



wwPDB X-ray Structure Validation Summary Report ⓘ

May 18, 2020 – 08:31 am BST

PDB ID : 5CDN
Title : 2.8A structure of etoposide with S.aureus DNA gyrase and DNA
Authors : Bax, B.D.; Srikannathasan, V.; Chan, P.F.
Deposited on : 2015-07-04
Resolution : 2.79 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

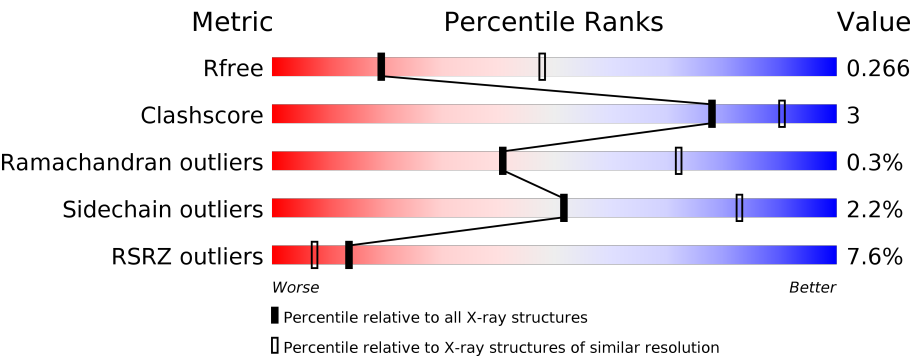
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.79 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	481	<div><div>5%</div><div><div></div><div>91%</div><div>8%</div></div></div>
1	C	481	<div><div>3%</div><div><div></div><div>91%</div><div>8%</div></div></div>
1	R	481	<div><div>7%</div><div><div></div><div>90%</div><div>8%</div><div>.</div></div></div>
1	T	481	<div><div>9%</div><div><div></div><div>92%</div><div>7%</div></div></div>
2	B	189	<div><div>7%</div><div><div></div><div>86%</div><div>13%</div><div>..</div></div></div>
2	D	189	<div><div>16%</div><div><div></div><div>85%</div><div>13%</div><div>..</div></div></div>

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Mol	Chain	Length	Quality of chain
2	S	189	 10% 89% 11%
2	U	189	 15% 88% 11%
3	E	8	 100%
3	F	8	 88% 13%
3	V	8	 100%
3	W	8	 88% 13%
4	G	12	 75% 25%
4	N	12	 50% 42% 8%
4	O	12	 83% 17%
4	P	12	 75% 25%

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 23069 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called DNA gyrase subunit A.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	481	Total	C	N	O	P	S	0	2	0
			3778	2348	682	731	1	16			
1	C	480	Total	C	N	O	P	S	0	0	0
			3775	2349	683	726	1	16			
1	R	475	Total	C	N	O	P	S	0	0	0
			3723	2320	670	716	1	16			
1	T	481	Total	C	N	O	P	S	0	5	0
			3798	2359	686	736	1	16			

- Molecule 2 is a protein called DNA gyrase subunit B,DNA gyrase subunit B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	188	Total	C	N	O	S	0	0	0
			1456	912	251	284	9			
2	D	187	Total	C	N	O	S	0	1	0
			1433	898	250	276	9			
2	S	188	Total	C	N	O	S	0	0	0
			1437	903	249	276	9			
2	U	189	Total	C	N	O	S	0	1	0
			1447	908	255	275	9			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	544	THR	-	linker	UNP P66937
B	545	GLY	-	linker	UNP P66937
D	544	THR	-	linker	UNP P66937
D	545	GLY	-	linker	UNP P66937
S	544	THR	-	linker	UNP P66937
S	545	GLY	-	linker	UNP P66937
U	544	THR	-	linker	UNP P66937
U	545	GLY	-	linker	UNP P66937

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	8	Total 162	C 78	N 33	O 44	P 7	0	0	0
3	F	8	Total 163	C 78	N 33	O 45	P 7	0	0	0
3	V	8	Total 163	C 78	N 33	O 45	P 7	0	0	0
3	W	8	Total 163	C 78	N 33	O 45	P 7	0	0	0

- Molecule 4 is a DNA chain called DNA (5'-D(P*GP*AP*GP*CP*GP*TP*AP*C*GP*GP*CP*CP*GP*TP*AP*CP*GP*CP*TP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	G	12	Total 240	C 115	N 44	O 70	P 11	0	0	0
4	O	12	Total 227	C 108	N 41	O 67	P 11	0	0	0
4	N	12	Total 259	C 124	N 47	O 76	P 12	0	1	0
4	P	12	Total 231	C 111	N 41	O 68	P 11	0	0	0

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O₄S).

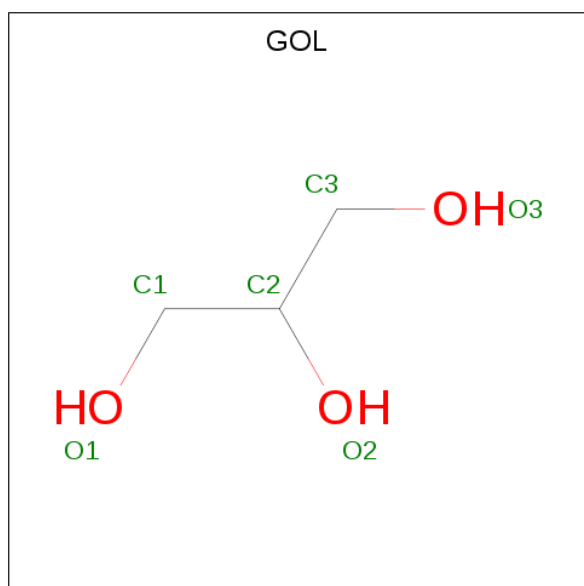


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	Mn	0	0
			1	1		
6	D	1	Total	Mn	0	0
			1	1		
6	S	1	Total	Mn	0	0
			1	1		
6	U	1	Total	Mn	0	0
			1	1		

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).

