wwPDB X-ray Structure Validation Summary Report (i)

Apr 27, 2024 – 03:30 pm BST

PDB ID	:	2XCR
Title	:	The 3.5A crystal structure of the catalytic core (B'A' region) of Staphylococcus aureus DNA Gyrase complexed with GSK299423 and DNA
Authors	:	Bax, B.D.; Chan, P.F.; Eggleston, D.S.; Fosberry, A.; Gentry, D.R.; Gorrec, F.; Giordano, I.; Hann, M.M.; Hennessy, A.; Hibbs, M.; Huang, J.; Jones, E.; Jones, J.; Brown, K.K.; Lewis, C.J.; May, E.W.; Singh, O.; Spitzfaden, C.; Shen, C.; Shillings, A.; Theobald, A.F.; Wohlkonig, A.; Pearson, N.D.; Gwynn, M.N.
Deposited on	:	2010-04-25
Resolution	:	3.50 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 (i) 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 (1)) were used in the production of this report:

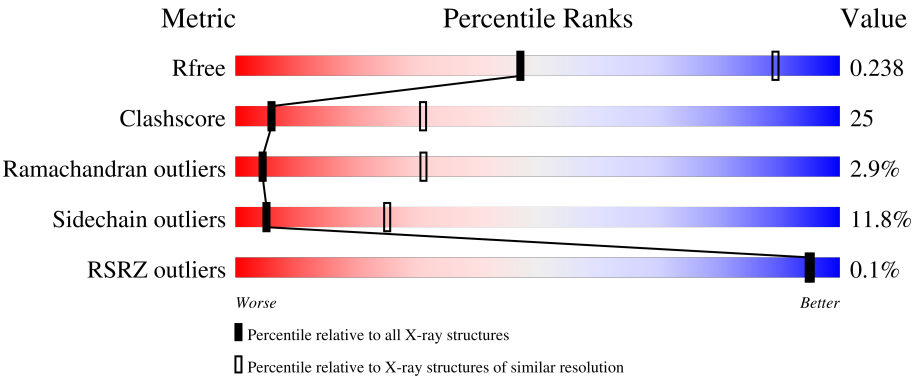
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)

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 3.50 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1659 (3.60-3.40)
Clashscore	141614	1036 (3.58-3.42)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)
RSRZ outliers	127900	1559 (3.60-3.40)

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 <=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	B	726	53% 39% 7%
1	D	726	55% 37% 7%
1	S	726	51% 40% 8%

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Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

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Mol	Chain	Length	Quality of chain
1	U	726	53% 37% 8%
2	E	20	25% 50% 25%
2	F	20	45% 25% 30%
3	V	20	5% 55% 40%
3	W	20	15% 55% 20% 10%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 24495 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 B, DNA GYRASE SUBUNIT A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	718	Total	C	N	O	S	0	0	0
			5689	3556	1018	1090	25			
1	D	719	Total	C	N	O	S	0	0	0
			5692	3556	1021	1090	25			
1	S	718	Total	C	N	O	S	0	0	0
			5694	3561	1022	1086	25			
1	U	717	Total	C	N	O	S	0	0	0
			5689	3558	1020	1086	25			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	409	MET	-	expression tag	UNP Q99XG5
B	1123	PHE	TYR	engineered mutation	UNP Q99XG5
D	409	MET	-	expression tag	UNP Q99XG5
D	1123	PHE	TYR	engineered mutation	UNP Q99XG5
S	409	MET	-	expression tag	UNP Q99XG5
S	1123	PHE	TYR	engineered mutation	UNP Q99XG5
U	409	MET	-	expression tag	UNP Q99XG5
U	1123	PHE	TYR	engineered mutation	UNP Q99XG5

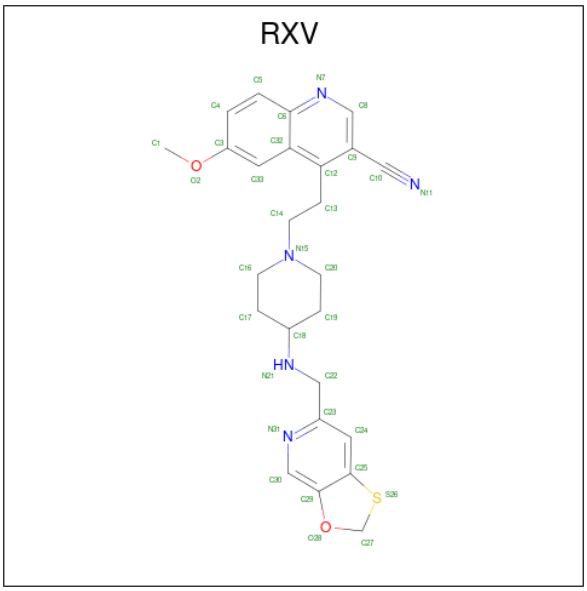
- Molecule 2 is a DNA chain called 5'-D(*5UA*GP*CP*CP*GP*TP*AP*GP*GP*GP*CP*CP*CP*TP*AP*CP*GP *GP*CP*TP)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	20	Total	C	N	O	P	0	0	0
			410	194	77	120	19			
2	F	20	Total	C	N	O	P	0	0	0
			410	194	77	120	19			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	V	20	Total	C	N	O	P	0	0	0
			410	193	77	120	20			
3	W	18	Total	C	N	O	P	0	0	0
			369	173	70	108	18			

- Molecule 4 is 6-METHOXY-4-(2-{4-[([1,3]OXATHIOLO[5,4-C]PYRIDIN-6-YLMETHYL) AMINO]PIPERIDIN-1-YL}ETHYL)QUINOLINE-3-CARBONITRILE (three-letter code: RXV) (formula: $C_{25}H_{27}N_5O_2S$).



