



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 12:20 PM UTC

PDB ID : 7NU3 / pdb_00007nu3
Title : Crystal Structure of Neisseria gonorrhoeae LeuRS E169G mutant in Complex with ATP and L-leucinol
Authors : Pang, L.; Strelkov, S.V.; Weeks, S.D.
Deposited on : 2021-03-11
Resolution : 2.27 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

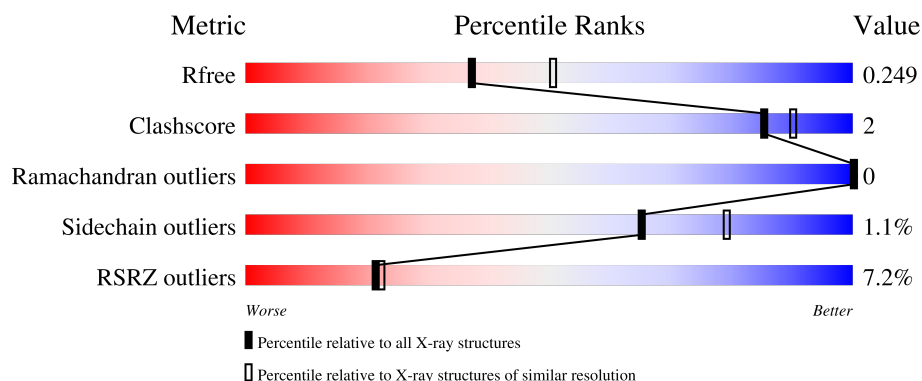
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.27 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	9078 (2.30-2.26)
Clashscore	190562	9802 (2.30-2.26)
Ramachandran outliers	187476	9690 (2.30-2.26)
Sidechain outliers	187428	9691 (2.30-2.26)
RSRZ outliers	180081	9085 (2.30-2.26)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	877	

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 6795 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
			Total	C	N	O	S			
1	A	848	6495	4140	1100	1216	39	0	3	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP B4RNT1
A	169	GLY	GLU	engineered mutation	UNP B4RNT1
A	454	ASN	ASP	conflict	UNP B4RNT1
A	508	ILE	MET	conflict	UNP B4RNT1

- Molecule 2 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

- DCL
-
- The diagram shows the chemical structure of D-glutamate (DCL). The central carbon atom is bonded to a hydrogen atom (H) and a carboxyl group (COOH). The carboxyl group consists of a carbon atom (C) double-bonded to an oxygen atom (O) and single-bonded to a hydroxyl group (OH). The central carbon is also bonded to an amino group (NH₂) and a side chain. The side chain consists of a methylene group (CH₂) bonded to a carboxyl group (COOH). The atoms are labeled as follows: C (central carbon), N (amino group), O (oxygen), H (hydrogen), and OH (hydroxyl group). The labels are in green. The amino group is shown in blue. The carboxyl group is shown in red. The side chain is shown in green.

ATP



WORLD WIDE
PDB
PROTEIN DATA BANK

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Mg	0	0
			1	1		

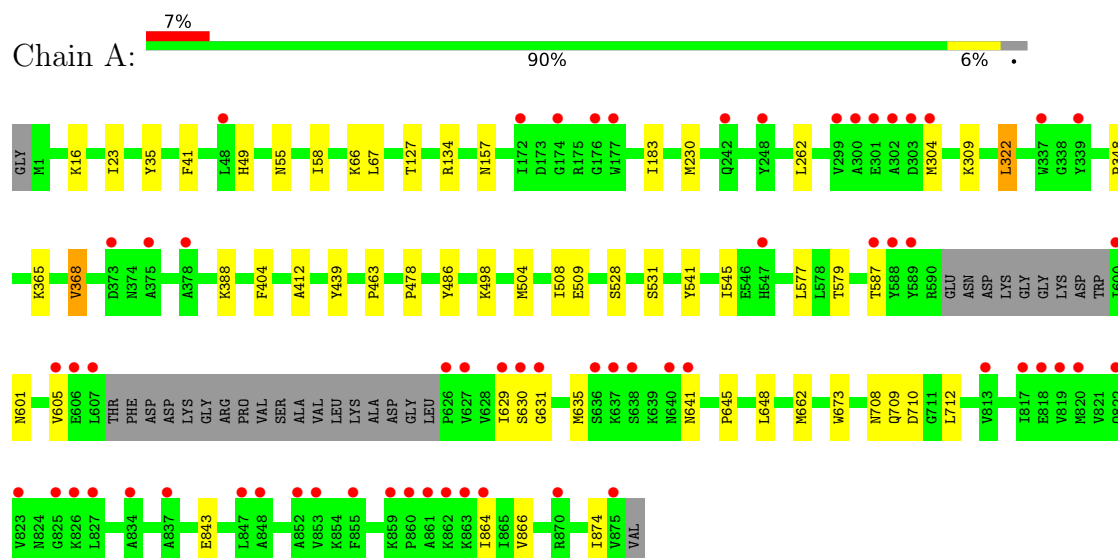
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	224	Total	O	0	0
			224	224		

