Oleg V Krokhin

List of Publications by Year
in descending order

58 papers	1,811 citations	304743 22 h-index	276875 41 g-index
59 all docs	59 docs citations	59 times ranked	2211 citing authors

#	Article	IF	Citations
1	Sequence-Specific Retention Calculator. Algorithm for Peptide Retention Prediction in Ion-Pair RP-HPLC:Â Application to 300- and 100-Ã... Pore Size C18 Sorbents. Analytical Chemistry, 2006, 78, 7785-7795.	6.5	213
2	Deamidation of -Asn-Gly- Sequences during Sample Preparation for Proteomics:Â Consequences for MALDI and HPLC-MALDI Analysis. Analytical Chemistry, 2006, 78, 6645-6650.	6.5	161
3	Practical Implementation of 2D HPLC Scheme with Accurate Peptide Retention Prediction in Both Dimensions for High-Throughput Bottom-Up Proteomics. Analytical Chemistry, 2008, 80, 7036-7042.	6.5	155
4	Peptide Retention Standards and Hydrophobicity Indexes in Reversed-Phase High-Performance Liquid Chromatography of Peptides. Analytical Chemistry, 2009, 81, 9522-9530.	6.5	137
5	Sequence-Specific Retention Calculator. A Family of Peptide Retention Time Prediction Algorithms in Reversed-Phase HPLC:â€‰ Applicability to Various Chromatographic Conditions and Columns. Analytical Chemistry, 2007, 79, 8762-8768.	6.5	89
6	Triticum mosaic virus: A New Virus Isolated from Wheat in Kansas. Plant Disease, 2008, 92, 808-817.	1.4	83
7	Use of Peptide Retention Time Prediction for Protein Identification by off-line Reversed-Phase HPLCâˆ’MALDI MS/MS. Analytical Chemistry, 2006, 78, 6265-6269.	6.5	75
8	Site-specificN-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
9	Retention projection enables accurate calculation of liquid chromatographic retention times across labs and methods. Journal of Chromatography A, 2015, 1412, 43-51.	3.7	47
10	3D HPLC-MS with Reversed-Phase Separation Functionality in All Three Dimensions for Large-Scale Bottom-Up Proteomics and Peptide Retention Data Collection. Analytical Chemistry, 2016, 88, 2847-2855.	6.5	43
11	Predicting Electrophoretic Mobility of Tryptic Peptides for High-Throughput CZE-MS Analysis. Analytical Chemistry, 2017, 89, 2000-2008.	6.5	43
12	Characterizing degradation products of peptides containing N-terminal Cys residues by (off-line) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 30 time-of-flight measurements. Rapid Communications in Mass Spectrometry, 2003, 17, 2528-2534.	1.5	38
13	Mass spectrometry analysis of gingival crevicular fluid in the presence of external root resorption. American Journal of Orthodontics and Dentofacial Orthopedics, 2014, 145, 787-798.	1.7	35
14	Global changes in the proteome of Cupriavidus necator H16 during poly-(3-hydroxybutyrate) synthesis from various biodiesel by-product substrates. AMB Express, 2016, 6, 36.	3.0	34
15	Predicting Retention Time Shifts Associated with Variation of the Gradient Slope in Peptide RP-HPLC. Analytical Chemistry, 2010, 82, 9678-9685.	6.5	33
16	Sequence-Specific Model for Peptide Retention Time Prediction in Strong Cation Exchange Chromatography. Analytical Chemistry, 2017, 89, 11795-11802.	6.5	32
17	Retention Time Prediction for Glycopeptides in Reversed-Phase Chromatography for Glycoproteomic Applications. Analytical Chemistry, 2019, 91, 13360-13366.	6.5	29
18	Capillary Zone Electrophoresisâ€"Tandem Mass Spectrometry for Large-Scale Phosphoproteomics with the Production of over 11,000 Phosphopeptides from the Colon Carcinoma HCT116 Cell Line. Analytical Chemistry, 2019, 91, 2201-2208.	6.5	27

