



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 07:19 PM UTC

PDB ID : 6OM4 / pdb_00006om4
Title : The structure of Microcin C7 biosynthetic enzyme MccB in complex with N-formylated MccA
Authors : Dong, S.-H.; Nair, S.K.
Deposited on : 2019-04-18
Resolution : 1.70 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

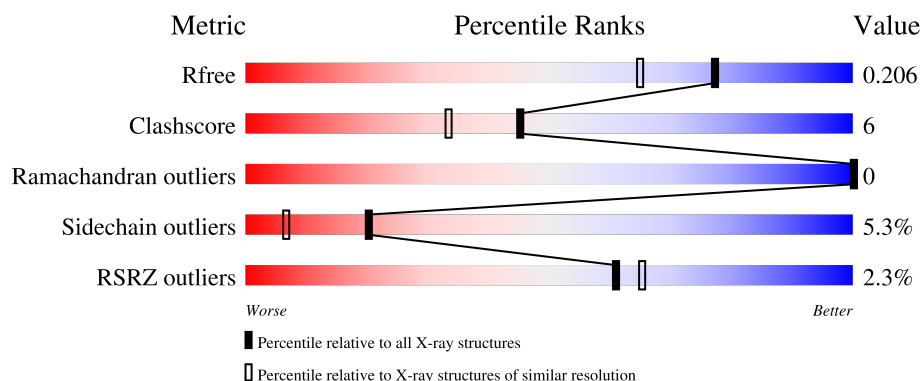
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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	348	2% 86% 12% ..
1	B	348	2% 86% 11% ..
2	C	7	86% 14%
2	D	7	86% 14%

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 6027 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 MccB protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	345	Total	C	N	O	S	0	0	0
			2713	1732	462	508	11			
1	B	344	Total	C	N	O	S	0	0	0
			2699	1725	457	506	11			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	81	SER	GLY	conflict	UNP Q47506
A	270	ALA	SER	conflict	UNP Q47506
B	81	SER	GLY	conflict	UNP Q47506
B	270	ALA	SER	conflict	UNP Q47506

- Molecule 2 is a protein called Microcin C7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	7	Total	C	N	O	S	0	0	0
			53	29	11	12	1			
2	D	7	Total	C	N	O	S	0	0	0
			53	29	11	12	1			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	7	ASP	ASN	conflict	UNP Q47505
D	7	ASP	ASN	conflict	UNP Q47505

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		

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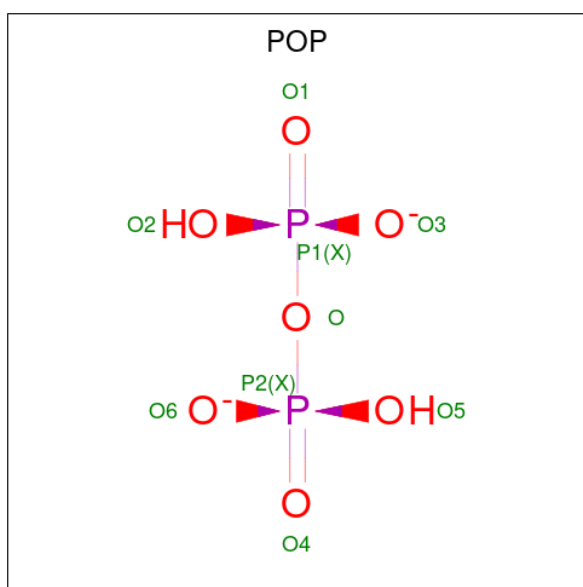
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Zn	0	0
			1	1		

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

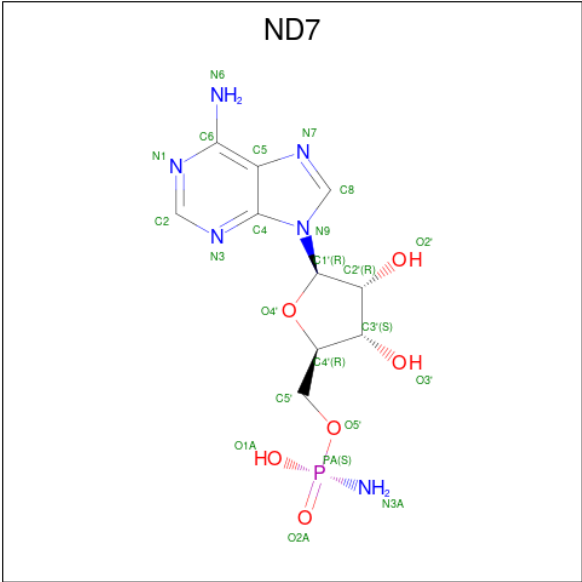
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Mg	0	0
			2	2		
4	B	2	Total	Mg	0	0
			2	2		

