

# Douglas V Laurents

## List of Publications by Citations

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103  
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49  
g-index

117  
ext. papers

3,022  
ext. citations

4.7  
avg, IF

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L-index

#	Paper	IF	Citations
103	pH dependence of the urea and guanidine hydrochloride denaturation of ribonuclease A and ribonuclease T1. <i>Biochemistry</i> , <b>1990</b> , 29, 2564-72	3.2	355
102	A new method for determining the heat capacity change for protein folding. <i>Biochemistry</i> , <b>1989</b> , 28, 2520-5	3.5	205
101	The cadherin cytoplasmic domain is unstructured in the absence of beta-catenin. A possible mechanism for regulating cadherin turnover. <i>Journal of Biological Chemistry</i> , <b>2001</b> , 276, 12301-9	5.4	199
100	Structural similarity of DNA-binding domains of bacteriophage repressors and the globin core. <i>Current Biology</i> , <b>1993</b> , 3, 141-8	6.3	160
99	Urea denaturation of barnase: pH dependence and characterization of the unfolded state. <i>Biochemistry</i> , <b>1992</b> , 31, 2728-34	3.2	129
98	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). <i>Journal of Molecular Biology</i> , <b>2003</b> , 325, 1077-92	6.5	90
97	The TDP-43 N-terminal domain structure at high resolution. <i>FEBS Journal</i> , <b>2016</b> , 283, 1242-60	5.7	82
96	NMR spectroscopy reveals that RNase A is chiefly denatured in 40% acetic acid: implications for oligomer formation by 3D domain swapping. <i>Journal of the American Chemical Society</i> , <b>2010</b> , 132, 1621-30	16.4	56
95	"Structural characterization of the minimal segment of TDP-43 competent for aggregation". <i>Archives of Biochemistry and Biophysics</i> , <b>2014</b> , 545, 53-62	4.1	54
94	Common features at the start of the neurodegeneration cascade. <i>PLoS Biology</i> , <b>2012</b> , 10, e1001335	9.7	52
93	Molecular Basis of Orb2 Amyloidogenesis and Blockade of Memory Consolidation. <i>PLoS Biology</i> , <b>2016</b> , 14, e1002361	9.7	50
92	Structural Evidence of Amyloid Fibril Formation in the Putative Aggregation Domain of TDP-43. <i>Journal of Physical Chemistry Letters</i> , <b>2015</b> , 6, 2608-15	6.4	47
91	Characterization of the unfolding pathway of hen egg white lysozyme. <i>Biochemistry</i> , <b>1997</b> , 36, 1496-504	3.2	47
90	Protein folding: matching theory and experiment. <i>Biophysical Journal</i> , <b>1998</b> , 75, 428-34	2.9	47
89	Charge substitution shows that repulsive electrostatic interactions impede the oligomerization of Alzheimer amyloid peptides. <i>FEBS Letters</i> , <b>2005</b> , 579, 3574-8	3.8	46
88	Point mutations in the N-terminal domain of transactive response DNA-binding protein 43 kDa (TDP-43) compromise its stability, dimerization, and functions. <i>Journal of Biological Chemistry</i> , <b>2017</b> , 292, 11992-12006	5.4	43
87	Double domain swapping in bovine seminal RNase: formation of distinct N- and C-swapped tetramers and multimers with increasing biological activities. <i>PLoS ONE</i> , <b>2012</b> , 7, e46804	3.7	34

