Igor F Tsigelny

List of Publications by Year
in descending order

53	1,884	304743 22	276875 41
papers	citations	h-index	g-index

58	58	58	3062
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Mechanisms of Hybrid Oligomer Formation in the Pathogenesis of Combined Alzheimer's and Parkinson's Diseases. PLoS ONE, 2008, 3, e3135.	2.5	233
2	Dynamics of Î±-synuclein aggregation and inhibition of pore-like oligomer development by Î²-synuclein. FEBS Journal, 2007, 274, 1862-1877.	4.7	149
3	Role of Î±â€synuclein penetration into the membrane in the mechanisms of oligomer pore formation. FEBS Journal, 2012, 279, 1000-1013.	4.7	146
4	Ade novocompound targeting Î±-synuclein improves deficits in models of Parkinsonâ€™s disease. Brain, 2016, 139, 3217-3236.	7.6	122
5	Kinetic Analyses of Mutations in the Glycine-Rich Loop of cAMP-Dependent Protein Kinaseâ€. Biochemistry, 1998, 37, 7708-7715.	2.5	82
6	Next-Generation Sequencing of Circulating Tumor DNA Reveals Frequent Alterations in Advanced Hepatocellular Carcinoma. Oncologist, 2018, 23, 586-593.	3.7	75
7	Role of Synucleins in Alzheimerâ€™s Disease. Neurotoxicity Research, 2009, 16, 306-317.	2.7	73
8	High expression of PD-1 ligands is associated with kataegis mutational signature and APOBEC3 alterations. OncoImmunology, 2017, 6, e1284719.	4.6	64
9	APOBEC-related mutagenesis and neo-peptide hydrophobicity: implications for response to immunotherapy. OncoImmunology, 2019, 8, 1550341.	4.6	60
10	Artificial intelligence in drug combination therapy. Briefings in Bioinformatics, 2019, 20, 1434-1448.	6.5	60
11	Interaction of Organic Cations with Organic Anion Transporters. Journal of Biological Chemistry, 2009, 284, 31422-31430.	3.4	58
12	Polycomb repressive 2 complexâ€”Molecular mechanisms of function. Protein Science, 2019, 28, 1387-1399.	7.6	57
13	Delineation of Selective Cyclic GMP-Dependent Protein Kinase Iα Substrate and Inhibitor Peptides Based on Combinatorial Peptide Libraries on Paper. , 1999, 82, 373-387.		52
14	600 ps Molecular dynamics reveals stable substructures and flexible hinge points in cAMP dependent protein kinase. , 1999, 50, 513-524.		49
15	Mechanism of alpha-synuclein oligomerization and membrane interaction: theoretical approach to unstructured proteins studies. Nanomedicine: Nanotechnology, Biology, and Medicine, 2008, 4, 350-357.	3.3	48
16	Potential COVID-19 papain-like protease PL^{pro} inhibitors: repurposing FDA-approved drugs. PeerJ, 2020, 8, e9965.	2.0	44
17	An All-Atom Model of the Structure of Human Copper Transporter 1. Cell Biochemistry and Biophysics, 2012, 63, 223-234.	1.8	40
18	Examination of an activeâ€site electrostatic node in the cAMPâ€dependent protein kinase catalytic subunit. Protein Science, 1996, 5, 1316-1324.	7.6	36

#	Article	IF	Citations
19	Recognition of early and late stages of bladder cancer using metabolites and machine learning. Metabolomics, 2019, 15, 94.	3.0	34
20	Finding distinctions between oral cancer and periodontitis using saliva metabolites and machine learning. Oral Diseases, 2021, 27, 484-493.	3.0	32
21	Analysis of Metagene Portraits Reveals Distinct Transitions During Kidney Organogenesis. Science Signaling, 2008, 1, ra16.	3.6	28
22	Conformational preferences and activities of peptides from the catecholamine release-inhibitory (catestatin) region of chromogranin A. Regulatory Peptides, 2004, 118, 75-87.	1.9	27
23	Adding a positive charge at residue 46 ofDrosophilaalcohol dehydrogenase increases cofactor specificity for NADP+. FEBS Letters, 1994, 356, 81-85.	2.8	26
24	Theoretical analysis of the structure of the peptide fasciculin and its docking to acetylcholinesterase. Protein Science, 1995, 4, 703-715.	7.6	23
25	Multiple spatially related pharmacophores define small molecule inhibitors of OLIG2 in glioblastoma. Oncotarget, 2017, 8, 22370-22384.	1.8	23
26	Finding needles in haystacks: Reranking DOT results by using shape complementarity, cluster analysis, and biological information. Proteins: Structure, Function and Bioinformatics, 2003, 52, 33-40.	2.6	20
27	MAPAS: a tool for predicting membrane-contacting protein surfaces. Nature Methods, 2008, 5, 119-119.	19.0	19
28	Conformational Changes of the Multispecific Transporter Organic Anion Transporter 1 (OAT1/SLC22A6) Suggests a Molecular Mechanism for Initial Stages of Drug and Metabolite Transport. Cell Biochemistry and Biophysics, 2011, 61, 251-259.	1.8	18
29	The copper transporter 1 (CTR1) is required to maintain the stability of copper transporter 2 (CTR2). Metallomics, 2015, 7, 1477-1487.	2.4	18
30	Catalytic subunit of cAMP-dependent protein kinase: Electrostatic features and peptide recognition. Biopolymers, 1996, 39, 353-365.	2.4	15
31	Elucidation of common pharmacophores from analysis of targeted metabolites transported by the multispecific drug transporterâ€"Organic anion transporter1 (Oat1). Bioorganic and Medicinal Chemistry, 2011, 19, 3320-3340.	3.0	14
32	Development of a pharmacophore model for the catecholamine release-inhibitory peptide catestatin: Virtual screening and functional testing identify novel small molecule therapeutics of hypertension. Bioorganic and Medicinal Chemistry, 2013, 21, 5855-5869.	3.0	13
33	Cripto stabilizes GRP78 on the cell membrane. Protein Science, 2018, 27, 653-661.	7.6	13
34	Complex Dynamics of Chaperoneâ€"Protein Interactions Under Cellular Stress. Cell Biochemistry and Biophysics, 2004, 40, 263-276.	1.8	12
35	MODELING OF GLYCEROL-3-PHOSPHATE TRANSPORTER SUGGESTS A POTENTIAL 'TILT' MECHANISM INVOLVED IN ITS FUNCTION. Journal of Bioinformatics and Computational Biology, 2008, 06, 885-904.	0.8	12
36	Bovine leukemia virus relation to human breast cancer: Meta-analysis. Microbial Pathogenesis, 2020, 149, 104417.	2.9	12

