Douglas V Laurents

List of Publications by Year in Descending Order

103 papers	2,703 citations	26 h-index	49 g-index
117 ext. papers	3,022 ext. citations	4.7 avg, IF	4.73 L-index

#	Paper	IF	Citations
103	Partial structure, dampened mobility, and modest impact of a His tag in the SARS-CoV-2 Nsp2 C-terminal region. *European Biophysics Journal*, **2021**, 50, 1129-1137	1.9	1
102	Divergent CPEB prion-like domains reveal different assembly mechanisms for a generic amyloid-like fold. *BMC Biology*, **2021**, 19, 43	7.3	6
101	Phe-Gly motifs drive fibrillization of TDP-43 prion-like domain condensates. *PLoS Biology*, **2021**, 19, e3001198	9.7	4
100	Large-Scale Recombinant Production of the SARS-CoV-2 Proteome for High-Throughput and Structural Biology Applications. *Frontiers in Molecular Biosciences*, **2021**, 8, 653148	5.6	12
99	Do polyproline II helix associations modulate biomolecular condensates?. *FEBS Open Bio*, **2021**, 11, 2390-2399	2.7	2
98	Cohesin-dockerin code in cellulosomal dual binding modes and its allosteric regulation by proline isomerization. *Structure*, **2021**, 29, 587-597.e8	5.2	1
97	Glycine rich segments adopt polyproline II helices: Implications for biomolecular condensate formation. *Archives of Biochemistry and Biophysics*, **2021**, 704, 108867	4.1	1
96	NMR assignments for the C-terminal domain of human TDP-43. *Biomolecular NMR Assignments*, **2021**, 15, 177-181	0.7	3
95	Disorder and partial folding in the regulatory subunit hinge region of Trypanosoma brucei protein kinase A: The C-linker portion inhibits the parasite protein kinase A. *Archives of Biochemistry and Biophysics*, **2021**, 698, 108731	4.1	0
94	Aromatic and aliphatic residues of the disordered region of TDP-43 are on a fast track for self-assembly. *Biochemical and Biophysical Research Communications*, **2021**, 578, 110-114	3.4	1
93	Conformational Priming of RepA-WH1 for Functional Amyloid Conversion Detected by NMR Spectroscopy. *Structure*, **2020**, 28, 336-347.e4	5.2	4
92	Structural transitions in Orb2 prion-like domain relevant for functional aggregation in memory consolidation. *Journal of Biological Chemistry*, **2020**, 295, 18122-18133	5.4	2
91	Probing structural changes during amyloid aggregation of the sweet protein MNEI. *FEBS Journal*, **2020**, 287, 2808-2822	5.7	2
90	Nucleotide-induced folding of cell division protein FtsZ from Staphylococcus aureus. *FEBS Journal*, **2020**, 287, 4048-4067	5.7	9
89	Molecular mechanism of the inhibition of TDP-43 amyloidogenesis by QBP1. *Archives of Biochemistry and Biophysics*, **2019**, 675, 108113	4.1	6
88	A new glucose biosensor based on Nickel/KH550 nanocomposite deposited on the GCE: An electrochemical study. *Journal of Electroanalytical Chemistry*, **2019**, 839, 9-15	4.1	6
87	RNA binding proteins: Diversity from microsurgeons to cowboys. *Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms*, **2019**, 1862, 194398	6	2

