



# Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 03:25 am BST

PDB ID : 5ON2  
Title : Quaternary complex of mutant T252A of E. coli leucyl-tRNA synthetase with tRNA(leu), leucyl-adenylate analogue, and post-transfer editing analogue of norvaline in the aminoacylation conformation  
Authors : Palencia, A.; Cusack, S.  
Deposited on : 2017-08-02  
Resolution : 3.10 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](mailto: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.

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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

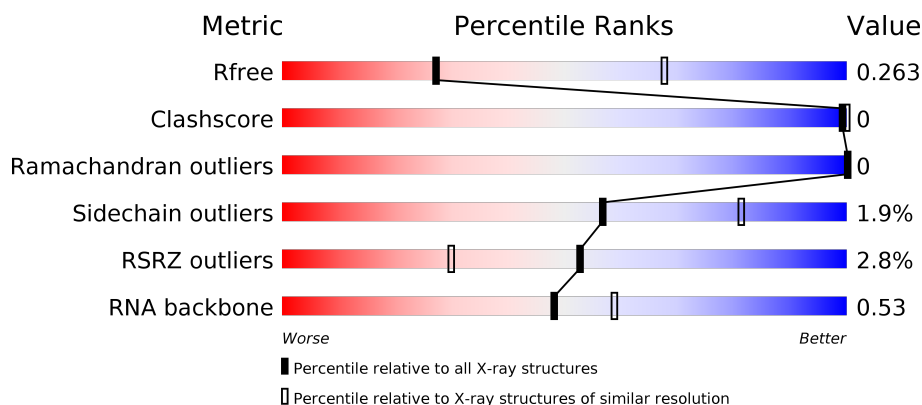
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.10 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	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)
RNA backbone	3102	1116 (3.40-2.80)

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  $\geq 3$ , 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	880	<div> <div>3%</div> <div>96%</div> <div>2%</div> </div>
1	D	880	<div> <div>3%</div> <div>96%</div> <div>2%</div> </div>
2	B	87	<div> <div>83%</div> <div>15%</div> <div>2%</div> </div>
2	E	87	<div> <div>76%</div> <div>17%</div> <div>7%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	ZN	D	900	-	-	-	X

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 17332 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 Leucine-tRNA ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	862	Total	C	N	O	S	0	0	0
			6843	4344	1161	1293	45			
1	D	860	Total	C	N	O	S	0	0	0
			6833	4338	1159	1291	45			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP P07813
A	-18	GLY	-	expression tag	UNP P07813
A	-17	SER	-	expression tag	UNP P07813
A	-16	SER	-	expression tag	UNP P07813
A	-15	HIS	-	expression tag	UNP P07813
A	-14	HIS	-	expression tag	UNP P07813
A	-13	HIS	-	expression tag	UNP P07813
A	-12	HIS	-	expression tag	UNP P07813
A	-11	HIS	-	expression tag	UNP P07813
A	-10	HIS	-	expression tag	UNP P07813
A	-9	SER	-	expression tag	UNP P07813
A	-8	SER	-	expression tag	UNP P07813
A	-7	GLY	-	expression tag	UNP P07813
A	-6	LEU	-	expression tag	UNP P07813
A	-5	VAL	-	expression tag	UNP P07813
A	-4	PRO	-	expression tag	UNP P07813
A	-3	ARG	-	expression tag	UNP P07813
A	-2	GLY	-	expression tag	UNP P07813
A	-1	SER	-	expression tag	UNP P07813
A	0	HIS	-	expression tag	UNP P07813
A	252	ALA	THR	engineered mutation	UNP P07813
D	-19	MET	-	initiating methionine	UNP P07813
D	-18	GLY	-	expression tag	UNP P07813
D	-17	SER	-	expression tag	UNP P07813
D	-16	SER	-	expression tag	UNP P07813

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-15	HIS	-	expression tag	UNP P07813
D	-14	HIS	-	expression tag	UNP P07813
D	-13	HIS	-	expression tag	UNP P07813
D	-12	HIS	-	expression tag	UNP P07813
D	-11	HIS	-	expression tag	UNP P07813
D	-10	HIS	-	expression tag	UNP P07813
D	-9	SER	-	expression tag	UNP P07813
D	-8	SER	-	expression tag	UNP P07813
D	-7	GLY	-	expression tag	UNP P07813
D	-6	LEU	-	expression tag	UNP P07813
D	-5	VAL	-	expression tag	UNP P07813
D	-4	PRO	-	expression tag	UNP P07813
D	-3	ARG	-	expression tag	UNP P07813
D	-2	GLY	-	expression tag	UNP P07813
D	-1	SER	-	expression tag	UNP P07813
D	0	HIS	-	expression tag	UNP P07813
D	252	ALA	THR	engineered mutation	UNP P07813

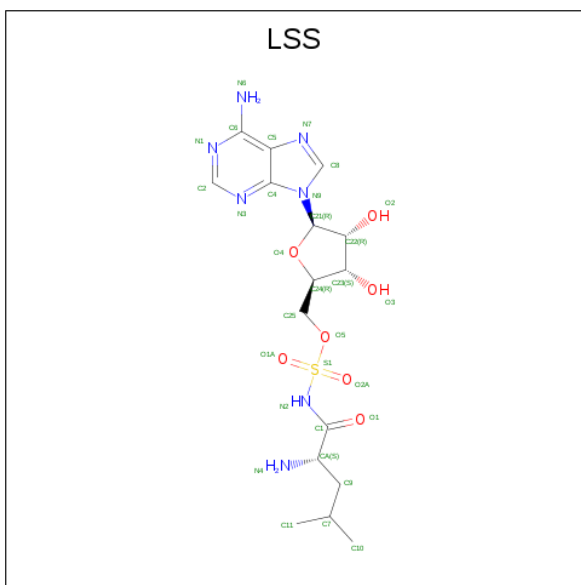
- Molecule 2 is a RNA chain called tRNA(leu).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	85	Total	C	N	O	P	0	0	0
			1819	810	329	595	85			
2	E	81	Total	C	N	O	P	0	0	0
			1719	763	313	562	81			