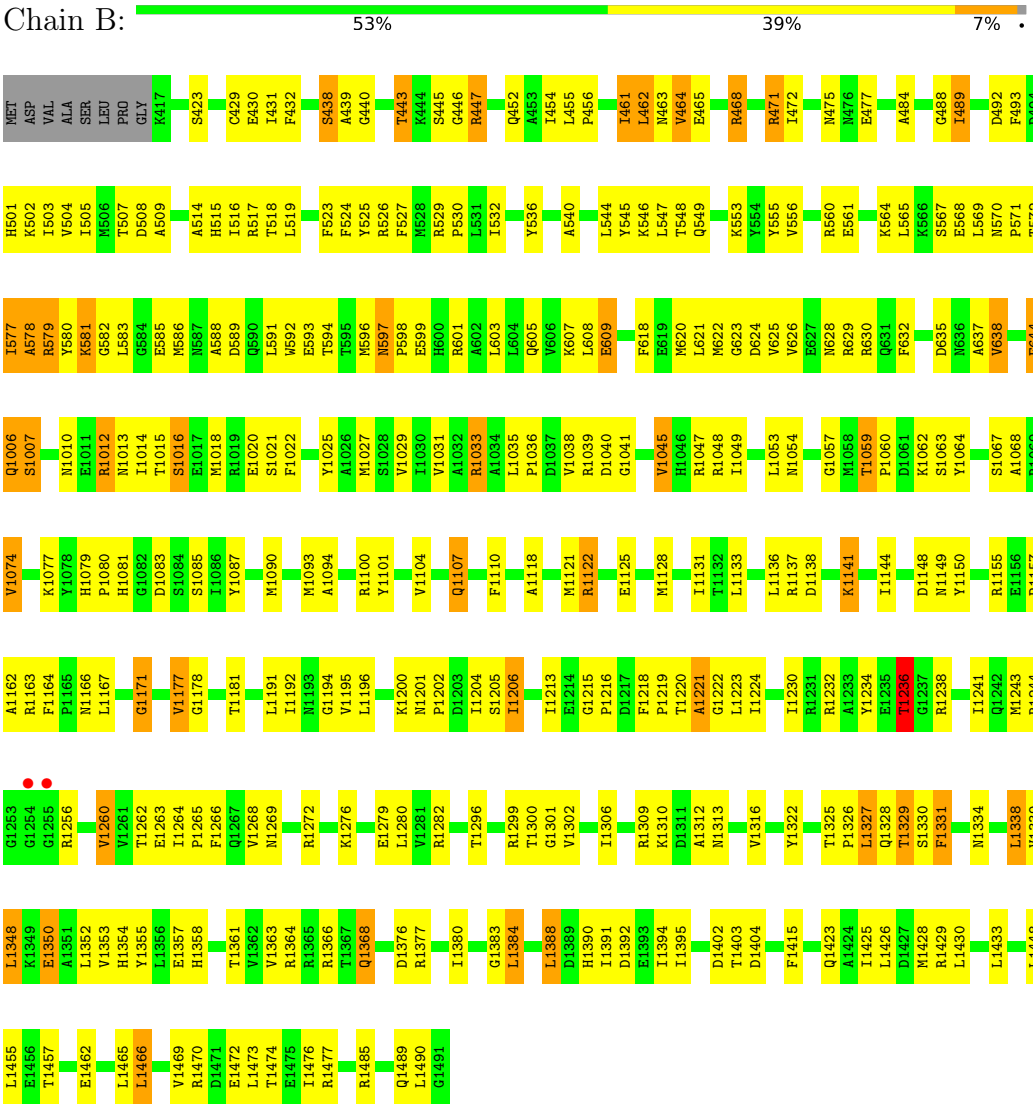
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	E	1	Total	C	N	O	S	0	1
			66	50	10	4	2		
4	W	1	Total	C	N	O	S	0	1
			66	50	10	4	2		

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.

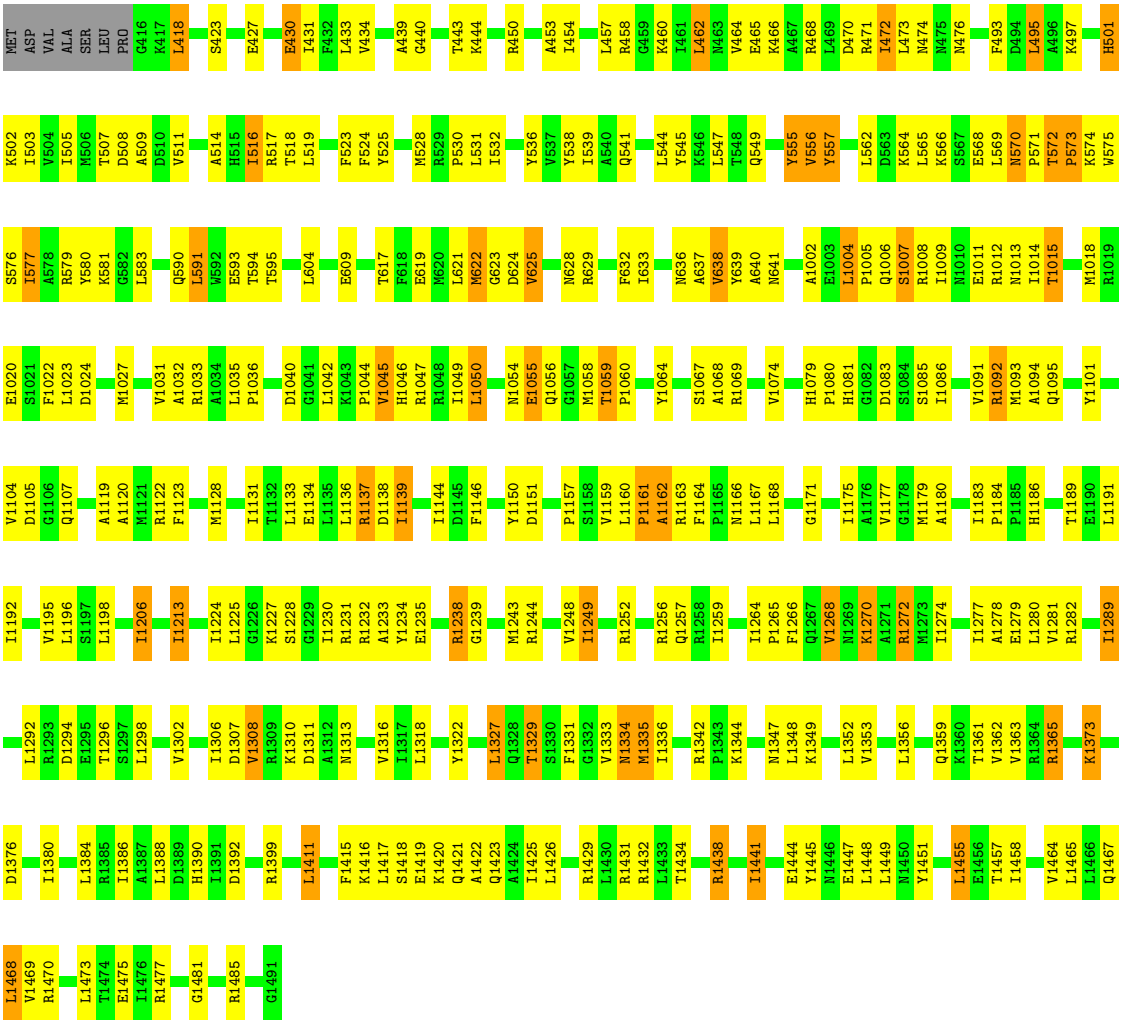
• Molecule 1: DNA GYRASE SUBUNIT B, DNA GYRASE SUBUNIT A

