

# Valeria A Risso

## List of Publications by Year in descending order

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36  
papers

1,246  
citations

471509

17  
h-index

395702

33  
g-index

44  
all docs

44  
docs citations

44  
times ranked

1340  
citing authors

#	ARTICLE	IF	CITATIONS
1	Hyperstability and Substrate Promiscuity in Laboratory Resurrections of Precambrian $\beta$ -Lactamases. <i>Journal of the American Chemical Society</i> , 2013, 135, 2899-2902.	13.7	212
2	Conformational dynamics and enzyme evolution. <i>Journal of the Royal Society Interface</i> , 2018, 15, 20180330.	3.4	140
3	Evolution of Conformational Dynamics Determines the Conversion of a Promiscuous Generalist into a Specialist Enzyme. <i>Molecular Biology and Evolution</i> , 2015, 32, 132-143.	8.9	125
4	Cooperativity and flexibility in enzyme evolution. <i>Current Opinion in Structural Biology</i> , 2018, 48, 83-92.	5.7	81
5	Mutational Studies on Resurrected Ancestral Proteins Reveal Conservation of Site-Specific Amino Acid Preferences throughout Evolutionary History. <i>Molecular Biology and Evolution</i> , 2015, 32, 440-455.	8.9	71
6	De novo active sites for resurrected Precambrian enzymes. <i>Nature Communications</i> , 2017, 8, 16113.	12.8	60
7	Biotechnological and protein-engineering implications of ancestral protein resurrection. <i>Current Opinion in Structural Biology</i> , 2018, 51, 106-115.	5.7	60
8	Phenotypic comparisons of consensus variants versus laboratory resurrections of Precambrian proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 887-896.	2.6	56
9	Hinge-shift mechanism as a protein design principle for the evolution of $\beta$ -lactamases from substrate promiscuity to specificity. <i>Nature Communications</i> , 2021, 12, 1852.	12.8	43
10	Manipulating Conformational Dynamics To Repurpose Ancient Proteins for Modern Catalytic Functions. <i>ACS Catalysis</i> , 2020, 10, 4863-4870.	11.2	42
11	Thermostable and promiscuous Precambrian proteins. <i>Environmental Microbiology</i> , 2014, 16, 1485-1489.	3.8	33
12	Radiation synthesis of seroalbumin nanoparticles. <i>Radiation Physics and Chemistry</i> , 2012, 81, 1417-1421.	2.8	29
13	Engineering ancestral protein hyperstability. <i>Biochemical Journal</i> , 2016, 473, 3611-3620.	3.7	29
14	Effects of Serine-to-Cysteine Mutations on $\beta$ -Lactamase Folding. <i>Biophysical Journal</i> , 2007, 93, 1707-1718.	0.5	26
15	Enhancing a <i>de novo</i> enzyme activity by computationally-focused ultra-low-throughput screening. <i>Chemical Science</i> , 2020, 11, 6134-6148.	7.4	24
16	Mapping the Distribution of Conformational Information Throughout a Protein Sequence. <i>Journal of Molecular Biology</i> , 2006, 358, 280-288.	4.2	23
17	Consensus Design of an Evolved High-Redox Potential Laccase. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 354.	4.1	22
18	Directed <i>in vitro</i> evolution of Precambrian and extant Rubiscos. <i>Scientific Reports</i> , 2018, 8, 5532.	3.3	20

#	ARTICLE	IF	CITATIONS
19	Heme-binding enables allosteric modulation in an ancient TIM-barrel glycosidase. <i>Nature Communications</i> , 2021, 12, 380.	12.8	20
20	Folding of an Abridged $\beta$ -Lactamase. <i>Biochemistry</i> , 2004, 43, 1715-1723.	2.5	17
21	Non-conservation of folding rates in the thioredoxin family reveals degradation of ancestral unassisted-folding. <i>Biochemical Journal</i> , 2019, 476, 3631-3647.	3.7	16
22	Selection for Protein Kinetic Stability Connects Denaturation Temperatures to Organismal Temperatures and Provides Clues to Archaeal Life. <i>PLoS ONE</i> , 2016, 11, e0156657.	2.5	16
23	Ancestral Resurrection and Directed Evolution of Fungal Mesozoic Laccases. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	14
24	Resurrected Ancestral Proteins as Scaffolds for Protein Engineering. , 2017, , 229-255.		8
25	Expression and physicochemical characterization of an extracellular segment of the receptor protein tyrosine phosphatase IA-2. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006, 1764, 174-181.	2.3	7
26	Biophysical Characterization of the Membrane-proximal Ectodomain of the Receptor-type Protein-tyrosine Phosphatase Phogrin. <i>Protein and Peptide Letters</i> , 2013, 20, 1009-1017.	0.9	7
27	Re-engineering a $\beta$ -lactamase using prototype peptides from a library of local structural motifs. <i>Protein Science</i> , 2009, 18, 440-449.	7.6	6
28	Protein-Protein Interactions in Crystals of the Human Receptor-Type Protein Tyrosine Phosphatase ICA512 Ectodomain. <i>PLoS ONE</i> , 2011, 6, e24191.	2.5	6
29	X-ray evidence of a native state with increased compactness populated by tryptophan-less <i>B. licheniformis</i> $\beta$ -lactamase. <i>Protein Science</i> , 2012, 21, 964-976.	7.6	6
30	Optical studies of single-tryptophan <i>B. licheniformis</i> $\beta$ -lactamase variants. <i>Biophysical Chemistry</i> , 2010, 151, 111-118.	2.8	5
31	Preparation and biophysical characterization of recombinant <i>Pseudomonas aeruginosa</i> phosphorylcholine phosphatase. <i>Protein Expression and Purification</i> , 2010, 71, 153-159.	1.3	5
32	Combining Ancestral Reconstruction with Folding-Landscape Simulations to Engineer Heterologous Protein Expression. <i>Journal of Molecular Biology</i> , 2021, 433, 167321.	4.2	5
33	Evidence for a role of phenotypic mutations in virus adaptation. <i>IScience</i> , 2021, 24, 102257.	4.1	2
34	Equilibrium partially folded states of <i>B. licheniformis</i> $\beta$ -lactamase. <i>European Biophysics Journal</i> , 2019, 48, 341-348.	2.2	1
35	A protocol to study bacteriophage adaptation to new hosts. <i>STAR Protocols</i> , 2021, 2, 100784.	1.2	1
36	Mechanistic Insights of $\beta$ -Lactamases Evolution. <i>Biophysical Journal</i> , 2014, 106, 663a.	0.5	0