

# Feng Ge

## List of Publications by Year in descending order

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93  
papers

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147566

31  
h-index

189595

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94  
all docs

94  
docs citations

94  
times ranked

4412  
citing authors

| #  | ARTICLE  | IF  | CITATIONS |
|----|--|-----|-----------|
| 1  | Systematic Survey of the Regulatory Networks of the Long Noncoding RNA BANCR in Cervical Cancer Cells. <i>Journal of Proteome Research</i> , 2022, 21, 1137-1152.  | 1.8 | 5         |
| 2  | Acetylation-dependent SAGA complex dimerization promotes nucleosome acetylation and gene transcription. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 261-273.  | 3.6 | 15        |
| 3  | Sinhcafa€dependent histone deacetylation is essential for primordial germ cell specification. <i>EMBO Reports</i> , 2022, 23, e54387.  | 2.0 | 4         |
| 4  | Proteogenomic Characterization of the Pathogenic Fungus <i>Aspergillus flavus</i> Reveals Novel Genes Involved in Aflatoxin Production. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100013.                 | 2.5 | 5         |
| 5  | A novel phosphoinositide kinase Fab1 regulates biosynthesis of pathogenic aflatoxin in <i>Aspergillus flavus</i> . <i>Virulence</i> , 2021, 12, 96-113.  | 1.8 | 11        |
| 6  | Nanoscale Imaging of RNA-Protein Interactions with a Photoactivatable Trimolecular Fluorescence Complementation System. <i>ACS Chemical Biology</i> , 2021, 16, 1003-1010.   | 1.6 | 3         |
| 7  | Ras subfamily GTPases regulate development, aflatoxin biosynthesis and pathogenicity in the fungus <i>Aspergillus flavus</i> . <i>Environmental Microbiology</i> , 2021, 23, 5334-5348.                              | 1.8 | 8         |
| 8  | Long noncoding RNA HOTAIR interacts with Y-Box Protein-1 (YBX1) to regulate cell proliferation. <i>Life Science Alliance</i> , 2021, 4, e202101139.  | 1.3 | 16        |
| 9  | Quantitative Proteomics Reveals the Protein Regulatory Network of <i>Anabaena</i> sp. PCC 7120 under Nitrogen Deficiency. <i>Journal of Proteome Research</i> , 2021, 20, 3963-3976.                                 | 1.8 | 6         |
| 10 | Proteogenomic Analysis Provides Novel Insight into Genome Annotation and Nitrogen Metabolism in <i>Nostoc</i> sp. PCC 7120. <i>Microbiology Spectrum</i> , 2021, 9, e0049021.  | 1.2 | 5         |
| 11 | Improving the Genome Annotation of <i>Rhizoctonia solani</i> Using Proteogenomics. <i>Current Genomics</i> , 2021, 22, 373-383.  | 0.7 | 1         |
| 12 | Structural and Functional Insights into a Lysine Deacylase in the Cyanobacterium <i>Synechococcus</i> sp. PCC 7002. <i>Plant Physiology</i> , 2020, 184, 762-776.  | 2.3 | 6         |
| 13 | Characterization of Lysine Monomethylome and Methyltransferase in Model Cyanobacterium <i>Synechocystis</i> sp. PCC 6803. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 289-304.                        | 3.0 | 6         |
| 14 | Antioxidant-related catalase CTA1 regulates development, aflatoxin biosynthesis, and virulence in pathogenic fungus <i>Aspergillus flavus</i> . <i>Environmental Microbiology</i> , 2020, 22, 2792-2810.             | 1.8 | 35        |
| 15 | The circular RNA CDR1as regulate cell proliferation via TMED2 and TMED10. <i>BMC Cancer</i> , 2020, 20, 312.   | 1.1 | 14        |
| 16 | Lysine acetylation contributes to development, aflatoxin biosynthesis and pathogenicity in <i>Aspergillus flavus</i> . <i>Environmental Microbiology</i> , 2019, 21, 4792-4807.                                      | 1.8 | 27        |
| 17 | Lysine Propionylation is a Widespread Post-Translational Modification Involved in Regulation of Photosynthesis and Metabolism in Cyanobacteria. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4792. | 1.8 | 12        |
| 18 | Comparative iTRAQ proteomics revealed proteins associated with lobed fin regeneration in Bichirs. <i>Proteome Science</i> , 2019, 17, 6.   | 0.7 | 0         |