Chain B:



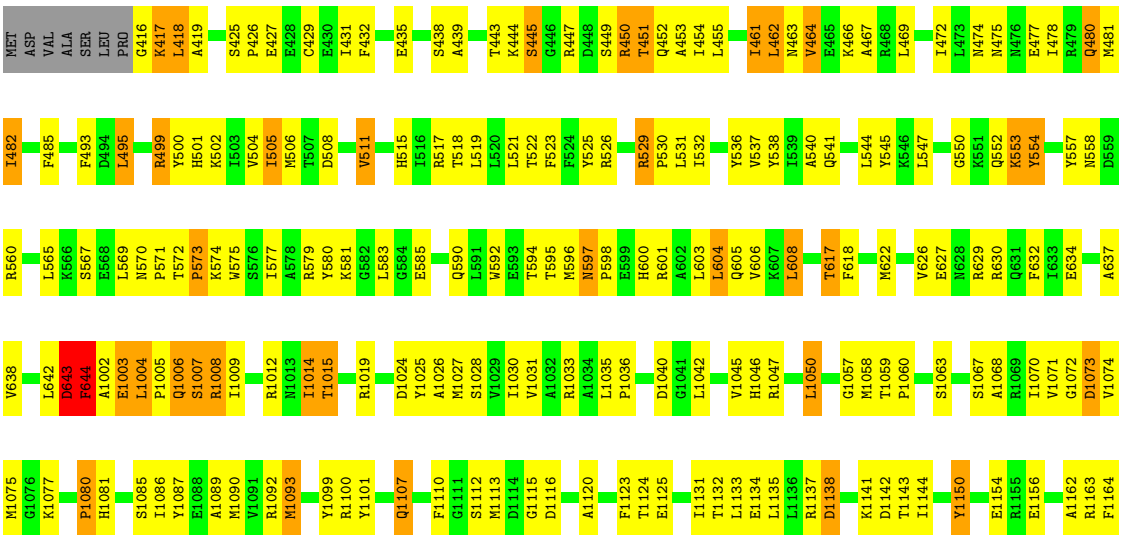
• Molecule 1: DNA GYRASE SUBUNIT B, DNA GYRASE SUBUNIT A

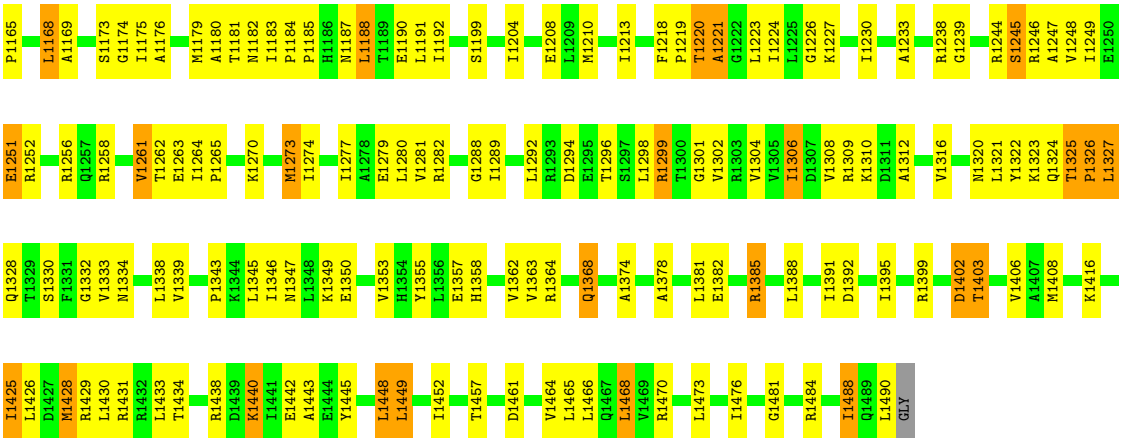
Chain D:



• Molecule 1: DNA GYRASE SUBUNIT B, DNA GYRASE SUBUNIT A

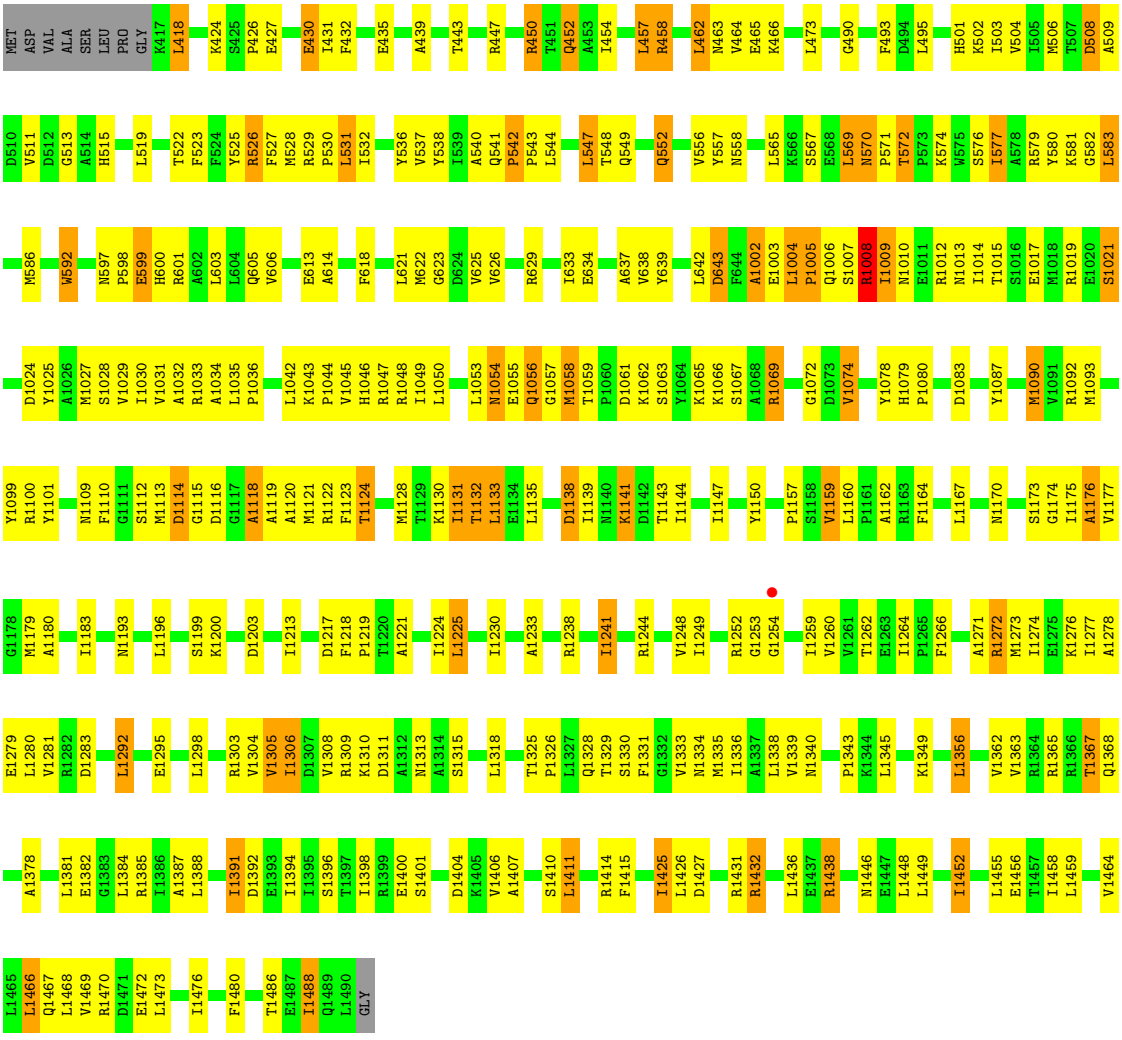
Chain S:





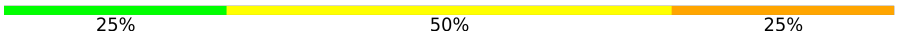
• Molecule 1: DNA GYRASE SUBUNIT B, DNA GYRASE SUBUNIT A

Chain U:



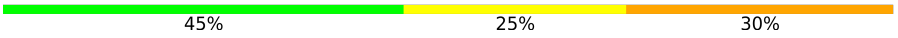
• Molecule 2: 5'-D(*5UA*GP*CP*CP*GP*TP*AP*GP*GP*GP*CP*CP*CP*TP*AP*CP*GP*GP*CP*TP)-3'

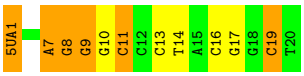
Chain E:



• Molecule 2: 5'-D(*5UA*GP*CP*CP*GP*TP*AP*GP*GP*GP*CP*CP*CP*TP*AP*CP*GP *GP*CP*TP)-3'

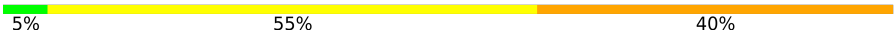
Chain F:





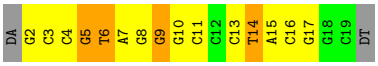
• Molecule 3: 5'-D(*AP*GP*CP*CP*GP*TP*AP*GP*GP*GP*CP*CP*CP*TP*AP*CP*GP *GP*CP*TP)-3'

Chain V:



• Molecule 3: 5'-D(*AP*GP*CP*CP*GP*TP*AP*GP*GP*GP*CP*CP*CP*TP*AP*CP*GP *GP*CP*TP)-3'

Chain W:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	113.26Å 165.38Å 308.43Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	23.99 – 3.50 23.99 – 3.50	Depositor EDS
% Data completeness (in resolution range)	84.5 (23.99-3.50) 84.6 (23.99-3.50)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.24 (at 3.54Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.208 , 0.258 0.176 , 0.238	Depositor DCC
R_{free} test set	2505 reflections (4.03%)	wwPDB-VP
Wilson B-factor (Å^2)	76.8	Xtriage
Anisotropy	1.010	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.24 , 52.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.41$, $< L^2 > = 0.23$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Reported twinning fraction	None for NONE	Depositor
Outliers	1 of 62227 reflections (0.002%)	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	24495	wwPDB-VP
Average B, all atoms (Å^2)	124.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.83% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: 5UA, RXV

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	B	0.40	0/5772	0.63	0/7784
1	D	0.42	0/5775	0.63	0/7792
1	S	0.43	0/5777	0.66	1/7789 (0.0%)
1	U	0.42	0/5772	0.64	0/7785
2	E	0.85	0/435	1.86	10/669 (1.5%)
2	F	0.84	0/435	1.70	9/669 (1.3%)
3	V	0.90	0/459	1.84	14/706 (2.0%)
3	W	0.94	1/413 (0.2%)	1.84	13/635 (2.0%)
All	All	0.47	1/24838 (0.0%)	0.80	47/33829 (0.1%)

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	S	0	1
1	U	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	W	14	DT	C1'-N1	5.28	1.56	1.49

The worst 5 of 47 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	8	DG	O4'-C1'-N9	-15.90	96.87	108.00
3	W	14	DT	O4'-C1'-N1	11.09	115.76	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	W	16	DC	O4'-C4'-C3'	-10.56	99.66	106.00
3	V	16	DC	O4'-C4'-C3'	-10.33	99.80	106.00
2	E	10	DG	O4'-C1'-N9	10.29	115.20	108.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	S	572	THR	Peptide
1	U	572	THR	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	B	5689	0	5712	310	0
1	D	5692	0	5704	271	0
1	S	5694	0	5731	296	0
1	U	5689	0	5721	296	0
2	E	410	0	225	24	0
2	F	410	0	225	19	0
3	V	410	0	224	26	0
3	W	369	0	201	16	0
4	E	66	0	54	9	0
4	W	66	0	54	12	0
All	All	24495	0	23851	1204	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 25.