- Molecule 5 is PYROPHOSPHATE 2- (CCD ID: POP) (formula: $\text{H}_2\text{O}_7\text{P}_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	P	0	0
			9	7	2		
5	B	1	Total	O	P	0	0
			9	7	2		

- Molecule 6 is 5'-O-[(S)-amino(hydroxy)phosphoryl]adenosine (CCD ID: ND7) (formula: $\text{C}_{10}\text{H}_{15}\text{N}_6\text{O}_6\text{P}$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	C	1	Total	C	N	O	P	0	0
			23	10	6	6	1		
6	D	1	Total	C	N	O	P	0	0
			23	10	6	6	1		

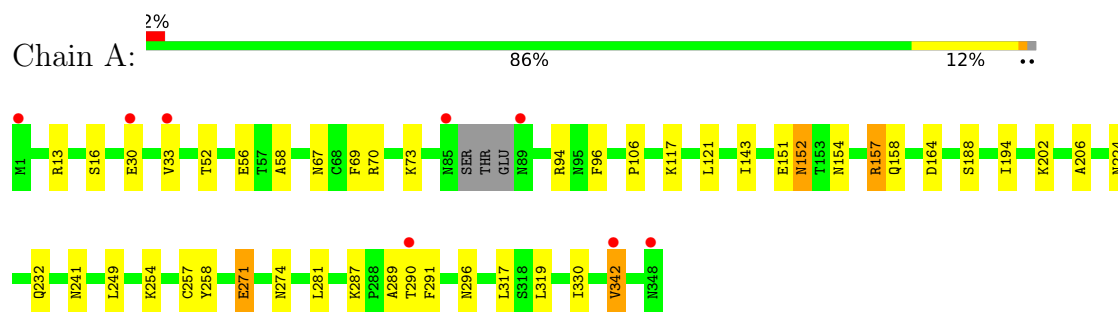
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	217	Total	O	0	0
			217	217		
7	B	208	Total	O	0	0
			208	208		
7	C	6	Total	O	0	0
			6	6		
7	D	8	Total	O	0	0
			8	8		

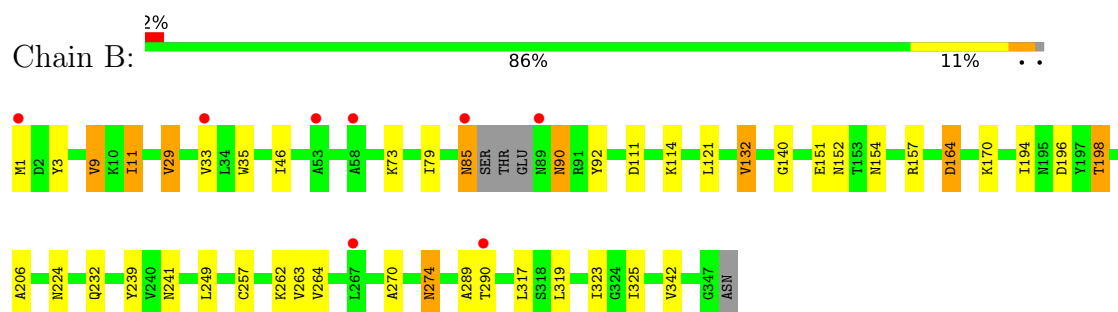
3 Residue-property plots [i](#)

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.

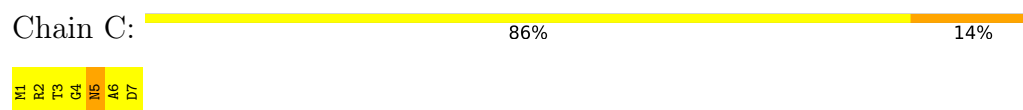
- Molecule 1: MccB protein



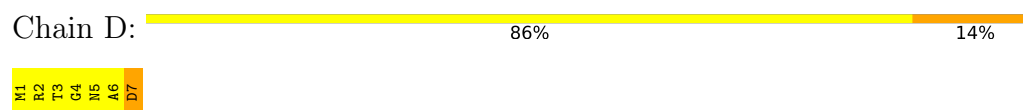
- Molecule 1: MccB protein



- Molecule 2: Microcin C7



- Molecule 2: Microcin C7



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	55.09Å 76.06Å 131.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	65.98 – 1.70 65.95 – 1.70	Depositor EDS
% Data completeness (in resolution range)	96.1 (65.98-1.70) 96.1 (65.95-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.36 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.8.0230	Depositor
R, R_{free}	0.155 , 0.199 0.165 , 0.206	Depositor DCC
R_{free} test set	2991 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å ²)	19.0	Xtriage
Anisotropy	0.094	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 30.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	6027	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.67% 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: FME, MG, ZN, POP, ND7