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: Leucine-tRNA ligase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	48.88Å 82.21Å 227.21Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	66.60 – 2.27 66.60 – 2.27	Depositor EDS
% Data completeness (in resolution range)	100.0 (66.60-2.27) 100.0 (66.60-2.27)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.63 (at 2.22Å)	Xtriage
Refinement program	PHENIX 1.17.1 _3660	Depositor
R, R_{free}	0.200 , 0.249 0.201 , 0.249	Depositor DCC
R_{free} test set	2170 reflections (4.77%)	wwPDB-VP
Wilson B-factor (Å ²)	43.3	Xtriage
Anisotropy	0.221	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 51.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6795	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.64% 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: MG, EDO, ATP, DCL, ZN

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	0.23	0/6668	0.41	1/9078 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	368	VAL	N-CA-C	-5.87	107.57	113.20

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	6495	0	6112	28	0
2	A	4	0	6	0	0
3	A	8	0	12	0	0
4	A	62	0	24	0	0
5	A	1	0	0	0	0
6	A	1	0	0	0	0
7	A	224	0	0	0	0
All	All	6795	0	6154	28	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 (28) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:528:SER:HG	1:A:531:SER:HG	1.41	0.68
1:A:545:ILE:HB	1:A:579:THR:HG21	1.76	0.66
1:A:709:GLN:HB2	1:A:712:LEU:HD12	1.84	0.59
1:A:439:TYR:HB2	1:A:478:PRO:HD2	1.84	0.58
1:A:348:PRO:HB2	1:A:365:LYS:HG2	1.85	0.58
1:A:262:LEU:HD23	1:A:322:LEU:HD22	1.85	0.57
1:A:587:THR:HG22	1:A:641:ASN:HB3	1.88	0.55
1:A:504:MET:HB3	1:A:508:ILE:HD12	1.89	0.54
1:A:134:ARG:HB3	1:A:463:PRO:HB3	1.90	0.53
1:A:230:MET:HE1	1:A:412:ALA:HB2	1.90	0.53
1:A:49:HIS:HA	1:A:645:PRO:HD3	1.93	0.51
1:A:843:GLU:HG3	1:A:866:VAL:HG21	1.93	0.50
1:A:708:ASN:HD21	1:A:710:ASP:HB2	1.78	0.49
1:A:648:LEU:HD22	1:A:673:TRP:HH2	1.77	0.49
1:A:58:ILE:HG13	1:A:662:MET:HE1	1.95	0.48
1:A:304:MET:O	1:A:309:LYS:NZ	2.47	0.48
1:A:630:SER:OG	1:A:631:GLY:N	2.47	0.46
1:A:157:ASN:HB3	1:A:183:ILE:HG21	1.98	0.46
1:A:127:THR:HB	1:A:509:GLU:HG2	1.97	0.45
1:A:304:MET:HE2	1:A:304:MET:HB3	1.89	0.45
1:A:55:ASN:C	1:A:55:ASN:HD22	2.25	0.45
1:A:864:ILE:HG23	1:A:874:ILE:HG12	1.99	0.44
1:A:541:TYR:HB3	1:A:577:LEU:HD12	1.99	0.44
1:A:35:TYR:CE2	1:A:66:LYS:HG3	2.53	0.43
1:A:486:TYR:O	1:A:498:LYS:HA	2.19	0.42
1:A:388:LYS:HD3	1:A:404:PHE:CZ	2.55	0.41
1:A:635:MET:HA	1:A:641:ASN:CG	2.46	0.41
1:A:23:ILE:HG22	1:A:67:LEU:HD11	2.03	0.41

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	845/877 (96%)	826 (98%)	19 (2%)	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	636/716 (89%)	629 (99%)	7 (1%)	65	79