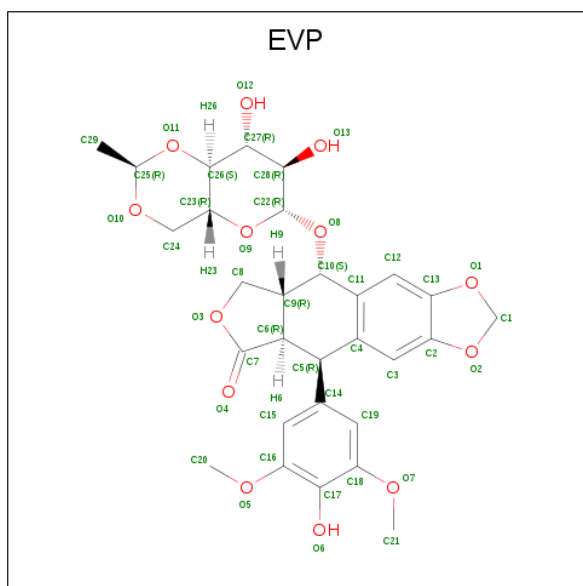


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	C	1	Total	C	O	0	0
			6	3	3		
7	C	1	Total	C	O	0	0
			6	3	3		
7	E	1	Total	C	O	0	0
			6	3	3		
7	T	1	Total	C	O	0	0
			6	3	3		

- Molecule 8 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	C	1	Total Na 1 1	0	0

- Molecule 9 is (5S,5aR,8aR,9R)-9-(4-hydroxy-3,5-dimethoxyphenyl)-8-oxo-5,5a,6,8,8a,9-hexahydrofuro[3',4':6,7]naphtho[2,3-d][1,3]dioxol-5-yl 4,6-O-[(1R)-ethylidene]-beta-D-glucopyranoside (three-letter code: EVP) (formula: C₂₉H₃₂O₁₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	G	1	Total C O 42 29 13	0	0
9	O	1	Total C O 42 29 13	0	0
9	N	1	Total C O 42 29 13	0	0
9	P	1	Total C O 42 29 13	0	0

- Molecule 10 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	75	Total O 75 75	0	0
10	B	27	Total O 27 27	0	0
10	C	76	Total O 76 76	0	0

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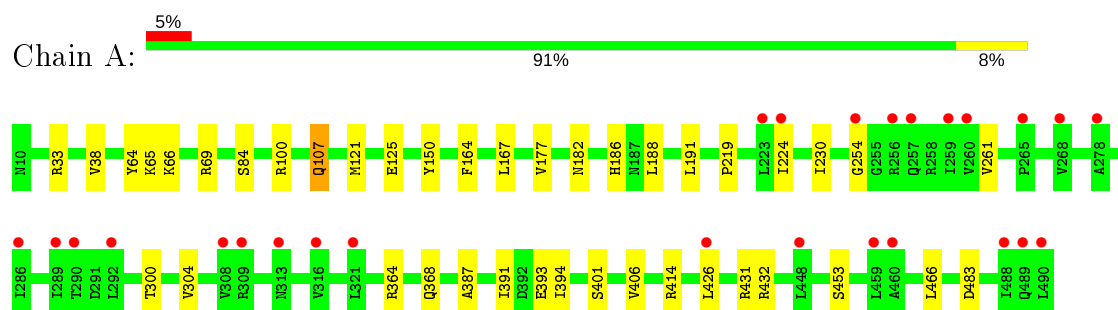
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	D	17	Total	O	0	0
			17	17		
10	E	8	Total	O	0	0
			8	8		
10	G	9	Total	O	0	0
			9	9		
10	F	5	Total	O	0	0
			5	5		
10	O	6	Total	O	0	0
			6	6		
10	R	64	Total	O	0	0
			64	64		
10	S	15	Total	O	0	0
			15	15		
10	T	79	Total	O	0	0
			79	79		
10	U	12	Total	O	0	0
			12	12		
10	V	4	Total	O	0	0
			4	4		
10	N	2	Total	O	0	0
			2	2		
10	W	7	Total	O	0	0
			7	7		
10	P	6	Total	O	0	0
			6	6		

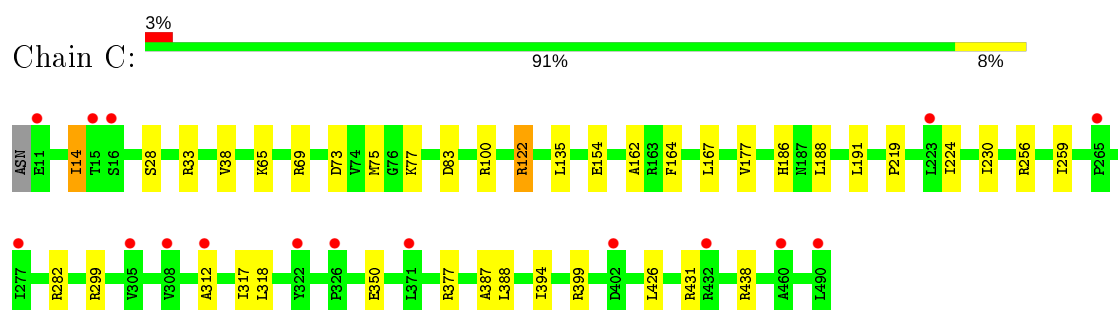
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