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	0.91	0/2769	1.01	3/3755 (0.1%)
1	B	0.92	1/2755 (0.0%)	1.05	4/3737 (0.1%)
2	C	3.71	7/42 (16.7%)	3.35	8/55 (14.5%)
2	D	3.47	6/42 (14.3%)	2.93	7/55 (12.7%)
All	All	1.01	14/5608 (0.2%)	1.09	22/7602 (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
1	A	0	2
1	B	0	1
All	All	0	3

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	5	ASN	C-N	9.57	1.46	1.33
2	C	2	ARG	C-N	9.11	1.45	1.33
2	D	2	ARG	C-N	9.10	1.45	1.33
2	D	2	ARG	NE-CZ	8.56	1.42	1.33
2	C	2	ARG	NE-CZ	8.50	1.42	1.33
2	C	2	ARG	CZ-NH1	8.40	1.44	1.32
2	D	4	GLY	C-N	7.71	1.44	1.33
2	C	3	THR	C-N	7.43	1.45	1.33
2	C	6	ALA	C-N	7.20	1.43	1.33
2	D	2	ARG	CZ-NH1	7.02	1.42	1.32
2	D	3	THR	C-N	6.50	1.43	1.33
2	D	6	ALA	C-N	6.47	1.42	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	4	GLY	C-N	6.45	1.42	1.33
1	B	79	ILE	N-CA	-5.29	1.41	1.46

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2	ARG	NE-CZ-NH1	-10.00	111.50	121.50
2	C	2	ARG	NE-CZ-NH2	9.67	127.91	119.20
2	D	7	ASP	CA-CB-CG	9.24	121.84	112.60
2	C	5	ASN	CA-CB-CG	8.38	120.98	112.60
1	B	132	VAL	CB-CA-C	-8.18	100.93	112.22
2	D	6	ALA	O-C-N	-7.45	113.78	123.16
2	D	6	ALA	N-CA-C	-7.39	98.20	109.95
1	B	132	VAL	N-CA-CB	7.25	121.46	110.58
1	A	342	VAL	N-CA-CB	-6.97	103.01	112.28
2	D	5	ASN	CA-CB-CG	6.91	119.51	112.60
2	D	5	ASN	CB-CA-C	-5.89	98.05	109.76
2	C	2	ARG	CA-CB-CG	-5.80	102.49	114.10
2	C	2	ARG	CG-CD-NE	-5.62	99.63	112.00
1	B	132	VAL	CA-CB-CG2	5.62	119.94	110.40
2	D	6	ALA	CA-C-O	5.34	127.19	121.16
2	D	3	THR	N-CA-C	-5.30	101.69	109.81
1	A	291	PHE	N-CA-CB	-5.20	102.30	110.77
1	B	9	VAL	N-CA-CB	5.16	117.68	110.56
2	C	6	ALA	N-CA-C	-5.12	102.61	110.14
2	C	4	GLY	CA-C-N	-5.09	111.84	122.07
2	C	4	GLY	C-N-CA	-5.09	111.84	122.07
1	A	158	GLN	CB-CG-CD	5.01	121.12	112.60

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	13	ARG	Sidechain
1	A	157	ARG	Sidechain
1	B	157	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	2713	0	2697	34	0
1	B	2699	0	2680	39	0
2	C	53	0	48	0	0
2	D	53	0	48	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
5	A	9	0	0	0	0
5	B	9	0	0	1	0
6	C	23	0	0	0	0
6	D	23	0	0	0	0
7	A	217	0	0	8	0
7	B	208	0	0	11	0
7	C	6	0	0	0	0
7	D	8	0	0	0	0
All	All	6027	0	5473	65	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 6.