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|----|---|-----|-----------|
| 19 | Effects of PSII Manganese-Stabilizing Protein Succinylation on Photosynthesis in the Model Cyanobacterium <i>Synechococcus</i> sp. PCC 7002. <i>Plant and Cell Physiology</i> , 2018, 59, 1466-1482.  | 1.5 | 8         |
| 20 | Lysine Succinylation Contributes to Aflatoxin Production and Pathogenicity in <i>Aspergillus flavus</i> . <i>Molecular and Cellular Proteomics</i> , 2018, 17, 457-471.   | 2.5 | 59        |
| 21 | Integrated Proteomic and Transcriptomic Analysis Reveals Long Noncoding RNA HOX Transcript Antisense Intergenic RNA (HOTAIR) Promotes Hepatocellular Carcinoma Cell Proliferation by Regulating Opioid Growth Factor Receptor (OGFr). <i>Molecular and Cellular Proteomics</i> , 2018, 17, 146-159. | 2.5 | 33        |
| 22 | Genome Annotation of a Model Diatom <i>Phaeodactylum tricornutum</i> Using an Integrated Proteogenomic Pipeline. <i>Molecular Plant</i> , 2018, 11, 1292-1307.  | 3.9 | 44        |
| 23 | Lysine Acetylome Analysis Reveals Photosystem II Manganese-stabilizing Protein Acetylation is Involved in Negative Regulation of Oxygen Evolution in Model Cyanobacterium <i>Synechococcus</i> sp. PCC 7002. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1297-1311.                        | 2.5 | 26        |
| 24 | Malonylome Analysis Reveals the Involvement of Lysine Malonylation in Metabolism and Photosynthesis in Cyanobacteria. <i>Journal of Proteome Research</i> , 2017, 16, 2030-2043.  | 1.8 | 28        |
| 25 | Properties of biodegradable poly(butylene succinate) (PBS) composites with carbon black. <i>Polymer Science - Series A</i> , 2017, 59, 416-424.   | 0.4 | 7         |
| 26 | Quantitative Proteomics Reveals the Regulatory Networks of Circular RNA CDR1as in Hepatocellular Carcinoma Cells. <i>Journal of Proteome Research</i> , 2017, 16, 3891-3902.  | 1.8 | 77        |
| 27 | Current Understanding of the TCTP Interactome. <i>Results and Problems in Cell Differentiation</i> , 2017, 64, 127-136.   | 0.2 | 9         |
| 28 | Quantitative Proteomics Analysis Reveals Novel Targets of miR-21 in Zebrafish Embryos. <i>Scientific Reports</i> , 2017, 7, 4022.   | 1.6 | 9         |
| 29 | Characterization of the Translationally Controlled Tumor Protein (TCTP) Interactome Reveals Novel Binding Partners in Human Cancer Cells. <i>Journal of Proteome Research</i> , 2016, 15, 3741-3751.  | 1.8 | 21        |
| 30 | GAPP: A Proteogenomic Software for Genome Annotation and Global Profiling of Post-translational Modifications in Prokaryotes. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3529-3539.   | 2.5 | 11        |
| 31 | Global Phosphoproteomic Analysis Reveals the Involvement of Phosphorylation in Aflatoxins Biosynthesis in the Pathogenic Fungus <i>Aspergillus flavus</i> . <i>Scientific Reports</i> , 2016, 6, 34078.   | 1.6 | 38        |
| 32 | Proteomic analysis of post translational modifications in cyanobacteria. <i>Journal of Proteomics</i> , 2016, 134, 57-64.   | 1.2 | 20        |
| 33 | Proteomics studies on stress responses in diatoms. <i>Proteomics</i> , 2015, 15, 3943-3953.   | 1.3 | 30        |
| 34 | CyanOmics: an integrated database of omics for the model cyanobacterium <i>Synechococcus</i> sp. PCC 7002. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, .  | 1.4 | 18        |
| 35 | Preparation of monoPEGylated Cyanovirin-N <sup>TM</sup> s derivative and its anti-influenza A virus bioactivity <i>in vitro</i> and <i>in vivo</i> . <i>Journal of Biochemistry</i> , 2015, 157, 539-548.   | 0.9 | 14        |
| 36 | Acetylome Analysis Reveals the Involvement of Lysine Acetylation in Photosynthesis and Carbon Metabolism in the Model Cyanobacterium <i>Synechocystis</i> sp. PCC 6803. <i>Journal of Proteome Research</i> , 2015, 14, 1275-1286.  | 1.8 | 119       |