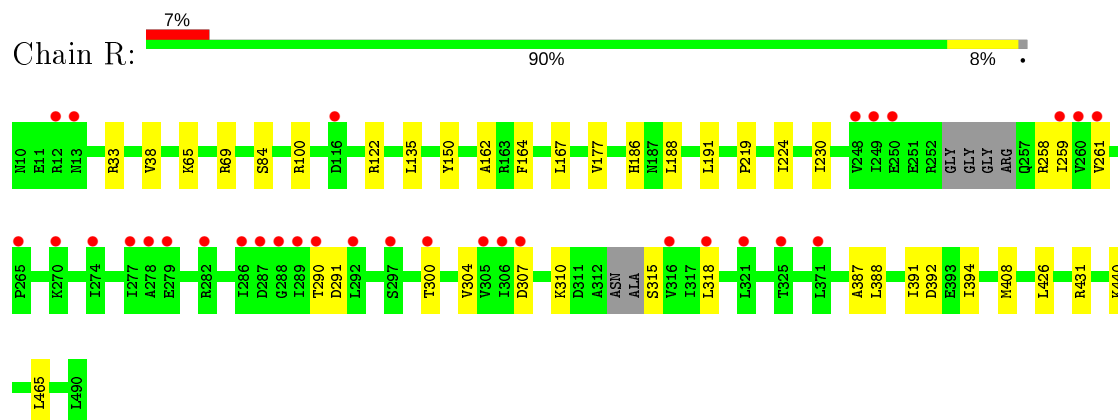
- Molecule 1: DNA gyrase subunit A



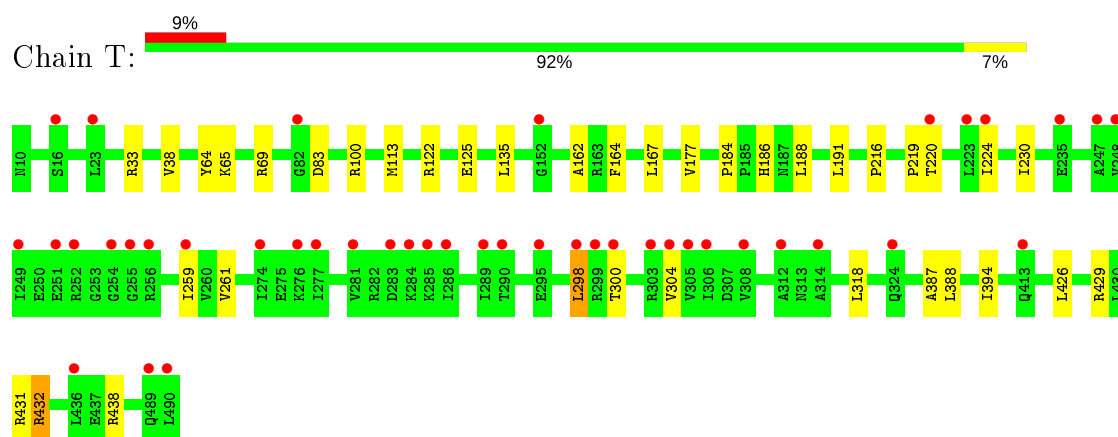
- Molecule 1: DNA gyrase subunit A



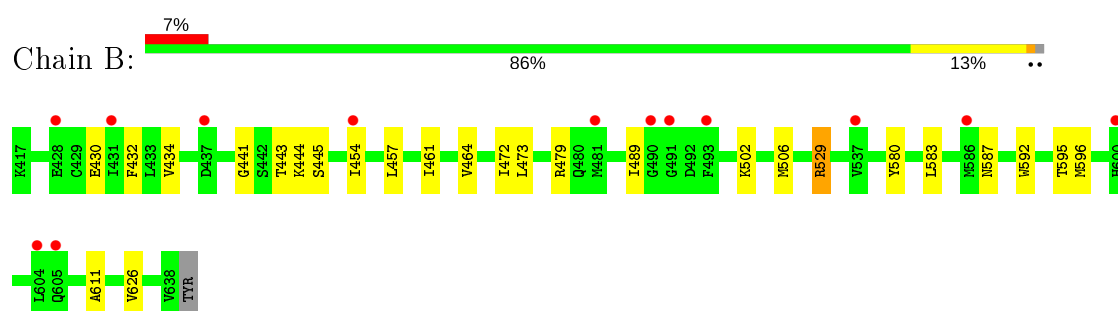
- Molecule 1: DNA gyrase subunit A



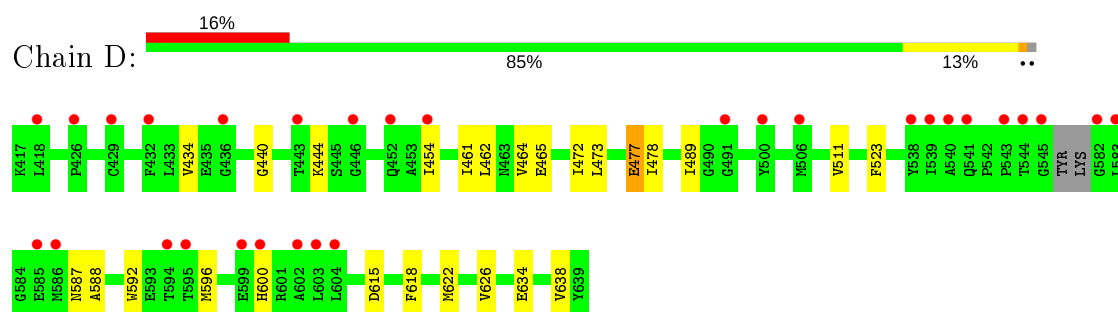
- Molecule 1: DNA gyrase subunit A



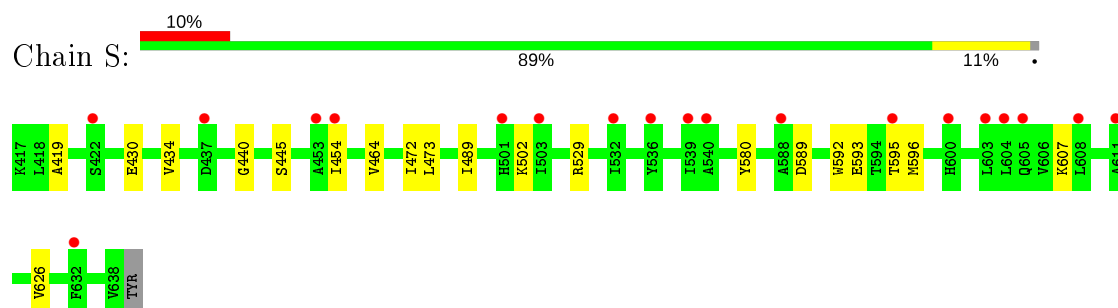
- Molecule 2: DNA gyrase subunit B,DNA gyrase subunit B



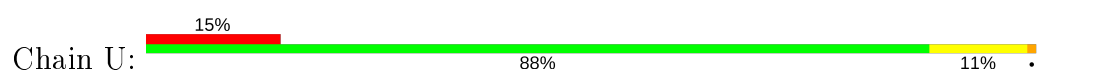
- Molecule 2: DNA gyrase subunit B,DNA gyrase subunit B

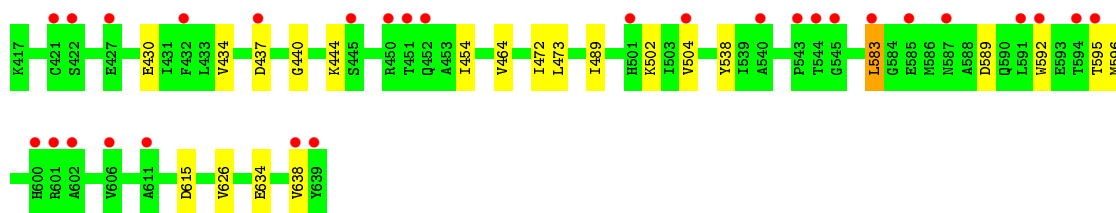


- Molecule 2: DNA gyrase subunit B,DNA gyrase subunit B



- Molecule 2: DNA gyrase subunit B,DNA gyrase subunit B



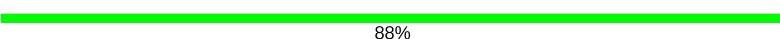
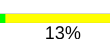


- Molecule 3: DNA (5'-D(P*GP*AP*GP*CP*GP*TP*AP**GP*GP*CP*CP*GP*TP*AP*CP*GP*CP*TP*C)-3')

Chain E:  100%

There are no outlier residues recorded for this chain.

