

Full wwPDB X-ray Structure Validation Report (i)

Aug 25, 2022 – 05:09 pm BST

PDB ID	:	7NU6
Title	:	Crystal Structure of Neisseria gonorrhoeae LeuRS in Complex with ATP in
		Conformation 1
Authors	:	Pang, L.; Strelkov, S.V.; Weeks, S.D.
Deposited on	:	2021-03-11
Resolution	:	2.20 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 (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	:	2.30
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.30

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 2.20 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R _{free}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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		
			9%		
1	А	877	88%	9%	•



2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 6705 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	А	848	Total 6454	C 4117	N 1094	O 1205	S 38	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	0	GLY	-	expression tag	UNP B4RNT1
А	454	ASN	ASP	conflict	UNP B4RNT1
А	508	ILE	MET	conflict	UNP B4RNT1

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



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



• Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
2	٨	1	Total	С	Ν	Ο	Р	0	0
J A	1	31	10	5	13	3	0	0	
2	٨	1	Total	С	Ν	0	Р	0	0
3 A	A	1	31	10	5	13	3	0	U

• Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	1	Total Zn 1 1	0	0

• Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	А	1	Total 1	Mg 1	0	0

• Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	183	Total O 183 183	0	0



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 (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	48.98Å 82.80Å 228.21Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Bosolution(A)	57.05 - 2.20	Depositor
Resolution (A)	114.11 - 2.17	EDS
% Data completeness	99.6 (57.05-2.20)	Depositor
(in resolution range)	$99.5\ (114.11-2.17)$	EDS
R_{merge}	0.09	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.44 (at 2.16 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
B B.	0.191 , 0.241	Depositor
Λ, Λ_{free}	0.191 , 0.241	DCC
R_{free} test set	2261 reflections $(4.51%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	46.1	Xtriage
Anisotropy	0.093	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	(Not available), (Not available)	EDS
L-test for twinning ²	$ < L > = 0.49, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6705	wwPDB-VP
Average B, all atoms $(Å^2)$	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.57% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

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: EDO, ATP, ZN, MG

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).

Mal	Chain	Bond	lengths	Bond angles		
	of Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.32	0/6619	0.49	0/9017	

There are no bond length outliers.

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	А	6454	0	6022	46	0
2	А	4	0	6	0	0
3	А	62	0	24	0	0
4	А	1	0	0	0	0
5	А	1	0	0	0	0
6	А	183	0	0	0	0
All	All	6705	0	6052	46	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 4.