86	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. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , <b>2006</b> , 1764, 44-54	4	34
85	Glycosylation and specific deamidation of ribonuclease B affect the formation of three-dimensional domain-swapped oligomers. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 46241-51	5.4	34
84	A pulse-chase-competition experiment to determine if a folding intermediate is on or off-pathway: application to ribonuclease A. <i>Journal of Molecular Biology</i> , <b>1998</b> , 283, 669-78	6.5	33
83	Different protein sequences can give rise to highly similar folds through different stabilizing interactions. <i>Protein Science</i> , <b>1994</b> , 3, 1938-44	6.3	31
82	Alzheimer's Aβ40 studied by NMR at low pH reveals that sodium 4,4-dimethyl-4-silapentane-1-sulfonate (DSS) binds and promotes beta-sheet oligomerization. <i>Journal of Biological Chemistry</i> , <b>2005</b> , 280, 3675-85	5.4	30
81	Purification of recombinant ribonuclease T1 expressed in Escherichia coli. <i>Journal of Proteomics</i> , <b>1990</b> , 20, 181-8		30
80	Interactions of gemini surfactants with two model proteins: NMR, CD, and fluorescence spectroscopies. <i>Journal of Colloid and Interface Science</i> , <b>2012</b> , 369, 245-55	9.3	29
79	Carbodiimide EDC induces cross-links that stabilize RNase A C-dimer against dissociation: EDC adducts can affect protein net charge, conformation, and activity. <i>Bioconjugate Chemistry</i> , <b>2009</b> , 20, 1459-73	6.3	27
78	Folding kinetics of phage 434 Cro protein. <i>Biochemistry</i> , <b>2000</b> , 39, 13963-73	3.2	26
77	Temperature dependence of ligand-protein complex formation as reflected by saturation transfer difference NMR experiments. <i>Magnetic Resonance in Chemistry</i> , <b>2007</b> , 45, 745-8	2.1	25
76	NMR structural determinants of eosinophil cationic protein binding to membrane and heparin mimetics. <i>Biophysical Journal</i> , <b>2010</b> , 98, 2702-11	2.9	24
75	The solution structure and dynamics of human pancreatic ribonuclease determined by NMR spectroscopy provide insight into its remarkable biological activities and inhibition. <i>Journal of Molecular Biology</i> , <b>2008</b> , 379, 953-65	6.5	24
74	Solution structure and dynamics of ribonuclease Sa. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2001</b> , 44, 200-11	4.2	24
73	Interaction of PiB-derivative metal complexes with beta-amyloid peptides: selective recognition of the aggregated forms. <i>Chemistry - A European Journal</i> , <b>2015</b> , 21, 5413-22	4.8	23
72	Electrostatic Repulsion Governs TDP-43 C-terminal Domain Aggregation. <i>PLoS Biology</i> , <b>2016</b> , 14, e1002447	4.7	23
71	Salt anions promote the conversion of HypF-N into amyloid-like oligomers and modulate the structure of the oligomers and the monomeric precursor state. <i>Journal of Molecular Biology</i> , <b>2012</b> , 424, 132-49	6.5	22
70	Formation, structure, and dissociation of the ribonuclease S three-dimensional domain-swapped dimer. <i>Journal of Biological Chemistry</i> , <b>2006</b> , 281, 9400-6	5.4	22
69	Pressure-jump-induced kinetics reveals a hydration dependent folding/unfolding mechanism of ribonuclease A. <i>Biophysical Journal</i> , <b>2006</b> , 91, 2264-74	2.9	22

