Monika Oberer

List of Publications by Year in descending order

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56
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126907
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docs citations

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5608
citing authors

#	Article	IF	Citations
1	Residues of the minimal sequence of G0S2 collectively contribute to ATGL inhibition while C-and N-terminal extensions promote binding to ATGL. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2022, 1867, 159105.	2.4	7
2	Small-Molecule Inhibitors Targeting Lipolysis in Human Adipocytes. Journal of the American Chemical Society, 2022, 144, 6237-6250.	13.7	16
3	ATGL is a biosynthetic enzyme for fatty acid esters of hydroxy fatty acids. Nature, 2022, 606, 968-975.	27.8	57
4	Structural Changes in the Cap of Rv0183/mtbMGL Modulate the Shape of the Binding Pocket. Biomolecules, 2021, 11, 1299.	4.0	2
5	Optimized expression and purification of adipose triglyceride lipase improved hydrolytic and transacylation activities inÂvitro. Journal of Biological Chemistry, 2021, 297, 101206.	3.4	13
6	Carboxylesterase 2 proteins are efficient diglyceride and monoglyceride lipases possibly implicated in metabolic disease. Journal of Lipid Research, 2021, 62, 100075.	4.2	23
7	Protein-protein interactions regulate the activity of Adipose Triglyceride Lipase in intracellular lipolysis. Biochimie, 2020, 169, 62-68.	2.6	22
8	The lipid-droplet-associated protein ABHD5 protects the heart through proteolysis of HDAC4. Nature Metabolism, 2019, 1, 1157-1167.	11.9	42
9	Characterization of Vibrio choleraeâ€™s Extracellular Nuclease Xds. Frontiers in Microbiology, 2019, 10, 2057.	3.5	13
10	The Î±/Î²-hydrolase domain-containing 4- and 5-related phospholipase Pummelig controls energy storage in Drosophila. Journal of Lipid Research, 2019, 60, 1365-1378.	4.2	7
11	Identification of lipases with activity towards monoacylglycerol by criterion of conserved cap architectures. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2018, 1863, 679-687.	2.4	8
12	Hypoxia-inducible lipid droplet-associated protein inhibits adipose triglyceride lipase. Journal of Lipid Research, 2018, 59, 531-541.	4.2	60
13	The crystal structure of monoacylglycerol lipase from M. tuberculosis reveals the basis for specific inhibition. Scientific Reports, 2018, 8, 8948.	3.3	23
14	Lipid droplet subset targeting of the Drosophila protein CG2254/dmLdsdh1. Journal of Cell Science, 2017, 130, 3141-3157.	2.0	21
15	Adipose Triglyceride Lipase Regulation: An Overview. Current Protein and Peptide Science, 2017, 19, 221-233.	1.4	70
16	GPIHBP1 and Plasma Triglyceride Metabolism. Trends in Endocrinology and Metabolism, 2016, 27, 455-469.	7.1	67
17	Monoacylglycerol Lipases Act as Evolutionarily Conserved Regulators of Non-oxidative Ethanol Metabolism. Journal of Biological Chemistry, 2016, 291, 11865-11875.	3.4	14
18	Crystal structure of the Saccharomyces cerevisiae monoglyceride lipase Yju3p. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2016, 1861, 462-470.	2.4	25

#	ARTICLE	IF	CITATIONS
19	Fatty Acid-binding Proteins Interact with Comparative Gene Identification-58 Linking Lipolysis with Lipid Ligand Shuttling. Journal of Biological Chemistry, 2015, 290, 18438-18453.	3.4	49
20	Purification, crystallization and preliminary X-ray diffraction analysis of a soluble variant of the monoglyceride lipase Yju3p from the yeastSaccharomyces cerevisiae. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 243-246.	0.8	2
21	<i>GPIHBP1</i> Missense Mutations Often Cause Multimerization of GPIHBP1 and Thereby Prevent Lipoprotein Lipase Binding. Circulation Research, 2015, 116, 624-632.	4.5	50
22	CGI-58/ABHD5 is phosphorylated on Ser239 by protein kinase A: control of subcellular localization. Journal of Lipid Research, 2015, 56, 109-121.	4.2	60
23	Structure of a CGI-58 Motif Provides the Molecular Basis of Lipid Droplet Anchoring. Journal of Biological Chemistry, 2015, 290, 26361-26372.	3.4	43
24	G0/G1 Switch Gene 2 Regulates Cardiac Lipolysis. Journal of Biological Chemistry, 2015, 290, 26141-26150.	3.4	28
25	A Peptide Derived from G0/G1 Switch Gene 2 Acts as Noncompetitive Inhibitor of Adipose Triglyceride Lipase. Journal of Biological Chemistry, 2014, 289, 32559-32570.	3.4	39
26	Identification of promiscuous ene-reductase activity by mining structural databases using active site constellations. Nature Communications, 2014, 5, 4150.	12.8	67
27	Adipose triglyceride lipase activity is inhibited by long-chain acyl-coenzyme A. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2014, 1841, 588-594.	2.4	50
28	Structure and Catalytic Regulatory Function of Ubiquitin Specific Protease 11 N-Terminal and Ubiquitin-like Domains. Biochemistry, 2014, 53, 2966-2978.	2.5	34
29	Resonance assignments of the microtubule-binding domain of the C. elegans spindle and kinetochore-associated protein 1. Biomolecular NMR Assignments, 2014, 8, 275-278.	0.8	5
30	The evolutionary conserved protein CG9186 is associated with lipid droplets, required for their positioning and for fat storage. Journal of Cell Science, 2013, 126, 2198-212.	2.0	48
31	Conformational Plasticity and Ligand Binding of Bacterial Monoacylglycerol Lipase. Journal of Biological Chemistry, 2013, 288, 31093-31104.	3.4	44
32	G0/G1 switch gene-2 regulates human adipocyte lipolysis by affecting activity and localization of adipose triglyceride lipase. Journal of Lipid Research, 2012, 53, 2307-2317.	4.2	88
33	The structure of monoacylglycerol lipase from Bacillus sp. H257 reveals unexpected conservation of the cap architecture between bacterial and human enzymes. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2012, 1821, 1012-1021.	2.4	40
34	Adiponutrin Functions as a Nutritionally Regulated Lysophosphatidic Acid Acyltransferase. Cell Metabolism, 2012, 15, 691-702.	16.2	258
35	The Kinetochore-Bound Ska1 Complex Tracks Depolymerizing Microtubules and Binds to Curved Protofilaments. Developmental Cell, 2012, 23, 968-980.	7.0	194
36	The Kinetochore-Bound Ska1 Complex Tracks Depolymerizing Microtubules and Binds to Curved Protofilaments. Developmental Cell, 2012, 23, 1081.	7.0	0

