



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 16, 2020 – 12:43 am BST

PDB ID : 6NRZ  
Title : Crystal Structure of Lysyl-tRNA Synthetase from Chlamydia trachomatis complexed with L-lysine and Adenosine  
Authors : Seattle Structural Genomics Center for Infectious Disease; Seattle Structural Genomics Center for Infectious Disease (SSGCID)  
Deposited on : 2019-01-24  
Resolution : 2.10 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

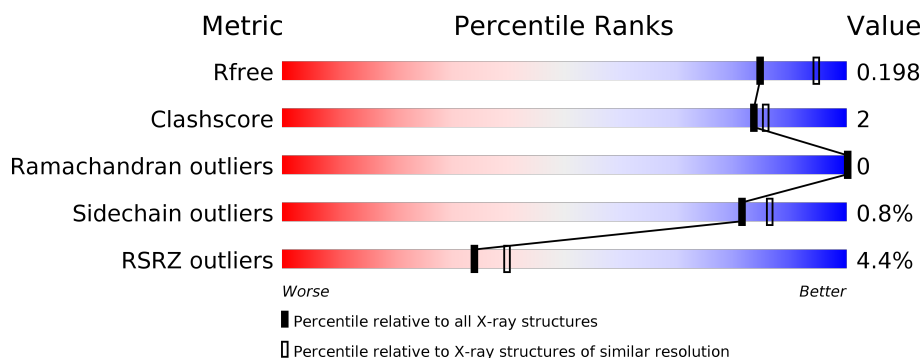
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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	534	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 1%, green 92%, grey 5%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>%</span> <span>92%</span> <span>5% .</span> </div> </div>
1	B	534	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 7%, orange 1%, yellow 1%, green 91%, grey 6%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>7%</span> <span>91%</span> <span>6% . .</span> </div> </div>

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 8897 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.

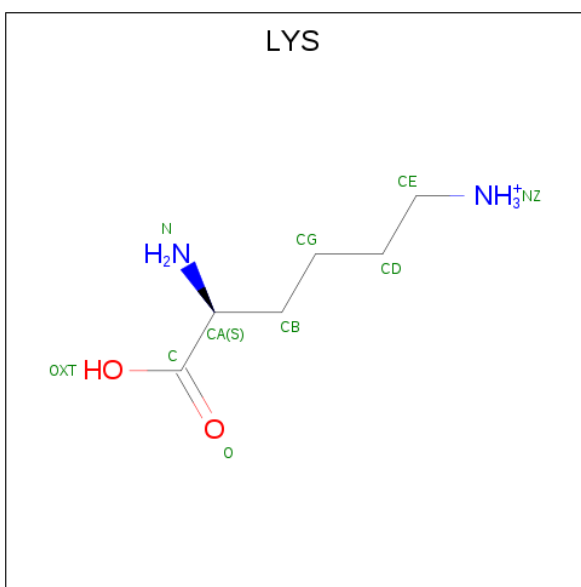
- Molecule 1 is a protein called Lysine-tRNA ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	517	Total	C	N	O	S	0	5	0
			4088	2610	689	766	23			
1	B	517	Total	C	N	O	S	0	6	0
			4041	2575	685	759	22			

There are 16 discrepancies between the modelled and reference sequences:

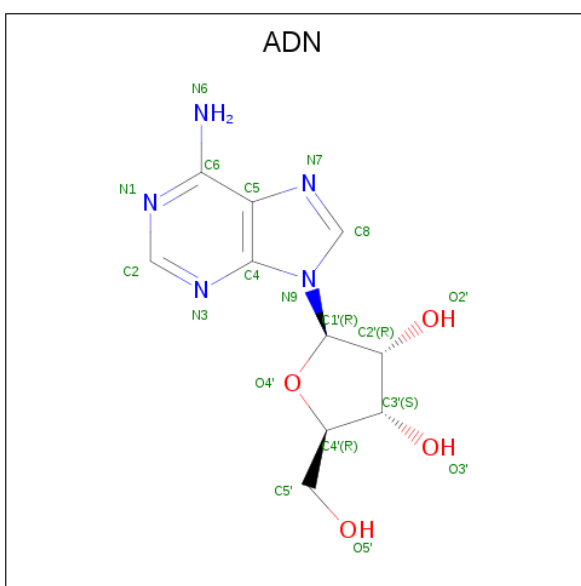
Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	initiating methionine	UNP B0BAN6
A	-6	ALA	-	expression tag	UNP B0BAN6
A	-5	HIS	-	expression tag	UNP B0BAN6
A	-4	HIS	-	expression tag	UNP B0BAN6
A	-3	HIS	-	expression tag	UNP B0BAN6
A	-2	HIS	-	expression tag	UNP B0BAN6
A	-1	HIS	-	expression tag	UNP B0BAN6
A	0	HIS	-	expression tag	UNP B0BAN6
B	-7	MET	-	initiating methionine	UNP B0BAN6
B	-6	ALA	-	expression tag	UNP B0BAN6
B	-5	HIS	-	expression tag	UNP B0BAN6
B	-4	HIS	-	expression tag	UNP B0BAN6
B	-3	HIS	-	expression tag	UNP B0BAN6
B	-2	HIS	-	expression tag	UNP B0BAN6
B	-1	HIS	-	expression tag	UNP B0BAN6
B	0	HIS	-	expression tag	UNP B0BAN6