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	LYS
1	A	41	PHE
1	A	322	LEU
1	A	368	VAL
1	A	601	ASN
1	A	605	VAL
1	A	629	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	163	GLN
1	A	374	ASN
1	A	390	ASN
1	A	418	GLN
1	A	708	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](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 2 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	$\# Z > 2$
2	EDO	A	1001	-	3,3,3	0.49	0	2,2,2	0.16	0
4	ATP	A	1005	-	32,33,33	0.28	0	48,52,52	0.33	0
4	ATP	A	1003	-	32,33,33	0.27	0	48,52,52	0.33	0
3	DCL	A	1002	-	7,7,7	0.10	0	6,8,8	0.14	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	EDO	A	1001	-	-	0/1/1/1	-
4	ATP	A	1005	-	-	6/22/38/38	0/3/3/3
4	ATP	A	1003	-	-	3/22/38/38	0/3/3/3
3	DCL	A	1002	-	-	1/6/6/6	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

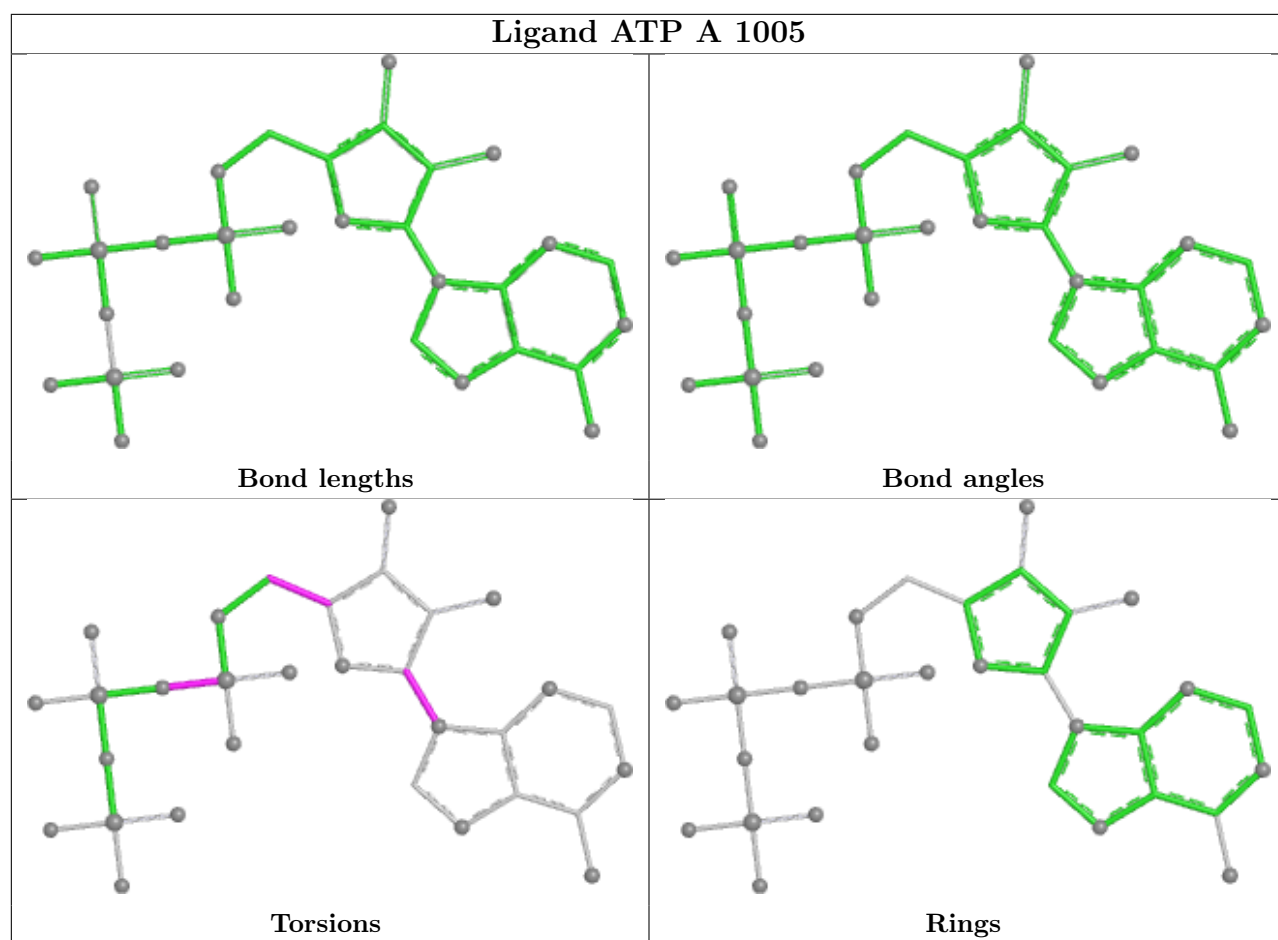
All (10) torsion outliers are listed below:

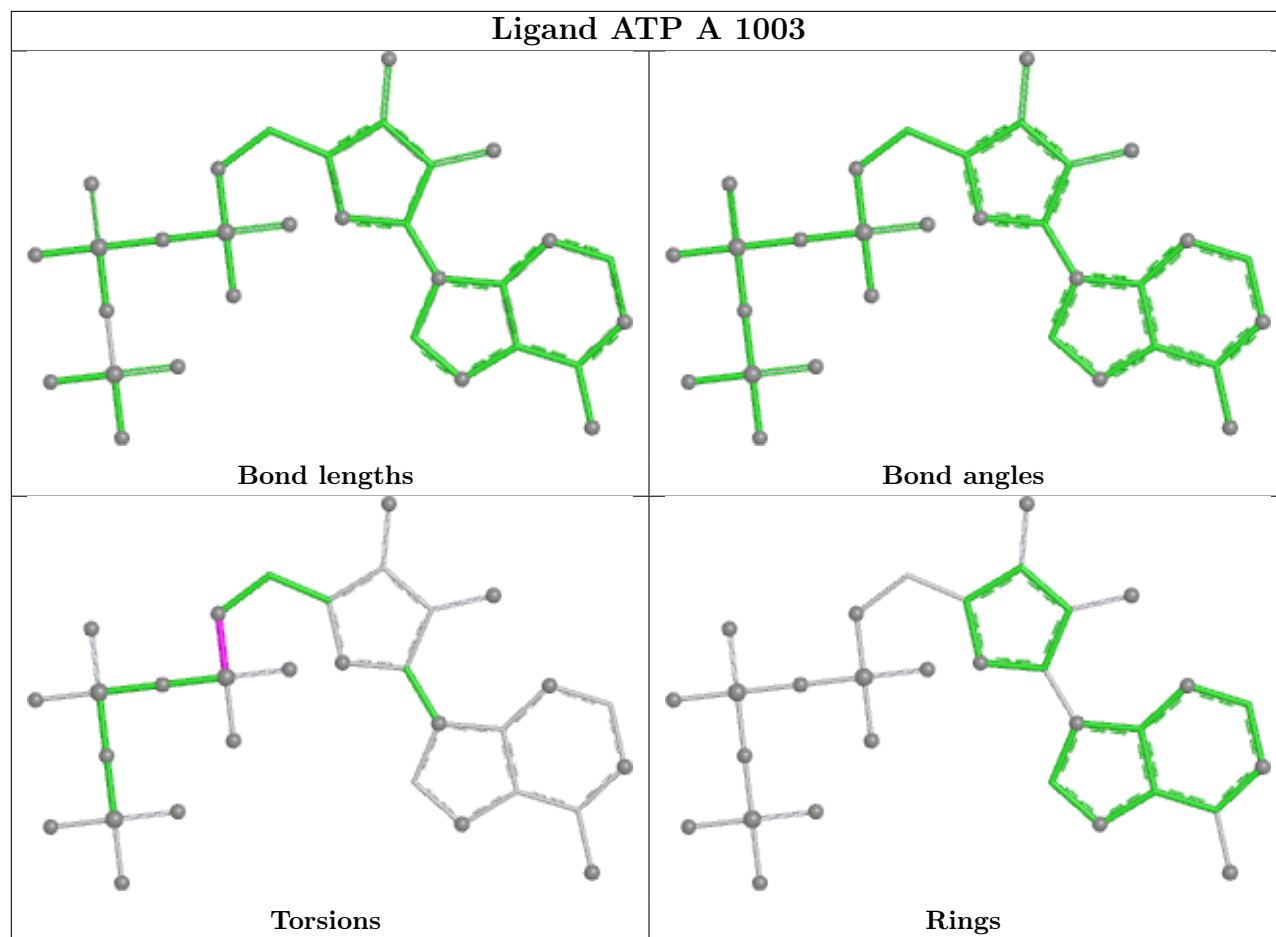
Mol	Chain	Res	Type	Atoms
4	A	1003	ATP	C5'-O5'-PA-O1A
4	A	1003	ATP	C5'-O5'-PA-O2A
4	A	1003	ATP	C5'-O5'-PA-O3A
4	A	1005	ATP	O4'-C4'-C5'-O5'
4	A	1005	ATP	C3'-C4'-C5'-O5'
4	A	1005	ATP	C2'-C1'-N9-C8
4	A	1005	ATP	PB-O3A-PA-O2A
3	A	1002	DCL	O-C-CA-N
4	A	1005	ATP	O4'-C1'-N9-C8
4	A	1005	ATP	PB-O3A-PA-O1A

