

Denis C Shields

List of Publications by Year in descending order

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Version: 2024-02-01

129
papers

10,329
citations

50276

46
h-index

37204

96
g-index

130
all docs

130
docs citations

130
times ranked

16699
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Molecular evidence for an ancient duplication of the entire yeast genome. <i>Nature</i> , 1997, 387, 708-713. | 27.8 | 1,702 |
| 2 | Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018, 50, 1412-1425. | 21.4 | 924 |
| 3 | Codon usage patterns in <i>Escherichia coli</i> , <i>Bacillus subtilis</i> , <i>Saccharomyces cerevisiae</i> , <i>Schizosaccharomyces pombe</i> , <i>Drosophila melanogaster</i> and <i>Homo sapiens</i> ; a review of the considerable within-species diversity. <i>Nucleic Acids Research</i> , 1988, 16, 8207-8211. | 14.5 | 569 |
| 4 | Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. <i>Nature Genetics</i> , 2017, 49, 403-415. | 21.4 | 492 |
| 5 | Towards the Improved Discovery and Design of Functional Peptides: Common Features of Diverse Classes Permit Generalized Prediction of Bioactivity. <i>PLoS ONE</i> , 2012, 7, e45012. | 2.5 | 322 |
| 6 | Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. <i>Nature Genetics</i> , 2013, 45, 621-631. | 21.4 | 282 |
| 7 | Synonymous codon usage in <i>Bacillus subtilis</i> reflects both translational selection and mutational biases. <i>Nucleic Acids Research</i> , 1987, 15, 8023-8040. | 14.5 | 277 |
| 8 | Large-Scale Gene-Centric Meta-Analysis across 39 Studies Identifies Type 2 Diabetes Loci. <i>American Journal of Human Genetics</i> , 2012, 90, 410-425. | 6.2 | 239 |
| 9 | Large-Scale Gene-Centric Meta-analysis across 32 Studies Identifies Multiple Lipid Loci. <i>American Journal of Human Genetics</i> , 2012, 91, 823-838. | 6.2 | 227 |
| 10 | The "Thermolabile" Variant of Methylene tetrahydrofolate Reductase and Neural Tube Defects: An Evaluation of Genetic Risk and the Relative Importance of the Genotypes of the Embryo and the Mother. <i>American Journal of Human Genetics</i> , 1999, 64, 1045-1055. | 6.2 | 219 |
| 11 | Pharmacogenetic meta-analysis of genome-wide association studies of LDL cholesterol response to statins. <i>Nature Communications</i> , 2014, 5, 5068. | 12.8 | 216 |
| 12 | Homocysteine and Risk of Premature Coronary Heart Disease. <i>Circulation</i> , 1996, 94, 2154-2158. | 1.6 | 196 |
| 13 | Gene-centric Association Signals for Lipids and Apolipoproteins Identified via the HumanCVD BeadChip. <i>American Journal of Human Genetics</i> , 2009, 85, 628-642. | 6.2 | 183 |
| 14 | A novel approach of homozygous haplotype sharing identifies candidate genes in autism spectrum disorder. <i>Human Genetics</i> , 2012, 131, 565-579. | 3.8 | 180 |
| 15 | Blood Pressure Loci Identified with a Gene-Centric Array. <i>American Journal of Human Genetics</i> , 2011, 89, 688-700. | 6.2 | 159 |
| 16 | SLIMFinder: A Probabilistic Method for Identifying Over-Represented, Convergently Evolved, Short Linear Motifs in Proteins. <i>PLoS ONE</i> , 2007, 2, e967. | 2.5 | 143 |
| 17 | CPPpred: prediction of cell penetrating peptides. <i>Bioinformatics</i> , 2013, 29, 3094-3096. | 4.1 | 125 |
| 18 | Inhibition of dipeptidyl peptidase IV and xanthine oxidase by amino acids and dipeptides. <i>Food Chemistry</i> , 2013, 141, 644-653. | 8.2 | 124 |