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

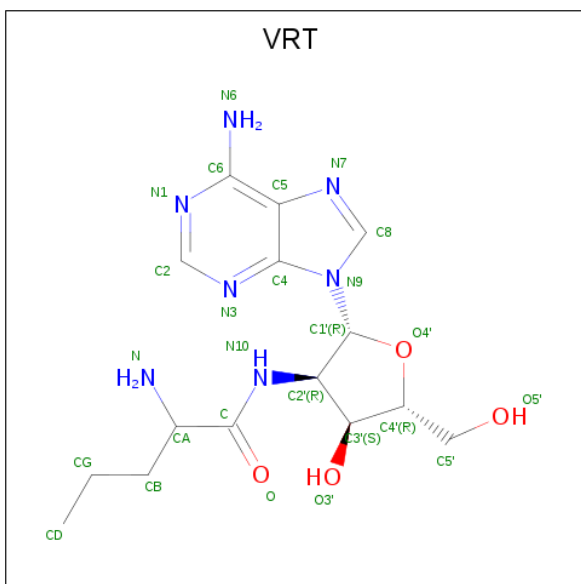
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		
3	D	1	Total	Zn	0	0
			1	1		

- Molecule 4 is 5'-O-(L-leucylsulfamoyl)adenosine (three-letter code: LSS) (formula: C<sub>16</sub>H<sub>25</sub>N<sub>7</sub>O<sub>7</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total 31	C 16	N 7	O 7	S 1	0	0
4	D	1	Total 31	C 16	N 7	O 7	S 1	0	0

- Molecule 5 is 2'-(L-NORVALYL)AMINO-2'-DEOXYADENOSINE (three-letter code: VRT) (formula: C<sub>15</sub>H<sub>23</sub>N<sub>7</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			26	15	7	4		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	D	1	Total	C	N	O	0	0
			26	15	7	4		

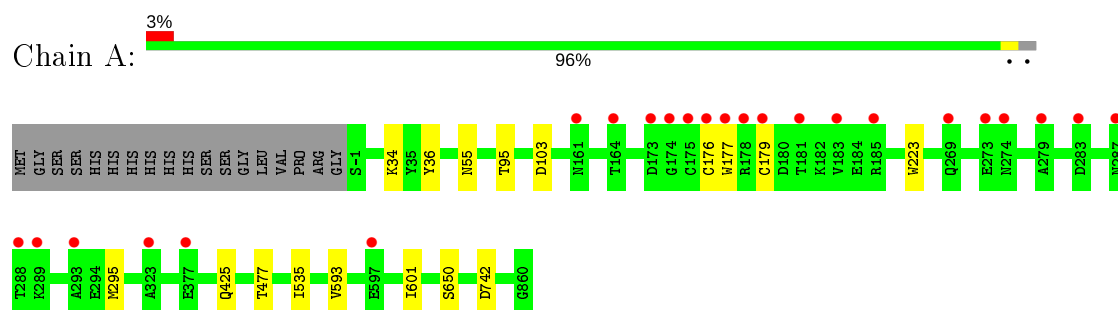
- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	Mg	0	0
			1	1		
6	E	1	Total	Mg	0	0
			1	1		

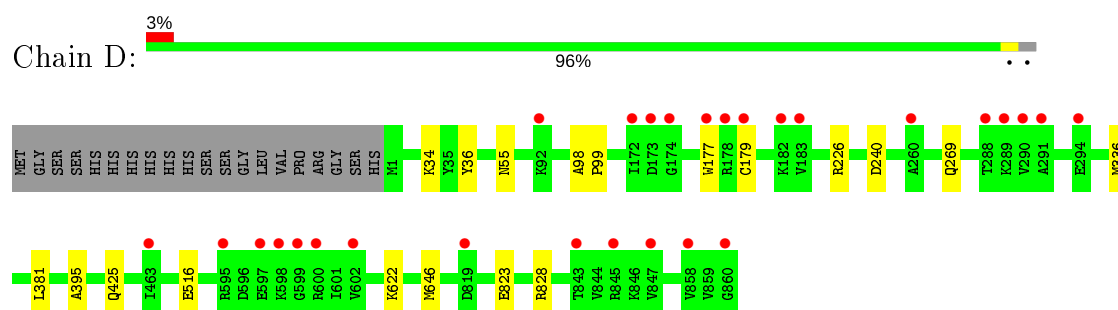
### 3 Residue-property plots [i](#)

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 ( $\text{RSRZ} > 2$ ). 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.