68	An Amyloid-Like Pathological Conformation of TDP-43 Is Stabilized by Hypercooperative Hydrogen Bonds. <i>Frontiers in Molecular Neuroscience</i> , <b>2016</b> , 9, 125	6.1	22
67	Structural and functional relationships of natural and artificial dimeric bovine ribonucleases: new scaffolds for potential antitumor drugs. <i>FEBS Letters</i> , <b>2013</b> , 587, 3601-8	3.8	21
66	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. <i>Biochemistry</i> , <b>2006</b> , 45, 10795-806	3.2	21
65	Crowding agents and osmolytes provide insight into the formation and dissociation of RNase A oligomers. <i>Archives of Biochemistry and Biophysics</i> , <b>2011</b> , 506, 123-9	4.1	20
64	Dimerization and folding processes of <i>Treponema denticola</i> cystalysin: the role of pyridoxal 5Qphosphate. <i>Biochemistry</i> , <b>2006</b> , 45, 14140-54	3.2	20
63	Thermodynamic analysis of the structural stability of phage 434 Cro protein. <i>Biochemistry</i> , <b>1999</b> , 38, 15536-47	3.6	19
62	The Singular NMR Fingerprint of a Polyproline II Helical Bundle. <i>Journal of the American Chemical Society</i> , <b>2018</b> , 140, 16988-17000	16.4	18
61	Kinetic analysis provides insight into the mechanism of ribonuclease A oligomer formation. <i>Archives of Biochemistry and Biophysics</i> , <b>2009</b> , 489, 41-7	4.1	16
60	Folding pathway of the pyridoxal 5Qphosphate C-S lyase MalY from <i>Escherichia coli</i> . <i>Biochemical Journal</i> , <b>2005</b> , 389, 885-98	3.8	16
59	Structure of the C-terminal domain of transcription factor IIB from <i>Trypanosoma brucei</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 13242-7	11.5	15
58	Getting specificity from simplicity in putative proteins from the prebiotic earth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 14941-6	11.5	15
57	Associating a negatively charged GdDOTA-derivative to the Pittsburgh compound B for targeting A $\beta$ amyloid aggregates. <i>Journal of Biological Inorganic Chemistry</i> , <b>2016</b> , 21, 83-99	3.7	14
56	Combining Classical MD and QM calculations to elucidate complex system nucleation: a twisted, three-stranded, parallel $\beta$ sheet seeds amyloid fibril conception. <i>Journal of Physical Chemistry B</i> , <b>2014</b> , 118, 7312-6	3.4	14
55	The structural determinants that lead to the formation of particular oligomeric structures in the pancreatic-type ribonuclease family. <i>Current Protein and Peptide Science</i> , <b>2008</b> , 9, 370-93	2.8	14
54	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. <i>Biopolymers</i> , <b>2009</b> , 91, 1018-28	2.2	13
53	pH-Dependent conformational stability of the ribotoxin alpha-sarcin and four active site charge substitution variants. <i>Biochemistry</i> , <b>2006</b> , 45, 13705-18	3.2	13
52	Large-Scale Recombinant Production of the SARS-CoV-2 Proteome for High-Throughput and Structural Biology Applications. <i>Frontiers in Molecular Biosciences</i> , <b>2021</b> , 8, 653148	5.6	12
51	Thermal stability and enzymatic activity of RNase A in the presence of cationic gemini surfactants. <i>International Journal of Biological Macromolecules</i> , <b>2012</b> , 50, 1151-7	7.9	11