- Molecule 3: DNA (5'-D(P*GP*AP*GP*CP*GP*TP*AP**GP*GP*CP*CP*GP*TP*AP*CP*GP*CP*TP*C)-3')

Chain F:  88%  13%



- Molecule 3: DNA (5'-D(P*GP*AP*GP*CP*GP*TP*AP**GP*GP*CP*CP*GP*TP*AP*CP*GP*CP*TP*C)-3')

Chain V:  100%

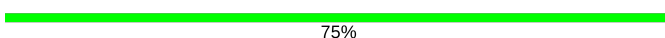
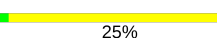
There are no outlier residues recorded for this chain.

- Molecule 3: DNA (5'-D(P*GP*AP*GP*CP*GP*TP*AP**GP*GP*CP*CP*GP*TP*AP*CP*GP*CP*TP*C)-3')

Chain W:  88%  13%

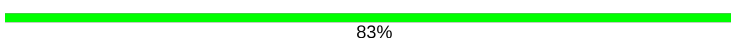
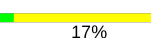


- Molecule 4: DNA (5'-D(P*GP*AP*GP*CP*GP*TP*AP*C*GP*GP*CP*CP*GP*TP*AP*CP*GP*CP*TP*C)-3')

Chain G:  75%  25%



- Molecule 4: DNA (5'-D(P*GP*AP*GP*CP*GP*TP*AP*C*GP*GP*CP*CP*GP*TP*AP*CP*GP*CP*TP*C)-3')

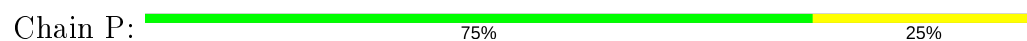
Chain O:  83%  17%



- Molecule 4: DNA (5'-D(P*GP*AP*GP*CP*GP*TP*AP*C*GP*GP*CP*CP*GP*TP*AP*CP*GP*CP*TP*C)-3')



- Molecule 4: DNA (5'-D(P*GP*AP*GP*CP*GP*TP*AP*C*GP*GP*CP*CP*GP*TP*AP*CP*GP*CP*TP*C)-3')



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	89.78Å 170.08Å 124.54Å 90.00° 102.27° 90.00°	Depositor
Resolution (Å)	39.35 – 2.79 39.35 – 2.79	Depositor EDS
% Data completeness (in resolution range)	96.1 (39.35-2.79) 96.2 (39.35-2.79)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.02 (at 2.81Å)	Xtriage
Refinement program	BUSTER 2.11.5	Depositor
R, R_{free}	0.213 , 0.242 0.230 , 0.266	Depositor DCC
R_{free} test set	3484 reflections (4.00%)	wwPDB-VP
Wilson B-factor (Å ²)	56.0	Xtriage
Anisotropy	0.868	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 47.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	23069	wwPDB-VP
Average B, all atoms (Å ²)	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 19.73% 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: GOL, NA, MN, SO4, EVP, PTR

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	0.38	0/3807	0.59	0/5135
1	C	0.38	0/3805	0.59	0/5131
1	R	0.40	0/3751	0.59	0/5062
1	T	0.39	0/3830	0.60	0/5168
2	B	0.39	0/1479	0.61	0/2000
2	D	0.39	0/1458	0.61	0/1973
2	S	0.38	0/1460	0.59	0/1975
2	U	0.39	0/1473	0.61	0/1994
3	E	0.91	0/182	0.90	0/280
3	F	0.87	0/183	0.83	0/281
3	V	0.91	0/183	0.89	0/281
3	W	0.93	0/183	0.86	0/281
4	G	1.04	0/268	0.95	0/412
4	N	1.15	1/288 (0.3%)	0.99	0/440
4	O	0.97	0/253	0.95	0/389
4	P	0.98	0/258	1.00	0/396
All	All	0.46	1/22861 (0.0%)	0.63	0/31198

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	N	2013	DG	O5'-C5'	-5.10	1.29	1.42

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3778	0	3768	19	0
1	C	3775	0	3799	25	0
1	R	3723	0	3720	19	0
1	T	3798	0	3777	21	0
2	B	1456	0	1413	12	0
2	D	1433	0	1376	17	0
2	S	1437	0	1388	9	0
2	U	1447	0	1400	13	0
3	E	162	0	88	0	0
3	F	163	0	91	2	0
3	V	163	0	91	0	0
3	W	163	0	91	1	0
4	G	240	0	133	4	0
4	N	259	0	145	8	0
4	O	227	0	123	2	0
4	P	231	0	126	3	0
5	A	5	0	0	0	0
6	B	1	0	0	0	0
6	D	1	0	0	0	0
6	S	1	0	0	0	0
6	U	1	0	0	0	0
7	C	12	0	16	1	0
7	E	6	0	8	0	0
7	T	6	0	8	0	0
8	C	1	0	0	0	0
9	G	42	0	32	0	0
9	N	42	0	32	0	0
9	O	42	0	32	0	0
9	P	42	0	32	0	0
10	A	75	0	0	1	0
10	B	27	0	0	0	0
10	C	76	0	0	1	0
10	D	17	0	0	0	0
10	E	8	0	0	0	0
10	F	5	0	0	0	0
10	G	9	0	0	0	0
10	N	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	O	6	0	0	0	0
10	P	6	0	0	0	0
10	R	64	0	0	0	0
10	S	15	0	0	0	0
10	T	79	0	0	0	0
10	U	12	0	0	0	0
10	V	4	0	0	0	0
10	W	7	0	0	0	0
All	All	23069	0	21689	127	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.

