3:A:142:TYR:OH	3:A:147:ASP:OD1	2.25	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:119:GLU:OE2	6:A:942:HOH:O	2.20	0.49
3:A:795:ASP:HB3	6:A:1000:HOH:O	2.12	0.49
3:A:897:LYS:HA	3:A:897:LYS:HZ2	1.72	0.49
2:P:928:DG:H2"	2:P:929:DA:C8	2.48	0.49
3:A:624:ASP:O	3:A:626:ASP:N	2.46	0.49
3:A:621:LEU:HD13	3:A:629:TYR:O	2.13	0.49
3:A:64:LEU:HB2	6:A:975:HOH:O	2.12	0.49
3:A:419:TYR:HA	3:A:422:ILE:HG13	1.95	0.49
3:A:795:ASP:O	3:A:796:VAL:HB	2.13	0.49
3:A:881:LYS:N	3:A:882:PRO:HD2	2.28	0.49
3:A:248:HIS:O	3:A:249:ARG:HB2	2.12	0.48
3:A:475:PRO:O	3:A:478:ILE:HG22	2.13	0.48
3:A:200:LEU:HD12	3:A:200:LEU:C	2.37	0.48
3:A:608:LEU:O	3:A:612:CYS:HB3	2.13	0.48
3:A:474:VAL:HB	3:A:475:PRO:HD3	1.94	0.48
3:A:346:LEU:HD22	3:A:350:MET:HE3	1.96	0.48
3:A:384:PRO:O	3:A:579:ARG:HD3	2.14	0.47
3:A:710:ARG:NH2	3:A:734:GLU:OE2	2.47	0.47
3:A:254:LYS:HB3	3:A:265:ILE:CD1	2.44	0.47
3:A:37:LYS:CE	6:A:977:HOH:O	2.62	0.47
3:A:174:GLN:HG2	3:A:180:GLU:OE2	2.15	0.47
3:A:65:PHE:CG	3:A:71:ALA:HB2	2.49	0.47
3:A:508:ASN:ND2	3:A:510:ASN:OD1	2.48	0.47
3:A:524:ASP:O	3:A:525:PHE:C	2.58	0.46
3:A:293:LEU:O	3:A:294:ASP:C	2.58	0.46
3:A:411:MET:HE3	3:A:654:LEU:HB3	1.98	0.46
3:A:507:HIS:N	3:A:507:HIS:ND1	2.63	0.46
3:A:662:MET:O	3:A:666:ILE:HG12	2.16	0.46
3:A:411:MET:CE	3:A:654:LEU:HB3	2.46	0.46
3:A:260:TYR:CD2	3:A:260:TYR:O	2.69	0.45
3:A:312:ILE:O	3:A:312:ILE:HD13	2.16	0.45
3:A:538:ALA:O	3:A:539:LYS:C	2.59	0.45
3:A:160:GLY:O	3:A:316:ARG:NH2	2.49	0.45
3:A:440:ALA:HB1	3:A:441:PRO:HD2	1.98	0.45
3:A:241:THR:O	3:A:244:ARG:HG3	2.16	0.45
3:A:813:THR:HB	3:A:816:ARG:NH2	2.32	0.45
3:A:346:LEU:HD11	3:A:561:ASN:CB	2.46	0.45
3:A:729:LYS:HE2	3:A:731:MET:SD	2.57	0.45
3:A:897:LYS:NZ	3:A:897:LYS:CA	2.74	0.45
3:A:851:TRP:CG	3:A:857:ILE:HG23	2.52	0.44
3:A:859:ASP:O	3:A:860:LEU:C	2.60	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:635:ILE:HD13	3:A:657:PHE:CE1	2.52	0.44
3:A:699:LYS:C	3:A:759:GLY:H	2.25	0.44
3:A:47:SER:O	3:A:49:ALA:N	2.50	0.44
3:A:96:LEU:HD23	3:A:96:LEU:HA	1.86	0.44
3:A:508:ASN:ND2	3:A:510:ASN:ND2	2.66	0.44
3:A:654:LEU:O	3:A:655:ASP:C	2.60	0.44
1:T:913:DA:C2	2:P:936:DA:C2	3.05	0.44
3:A:341:ARG:O	3:A:557:THR:HG21	2.16	0.44
3:A:117:ASP:OD2	3:A:327:ASN:ND2	2.51	0.44
3:A:154:LEU:HB2	3:A:200:LEU:HD23	1.98	0.44