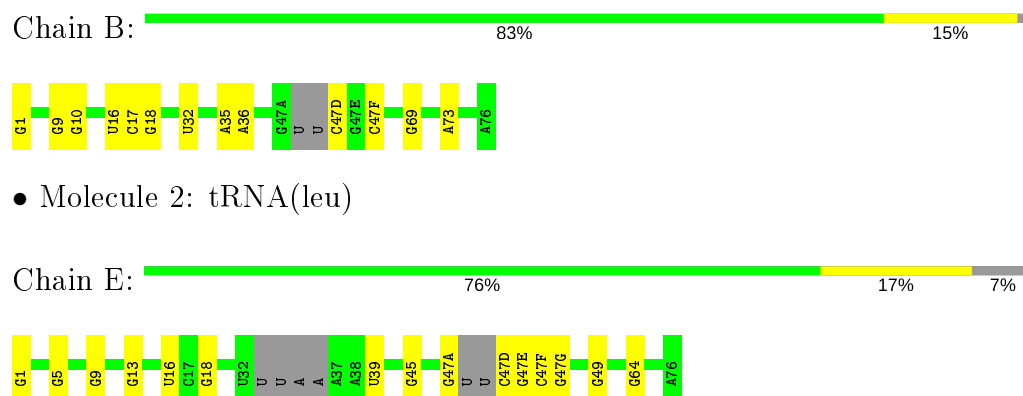
- Molecule 1: Leucine-tRNA ligase



- Molecule 1: Leucine-tRNA ligase



- Molecule 2: tRNA(leu)



- Molecule 2: tRNA(leu)



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	159.65Å 70.62Å 230.34Å 90.00° 104.52° 90.00°	Depositor
Resolution (Å)	50.00 – 3.10 47.90 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.6 (50.00-3.10) 99.7 (47.90-3.10)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.01	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.32 (at 3.12Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, $R_{free}$	0.226 , 0.263 0.228 , 0.263	Depositor DCC
$R_{free}$ test set	2193 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	86.7	Xtriage
Anisotropy	0.086	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 33.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	17332	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	99.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.30% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN, LSS, VRT

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	0.35	0/7004	0.51	0/9508
1	D	0.35	0/6994	0.51	0/9494
2	B	0.30	1/2032 (0.0%)	0.65	0/3163
2	E	0.30	1/1919 (0.1%)	0.65	0/2986
All	All	0.34	2/17949 (0.0%)	0.55	0/25151

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	1	G	OP3-P	-10.11	1.49	1.61
2	B	1	G	OP3-P	-10.03	1.49	1.61

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 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	A	6843	0	6687	2	0
1	D	6833	0	6683	2	0
2	B	1819	0	921	1	0
2	E	1719	0	869	2	0
3	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	1	0	0	0	0
4	A	31	0	25	0	0
4	D	31	0	25	0	0
5	A	26	0	0	0	0
5	D	26	0	0	0	0
6	B	1	0	0	0	0
6	E	1	0	0	0	0
All	All	17332	0	15210	7	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 0.

All (7) 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)
2:B:47(D):C:O2	2:B:47(D):C:O4'	2.30	0.50
2:E:47(D):C:O2	2:E:47(D):C:O4'	2.28	0.50
1:D:381:LEU:HD11	1:D:395:ALA:HB1	1.96	0.48
1:D:98:ALA:HB3	1:D:99:PRO:HD3	1.95	0.48
1:A:223:TRP:CD2	1:A:535:ILE:HG21	2.54	0.42
1:A:593:VAL:HG13	1:A:601:ILE:HG23	2.02	0.41
2:E:47(A):G:C2	2:E:47(G):G:C2	3.09	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	860/880 (98%)	826 (96%)	34 (4%)	0	100	100
1	D	858/880 (98%)	823 (96%)	35 (4%)	0	100	100
All	All	1718/1760 (98%)	1649 (96%)	69 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 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	723/740 (98%)	710 (98%)	13 (2%)	59	82
1	D	723/740 (98%)	708 (98%)	15 (2%)	53	79
All	All	1446/1480 (98%)	1418 (98%)	28 (2%)	57	81

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	LYS
1	A	36	TYR
1	A	55	ASN
1	A	95	THR
1	A	103	ASP
1	A	176	CYS
1	A	177	TRP
1	A	179	CYS
1	A	295	MET
1	A	425	GLN
1	A	477	THR
1	A	650	SER
1	A	742	ASP
1	D	34	LYS
1	D	36	TYR
1	D	55	ASN
1	D	177	TRP
1	D	179	CYS
1	D	226	ARG
1	D	240	ASP
1	D	269	GLN
1	D	336	MET
1	D	425	GLN
1	D	516	GLU
1	D	622	LYS

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Mol	Chain	Res	Type
1	D	646	MET
1	D	823	GLU
1	D	828	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	449	GLN
1	A	555	ASN
1	A	584	ASN
1	D	355	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	83/87 (95%)	10 (12%)	1 (1%)
2	E	77/87 (88%)	11 (14%)	0
All	All	160/174 (91%)	21 (13%)	1 (0%)

All (21) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	9	G
2	B	10	G
2	B	16	U
2	B	18	G
2	B	32	U
2	B	35	A
2	B	36	A
2	B	47(F)	C
2	B	69	G
2	B	73	A
2	E	5	G
2	E	9	G
2	E	13	G
2	E	16	U
2	E	18	G
2	E	39	U
2	E	45	G
2	E	47(E)	G

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Mol	Chain	Res	Type
2	E	47(F)	C
2	E	49	G
2	E	64	G

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	17	C

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 4 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	$\# Z  > 2$
4	LSS	A	901	-	30,33,33	1.29	4 (13%)	33,49,49	1.80	3 (9%)
4	LSS	D	901	-	30,33,33	1.27	2 (6%)	33,49,49	1.84	3 (9%)
5	VRT	D	902	-	25,28,28	2.60	3 (12%)	23,40,40	2.06	3 (13%)
5	VRT	A	902	-	25,28,28	2.60	3 (12%)	23,40,40	2.12	3 (13%)

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	LSS	A	901	-	-	2/18/39/39	0/3/3/3
4	LSS	D	901	-	-	5/18/39/39	0/3/3/3
5	VRT	D	902	-	-	3/13/33/33	0/3/3/3
5	VRT	A	902	-	-	0/13/33/33	0/3/3/3