The worst 5 of 1204 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:D:439:ALA:HB1	1:D:583:LEU:HB2	1.27	1.14
1:B:468:ARG:HH21	1:B:468:ARG:HG3	1.12	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:471:ARG:HH11	1:B:471:ARG:HG2	0.92	1.08
1:S:1005:PRO:HA	1:S:1006:GLN:CB	1.85	1.07
1:S:1003:GLU:HA	1:S:1004:LEU:HB3	1.12	1.05

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	B	716/726 (99%)	596 (83%)	102 (14%)	18 (2%)	5	34
1	D	717/726 (99%)	599 (84%)	97 (14%)	21 (3%)	4	31
1	S	716/726 (99%)	598 (84%)	95 (13%)	23 (3%)	4	29
1	U	715/726 (98%)	607 (85%)	86 (12%)	22 (3%)	4	30
All	All	2864/2904 (99%)	2400 (84%)	380 (13%)	84 (3%)	4	31

5 of 84 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	579	ARG
1	B	644	PHE
1	B	1004	LEU
1	B	1005	PRO
1	B	1007	SER

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	B	611/624 (98%)	543 (89%)	68 (11%)	6 28
1	D	610/624 (98%)	541 (89%)	69 (11%)	6 27
1	S	611/624 (98%)	531 (87%)	80 (13%)	4 21
1	U	611/624 (98%)	539 (88%)	72 (12%)	5 25
All	All	2443/2496 (98%)	2154 (88%)	289 (12%)	5 25

5 of 289 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	U	569	LEU
1	U	1468	LEU
1	U	1012	ARG
1	U	1167	LEU
1	D	1059	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 48 such sidechains are listed below:

Mol	Chain	Res	Type
1	S	605	GLN
1	S	1368	GLN
1	S	1056	GLN
1	S	1109	ASN
1	S	1450	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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	5UA	E	1	-	21,23,23	2.74	3 (14%)	20,33,33	2.54	5 (25%)
2	5UA	F	1	-	21,23,23	2.73	3 (14%)	20,33,33	2.57	5 (25%)

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	5UA	E	1	-	-	3/4/21/21	0/3/3/3
2	5UA	F	1	-	-	1/4/21/21	0/3/3/3

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	1	5UA	C2-N3	8.92	1.46	1.32
2	F	1	5UA	C2-N3	8.78	1.46	1.32
2	F	1	5UA	C2-N1	6.74	1.46	1.33
2	E	1	5UA	C2-N1	6.67	1.46	1.33
2	F	1	5UA	O5'-C6'	4.71	1.46	1.33

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	F	1	5UA	N3-C2-N1	-9.39	114.00	128.68
2	E	1	5UA	N3-C2-N1	-9.11	114.44	128.68
2	E	1	5UA	O5'-C6'-OP3	-3.70	118.03	126.62
2	F	1	5UA	C4-C5-N7	-3.39	105.86	109.40
2	E	1	5UA	C4-C5-N7	-3.37	105.88	109.40

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	1	5UA	C3'-C4'-C5'-O5'
2	F	1	5UA	OP3-C6'-O5'-C5'
2	E	1	5UA	O4'-C4'-C5'-O5'
2	E	1	5UA	OP3-C6'-O5'-C5'

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	1	5UA	1	0
2	F	1	5UA	2	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	RXV	W	1020[B]	-	36,37,37	2.27	6 (16%)	45,51,51	1.98	8 (17%)
4	RXV	E	1021[A]	-	36,37,37	2.55	5 (13%)	45,51,51	3.03	16 (35%)
4	RXV	W	1020[A]	-	36,37,37	2.38	5 (13%)	45,51,51	1.61	10 (22%)
4	RXV	E	1021[B]	-	36,37,37	2.47	5 (13%)	45,51,51	1.86	13 (28%)

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	RXV	W	1020[B]	-	-	6/14/30/30	0/5/5/5
4	RXV	E	1021[A]	-	-	6/14/30/30	0/5/5/5
4	RXV	W	1020[A]	-	-	6/14/30/30	0/5/5/5
4	RXV	E	1021[B]	-	-	3/14/30/30	0/5/5/5

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	1021[A]	RXV	C9-C10	-11.77	1.26	1.44
4	E	1021[B]	RXV	C9-C10	-10.10	1.29	1.44
4	W	1020[B]	RXV	C9-C10	-9.68	1.29	1.44
4	W	1020[A]	RXV	C9-C10	-9.46	1.30	1.44
4	W	1020[A]	RXV	C25-S26	-7.10	1.68	1.76

The worst 5 of 47 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	E	1021[A]	RXV	C9-C8-N7	-12.15	116.65	125.68
4	E	1021[B]	RXV	C22-N21-C18	7.31	124.60	114.14
4	W	1020[B]	RXV	C9-C8-N7	-7.22	120.31	125.68
4	E	1021[A]	RXV	C8-N7-C6	6.23	124.41	116.91
4	E	1021[A]	RXV	C9-C10-N11	-6.00	167.99	177.88

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	E	1021[A]	RXV	C9-C12-C13-C14
4	E	1021[A]	RXV	C19-C18-N21-C22
4	W	1020[A]	RXV	N11-C10-C9-C8
4	W	1020[A]	RXV	C9-C12-C13-C14
4	W	1020[B]	RXV	C9-C12-C13-C14

There are no ring outliers.