1:T:907:DA:H5'	1:T:907:DA:N3	2.32	0.44
3:A:640:GLY:C	3:A:642:SER:H	2.26	0.44
3:A:645:ARG:H	3:A:645:ARG:HG3	1.59	0.43
3:A:837:PRO:CG	3:A:874:LEU:HD23	2.48	0.43
3:A:615:GLU:HA	3:A:615:GLU:OE1	2.18	0.43
2:P:927:DG:H2''	2:P:928:DG:OP2	2.18	0.43
3:A:287:ASN:OD1	3:A:832:LYS:NZ	2.51	0.43
3:A:474:VAL:HG13	3:A:569:LEU:HD21	2.01	0.43
3:A:822:ILE:HD13	3:A:822:ILE:H	1.83	0.43
1:T:914:DA:H2'	1:T:915:DG:C8	2.53	0.43
1:T:909:8OG:OP2	3:A:364:PRO:HD2	2.19	0.43
3:A:564:LEU:HD23	6:A:951:HOH:O	2.19	0.43
3:A:655:ASP:OD1	3:A:688:ARG:NH1	2.50	0.43
3:A:858:THR:HG22	3:A:860:LEU:H	1.84	0.43
3:A:376:LEU:HD13	3:A:473:VAL:HG11	2.01	0.43
3:A:508:ASN:O	3:A:510:ASN:OD1	2.35	0.43
3:A:41:PHE:CD1	3:A:41:PHE:N	2.87	0.42
3:A:194:PHE:CD1	3:A:200:LEU:HB2	2.54	0.42
3:A:502:ILE:HD13	3:A:544:MET:HB2	2.02	0.42
3:A:358:ILE:O	3:A:361:VAL:HG22	2.19	0.42
3:A:416:THR:O	3:A:417:SER:C	2.63	0.42
3:A:622:TYR:CG	3:A:623:GLY:N	2.88	0.42
3:A:311:PRO:HG2	3:A:314:LYS:HG3	2.02	0.42
3:A:511:LEU:HD22	3:A:511:LEU:HA	1.95	0.42
3:A:397:ALA:CB	3:A:625:THR:HB	2.50	0.42
3:A:418:LEU:O	3:A:422:ILE:HG13	2.19	0.42
3:A:367:THR:HG21	3:A:565:LEU:HD11	2.02	0.42
3:A:156:ASN:HA	3:A:161:ASN:HD22	1.85	0.41
3:A:570:TYR:CD1	3:A:570:TYR:C	2.96	0.41
3:A:688:ARG:HG2	3:A:689:GLU:N	2.34	0.41
3:A:899:SER:OG	3:A:902:ASP:OD1	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:5:LYS:NZ	3:A:5:LYS:CB	2.76	0.41
2:P:936:DA:H5'	3:A:737:LYS:HA	2.02	0.41
3:A:54:ASP:OD1	3:A:54:ASP:C	2.64	0.41
3:A:294:ASP:OD2	3:A:305:LYS:O	2.37	0.41
3:A:307:LYS:O	3:A:308:TYR:HB3	2.21	0.41
3:A:152:PHE:HB3	3:A:200:LEU:HD13	2.02	0.41
3:A:256:ILE:O	3:A:256:ILE:HG22	2.21	0.41
3:A:255:VAL:O	3:A:256:ILE:C	2.63	0.41
4:P:939:DCP:O2G	3:A:485:ARG:NH2	2.54	0.41
3:A:44:CYS:HB2	3:A:45:PRO:CD	2.46	0.41
3:A:506:LEU:HD23	3:A:541:LEU:HD12	2.02	0.41
3:A:754:ARG:CZ	3:A:766:TYR:HB2	2.50	0.41
3:A:37:LYS:HE2	6:A:977:HOH:O	2.20	0.41
3:A:305:LYS:O	3:A:306:LEU:HB2	2.18	0.40
3:A:529:ILE:HG22	3:A:533:ILE:HD12	2.03	0.40
3:A:614:THR:HG23	3:A:615:GLU:H	1.85	0.40
3:A:806:PHE:CZ	3:A:877:LYS:NZ	2.89	0.40
3:A:818:ILE:O	3:A:819:LYS:C	2.64	0.40
3:A:219:TRP:O	3:A:220:ASN:CB	2.68	0.40
3:A:276:TYR:OH	3:A:338:ASP:HA	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
3	A	900/906 (99%)	813 (90%)	68 (8%)	19 (2%)	5 20