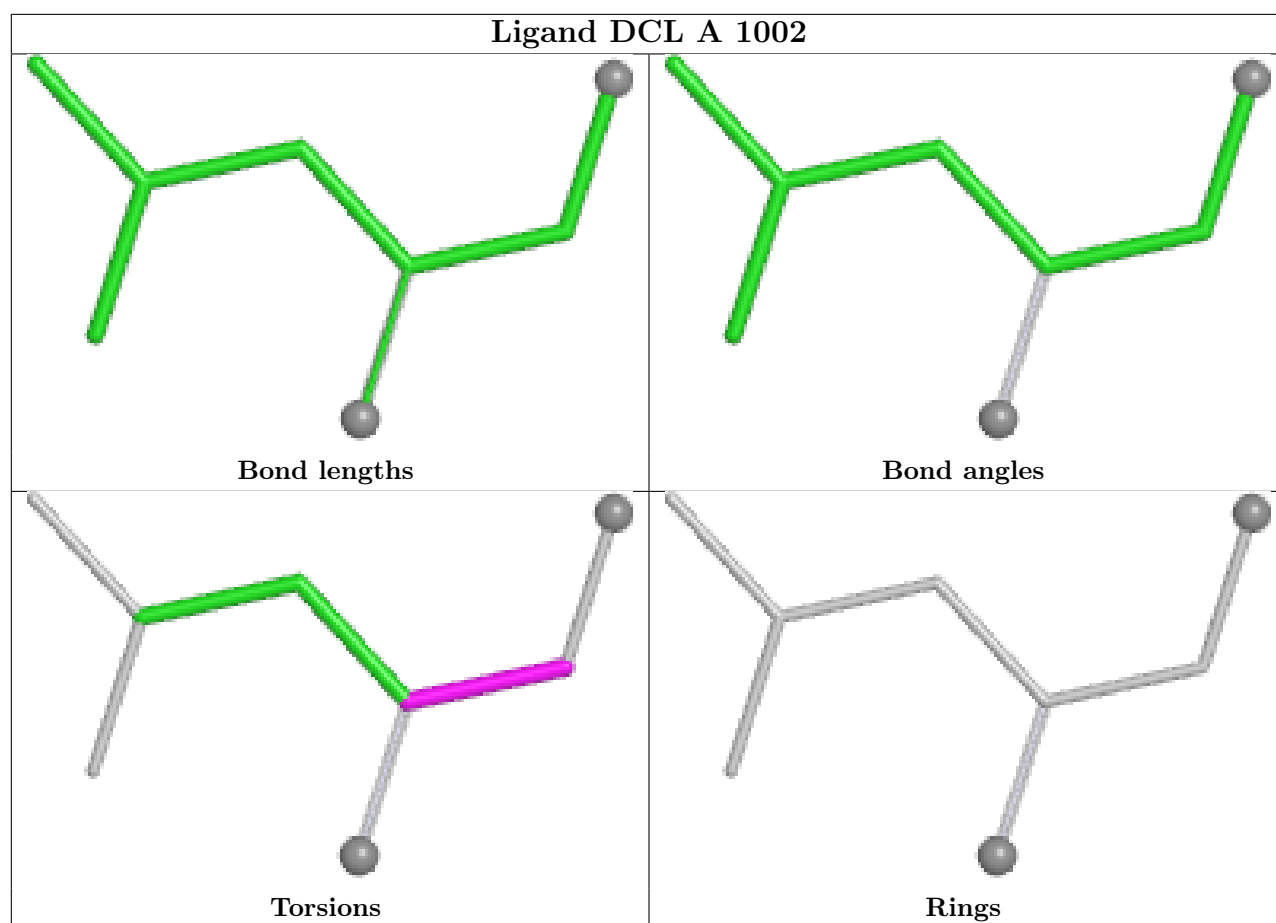
There are no ring outliers.