50	Putative one-pot prebiotic polypeptides with ribonucleolytic activity. <i>Chemistry - A European Journal</i> , <b>2010</b> , 16, 5314-23	4.8	11
49	Destabilizing mutations alter the hydrogen exchange mechanism in ribonuclease A. <i>Biophysical Journal</i> , <b>2008</b> , 94, 2297-305	2.9	11
48	Complex System Assembly Underlies a Two-Tiered Model of Highly Delocalized Electrons. <i>Journal of Physical Chemistry Letters</i> , <b>2016</b> , 7, 1859-64	6.4	10
47	NMR spectroscopy reveals a preferred conformation with a defined hydrophobic cluster for polyglutamine binding peptide 1. <i>Archives of Biochemistry and Biophysics</i> , <b>2014</b> , 558, 104-10	4.1	9
46	Nucleotide-induced folding of cell division protein FtsZ from <i>Staphylococcus aureus</i> . <i>FEBS Journal</i> , <b>2020</b> , 287, 4048-4067	5.7	9
45	Gemini surfactants affect the structure, stability, and activity of ribonuclease Sa. <i>Journal of Physical Chemistry B</i> , <b>2014</b> , 118, 10633-42	3.4	8
44	Cytotoxicity of polyspermine-ribonuclease A and polyspermine-dimeric ribonuclease A. <i>Bioconjugate Chemistry</i> , <b>2007</b> , 18, 1946-55	6.3	8
43	Ribonuclease Sa conformational stability studied by NMR-monitored hydrogen exchange. <i>Biochemistry</i> , <b>2005</b> , 44, 7644-55	3.2	8
42	Tautomeric state of alpha-sarcin histidines. Ndelta tautomers are a common feature in the active site of extracellular microbial ribonucleases. <i>FEBS Letters</i> , <b>2003</b> , 534, 197-201	3.8	8
41	The Y9P Variant of the Titin I27 Module: Structural Determinants of Its Revisited Nanomechanics. <i>Structure</i> , <b>2016</b> , 24, 606-616	5.2	7
40	Dysregulation of TDP-43 intracellular localization and early onset ALS are associated with a TARDBP S375G variant. <i>Brain Pathology</i> , <b>2019</b> , 29, 397-413	6	7
39	A truncated apoptin protein variant selectively kills cancer cells. <i>Investigational New Drugs</i> , <b>2017</b> , 35, 260-268	4.3	6
38	Molecular mechanism of the inhibition of TDP-43 amyloidogenesis by QBP1. <i>Archives of Biochemistry and Biophysics</i> , <b>2019</b> , 675, 108113	4.1	6
37	A new glucose biosensor based on Nickel/KH550 nanocomposite deposited on the GCE: An electrochemical study. <i>Journal of Electroanalytical Chemistry</i> , <b>2019</b> , 839, 9-15	4.1	6
36	DMSO affects A $\beta$ 40 conformation and interactions with aggregation inhibitors as revealed by NMR. <i>RSC Advances</i> , <b>2015</b> , 5, 69761-69764	3.7	6
35	An Arg-rich putative prebiotic protein is as stable as its Lys-rich variant. <i>Archives of Biochemistry and Biophysics</i> , <b>2012</b> , 528, 118-26	4.1	6
34	Sequential assignment and solution secondary structure of doubly labelled ribonuclease Sa. <i>Journal of Biomolecular NMR</i> , <b>1999</b> , 14, 89-90	3	6
33	Intrinsically Disordered Domains, Amyloids and Protein Liquid Phases: Evolving Concepts and Open Questions. <i>Protein and Peptide Letters</i> , <b>2017</b> , 24, 281-293	1.9	6

32	Divergent CPEB prion-like domains reveal different assembly mechanisms for a generic amyloid-like fold. <i>BMC Biology</i> , <b>2021</b> , 19, 43	7.3	6
31	Efficient and simplified nanomechanical analysis of intrinsically disordered proteins. <i>Nanoscale</i> , <b>2018</b> , 10, 16857-16867	7.7	5
30	Towards tricking a pathogen@protease into fighting infection: the 3D structure of a stable circularly permuted onconase variant cleavedby HIV-1 protease. <i>PLoS ONE</i> , <b>2013</b> , 8, e54568	3.7	5
29	Preparation of ribonuclease S domain-swapped dimers conjugated with DNA and PNA: modulating the activity of ribonucleases. <i>Bioconjugate Chemistry</i> , <b>2008</b> , 19, 263-70	6.3	5
28	Molecular Determinants of Liquid Demixing and Amyloidogenesis in Human CPEB3		5
27	Conformational Priming of RepA-WH1 for Functional Amyloid Conversion Detected by NMR Spectroscopy. <i>Structure</i> , <b>2020</b> , 28, 336-347.e4	5.2	4
26	Conformation specificity and arene binding in a peptide composed only of Lys, Ile, Ala and Gly. <i>European Biophysics Journal</i> , <b>2012</b> , 41, 63-72	1.9	4
25	Structure of a simplified Hairpin and its ATP complex. <i>Archives of Biochemistry and Biophysics</i> , <b>2013</b> , 537, 62-71	4.1	4
24	Characterization of the structure and self-recognition of the human centrosomal protein NA14: implications for stability and function. <i>Protein Engineering, Design and Selection</i> , <b>2011</b> , 24, 883-92	1.9	4
23	Holo- and apo-cystalsin from <i>Treponema denticola</i> : two different conformations. <i>Archives of Biochemistry and Biophysics</i> , <b>2006</b> , 455, 31-9	4.1	4
22	Preferred Conformations in the Intrinsically Disordered Region of Human CPEB3 Explain its Role in Memory Consolidation		4
21	Phe-Gly motifs drive fibrillization of TDP-43@prion-like domain condensates. <i>PLoS Biology</i> , <b>2021</b> , 19, e3001198	9.7	4
20	Insights into the mechanism of Apoptin@exquisitely selective anti-tumor action from atomic level characterization of its conformation and dynamics. <i>Archives of Biochemistry and Biophysics</i> , <b>2017</b> , 614, 53-64	4.1	3
19	Interactions crucial for three-dimensional domain swapping in the HP-RNase variant PM8. <i>Biophysical Journal</i> , <b>2011</b> , 101, 459-67	2.9	3
18	Divergent CPEB prion-like domains reveal different assembly mechanisms for a generic amyloid-like fold		3
17	NMR assignments for the C-terminal domain of human TDP-43. <i>Biomolecular NMR Assignments</i> , <b>2021</b> , 15, 177-181	0.7	3
16	Extensive deamidation of RNase A inhibits its oligomerization through 3D domain swapping. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , <b>2017</b> , 1865, 76-87	4	2
15	Solution conformation of a cohesin module and its scaffoldin linker from a prototypical cellulosome. <i>Archives of Biochemistry and Biophysics</i> , <b>2018</b> , 644, 1-7	4.1	2