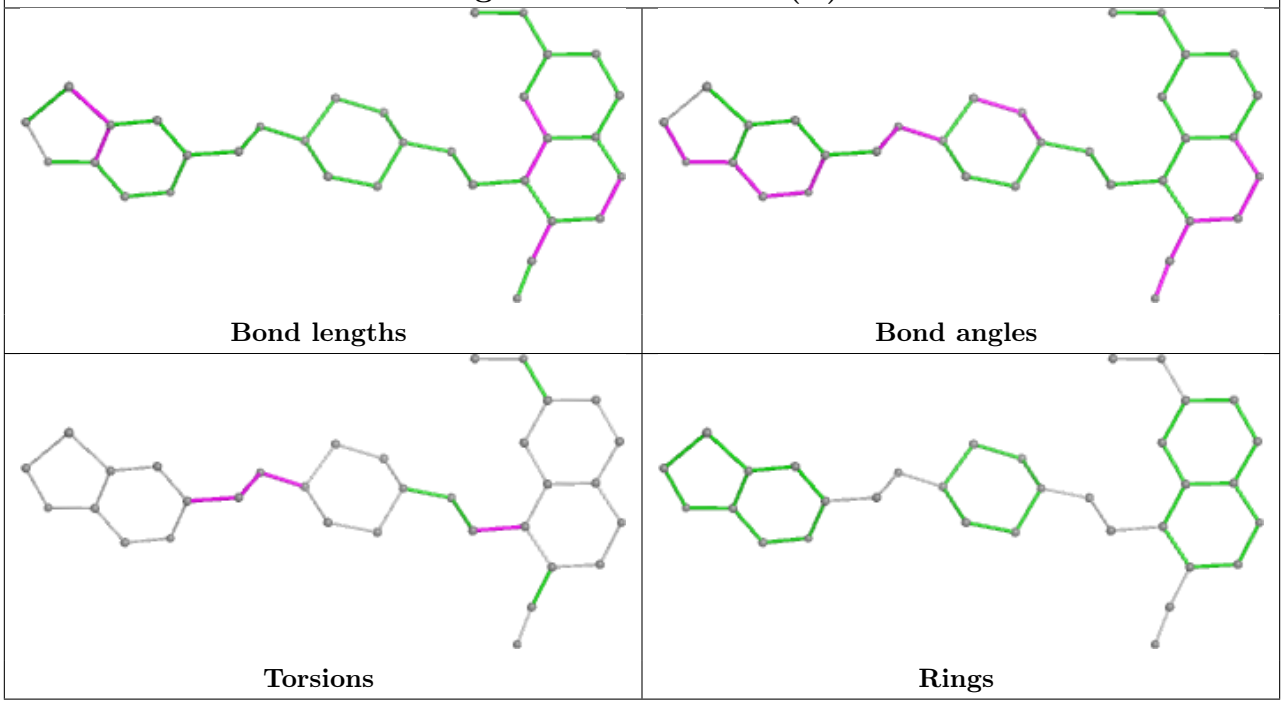
4 monomers are involved in 21 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	W	1020[B]	RXV	5	0
4	E	1021[A]	RXV	5	0
4	W	1020[A]	RXV	7	0
4	E	1021[B]	RXV	4	0

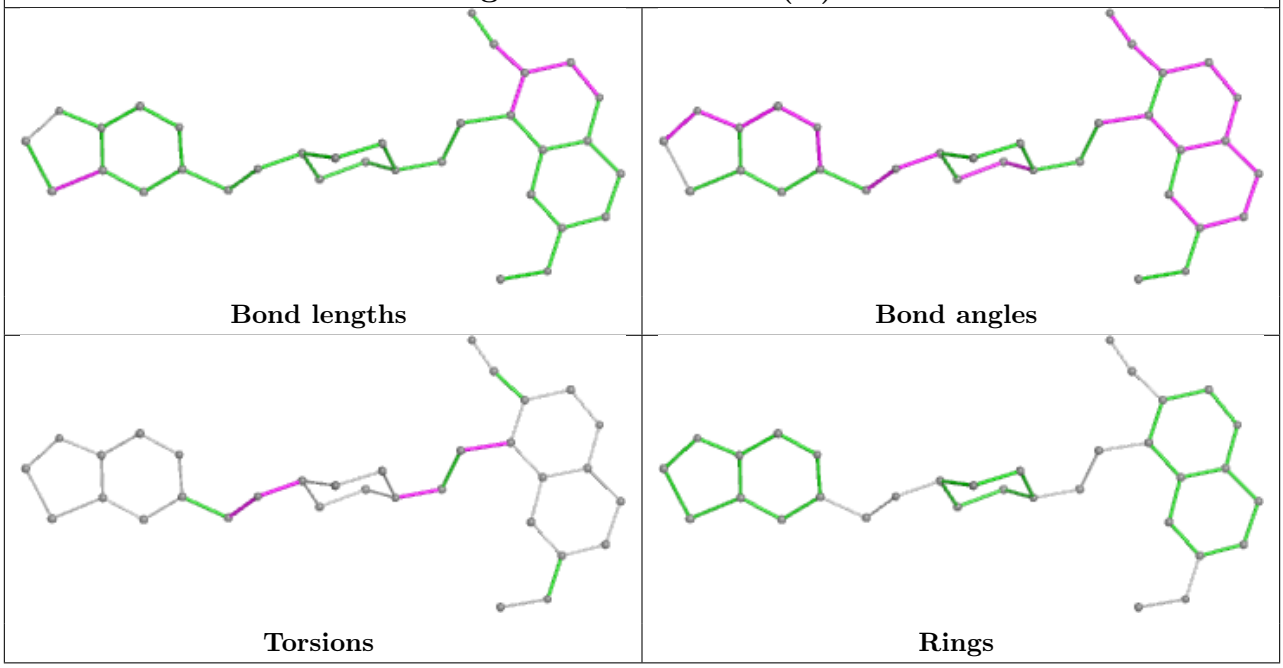
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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.

