Veronika Obsilov

List of Publications by Year in Descending Order

53 papers	1,408 citations	21 h-index	36 g-index
56 ext. papers	1,673 ext. citations	4.7 avg, IF	4.6 L-index

#	Paper	IF	Citations
53	FOXO4 interacts with p53 TAD and CRD and inhibits its binding to DNA.. *Protein Science*, **2022**, 31, e4287	6.3	1
52	14-3-3-protein regulates Nedd4-2 by modulating interactions between HECT and WW domains. *Communications Biology*, **2021**, 4, 899	6.7	4
51	14-3-3 proteins inactivate DAPK2 by promoting its dimerization and protecting key regulatory phosphosites. *Communications Biology*, **2021**, 4, 986	6.7	1
50	Structural Insights Support Targeting ASK1 Kinase for Therapeutic Interventions.. *International Journal of Molecular Sciences*, **2021**, 22,	6.3	2
49	Stabilization of Protein-Protein Interactions between CaMKK2 and 14-3-3 by Fusicoccins. *ACS Chemical Biology*, **2020**, 15, 3060-3071	4.9	5
48	14-3-3 protein binding blocks the dimerization interface of caspase-2. *FEBS Journal*, **2020**, 287, 3494-3510	5.7	7
47	The redox-active site of thioredoxin is directly involved in apoptosis signal-regulating kinase 1 binding that is modulated by oxidative stress. *FEBS Journal*, **2020**, 287, 1626-1644	5.7	9
46	The 14-3-3 Proteins as Important Allosteric Regulators of Protein Kinases. *International Journal of Molecular Sciences*, **2020**, 21,	6.3	9
45	A new role for 14-3-3 protein in steroidogenesis. *FEBS Journal*, **2020**, 287, 3921-3924	5.7	1
44	The activity of Saccharomyces cerevisiae Na, K/H antiporter Nha1 is negatively regulated by 14-3-3 protein binding at serine 481. *Biochimica Et Biophysica Acta - Molecular Cell Research*, **2019**, 1866, 118534	4.9	3
43	Forkhead Domains of FOXO Transcription Factors Differ in both Overall Conformation and Dynamics. *Cells*, **2019**, 8,	7.9	16
42	Allosteric activation of yeast enzyme neutral trehalase by calcium and 14-3-3 protein. *Physiological Research*, **2019**, 68, 147-160	2.1	5
41	Modulating FOXO3 transcriptional activity by small, DBD-binding molecules. *ELife*, **2019**, 8,	8.9	5
40	14-3-3 protein directly interacts with the kinase domain of calcium/calmodulin-dependent protein kinase kinase (CaMKK2). *Biochimica Et Biophysica Acta - General Subjects*, **2018**, 1862, 1612-1625	4	18
39	CaMKK2 kinase domain interacts with the autoinhibitory region through the N-terminal lobe including the RP insert. *Biochimica Et Biophysica Acta - General Subjects*, **2018**, 1862, 2304-2313	4	2
38	14-3-3 protein masks the nuclear localization sequence of caspase-2. *FEBS Journal*, **2018**, 285, 4196-4213	5.7	13
37	Structural Basis for the 14-3-3 Protein-Dependent Inhibition of Phosducin Function. *Biophysical Journal*, **2017**, 112, 1339-1349	2.9	6

36	Molecular basis of the 14-3-3 protein-dependent activation of yeast neutral trehalase Nth1. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, E9811-E9820	11.5	36
35	Human procaspase-2 phosphorylation at both S139 and S164 is required for 14-3-3 binding. *Biochemical and Biophysical Research Communications*, **2017**, 493, 940-945	3.4	10
34	Structural aspects of protein kinase ASK1 regulation. *Advances in Biological Regulation*, **2017**, 66, 31-36	6.2	16
33	Artificial proteins as allosteric modulators of PDZ3 and SH3 in two-domain constructs: A computational characterization of novel chimeric proteins. *Proteins: Structure, Function and Bioinformatics*, **2016**, 84, 1358-74	4.2	3
32	Cysteine residues mediate high-affinity binding of thioredoxin to ASK1. *FEBS Journal*, **2016**, 283, 3821-3838	5.4	21
31	Structural Insight into the 14-3-3 Protein-dependent Inhibition of Protein Kinase ASK1 (Apoptosis Signal-regulating kinase 1). *Journal of Biological Chemistry*, **2016**, 291, 20753-65	5.4	36
30	Structural Characterization of Phosducin and Its Complex with the 14-3-3 Protein. *Journal of Biological Chemistry*, **2015**, 290, 16246-60	5.4	18
29	Mechanistic Insight into the 14-3-3 Protein-Dependent Activation of Yeast Neutral Trehalase Nth1. *FASEB Journal*, **2015**, 29, 572.2	0.9	
28	Biophysical Characterization of Interaction between the Thioredoxin-Binding Domain of Protein Kinase ASK1 and Reduced Thioredoxin. *FASEB Journal*, **2015**, 29, 724.3	0.9	
27	Role of the EF-hand-like motif in the 14-3-3 protein-mediated activation of yeast neutral trehalase Nth1. *Journal of Biological Chemistry*, **2014**, 289, 13948-61	5.4	19
26	Biophysical and structural characterization of the thioredoxin-binding domain of protein kinase ASK1 and its interaction with reduced thioredoxin. *Journal of Biological Chemistry*, **2014**, 289, 24463-74	5.4	29
25	Structural basis of the 14-3-3 protein-dependent activation of yeast neutral trehalase Nth1. *Biochimica Et Biophysica Acta - General Subjects*, **2013**, 1830, 4491-9	4	28
24	Detailed kinetic analysis of the interaction between the FOXO4-DNA-binding domain and DNA. *Biophysical Chemistry*, **2013**, 184, 68-78	3.5	7
23	Structural modulation of phosducin by phosphorylation and 14-3-3 protein binding. *Biophysical Journal*, **2012**, 103, 1960-9	2.9	12
22	In-situ enrichment of phosphopeptides on MALDI plates modified by ambient ion landing. *Journal of Mass Spectrometry*, **2012**, 47, 1294-302	2.2	18
21	Role of individual phosphorylation sites for the 14-3-3-protein-dependent activation of yeast neutral trehalase Nth1. *Biochemical Journal*, **2012**, 443, 663-70	3.8	35
20	Structural basis of 14-3-3 protein functions. *Seminars in Cell and Developmental Biology*, **2011**, 22, 663-72	7.5	192
19	Structural basis for DNA recognition by FOXO proteins. *Biochimica Et Biophysica Acta - Molecular Cell Research*, **2011**, 1813, 1946-53	4.9	60

