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	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
2	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
3	Modeling of mutant superoxide dismutase 1 octamers with cross-linked disulfide bonds. Journal of Molecular Modeling, 2022, 28, 89.	1.8	0
4	<scp>Machineâ€learningâ€based</scp> virtual screening to repurpose drugs for treatment of Candida albicans infection. Mycoses, 2022, 65, 794-805.	4.0	5
5	Finding distinctions between oral cancer and periodontitis using saliva metabolites and machine learning. Oral Diseases, 2021, 27, 484-493.	3.0	32
6	Potential SARS-CoV-2 protease M^{pro} inhibitors: repurposing FDA-approved drugs. Physical Biology, 2021, 18, 025001.	1.8	4
7	Implications of viral infection in cancer development. Biochimica Et Biophysica Acta: Reviews on Cancer, 2021, 1876, 188622.	7.4	5
8	Machine Learning Strategies to Distinguish Oral Cancer from Periodontitis Using Salivary Metabolites. Advances in Intelligent Systems and Computing, 2021, , 511-526.	0.6	3
9	Targeting Epigenetic Regulators Using Machine Learning: Potential Sirtuin 2 Inhibitors. Journal of Computational Biophysics and Chemistry, 2021, 20, 841-851.	1.7	1
10	Deep-learning- and pharmacophore-based prediction of RAGE inhibitors. Physical Biology, 2020, 17, 036003.	1.8	11
11	Bovine leukemia virus relation to human breast cancer: Meta-analysis. Microbial Pathogenesis, 2020, 149, 104417.	2.9	12
12	Prediction of Premature Termination Codon Suppressing Compounds for Treatment of Duchenne Muscular Dystrophy Using Machine Learning. Molecules, 2020, 25, 3886.	3.8	1
13	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
14	Potential COVID-19 papain-like protease PL^{pro} inhibitors: repurposing FDA-approved drugs. PeerJ, 2020, 8, e9965.	2.0	44
15	Recognition of early and late stages of bladder cancer using metabolites and machine learning. Metabolomics, 2019, 15, 94.	3.0	34
16	Polycomb repressive 2 complexâ€"Molecular mechanisms of function. Protein Science, 2019, 28, 1387-1399.	7.6	57
17	APOBEC-related mutagenesis and neo-peptide hydrophobicity: implications for response to immunotherapy. Oncolmmunology, 2019, 8, 1550341.	4.6	60
18	Artificial intelligence in drug combination therapy. Briefings in Bioinformatics, 2019, 20, 1434-1448.	6.5	60

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19	Next-Generation Sequencing of Circulating Tumor DNA Reveals Frequent Alterations in Advanced Hepatocellular Carcinoma. Oncologist, 2018, 23, 586-593.	3.7	75
20	Cripto stabilizes GRP78 on the cell membrane. Protein Science, 2018, 27, 653-661.	7.6	13
21	High expression of PD-1 ligands is associated with kataegis mutational signature and APOBEC3 alterations. OncoImmunology, 2017, 6, e1284719.	4.6	64
22	Multiple spatially related pharmacophores define small molecule inhibitors of OLIG2 in glioblastoma. Oncotarget, 2017, 8, 22370-22384.	1.8	23
23	Ade novocompound targeting Î±-synuclein improves deficits in models of Parkinsonâ€™s disease. Brain, 2016, 139, 3217-3236.	7.6	122
24	The copper transporter 1 (CTR1) is required to maintain the stability of copper transporter 2 (CTR2). Metallomics, 2015, 7, 1477-1487.	2.4	18
25	Hierarchical control of coherent gene clusters defines the molecular mechanisms of glioblastoma. Molecular BioSystems, 2015, 11, 1012-1028.	2.9	0
26	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
27	An All-Atom Model of the Structure of Human Copper Transporter 1. Cell Biochemistry and Biophysics, 2012, 63, 223-234.	1.8	40
28	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
29	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
30	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
31	Interaction of Organic Cations with Organic Anion Transporters. Journal of Biological Chemistry, 2009, 284, 31422-31430.	3.4	58
32	Role of Synucleins in Alzheimerâ€™s Disease. Neurotoxicity Research, 2009, 16, 306-317.	2.7	73
33	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
34	MAPAS: a tool for predicting membrane-contacting protein surfaces. Nature Methods, 2008, 5, 119-119.	19.0	19
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	Analysis of Metagene Portraits Reveals Distinct Transitions During Kidney Organogenesis. Science Signaling, 2008, 1, ra16.	3.6	28

#	Article	IF	Citations
37	Mechanisms of Hybrid Oligomer Formation in the Pathogenesis of Combined Alzheimer's and Parkinson's Diseases. PLoS ONE, 2008, 3, e3135.	2.5	233
38	Dynamics of Î±-synuclein aggregation and inhibition of pore-like oligomer development by Î²-synuclein. FEBS Journal, 2007, 274, 1862-1877.	4.7	149
39	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
40	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
41	Complex Dynamics of Chaperoneâ€“Protein Interactions Under Cellular Stress. Cell Biochemistry and Biophysics, 2004, 40, 263-276.	1.8	12
42	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
43	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
44	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
45	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
46	600 ps Molecular dynamics reveals stable substructures and flexible hinge points in cAMP dependent protein kinase. , 1999, 50, 513-524.		49
47	Kinetic Analyses of Mutations in the Glycine-Rich Loop of cAMP-Dependent Protein Kinaseâ€. Biochemistry, 1998, 37, 7708-7715.	2.5	82
48	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
49	Examination of an activeâ€site electrostatic node in the cAMPâ€dependent protein kinase catalytic subunit. Protein Science, 1996, 5, 1316-1324.	7.6	36
50	Catalytic subunit of cAMP-dependent protein kinase: Electrostatic features and peptide recognition. Biopolymers, 1996, 39, 353-365.	2.4	15
51	Catalytic subunit of cAMPâ€dependent protein kinase: Electrostatic features and peptide recognition. Biopolymers, 1996, 39, 353-365.	2.4	9
52	Theoretical analysis of the structure of the peptide fasciculin and its docking to acetylcholinesterase. Protein Science, 1995, 4, 703-715.	7.6	23
53	Adding a positive charge at residue 46 ofDrosophilaalcohol dehydrogenase increases cofactor specificity for NADP+. FEBS Letters, 1994, 356, 81-85.	2.8	26