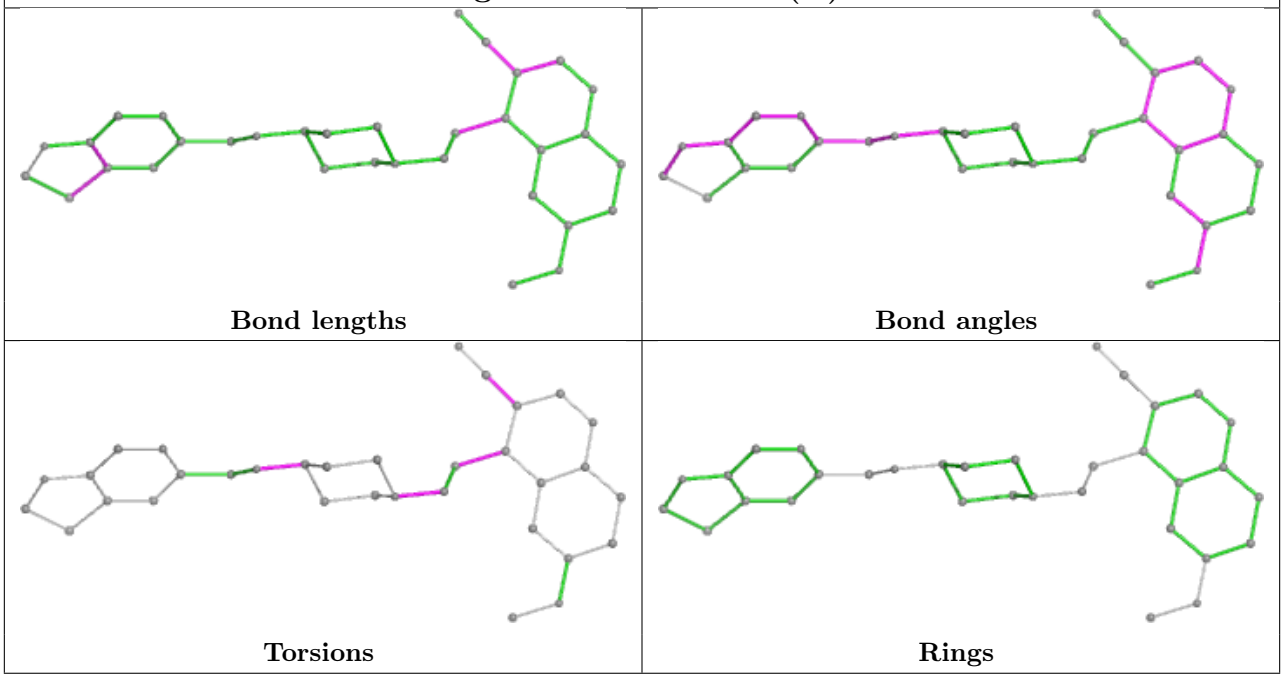
Ligand RXV W 1020 (B)



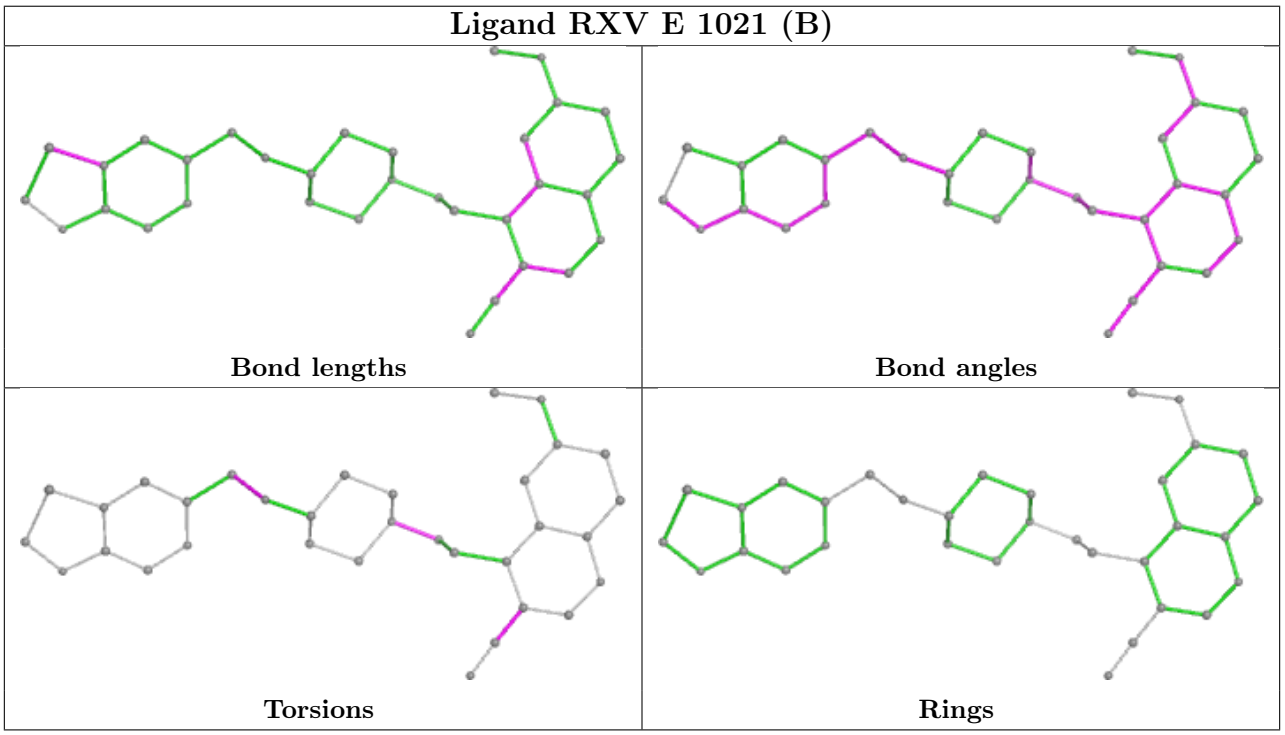
Ligand RXV E 1021 (A)



Ligand RXV W 1020 (A)



Ligand RXV E 1021 (B)



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	E	1
2	F	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	1:5UA	O3'	2:DG	P	3.52
1	F	1:5UA	O3'	2:DG	P	3.24

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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, 95^{th} 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	B	718/726 (98%)	-0.67	2 (0%) 94 91	78, 126, 188, 218	0
1	D	719/726 (99%)	-0.68	0 100 100	63, 111, 184, 221	0
1	S	718/726 (98%)	-0.73	0 100 100	64, 116, 171, 203	0
1	U	717/726 (98%)	-0.72	1 (0%) 95 95	64, 123, 171, 222	0
2	E	19/20 (95%)	-0.48	0 100 100	103, 115, 196, 218	0
2	F	19/20 (95%)	-0.53	0 100 100	96, 112, 188, 193	0
3	V	20/20 (100%)	-0.33	0 100 100	91, 116, 209, 268	0
3	W	18/20 (90%)	-0.43	0 100 100	100, 119, 173, 202	0
All	All	2948/2984 (98%)	-0.69	3 (0%) 95 95	63, 120, 181, 268	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1254	GLY	2.6
1	B	1255	GLY	2.3
1	U	1254	GLY	2.1

6.2 Non-standard residues in protein, DNA, RNA chains

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, 95^{th} 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	5UA	E	1	21/21	0.89	0.29	193,198,206,208	0
2	5UA	F	1	21/21	0.89	0.42	220,235,239,241	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