- Molecule 2 is LYSINE (three-letter code: LYS) (formula:  $C_6H_{15}N_2O_2$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			10	6	2	2		
2	B	1	Total	C	N	O	0	0
			10	6	2	2		

- Molecule 3 is ADENOSINE (three-letter code: ADN) (formula:  $C_{10}H_{13}N_5O_4$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			19	10	5	4		
3	B	1	Total	C	N	O	0	0
			19	10	5	4		

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0

- Molecule 5 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: C<sub>8</sub>H<sub>18</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			13	8	5		
5	B	1	Total	C	O	0	0
			13	8	5		

- Molecule 6 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	2	Total	Na	0	0
			2	2		

- Molecule 7 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	1	Total	Cl	0	0
			1	1		

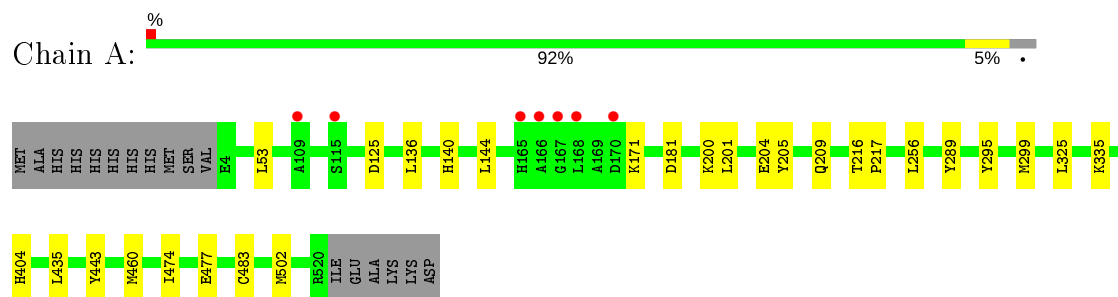
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	341	Total	O	0	2
			343	343		
8	B	224	Total	O	0	2
			226	226		

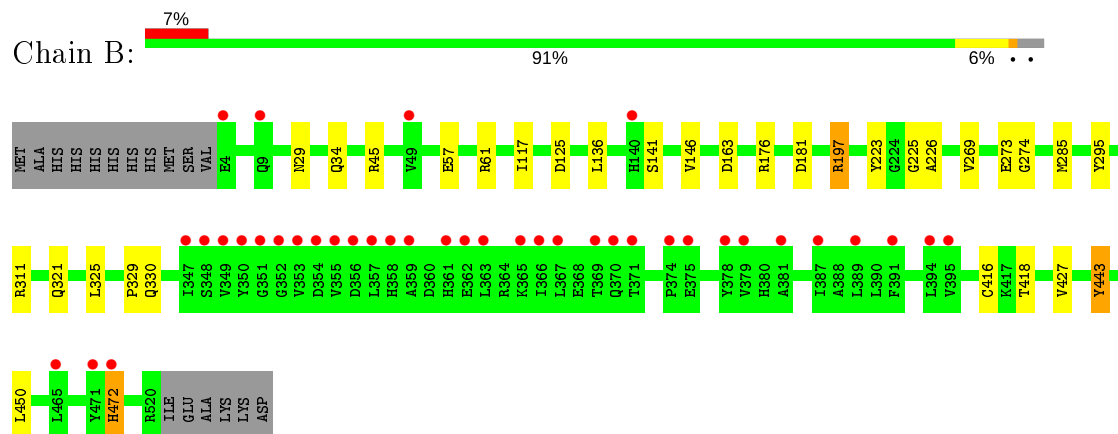
### 3 Residue-property plots [i](#)

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: Lysine-tRNA ligase



#### • Molecule 1: Lysine-tRNA ligase





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	96.17Å 57.52Å 139.09Å 90.00° 96.68° 90.00°	Depositor
Resolution (Å)	49.27 – 2.10 49.28 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (49.27-2.10) 99.8 (49.28-2.10)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.30 (at 2.10Å)	Xtriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.160 , 0.197 0.160 , 0.198	Depositor DCC
$R_{free}$ test set	1995 reflections (2.25%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	37.6	Xtriage
Anisotropy	0.102	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 55.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	8897	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.88% 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: ADN, NA, PG4, EDO, CL

