

Roberto A Chica

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.

38
papers

1,184
citations

18
h-index

34
g-index

43
ext. papers

1,368
ext. citations

8.4
avg, IF

4.5
L-index

#	Paper	IF	Citations
38	Generation of bright monomeric red fluorescent proteins computational design of enhanced chromophore packing.. <i>Chemical Science</i> , 2022 , 13, 1408-1418	9.4	1
37	Personalized oncology and BRAF melanoma: model development, drug discovery, and clinical correlation. <i>Journal of Cancer Research and Clinical Oncology</i> , 2021 , 147, 1365-1378	4.9	0
36	Genetically Encoded Fluorescent Biosensor for Rapid Detection of Protein Expression. <i>ACS Synthetic Biology</i> , 2020 , 9, 2955-2963	5.7	2
35	Ensemble-based enzyme design can recapitulate the effects of laboratory directed evolution in silico. <i>Nature Communications</i> , 2020 , 11, 4808	17.4	27
34	Computational Design of Multisubstrate Enzyme Specificity. <i>ACS Catalysis</i> , 2019 , 9, 5480-5485	13.1	18
33	One-Pot Biocatalytic Synthesis of Substituted d-Tryptophans from Indoles Enabled by an Engineered Aminotransferase. <i>ACS Catalysis</i> , 2019 , 9, 3482-3486	13.1	27
32	Biocatalytic retrosynthesis approaches to D-(2,4,5-trifluorophenyl)alanine, key precursor of the antidiabetic sitagliptin. <i>Green Chemistry</i> , 2019 , 21, 4368-4379	10	10
31	Designer sense-response systems. <i>Science</i> , 2019 , 366, 952-953	33.3	
30	Origin of conformational dynamics in a globular protein. <i>Communications Biology</i> , 2019 , 2, 433	6.7	6
29	ProtaBank: A repository for protein design and engineering data. <i>Protein Science</i> , 2018 , 27, 1113-1124	6.3	22
28	Chapter 4:Computational Enzyme Design: Successes, Challenges, and Future Directions. <i>RSC Catalysis Series</i> , 2018 , 88-116	0.3	4
27	Engineered Aminotransferase for the Production of d-Phenylalanine Derivatives Using Biocatalytic Cascades. <i>ChemCatChem</i> , 2018 , 10, 470-474	5.2	17
26	Structural Determinants of the Stereoinverting Activity of <i>Pseudomonas stutzeri</i> d-Phenylglycine Aminotransferase. <i>Biochemistry</i> , 2018 , 57, 5437-5446	3.2	4
25	Structure-guided rational design of red fluorescent proteins: towards designer genetically-encoded fluorophores. <i>Current Opinion in Structural Biology</i> , 2017 , 45, 91-99	8.1	17
24	Multistate Computational Protein Design with Backbone Ensembles. <i>Methods in Molecular Biology</i> , 2017 , 1529, 161-179	1.4	14
23	Rational design of proteins that exchange on functional timescales. <i>Nature Chemical Biology</i> , 2017 , 13, 1280-1285	11.7	54
22	Brighter Red Fluorescent Proteins by Rational Design of Triple-Decker Motif. <i>ACS Chemical Biology</i> , 2016 , 11, 508-17	4.9	18

21	Specificity of transglutaminase-catalyzed peptide synthesis. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2016 , 123, 53-61		2
20	Turning a Negative into a Positive: Conversion of a Homodimer into a Heterodimer Using Negative State Repertoires. <i>Structure</i> , 2016 , 24, 496-497	5.2	1
19	Prediction of Stable Globular Proteins Using Negative Design with Non-native Backbone Ensembles. <i>Structure</i> , 2015 , 23, 2011-21	5.2	19
18	Optimization of rotamers prior to template minimization improves stability predictions made by computational protein design. <i>Protein Science</i> , 2015 , 24, 545-60	6.3	7
17	Discovery of substrates for a SET domain lysine methyltransferase predicted by multistate computational protein design. <i>Structure</i> , 2015 , 23, 206-215	5.2	28
16	Protein engineering in the 21st century. <i>Protein Science</i> , 2015 , 24, 431-3	6.3	7
15	Improving the accuracy of protein stability predictions with multistate design using a variety of backbone ensembles. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014 , 82, 771-84	4.2	36
14	Continuous colorimetric screening assay for detection of d-amino acid aminotransferase mutants displaying altered substrate specificity. <i>Analytical Biochemistry</i> , 2014 , 463, 23-30	3.1	12
13	A high-throughput assay for screening L- or D-amino acid specific aminotransferase mutant libraries. <i>Analytical Biochemistry</i> , 2013 , 441, 190-8	3.1	11
12	Bioanalysis for biocatalysis: multiplexed capillary electrophoresis-mass spectrometry assay for aminotransferase substrate discovery and specificity profiling. <i>Journal of the American Chemical Society</i> , 2013 , 135, 13728-36	16.4	13
11	Iterative approach to computational enzyme design. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 3790-5	11.5	245
10	Multistate approaches in computational protein design. <i>Protein Science</i> , 2012 , 21, 1241-52	6.3	51
9	Recovery of red fluorescent protein chromophore maturation deficiency through rational design. <i>PLoS ONE</i> , 2012 , 7, e52463	3.7	15
8	Nerve agent hydrolysis activity designed into a human drug metabolism enzyme. <i>PLoS ONE</i> , 2011 , 6, e17441	3.7	18
7	Generation of longer emission wavelength red fluorescent proteins using computationally designed libraries. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 20257-62	11.5	71
6	Photolabeling of tissue transglutaminase reveals the binding mode of potent cinnamoyl inhibitors. <i>Biochemistry</i> , 2009 , 48, 3346-53	3.2	22
5	The bioorganic chemistry of transglutaminase II from mechanism to inhibition and engineering. <i>Canadian Journal of Chemistry</i> , 2008 , 86, 271-276	0.9	36
4	Semi-rational approaches to engineering enzyme activity: combining the benefits of directed evolution and rational design. <i>Current Opinion in Biotechnology</i> , 2005 , 16, 378-84	11.4	285

3	Tissue transglutaminase acylation: Proposed role of conserved active site Tyr and Trp residues revealed by molecular modeling of peptide substrate binding. <i>Protein Science</i> , 2004 , 13, 979-91	6.3	36
2	Expression and rapid purification of highly active hexahistidine-tagged guinea pig liver transglutaminase. <i>Protein Expression and Purification</i> , 2004 , 33, 256-64	2	20
1	Evolution of an enzyme conformational ensemble guides design of an efficient biocatalyst		5