All (65) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:58:ALA:HB1	7:A:697:HOH:O	1.43	1.16
1:B:270:ALA:HB1	7:B:663:HOH:O	0.75	0.92
1:B:164:ASP:HB3	7:B:502:HOH:O	1.71	0.90
1:B:262:LYS:HE2	7:B:639:HOH:O	1.79	0.83
1:A:16:SER:HB2	1:A:30:GLU:OE1	1.78	0.81
1:A:67:ASN:ND2	1:A:70:ARG:NH1	2.30	0.78
1:A:69:PHE:CE2	1:A:73:LYS:HD2	2.18	0.78
1:A:224:ASN:HD21	1:A:257:CYS:HB2	1.50	0.75
1:B:11:ILE:CD1	1:B:35:TRP:CZ2	2.70	0.74
1:A:290:THR:HG21	7:A:524:HOH:O	1.88	0.73
1:A:330:ILE:HD11	1:B:323:ILE:HD13	1.73	0.70
1:A:58:ALA:CB	7:A:697:HOH:O	2.16	0.69
1:B:33:VAL:HG23	7:B:683:HOH:O	1.93	0.69
1:B:121:LEU:HD11	1:B:194:ILE:HD11	1.73	0.69
1:A:290:THR:CG2	7:A:524:HOH:O	2.42	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:90:ASN:HD22	1:B:92:TYR:H	1.41	0.66
1:B:290:THR:CG2	7:B:528:HOH:O	2.44	0.65
1:A:281:LEU:CD1	1:B:46:ILE:CD1	2.75	0.64
1:A:121:LEU:HD11	1:A:194:ILE:CD1	2.28	0.64
1:A:33:VAL:HG13	7:A:614:HOH:O	1.98	0.64
1:B:29:VAL:HG22	1:B:35:TRP:HB2	1.81	0.62
1:A:281:LEU:HD12	1:B:46:ILE:CD1	2.29	0.61
1:B:11:ILE:HD12	1:B:35:TRP:CZ2	2.35	0.61
1:B:224:ASN:HD21	1:B:257:CYS:HB2	1.66	0.60
1:B:11:ILE:HD12	1:B:35:TRP:HZ2	1.67	0.60
1:B:90:ASN:OD1	7:B:501:HOH:O	2.15	0.59
1:B:290:THR:HG21	7:B:528:HOH:O	2.00	0.59
1:B:206:ALA:H	1:B:232:GLN:HE22	1.50	0.59
1:A:281:LEU:CD1	1:B:46:ILE:HD13	2.34	0.57
1:A:330:ILE:CD1	1:B:323:ILE:HD13	2.34	0.57
1:A:67:ASN:HD21	1:A:70:ARG:NH1	2.01	0.57
1:A:67:ASN:ND2	1:A:70:ARG:HH11	2.03	0.57
1:B:11:ILE:HD11	1:B:35:TRP:CZ2	2.41	0.55
1:A:117:LYS:NZ	7:A:501:HOH:O	2.22	0.55
1:A:206:ALA:H	1:A:232:GLN:HE22	1.53	0.55
1:A:254:LYS:NZ	7:A:502:HOH:O	2.34	0.55
1:A:67:ASN:HD22	1:A:70:ARG:NH1	2.05	0.54
1:B:151:GLU:H	1:B:154:ASN:ND2	2.05	0.53
1:A:330:ILE:HD11	1:B:323:ILE:CD1	2.39	0.51
1:B:90:ASN:ND2	1:B:92:TYR:H	2.09	0.50
1:A:271:GLU:H	1:A:271:GLU:CD	2.19	0.49
1:B:241:ASN:ND2	1:B:289:ALA:H	2.10	0.49
1:A:67:ASN:HD22	1:A:70:ARG:HH11	1.59	0.48
1:B:342:VAL:O	1:B:342:VAL:HG12	2.13	0.48
1:B:290:THR:HG23	7:B:528:HOH:O	2.11	0.48
1:A:241:ASN:ND2	1:A:289:ALA:H	2.12	0.47
1:B:196:ASP:OD2	1:B:198:THR:HG22	2.15	0.47
1:A:281:LEU:HD11	1:B:46:ILE:HD13	1.96	0.46
1:A:152:ASN:HD22	1:A:152:ASN:N	2.13	0.46
1:B:325:ILE:N	1:B:325:ILE:HD12	2.31	0.46
1:B:170:LYS:NZ	5:B:404:POP:O2	2.50	0.45
1:A:151:GLU:H	1:A:154:ASN:ND2	2.15	0.45
1:A:52:THR:HG23	7:A:686:HOH:O	2.16	0.44
1:A:94:ARG:HB3	1:B:290:THR:OG1	2.18	0.44
1:A:143:ILE:HD12	1:A:188:SER:OG	2.18	0.44
1:A:224:ASN:ND2	1:A:258:TYR:H	2.16	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:270:ALA:CB	7:B:663:HOH:O	1.67	0.42
1:B:239:TYR:CE1	1:B:290:THR:HG22	2.54	0.42
1:B:121:LEU:HD11	1:B:194:ILE:CD1	2.48	0.42
1:A:296:ASN:N	1:A:296:ASN:HD22	2.18	0.42
1:B:85:ASN:C	7:B:644:HOH:O	2.62	0.42
1:A:96:PHE:CG	1:A:106:PRO:HB2	2.55	0.41
1:B:274:ASN:HB3	7:B:703:HOH:O	2.19	0.41
1:B:3:TYR:OH	1:B:73:LYS:HE3	2.20	0.41
1:B:114:LYS:O	1:B:140:GLY:HA3	2.21	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	
1	A	341/348 (98%)	332 (97%)	9 (3%)	0	100	100
1	B	340/348 (98%)	334 (98%)	6 (2%)	0	100	100
2	C	5/7 (71%)	5 (100%)	0	0	100	100
2	D	5/7 (71%)	5 (100%)	0	0	100	100
All	All	691/710 (97%)	676 (98%)	15 (2%)	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	297/300 (99%)	285 (96%)	12 (4%)	28	12
1	B	295/300 (98%)	278 (94%)	17 (6%)	18	5
2	C	4/4 (100%)	2 (50%)	2 (50%)	0	0
2	D	4/4 (100%)	3 (75%)	1 (25%)	0	0
All	All	600/608 (99%)	568 (95%)	32 (5%)	20	7

