

# Konstantin Denessiouk

## List of Publications by Year in descending order

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Version: 2024-02-01

23  
papers

540  
citations

933447

10  
h-index

713466

21  
g-index

23  
all docs

23  
docs citations

23  
times ranked

917  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural leitmotif and functional variations of the structural catalytic core in (chymo)trypsin-like serine/cysteine fold proteinases. <i>International Journal of Biological Macromolecules</i> , 2021, 179, 601-609.	7.5	2
2	Structural and functional significance of the amino acid differences Val35Thr, Ser46Ala, Asn65Ser, and Ala94Ser in 3C-like proteinases from SARS-CoV-2 and SARS-CoV. <i>International Journal of Biological Macromolecules</i> , 2021, 193, 2113-2113.	7.5	3
3	Papain-like cysteine proteinase zone (PCP-zone) and PCP structural catalytic core (PCP-SCC) of enzymes with cysteine proteinase fold. <i>International Journal of Biological Macromolecules</i> , 2020, 165, 1438-1446.	7.5	5
4	NBCZone: Universal three-dimensional construction of eleven amino acids near the catalytic nucleophile and base in the superfamily of (chymo)trypsin-like serine fold proteases. <i>International Journal of Biological Macromolecules</i> , 2020, 153, 399-411.	7.5	5
5	The acid-base-nucleophile catalytic triad in ABH-fold enzymes is coordinated by a set of structural elements. <i>PLoS ONE</i> , 2020, 15, e0229376.	2.5	18
6	A conserved strategy of chalcone isomerase-like protein to rectify promiscuous chalcone synthase specificity. <i>Nature Communications</i> , 2020, 11, 870.	12.8	71
7	System Approach for Building of Calcium-Binding Sites in Proteins. <i>Biomolecules</i> , 2020, 10, 588.	4.0	1
8	Experimental Insight into the Structural and Functional Roles of the $\sim$ Black $\text{\textcircled{TM}}$ and $\sim$ Gray $\text{\textcircled{TM}}$ Clusters in Recoverin, a Calcium Binding Protein with Four EF-Hand Motifs. <i>Molecules</i> , 2019, 24, 2494.	3.8	2
9	Analyzing the structural and functional roles of residues from the $\sim$ black $\text{\textcircled{TM}}$ and $\sim$ gray $\text{\textcircled{TM}}$ clusters of human S100P protein. <i>Cell Calcium</i> , 2019, 80, 46-55.	2.4	4
10	Distinctive structural motifs coordinate the catalytic nucleophile and the residues of the oxyanion hole in the alpha/beta-hydrolase fold enzymes. <i>Protein Science</i> , 2019, 28, 344-364.	7.6	25
11	Physical interactions among flavonoid enzymes in snapdragon and torenia reveal the diversity in the flavonoid metabolon organization of different plant species. <i>Plant Journal</i> , 2018, 94, 372-392.	5.7	84
12	Top surface blade residues and the central channel water molecules are conserved in every repeat of the integrin-like $\beta$ -propeller structures. <i>Journal of Structural Biology</i> , 2018, 201, 155-161.	2.8	2
13	The Receptor-like Pseudokinase GHR1 Is Required for Stomatal Closure. <i>Plant Cell</i> , 2018, 30, 2813-2837.	6.6	95
14	Comprehensive analysis of the roles of $\sim$ black $\text{\textcircled{TM}}$ and $\sim$ gray $\text{\textcircled{TM}}$ clusters in structure and function of rat $\beta$ -parvalbumin. <i>Cell Calcium</i> , 2018, 75, 64-78.	2.4	8
15	On the relationship between the conserved $\sim$ black $\text{\textcircled{TM}}$ and $\sim$ gray $\text{\textcircled{TM}}$ structural clusters and intrinsic disorder in parvalbumins. <i>International Journal of Biological Macromolecules</i> , 2018, 120, 1055-1062.	7.5	5
16	Novel calcium recognition constructions in proteins: Calcium blade and EF-hand zone. <i>Biochemical and Biophysical Research Communications</i> , 2017, 483, 958-963.	2.1	4
17	Building kit for metal cation binding sites in proteins. <i>Biochemical and Biophysical Research Communications</i> , 2017, 494, 311-317.	2.1	3
18	Alpha/beta-hydrolases: A unique structural motif coordinates catalytic acid residue in 40 protein fold families. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 1845-1855.	2.6	25

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19	Identification of protein-protein interactions of isoflavonoid biosynthetic enzymes with 2-hydroxyisoflavanone synthase in soybean ( <i>Glycine max</i> (L.) Merr.). <i>Biochemical and Biophysical Research Communications</i> , 2016, 469, 546-551.	2.1	40
20	Two Structural Motifs within Canonical EF-Hand Calcium-Binding Domains Identify Five Different Classes of Calcium Buffers and Sensors. <i>PLoS ONE</i> , 2014, 9, e109287.	2.5	61
21	Effects of light and the regulatory B-subunit composition of protein phosphatase 2A on the susceptibility of <i>Arabidopsis thaliana</i> to aphid ( <i>Myzus persicae</i> ) infestation. <i>Frontiers in Plant Science</i> , 2014, 5, 405.	3.6	27
22	Conservation of the Human Integrin-Type Beta-Propeller Domain in Bacteria. <i>PLoS ONE</i> , 2011, 6, e25069.	2.5	22
23	Finding local structural similarities among families of unrelated protein structures: A generic non-linear alignment algorithm. , 1999, 34, 341-355.		28