86	Dysregulation of TDP-43 intracellular localization and early onset ALS are associated with a TARDBP S375G variant. *Brain Pathology*, **2019**, 29, 397-413	6	7
85	Solution conformation of a cohesin module and its scaffoldin linker from a prototypical cellulosome. *Archives of Biochemistry and Biophysics*, **2018**, 644, 1-7	4.1	2
84	Efficient and simplified nanomechanical analysis of intrinsically disordered proteins. *Nanoscale*, **2018**, 10, 16857-16867	7.7	5
83	The Singular NMR Fingerprint of a Polyproline II Helical Bundle. *Journal of the American Chemical Society*, **2018**, 140, 16988-17000	16.4	18
82	Insights into the mechanism of Apoptin's exquisitely selective anti-tumor action from atomic level characterization of its conformation and dynamics. *Archives of Biochemistry and Biophysics*, **2017**, 614, 53-64	4.1	3
81	A truncated apoptin protein variant selectively kills cancer cells. *Investigational New Drugs*, **2017**, 35, 260-268	4.3	6
80	Point mutations in the N-terminal domain of transactive response DNA-binding protein 43 kDa (TDP-43) compromise its stability, dimerization, and functions. *Journal of Biological Chemistry*, **2017**, 292, 11992-12006	5.4	43
79	Extensive deamidation of RNase A inhibits its oligomerization through 3D domain swapping. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2017**, 1865, 76-87	4	2
78	Intrinsically Disordered Domains, Amyloids and Protein Liquid Phases: Evolving Concepts and Open Questions. *Protein and Peptide Letters*, **2017**, 24, 281-293	1.9	6
77	Associating a negatively charged GdDOTA-derivative to the Pittsburgh compound B for targeting Aβ amyloid aggregates. *Journal of Biological Inorganic Chemistry*, **2016**, 21, 83-99	3.7	14
76	An Amyloid-Like Pathological Conformation of TDP-43 Is Stabilized by Hypercooperative Hydrogen Bonds. *Frontiers in Molecular Neuroscience*, **2016**, 9, 125	6.1	22
75	Molecular Basis of Orb2 Amyloidogenesis and Blockade of Memory Consolidation. *PLoS Biology*, **2016**, 14, e1002361	9.7	50
74	Electrostatic Repulsion Governs TDP-43 C-terminal Domain Aggregation. *PLoS Biology*, **2016**, 14, e1002447	9.7	23
73	The Y9P Variant of the Titin I27 Module: Structural Determinants of Its Revisited Nanomechanics. *Structure*, **2016**, 24, 606-616	5.2	7
72	The TDP-43 N-terminal domain structure at high resolution. *FEBS Journal*, **2016**, 283, 1242-60	5.7	82
71	Complex System Assembly Underlies a Two-Tiered Model of Highly Delocalized Electrons. *Journal of Physical Chemistry Letters*, **2016**, 7, 1859-64	6.4	10
70	Interaction of PiB-derivative metal complexes with beta-amyloid peptides: selective recognition of the aggregated forms. *Chemistry - A European Journal*, **2015**, 21, 5413-22	4.8	23
69	Structural Evidence of Amyloid Fibril Formation in the Putative Aggregation Domain of TDP-43. *Journal of Physical Chemistry Letters*, **2015**, 6, 2608-15	6.4	47

68	DMSO affects A□40 conformation and interactions with aggregation inhibitors as revealed by NMR. *RSC Advances*, **2015**, 5, 69761-69764	3.7	6
67	"Structural characterization of the minimal segment of TDP-43 competent for aggregation". *Archives of Biochemistry and Biophysics*, **2014**, 545, 53-62	4.1	54
66	NMR spectroscopy reveals a preferred conformation with a defined hydrophobic cluster for polyglutamine binding peptide 1. *Archives of Biochemistry and Biophysics*, **2014**, 558, 104-10	4.1	9
65	Combining Classical MD and QM calculations to elucidate complex system nucleation: a twisted, three-stranded, parallel □sheet seeds amyloid fibril conception. *Journal of Physical Chemistry B*, **2014**, 118, 7312-6	3.4	14
64	Gemini surfactants affect the structure, stability, and activity of ribonuclease Sa. *Journal of Physical Chemistry B*, **2014**, 118, 10633-42	3.4	8
63	Nanomechanics of Neurotoxic Proteins: Insights at the Start of the Neurodegeneration Cascade **2014**, 57-68		
62	(1)H, (13)C and (15)N resonance assignments of the Onconase FL-G zymogen. *Biomolecular NMR Assignments*, **2013**, 7, 13-5	0.7	1
61	Structure of a simplified □hairpin and its ATP complex. *Archives of Biochemistry and Biophysics*, **2013**, 537, 62-71	4.1	4
60	Structural and functional relationships of natural and artificial dimeric bovine ribonucleases: new scaffolds for potential antitumor drugs. *FEBS Letters*, **2013**, 587, 3601-8	3.8	21
59	Towards tricking a pathogen□ protease into fighting infection: the 3D structure of a stable circularly permuted onconase variant cleavedby HIV-1 protease. *PLoS ONE*, **2013**, 8, e54568	3.7	5
58	Interactions of gemini surfactants with two model proteins: NMR, CD, and fluorescence spectroscopies. *Journal of Colloid and Interface Science*, **2012**, 369, 245-55	9.3	29
57	Conformation specificity and arene binding in a peptide composed only of Lys, Ile, Ala and Gly. *European Biophysics Journal*, **2012**, 41, 63-72	1.9	4
56	An Arg-rich putative prebiotic protein is as stable as its Lys-rich variant. *Archives of Biochemistry and Biophysics*, **2012**, 528, 118-26	4.1	6
55	Thermal stability and enzymatic activity of RNase A in the presence of cationic gemini surfactants. *International Journal of Biological Macromolecules*, **2012**, 50, 1151-7	7.9	11
54	Salt anions promote the conversion of HypF-N into amyloid-like oligomers and modulate the structure of the oligomers and the monomeric precursor state. *Journal of Molecular Biology*, **2012**, 424, 132-49	6.5	22
53	Double domain swapping in bovine seminal RNase: formation of distinct N- and C-swapped tetramers and multimers with increasing biological activities. *PLoS ONE*, **2012**, 7, e46804	3.7	34
52	Common features at the start of the neurodegeneration cascade. *PLoS Biology*, **2012**, 10, e1001335	9.7	52
51	Interactions crucial for three-dimensional domain swapping in the HP-RNase variant PM8. *Biophysical Journal*, **2011**, 101, 459-67	2.9	3