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37	Deep-learning- and pharmacophore-based prediction of RAGE inhibitors. Physical Biology, 2020, 17, 036003.	1.8	11
38	Catalytic subunit of cAMPâ€dependent protein kinase: Electrostatic features and peptide recognition. Biopolymers, 1996, 39, 353-365.	2.4	9
39	Identification of Molecular Determinants That Modulate Trafficking of Î”F508 CFTR, the Mutant ABC Transporter Associated With Cystic Fibrosis. Cell Biochemistry and Biophysics, 2005, 42, 041-054.	1.8	8
40	Solution structure of synthetic peptide inhibitor and substrate of cAMPâ€dependent protein kinase. A study by 2D ¹H NMR and molecular dynamics. Chemical Biology and Drug Design, 1997, 49, 210-220.	1.1	7
41	Hidden Markov Models-based system (HMMSPECTR) for detecting structural homologies on the basis of sequential information. Protein Engineering, Design and Selection, 2002, 15, 347-352.	2.1	6
42	Implications of viral infection in cancer development. Biochimica Et Biophysica Acta: Reviews on Cancer, 2021, 1876, 188622.	7.4	5
43	Potential SARS-CoV-2 Spike Protein-ACE2 Interface Inhibitors: Repurposing FDA-approved Drugs. Journal of Exploratory Research in Pharmacology, 2022, 7, 17-29.	0.4	5
44	<scp>Machineâ€learningâ€based</scp> virtual screening to repurpose drugs for treatment of Candida albicans infection. Mycoses, 2022, 65, 794-805.	4.0	5
45	Interactions of large T-Antigen (LT) protein of polyomaviruses with p53 unfold their cancerogenic potential. Journal of Biomolecular Structure and Dynamics, 2022, 40, 5243-5252.	3.5	4
46	Potential SARS-CoV-2 protease M^{pro} inhibitors: repurposing FDA-approved drugs. Physical Biology, 2021, 18, 025001.	1.8	4
47	Machine Learning Strategies to Distinguish Oral Cancer from Periodontitis Using Salivary Metabolites. Advances in Intelligent Systems and Computing, 2021, , 511-526.	0.6	3
48	Human Papillomavirus (HPV) Viral Proteins Substitute for the Impact of Somatic Mutations by Affecting Cancer-Related Genes: Meta-analysis and Perspectives. Journal of Infectiology, 2020, 3, 29-47.	0.8	2
49	Prediction of Premature Termination Codon Suppressing Compounds for Treatment of Duchenne Muscular Dystrophy Using Machine Learning. Molecules, 2020, 25, 3886.	3.8	1
50	Targeting Epigenetic Regulators Using Machine Learning: Potential Sirtuin 2 Inhibitors. Journal of Computational Biophysics and Chemistry, 2021, 20, 841-851.	1.7	1
51	Hierarchical control of coherent gene clusters defines the molecular mechanisms of glioblastoma. Molecular BioSystems, 2015, 11, 1012-1028.	2.9	0
52	Structure â€“ activity relationships and determinants of selectivity for congeners of the selective Î±7 partial agonist 3â€(2,4â€dimethoxybenzylidene)â€anabaseine (DMXBA or GTSâ€21) with the ACh binding proteins (AChBPs). FASEB Journal, 2006, 20, A244.	0.5	0
53	Modeling of mutant superoxide dismutase 1 octamers with cross-linked disulfide bonds. Journal of Molecular Modeling, 2022, 28, 89.	1.8	0