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	902	VRT	C2-N3	9.77	1.47	1.32
5	A	902	VRT	C2-N3	9.70	1.47	1.32
5	A	902	VRT	C2-N1	7.60	1.48	1.33
5	D	902	VRT	C2-N1	7.55	1.48	1.33
4	D	901	LSS	S1-N2	-3.96	1.52	1.59
4	A	901	LSS	S1-N2	-3.82	1.53	1.59
4	A	901	LSS	O5-S1	-2.99	1.53	1.59
4	D	901	LSS	O5-S1	-2.77	1.53	1.59
5	A	902	VRT	C5-C4	2.68	1.48	1.40
5	D	902	VRT	C5-C4	2.60	1.47	1.40
4	A	901	LSS	O2A-S1	2.10	1.44	1.42
4	A	901	LSS	O1A-S1	2.03	1.44	1.42

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	902	VRT	N3-C2-N1	-8.65	115.16	128.68
5	D	902	VRT	N3-C2-N1	-8.55	115.32	128.68
4	D	901	LSS	O2A-S1-O1A	-7.76	108.68	120.76
4	A	901	LSS	O2A-S1-O1A	-7.65	108.85	120.76
4	D	901	LSS	N3-C2-N1	-4.58	121.52	128.68
4	A	901	LSS	N3-C2-N1	-4.56	121.55	128.68
4	D	901	LSS	C25-O5-S1	3.32	124.22	117.37
5	A	902	VRT	C2-N1-C6	2.95	123.80	118.75
5	A	902	VRT	C4-C5-N7	-2.91	106.37	109.40
5	D	902	VRT	C2-N1-C6	2.88	123.68	118.75
4	A	901	LSS	C25-O5-S1	2.87	123.30	117.37
5	D	902	VRT	C4-C5-N7	-2.54	106.76	109.40

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	901	LSS	C25-O5-S1-N2

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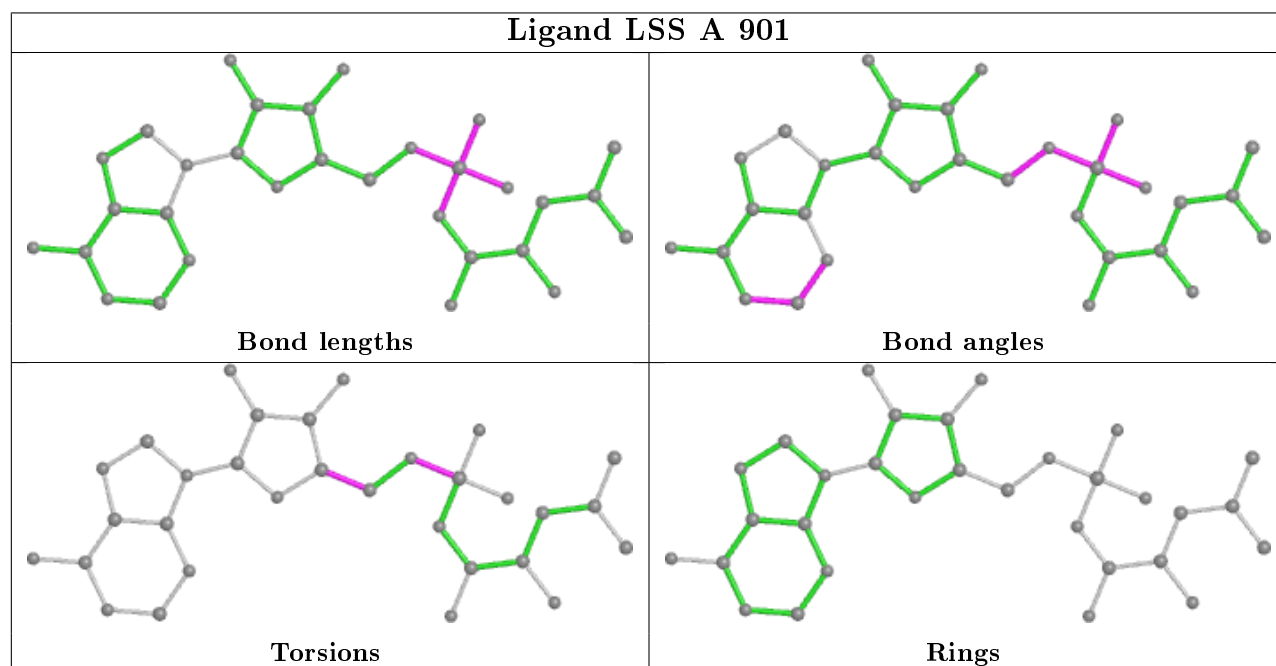
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Mol	Chain	Res	Type	Atoms
5	D	902	VRT	C3'-C4'-C5'-O5'
5	D	902	VRT	O4'-C4'-C5'-O5'
4	D	901	LSS	C23-C24-C25-O5
5	D	902	VRT	N-CA-CB-CG
4	A	901	LSS	C25-O5-S1-N2
4	D	901	LSS	O1-C1-CA-N4
4	D	901	LSS	N2-C1-CA-N4
4	A	901	LSS	C23-C24-C25-O5
4	D	901	LSS	C25-O5-S1-O2A

There are no ring outliers.

