

# Oleg V Krokhin

## List of Publications by Year in descending order

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58  
papers

1,811  
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304743

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276875

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59  
docs citations

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times ranked

2211  
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteomic Shifts Reflecting Oxidative Stress and Reduced Capacity for Protein Synthesis, and Alterations to Mitochondrial Membranes in <i>Neurospora crassa</i> Lacking VDAC. <i>Microorganisms</i> , 2022, 10, 198.	3.6	2
2	Retention Time Prediction for TMT-Labeled Peptides in Proteomic LC-MS Experiments. <i>Journal of Proteome Research</i> , 2022, 21, 1218-1228.	3.7	5
3	Confident Identification of Citrullination and Carbamylation Assisted by Peptide Retention Time Prediction. <i>Journal of Proteome Research</i> , 2021, 20, 1571-1581.	3.7	12
4	Analysis of the <i>Yarrowia lipolytica</i> proteome reveals subtle variations in expression levels between lipogenic and non-lipogenic conditions. <i>FEMS Yeast Research</i> , 2021, 21, .	2.3	1
5	Disrupting Tryptophan in the Central Hydrophobic Region Selectively Mitigates Immunomodulatory Activities of the Innate Defence Regulator Peptide IDR-1002. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 6696-6705.	6.4	4
6	Sequence-Specific Model for Predicting Peptide Collision Cross Section Values in Proteomic Ion Mobility Spectrometry. <i>Journal of Proteome Research</i> , 2021, 20, 3600-3610.	3.7	12
7	Peptide retention time prediction for peptides with post-translational modifications: N-terminal ( $\beta$ -amine) and lysine ( $\beta$ -amine) acetylation. <i>Journal of Chromatography A</i> , 2021, 1657, 462584.	3.7	6
8	Peptide separation selectivity in proteomics LC-MS experiments: Comparison of formic and mixed formic/heptafluorobutyric acids ion-pairing modifiers. <i>Journal of Separation Science</i> , 2020, 43, 3830-3839.	2.5	7
9	Separation Orthogonality in Liquid Chromatography-Mass Spectrometry for Proteomic Applications: Comparison of 16 Different Two-Dimensional Combinations. <i>Analytical Chemistry</i> , 2020, 92, 3904-3912.	6.5	25
10	Peptide retention time prediction in hydrophilic interaction liquid chromatography: Zwitter-ionic sulfoalkylbetaine and phosphorylcholine stationary phases. <i>Journal of Chromatography A</i> , 2020, 1619, 460909.	3.7	16
11	Immunomodulatory Functions of the Human Cathelicidin LL-37 (aa 13-31)-Derived Peptides are Associated with Predicted $\beta$ -Helical Propensity and Hydrophobic Index. <i>Biomolecules</i> , 2019, 9, 501.	4.0	12
12	Retention Time Prediction for Glycopeptides in Reversed-Phase Chromatography for Glycoproteomic Applications. <i>Analytical Chemistry</i> , 2019, 91, 13360-13366.	6.5	29
13	Genomic comparison of facultatively anaerobic and obligatory aerobic <i>Caldibacillus debilis</i> strains GB1 and Tf helps explain physiological differences. <i>Canadian Journal of Microbiology</i> , 2019, 65, 421-428.	1.7	0
14	Universal retention standard for peptide separations using various modes of high-performance liquid chromatography. <i>Journal of Chromatography A</i> , 2019, 1588, 163-168.	3.7	14
15	Capillary Zone Electrophoresis-Tandem Mass Spectrometry for Large-Scale Phosphoproteomics with the Production of over 11,000 Phosphopeptides from the Colon Carcinoma HCT116 Cell Line. <i>Analytical Chemistry</i> , 2019, 91, 2201-2208.	6.5	27
16	Description of a cryptic thermophilic (pro)phage, CBP1 from <i>Caldibacillus debilis</i> strain GB1. <i>Extremophiles</i> , 2018, 22, 203-209.	2.3	1
17	Peptide retention time prediction in hydrophilic interaction liquid chromatography. Comparison of separation selectivity between bare silica and bonded stationary phases. <i>Journal of Chromatography A</i> , 2018, 1534, 75-84.	3.7	20
18	Retention Order Reversal of Phosphorylated and Unphosphorylated Peptides in Reversed-Phase LC/MS. <i>Analytical Sciences</i> , 2018, 34, 1037-1041.	1.6	8

