

# Tea Pavkov-Keller

## List of Publications by Year in descending order

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54  
papers

4,463  
citations

257450

24  
h-index

161849

54  
g-index

57  
all docs

57  
docs citations

57  
times ranked

5076  
citing authors

#	ARTICLE	IF	CITATIONS
1	Residue-Specific Incorporation of the Non-Canonical Amino Acid Norleucine Improves Lipase Activity on Synthetic Polyesters. <i>Frontiers in Bioengineering and Biotechnology</i> , 2022, 10, 769830.	4.1	3
2	Small Things Matter: The 11.6-kDa TraB Protein is Crucial for Antibiotic Resistance Transfer Among Enterococci. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 867136.	3.5	2
3	The periplasmic domains of <i>Vibrio cholerae</i> ToxR and ToxS are forming a strong heterodimeric complex independent on the redox state of ToxR cysteines. <i>Molecular Microbiology</i> , 2021, 115, 1277-1291.	2.5	7
4	Accurate prediction of protein structures and interactions using a three-track neural network. <i>Science</i> , 2021, 373, 871-876.	12.6	2,843
5	Structural Changes in the Cap of Rv0183/mtbMGL Modulate the Shape of the Binding Pocket. <i>Biomolecules</i> , 2021, 11, 1299.	4.0	2
6	Structural and DNA-binding properties of the cytoplasmic domain of <i>Vibrio cholerae</i> transcription factor ToxR. <i>Journal of Biological Chemistry</i> , 2021, 297, 101167.	3.4	5
7	Rational Engineered C-Acyltransferase Transforms Sterically Demanding Acyl Donors. <i>ACS Catalysis</i> , 2020, 10, 1094-1101.	11.2	10
8	Substituting the catalytic proline of 4-oxalocrotonate tautomerase with non-canonical analogues reveals a finely tuned catalytic system. <i>Scientific Reports</i> , 2019, 9, 2697.	3.3	6
9	Structure and Catalytic Mechanism of a Bacterial Friedel-Crafts Acylase. <i>ChemBioChem</i> , 2019, 20, 88-95.	2.6	27
10	Oxidative cyclization of N-methyl-dopa by a fungal flavoenzyme of the amine oxidase family. <i>Journal of Biological Chemistry</i> , 2018, 293, 17021-17032.	3.4	4
11	TraN: A novel repressor of an <i>Enterococcus</i> conjugative type IV secretion system. <i>Nucleic Acids Research</i> , 2018, 46, 9201-9219.	14.5	11
12	Identification of Key Residues for Enzymatic Carboxylate Reduction. <i>Frontiers in Microbiology</i> , 2018, 9, 250.	3.5	29
13	The crystal structure of monoacylglycerol lipase from <i>M. tuberculosis</i> reveals the basis for specific inhibition. <i>Scientific Reports</i> , 2018, 8, 8948.	3.3	23
14	Enzyme discovery beyond homology: a unique hydroxynitrile lyase in the Bet v1 superfamily. <i>Scientific Reports</i> , 2017, 7, 46738.	3.3	21
15	Biocatalytic Friedel-Crafts Acylation and Fries Reaction. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 7615-7619.	13.8	54
16	Biocatalytic Friedel-Crafts Acylation and Fries Reaction. <i>Angewandte Chemie</i> , 2017, 129, 7723-7727.	2.0	11
17	Regioselective <i>para</i> -Carboxylation of Catechols with a Prenylated Flavin Dependent Decarboxylase. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 13893-13897.	13.8	64
18	Regioselektive <i>para</i> -Carboxylierung von Catecholen mit einer Prenylflavin-abhängigen Decarboxylase. <i>Angewandte Chemie</i> , 2017, 129, 14081-14085.	2.0	6