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	56	GLU
1	A	152	ASN
1	A	157	ARG
1	A	164	ASP
1	A	202	LYS
1	A	249	LEU
1	A	271	GLU
1	A	274	ASN
1	A	287	LYS
1	A	317	LEU
1	A	319	LEU
1	A	342	VAL
1	B	1	MET
1	B	9	VAL
1	B	11	ILE
1	B	29	VAL
1	B	85	ASN
1	B	90	ASN
1	B	111	ASP
1	B	132	VAL
1	B	152	ASN
1	B	164	ASP
1	B	198	THR
1	B	249	LEU
1	B	263	VAL
1	B	264	VAL
1	B	274	ASN
1	B	317	LEU
1	B	319	LEU
2	C	5	ASN
2	C	7	ASP
2	D	7	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	67	ASN
1	A	75	ASN
1	A	84	ASN
1	A	110	GLN
1	A	129	HIS
1	A	149	GLN
1	A	152	ASN
1	A	215	HIS
1	A	224	ASN
1	A	232	GLN
1	A	236	ASN
1	A	241	ASN
1	A	295	ASN
1	A	296	ASN
1	B	75	ASN
1	B	85	ASN
1	B	90	ASN
1	B	100	GLN
1	B	129	HIS
1	B	152	ASN
1	B	154	ASN
1	B	215	HIS
1	B	218	ASN
1	B	224	ASN
1	B	232	GLN
1	B	241	ASN
1	B	277	HIS
1	B	295	ASN
1	B	296	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	FME	C	1	2	8,9,10	1.52	1 (12%)	8,9,11	1.41	1 (12%)
2	FME	D	1	2	8,9,10	1.33	1 (12%)	8,9,11	1.21	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
2	FME	C	1	2	-	2/7/9/11	-
2	FME	D	1	2	-	1/7/9/11	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1	FME	CN-N	3.62	1.45	1.33
2	D	1	FME	CN-N	3.08	1.43	1.33

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1	FME	CA-N-CN	-2.75	118.59	122.82

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	1	FME	O-C-CA-CB
2	D	1	FME	O-C-CA-CB
2	C	1	FME	CB-CG-SD-CE

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 6 are monoatomic - leaving 4 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
5	POP	B	404	4	6,8,8	1.11	1 (16%)	12,13,13	1.15	1 (8%)
6	ND7	C	101	2,4	24,25,25	3.18	11 (45%)	35,38,38	1.93	9 (25%)
6	ND7	D	101	2,4	24,25,25	2.84	6 (25%)	35,38,38	1.97	14 (40%)
5	POP	A	403	4	6,8,8	1.13	1 (16%)	12,13,13	1.16	1 (8%)

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
5	POP	B	404	4	-	0/6/6/6	-
6	ND7	C	101	2,4	-	2/8/26/26	0/3/3/3
6	ND7	D	101	2,4	-	0/8/26/26	0/3/3/3
5	POP	A	403	4	-	2/6/6/6	-