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|----|--|-----|-----------|
| 37 | Succinylome Analysis Reveals the Involvement of Lysine Succinylation in Metabolism in Pathogenic <i>Mycobacterium tuberculosis</i> *. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 796-811.                                      | 2.5 | 117       |
| 38 | Unique diversity of the venom peptides from the scorpion <i>Androctonus bicolor</i> revealed by transcriptomic and proteomic analysis. <i>Journal of Proteomics</i> , 2015, 128, 231-250.  | 1.2 | 56        |
| 39 | Quantitative Proteomics Analysis Reveals Novel Insights into Mechanisms of Action of Long Noncoding RNA Hox Transcript Antisense Intergenic RNA (HOTAIR) in HeLa Cells*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1447-1463. | 2.5 | 44        |
| 40 | Integrated Transcriptomic and Proteomic Analysis of the Global Response of <i>Synechococcus</i> to High Light Stress*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1038-1053.   | 2.5 | 44        |
| 41 | Effects of Phosphorylation of $\hat{I}^2$ Subunits of Phycocyanins on State Transition in the Model Cyanobacterium <i>Synechocystis</i> sp. PCC 6803. <i>Plant and Cell Physiology</i> , 2015, 56, 1997-2013.                            | 1.5 | 37        |
| 42 | Systematic identification of arsenic-binding proteins reveals that hexokinase-2 is inhibited by arsenic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15084-15089.                | 3.3 | 126       |
| 43 | Desiccation enhances phosphorylation of <i>psbA</i> and affects the distribution of protein complexes in the thylakoid membrane. <i>Physiologia Plantarum</i> , 2015, 153, 492-502.  | 2.6 | 18        |
| 44 | YcgC represents a new protein deacetylase family in prokaryotes. <i>ELife</i> , 2015, 4, .   | 2.8 | 52        |
| 45 | <i>Mycobacterium Tuberculosis</i> Proteome Microarray for Global Studies of Protein Function and Immunogenicity. <i>Cell Reports</i> , 2014, 9, 2317-2329.   | 2.9 | 77        |
| 46 | Proteogenomic analysis and global discovery of posttranslational modifications in prokaryotes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E5633-42.                             | 3.3 | 55        |
| 47 | Acetylome Analysis Reveals Diverse Functions of Lysine Acetylation in <i>Mycobacterium tuberculosis</i> . <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3352-3366.  | 2.5 | 170       |
| 48 | Methylcrotonyl-CoA Carboxylase Regulates Triacylglycerol Accumulation in the Model Diatom <i>Phaeodactylum tricorutum</i> . <i>Plant Cell</i> , 2014, 26, 1681-1697.   | 3.1 | 136       |
| 49 | Phosphoproteomic Analysis of Protein Phosphorylation Networks in <i>Tetrahymena thermophila</i> , a Model Single-celled Organism. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 503-519.  | 2.5 | 21        |
| 50 | Phosphoproteomic Analysis Provides Novel Insights into Stress Responses in <i>Phaeodactylum tricorutum</i> , a Model Diatom. <i>Journal of Proteome Research</i> , 2014, 13, 2511-2523.  | 1.8 | 39        |
| 51 | Reduced plant nutrition under elevated CO <sub>2</sub> depresses the immunocompetence of cotton bollworm against its endoparasite. <i>Scientific Reports</i> , 2014, 4, 4538.  | 1.6 | 5         |
| 52 | Global Phosphoproteomic Analysis Reveals Diverse Functions of Serine/Threonine/Tyrosine Phosphorylation in the Model Cyanobacterium <i>Synechococcus</i> sp. Strain PCC 7002. <i>Journal of Proteome Research</i> , 2013, 12, 1909-1923. | 1.8 | 72        |
| 53 | Bcl2-associated Athanogene 3 Interactome Analysis Reveals a New Role in Modulating Proteasome Activity. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2804-2819.  | 2.5 | 62        |
| 54 | Quantitative proteomic strategies for the identification of microRNA targets. <i>Expert Review of Proteomics</i> , 2012, 9, 549-559.   | 1.3 | 22        |