14	RNA binding proteins: Diversity from microsurgions to cowboys. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , <b>2019</b> , 1862, 194398	6	2
13	Structural transitions in Orb2 prion-like domain relevant for functional aggregation in memory consolidation. <i>Journal of Biological Chemistry</i> , <b>2020</b> , 295, 18122-18133	5.4	2
12	Towards Targeting the Disordered SARS-CoV-2 Nsp2 C-terminal Region: Partial Structure and Dampened Mobility Revealed by NMR Spectroscopy		2
11	Probing structural changes during amyloid aggregation of the sweet protein MNEI. <i>FEBS Journal</i> , <b>2020</b> , 287, 2808-2822	5.7	2
10	Do polyproline II helix associations modulate biomolecular condensates?. <i>FEBS Open Bio</i> , <b>2021</b> , 11, 2390-2399	2	
9	(1)H, (13)C and (15)N resonance assignments of the Onconase FL-G zymogen. <i>Biomolecular NMR Assignments</i> , <b>2013</b> , 7, 13-5	0.7	1
8	3D domain swapping provides a minor alternative refolding pathway for ribonuclease A. <i>Protein and Peptide Letters</i> , <b>2011</b> , 18, 467-70	1.9	1
7	Partial structure, dampened mobility, and modest impact of a His tag in the SARS-CoV-2 Nsp2 C-terminal region. <i>European Biophysics Journal</i> , <b>2021</b> , 50, 1129-1137	1.9	1
6	Tau amyloidogenesis begins with a loss of its conformational polymorphism		1
5	Cohesin-dockerin code in cellulosomal dual binding modes and its allosteric regulation by proline isomerization. <i>Structure</i> , <b>2021</b> , 29, 587-597.e8	5.2	1
4	Glycine rich segments adopt polyproline II helices: Implications for biomolecular condensate formation. <i>Archives of Biochemistry and Biophysics</i> , <b>2021</b> , 704, 108867	4.1	1
3	Aromatic and aliphatic residues of the disordered region of TDP-43 are on a fast track for self-assembly. <i>Biochemical and Biophysical Research Communications</i> , <b>2021</b> , 578, 110-114	3.4	1
2	Disorder and partial folding in the regulatory subunit hinge region of Trypanosoma brucei protein kinase A: The C-linker portion inhibits the parasite's protein kinase A. <i>Archives of Biochemistry and Biophysics</i> , <b>2021</b> , 698, 108731	4.1	0
1	Nanomechanics of Neurotoxic Proteins: Insights at the Start of the Neurodegeneration Cascade <b>2014</b> , 57-68		