50	Crowding agents and osmolytes provide insight into the formation and dissociation of RNase A oligomers. *Archives of Biochemistry and Biophysics*, **2011**, 506, 123-9	4.1	20
49	3D domain swapping provides a minor alternative refolding pathway for ribonuclease A. *Protein and Peptide Letters*, **2011**, 18, 467-70	1.9	1
48	Characterization of the structure and self-recognition of the human centrosomal protein NA14: implications for stability and function. *Protein Engineering, Design and Selection*, **2011**, 24, 883-92	1.9	4
47	NMR structural determinants of eosinophil cationic protein binding to membrane and heparin mimetics. *Biophysical Journal*, **2010**, 98, 2702-11	2.9	24
46	NMR spectroscopy reveals that RNase A is chiefly denatured in 40% acetic acid: implications for oligomer formation by 3D domain swapping. *Journal of the American Chemical Society*, **2010**, 132, 1621-30	16.4	56
45	Putative one-pot prebiotic polypeptides with ribonucleolytic activity. *Chemistry - A European Journal*, **2010**, 16, 5314-23	4.8	11
44	Structure of the C-terminal domain of transcription factor IIB from Trypanosoma brucei. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 13242-7	11.5	15
43	The (1)H, (13)C, (15)N resonance assignment, solution structure, and residue level stability of eosinophil cationic protein/RNase 3 determined by NMR spectroscopy. *Biopolymers*, **2009**, 91, 1018-28	2.2	13
42	Carbodiimide EDC induces cross-links that stabilize RNase A C-dimer against dissociation: EDC adducts can affect protein net charge, conformation, and activity. *Bioconjugate Chemistry*, **2009**, 20, 1459-73	6.3	27
41	Kinetic analysis provides insight into the mechanism of ribonuclease A oligomer formation. *Archives of Biochemistry and Biophysics*, **2009**, 489, 41-7	4.1	16
40	Preparation of ribonuclease S domain-swapped dimers conjugated with DNA and PNA: modulating the activity of ribonucleases. *Bioconjugate Chemistry*, **2008**, 19, 263-70	6.3	5
39	Destabilizing mutations alter the hydrogen exchange mechanism in ribonuclease A. *Biophysical Journal*, **2008**, 94, 2297-305	2.9	11
38	The solution structure and dynamics of human pancreatic ribonuclease determined by NMR spectroscopy provide insight into its remarkable biological activities and inhibition. *Journal of Molecular Biology*, **2008**, 379, 953-65	6.5	24
37	The structural determinants that lead to the formation of particular oligomeric structures in the pancreatic-type ribonuclease family. *Current Protein and Peptide Science*, **2008**, 9, 370-93	2.8	14
36	Cytotoxicity of polyspermine-ribonuclease A and polyspermine-dimeric ribonuclease A. *Bioconjugate Chemistry*, **2007**, 18, 1946-55	6.3	8
35	Temperature dependence of ligand-protein complex formation as reflected by saturation transfer difference NMR experiments. *Magnetic Resonance in Chemistry*, **2007**, 45, 745-8	2.1	25
34	Getting specificity from simplicity in putative proteins from the prebiotic earth. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 14941-6	11.5	15
33	Formation, structure, and dissociation of the ribonuclease S three-dimensional domain-swapped dimer. *Journal of Biological Chemistry*, **2006**, 281, 9400-6	5.4	22