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	101	ND7	O4'-C1'	8.88	1.62	1.42
6	D	101	ND7	O4'-C1'	7.76	1.59	1.42
6	C	101	ND7	O4'-C4'	-6.72	1.30	1.45
6	D	101	ND7	C2'-C1'	-6.31	1.33	1.53
6	C	101	ND7	C2'-C1'	-6.06	1.34	1.53
6	D	101	ND7	O4'-C4'	-5.93	1.31	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	D	101	ND7	C6-N6	4.50	1.45	1.34
6	C	101	ND7	C6-N6	4.48	1.45	1.34
6	C	101	ND7	PA-O2A	4.29	1.52	1.46
6	D	101	ND7	O3'-C3'	-2.37	1.37	1.43
6	C	101	ND7	PA-O1A	-2.32	1.50	1.56
6	C	101	ND7	O2'-C2'	2.23	1.48	1.43
6	C	101	ND7	C2'-C3'	2.15	1.59	1.53
5	A	403	POP	P2-O6	-2.09	1.47	1.54
6	D	101	ND7	O2'-C2'	2.08	1.48	1.43
6	C	101	ND7	C5-C4	-2.08	1.35	1.39
5	B	404	POP	P1-O2	-2.05	1.47	1.54
6	C	101	ND7	O3'-C3'	-2.03	1.37	1.43
6	C	101	ND7	C2-N3	-2.02	1.30	1.33

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	101	ND7	N1-C2-N3	-5.01	121.00	128.58
6	D	101	ND7	O1A-PA-O2A	4.10	120.87	110.26
6	D	101	ND7	N1-C2-N3	-4.07	122.42	128.58
6	C	101	ND7	C5-C4-N3	-3.96	121.26	126.72
6	D	101	ND7	N9-C8-N7	-3.58	108.85	113.94
6	C	101	ND7	O5'-PA-O2A	-3.28	105.25	115.71
6	D	101	ND7	C5-C4-N3	-3.06	122.50	126.72
6	D	101	ND7	C4-N9-C8	3.00	108.88	105.74
6	C	101	ND7	C2-N3-C4	2.98	119.11	111.83
6	C	101	ND7	O1A-PA-O2A	2.91	117.78	110.26
5	B	404	POP	O2-P1-O1	2.75	121.54	110.83
6	D	101	ND7	C2-N1-C6	2.68	123.14	118.73
6	D	101	ND7	O5'-PA-N3A	-2.67	100.42	107.63
6	C	101	ND7	O4'-C4'-C3'	2.66	110.44	105.15
6	D	101	ND7	C3'-C2'-C1'	2.59	106.37	101.46
6	C	101	ND7	N9-C8-N7	-2.56	110.31	113.94
6	D	101	ND7	C5-N7-C8	2.48	107.35	103.45
6	C	101	ND7	N3-C4-N9	2.44	131.32	127.17
6	C	101	ND7	C5-N7-C8	2.40	107.23	103.45
6	D	101	ND7	O4'-C1'-N9	-2.37	103.54	108.09
6	D	101	ND7	N6-C6-N1	2.19	123.26	118.38
6	D	101	ND7	C2-N3-C4	2.18	117.17	111.83
6	D	101	ND7	N3-C4-N9	2.17	130.86	127.17
6	D	101	ND7	C4-C5-N7	-2.12	108.15	110.58
5	A	403	POP	O-P1-O1	-2.10	99.97	111.04

There are no chirality outliers.

All (4) torsion outliers are listed below:

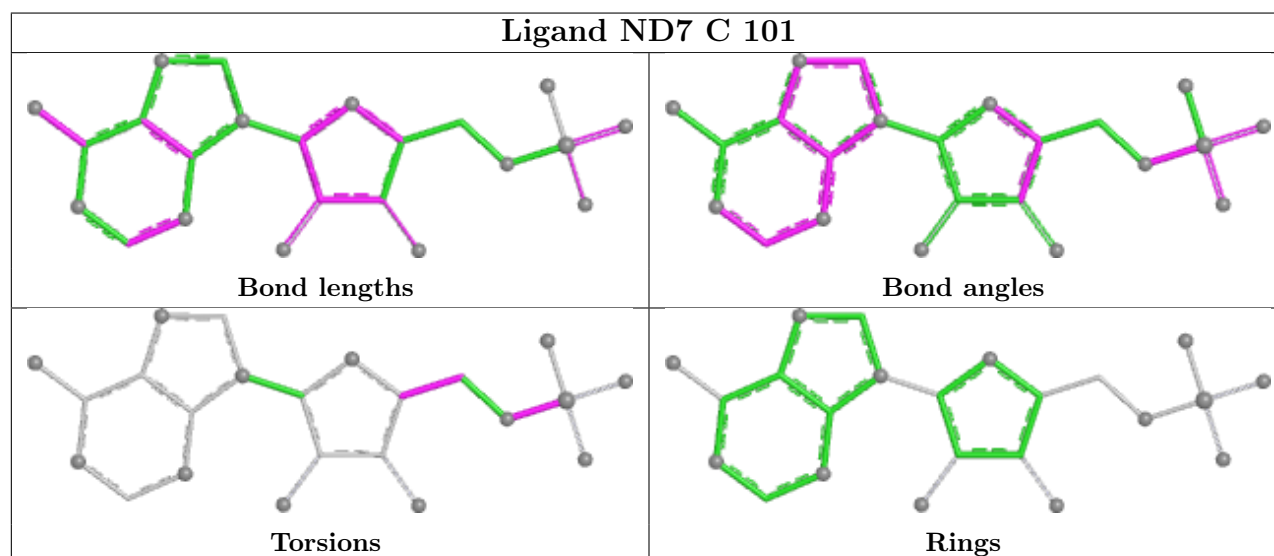
Mol	Chain	Res	Type	Atoms
5	A	403	POP	P1-O-P2-O4
5	A	403	POP	P1-O-P2-O5
6	C	101	ND7	C5'-O5'-PA-O2A
6	C	101	ND7	O4'-C4'-C5'-O5'

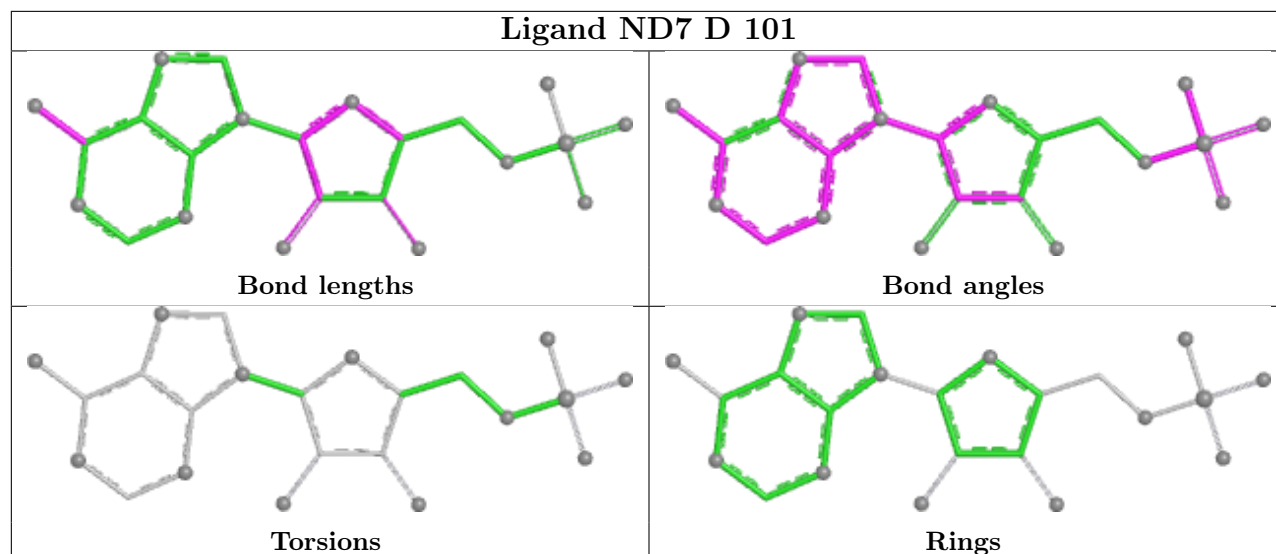
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	404	POP	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	345/348 (99%)	-0.12	8 (2%) 61 65	12, 19, 33, 63	0
1	B	344/348 (98%)	-0.10	8 (2%) 61 65	12, 19, 35, 70	0
2	C	6/7 (85%)	0.13	0 100 100	17, 18, 26, 32	0
2	D	6/7 (85%)	-0.31	0 100 100	17, 17, 23, 24	0
All	All	701/710 (98%)	-0.11	16 (2%) 61 65	12, 19, 34, 70	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1	MET	3.7
1	B	89	ASN	3.7
1	B	58	ALA	3.6
1	A	348	ASN	3.4
1	A	85	ASN	3.4
1	A	290	THR	2.8
1	B	290	THR	2.7
1	A	1	MET	2.7
1	B	33	VAL	2.6
1	A	33	VAL	2.3
1	B	267	LEU	2.2
1	A	30	GLU	2.2
1	B	85	ASN	2.2
1	A	89	ASN	2.0
1	B	53	ALA	2.0
1	A	342	VAL	2.0