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	0.39	0/4184	0.55	0/5667
1	B	0.36	0/4139	0.54	0/5614
All	All	0.38	0/8323	0.55	0/11281

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	443	TYR	Peptide
1	B	443	TYR	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	A	4088	0	4015	18	0
1	B	4041	0	3918	21	0
2	A	10	0	12	0	0
2	B	10	0	12	0	0
3	A	19	0	13	0	0
3	B	19	0	13	0	0
4	A	56	0	84	7	0
4	B	56	0	84	6	0
5	A	13	0	18	1	0
5	B	13	0	18	2	0
6	A	2	0	0	0	0
7	B	1	0	0	0	0
8	A	343	0	0	1	0
8	B	226	0	0	4	0
All	All	8897	0	8187	40	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 2.

All (40) 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:B:225:GLY:H	5:B:1708:PG4:H62	1.28	0.97
1:B:29:ASN:HA	4:B:1706:EDO:H22	1.83	0.60
1:A:200:LYS:NZ	4:A:615:EDO:O2	2.34	0.58
1:B:34:GLN:HG2	4:B:1713:EDO:H22	1.86	0.57
1:A:256:LEU:HD11	1:A:289:TYR:HB3	1.87	0.56
1:B:450:LEU:HD23	4:B:1707:EDO:H22	1.86	0.56
1:B:311:ARG:HH11	4:B:1704:EDO:H11	1.70	0.55
1:B:141:SER:N	8:B:1802:HOH:O	2.24	0.55
1:A:201:LEU:HD21	4:A:605:EDO:H11	1.91	0.53
1:A:435:LEU:HD12	1:A:502:MET:HG2	1.91	0.52
1:A:335:LYS:NZ	8:A:702:HOH:O	2.37	0.51
1:B:45:ARG:NH2	8:B:1814:HOH:O	2.44	0.49
1:B:197[A]:ARG:NH2	8:B:1803:HOH:O	2.24	0.49
4:B:1709:EDO:O2	8:B:1801:HOH:O	2.20	0.49
1:A:299:MET:HG2	1:A:404:HIS:CD2	2.48	0.48
1:B:136:LEU:HD23	1:B:146:VAL:HG22	1.95	0.48
1:B:125:ASP:HA	4:B:1709:EDO:H22	1.95	0.48
1:A:460:MET:HE3	1:A:474:ILE:HG13	1.97	0.46
1:A:325:LEU:HD21	4:A:609:EDO:H11	1.98	0.46
5:A:607:PG4:H31	5:A:607:PG4:H51	1.48	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:216:THR:HB	1:A:217:PRO:HD2	1.99	0.45
1:A:483:CYS:SG	4:A:611:EDO:H11	2.56	0.45
1:B:226:ALA:N	5:B:1708:PG4:H32	2.33	0.44
1:B:117:ILE:HA	1:B:117:ILE:HD12	1.85	0.43
1:A:200:LYS:HG2	4:A:615:EDO:H12	2.01	0.43
1:A:477:GLU:OE2	1:B:176:ARG:NH1	2.48	0.43
1:A:125:ASP:HA	4:A:603:EDO:H21	2.00	0.42
1:B:325:LEU:HD12	1:B:330:GLN:HG3	2.01	0.42
1:B:269:VAL:HG11	1:B:285:MET:HE2	2.02	0.42
1:B:418:THR:HA	1:B:427:VAL:HA	2.02	0.42
1:A:205:TYR:O	1:A:209:GLN:HG2	2.19	0.42
1:A:171:LYS:NZ	1:A:181:ASP:OD2	2.51	0.41
1:A:53:LEU:HD12	1:A:53:LEU:HA	1.91	0.41
1:B:57:GLU:O	1:B:61[A]:ARG:HG3	2.20	0.41
1:A:204:GLU:OE1	4:A:615:EDO:H21	2.21	0.41
1:A:136:LEU:HD22	1:A:144:LEU:HD11	2.02	0.41
1:B:223:TYR:O	1:B:472:HIS:CE1	2.74	0.41
1:B:273:GLU:HB3	1:B:274:GLY:H	1.75	0.40
1:B:321:GLN:HE22	1:B:329:PRO:HB3	1.85	0.40
1:B:416:CYS:SG	1:B:443:TYR:HB3	2.61	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	520/534 (97%)	514 (99%)	6 (1%)	0	100	100
1	B	521/534 (98%)	515 (99%)	6 (1%)	0	100	100
All	All	1041/1068 (98%)	1029 (99%)	12 (1%)	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	434/469 (92%)	432 (100%)	2 (0%)	88	92
1	B	422/469 (90%)	416 (99%)	6 (1%)	67	73
All	All	856/938 (91%)	848 (99%)	8 (1%)	81	84

