

Onur Dagliyan

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8054807/publications.pdf>

Version: 2024-02-01

26
papers

1,166
citations

361413

20
h-index

580821

25
g-index

30
all docs

30
docs citations

30
times ranked

1829
citing authors

#	ARTICLE	IF	CITATIONS
1	Engineering a switchable single-chain TEV protease to control protein maturation in living neurons. <i>Bioengineering and Translational Medicine</i> , 2022, 7, .	7.1	7
2	Expression of the transcription factor PU.1 induces the generation of microglia-like cells in human cortical organoids. <i>Nature Communications</i> , 2022, 13, 430.	12.8	49
3	Bidirectional perisomatic inhibitory plasticity of a Fos neuronal network. <i>Nature</i> , 2021, 590, 115-121.	27.8	70
4	Biosensors based on peptide exposure show single molecule conformations in live cells. <i>Cell</i> , 2021, 184, 5670-5685.e23.	28.9	15
5	Low-Dose Vertical Inhibition of the RAF-MEK-ERK Cascade Causes Apoptotic Death of KRAS Mutant Cancers. <i>Cell Reports</i> , 2020, 31, 107764.	6.4	69
6	Rational design and implementation of a chemically inducible heterotrimerization system. <i>Nature Methods</i> , 2020, 17, 928-936.	19.0	30
7	Engineering proteins for allosteric control by light or ligands. <i>Nature Protocols</i> , 2019, 14, 1863-1883.	12.0	46
8	Controlling protein conformation with light. <i>Current Opinion in Structural Biology</i> , 2019, 57, 17-22.	5.7	25
9	Computational design of chemogenetic and optogenetic split proteins. <i>Nature Communications</i> , 2018, 9, 4042.	12.8	75
10	Profiling cellular morphodynamics by spatiotemporal spectrum decomposition. <i>PLoS Computational Biology</i> , 2018, 14, e1006321.	3.2	34
11	Probe the Conformational Changes of Individual Molecules in Living Cells. <i>Biophysical Journal</i> , 2018, 114, 21a.	0.5	0
12	Morphodynamic Profiling of Cell Protrusion Based on Spatiotemporal Spectrum Decomposition and Unsupervised Clustering. <i>Biophysical Journal</i> , 2017, 112, 45a.	0.5	4
13	Engineering Pak1 Allosteric Switches. <i>ACS Synthetic Biology</i> , 2017, 6, 1257-1262.	3.8	26
14	Engineering extrinsic disorder to control protein activity in living cells. <i>Science</i> , 2016, 354, 1441-1444.	12.6	185
15	FRET binding antenna reports spatiotemporal dynamics of GDI-Cdc42 GTPase interactions. <i>Nature Chemical Biology</i> , 2016, 12, 802-809.	8.0	45
16	Gain-of-Function Mutation W493R in the Epithelial Sodium Channel Allosterically Reconfigures Intersubunit Coupling. <i>Journal of Biological Chemistry</i> , 2016, 291, 3682-3692.	3.4	6
17	Computational approaches to understanding protein aggregation in neurodegeneration. <i>Journal of Molecular Cell Biology</i> , 2014, 6, 104-115.	3.3	43
18	Intrinsic Disorder Mediates Cooperative Signal Transduction in STIM1. <i>Journal of Molecular Biology</i> , 2014, 426, 2082-2097.	4.2	24

#	ARTICLE	IF	CITATIONS
19	Engineered kinase activation reveals unique morphodynamic phenotypes and associated trafficking for Src family isoforms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 12420-12425.	7.1	47
20	Identification of Novel Integrin Binding Partners for Calcium and Integrin Binding Protein 1 (CIB1): Structural and Thermodynamic Basis of CIB1 Promiscuity. <i>Biochemistry</i> , 2013, 52, 7082-7090.	2.5	21
21	Knowledge-Based Design of a Biosensor to Quantify Localized ERK Activation in Living Cells. <i>Chemistry and Biology</i> , 2013, 20, 847-856.	6.0	49
22	Rational design of a ligand-controlled protein conformational switch. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 6800-6804.	7.1	111
23	Structure Based Discovery of Small Molecules to Regulate the Activity of Human Insulin Degrading Enzyme. <i>PLoS ONE</i> , 2012, 7, e31787.	2.5	27
24	Structural and Dynamic Determinants of Protein-Peptide Recognition. <i>Structure</i> , 2011, 19, 1837-1845.	3.3	79
25	Optimization Based Tumor Classification from Microarray Gene Expression Data. <i>PLoS ONE</i> , 2011, 6, e14579.	2.5	60
26	Classification of Cytochrome P450 Inhibitors with Respect to Binding Free Energy and $pI C_{50}$ Using Common Molecular Descriptors. <i>Journal of Chemical Information and Modeling</i> , 2009, 49, 2403-2411.	5.4	19