Olga Vinogradova

List of Publications by Year
in descending order

45 papers	2,163 citations	279701 23 h-index	233338 45 g-index
46 all docs	46 docs citations	46 times ranked	2273 citing authors

#	Article	IF	Citations
1	A Structural Mechanism of Integrin Î±IIbÎ²3 â€œInside-Outâ€•Activation as Regulated by Its Cytoplasmic Face. Cell, 2002, 110, 587-597.	13.5	491
2	Integrin Bidirectional Signaling: A Molecular View. PLoS Biology, 2004, 2, e169.	2.6	146
3	A structural basis for integrin activation by the cytoplasmic tail of the alpha IIb-subunit. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 1450-1455.	3.3	134
4	Structural characterization and immunochemical detection of a fluorophore derived from 4-hydroxy-2-nonenal and lysine. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 7975-7980.	3.3	124
5	Structure of an Ultraweak Protein-Protein Complex and Its Crucial Role in Regulation of Cell Morphology and Motility. Molecular Cell, 2005, 17, 513-523.	4.5	116
6	Membrane-mediated structural transitions at the cytoplasmic face during integrin activation. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 4094-4099.	3.3	115
7	On choosing a detergent for solution NMR studies of membrane proteins. Journal of Biomolecular NMR, 1998, 11, 381-386.	1.6	107
8	Synthesis of a Phosphoantigen Prodrug that Potently Activates VÎ³9VÎ´2 T-Lymphocytes. Chemistry and Biology, 2014, 21, 945-954.	6.2	86
9	Escherichia coli diacylglycerol kinase: a case study in the application of solution NMR methods to an integral membrane protein. Biophysical Journal, 1997, 72, 2688-2701.	0.2	68
10	Structural and functional insights into PINCH LIM4 domainâ€“mediated integrin signaling. Nature Structural and Molecular Biology, 2003, 10, 558-564.	3.6	64
11	Escherichia coli Diacylglycerol Kinase Is an Î±-Helical Polytopic Membrane Protein and Can Spontaneously Insert into Preformed Lipid Vesicles. Biochemistry, 1996, 35, 8610-8618.	1.2	61
12	Solution NMR: A powerful tool for structural and functional studies of membrane proteins in reconstituted environments. Journal of Biological Chemistry, 2019, 294, 15914-15931.	1.6	59
13	Regulation of Integrin Î±IIbÎ²3 Activation by Distinct Regions of Its Cytoplasmic Tails. Biochemistry, 2006, 45, 6656-6662.	1.2	58
14	Nanodiscs and solution NMR: preparation, application and challenges. Nanotechnology Reviews, 2017, 6, 111-125.	2.6	50
15	NMR as a Unique Tool in Assessment and Complex Determination of Weak Proteinâ€“Protein Interactions. Topics in Current Chemistry, 2011, 326, 35-45.	4.0	48
16	The butyrophilin 3A1 intracellular domain undergoes a conformational change involving the juxtamembrane region. FASEB Journal, 2017, 31, 4697-4706.	0.2	41
17	Proteinâ€“protein interactions probed by nuclear magnetic resonance spectroscopy. Methods in Enzymology, 2001, 339, 377-389.	0.4	34
18	Integrin Î²3 Crosstalk with VEGFR Accommodating Tyrosine Phosphorylation as a Regulatory Switch. PLoS ONE, 2012, 7, e31071.	1.1	34