18	Structural basis for the 14-3-3 protein-dependent inhibition of the regulator of G protein signaling 3 (RGS3) function. *Journal of Biological Chemistry*, **2011**, 286, 43527-36	5.4	24
17	The C-terminal segment of yeast BMH proteins exhibits different structure compared to other 14-3-3 protein isoforms. *Biochemistry*, **2010**, 49, 3853-61	3.2	23
16	The interactions of the C-terminal region of the TRPC6 channel with calmodulin. *Neurochemistry International*, **2010**, 56, 363-6	4.4	13
15	14-3-3 protein interacts with and affects the structure of RGS domain of regulator of G protein signaling 3 (RGS3). *Journal of Structural Biology*, **2010**, 170, 451-61	3.4	30
14	Structure of the human FOXO4-DBD-DNA complex at 1.9 Å resolution reveals new details of FOXO binding to the DNA. *Acta Crystallographica Section D: Biological Crystallography*, **2010**, 66, 1351-7		44
13	14-3-3 protein masks the DNA binding interface of forkhead transcription factor FOXO4. *Journal of Biological Chemistry*, **2009**, 284, 19349-60	5.4	47
12	Structure/function relationships underlying regulation of FOXO transcription factors. *Oncogene*, **2008**, 27, 2263-75	9.2	170
11	Ionic interactions are essential for TRPV1 C-terminus binding to calmodulin. *Biochemical and Biophysical Research Communications*, **2008**, 375, 680-3	3.4	25
10	The 14-3-3 protein affects the conformation of the regulatory domain of human tyrosine hydroxylase. *Biochemistry*, **2008**, 47, 1768-77	3.2	42
9	The role of proline residues in the structure and function of human MT2 melatonin receptor. *Journal of Pineal Research*, **2008**, 45, 361-72	10.4	17
8	Both the N-terminal loop and wing W2 of the forkhead domain of transcription factor Foxo4 are important for DNA binding. *Journal of Biological Chemistry*, **2007**, 282, 8265-75	5.4	58
7	ATP binding site on the C-terminus of the vanilloid receptor. *Archives of Biochemistry and Biophysics* , **2007**, 465, 389-98	4.1	13
6	14-3-3 Protein interacts with nuclear localization sequence of forkhead transcription factor FoxO4. *Biochemistry*, **2005**, 44, 11608-17	3.2	86
5	Ligand binding to the human MT2 melatonin receptor: the role of residues in transmembrane domains 3, 6, and 7. *Biochemical and Biophysical Research Communications*, **2005**, 332, 726-34	3.4	25
4	14-3-3zeta C-terminal stretch changes its conformation upon ligand binding and phosphorylation at Thr232. *Journal of Biological Chemistry*, **2004**, 279, 4531-40	5.4	62
3	14-3-3 protein C-terminal stretch occupies ligand binding groove and is displaced by phosphopeptide binding. *Journal of Biological Chemistry*, **2004**, 279, 49113-9	5.4	41
2	Molecular modeling of human MT2 melatonin receptor: the role of Val204, Leu272 and Tyr298 in ligand binding. *Journal of Neurochemistry*, **2004**, 91, 836-42	6	31
1	Effect of aminophospholipid glycation on order parameter and hydration of phospholipid bilayer. *Biophysical Chemistry*, **1999**, 80, 165-77	3.5	8