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	256	ILE

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Mol	Chain	Res	Type
3	A	258	ASN
3	A	306	LEU
3	A	625	THR
3	A	759	GLY
3	A	795	ASP
3	A	798	GLY
3	A	195	ASP
3	A	525	PHE
3	A	614	THR
3	A	48	GLN
3	A	50	THR
3	A	642	SER
3	A	815	ASN
3	A	819	LYS
3	A	796	VAL
3	A	860	LEU
3	A	262	SER
3	A	539	LYS

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
3	A	798/802 (100%)	659 (83%)	139 (17%)	2 7

All (139) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	4	MET
3	A	5	LYS
3	A	9	LEU
3	A	18	ILE
3	A	25	SER
3	A	58	LYS
3	A	61	THR
3	A	64	LEU

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Mol	Chain	Res	Type
3	A	69	ARG
3	A	73	GLN
3	A	79	GLU
3	A	105	LYS
3	A	110	LYS
3	A	115	ASN
3	A	117	ASP
3	A	124	ASP
3	A	148	ARG
3	A	157	SER
3	A	168	GLU
3	A	172	LYS
3	A	173	LEU
3	A	174	GLN
3	A	180	GLU
3	A	185	ILE
3	A	190	ILE
3	A	192	MET
3	A	199	GLU
3	A	200	LEU
3	A	202	MET
3	A	221	VAL
3	A	222	GLU
3	A	229	VAL
3	A	239	GLU
3	A	240	SER
3	A	241	THR
3	A	243	LYS
3	A	244	ARG
3	A	249	ARG
3	A	250	LYS
3	A	254	LYS
3	A	255	VAL
3	A	260	TYR
3	A	262	SER
3	A	264	GLU
3	A	265	ILE
3	A	282	LYS
3	A	290	SER
3	A	298	GLU
3	A	307	LYS
3	A	312	ILE

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Mol	Chain	Res	Type
3	A	313	SER
3	A	333	ARG
3	A	335	LEU
3	A	346	LEU
3	A	372	ILE
3	A	376	LEU
3	A	377	LYS
3	A	414	ASP
3	A	417	SER
3	A	422	ILE
3	A	429	SER
3	A	438	LYS
3	A	439	VAL
3	A	451	GLU
3	A	456	VAL
3	A	468	LYS
3	A	469	ASP
3	A	473	VAL
3	A	476	THR
3	A	480	LYS
3	A	485	ARG
3	A	487	GLU
3	A	507	HIS
3	A	508	ASN
3	A	511	LEU
3	A	514	ASP
3	A	517	LEU
3	A	528	GLU
3	A	531	GLU
3	A	532	LYS
3	A	533	ILE
3	A	534	LYS
3	A	535	LYS
3	A	536	LEU
3	A	539	LYS
3	A	540	SER
3	A	544	MET
3	A	557	THR
3	A	559	GLN
3	A	560	ILE
3	A	579	ARG
3	A	583	LEU