32	Pressure-jump-induced kinetics reveals a hydration dependent folding/unfolding mechanism of ribonuclease A. *Biophysical Journal*, **2006**, 91, 2264-74	2.9	22
31	Dimerization and folding processes of Treponema denticola cystalysin: the role of pyridoxal 5Qphosphate. *Biochemistry*, **2006**, 45, 14140-54	3.2	20
30	Increase of RNase a N-terminus polarity or C-terminus apolarity changes the two domainsQ propensity to swap and form the two dimeric conformers of the protein. *Biochemistry*, **2006**, 45, 10795-806	3.2	21
29	pH-Dependent conformational stability of the ribotoxin alpha-sarcin and four active site charge substitution variants. *Biochemistry*, **2006**, 45, 13705-18	3.2	13
28	Holo- and apo-cystalysin from Treponema denticola: two different conformations. *Archives of Biochemistry and Biophysics*, **2006**, 455, 31-9	4.1	4
27	Three-dimensional domain-swapped oligomers of ribonuclease A: identification of a fifth tetramer, pentamers and hexamers, and detection of trace heptameric, octameric and nonameric species. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2006**, 1764, 44-54	4	34
26	Ribonuclease Sa conformational stability studied by NMR-monitored hydrogen exchange. *Biochemistry*, **2005**, 44, 7644-55	3.2	8
25	Charge substitution shows that repulsive electrostatic interactions impede the oligomerization of Alzheimer amyloid peptides. *FEBS Letters*, **2005**, 579, 3574-8	3.8	46
24	Folding pathway of the pyridoxal 5Qphosphate C-S lyase MalY from Escherichia coli. *Biochemical Journal*, **2005**, 389, 885-98	3.8	16
23	AlzheimerQ Abeta40 studied by NMR at low pH reveals that sodium 4,4-dimethyl-4-silapentane-1-sulfonate (DSS) binds and promotes beta-ball oligomerization. *Journal of Biological Chemistry*, **2005**, 280, 3675-85	5.4	30
22	Charge-charge interactions are key determinants of the pK values of ionizable groups in ribonuclease Sa (pI=3.5) and a basic variant (pI=10.2). *Journal of Molecular Biology*, **2003**, 325, 1077-92	6.5	90
21	Tautomeric state of alpha-sarcin histidines. Ndelta tautomers are a common feature in the active site of extracellular microbial ribonucleases. *FEBS Letters*, **2003**, 534, 197-201	3.8	8
20	Glycosylation and specific deamidation of ribonuclease B affect the formation of three-dimensional domain-swapped oligomers. *Journal of Biological Chemistry*, **2003**, 278, 46241-51	5.4	34
19	Solution structure and dynamics of ribonuclease Sa. *Proteins: Structure, Function and Bioinformatics*, **2001**, 44, 200-11	4.2	24
18	The cadherin cytoplasmic domain is unstructured in the absence of beta-catenin. A possible mechanism for regulating cadherin turnover. *Journal of Biological Chemistry*, **2001**, 276, 12301-9	5.4	199
17	Folding kinetics of phage 434 Cro protein. *Biochemistry*, **2000**, 39, 13963-73	3.2	26
16	Sequential assignment and solution secondary structure of doubly labelled ribonuclease Sa. *Journal of Biomolecular NMR*, **1999**, 14, 89-90	3	6
15	Thermodynamic analysis of the structural stability of phage 434 Cro protein. *Biochemistry*, **1999**, 38, 15536-47	3.2	19

14	A pulse-chase-competition experiment to determine if a folding intermediate is on or off-pathway: application to ribonuclease A. *Journal of Molecular Biology*, **1998**, 283, 669-78	6.5	33
13	Protein folding: matching theory and experiment. *Biophysical Journal*, **1998**, 75, 428-34	2.9	47
12	Characterization of the unfolding pathway of hen egg white lysozyme. *Biochemistry*, **1997**, 36, 1496-504	3.2	47
11	Different protein sequences can give rise to highly similar folds through different stabilizing interactions. *Protein Science*, **1994**, 3, 1938-44	6.3	31
10	Structural similarity of DNA-binding domains of bacteriophage repressors and the globin core. *Current Biology*, **1993**, 3, 141-8	6.3	160
9	Urea denaturation of barnase: pH dependence and characterization of the unfolded state. *Biochemistry*, **1992**, 31, 2728-34	3.2	129
8	pH dependence of the urea and guanidine hydrochloride denaturation of ribonuclease A and ribonuclease T1. *Biochemistry*, **1990**, 29, 2564-72	3.2	355
7	Purification of recombinant ribonuclease T1 expressed in Escherichia coli. *Journal of Proteomics*, **1990**, 20, 181-8		30
6	A new method for determining the heat capacity change for protein folding. *Biochemistry*, **1989**, 28, 2520-5	3.2	205
5	Divergent CPEB prion-like domains reveal different assembly mechanisms for a generic amyloid-like fold		3
4	Preferred Conformations in the Intrinsically Disordered Region of Human CPEB3 Explain its Role in Memory Consolidation		4
3	Molecular Determinants of Liquid Demixing and Amyloidogenesis in Human CPEB3		5
2	Tau amyloidogenesis begins with a loss of its conformational polymorphism		1
1	Towards Targeting the Disordered SARS-CoV-2 Nsp2 C-terminal Region: Partial Structure and Dampened Mobility Revealed by NMR Spectroscopy		2