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19	Crystal Structure and Catalytic Mechanism of CouO, a Versatile C-Methyltransferase from <i>Streptomyces rishiriensis</i> . PLoS ONE, 2017, 12, e0171056.	2.5	16
20	Discovery and structural characterisation of new fold type IV-transaminases exemplify the diversity of this enzyme fold. Scientific Reports, 2016, 6, 38183.	3.3	36
21	Structures of almond hydroxynitrile lyase isoenzyme 5 provide a rationale for the lack of oxidoreductase activity in flavin dependent HNLs. Journal of Biotechnology, 2016, 235, 24-31.	3.8	3
22	Structure and biochemical properties of recombinant human dimethylglycine dehydrogenase and comparison to the disease-related H109R variant. FEBS Journal, 2016, 283, 3587-3603.	4.7	14
23	Substrate complexes of human dipeptidyl peptidase III reveal the mechanism of enzyme inhibition. Scientific Reports, 2016, 6, 23787.	3.3	41
24	Characterization of a poly(butylene adipate-co-terephthalate)-hydrolyzing lipase from <i>Pelosinus fermentans</i> . Applied Microbiology and Biotechnology, 2016, 100, 1753-1764.	3.6	75
25	An Esterase from Anaerobic <i>Clostridium hathewayi</i> Can Hydrolyze Aliphatic Aromatic Polyesters. Environmental Science & Technology, 2016, 50, 2899-2907.	10.0	39
26	Regioselective Enzymatic $\beta$ -Carboxylation of <i>para</i> -Hydroxy-styrene Derivatives Catalyzed by Phenolic Acid Decarboxylases. Advanced Synthesis and Catalysis, 2015, 357, 1909-1918.	4.3	47
27	Structure-Based Mechanism of Oleate Hydratase from <i>Elizabethkingia meningoseptica</i> . ChemBioChem, 2015, 16, 1730-1734.	2.6	66
28	The Nitrile-Forming Enzyme $\gamma$ -Cyano- $\gamma$ -Deazaguanine Synthase from <i>Geobacillus kaustophilus</i> : A Reverse Nitrilase?. ChemBioChem, 2015, 16, 2373-2378.	2.6	7
29	Complete switch from $\beta$ -2,3- to $\beta$ -2,6-regioselectivity in <i>Pasteurella dagmatis</i> -galactoside sialyltransferase by active-site redesign. Chemical Communications, 2015, 51, 3083-3086.	4.1	41
30	Improving the Properties of Bacterial $\alpha$ -Selective Hydroxynitrile Lyases for Industrial Applications. ChemCatChem, 2015, 7, 325-332.	3.7	27
31	Anthranoyl-CoA monooxygenase/reductase from <i>Azoarcus evansii</i> possesses both FMN and FAD in two distinct and independent active sites. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2015, 1854, 890-896.	2.3	4
32	Oxidation of Monolignols by Members of the Berberine Bridge Enzyme Family Suggests a Role in Plant Cell Wall Metabolism. Journal of Biological Chemistry, 2015, 290, 18770-18781.	3.4	83
33	Identification of promiscuous ene-reductase activity by mining structural databases using active site constellations. Nature Communications, 2014, 5, 4150.	12.8	67
34	Dissection of the IgE and T-cell recognition of the major group 5 grass pollen allergen Phl p 5. Journal of Allergy and Clinical Immunology, 2014, 133, 836-845.e11.	2.9	36
35	Structure of allergens and structure based epitope predictions. Methods, 2014, 66, 3-21.	3.8	82
36	S-adenosyl-L-homocysteine hydrolase and methylation disorders: Yeast as a model system. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2013, 1832, 204-215.	3.8	122

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37	Crystallization and preliminary structure determination of the transfer protein TraM from the Gram-positive conjugative plasmid pIP501. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 178-183.	0.7	6
38	The 2.5 Å... Structure of the Enterococcus Conjugation Protein TraM resembles VirB8 Type IV Secretion Proteins. <i>Journal of Biological Chemistry</i> , 2013, 288, 2018-2028.	3.4	50
39	Crystallization of domains involved in self-assembly of the S-layer protein SbsC. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1511-1514.	0.7	7
40	The Structure of Bacterial S-Layer Proteins. <i>Progress in Molecular Biology and Translational Science</i> , 2011, 103, 73-130.	1.7	58
41	Recombinant monoclonal human immunoglobulin E to investigate the allergenic activity of major grass pollen allergen Phl p 5. <i>Clinical and Experimental Allergy</i> , 2011, 41, 270-280.	2.9	17
42	Structure of Human Na <sup>+</sup> /H <sup>+</sup> Exchanger NHE1 Regulatory Region in Complex with Calmodulin and Ca <sup>2+</sup> . <i>Journal of Biological Chemistry</i> , 2011, 286, 40954-40961.	3.4	47
43	Visualization of clustered IgE epitopes on $\hat{\pm}$ -lactalbumin. <i>Journal of Allergy and Clinical Immunology</i> , 2010, 125, 1279-1285.e9.	2.9	48
44	Identification of the reactive cysteine residues in yeast dipeptidyl peptidase III. <i>Biochimie</i> , 2010, 92, 89-96.	2.6	15
45	Towards the structure of the C-terminal part of the S-layer protein SbsC. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 1042-1047.	0.7	5
46	The high-molecular-mass amylase (HMMA) of <i>Geobacillus stearothermophilus</i> ATCC 12980 interacts with the cell wall components by virtue of three specific binding regions. <i>Molecular Microbiology</i> , 2009, 72, 1448-1461.	2.5	15
47	The Structure and Binding Behavior of the Bacterial Cell Surface Layer Protein SbsC. <i>Structure</i> , 2008, 16, 1226-1237.	3.3	79
48	Mimotopes identify conformational B-cell epitopes on the two major house dust mite allergens Der p 1 and Der p 2. <i>Molecular Immunology</i> , 2008, 45, 1308-1317.	2.2	30
49	Reduction of the in vivo allergenicity of Der p 2, the major house-dust mite allergen, by genetic engineering. <i>Molecular Immunology</i> , 2008, 45, 2486-2498.	2.2	53
50	S-Adenosylhomocysteine hydrolase (AdoHcyase) deficiency: Enzymatic capabilities of human AdoHcyase are highly effected by changes to codon 89 and its surrounding residues. <i>Biochemical and Biophysical Research Communications</i> , 2008, 368, 30-36.	2.1	9
51	Functional analysis of human S-adenosylhomocysteine hydrolase isoforms SAHH-2 and SAHH-3. <i>European Journal of Human Genetics</i> , 2007, 15, 347-351.	2.8	9
52	A single mutation at Tyr143 of human S-adenosylhomocysteine hydrolase renders the enzyme thermosensitive and affects the oxidation state of bound cofactor nicotinamide-adenine dinucleotide. <i>Biochemical Journal</i> , 2006, 400, 245-253.	3.7	18
53	Crystallization and preliminary structure determination of the plant food allergen Pru av 2. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 186-188.	0.7	15
54	Crystallization and preliminary structure determination of the C-terminal truncated domain of the S-layer protein SbsC. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1466-1468.	2.5	22