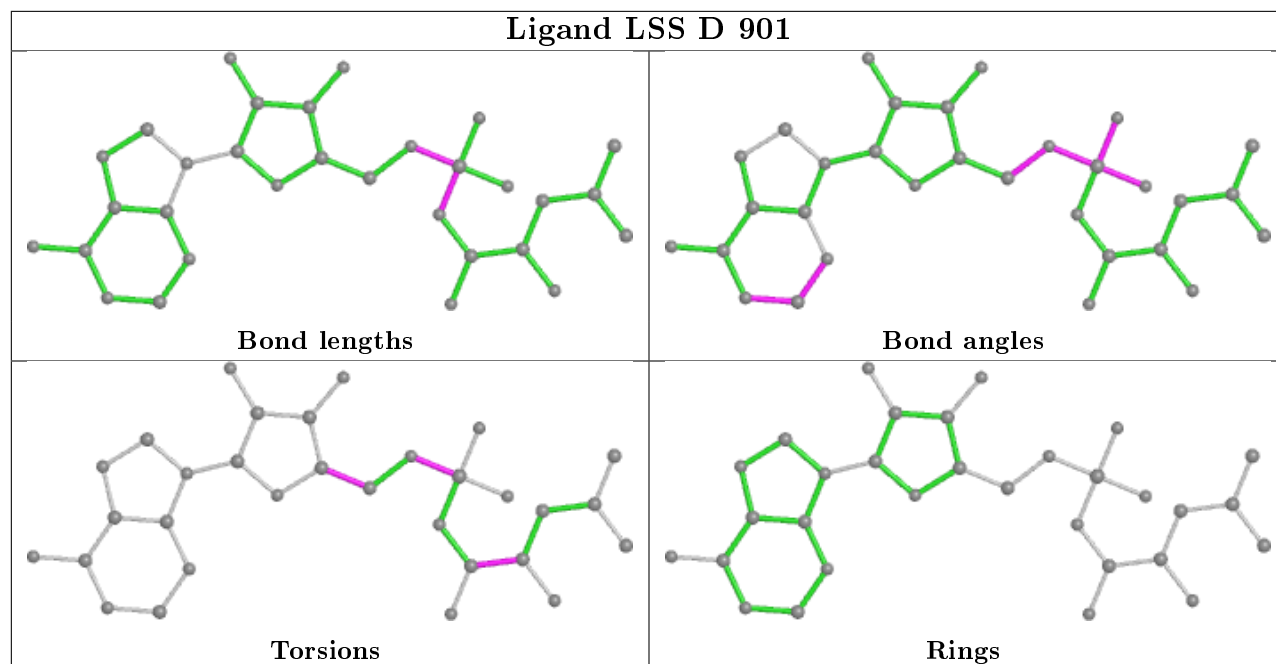
No monomer is involved in short contacts.

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.