All (46) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



Atom_1	Atom_2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:276:LEU:HD22	1:A:329:VAL:HG11	1.71	0.73
1:A:41:PHE:CD2	1:A:513:TYR:CE2	2.84	0.65
1:A:819:VAL:HG21	1:A:842:LEU:HD11	1.78	0.65
1:A:843:GLU:HG3	1:A:864:ILE:HG21	1.80	0.63
1:A:439:TYR:HB2	1:A:478:PRO:HD2	1.80	0.62
1:A:648:LEU:HD12	1:A:657:ALA:HB2	1.84	0.60
1:A:817:ILE:HD12	1:A:869:GLY:HA2	1.85	0.57
1:A:193:PHE:HD2	1:A:434:ILE:HD11	1.70	0.57
1:A:630:SER:OG	1:A:631:GLY:N	2.35	0.56
1:A:41:PHE:CE1	1:A:80:ASP:HB2	2.42	0.55
1:A:301:GLU:HA	1:A:304:MET:HB2	1.89	0.54
1:A:587:THR:HB	1:A:599:TRP:HZ3	1.73	0.54
1:A:41:PHE:CD2	1:A:513:TYR:CZ	2.96	0.53
1:A:682:HIS:CD2	1:A:686:ARG:HD2	2.43	0.53
1:A:798:LYS:HB2	1:A:801:GLU:HG3	1.89	0.52
1:A:106:GLU:HG3	1:A:107:TYR:N	2.26	0.51
1:A:350:HIS:CE1	1:A:369:ILE:HB	2.47	0.50
1:A:633:GLU:HG2	1:A:634:LYS:N	2.29	0.48
1:A:273:GLU:HG3	1:A:295:LYS:HE2	1.96	0.47
1:A:49:HIS:HA	1:A:645:PRO:HD3	1.96	0.47
1:A:134:ARG:HB3	1:A:463:PRO:HB3	1.96	0.47
1:A:164:THR:HG22	1:A:165:VAL:O	2.16	0.45
1:A:191:TYR:OH	1:A:446:ILE:HG21	2.17	0.45
1:A:268:VAL:HG13	1:A:344:VAL:O	2.17	0.45
1:A:589:TYR:HE1	1:A:630:SER:HB2	1.82	0.44
1:A:193:PHE:CD2	1:A:434:ILE:HD11	2.51	0.44
1:A:240:SER:HB3	1:A:316:ARG:HD2	2.00	0.43
1:A:867:VAL:CG1	1:A:871:LEU:HG	2.48	0.43
1:A:682:HIS:NE2	1:A:686:ARG:HD2	2.34	0.43
1:A:42:PRO:HD2	1:A:78:GLY:O	2.18	0.43
1:A:40:MET:HE3	1:A:543:GLY:HA3	2.01	0.43
1:A:40:MET:HE2	1:A:40:MET:HB2	1.91	0.42
1:A:41:PHE:HD2	1:A:41:PHE:H	1.67	0.42
1:A:157:ASN:HB3	1:A:183:ILE:HG21	2.01	0.42
1:A:543:GLY:O	1:A:579:THR:HA	2.19	0.42
1:A:587:THR:HB	1:A:599:TRP:CZ3	2.54	0.42
1:A:374:ASN:HB3	1:A:384:TRP:CE2	2.55	0.41
1:A:709:GLN:HB2	1:A:712:LEU:HD12	2.01	0.41
1:A:833:VAL:HG21	1:A:842:LEU:HD21	2.01	0.41
1:A:348:PRO:HB2	1:A:365:LYS:HG2	2.01	0.41
1:A:62:LEU:HD13	1:A:540:GLN:HG2	2.02	0.41
1:A:545:ILE:N	1:A:579:THR:OG1	2.55	0.41

Continued on next page...



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:867:VAL:HG13	1:A:871:LEU:H	1.86	0.41
1:A:584:VAL:HG12	1:A:634:LYS:HA	2.02	0.40
1:A:486:TYR:O	1:A:498:LYS:HA	2.21	0.40
1:A:171:VAL:HG13	1:A:171:VAL:O	2.20	0.40

Continued from previous page...

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	А	842/877~(96%)	821 (98%)	20~(2%)	1 (0%)	51 60	

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	630	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	А	622/717~(87%)	614 (99%)	8 (1%)	69 81	

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



Mol	Chain	Res	Type
1	А	34	LYS
1	А	36	TYR
1	А	41	PHE
1	А	45	SER
1	А	55	ASN
1	А	309	LYS
1	А	360	LYS
1	А	569	ASN

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

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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 Chai	Chain	Dog	Tiple	Bond lengths				Bond angles		
MOI	туре	Unain	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	ATP	А	1003	-	26,33,33	0.56	0	31,52,52	0.73	1 (3%)
3	ATP	А	1002	-	26,33,33	0.60	1 (3%)	31,52,52	0.72	1 (3%)
2	EDO	А	1001	-	3,3,3	0.48	0	2,2,2	0.25	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
3	ATP	А	1003	-	-	1/18/38/38	0/3/3/3
3	ATP	А	1002	-	-	6/18/38/38	0/3/3/3
2	EDO	А	1001	-	-	0/1/1/1	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	А	1002	ATP	C8-N7	-2.02	1.31	1.34

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	А	1003	ATP	C5-C6-N6	2.60	124.31	120.35
3	А	1002	ATP	C5-C6-N6	2.16	123.64	120.35

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	А	1002	ATP	O4'-C4'-C5'-O5'
3	А	1002	ATP	C3'-C4'-C5'-O5'
3	А	1003	ATP	PB-O3A-PA-O5'
3	А	1002	ATP	PB-O3A-PA-O2A
3	А	1002	ATP	PB-O3B-PG-O2G
3	А	1002	ATP	PA-O3A-PB-O2B
3	А	1002	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 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.