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	140	HIS
1	A	295	TYR
1	B	163	ASP
1	B	181	ASP
1	B	197[A]	ARG
1	B	197[B]	ARG
1	B	295	TYR
1	B	472	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

Of 37 ligands modelled in this entry, 3 are monoatomic - leaving 34 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	EDO	B	1715	-	3,3,3	0.49	0	2,2,2	0.31	0
4	EDO	A	606	-	3,3,3	0.49	0	2,2,2	0.19	0
4	EDO	B	1714	-	3,3,3	0.66	0	2,2,2	0.13	0
4	EDO	A	603	-	3,3,3	0.57	0	2,2,2	0.28	0
4	EDO	B	1701	-	3,3,3	0.50	0	2,2,2	0.13	0
4	EDO	B	1709	-	3,3,3	0.83	0	2,2,2	0.55	0
4	EDO	A	615	-	3,3,3	0.47	0	2,2,2	0.36	0
4	EDO	A	614	-	3,3,3	0.46	0	2,2,2	0.24	0
4	EDO	A	608	-	3,3,3	0.53	0	2,2,2	0.26	0
4	EDO	B	1704	-	3,3,3	0.51	0	2,2,2	0.12	0
4	EDO	B	1716	-	3,3,3	0.45	0	2,2,2	0.37	0
4	EDO	A	612	-	3,3,3	0.47	0	2,2,2	0.48	0
4	EDO	A	616	-	3,3,3	0.42	0	2,2,2	0.53	0
4	EDO	A	605	-	3,3,3	0.51	0	2,2,2	0.16	0
4	EDO	B	1706	-	3,3,3	0.58	0	2,2,2	0.14	0
4	EDO	A	610	-	3,3,3	0.55	0	2,2,2	0.20	0
4	EDO	B	1710	-	3,3,3	0.51	0	2,2,2	0.23	0
4	EDO	B	1707	-	3,3,3	0.42	0	2,2,2	0.46	0
4	EDO	A	613	-	3,3,3	0.42	0	2,2,2	0.53	0
4	EDO	B	1712	-	3,3,3	0.42	0	2,2,2	0.55	0
5	PG4	B	1708	-	12,12,12	0.09	0	11,11,11	0.16	0
4	EDO	B	1711	-	3,3,3	0.51	0	2,2,2	0.19	0
4	EDO	A	611	-	3,3,3	0.39	0	2,2,2	0.35	0
3	ADN	A	602	-	18,21,21	0.60	0	18,31,31	0.81	1 (5%)
3	ADN	B	1703	-	18,21,21	0.61	0	18,31,31	0.83	1 (5%)
5	PG4	A	607	-	12,12,12	0.17	0	11,11,11	0.23	0
4	EDO	B	1713	-	3,3,3	0.55	0	2,2,2	0.42	0
4	EDO	A	617	-	3,3,3	0.42	0	2,2,2	0.52	0
4	EDO	B	1717	-	3,3,3	0.51	0	2,2,2	0.25	0
4	EDO	A	604	-	3,3,3	0.50	0	2,2,2	0.29	0
4	EDO	B	1705	-	3,3,3	0.47	0	2,2,2	0.42	0
4	EDO	A	609	-	3,3,3	0.45	0	2,2,2	0.30	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	B	1715	-	-	0/1/1/1	-
4	EDO	A	606	-	-	0/1/1/1	-
4	EDO	B	1714	-	-	0/1/1/1	-
4	EDO	A	603	-	-	0/1/1/1	-
4	EDO	B	1701	-	-	1/1/1/1	-
4	EDO	B	1709	-	-	1/1/1/1	-
4	EDO	A	615	-	-	0/1/1/1	-
4	EDO	A	614	-	-	1/1/1/1	-
4	EDO	A	608	-	-	1/1/1/1	-
4	EDO	B	1704	-	-	1/1/1/1	-
4	EDO	B	1716	-	-	0/1/1/1	-
4	EDO	A	612	-	-	0/1/1/1	-
4	EDO	A	616	-	-	0/1/1/1	-
4	EDO	A	605	-	-	0/1/1/1	-
4	EDO	B	1706	-	-	1/1/1/1	-
4	EDO	A	610	-	-	1/1/1/1	-
4	EDO	B	1710	-	-	1/1/1/1	-
4	EDO	B	1707	-	-	1/1/1/1	-
4	EDO	A	613	-	-	0/1/1/1	-
4	EDO	B	1712	-	-	0/1/1/1	-
5	PG4	B	1708	-	-	8/10/10/10	-
4	EDO	B	1711	-	-	0/1/1/1	-
4	EDO	A	611	-	-	0/1/1/1	-
3	ADN	A	602	-	-	0/2/22/22	0/3/3/3
3	ADN	B	1703	-	-	0/2/22/22	0/3/3/3
5	PG4	A	607	-	-	6/10/10/10	-
4	EDO	B	1713	-	-	1/1/1/1	-
4	EDO	A	617	-	-	0/1/1/1	-
4	EDO	B	1717	-	-	1/1/1/1	-
4	EDO	A	604	-	-	1/1/1/1	-
4	EDO	B	1705	-	-	1/1/1/1	-
4	EDO	A	609	-	-	0/1/1/1	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1703	ADN	C5-C6-N6	2.38	123.97	120.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	602	ADN	C5-C6-N6	2.28	123.81	120.35