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19	Separation Orthogonality in Liquid Chromatographyâ€"Mass Spectrometry for Proteomic Applications: Comparison of 16 Different Two-Dimensional Combinations. Analytical Chemistry, 2020, 92, 3904-3912.	6.5	25
20	Peptide Retention Time Prediction in Hydrophilic Interaction Liquid Chromatography: Data Collection Methods and Features of Additive and Sequence-Specific Models. Analytical Chemistry, 2017, 89, 5526-5533.	6.5	24
21	N-Capping Motifs Promote Interaction of Amphipathic Helical Peptides with Hydrophobic Surfaces and Drastically Alter Hydrophobicity Values of Individual Amino Acids. Analytical Chemistry, 2014, 86, 11498-11502.	6.5	23
22	Reduced catabolic protein expression in Clostridium butyricum DSM 10702 correlate with reduced 1,3-propanediol synthesis at high glycerol loading. AMB Express, 2014, 4, 63.	3.0	23
23	Transcriptomic and proteomic analyses of core metabolism in Clostridium termitidis CT1112 during growth on Î±-cellulose, xylan, cellobiose and xylose. BMC Microbiology, 2016, 16, 91.	3.3	22
24	Quantitative â€˜Omics Analyses of Medium Chain Length Polyhydroxyalkanaote Metabolism in Pseudomonas putida LS46 Cultured with Waste Glycerol and Waste Fatty Acids. PLoS ONE, 2015, 10, e0142322.	2.5	21
25	Predicting Peptide Retention Times for Proteomics. Current Protocols in Bioinformatics, 2010, 31, Unit 13.14.	25.8	20
26	Chromatographic behavior of peptides containing oxidized methionine residues in proteomic LCâ€"MS experiments: Complex tale of a simple modification. Journal of Proteomics, 2015, 125, 131-139.	2.4	20
27	Investigating Acquisition Performance on the Orbitrap Fusion When Using Tandem MS/MS/MS Scanning with Isobaric Tags. Journal of Proteome Research, 2017, 16, 1839-1846.	3.7	20
28	Peptide retention time prediction in hydrophilic interaction liquid chromatography. Comparison of separation selectivity between bare silica and bonded stationary phases. Journal of Chromatography A, 2018, 1534, 75-84.	3.7	20
29	Effect of cyclization of N-terminal glutamine and carbamidomethyl-cysteine (residues) on the chromatographic behavior of peptides in reversed-phase chromatography. Journal of Chromatography A, 2011, 1218, 5101-5107.	3.7	19
30	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
31	Peptide retention time prediction in hydrophilic interaction liquid chromatography: Zwitter-ionic sulfoalkylbetaine and phosphorylcholine stationary phases. Journal of Chromatography A, 2020, 1619, 460909.	3.7	16
32	Defining intrinsic hydrophobicity of amino acidsâ€™ side chains in random coil conformation. Reversed-phase liquid chromatography of designed synthetic peptides vs. random peptide data sets. Journal of Chromatography A, 2011, 1218, 6348-6355.	3.7	15
33	The effect of various S-alkylating agents on the chromatographic behavior of cysteine-containing peptides in reversed-phase chromatography. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2013, 915-916, 57-63.	2.3	14
34	Universal retention standard for peptide separations using various modes of high-performance liquid chromatography. Journal of Chromatography A, 2019, 1588, 163-168.	3.7	14
35	Absolute Quantitation of Glycoforms of Two Human IgG Subclasses Using Synthetic Fc Peptides and Glycopeptides. Journal of the American Society for Mass Spectrometry, 2018, 29, 1086-1098.	2.8	13
36	Quantitative proteomic analysis of the cellulolytic system of Clostridium termitidis CT1112 reveals distinct protein expression profiles upon growth on Î±-cellulose and cellobiose. Journal of Proteomics, 2015, 125, 41-53.	2.4	12

