

# David Rodriguez-Larrea

## List of Publications by Year in descending order

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29  
papers

1,562  
citations

471509

17  
h-index

501196

28  
g-index

30  
all docs

30  
docs citations

30  
times ranked

2006  
citing authors

#	ARTICLE	IF	CITATIONS
1	Use of pore-forming toxins to study co-translocational protein folding. <i>Methods in Enzymology</i> , 2021, 649, 635-649.	1.0	0
2	Single-aminoacid discrimination in proteins with homogeneous nanopore sensors and neural networks. <i>Biosensors and Bioelectronics</i> , 2021, 180, 113108.	10.1	14
3	The emerging landscape of single-molecule protein sequencing technologies. <i>Nature Methods</i> , 2021, 18, 604-617.	19.0	198
4	Oligonucleotide-Directed Protein Threading Through a Rigid Nanopore. <i>Methods in Molecular Biology</i> , 2021, 2186, 135-144.	0.9	1
5	Transmembrane protein rotaxanes reveal kinetic traps in the refolding of translocated substrates. <i>Communications Biology</i> , 2020, 3, 159.	4.4	12
6	Free-energy landscapes of membrane co-translocational protein unfolding. <i>Communications Biology</i> , 2020, 3, 160.	4.4	13
7	DNA-binding miniproteins based on zinc fingers. Assessment of the interaction using nanopores. <i>Chemical Science</i> , 2018, 9, 4118-4123.	7.4	10
8	Label-Free, Multiplexed, Single-Molecule Analysis of Protein-DNA Complexes with Nanopores. <i>ACS Nano</i> , 2017, 11, 5815-5825.	14.6	37
9	Protein co-translocational unfolding depends on the direction of pulling. <i>Nature Communications</i> , 2014, 5, 4841.	12.8	62
10	Single-molecule site-specific detection of protein phosphorylation with a nanopore. <i>Nature Biotechnology</i> , 2014, 32, 179-181.	17.5	229
11	Multistep protein unfolding during nanopore translocation. <i>Nature Nanotechnology</i> , 2013, 8, 288-295.	31.5	275
12	Intrinsically Disordered Protein Threads Through the Bacterial Outer-Membrane Porin OmpF. <i>Science</i> , 2013, 340, 1570-1574.	12.6	109
13	The Peripheral Binding of 14-3-3 $\beta$ to Membranes Involves Isoform-Specific Histidine Residues. <i>PLoS ONE</i> , 2012, 7, e49671.	2.5	15
14	Role of conservative mutations in protein multi-property adaptation. <i>Biochemical Journal</i> , 2010, 429, 243-249.	3.7	20
15	Using multi-objective computational design to extend protein promiscuity. <i>Biophysical Chemistry</i> , 2010, 147, 13-19.	2.8	16
16	Protein-protein interactions at an enzyme-substrate interface: Characterization of transient reaction intermediates throughout a full catalytic cycle of <i>Escherichia coli</i> thioredoxin reductase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 36-51.	2.6	17
17	Proteolytic Scanning Calorimetry: A Novel Methodology that Probes the Fundamental Features of Protein Kinetic Stability. <i>Biophysical Journal</i> , 2010, 98, L12-L14.	0.5	21
18	Modulation of Buried Ionizable Groups in Proteins with Engineered Surface Charge. <i>Journal of the American Chemical Society</i> , 2010, 132, 1218-1219.	13.7	31

#	ARTICLE	IF	CITATIONS
19	Three-way Interaction between 14-3-3 Proteins, the N-terminal Region of Tyrosine Hydroxylase, and Negatively Charged Membranes. <i>Journal of Biological Chemistry</i> , 2009, 284, 32758-32769.	3.4	40
20	Diversity of chemical mechanisms in thioredoxin catalysis revealed by single-molecule force spectroscopy. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 890-896.	8.2	91
21	Between-Species Variation in the Kinetic Stability of TIM Proteins Linked to Solvation-Barrier Free Energies. <i>Journal of Molecular Biology</i> , 2009, 385, 924-937.	4.2	44
22	Super-proteins From Fitness-threshold Selection Statistics. <i>Biophysical Journal</i> , 2009, 96, 591a.	0.5	0
23	Beyond Lumry&Eyring: An unexpected pattern of operational reversibility/irreversibility in protein denaturation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 19-24.	2.6	12
24	Engineering proteins with tunable thermodynamic and kinetic stabilities. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 165-174.	2.6	39
25	Structural Basis of Human Triosephosphate Isomerase Deficiency. <i>Journal of Biological Chemistry</i> , 2008, 283, 23254-23263.	3.4	68
26	Force-Clamp Spectroscopy Detects Residue Co-evolution in Enzyme Catalysis. <i>Journal of Biological Chemistry</i> , 2008, 283, 27121-27129.	3.4	16
27	Energetic and Structural Consequences of Desolvation/Solvation Barriers to Protein Folding/Unfolding Assessed from Experimental Unfolding Rates. <i>Biophysical Journal</i> , 2006, 91, L48-L50.	0.5	19
28	Role of Solvation Barriers in Protein Kinetic Stability. <i>Journal of Molecular Biology</i> , 2006, 360, 715-724.	4.2	86
29	Natural Selection for Kinetic Stability Is a Likely Origin of Correlations between Mutational Effects on Protein Energetics and Frequencies of Amino Acid Occurrences in Sequence Alignments. <i>Journal of Molecular Biology</i> , 2006, 362, 966-978.	4.2	65