The worst 5 of 127 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:R:388:LEU:HD23	1:R:391:ILE:HD11	1.70	0.73
1:A:401:SER:HB3	1:A:406:VAL:HG23	1.73	0.71
4:G:2020:DC:H2"	3:F:1:DG:H1	1.57	0.70
2:U:502:LYS:HG2	2:U:538:TYR:HE2	1.56	0.70
2:B:432:PHE:HB2	2:B:454:ILE:CD1	2.23	0.69

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	480/481 (100%)	463 (96%)	14 (3%)	3 (1%)	25	56
1	C	477/481 (99%)	462 (97%)	14 (3%)	1 (0%)	47	78
1	R	468/481 (97%)	451 (96%)	15 (3%)	2 (0%)	34	66

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	T	483/481 (100%)	464 (96%)	18 (4%)	1 (0%)	47	78
2	B	186/189 (98%)	183 (98%)	3 (2%)	0	100	100
2	D	184/189 (97%)	177 (96%)	6 (3%)	1 (0%)	29	61
2	S	186/189 (98%)	183 (98%)	3 (2%)	0	100	100
2	U	188/189 (100%)	180 (96%)	7 (4%)	1 (0%)	29	61
All	All	2652/2680 (99%)	2563 (97%)	80 (3%)	9 (0%)	41	72

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	R	310	LYS
2	U	583	LEU
2	D	588	ALA
1	A	33	ARG
1	C	33	ARG

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	401/415 (97%)	393 (98%)	8 (2%)	55	84
1	C	404/415 (97%)	397 (98%)	7 (2%)	60	87
1	R	396/415 (95%)	387 (98%)	9 (2%)	50	82
1	T	403/415 (97%)	399 (99%)	4 (1%)	76	93
2	B	152/158 (96%)	145 (95%)	7 (5%)	27	60
2	D	146/158 (92%)	142 (97%)	4 (3%)	44	78
2	S	146/158 (92%)	141 (97%)	5 (3%)	37	71
2	U	147/158 (93%)	143 (97%)	4 (3%)	44	78
All	All	2195/2292 (96%)	2147 (98%)	48 (2%)	52	83

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	299	ARG
1	R	84	SER
2	U	583	LEU
2	D	477	GLU
2	D	600	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	597	ASN
1	T	153	ASN
2	S	628	ASN
2	D	476	ASN
2	D	600	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 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$
1	PTR	T	123	1,4	15,16,17	1.26	2 (13%)	19,22,24	1.34	2 (10%)
1	PTR	A	123	1	15,16,17	1.73	4 (26%)	19,22,24	1.87	6 (31%)
1	PTR	C	123	1	15,16,17	1.43	2 (13%)	19,22,24	1.40	3 (15%)
1	PTR	R	123	1,4	15,16,17	1.38	1 (6%)	19,22,24	1.08	1 (5%)

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
1	PTR	T	123	1,4	-	1/10/11/13	0/1/1/1
1	PTR	A	123	1	-	0/10/11/13	0/1/1/1
1	PTR	C	123	1	-	0/10/11/13	0/1/1/1
1	PTR	R	123	1,4	-	0/10/11/13	0/1/1/1

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	123	PTR	CE2-CZ	3.87	1.46	1.38
1	A	123	PTR	CE2-CD2	3.42	1.45	1.38
1	C	123	PTR	CE1-CZ	3.23	1.45	1.38
1	R	123	PTR	CE1-CZ	2.80	1.44	1.38
1	A	123	PTR	CD2-CG	2.61	1.44	1.38

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	123	PTR	O3P-P-O1P	-4.09	94.67	110.68
1	T	123	PTR	O2P-P-OH	3.87	117.33	105.24
1	C	123	PTR	O3P-P-OH	2.87	114.23	105.24
1	A	123	PTR	CD1-CE1-CZ	2.62	122.94	119.73
1	A	123	PTR	P-OH-CZ	-2.60	115.42	123.75

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	T	123	PTR	N-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 5 are monoatomic - leaving 9 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
7	GOL	E	101	-	5,5,5	0.08	0	5,5,5	0.33	0
7	GOL	C	501	-	5,5,5	0.06	0	5,5,5	0.12	0
9	EVP	N	2101	-	48,48,48	0.77	1 (2%)	72,73,73	1.91	12 (16%)
9	EVP	O	2101	-	48,48,48	0.79	1 (2%)	72,73,73	1.77	16 (22%)
9	EVP	G	2101	-	48,48,48	0.78	1 (2%)	72,73,73	1.98	18 (25%)
7	GOL	T	501	-	5,5,5	0.07	0	5,5,5	0.14	0
7	GOL	C	503	-	5,5,5	0.08	0	5,5,5	0.20	0
5	SO4	A	501	-	4,4,4	0.19	0	6,6,6	0.16	0
9	EVP	P	2101	-	48,48,48	0.81	1 (2%)	72,73,73	2.11	15 (20%)

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
7	GOL	E	101	-	-	0/4/4/4	-
7	GOL	C	501	-	-	0/4/4/4	-
9	EVP	N	2101	-	-	2/12/76/76	0/7/7/7
9	EVP	O	2101	-	-	2/12/76/76	0/7/7/7
9	EVP	G	2101	-	-	2/12/76/76	0/7/7/7
7	GOL	T	501	-	-	2/4/4/4	-
7	GOL	C	503	-	-	0/4/4/4	-
9	EVP	P	2101	-	-	4/12/76/76	0/7/7/7

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	O	2101	EVP	C6-C9	-2.36	1.49	1.54
9	P	2101	EVP	C6-C9	-2.30	1.50	1.54
9	G	2101	EVP	C6-C9	-2.19	1.50	1.54
9	N	2101	EVP	C6-C9	-2.04	1.50	1.54

The worst 5 of 61 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	P	2101	EVP	C20-O5-C16	-6.97	107.00	117.53
9	G	2101	EVP	C20-O5-C16	-6.92	107.08	117.53
9	N	2101	EVP	C20-O5-C16	-6.47	107.77	117.53
9	P	2101	EVP	O5-C16-C17	6.28	120.87	114.54
9	N	2101	EVP	O5-C16-C17	5.90	120.49	114.54

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	N	2101	EVP	C17-C16-O5-C20
9	G	2101	EVP	C17-C16-O5-C20
9	P	2101	EVP	C17-C16-O5-C20
9	G	2101	EVP	C15-C16-O5-C20
9	P	2101	EVP	C15-C16-O5-C20

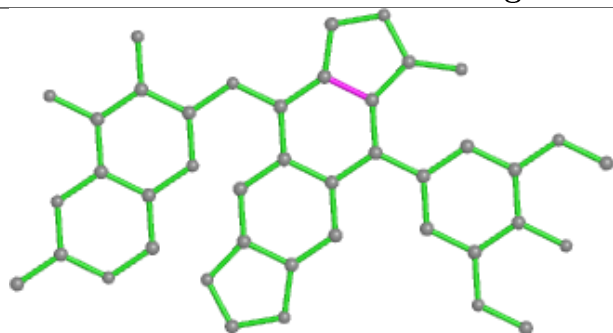
There are no ring outliers.