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|----|---|------|-----------|
| 19 | Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. <i>American Journal of Human Genetics</i> , 2011, 88, 6-18. | 6.2 | 122 |
| 20 | The Evolution of the MAP Kinase Pathways: Coduplication of Interacting Proteins Leads to New Signaling Cascades. <i>Journal of Molecular Evolution</i> , 1999, 49, 567-582. | 1.8 | 117 |
| 21 | Structures of YAP protein domains reveal promising targets for development of new cancer drugs. <i>Seminars in Cell and Developmental Biology</i> , 2012, 23, 827-833. | 5.0 | 113 |
| 22 | In silico approaches to predict the potential of milk protein-derived peptides as dipeptidyl peptidase IV (DPP-IV) inhibitors. <i>Peptides</i> , 2014, 57, 43-51. | 2.4 | 113 |
| 23 | Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. <i>Journal of Clinical Investigation</i> , 2017, 127, 1798-1812. | 8.2 | 106 |
| 24 | MORGAM (an international pooling of cardiovascular cohorts). <i>International Journal of Epidemiology</i> , 2004, 34, 21-27. | 1.9 | 105 |
| 25 | SLiMDisc: short, linear motif discovery, correcting for common evolutionary descent. <i>Nucleic Acids Research</i> , 2006, 34, 3546-3554. | 14.5 | 101 |
| 26 | Preferential Transmission of Paternal Alleles at Risk Genes in Attention-Deficit/Hyperactivity Disorder. <i>American Journal of Human Genetics</i> , 2005, 77, 958-965. | 6.2 | 100 |
| 27 | Genome-wide association study of genetic determinants of LDL-c response to atorvastatin therapy: importance of Lp(a). <i>Journal of Lipid Research</i> , 2012, 53, 1000-1011. | 4.2 | 97 |
| 28 | SLiMPrints: conservation-based discovery of functional motif fingerprints in intrinsically disordered protein regions. <i>Nucleic Acids Research</i> , 2012, 40, 10628-10641. | 14.5 | 92 |
| 29 | Human Tissue Profiling with Multidimensional Protein Identification Technology. <i>Journal of Proteome Research</i> , 2005, 4, 1757-1767. | 3.7 | 81 |
| 30 | Bioinformatic discovery of novel bioactive peptides. , 2007, 3, 108-112. | | 73 |
| 31 | Predictive modelling of angiotensin converting enzyme inhibitory dipeptides. <i>Food Chemistry</i> , 2012, 133, 1349-1354. | 8.2 | 73 |
| 32 | Peptigram: A Web-Based Application for Peptidomics Data Visualization. <i>Journal of Proteome Research</i> , 2017, 16, 712-719. | 3.7 | 73 |
| 33 | Prediction of Short Linear Protein Binding Regions. <i>Journal of Molecular Biology</i> , 2012, 415, 193-204. | 4.2 | 71 |
| 34 | Evolutionary instability of CUG-Leu in the genetic code of budding yeasts. <i>Nature Communications</i> , 2018, 9, 1887. | 12.8 | 70 |
| 35 | Evidence for an allelic association between bipolar disorder and a Na ⁺ , K ⁺ adenosine triphosphatase alpha subunit gene (ATP1A3). <i>Biological Psychiatry</i> , 1998, 44, 47-51. | 1.3 | 69 |
| 36 | SLiMSearch 2.0: biological context for short linear motifs in proteins. <i>Nucleic Acids Research</i> , 2011, 39, W56-W60. | 14.5 | 68 |