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Mol	Chain	Res	Type
3	A	597	LEU
3	A	598	GLN
3	A	600	ILE
3	A	610	GLU
3	A	611	VAL
3	A	612	CYS
3	A	614	THR
3	A	621	LEU
3	A	625	THR
3	A	627	SER
3	A	634	LYS
3	A	638	LYS
3	A	643	LYS
3	A	645	ARG
3	A	656	LYS
3	A	662	MET
3	A	696	LEU
3	A	719	GLU
3	A	727	LYS
3	A	740	THR
3	A	742	LYS
3	A	761	GLU
3	A	763	LEU
3	A	768	LYS
3	A	771	GLU
3	A	772	LYS
3	A	775	ARG
3	A	780	ILE
3	A	782	ILE
3	A	813	THR
3	A	819	LYS
3	A	821	ASN
3	A	822	ILE
3	A	831	GLU
3	A	838	LEU
3	A	847	LYS
3	A	857	ILE
3	A	865	VAL
3	A	874	LEU
3	A	875	LEU
3	A	876	GLU
3	A	877	LYS

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Mol	Chain	Res	Type
3	A	881	LYS
3	A	883	LEU
3	A	895	GLU
3	A	896	LYS
3	A	897	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	161	ASN
3	A	174	GLN
3	A	206	ASN
3	A	220	ASN
3	A	302	ASN
3	A	327	ASN
3	A	336	GLN
3	A	357	GLN
3	A	379	GLN
3	A	508	ASN
3	A	542	ASN
3	A	567	ASN
3	A	649	HIS
3	A	764	GLN
3	A	789	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues 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	DOC	P	938	1,2	16,19,20	1.07	1 (6%)	20,26,29	0.90	0
1	8OG	T	909	1	22,25,26	1.65	2 (9%)	26,37,40	2.42	4 (15%)

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	DOC	P	938	1,2	-	2/7/18/19	0/2/2/2
1	8OG	T	909	1	-	4/7/21/22	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	T	909	8OG	C8-N7	-6.17	1.27	1.38
1	T	909	8OG	C8-N9	-3.85	1.33	1.40
2	P	938	DOC	C4-N3	-2.64	1.29	1.34

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	T	909	8OG	N7-C8-N9	8.88	116.49	106.61
1	T	909	8OG	O8-C8-N9	-6.49	117.18	126.00
1	T	909	8OG	C5-N7-C8	-3.38	104.82	109.47
1	T	909	8OG	C1'-N9-C4	2.65	131.54	126.88

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	T	909	8OG	O4'-C1'-N9-C8
1	T	909	8OG	O4'-C1'-N9-C4
1	T	909	8OG	C2'-C1'-N9-C4
2	P	938	DOC	C3'-C4'-C5'-O5'
2	P	938	DOC	O4'-C4'-C5'-O5'
1	T	909	8OG	C2'-C1'-N9-C8

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	P	938	DOC	1	0
1	T	909	8OG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 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$
4	DCP	P	939	5	28,29,29	1.25	3 (10%)	41,45,45	1.62	9 (21%)

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
4	DCP	P	939	5	-	4/22/34/34	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	P	939	DCP	PB-O3A	2.98	1.62	1.59
4	P	939	DCP	C6-C5	2.90	1.41	1.35
4	P	939	DCP	PA-O3A	2.14	1.61	1.59

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	P	939	DCP	O4'-C1'-N1	3.73	114.48	107.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	P	939	DCP	O2-C2-N3	-3.49	116.83	122.33
4	P	939	DCP	N1-C2-N3	2.95	123.92	118.80
4	P	939	DCP	O3B-PB-O1B	-2.82	102.21	110.70
4	P	939	DCP	C2'-C1'-N1	-2.64	107.22	113.81
4	P	939	DCP	C5-C4-N4	2.64	125.25	120.63
4	P	939	DCP	O2B-PB-O3A	2.42	113.82	107.27
4	P	939	DCP	C1'-N1-C6	2.28	126.02	121.53
4	P	939	DCP	C5-C6-N1	-2.02	118.56	121.84

There are no chirality outliers.