1 monomer is involved in 1 short contact:

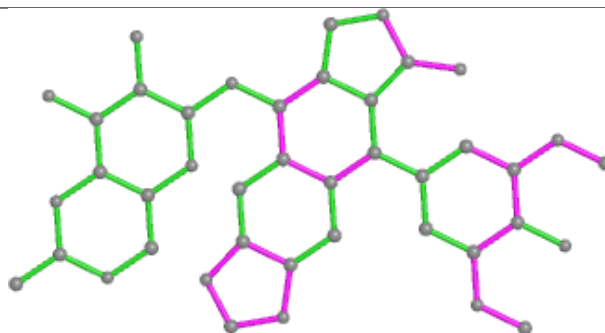
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	C	503	GOL	1	0

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.

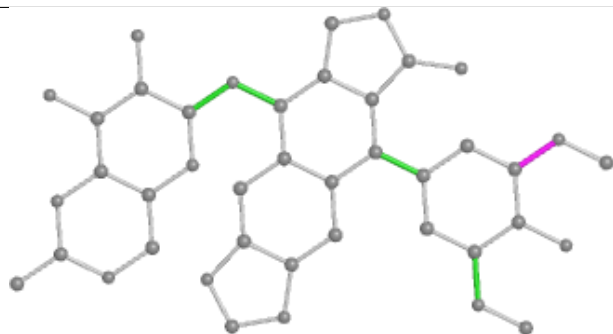
Ligand EVP N 2101



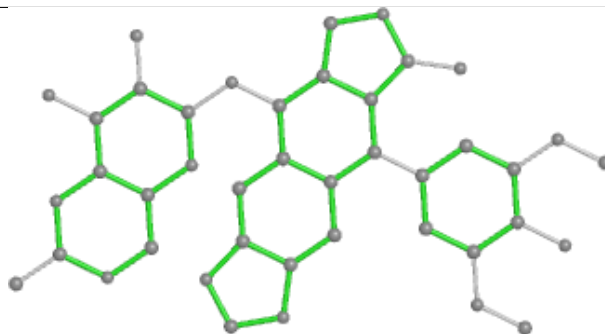
Bond lengths



Bond angles

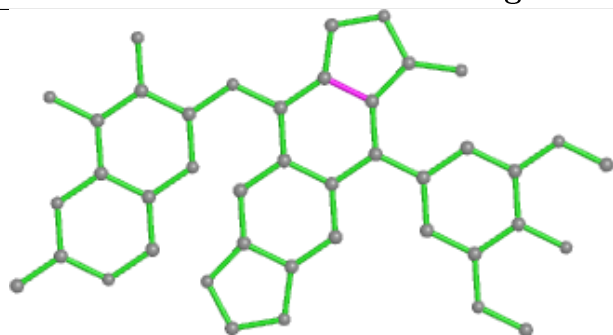


Torsions

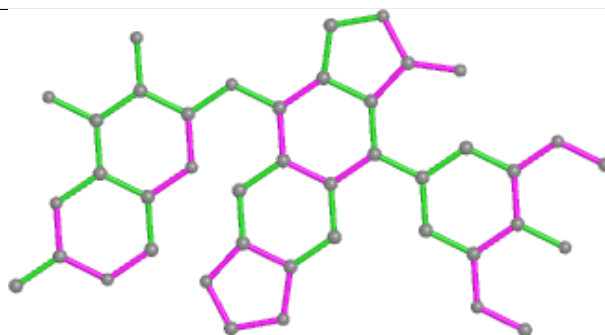


Rings

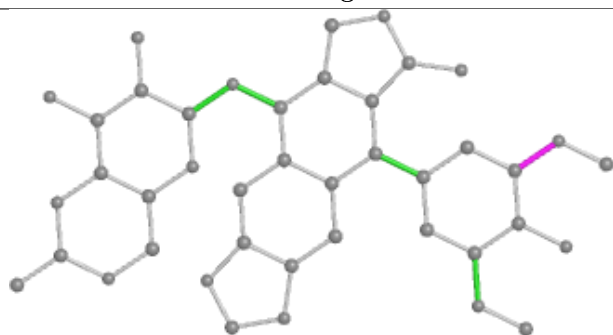
Ligand EVP O 2101



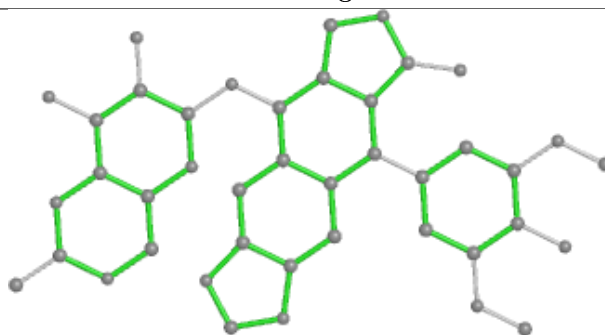
Bond lengths



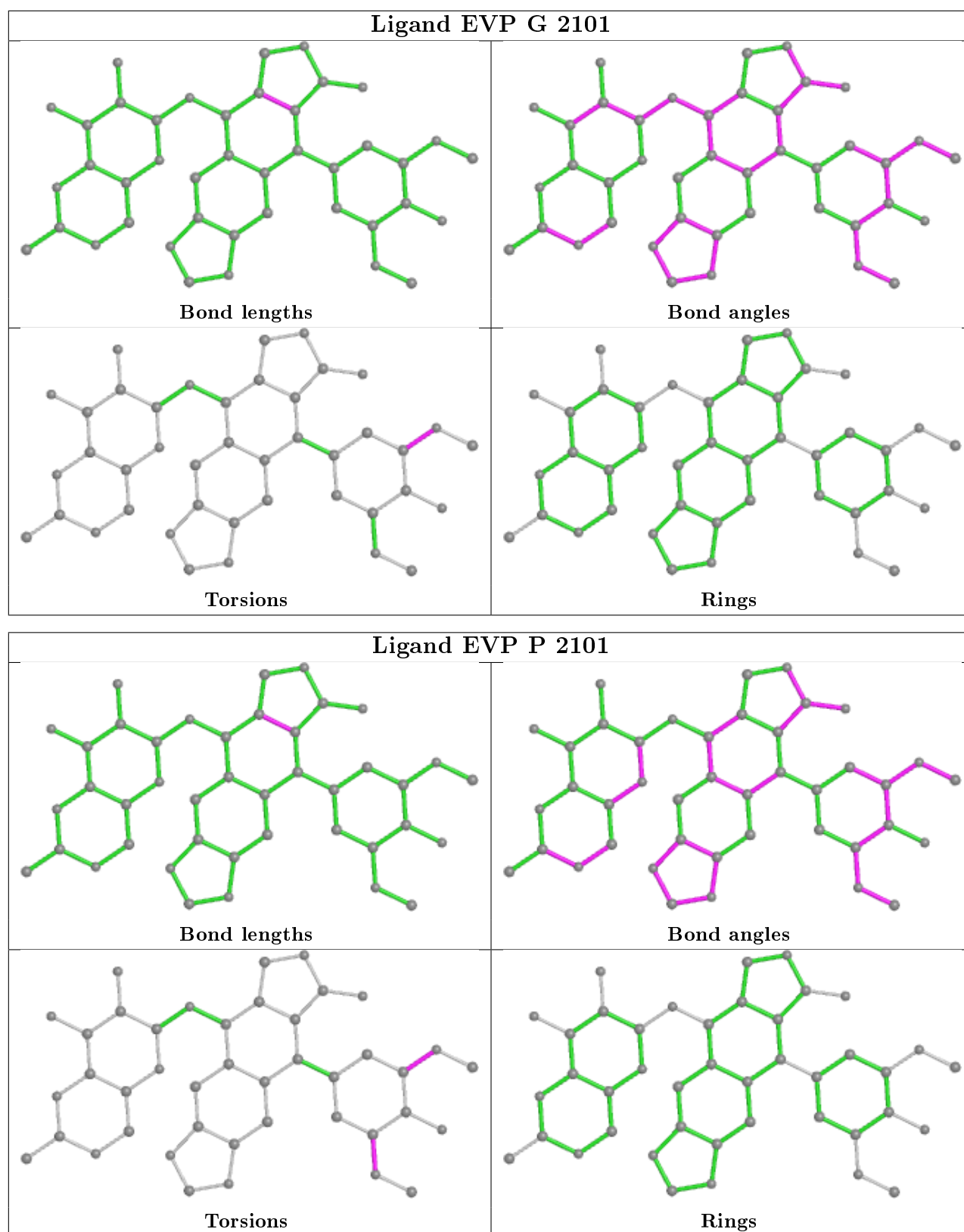
Bond angles



Torsions



Rings



5.7 Other polymers [i](#)

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	480/481 (99%)	0.47	26 (5%) 25 17	48, 69, 101, 115	0
1	C	479/481 (99%)	0.43	16 (3%) 46 36	43, 65, 95, 132	0
1	R	474/481 (98%)	0.53	32 (6%) 17 10	45, 70, 120, 155	0
1	T	480/481 (99%)	0.54	43 (8%) 9 5	47, 70, 125, 152	0
2	B	188/189 (99%)	0.68	13 (6%) 16 10	53, 85, 112, 121	0
2	D	187/189 (98%)	1.10	30 (16%) 1 1	49, 95, 142, 161	0
2	S	188/189 (99%)	0.80	19 (10%) 7 4	62, 102, 134, 149	0
2	U	189/189 (100%)	0.85	29 (15%) 2 1	58, 90, 125, 144	0
3	E	8/8 (100%)	0.47	0 100 100	52, 64, 76, 78	0
3	F	8/8 (100%)	0.44	0 100 100	52, 59, 87, 93	0
3	V	8/8 (100%)	0.48	0 100 100	54, 63, 86, 88	0
3	W	8/8 (100%)	0.34	0 100 100	56, 66, 91, 99	0
4	G	12/12 (100%)	0.09	0 100 100	54, 74, 89, 91	0
