

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 | The Receptor-like Pseudokinase GHR1 Is Required for Stomatal Closure. <i>Plant Cell</i> , 2018, 30, 2813-2837. | 6.6 | 95 |
| 2 | 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 |
| 3 | A conserved strategy of chalcone isomerase-like protein to rectify promiscuous chalcone synthase specificity. <i>Nature Communications</i> , 2020, 11, 870. | 12.8 | 71 |
| 4 | 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 |
| 5 | 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 |
| 6 | Finding local structural similarities among families of unrelated protein structures: A generic non-linear alignment algorithm. , 1999, 34, 341-355. | | 28 |
| 7 | 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 |
| 8 | 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 |
| 9 | 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 |
| 10 | Conservation of the Human Integrin-Type Beta-Propeller Domain in Bacteria. <i>PLoS ONE</i> , 2011, 6, e25069. | 2.5 | 22 |
| 11 | 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 |
| 12 | Comprehensive analysis of the roles of β -black TM and β -gray TM clusters in structure and function of rat β 2-parvalbumin. <i>Cell Calcium</i> , 2018, 75, 64-78. | 2.4 | 8 |
| 13 | On the relationship between the conserved β -black TM and β -gray TM structural clusters and intrinsic disorder in parvalbumins. <i>International Journal of Biological Macromolecules</i> , 2018, 120, 1055-1062. | 7.5 | 5 |
| 14 | 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 |
| 15 | 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 |
| 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 | Analyzing the structural and functional roles of residues from the β -black TM and β -gray TM clusters of human S100P protein. <i>Cell Calcium</i> , 2019, 80, 46-55. | 2.4 | 4 |
| 18 | Building kit for metal cation binding sites in proteins. <i>Biochemical and Biophysical Research Communications</i> , 2017, 494, 311-317. | 2.1 | 3 |

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|----|--|-----|-----------|
| 19 | 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 |
| 20 | Top surface blade residues and the central channel water molecules are conserved in every repeat of the integrin-like Î²-propeller structures. <i>Journal of Structural Biology</i> , 2018, 201, 155-161. | 2.8 | 2 |
| 21 | Experimental Insight into the Structural and Functional Roles of the "Black"™ and "Gray"™ Clusters in Recoverin, a Calcium Binding Protein with Four EF-Hand Motifs. <i>Molecules</i> , 2019, 24, 2494. | 3.8 | 2 |
| 22 | 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 |
| 23 | System Approach for Building of Calcium-Binding Sites in Proteins. <i>Biomolecules</i> , 2020, 10, 588. | 4.0 | 1 |