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.







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, 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	848/877 (96%)	0.35	61 (7%) 21 22	25, 53, 104, 157	3 (0%)

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	589	TYR	5.0
1	A	607	LEU	4.8
1	A	626	PRO	4.8
1	A	600	ILE	4.7
1	A	629	ILE	4.3
1	A	302	ALA	4.2
1	A	177	TRP	4.0
1	A	852	ALA	3.9
1	A	641	ASN	3.9
1	A	640	ASN	3.9
1	A	627	VAL	3.6
1	A	820	MET	3.5
1	A	303	ASP	3.5
1	A	819	VAL	3.3
1	A	834	ALA	3.2
1	A	48	LEU	3.2
1	A	605	VAL	3.2
1	A	300	ALA	3.1
1	A	861	ALA	3.1
1	A	301	GLU	3.1
1	A	588	TYR	3.1
1	A	817	ILE	3.1
1	A	860	PRO	3.1
1	A	606	GLU	3.0
1	A	304	MET	2.8
1	A	826	LYS	2.8
1	A	587	THR	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	823	VAL	2.8
1	A	174	GLY	2.7
1	A	637	LYS	2.7
1	A	631	GLY	2.7
1	A	242	GLN	2.6
1	A	822	GLN	2.6
1	A	875	VAL	2.6
1	A	864	ILE	2.6
1	A	248	TYR	2.6
1	A	172	ILE	2.6
1	A	299	VAL	2.6
1	A	853	VAL	2.6
1	A	339	TYR	2.6
1	A	825	GLY	2.5
1	A	176	GLY	2.4
1	A	813	VAL	2.4
1	A	862	LYS	2.4
1	A	870	ARG	2.4
1	A	630	SER	2.4
1	A	636	SER	2.3
1	A	373	ASP	2.3
1	A	337	TRP	2.3
1	A	848	ALA	2.3
1	A	855	PHE	2.2
1	A	837	ALA	2.2
1	A	863	LYS	2.2
1	A	847	LEU	2.2
1	A	375	ALA	2.2
1	A	827	LEU	2.1
1	A	378	ALA	2.1
1	A	547	HIS	2.1
1	A	818	GLU	2.1
1	A	859	LYS	2.0
1	A	638	SER	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 [i](#)

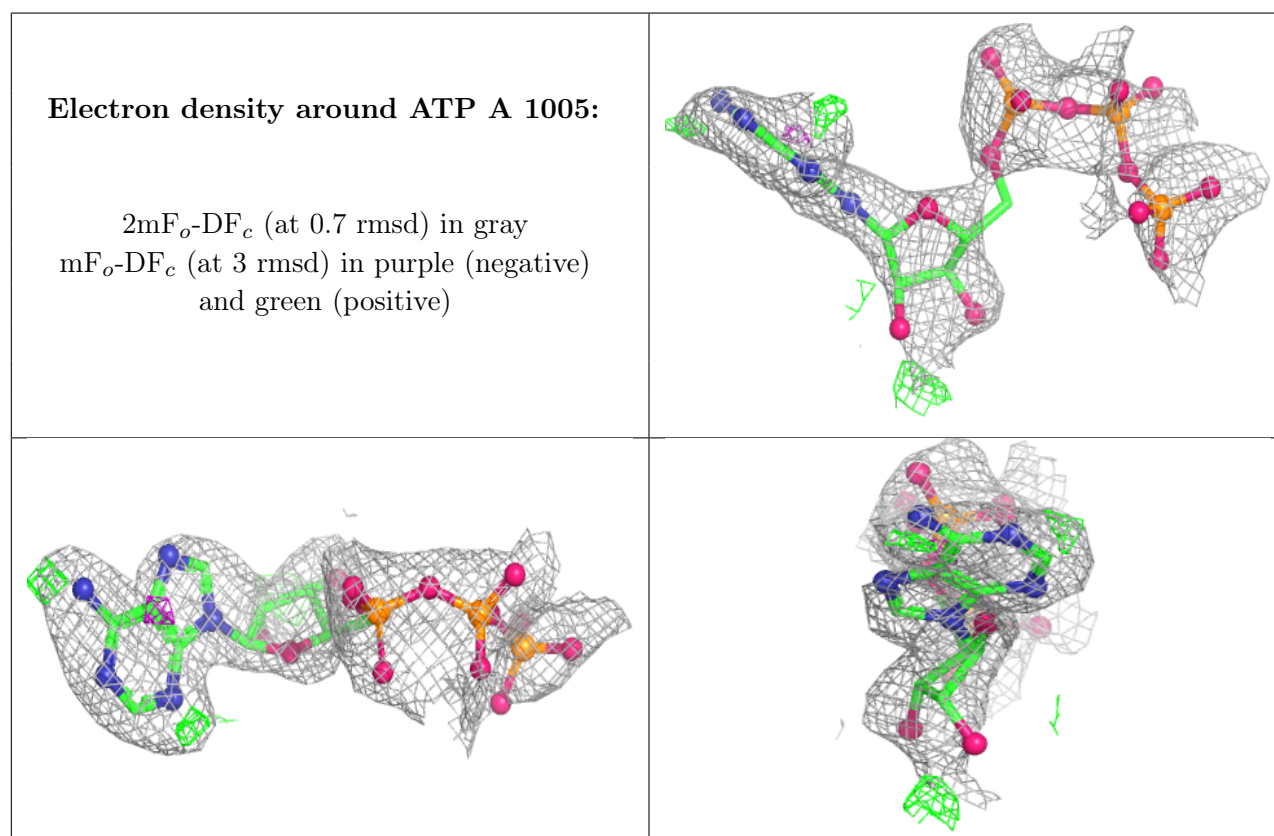
There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