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|----|--|-----|-----------|
| 55 | QUICK identification and SPR validation of signal transducers and activators of transcription 3 (Stat3) interacting proteins. <i>Journal of Proteomics</i> , 2012, 75, 1055-1066.        | 1.2 | 17        |
| 56 | Identification of Novel miR-21 Target Proteins in Multiple Myeloma Cells by Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2012, 11, 2078-2090.                          | 1.8 | 66        |
| 57 | 14-3-3 $\eta$ Interacts with Stat3 and Regulates Its Constitutive Activation in Multiple Myeloma Cells. <i>PLoS ONE</i> , 2012, 7, e29554.   | 1.1 | 25        |
| 58 | Phosphoproteome profile of human lung cancer cell line A549. <i>Molecular BioSystems</i> , 2011, 7, 472-479.   | 2.9 | 13        |
| 59 | Identification and evaluation of a panel of serum biomarkers for predicting response to thalidomide in multiple myeloma patients. <i>Expert Review of Proteomics</i> , 2011, 8, 439-442. | 1.3 | 3         |
| 60 | Quantitative Proteomic Analysis of Tumor Reversion in Multiple Myeloma Cells. <i>Journal of Proteome Research</i> , 2011, 10, 845-855.   | 1.8 | 22        |
| 61 | The C-terminus of MIP-T3 protein is required for ubiquitin-proteasome-mediated degradation in human cells. <i>FEBS Letters</i> , 2011, 585, 1350-1356.                                   | 1.3 | 4         |
| 62 | Antiviral activity and possible mechanisms of action of pentagalloylglucose (PGG) against influenza A virus. <i>Archives of Virology</i> , 2011, 156, 1359-1369.                         | 0.9 | 72        |
| 63 | Proteomic analysis of multiple myeloma: Current status and future perspectives. <i>Proteomics - Clinical Applications</i> , 2011, 5, 30-37.  | 0.8 | 11        |
| 64 | Subcellular proteomics revealed the epithelial $\rightarrow$ mesenchymal transition phenotype in lung cancer. <i>Proteomics</i> , 2011, 11, 429-439.                                     | 1.3 | 44        |
| 65 | Proteomics: addressing the challenges of multiple myeloma. <i>Acta Biochimica Et Biophysica Sinica</i> , 2011, 43, 89-95.  | 0.9 | 8         |
| 66 | Identification of ubiquitinated proteins from human multiple myeloma U266 cells by proteomics. <i>Biomedical and Environmental Sciences</i> , 2011, 24, 422-30.                          | 0.2 | 8         |
| 67 | Soluble cytoplasmic expression, rapid purification, and characterization of cyanovirin-N as a His-SUMO fusion. <i>Applied Microbiology and Biotechnology</i> , 2010, 85, 1051-1060.      | 1.7 | 35        |
| 68 | Phosphoproteomic analysis of primary human multiple myeloma cells. <i>Journal of Proteomics</i> , 2010, 73, 1381-1390.   | 1.2 | 25        |
| 69 | Proteomic analysis reveals novel binding partners of MIP $\alpha$ T3 in human cells. <i>Proteomics</i> , 2010, 10, 2337-2347.  | 1.3 | 14        |
| 70 | <i>In vitro</i> and <i>in vivo</i> antineoplastic activity of a novel bromopyrrole and its potential mechanism of action. <i>British Journal of Pharmacology</i> , 2010, 159, 909-918.   | 2.7 | 15        |
| 71 | Quantitative Phosphoproteomics of Proteasome Inhibition in Multiple Myeloma Cells. <i>PLoS ONE</i> , 2010, 5, e13095.  | 1.1 | 28        |
| 72 | A Cys/Ser mutation of NDPK-A stabilizes its oligomerization state and enhances its activity. <i>Journal of Biochemistry</i> , 2010, 148, 149-155.  | 0.9 | 5         |

