

# Ramesh K Jha

## List of Publications by Year in descending order

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20  
papers

592  
citations

687363

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h-index

752698

20  
g-index

29  
all docs

29  
docs citations

29  
times ranked

1024  
citing authors

#	ARTICLE	IF	CITATIONS
1	Engineered pH-Sensitive Protein G/IgG Interaction. ACS Chemical Biology, 2021, 16, 1142-1146.	3.4	0
2	Identifying key determinants and dynamics of SARS-CoV-2/ACE2 tight interaction. PLoS ONE, 2021, 16, e0257905.	2.5	6
3	Engineering glucose metabolism for enhanced muconic acid production in <i>Pseudomonas putida</i> KT2440. Metabolic Engineering, 2020, 59, 64-75.	7.0	76
4	Gene amplification, laboratory evolution, and biosensor screening reveal MucK as a terephthalic acid transporter in <i>Acinetobacter baylyi</i> ADP1. Metabolic Engineering, 2020, 62, 260-274.	7.0	35
5	Smart Microbial Cells Couple Catalysis and Sensing to Provide High-Throughput Selection of an Organophosphate Hydrolase. ACS Synthetic Biology, 2020, 9, 1234-1239.	3.8	7
6	Sensor-Enabled Alleviation of Product Inhibition in Chorismate Pyruvate-Lyase. ACS Synthetic Biology, 2019, 8, 775-786.	3.8	23
7	A protocatechuate biosensor for <i>Pseudomonas putida</i> KT2440 via promoter and protein evolution. Metabolic Engineering Communications, 2018, 6, 33-38.	3.6	29
8	Rapid Thermostabilization of <i>Bacillus thuringiensis</i> Serovar Konkukian 97â€²27 Dehydroshikimate Dehydratase through a Structure-Based Enzyme Design and Whole Cell Activity Assay. ACS Synthetic Biology, 2017, 6, 120-129.	3.8	14
9	A microbial sensor for organophosphate hydrolysis exploiting an engineered specificity switch in a transcription factor. Nucleic Acids Research, 2016, 44, 8490-8500.	14.5	31
10	Rosetta comparative modeling for library design: Engineering alternative inducer specificity in a transcription factor. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1327-1340.	2.6	51
11	Genome Sequence and Transcriptome Analyses of <i>Chrysochromulina tobin</i> : Metabolic Tools for Enhanced Algal Fitness in the Prominent Order Prymnesiales (Haptophyceae). PLoS Genetics, 2015, 11, e1005469.	3.5	58
12	Engineering an <i>Acinetobacter</i> regulon for biosensing and high-throughput enzyme screening in <i>E. coli</i> via flow cytometry. Nucleic Acids Research, 2014, 42, 8150-8160.	14.5	59
13	The mitochondrial and chloroplast genomes of the haptophyte <i>Chrysochromulina tobin</i> contain unique repeat structures and gene profiles. BMC Genomics, 2014, 15, 604.	2.8	30
14	An improved Protein G with higher affinity for human/rabbit IgG Fc domains exploiting a computationally designed polar network. Protein Engineering, Design and Selection, 2014, 27, 127-134.	2.1	21
15	A pangenomic analysis of the <i>Nannochloropsis</i> organellar genomes reveals novel genetic variations in key metabolic genes. BMC Genomics, 2014, 15, 212.	2.8	41
16	Combined computational design of a zinc-binding site and a protein-protein interaction: One open zinc coordination site was not a robust hotspot for de novo ubiquitin binding. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1245-1255.	2.6	10
17	3D structure analysis of PAKs. Cellular Logistics, 2012, 2, 69-77.	0.9	16
18	Exploring the sequence-function relationship in transcriptional regulation by the <i>lac</i> O <sub>1</sub> operator. FEBS Journal, 2012, 279, 2534-2543.	4.7	3

#	ARTICLE	IF	CITATIONS
19	Redesign of the PAK1 Autoinhibitory Domain for Enhanced Stability and Affinity in Biosensor Applications. Journal of Molecular Biology, 2011, 413, 513-522.	4.2	10
20	Computational Design of a PAK1 Binding Protein. Journal of Molecular Biology, 2010, 400, 257-270.	4.2	69