There are no chirality outliers.

All (27) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	607	PG4	C3-C4-O3-C5
5	A	607	PG4	C4-C3-O2-C2
5	B	1708	PG4	O3-C5-C6-O4
4	B	1709	EDO	O1-C1-C2-O2
4	A	614	EDO	O1-C1-C2-O2
4	B	1706	EDO	O1-C1-C2-O2
4	A	604	EDO	O1-C1-C2-O2
4	B	1713	EDO	O1-C1-C2-O2
4	B	1704	EDO	O1-C1-C2-O2
4	B	1710	EDO	O1-C1-C2-O2
5	B	1708	PG4	C1-C2-O2-C3
5	A	607	PG4	C1-C2-O2-C3
5	A	607	PG4	O2-C3-C4-O3
5	B	1708	PG4	C6-C5-O3-C4
5	B	1708	PG4	O1-C1-C2-O2
5	B	1708	PG4	C3-C4-O3-C5
5	A	607	PG4	O3-C5-C6-O4
5	A	607	PG4	C5-C6-O4-C7
4	B	1701	EDO	O1-C1-C2-O2
4	A	610	EDO	O1-C1-C2-O2
4	B	1705	EDO	O1-C1-C2-O2
5	B	1708	PG4	C4-C3-O2-C2
5	B	1708	PG4	C5-C6-O4-C7
5	B	1708	PG4	O2-C3-C4-O3
4	B	1707	EDO	O1-C1-C2-O2
4	B	1717	EDO	O1-C1-C2-O2
4	A	608	EDO	O1-C1-C2-O2

There are no ring outliers.

12 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	603	EDO	1	0
4	B	1709	EDO	2	0
4	A	615	EDO	3	0