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19	A metabolic and genomic assessment of sugar fermentation profiles of the thermophilic Thermotogales, <i>Fervidobacterium pennivorans</i> . <i>Extremophiles</i> , 2018, 22, 965-974.	2.3	6
20	Absolute Quantitation of Glycoforms of Two Human IgG Subclasses Using Synthetic Fc Peptides and Glycopeptides. <i>Journal of the American Society for Mass Spectrometry</i> , 2018, 29, 1086-1098.	2.8	13
21	Predicting Electrophoretic Mobility of Tryptic Peptides for High-Throughput CZE-MS Analysis. <i>Analytical Chemistry</i> , 2017, 89, 2000-2008.	6.5	43
22	A deletion variant partially complements a porin-less strain of <i>Neurospora crassa</i> . <i>Biochemistry and Cell Biology</i> , 2017, 95, 318-327.	2.0	5
23	Investigating Acquisition Performance on the Orbitrap Fusion When Using Tandem MS/MS/MS Scanning with Isobaric Tags. <i>Journal of Proteome Research</i> , 2017, 16, 1839-1846.	3.7	20
24	Evaluating the Characteristics of Reporter Ion Signal Acquired in the Orbitrap Analyzer for Isobaric Mass Tag Proteome Quantification Experiments. <i>Journal of Proteome Research</i> , 2017, 16, 1831-1838.	3.7	8
25	Peptide Retention Time Prediction in Hydrophilic Interaction Liquid Chromatography: Data Collection Methods and Features of Additive and Sequence-Specific Models. <i>Analytical Chemistry</i> , 2017, 89, 5526-5533.	6.5	24
26	Understanding aerobic/anaerobic metabolism in <i>Caldibacillus debilis</i> through a comparison with model organisms. <i>Systematic and Applied Microbiology</i> , 2017, 40, 245-253.	2.8	8
27	Comparison of peptide retention prediction algorithm in reversed-phase chromatography. Comment on "Predictive chromatography of peptides and proteins as a complementary tool for proteomics" by I. A. Tarasova, C. D. Masselon, A. V. Gorshkov and M. V. Gorshkov, <i>Analyst</i> , 2016, 141, 4816. <i>Analyst</i> , The, 2017, 142, 2050-2051.	3.5	1
28	Sequence-Specific Model for Peptide Retention Time Prediction in Strong Cation Exchange Chromatography. <i>Analytical Chemistry</i> , 2017, 89, 11795-11802.	6.5	32
29	A proteomic evaluation of urinary changes associated with cardiopulmonary bypass. <i>Clinical Proteomics</i> , 2016, 13, 17.	2.1	8
30	Transcriptomic and proteomic analyses of core metabolism in <i>Clostridium termitidis</i> CT1112 during growth on $\beta$ -cellulose, xylan, cellobiose and xylose. <i>BMC Microbiology</i> , 2016, 16, 91.	3.3	22
31	Global changes in the proteome of <i>Cupriavidus necator</i> H16 during poly-(3-hydroxybutyrate) synthesis from various biodiesel by-product substrates. <i>AMB Express</i> , 2016, 6, 36.	3.0	34
32	Generation of accurate peptide retention data for targeted and data independent quantitative LC-MS analysis: Chromatographic lessons in proteomics. <i>Proteomics</i> , 2016, 16, 2931-2936.	2.2	7
33	3D HPLC-MS with Reversed-Phase Separation Functionality in All Three Dimensions for Large-Scale Bottom-Up Proteomics and Peptide Retention Data Collection. <i>Analytical Chemistry</i> , 2016, 88, 2847-2855.	6.5	43
34	Chromatographic behavior of peptides containing oxidized methionine residues in proteomic LC-MS experiments: Complex tale of a simple modification. <i>Journal of Proteomics</i> , 2015, 125, 131-139.	2.4	20
35	Retention projection enables accurate calculation of liquid chromatographic retention times across labs and methods. <i>Journal of Chromatography A</i> , 2015, 1412, 43-51.	3.7	47
36	Quantitative proteomic analysis of the cellulolytic system of <i>Clostridium termitidis</i> CT1112 reveals distinct protein expression profiles upon growth on $\beta$ -cellulose and cellobiose. <i>Journal of Proteomics</i> , 2015, 125, 41-53.	2.4	12