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19	Bipartite Topology of Treponema pallidum Repeat Proteins C/D and I. Journal of Biological Chemistry, 2015, 290, 12313-12331.	1.6	30
20	Optimization of the design and preparation of nanoscale phospholipid bilayers for its application to solution NMR. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1222-1231.	1.5	28
21	Phosphinophosphonates and Their Tris-pivaloyloxymethyl Prodrugs Reveal a Negatively Cooperative Butyrophilin Activation Mechanism. Journal of Medicinal Chemistry, 2017, 60, 2373-2382.	2.9	28
22	Integrin Î²3 Phosphorylation Dictates Its Complex with the Shc Phosphotyrosine-binding (PTB) Domain. Journal of Biological Chemistry, 2010, 285, 34875-34884.	1.6	27
23	Tyrosine Phosphorylation as a Conformational Switch. Journal of Biological Chemistry, 2011, 286, 40943-40953.	1.6	27
24	Ligand-induced interactions between butyrophilin 2A1 and 3A1 internal domains in the HMBPP receptor complex. Cell Chemical Biology, 2022, 29, 985-995.e5.	2.5	19
25	NMR-Based Amide Hydrogenâ€“Deuterium Exchange Measurements for Complex Membrane Proteins: Development and Critical Evaluation. Journal of Magnetic Resonance, 2000, 142, 111-119.	1.2	18
26	NMR solution structure of human cannabinoid receptor-1 helix 7/8 peptide: Candidate electrostatic interactions and microdomain formation. Biochemical and Biophysical Research Communications, 2009, 390, 441-446.	1.0	18
27	A Membrane Setting for the Sorting Motifs Present in the Adenovirus E3-13.7 Protein Which Down-regulates the Epidermal Growth Factor Receptor. Journal of Biological Chemistry, 1998, 273, 17343-17350.	1.6	17
28	Structural biology of human cannabinoid receptor-2 helix 6 in membrane-mimetic environments. Biochemical and Biophysical Research Communications, 2009, 384, 243-248.	1.0	17
29	The Solution Structure of <i>Bacillus anthracis</i> Dihydrofolate Reductase Yields Insight into the Analysis of Structureâˆ’Activity Relationships for Novel Inhibitors. Biochemistry, 2009, 48, 4100-4108.	1.2	13
30	Characterization of the Neuron-Specific L1-CAM Cytoplasmic Tail: Naturally Disordered in Solution It Exercises Different Binding Modes for Different Adaptor Proteins. Biochemistry, 2008, 47, 4160-4168.	1.2	12
31	Structural Insight into the Interaction between Platelet Integrin Î±IIbÎ²3 and Cytoskeletal Protein Skelemin. Journal of Biological Chemistry, 2007, 282, 32349-32356.	1.6	11
32	The major outer sheath protein forms distinct conformers and multimeric complexes in the outer membrane and periplasm of Treponema denticola. Scientific Reports, 2017, 7, 13260.	1.6	10
33	Investigation of the adaptor protein PLIC-2 in multiple pathways. Biochemistry and Biophysics Reports, 2017, 9, 341-348.	0.7	8
34	Structural studies of a signal peptide in complex with signal peptidase I cytoplasmic domain: The stabilizing effect of membraneâ€mimetics on the acquired fold. Proteins: Structure, Function and Bioinformatics, 2012, 80, 807-817.	1.5	7
35	New Horizons in Structural Biology of Membrane Proteins: Experimental Evaluation of the Role of Conformational Dynamics and Intrinsic Flexibility. Membranes, 2022, 12, 227.	1.4	6
36	NMR structural characterization of the pentaâ€peptide calpain inhibitor. FEBS Letters, 2009, 583, 135-140.	1.3	5

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37	Phospho-Tyrosine(s) vs. Phosphatidylinositol Binding in Shc Mediated Integrin Signaling. American Journal of Molecular Biology, 2015, 05, 17-31.	0.1	5
38	Structural insights into the recognition of Î²₃ integrin cytoplasmic tail by the SH3 domain of Src kinase. Protein Science, 2013, 22, 1358-1365.	3.1	4
39	The Anti-Inflammatory Protein TNIP1 Is Intrinsically Disordered with Structural Flexibility Contributed by Its AHD1-UBAN Domain. Biomolecules, 2020, 10, 1531.	1.8	4
40	Targeting Integrin-Dependent Adhesion and Signaling with 3-Arylquinoline and 3-Aryl-2-Quinolone Derivatives: A new Class of Integrin Antagonists. PLoS ONE, 2015, 10, e0141205.	1.1	4
41	Skelemin Association with Î±_{IIb}Î²₃ Integrin: A Structural Model. Biochemistry, 2014, 53, 6766-6775.	1.2	3
42	Expression of Cellulolytic Enzyme as a Fusion Protein That Reacts Specifically With a Polymeric Scaffold. Methods in Enzymology, 2017, 590, 259-276.	0.4	2
43	Binding and backbone dynamics of protein under topological constraint: calmodulin as a model system. Chemical Communications, 2018, 54, 8917-8920.	2.2	2
44	Synthesis and Biological Evaluation of a Phosphonate Phosphoantigen Prodrug. Phosphorus, Sulfur and Silicon and the Related Elements, 2015, 190, 751-753.	0.8	1
45	Intrinsic disorder in integral membrane proteins. Progress in Molecular Biology and Translational Science, 2021, 183, 101-134.	0.9	1