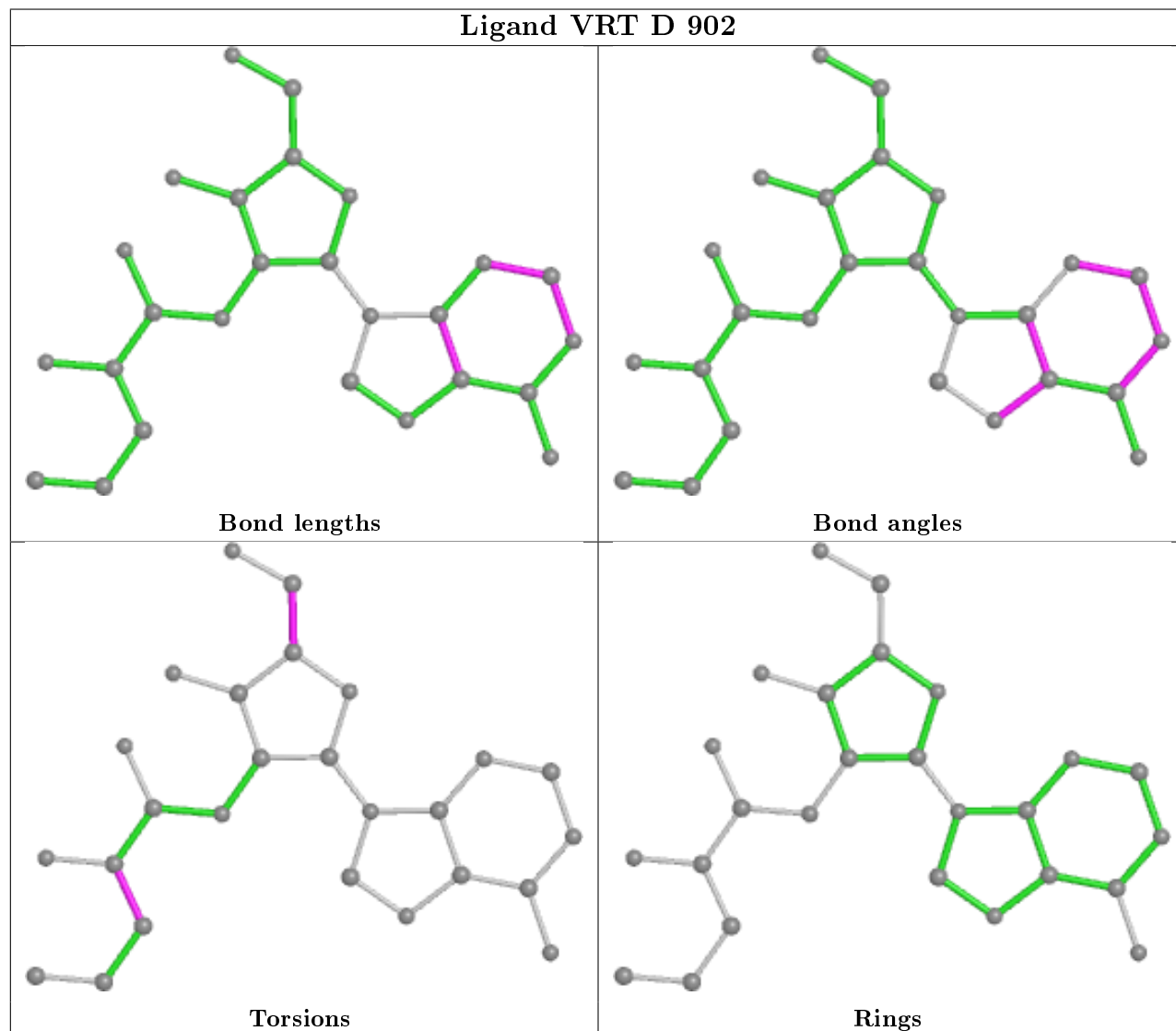


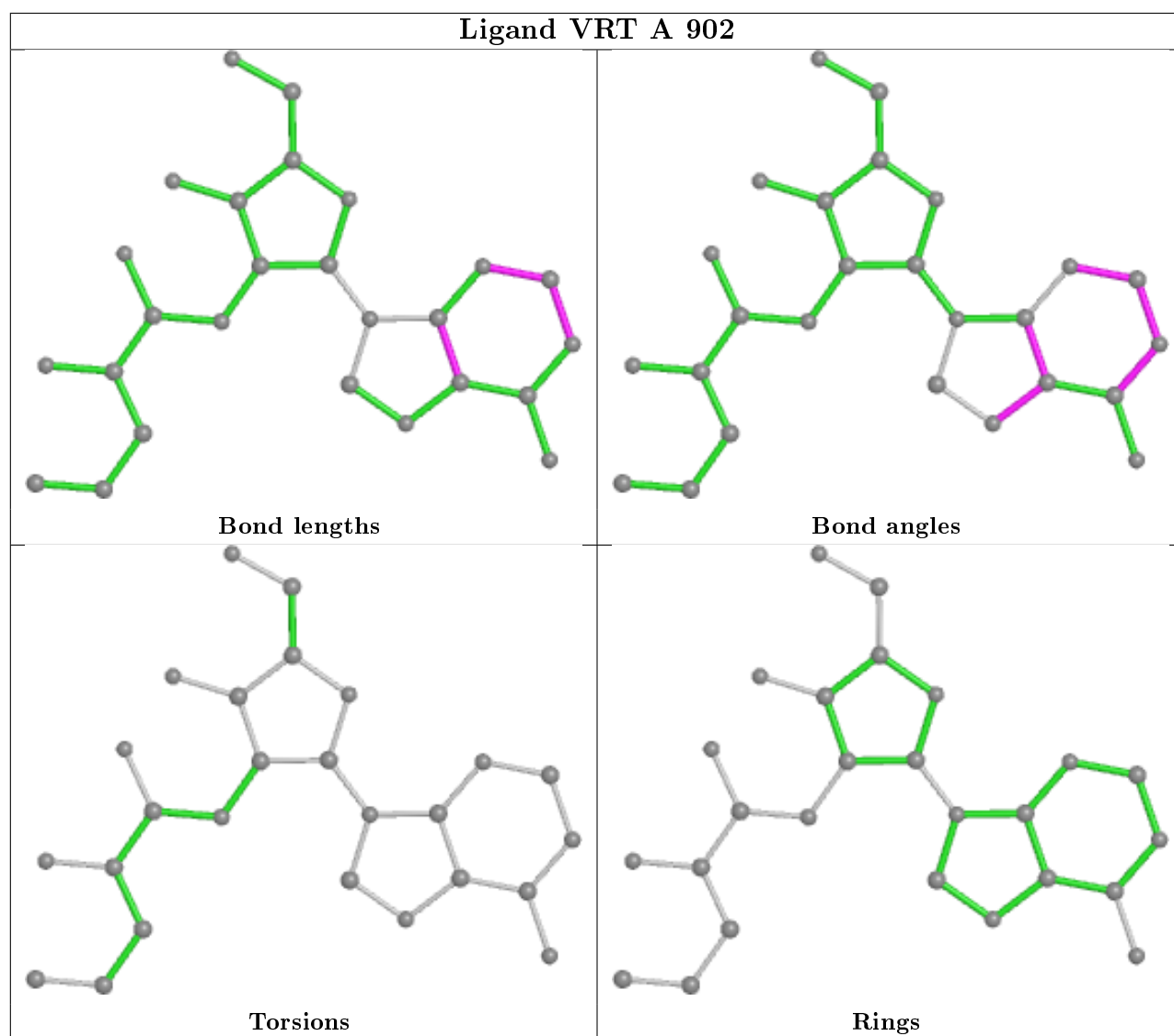


## Ligand LSS D 901



## Ligand VRT D 902





## 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

### 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	862/880 (97%)	-0.13	24 (2%)	53	30	50, 86, 155, 204	0
1	D	860/880 (97%)	-0.02	28 (3%)	46	24	59, 97, 158, 209	0
2	B	85/87 (97%)	-0.18	0	100	100	57, 88, 175, 210	0
2	E	81/87 (93%)	-0.15	0	100	100	72, 112, 165, 194	0
All	All	1888/1934 (97%)	-0.08	52 (2%)	53	30	50, 92, 159, 210	0

