

Nicolas Leulliot

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

66

papers

2,327

citations

28

h-index

46

g-index

70

ext. papers

2,580

ext. citations

8

avg, IF

4.34

L-index

| # | Paper | IF | Citations |
|----|---|------|-----------|
| 66 | Genetic, structural, and functional characterization of POLE polymerase proofreading variants allows cancer risk prediction. <i>Genetics in Medicine</i> , 2020 , 22, 1533-1541 | 8.1 | 9 |
| 65 | The Npa1p complex chaperones the assembly of the earliest eukaryotic large ribosomal subunit precursor. <i>PLoS Genetics</i> , 2018 , 14, e1007597 | 6 | 11 |
| 64 | Shared genetic predisposition in rheumatoid arthritis-interstitial lung disease and familial pulmonary fibrosis. <i>European Respiratory Journal</i> , 2017 , 49, | 13.6 | 89 |
| 63 | Functional link between DEAH/RHA helicase Prp43 activation and ATP base binding. <i>Nucleic Acids Research</i> , 2017 , 45, 1539-1552 | 20.1 | 16 |
| 62 | Insertion of the Biogenesis Factor Rei1 Probes the Ribosomal Tunnel during 60S Maturation. <i>Cell</i> , 2016 , 164, 91-102 | 56.2 | 75 |
| 61 | and screen in the Sotos-like syndrome French cohort. <i>Journal of Medical Genetics</i> , 2016 , 53, 743-751 | 5.8 | 36 |
| 60 | Sequential domain assembly of ribosomal protein S3 drives 40S subunit maturation. <i>Nature Communications</i> , 2016 , 7, 10336 | 17.4 | 39 |
| 59 | Chaperoning 5S RNA assembly. <i>Genes and Development</i> , 2015 , 29, 1432-46 | 12.6 | 35 |
| 58 | Structure of Escherichia coli tryptophanase purified from an alkaline-stressed bacterial culture. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015 , 71, 1378-83 | 1.1 | 0 |
| 57 | Regulation of DEAH/RHA helicases by G-patch proteins. <i>BioMed Research International</i> , 2015 , 2015, 931857 | 5.7 | 40 |
| 56 | RNA mimicry by the fap7 adenylate kinase in ribosome biogenesis. <i>PLoS Biology</i> , 2014 , 12, e1001860 | 9.7 | 33 |
| 55 | Structure and function of AvtR, a novel transcriptional regulator from a hyperthermophilic archaeal lipothrixvirus. <i>Journal of Virology</i> , 2013 , 87, 124-36 | 6.6 | 15 |
| 54 | Hydroxamic acids as potent inhibitors of Fe(II) and Mn(II) E. coli methionine aminopeptidase: biological activities and X-ray structures of oxazole hydroxamate-EcMetAP-Mn complexes. <i>ChemMedChem</i> , 2012 , 7, 1020-30 | 3.7 | 28 |
| 53 | Mechanism of the AAA+ ATPases pontin and reptin in the biogenesis of H/ACA RNPs. <i>Rna</i> , 2012 , 18, 1833-45 | 5.85 | 54 |
| 52 | The H/ACA RNP assembly factor SHQ1 functions as an RNA mimic. <i>Genes and Development</i> , 2011 , 25, 2398-408 | 12.6 | 33 |
| 51 | Prp43p contains a processive helicase structural architecture with a specific regulatory domain. <i>EMBO Journal</i> , 2010 , 29, 2194-204 | 13 | 107 |
| 50 | ORF157 from the archaeal virus Acidianus filamentous virus 1 defines a new class of nuclease. <i>Journal of Virology</i> , 2010 , 84, 5025-31 | 6.6 | 14 |