All (4) torsion outliers are listed below:

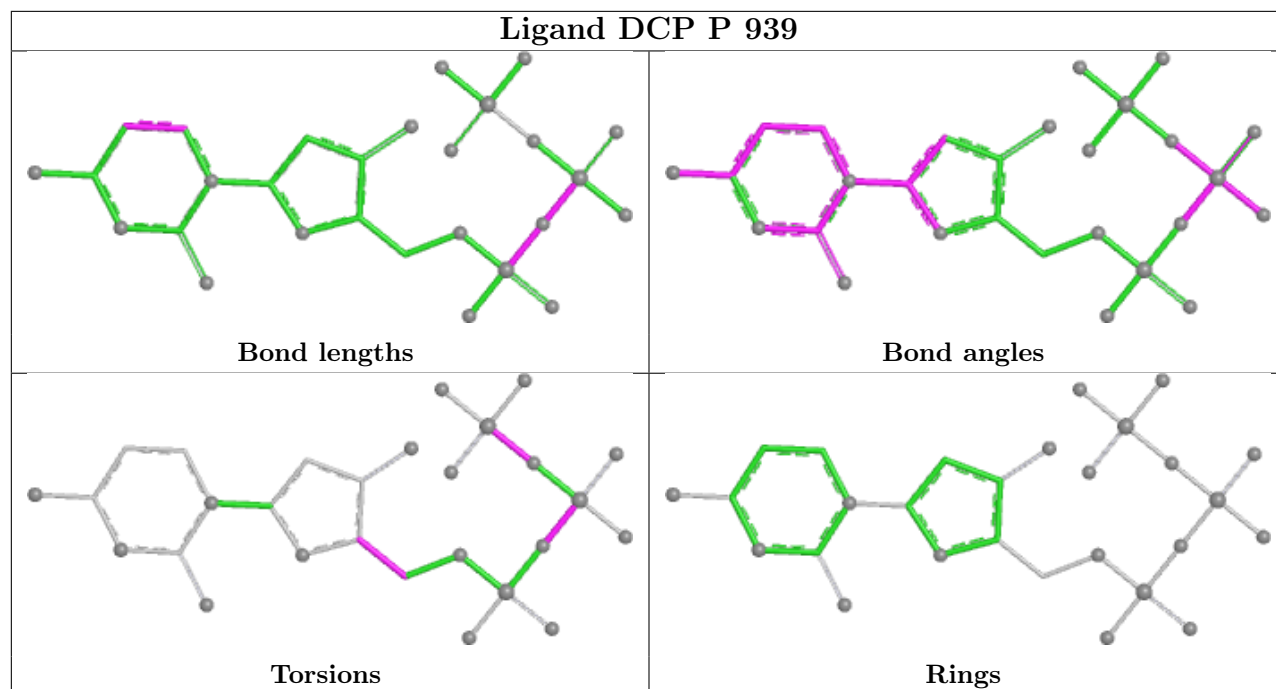
Mol	Chain	Res	Type	Atoms
4	P	939	DCP	PB-O3B-PG-O2G
4	P	939	DCP	PA-O3A-PB-O2B
4	P	939	DCP	O4'-C4'-C5'-O5'
4	P	939	DCP	PB-O3B-PG-O1G

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	P	939	DCP	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	T	17/18 (94%)	-0.72	0	100 100	17, 32, 51, 60	0
2	P	13/14 (92%)	-0.55	0	100 100	20, 33, 51, 56	0
3	A	902/906 (99%)	-0.23	4 (0%)	88 84	14, 35, 64, 90	0
All	All	932/938 (99%)	-0.25	4 (0%)	88 84	14, 35, 64, 90	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	A	1	HIS	2.4
3	A	256	ILE	2.4
3	A	4	MET	2.2
3	A	64	LEU	2.2

6.2 Non-standard residues in protein, DNA, RNA chains [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	DOC	P	938	18/19	0.95	0.08	12,21,33,36	0
1	8OG	T	909	23/24	0.98	0.06	9,14,18,22	0