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|----|---|-----|-----------|
| 73 | Quantitative Proteomics Analysis Reveals BAG3 as a Potential Target To Suppress Severe Acute Respiratory Syndrome Coronavirus Replication. <i>Journal of Virology</i> , 2010, 84, 6050-6059.        | 1.5 | 52        |
| 74 | Identification of Novel 14-3-3 $\sigma$ Interacting Proteins by Quantitative Immunoprecipitation Combined with Knockdown (QUICK). <i>Journal of Proteome Research</i> , 2010, 9, 5848-5858.         | 1.8 | 40        |
| 75 | Phosphoproteomic Analysis Reveals the Multiple Roles of Phosphorylation in Pathogenic Bacterium <i>Streptococcus pneumoniae</i> . <i>Journal of Proteome Research</i> , 2010, 9, 275-282.           | 1.8 | 164       |
| 76 | Proteomics of apoptosis of multiple myeloma cells induced by proteasome inhibitor PS-341. <i>Journal of Central South University (Medical Sciences)</i> , 2010, 35, 784-91.                         | 0.1 | 3         |
| 77 | Detection of Abundant Proteins in Multiple Myeloma Cells by Proteomics. <i>Journal of Proteomics and Bioinformatics</i> , 2010, 03, 005-009.  | 0.4 | 6         |
| 78 | Transcriptomic and proteomic approach to studying SNX2112-induced K562 cells apoptosis and anti-leukemia activity in K562 $\alpha$ NOD/SCID mice. <i>FEBS Letters</i> , 2009, 583, 1859-1866.       | 1.3 | 40        |
| 79 | Comparative proteomic analysis to discover potential therapeutic targets in human multiple myeloma. <i>Proteomics - Clinical Applications</i> , 2009, 3, 1348-1360.                                 | 0.8 | 21        |
| 80 | Proteomic and Functional Analyses Reveal a Dual Molecular Mechanism Underlying Arsenic-Induced Apoptosis in Human Multiple Myeloma Cells. <i>Journal of Proteome Research</i> , 2009, 8, 3006-3019. | 1.8 | 53        |
| 81 | Nm23-H1 regulates the proliferation and differentiation of the human chronic myeloid leukemia K562 cell line: A functional proteomics study. <i>Life Sciences</i> , 2009, 84, 458-467.              | 2.0 | 20        |
| 82 | Genomic and proteomic approaches for predicting toxicity and adverse drug reactions. <i>Expert Opinion on Drug Metabolism and Toxicology</i> , 2009, 5, 29-37.                                      | 1.5 | 19        |
| 83 | Ku86 exists as both a full-length and a protease-sensitive natural variant in multiple myeloma cells. <i>Cancer Cell International</i> , 2008, 8, 4.  | 1.8 | 9         |
| 84 | High-throughput assay using a GFP-expressing replicon for SARS-CoV drug discovery. <i>Antiviral Research</i> , 2008, 80, 107-113.   | 1.9 | 14        |
| 85 | Derivation of a novel SARS $\alpha$ coronavirus replicon cell line and its application for anti-SARS drug screening. <i>Virology</i> , 2007, 360, 150-158.  | 1.1 | 38        |
| 86 | Effects of Rare Earth Elements on the Growth of <i>Arnebia euchroma</i> Cells and the Biosynthesis of Shikonin. <i>Plant Growth Regulation</i> , 2006, 48, 283-290.                                 | 1.8 | 20        |
| 87 | Cell Growth and Shikonin Production of <i>Arnebia euchroma</i> in a Periodically Submerged Airlift Bioreactor. <i>Biotechnology Letters</i> , 2006, 28, 525-529.                                    | 1.1 | 16        |
| 88 | Construction of Double-Copy Glucose Isomerase Gene Engineering Strain of <i>Streptomyces diastaticus</i> by Homologous Recombination. <i>Current Microbiology</i> , 2002, 44, 273-279.              | 1.0 | 2         |
| 89 | Site-Specific Integration of the Double-Mutation Glucose Isomerase (GIG138PG247D) Gene in <i>Streptomyces lividans</i> and Its Stable Expression. <i>Current Microbiology</i> , 2002, 44, 18-24.    | 1.0 | 1         |
| 90 | Heterologous Expression of the Single-Mutation Glucose Isomerase (GIG138P) Gene in <i>Streptomyces lividans</i> and Its Genetic Instability. <i>Current Microbiology</i> , 2001, 42, 241-247.       | 1.0 | 3         |

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|----|--|-----|-----------|
| 91 | SIMULTANEOUS DETERMINATION OF GLUCOAMYLASE ACTIVITY AND GLUCOSE IN FERMENTATION PROCESS BASED ON SCREEN-PRINTED DISPOSABLE BIOSENSOR. <i>Analytical Letters</i> , 2001, 34, 79-90. | 1.0 | 5         |
| 92 | Simultaneous determination of maltose and glucose using a screen-printed electrode system. <i>Biosensors and Bioelectronics</i> , 1998, 13, 333-339.                               | 5.3 | 43        |
| 93 | Potassium Ferricyanide Mediated Disposable Biosensor for Determination of Maltose and Glucose. <i>Analytical Letters</i> , 1998, 31, 383-394.                                      | 1.0 | 11        |