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37	Immunomodulatory Functions of the Human Cathelicidin LL-37 (aa 13–31)-Derived Peptides are Associated with Predicted α-Helical Propensity and Hydrophobic Index. Biomolecules, 2019, 9, 501.	4.0	12
38	Confident Identification of Citrullination and Carbamylation Assisted by Peptide Retention Time Prediction. Journal of Proteome Research, 2021, 20, 1571-1581.	3.7	12
39	Sequence-Specific Model for Predicting Peptide Collision Cross Section Values in Proteomic Ion Mobility Spectrometry. Journal of Proteome Research, 2021, 20, 3600-3610.	3.7	12
40	Unifying Expression Scale for Peptide Hydrophobicity in Proteomic Reversed Phase High-Pressure Liquid Chromatography Experiments. Analytical Chemistry, 2013, 85, 10878-10886.	6.5	10
41	A proteomic evaluation of urinary changes associated with cardiopulmonary bypass. Clinical Proteomics, 2016, 13, 17.	2.1	8
42	Evaluating the Characteristics of Reporter Ion Signal Acquired in the Orbitrap Analyzer for Isobaric Mass Tag Proteome Quantification Experiments. Journal of Proteome Research, 2017, 16, 1831-1838.	3.7	8
43	Understanding aerobic/anaerobic metabolism in Caldibacillus debilis through a comparison with model organisms. Systematic and Applied Microbiology, 2017, 40, 245-253.	2.8	8
44	Retention Order Reversal of Phosphorylated and Unphosphorylated Peptides in Reversed-Phase LC/MS. Analytical Sciences, 2018, 34, 1037-1041.	1.6	8
45	Generation of accurate peptide retention data for targeted and data independent quantitative LC-MS analysis: Chromatographic lessons in proteomics. Proteomics, 2016, 16, 2931-2936.	2.2	7
46	Peptide separation selectivity in proteomics LC–MS experiments: Comparison of formic and mixed formic/heptafluorobutyric acids ion–pairing modifiers. Journal of Separation Science, 2020, 43, 3830-3839.	2.5	7
47	A metabolic and genomic assessment of sugar fermentation profiles of the thermophilic Thermotogales, Fervidobacterium pennivorans. Extremophiles, 2018, 22, 965-974.	2.3	6
48	Peptide retention time prediction for peptides with post-translational modifications: N-terminal (α-amine) and lysine (ε-amine) acetylation. Journal of Chromatography A, 2021, 1657, 462584.	3.7	6
49	A deletion variant partially complements a porin-less strain of Neurospora crassa. Biochemistry and Cell Biology, 2017, 95, 318-327.	2.0	5
50	Retention Time Prediction for TMT-Labeled Peptides in Proteomic LC-MS Experiments. Journal of Proteome Research, 2022, 21, 1218-1228.	3.7	5
51	In situ activity-based protein profiling of serine hydrolases in E. coli. EuPA Open Proteomics, 2014, 4, 18-24.	2.5	4
52	Disrupting Tryptophan in the Central Hydrophobic Region Selectively Mitigates Immunomodulatory Activities of the Innate Defence Regulator Peptide IDR-1002. Journal of Medicinal Chemistry, 2021, 64, 6696-6705.	6.4	4
53	Proteomic Shifts Reflecting Oxidative Stress and Reduced Capacity for Protein Synthesis, and Alterations to Mitochondrial Membranes in Neurospora crassa Lacking VDAC. Microorganisms, 2022, 10, 198.	3.6	2
54	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, Analyst, 2016, 141, 4816. Analyst, The, 2017, 142, 2050-2051.	3.5	1

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55	Description of a cryptic thermophilic (pro)phage, CBP1 from Caldibacillus debilis strain GB1. Extremophiles, 2018, 22, 203-209.	2.3	1
56	Analysis of the Yarrowia lipolytica proteome reveals subtle variations in expression levels between lipogenic and non-lipogenic conditions. FEMS Yeast Research, 2021, 21, .	2.3	1
57	Proteomic Analysis of Reprograming of Mesenchymal Stem/Stromal Cells (MSC) Following Interferon Gamma Identifies Pathways That Are Upregulated in Suppression. Blood, 2015, 126, 384-384.	1.4	1
58	Genomic comparison of facultatively anaerobic and obligatory aerobic Caldibacillus debilis strains GB1 and Tf helps explain physiological differences. Canadian Journal of Microbiology, 2019, 65, 421-428.	1.7	0