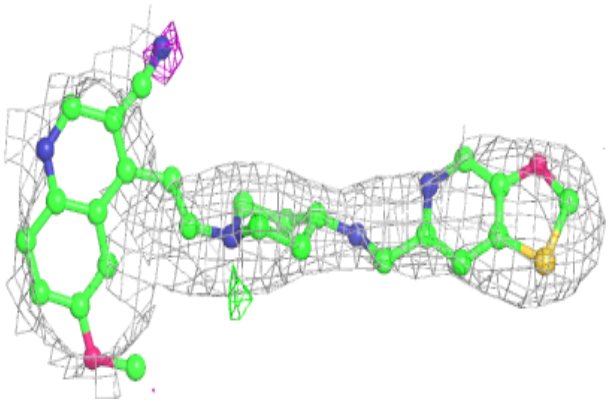
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

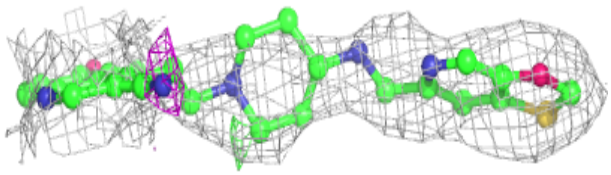
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	RXV	E	1021[A]	33/33	0.88	0.29	111,129,144,148	33
4	RXV	E	1021[B]	33/33	0.88	0.29	110,128,143,146	33
4	RXV	W	1020[A]	33/33	0.94	0.20	100,108,111,111	33
4	RXV	W	1020[B]	33/33	0.94	0.20	100,108,110,110	33

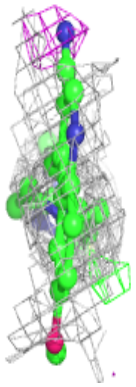
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around RXV E 1021 (A):

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

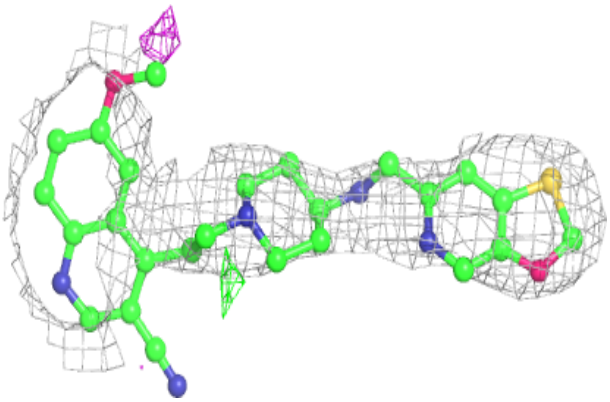


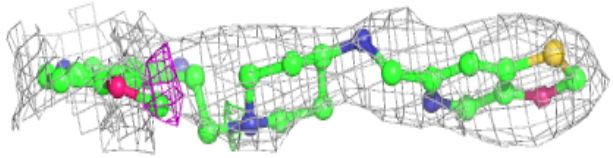


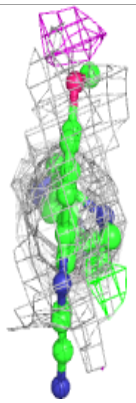


Electron density around RXV E 1021 (B):

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

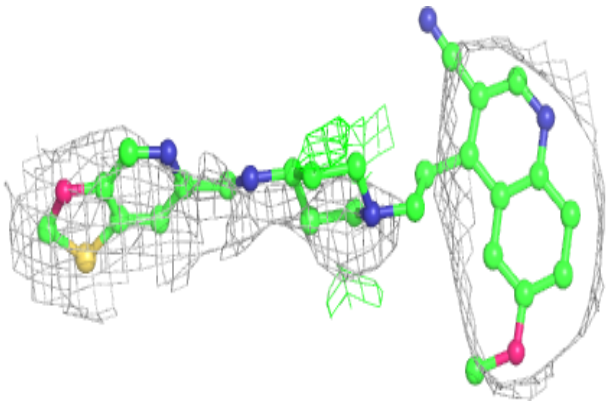


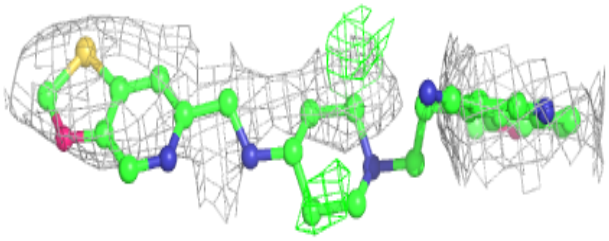


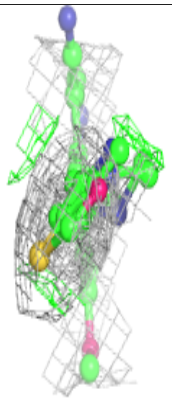


Electron density around RXV W 1020 (A):

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

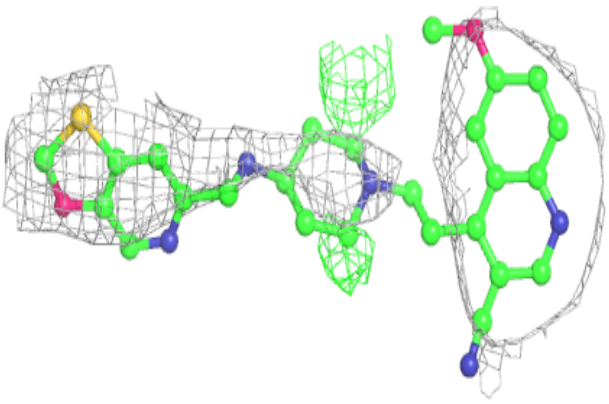


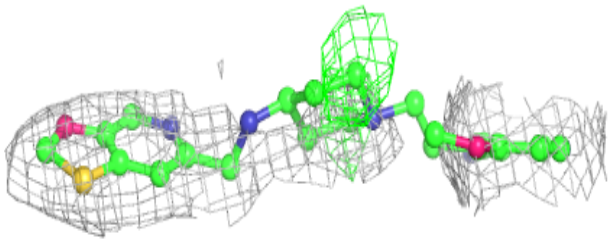


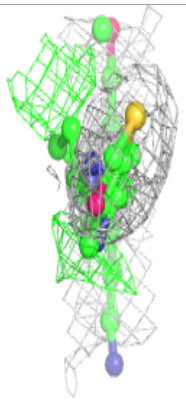


Electron density around RXV W 1020 (B):

$2mF_o$-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.