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	173	ASP	13.8
1	A	173	ASP	8.7
1	D	174	GLY	8.5
1	A	175	CYS	6.1
1	D	291	ALA	5.8
1	A	174	GLY	5.7
1	A	283	ASP	5.6
1	D	172	ILE	5.2
1	D	598	LYS	5.1
1	D	600	ARG	5.1
1	D	177	TRP	4.8
1	D	860	GLY	4.4
1	A	178	ARG	4.4
1	D	595	ARG	4.2
1	D	178	ARG	4.2
1	A	274	ASN	4.1
1	D	843	THR	4.1
1	A	597	GLU	3.9
1	A	177	TRP	3.7
1	D	845	ARG	3.7
1	D	182	LYS	3.6

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	181	THR	3.5
1	A	289	LYS	3.4
1	D	602	VAL	3.2
1	D	599	GLY	3.1
1	A	279	ALA	3.1
1	A	287	ASN	3.1
1	A	164	THR	3.0
1	D	290	VAL	2.9
1	D	597	GLU	2.9
1	A	273	GLU	2.9
1	D	183	VAL	2.8
1	D	289	LYS	2.7
1	D	858	VAL	2.7
1	A	183	VAL	2.6
1	A	288	THR	2.6
1	A	293	ALA	2.5
1	A	377	GLU	2.5
1	A	176	CYS	2.4
1	A	161	ASN	2.4
1	A	269	GLN	2.3
1	D	294	GLU	2.3
1	D	288	THR	2.3
1	D	260	ALA	2.3
1	A	179	CYS	2.3
1	A	185	ARG	2.2
1	D	847	VAL	2.2
1	D	92	LYS	2.1
1	D	179	CYS	2.1
1	D	819	ASP	2.1
1	D	463	ILE	2.0
1	A	323	ALA	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates ⓘ

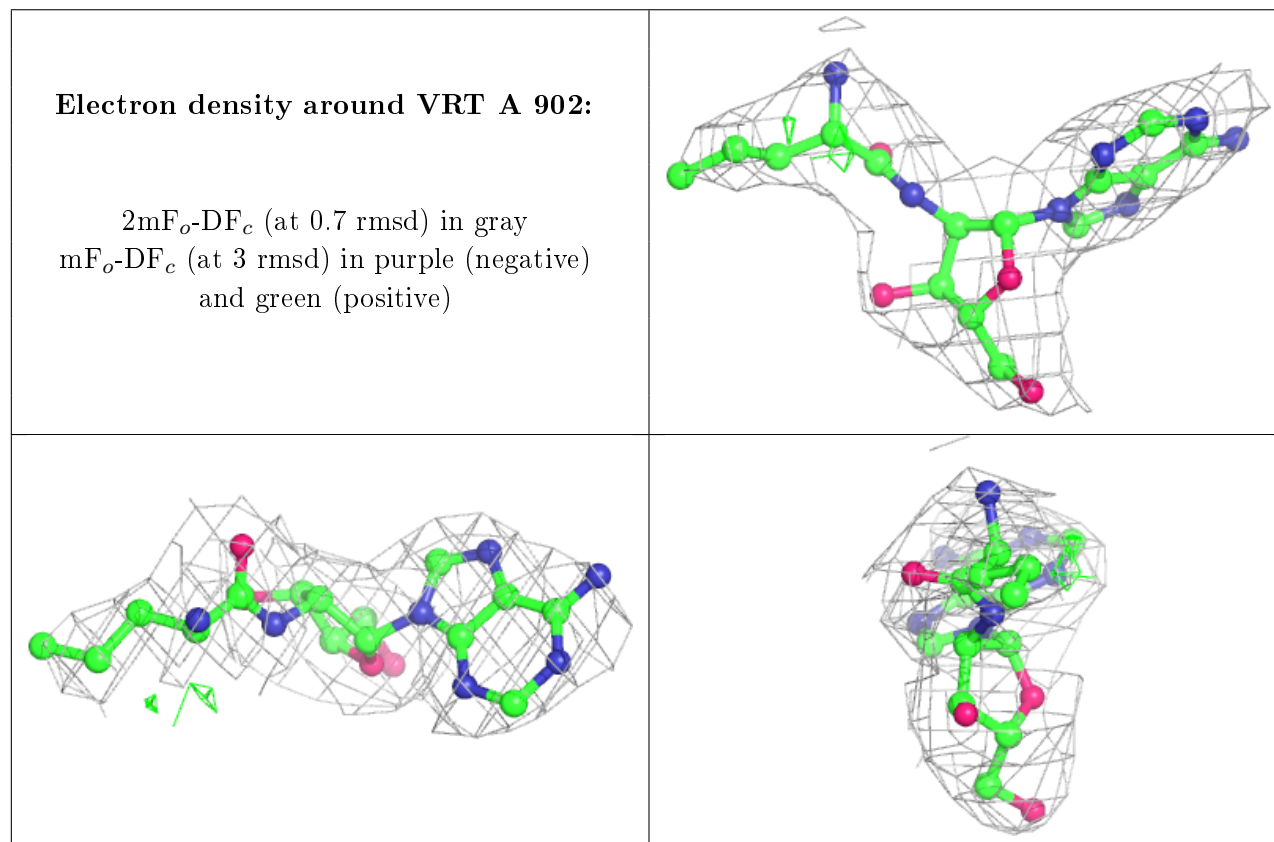
There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

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<sup>th</sup> 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.