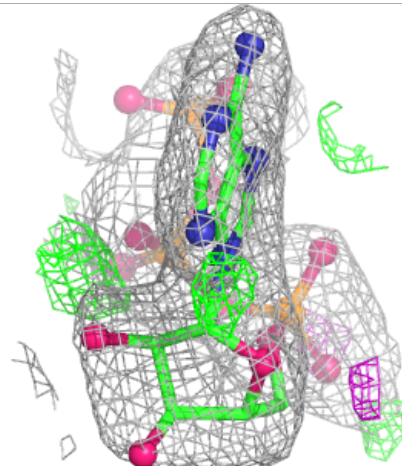
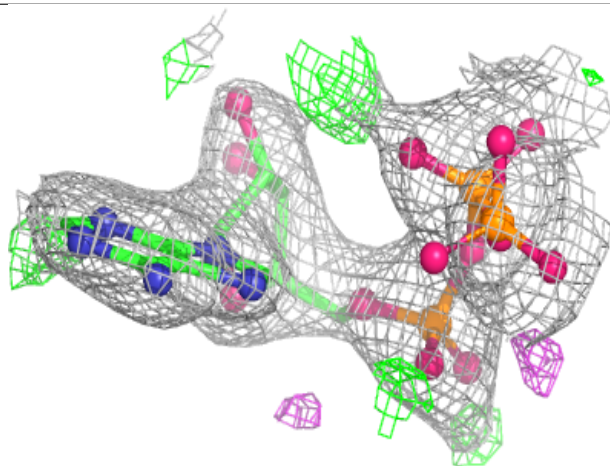
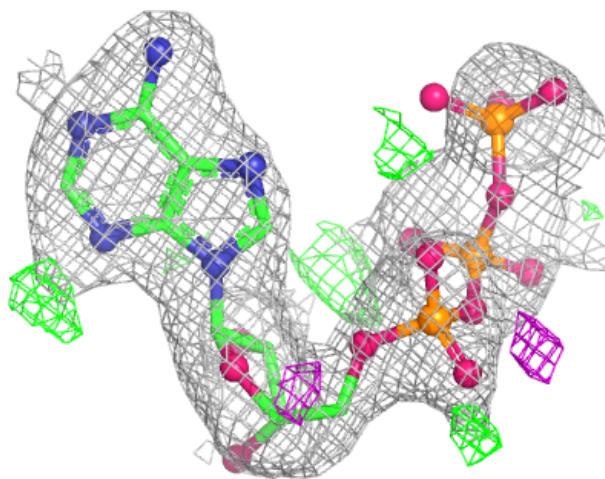
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	ATP	A	1005	31/31	0.70	0.15	86,109,156,157	0
4	ATP	A	1003	31/31	0.81	0.13	45,57,110,115	31
6	MG	A	1006	1/1	0.86	0.13	65,65,65,65	0
3	DCL	A	1002	8/8	0.91	0.13	44,51,62,74	0
2	EDO	A	1001	4/4	0.91	0.12	52,54,55,55	0
5	ZN	A	1004	1/1	0.99	0.03	46,46,46,46	0