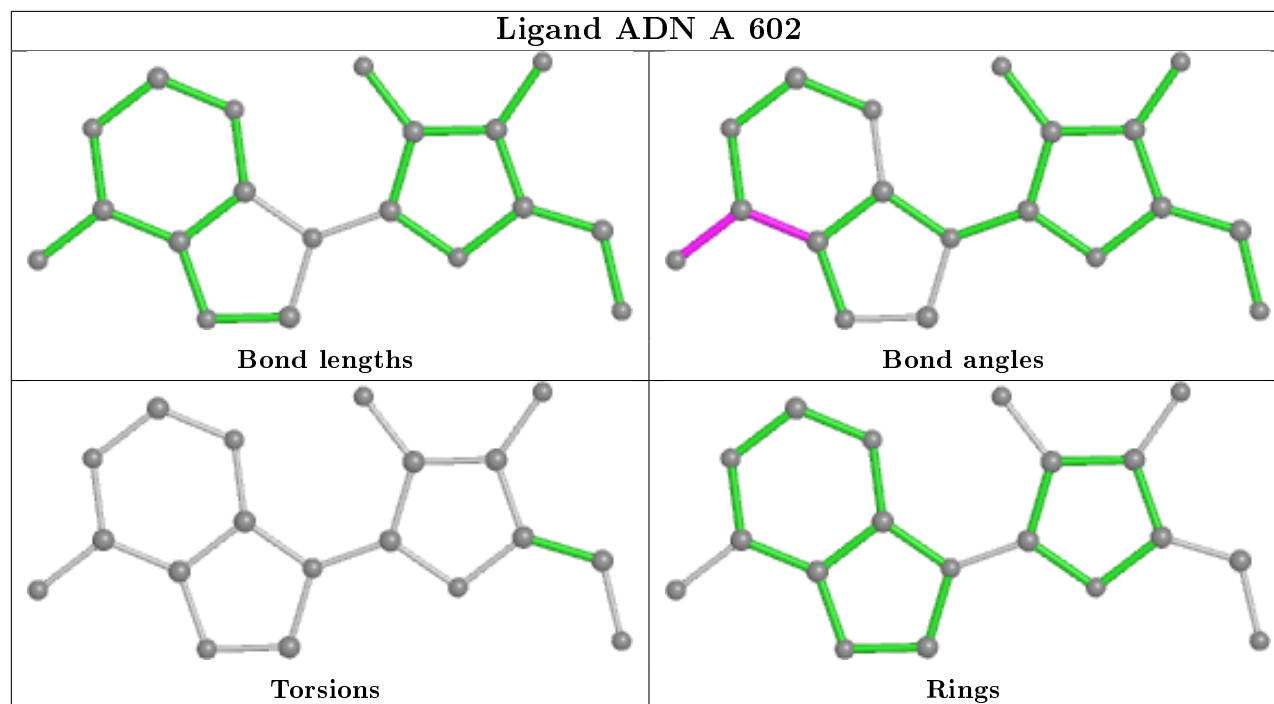
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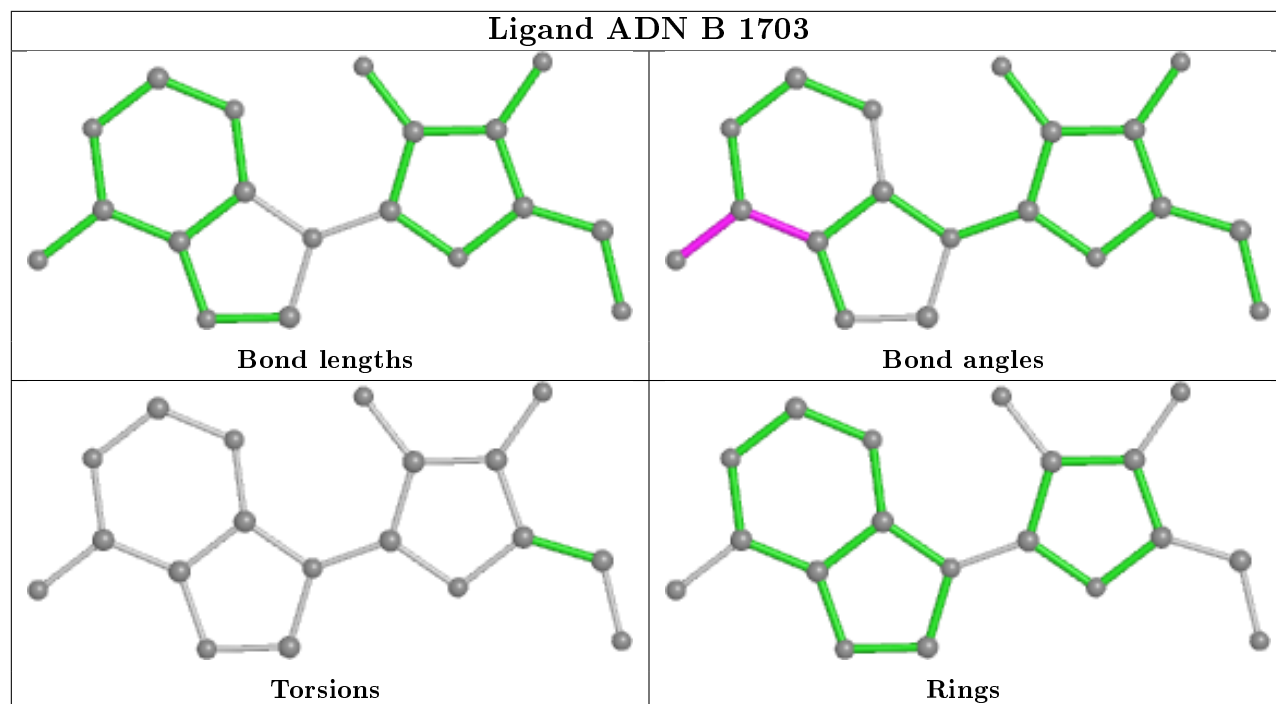


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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1704	EDO	1	0
4	A	605	EDO	1	0
4	B	1706	EDO	1	0
4	B	1707	EDO	1	0
5	B	1708	PG4	2	0
4	A	611	EDO	1	0
5	A	607	PG4	1	0
4	B	1713	EDO	1	0
4	A	609	EDO	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 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	517/534 (96%)	-0.12	7 (1%) 75 78	24, 45, 83, 127	2 (0%)
1	B	517/534 (96%)	0.12	39 (7%) 14 18	24, 50, 101, 120	0
All	All	1034/1068 (96%)	0.00	46 (4%) 34 40	24, 48, 95, 127	2 (0%)