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| 49 | Crystal structure of yeast FAD synthetase (Fad1) in complex with FAD. <i>Journal of Molecular Biology</i> , 2010 , 398, 641-6 | 6.5 | 22 |
| 48 | The family X DNA polymerase from <i>Deinococcus radiodurans</i> adopts a non-standard extended conformation. <i>Journal of Biological Chemistry</i> , 2009 , 284, 11992-9 | 5.4 | 25 |
| 47 | Evf, a virulence factor produced by the <i>Drosophila</i> pathogen <i>Erwinia carotovora</i> , is an S-palmitoylated protein with a new fold that binds to lipid vesicles. <i>Journal of Biological Chemistry</i> , 2009 , 284, 3552-62 | 5.4 | 25 |
| 46 | The crystal structure of ORF14 from <i>Sulfolobus islandicus</i> filamentous virus. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 76, 1020-2 | 4.2 | 7 |
| 45 | The thermo- and acido-stable ORF-99 from the archaeal virus AFV1. <i>Protein Science</i> , 2009 , 18, 1316-20 | 6.3 | 12 |
| 44 | A protein encoded by a new family of mobile elements from Euryarchaea exhibits three domains with novel folds. <i>Protein Science</i> , 2009 , 18, 850-5 | 6.3 | 14 |
| 43 | Crystal structure of AFV1-102, a protein from the acidianus filamentous virus 1. <i>Protein Science</i> , 2009 , 18, 845-9 | 6.3 | 7 |
| 42 | The box H/ACA snoRNP assembly factor Shq1p is a chaperone protein homologous to Hsp90 cochaperones that binds to the Cbf5p enzyme. <i>Journal of Molecular Biology</i> , 2009 , 390, 231-44 | 6.5 | 18 |
| 41 | Structure of the yeast tRNA m7G methylation complex. <i>Structure</i> , 2008 , 16, 52-61 | 5.2 | 73 |
| 40 | The crystal structure of <i>Pyrococcus abyssi</i> tRNA (uracil-54, C5)-methyltransferase provides insights into its tRNA specificity. <i>Nucleic Acids Research</i> , 2008 , 36, 4929-40 | 20.1 | 14 |
| 39 | The yeast ribosome synthesis factor Emg1 is a novel member of the superfamily of alpha/beta knot fold methyltransferases. <i>Nucleic Acids Research</i> , 2008 , 36, 629-39 | 20.1 | 45 |
| 38 | Production and crystallization of protein domains: how useful are disorder predictions?. <i>Current Protein and Peptide Science</i> , 2007 , 8, 151-60 | 2.8 | 7 |
| 37 | An archaeal orthologue of the universal protein Kae1 is an iron metalloprotein which exhibits atypical DNA-binding properties and apurinic-endonuclease activity in vitro. <i>Nucleic Acids Research</i> , 2007 , 35, 6042-51 | 20.1 | 54 |
| 36 | The box H/ACA RNP assembly factor Naf1p contains a domain homologous to Gar1p mediating its interaction with Cbf5p. <i>Journal of Molecular Biology</i> , 2007 , 371, 1338-53 | 6.5 | 34 |
| 35 | Crystal structure of AFV3-109, a highly conserved protein from crenarchaeal viruses. <i>Virology Journal</i> , 2007 , 4, 12 | 6.1 | 26 |
| 34 | Cloning, production, and purification of proteins for a medium-scale structural genomics project. <i>Methods in Molecular Biology</i> , 2007 , 363, 21-37 | 1.4 | 12 |
| 33 | Structure-based functional annotation: yeast ymr099c codes for a D-hexose-6-phosphate mutarotase. <i>Journal of Biological Chemistry</i> , 2006 , 281, 30175-85 | 5.4 | 20 |
| 32 | Structure of the human multidrug resistance protein 1 nucleotide binding domain 1 bound to Mg ²⁺ /ATP reveals a non-productive catalytic site. <i>Journal of Molecular Biology</i> , 2006 , 359, 940-9 | 6.5 | 70 |

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| 31 | Structural characterization of Set1 RNA recognition motifs and their role in histone H3 lysine 4 methylation. <i>Journal of Molecular Biology</i> , 2006 , 359, 1170-81 | 6.5 | 45 |
| 30 | Crystal structure of the PP2A phosphatase activator: implications for its PP2A-specific PPlase activity. <i>Molecular Cell</i> , 2006 , 23, 413-24 | 17.6 | 43 |
| 29 | Crystallization and preliminary X-ray diffraction analysis of protein 14 from <i>Sulfolobus islandicus</i> filamentous virus (SIFV). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006 , 62, 884-6 | | 4 |
| 28 | Crystal structure of the yeast His6 enzyme suggests a reaction mechanism. <i>Protein Science</i> , 2006 , 15, 1516-21 | 6.3 | 7 |
| 27 | Crystal structure of the YML079w protein from <i>Saccharomyces cerevisiae</i> reveals a new sequence family of the jelly-roll fold. <i>Protein Science</i> , 2005 , 14, 209-15 | 6.3 | 9 |
| 26 | Crystal structure of the <i>S. cerevisiae</i> D-ribose-5-phosphate isomerase: comparison with the archaeal and bacterial enzymes. <i>Biochimie</i> , 2005 , 87, 763-9 | 4.6 | 15 |
| 25 | Crystal structure and confirmation of the alanine:glyoxylate aminotransferase activity of the YFL030w yeast protein. <i>Biochimie</i> , 2005 , 87, 1041-7 | 4.6 | 10 |
| 24 | Crystal structure of yeast YHR049W/FSH1, a member of the serine hydrolase family. <i>Protein Science</i> , 2005 , 14, 1350-6 | 6.3 | 18 |
| 23 | Crystal structure of yeast YER010Cp, a knotable member of the RraA protein family. <i>Protein Science</i> , 2005 , 14, 2751-8 | 6.3 | 4 |
| 22 | High-throughput crystal-optimization strategies in the South Paris Yeast Structural Genomics Project: one size fits all?. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005 , 61, 664-70 | | 13 |
| 21 | HalX: an open-source LIMS (Laboratory Information Management System) for small- to large-scale laboratories. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005 , 61, 671-8 | | 18 |
| 20 | Crystal structure of YHI9, the yeast member of the phenazine biosynthesis PhzF enzyme superfamily. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 60, 778-86 | 4.2 | 10 |
| 19 | Crystal structure of the bifunctional chorismate synthase from <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2004 , 279, 619-25 | 5.4 | 22 |
| 18 | Crystal structure of yeast allantoicase reveals a repeated jelly roll motif. <i>Journal of Biological Chemistry</i> , 2004 , 279, 23447-52 | 5.4 | 19 |
| 17 | Structure of protein phosphatase methyltransferase 1 (PPM1), a leucine carboxyl methyltransferase involved in the regulation of protein phosphatase 2A activity. <i>Journal of Biological Chemistry</i> , 2004 , 279, 8351-8 | 5.4 | 65 |
| 16 | Crystal structure and functional characterization of yeast YLR011wp, an enzyme with NAD(P)H-FMN and ferric iron reductase activities. <i>Journal of Biological Chemistry</i> , 2004 , 279, 34890-7 | 5.4 | 62 |
| 15 | A new alpha-helical extension promotes RNA binding by the dsRBD of Rnt1p RNAse III. <i>EMBO Journal</i> , 2004 , 23, 2468-77 | 13 | 53 |
| 14 | Crystal structure of the YDR533c <i>S. cerevisiae</i> protein, a class II member of the Hsp31 family. <i>Structure</i> , 2004 , 12, 839-47 | 5.2 | 28 |