4	N	12/12 (100%)	0.08	0 100 100	61, 76, 93, 98	0
4	O	12/12 (100%)	0.31	0 100 100	53, 66, 90, 93	0
4	P	12/12 (100%)	-0.09	0 100 100	56, 76, 88, 93	0
All	All	2745/2760 (99%)	0.58	208 (7%) 13 7	43, 73, 121, 161	0

The worst 5 of 208 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	U	587	ASN	6.9
2	D	585	GLU	6.3
1	R	259	ILE	6.1
1	T	305	VAL	5.3
2	D	586	MET	5.3

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(\AA^2)	Q<0.9
1	PTR	A	123	16/17	0.89	0.22	71,82,98,99	0
1	PTR	R	123	16/17	0.89	0.20	70,80,94,94	0
1	PTR	C	123	16/17	0.94	0.17	65,73,84,85	0
1	PTR	T	123	16/17	0.96	0.21	63,67,77,79	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

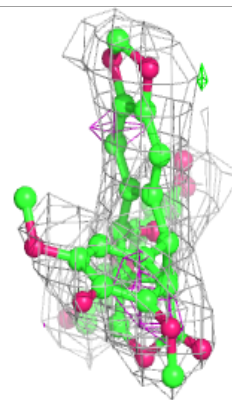
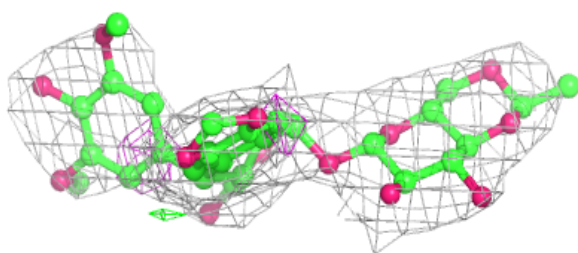
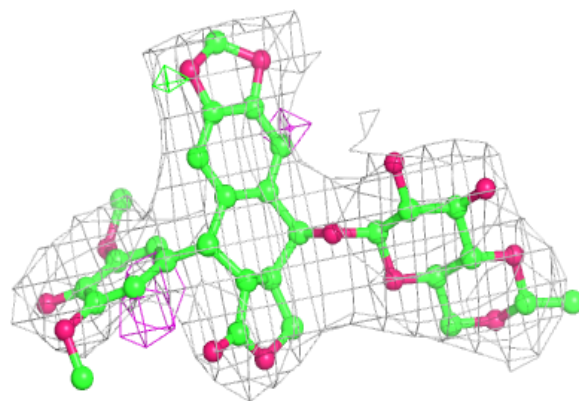
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
7	GOL	C	503	6/6	0.75	0.34	66,72,74,75	0
7	GOL	C	501	6/6	0.81	0.37	76,81,82,83	0
8	NA	C	502	1/1	0.86	0.19	61,61,61,61	0
5	SO4	A	501	5/5	0.87	0.25	113,114,115,115	0
7	GOL	T	501	6/6	0.89	0.24	57,58,59,61	0
9	EVP	P	2101	42/42	0.89	0.23	73,82,92,94	0
9	EVP	O	2101	42/42	0.90	0.21	81,86,91,96	0
7	GOL	E	101	6/6	0.90	0.43	80,82,83,84	0
9	EVP	G	2101	42/42	0.94	0.17	62,73,83,86	0
9	EVP	N	2101	42/42	0.95	0.17	63,69,75,76	0
6	MN	B	1001	1/1	0.98	0.17	57,57,57,57	0
6	MN	U	1001	1/1	0.99	0.16	64,64,64,64	0
6	MN	D	1001	1/1	0.99	0.15	84,84,84,84	0
6	MN	S	6001	1/1	1.00	0.18	61,61,61,61	0