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	FME	C	1	10/11	0.97	0.06	18,19,22,24	0
2	FME	D	1	10/11	0.98	0.05	15,16,17,18	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

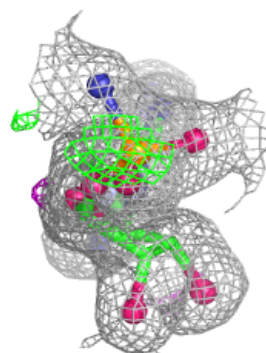
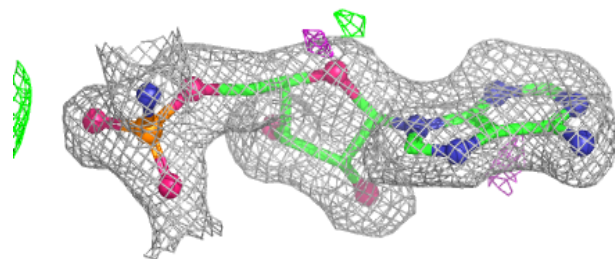
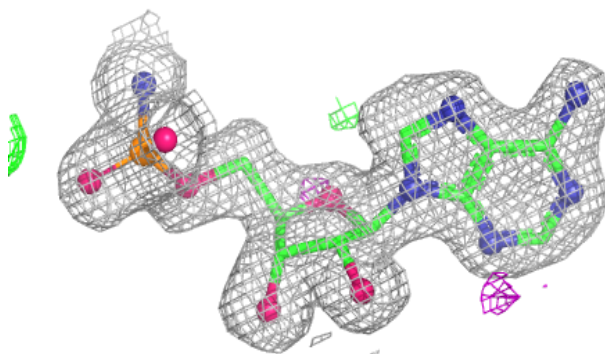
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	MG	B	402	1/1	0.97	0.12	30,30,30,30	0
6	ND7	D	101	23/23	0.97	0.05	17,19,20,22	0
5	POP	B	404	9/9	0.98	0.04	22,24,26,26	0
6	ND7	C	101	23/23	0.98	0.05	18,19,21,23	0
4	MG	A	404	1/1	0.98	0.02	17,17,17,17	0
4	MG	B	403	1/1	0.99	0.07	20,20,20,20	0
5	POP	A	403	9/9	0.99	0.02	15,17,18,18	0
4	MG	A	402	1/1	0.99	0.03	17,17,17,17	0
3	ZN	A	401	1/1	0.99	0.02	18,18,18,18	0
3	ZN	B	401	1/1	0.99	0.05	23,23,23,23	0

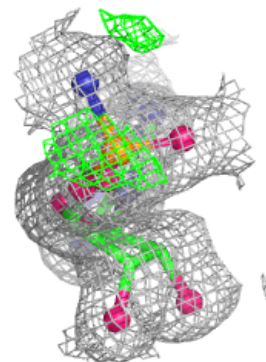
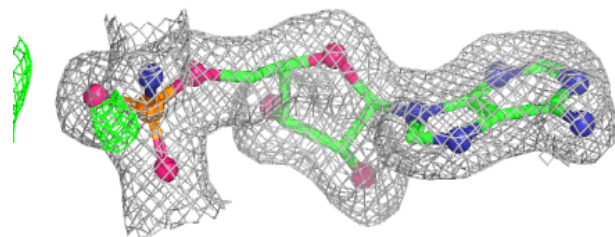
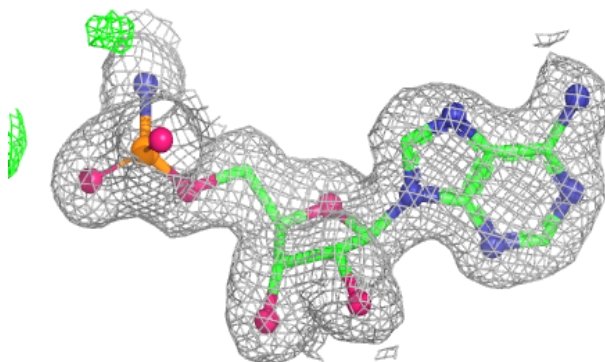
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ND7 D 101:

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

**Electron density around ND7 C 101:**

$2mF_o-DF_c$ (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.