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|----|---|------|-----|
| 13 | Crystal structure of the YGR205w protein from <i>Saccharomyces cerevisiae</i> : close structural resemblance to <i>E. coli</i> pantothenate kinase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 54, 776-83 | 4.2 | 12 |
| 12 | The Paris-Sud yeast structural genomics pilot-project: from structure to function. <i>Biochimie</i> , 2004 , 86, 617-23 | 4.6 | 17 |
| 11 | Thermodynamic and structural features of ultrastable DNA and RNA hairpins. <i>Journal of Molecular Structure</i> , 2003 , 651-653, 67-74 | 3.4 | 8 |
| 10 | A structural genomics initiative on yeast proteins. <i>Journal of Synchrotron Radiation</i> , 2003 , 10, 4-8 | 2.4 | 17 |
| 9 | Crystal structure of the yeast Phox homology (PX) domain protein Grd19p complexed to phosphatidylinositol-3-phosphate. <i>Journal of Biological Chemistry</i> , 2003 , 278, 50371-6 | 5.4 | 55 |
| 8 | The solution structure of an essential stem-loop of human telomerase RNA. <i>Nucleic Acids Research</i> , 2003 , 31, 2614-21 | 20.1 | 36 |
| 7 | Current topics in RNA-protein recognition: control of specificity and biological function through induced fit and conformational capture. <i>Biochemistry</i> , 2001 , 40, 7947-56 | 3.2 | 297 |
| 6 | Analysis of the structural and vibrational properties of RNA building blocks by means of neutron inelastic scattering and density functional theory calculations. <i>Chemical Physics</i> , 2000 , 261, 217-237 | 2.3 | 64 |
| 5 | Ground-State Properties of Nucleic Acid Constituents Studied by Density Functional Calculations. 3. Role of Sugar Puckering and Base Orientation on the Energetics and Geometry of 2-Deoxyribonucleosides and Ribonucleosides. <i>Journal of Physical Chemistry B</i> , 2000 , 104, 4560-4568 | 3.4 | 90 |
| 4 | Unusual nucleotide conformations in GNRA and UNCG type tetraloop hairpins: evidence from Raman markers assignments. <i>Nucleic Acids Research</i> , 1999 , 27, 1398-404 | 20.1 | 33 |
| 3 | Aqueous phase structural features of GNRA tetraloops formed in short hairpins as evidenced by UV absorption and Raman spectroscopy. <i>Vibrational Spectroscopy</i> , 1999 , 19, 335-340 | 2.1 | 12 |
| 2 | Ground State Properties of the Nucleic Acid Constituents Studied by Density Functional Calculations. 2. Comparison between Calculated and Experimental Vibrational Spectra of Uridine and Cytidine. <i>Journal of Physical Chemistry B</i> , 1999 , 103, 10934-10944 | 3.4 | 60 |
| 1 | Ground State Properties of the Nucleic Acid Constituents Studied by Density Functional Calculations. I. Conformational Features of Ribose, Dimethyl Phosphate, Uridine, Cytidine, 5-Methyl Phosphate-Uridine, and 3-Methyl Phosphate-Uridine. <i>Journal of Physical Chemistry A</i> , 1999 , 103, 8716-8724 | 2.8 | 61 |