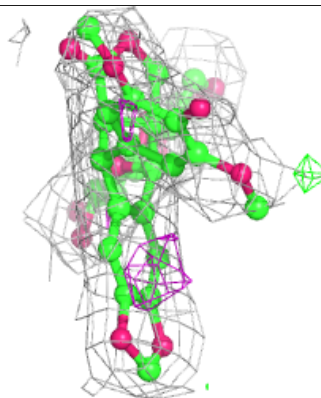
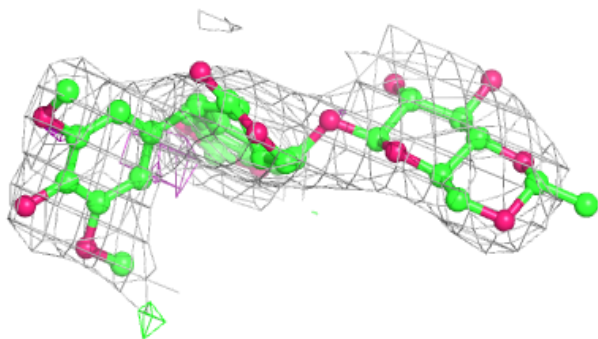
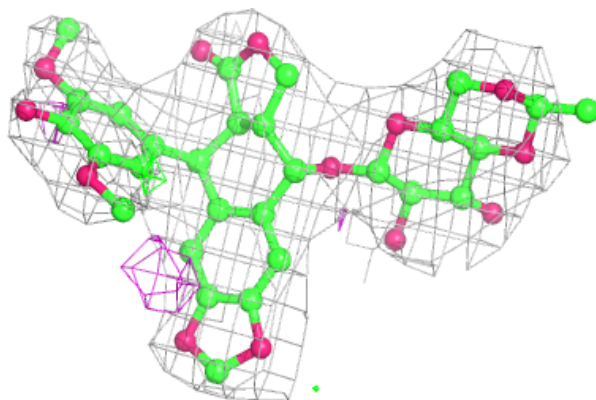
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around EVP P 2101:

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

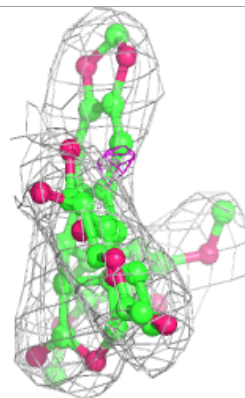
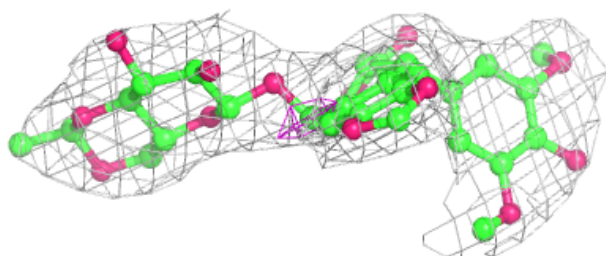
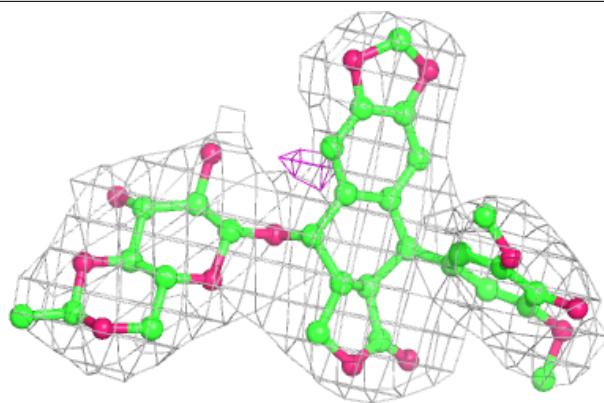
**Electron density around EVP O 2101:**

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

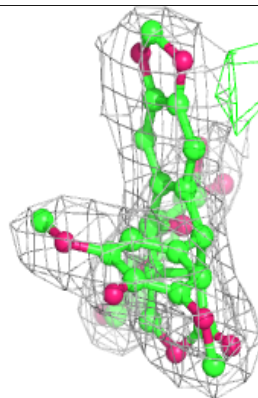
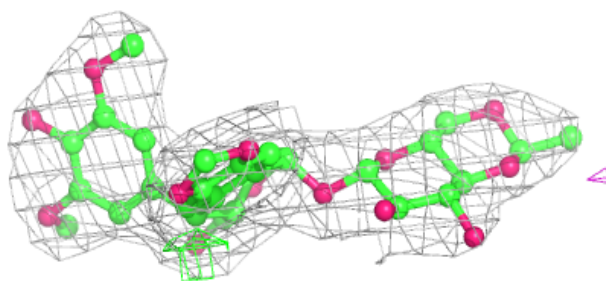
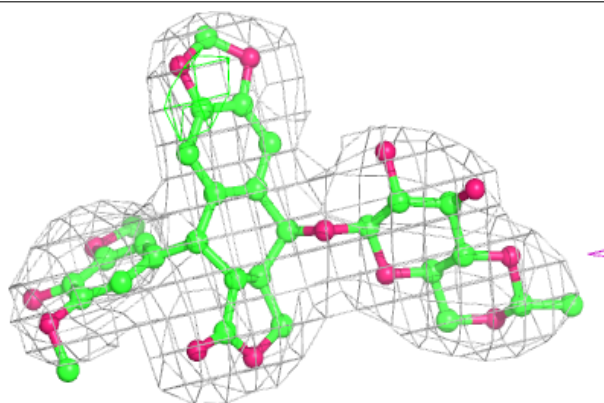


Electron density around EVP G 2101:

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

**Electron density around EVP N 2101:**

$2mF_o-DF_c$ (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.