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37	Proteomic Analysis of Reprogramming of Mesenchymal Stem/Stromal Cells (MSC) Following Interferon Gamma Identifies Pathways That Are Upregulated in Suppression. <i>Blood</i> , 2015, 126, 384-384.	1.4	1
38	Quantitative $\omega$ -Omics Analyses of Medium Chain Length Polyhydroxyalkanoate Metabolism in <i>Pseudomonas putida</i> LS46 Cultured with Waste Glycerol and Waste Fatty Acids. <i>PLoS ONE</i> , 2015, 10, e0142322.	2.5	21
39	N-Capping Motifs Promote Interaction of Amphipathic Helical Peptides with Hydrophobic Surfaces and Drastically Alter Hydrophobicity Values of Individual Amino Acids. <i>Analytical Chemistry</i> , 2014, 86, 11498-11502.	6.5	23
40	In situ activity-based protein profiling of serine hydrolases in <i>E. coli</i> . <i>EuPA Open Proteomics</i> , 2014, 4, 18-24.	2.5	4
41	Reduced catabolic protein expression in <i>Clostridium butyricum</i> DSM 10702 correlate with reduced 1,3-propanediol synthesis at high glycerol loading. <i>AMB Express</i> , 2014, 4, 63.	3.0	23
42	Mass spectrometry analysis of gingival crevicular fluid in the presence of external root resorption. <i>American Journal of Orthodontics and Dentofacial Orthopedics</i> , 2014, 145, 787-798.	1.7	35
43	The effect of various S-alkylating agents on the chromatographic behavior of cysteine-containing peptides in reversed-phase chromatography. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2013, 915-916, 57-63.	2.3	14
44	Unifying Expression Scale for Peptide Hydrophobicity in Proteomic Reversed Phase High-Pressure Liquid Chromatography Experiments. <i>Analytical Chemistry</i> , 2013, 85, 10878-10886.	6.5	10
45	Defining intrinsic hydrophobicity of amino acids' side chains in random coil conformation. Reversed-phase liquid chromatography of designed synthetic peptides vs. random peptide data sets. <i>Journal of Chromatography A</i> , 2011, 1218, 6348-6355.	3.7	15
46	Effect of cyclization of N-terminal glutamine and carbamidomethyl-cysteine (residues) on the chromatographic behavior of peptides in reversed-phase chromatography. <i>Journal of Chromatography A</i> , 2011, 1218, 5101-5107.	3.7	19
47	Predicting Peptide Retention Times for Proteomics. <i>Current Protocols in Bioinformatics</i> , 2010, 31, Unit 13.14.	25.8	20
48	Predicting Retention Time Shifts Associated with Variation of the Gradient Slope in Peptide RP-HPLC. <i>Analytical Chemistry</i> , 2010, 82, 9678-9685.	6.5	33
49	Peptide Retention Standards and Hydrophobicity Indexes in Reversed-Phase High-Performance Liquid Chromatography of Peptides. <i>Analytical Chemistry</i> , 2009, 81, 9522-9530.	6.5	137
50	Practical Implementation of 2D HPLC Scheme with Accurate Peptide Retention Prediction in Both Dimensions for High-Throughput Bottom-Up Proteomics. <i>Analytical Chemistry</i> , 2008, 80, 7036-7042.	6.5	155
51	Triticum mosaic virus: A New Virus Isolated from Wheat in Kansas. <i>Plant Disease</i> , 2008, 92, 808-817.	1.4	83
52	Sequence-Specific Retention Calculator. A Family of Peptide Retention Time Prediction Algorithms in Reversed-Phase HPLC: Applicability to Various Chromatographic Conditions and Columns. <i>Analytical Chemistry</i> , 2007, 79, 8762-8768.	6.5	89
53	Deamidation of -Asn-Gly- Sequences during Sample Preparation for Proteomics: Consequences for MALDI and HPLC-MALDI Analysis. <i>Analytical Chemistry</i> , 2006, 78, 6645-6650.	6.5	161
54	Sequence-Specific Retention Calculator. Algorithm for Peptide Retention Prediction in Ion-Pair RP-HPLC: Application to 300- and 100-Å... Pore Size C18 Sorbents. <i>Analytical Chemistry</i> , 2006, 78, 7785-7795.	6.5	213

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55	Use of Peptide Retention Time Prediction for Protein Identification by off-line Reversed-Phase HPLC-MALDI MS/MS. Analytical Chemistry, 2006, 78, 6265-6269.	6.5	75
56	MALDI QqTOF MS combined with off-line HPLC for characterization of protein primary structure and post-translational modifications. Journal of Biomolecular Techniques, 2005, 16, 429-40.	1.5	18
57	Site-specific N-glycosylation analysis: matrix-assisted laser desorption/ionization quadrupole-quadrupole time-of-flight tandem mass spectral signatures for recognition and identification of glycopeptides. Rapid Communications in Mass Spectrometry, 2004, 18, 2020-2030.	1.5	70
58	Characterizing degradation products of peptides containing N-terminal Cys residues by (off-line) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6 time-of-flight measurements. Rapid Communications in Mass Spectrometry, 2003, 17, 2528-2534.	1.5	38