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	366	ILE	6.0
1	B	465	LEU	5.5
1	B	363	LEU	4.8
1	B	355	VAL	4.5
1	A	166	ALA	4.2
1	B	357	LEU	4.2
1	B	353	VAL	4.0
1	B	352	GLY	3.9
1	B	349	VAL	3.8
1	B	472	HIS	3.8
1	B	347	ILE	3.6
1	B	49	VAL	3.5
1	B	351	GLY	3.4
1	B	358	HIS	3.4
1	A	165	HIS	3.3
1	B	350	TYR	3.3
1	B	374	PRO	3.2
1	B	367	LEU	3.2
1	B	394	LEU	3.1
1	A	168	LEU	3.1
1	B	389	LEU	3.1
1	A	167	GLY	3.1
1	B	381	ALA	3.0
1	B	362	GLU	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	4	GLU	3.0
1	B	356	ASP	3.0
1	B	379	VAL	2.9
1	B	348	SER	2.9
1	B	370	GLN	2.9
1	B	369	THR	2.6
1	B	354	ASP	2.6
1	B	365	LYS	2.6
1	B	395	VAL	2.6
1	B	361	HIS	2.6
1	B	391	PHE	2.5
1	B	378	TYR	2.5
1	B	375	GLU	2.5
1	B	359	ALA	2.4
1	A	109	ALA	2.3
1	B	140	HIS	2.3
1	A	115	SER	2.3
1	B	471	TYR	2.3
1	A	170	ASP	2.2
1	B	9	GLN	2.1
1	B	387	ILE	2.0
1	B	371	THR	2.0

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

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

## 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, 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( $\text{\AA}^2$ )	Q<0.9
4	EDO	A	603	4/4	0.59	0.23	59,63,73,75	0

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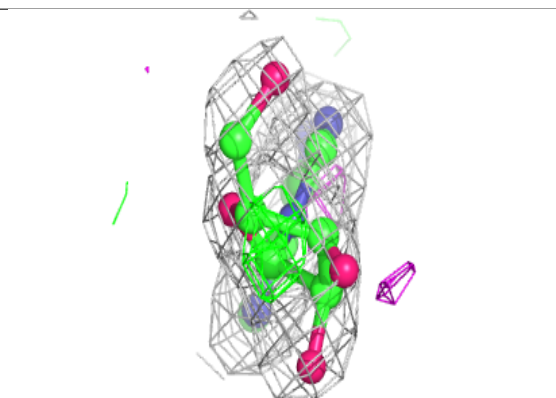
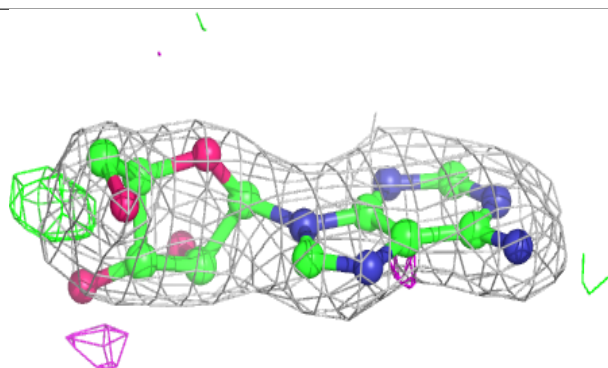
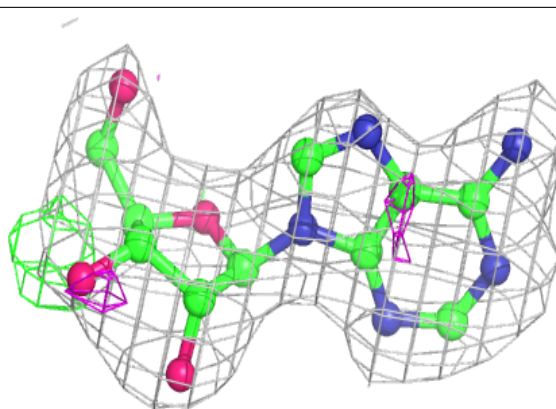
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	EDO	B	1717	4/4	0.66	0.24	75,85,87,90	0
4	EDO	A	615	4/4	0.68	0.22	70,70,73,73	0
4	EDO	B	1704	4/4	0.71	0.30	63,70,73,78	0
4	EDO	B	1709	4/4	0.76	0.16	36,37,39,41	0
4	EDO	B	1706	4/4	0.79	0.18	42,55,55,66	0
4	EDO	B	1705	4/4	0.80	0.10	75,80,82,86	0
4	EDO	A	605	4/4	0.81	0.21	66,69,72,73	0
4	EDO	B	1715	4/4	0.82	0.15	68,75,81,88	0
4	EDO	B	1710	4/4	0.83	0.34	60,73,83,87	0
4	EDO	A	609	4/4	0.83	0.28	71,75,80,84	0
5	PG4	B	1708	13/13	0.86	0.16	56,69,83,84	0
4	EDO	B	1716	4/4	0.86	0.36	85,87,88,90	0
4	EDO	B	1713	4/4	0.87	0.21	44,44,68,69	0
4	EDO	A	604	4/4	0.87	0.15	56,61,65,67	0
3	ADN	B	1703	19/19	0.88	0.15	49,67,82,89	0
4	EDO	B	1714	4/4	0.88	0.18	45,45,51,54	0
4	EDO	B	1701	4/4	0.88	0.21	45,49,49,51	0
3	ADN	A	602	19/19	0.91	0.11	43,55,60,62	0
4	EDO	A	606	4/4	0.92	0.21	40,47,52,64	0
4	EDO	B	1711	4/4	0.92	0.11	41,53,63,64	0
4	EDO	A	614	4/4	0.92	0.21	38,46,57,66	0
4	EDO	A	613	4/4	0.92	0.20	57,58,62,66	0
4	EDO	A	617	4/4	0.93	0.27	58,79,79,82	0
4	EDO	A	616	4/4	0.94	0.23	66,68,75,80	0
5	PG4	A	607	13/13	0.94	0.16	44,55,85,96	0
6	NA	A	619	1/1	0.94	0.10	76,76,76,76	0
4	EDO	B	1707	4/4	0.94	0.28	66,71,73,80	0
4	EDO	B	1712	4/4	0.95	0.20	49,56,63,69	0
4	EDO	A	608	4/4	0.96	0.09	43,44,45,47	0
4	EDO	A	610	4/4	0.97	0.14	35,41,41,56	0
4	EDO	A	611	4/4	0.97	0.12	39,43,44,45	0
4	EDO	A	612	4/4	0.97	0.14	37,38,47,50	0
2	LYS	B	1702	10/10	0.97	0.12	40,44,50,50	0
7	CL	B	1718	1/1	0.97	0.17	39,39,39,39	0
6	NA	A	618	1/1	0.98	0.06	52,52,52,52	0
2	LYS	A	601	10/10	0.99	0.16	23,28,33,37	0