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 (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	$\mathbf{OWAB}(\mathbf{\AA}^2)$	Q < 0.9
1	А	848/877~(96%)	0.73	77 (9%) 9 8	29, 54, 97, 132	0

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ	
1	А	548	ALA	10.4	
1	А	853	VAL	10.0	
1	А	302	ALA	8.0	
1	А	848	ALA	7.4	
1	А	838	SER	6.5	
1	А	545	ILE	6.0	
1	А	300	ALA	5.9	
1	А	629	ILE	5.8	
1	А	599	TRP	5.7	
1	А	474	GLY	5.4	
1	А	166	LEU	5.3	
1	А	589	TYR	5.2	
1	А	851	GLY	5.1	
1	А	598	ASP	4.9	
1	А	587	THR	4.9	
1	А	874	ILE	4.8	
1	А	588	TYR	4.6	
1	А	174	GLY	4.5	
1	А	375	ALA	4.3	
1	А	301	GLU	4.3	
1	А	852	ALA	4.2	
1	А	832	THR	3.9	
1	А	837	ALA	3.8	
1	А	826	LYS	3.8	
1	А	640	ASN	3.6	
1	А	177	TRP	3.6	
1	А	277	ALA	3.6	

Continued on next page...



7NI	U6
-----	----

Mol	Chain	Res	Type	RSRZ
1	А	815	SER	3.5
1	А	863	LYS	3.4
1	А	1	MET	3.4
1	А	817	ILE	3.4
1	А	628	VAL	3.4
1	А	864	ILE	3.4
1	А	697	LYS	3.3
1	А	856	MET	3.3
1	А	840	ALA	3.3
1	А	642	GLY	3.2
1	А	282	ALA	3.1
1	А	299	VAL	3.0
1	А	825	GLY	2.9
1	А	827	LEU	2.9
1	А	605	VAL	2.8
1	А	476	GLY	2.7
1	А	374	ASN	2.7
1	А	276	LEU	2.7
1	А	849	ASN	2.7
1	А	373	ASP	2.6
1	А	641	ASN	2.6
1	А	870	ARG	2.5
1	А	582	MET	2.5
1	А	235	ALA	2.5
1	А	835	ALA	2.5
1	А	858	GLY	2.4
1	А	246	GLY	2.4
1	А	822	GLN	2.3
1	А	861	ALA	2.3
1	A	806	THR	2.3
1	А	345	MET	2.3
1	A	321	PRO	2.3
1	А	183	ILE	2.3
1	А	758	ASP	2.2
1	А	482	MET	2.2
1	A	171	VAL	2.2
1	А	833	VAL	2.2
1	A	839	LYS	2.2
1	А	850	GLU	2.2
1	A	859	LYS	2.2
1	А	404	PHE	2.1
1	А	347	VAL	2.1

Continued from previous page...

Continued on next page...



Mol	Chain	Res	Type	RSRZ
1	А	234	PHE	2.1
1	А	735	GLY	2.1
1	А	847	LEU	2.1
1	А	238	ASP	2.1
1	А	239	ASP	2.1
1	А	31	SER	2.1
1	А	182	LEU	2.0
1	А	383	GLU	2.0

Continued from previous page...

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 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	$\mathbf{B} ext{-factors}(\mathbf{A}^2)$	$\mathbf{Q} < 0.9$
5	MG	А	1005	1/1	0.40	0.39	87,87,87,87	0
3	ATP	А	1003	31/31	0.70	0.24	43,67,159,161	0
3	ATP	А	1002	31/31	0.77	0.19	50,62,124,125	0
2	EDO	А	1001	4/4	0.90	0.20	48,57,64,70	0
4	ZN	А	1004	1/1	1.00	0.15	50,50,50,50	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.







6.5 Other polymers (i)

There are no such residues in this entry.