6.3 Carbohydrates [i](#)

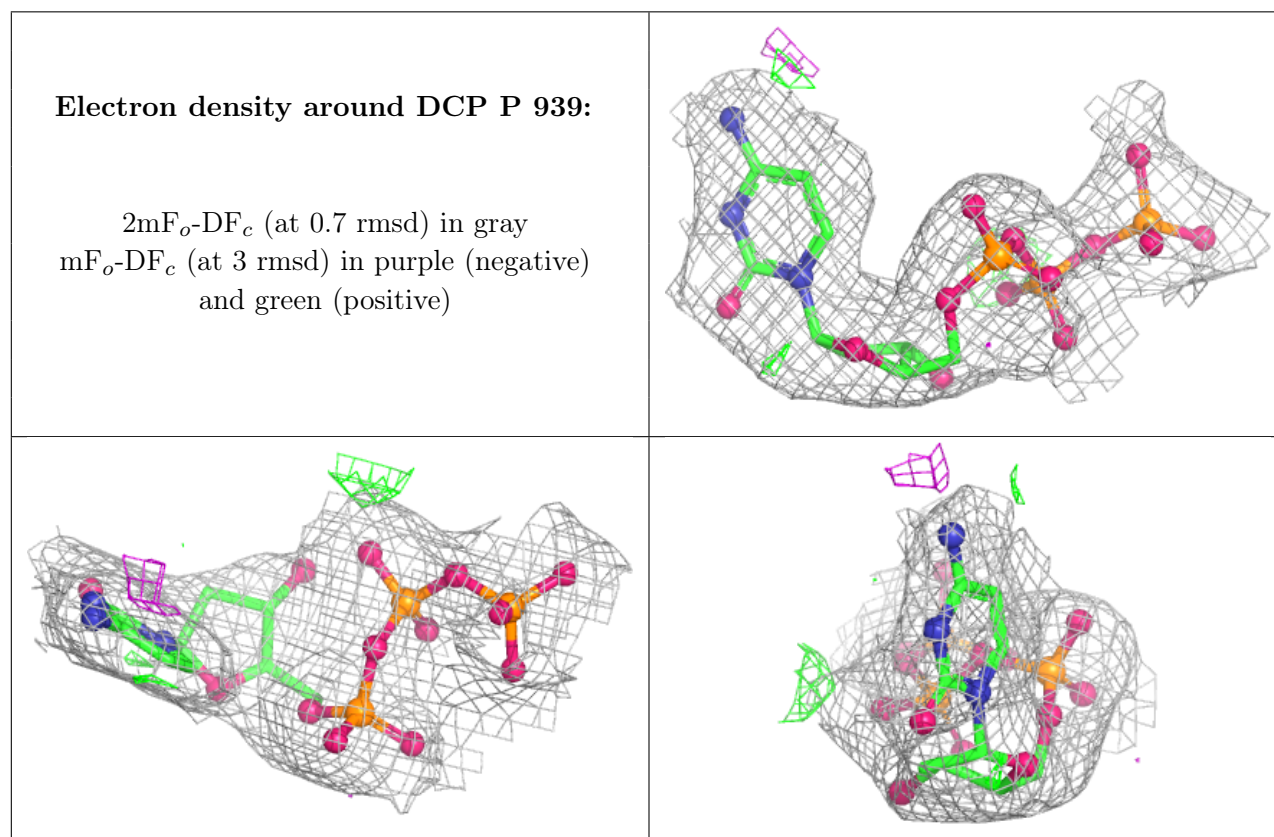
There are no oligosaccharides in this entry.

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
5	CA	A	941	1/1	0.88	0.08	51,51,51,51	0
5	CA	A	940	1/1	0.89	0.14	55,55,55,55	0
4	DCP	P	939	28/28	0.98	0.06	1,19,25,31	0
5	CA	A	939	1/1	0.99	0.04	30,30,30,30	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.