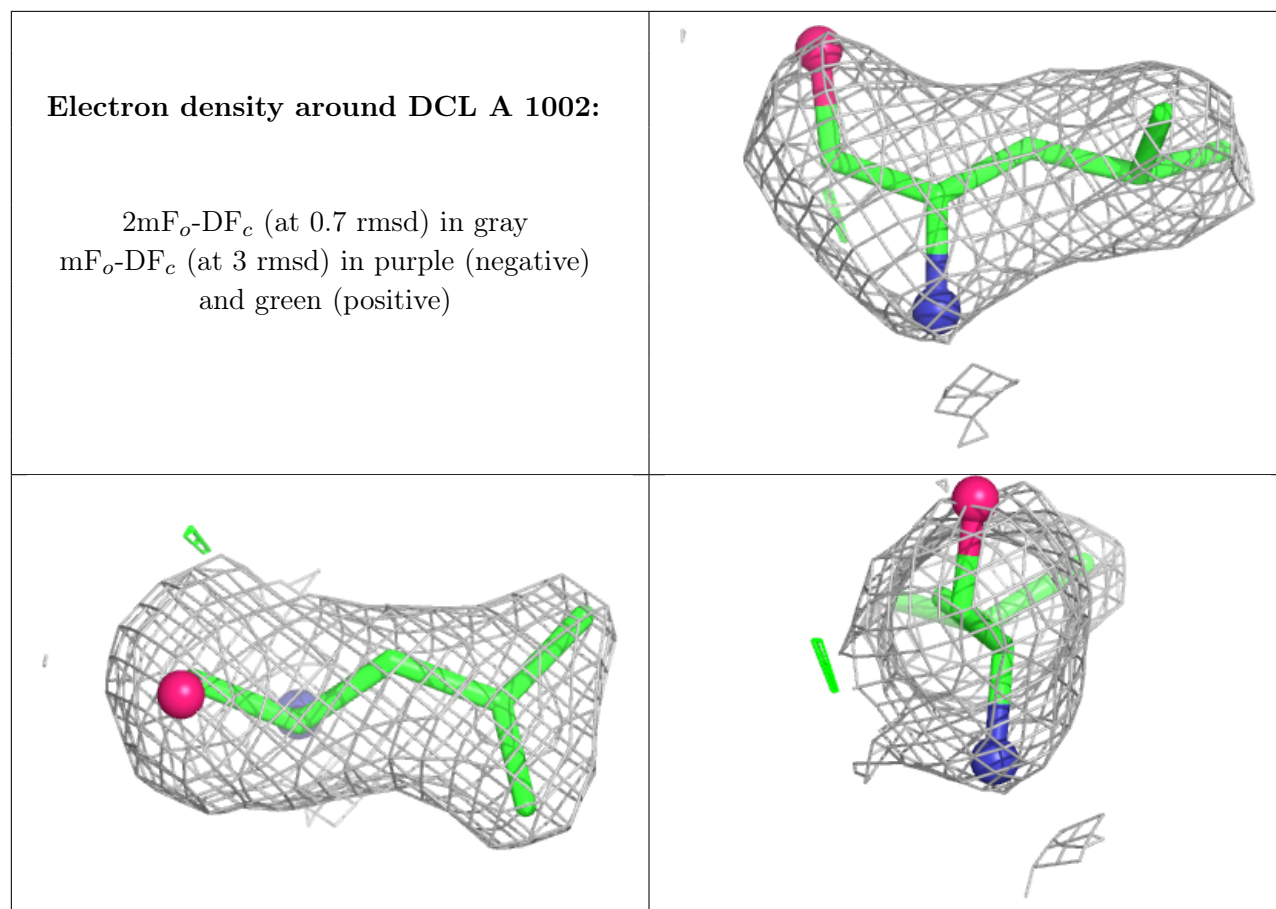
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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



Electron density around ATP A 1003:

$2mF_o-DF_c$ (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.