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37	Lipolysis â€“ A highly regulated multi-enzyme complex mediates the catabolism of cellular fat stores. Progress in Lipid Research, 2011, 50, 14-27.	11.6	519
38	The Minimal Domain of Adipose Triglyceride Lipase (ATGL) Ranges until Leucine 254 and Can Be Activated and Inhibited by CGI-58 and G0S2, Respectively. PLoS ONE, 2011, 6, e26349.	2.5	76
39	Recent insights into the structure and function of comparative gene identification-58. Current Opinion in Lipidology, 2011, 22, 149-158.	2.7	36
40	The N-terminal Region of Comparative Gene Identification-58 (CGI-58) Is Important for Lipid Droplet Binding and Activation of Adipose Triglyceride Lipase. Journal of Biological Chemistry, 2010, 285, 12289-12298.	3.4	94
41	Identification of Yju3p as functional orthologue of mammalian monoglyceride lipase in the yeast Saccharomyces cerevisiae. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2010, 1801, 1063-1071.	2.4	54
42	Mammalian patatin domain containing proteins: a family with diverse lipolytic activities involved in multiple biological functions. Journal of Lipid Research, 2009, 50, S63-S68.	4.2	275
43	Topology and Regulation of the Human eIF4A/4G/4H Helicase Complex in Translation Initiation. Cell, 2009, 136, 447-460.	28.9	205
44	The C-terminal Region of Human Adipose Triglyceride Lipase Affects Enzyme Activity and Lipid Droplet Binding. Journal of Biological Chemistry, 2008, 283, 17211-17220.	3.4	133
45	Selective Pharmacological Targeting of a DEAD Box RNA Helicase. PLoS ONE, 2008, 3, e1583.	2.5	111
46	The solution structure of ParD, the antidote of the ParDE toxinâ€“antitoxin module, provides the structural basis for DNA and toxin binding. Protein Science, 2007, 16, 1676-1688.	7.6	66
47	Structural Basis for Nucleic Acid and Toxin Recognition of the Bacterial Antitoxin CcdA. Journal of Molecular Biology, 2006, 364, 170-185.	4.2	119
48	Functional characterization of IRESes by an inhibitor of the RNA helicase eIF4A. Nature Chemical Biology, 2006, 2, 213-220.	8.0	317
49	RNA-Mediated Sequestration of the RNA Helicase eIF4A by Pateamine A Inhibits Translation Initiation. Chemistry and Biology, 2006, 13, 1287-1295.	6.0	144
50	Structural basis for the enhancement of eIF4A helicase activity by eIF4G. Genes and Development, 2005, 19, 2212-2223.	5.9	137
51	Crystallization and preliminary structure determination of the C-terminal truncated domain of the S-layer protein SbsC. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1466-1468.	2.5	22
52	X-filtering for a range of coupling constants: application to the detection of intermolecular NOEs. Journal of Magnetic Resonance, 2003, 160, 97-106.	2.1	10
53	The anti-toxin ParD of plasmid RK2 consists of two structurally distinct moieties and belongs to the ribbon-helix-helix family of DNA-binding proteins. Biochemical Journal, 2002, 361, 41-47.	3.7	36
54	The anti-toxin ParD of plasmid RK2 consists of two structurally distinct moieties and belongs to the ribbon-helix-helix family of DNA-binding proteins. Biochemical Journal, 2002, 361, 41.	3.7	27

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55	Pure-Phase Selective Excitation in Fast-Relaxing Systems. Journal of Magnetic Resonance, 2001, 152, 48-56.	2.1	12
56	Thermodynamic Properties and DNA Binding of the ParD Protein from the Broad Host-Range Plasmid RK2/RP4 Killing System. Biological Chemistry, 1999, 380, 1413-20.	2.5	30