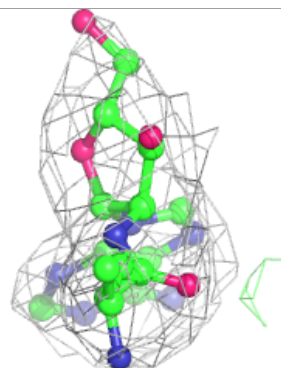
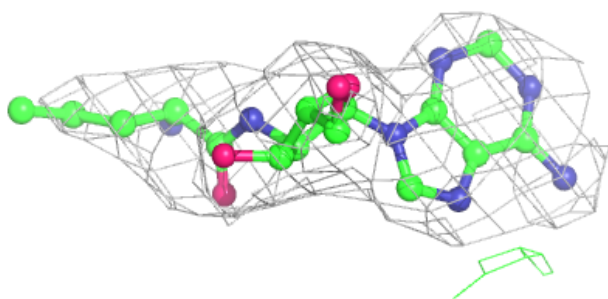
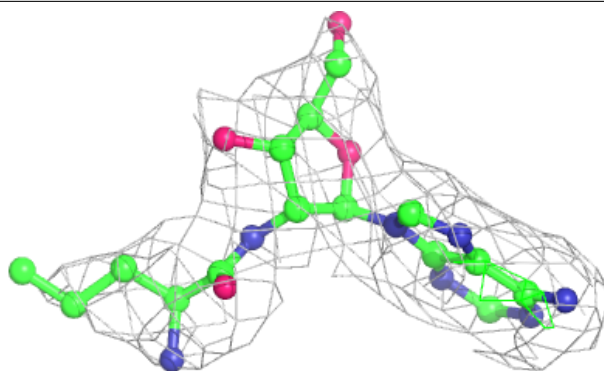
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	ZN	D	900	1/1	0.77	0.54	210,210,210,210	0
3	ZN	A	900	1/1	0.82	0.39	201,201,201,201	0
5	VRT	A	902	26/26	0.91	0.17	92,93,95,95	0
5	VRT	D	902	26/26	0.94	0.18	82,83,89,89	0
6	MG	E	101	1/1	0.94	0.09	56,56,56,56	0
4	LSS	D	901	31/31	0.96	0.19	68,70,73,73	0
6	MG	B	101	1/1	0.96	0.15	43,43,43,43	0
4	LSS	A	901	31/31	0.98	0.19	56,57,58,58	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.

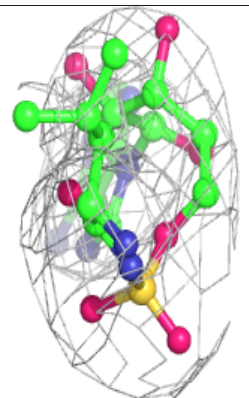
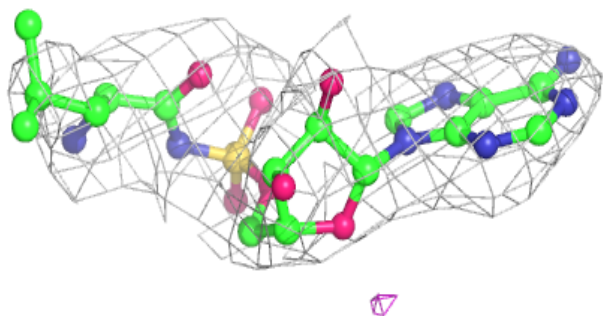
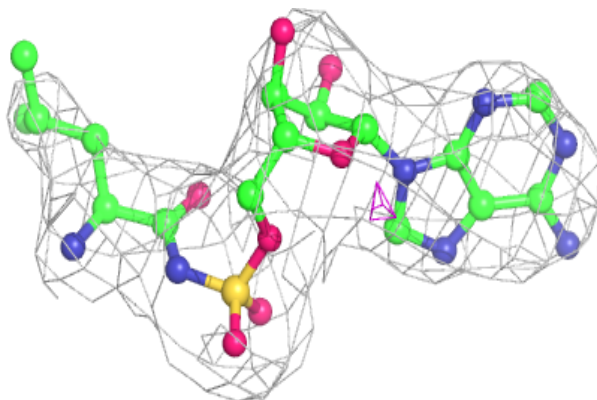


**Electron density around VRT D 902:**

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

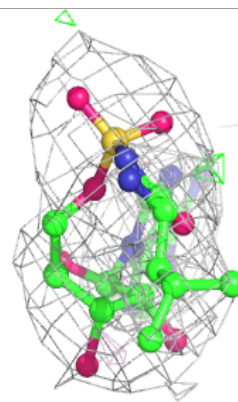
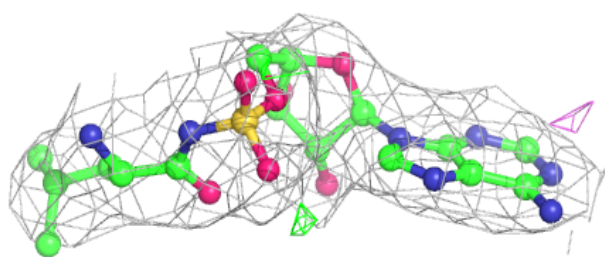
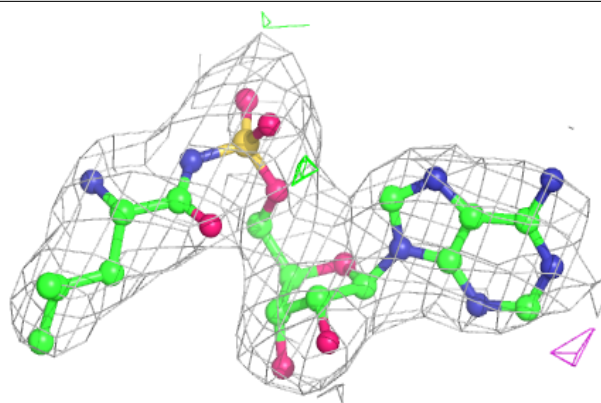
**Electron density around LSS D 901:**

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



**Electron density around LSS A 901:**

$2mF_o-DF_c$  (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.