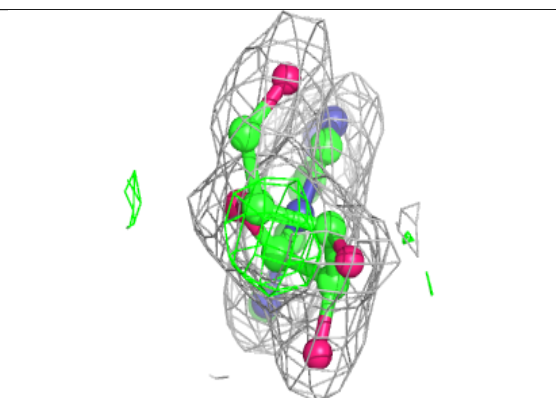
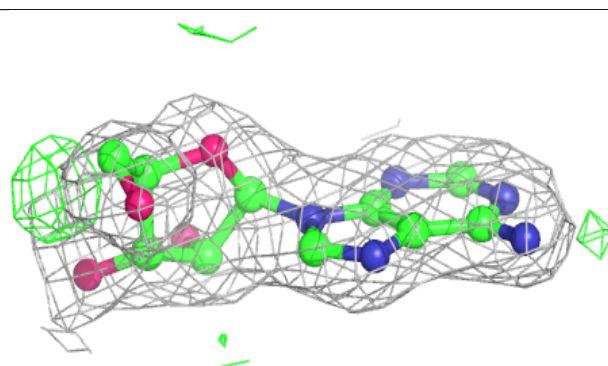
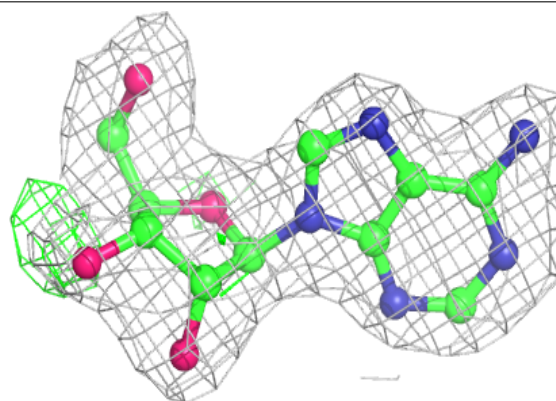
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around ADN B 1703:**

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

**Electron density around ADN A 602:**

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



## 6.5 Other polymers

There are no such residues in this entry.