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|----|---|------|-----------|
| 37 | ProVizâ€”a web-based visualization tool to investigate the functional and evolutionary features of protein sequences. <i>Nucleic Acids Research</i> , 2016, 44, W11-W15. | 14.5 | 68 |
| 38 | PeptideLocator: prediction of bioactive peptides in protein sequences. <i>Bioinformatics</i> , 2013, 29, 1120-1126. | 4.1 | 66 |
| 39 | SLiMFinder: a web server to find novel, significantly over-represented, short protein motifs. <i>Nucleic Acids Research</i> , 2010, 38, W534-W539. | 14.5 | 64 |
| 40 | Genetic Analysis of the Thermolabile Variant of 5,10-Methylenetetrahydrofolate Reductase as a Risk Factor for Ischemic Stroke. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 1999, 19, 208-211. | 2.4 | 63 |
| 41 | Genetic variation in glycoprotein IIb/IIIa (GPIIb/IIIa) as a determinant of the responses to an oral GPIIb/IIIa antagonist in patients with unstable coronary syndromes. <i>Blood</i> , 2001, 98, 3256-3260. | 1.4 | 61 |
| 42 | Short linear motif candidates in the cell entry system used by SARS-CoV-2 and their potential therapeutic implications. <i>Science Signaling</i> , 2021, 14, . | 3.6 | 61 |
| 43 | Switches in species-specific codon preferences: The influence of mutation biases. <i>Journal of Molecular Evolution</i> , 1990, 31, 71-80. | 1.8 | 60 |
| 44 | Masking residues using context-specific evolutionary conservation significantly improves short linear motif discovery. <i>Bioinformatics</i> , 2009, 25, 443-450. | 4.1 | 60 |
| 45 | Predicting the Important Enzymes in Human Breast Milk Digestion. <i>Journal of Agricultural and Food Chemistry</i> , 2014, 62, 7225-7232. | 5.2 | 55 |
| 46 | The SLiMDisc server: short, linear motif discovery in proteins. <i>Nucleic Acids Research</i> , 2007, 35, W455-W459. | 14.5 | 51 |
| 47 | Marked Variability in the Extent of Protein Disorder within and between Viral Families. <i>PLoS ONE</i> , 2013, 8, e60724. | 2.5 | 50 |
| 48 | EnzymePredictor: A Tool for Predicting and Visualizing Enzymatic Cleavages of Digested Proteins. <i>Journal of Proteome Research</i> , 2012, 11, 6056-6065. | 3.7 | 48 |
| 49 | CompariMotif: quick and easy comparisons of sequence motifs. <i>Bioinformatics</i> , 2008, 24, 1307-1309. | 4.1 | 47 |
| 50 | Renin Gene Polymorphisms and Haplotypes, Blood Pressure, and Responses to Renin-Angiotensin System Inhibition. <i>Hypertension</i> , 2007, 50, 340-347. | 2.7 | 41 |
| 51 | Following the Digestion of Milk Proteins from Mother to Baby. <i>Journal of Proteome Research</i> , 2014, 13, 5777-5783. | 3.7 | 41 |
| 52 | Integrating biomarkers across omic platforms: an approach to improve stratification of patients with indolent and aggressive prostate cancer. <i>Molecular Oncology</i> , 2018, 12, 1513-1525. | 4.6 | 41 |
| 53 | Gene conversion among chemokine receptors. <i>Gene</i> , 2000, 246, 239-245. | 2.2 | 39 |
| 54 | A genomeâ€”wide association study of recipient genotype and mediumâ€”term kidney allograft function. <i>Clinical Transplantation</i> , 2013, 27, 379-387. | 1.6 | 39 |

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|----|--|-----|-----------|
| 55 | Significantly Different Patterns of Amino Acid Replacement After Gene Duplication as Compared to After Speciation. <i>Molecular Biology and Evolution</i> , 2003, 20, 484-490. | 8.9 | 38 |
| 56 | Association of Methylenetetrahydrofolate Reductase Polymorphism and the Risk of Squamous Cell Carcinoma in Renal Transplant Patients. <i>Transplantation</i> , 2007, 84, 113-116. | 1.0 | 37 |
| 57 | Approved Drug Mimics of Short Peptide Ligands from Protein Interaction Motifs. <i>Journal of Chemical Information and Modeling</i> , 2008, 48, 1943-1948. | 5.4 | 35 |
| 58 | Shift in the isoelectric-point of milk proteins as a consequence of adaptive divergence between the milks of mammalian species. <i>Biology Direct</i> , 2011, 6, 40. | 4.6 | 35 |
| 59 | CycloPs: Generating Virtual Libraries of Cyclized and Constrained Peptides Including Nonnatural Amino Acids. <i>Journal of Chemical Information and Modeling</i> , 2011, 51, 829-836. | 5.4 | 34 |
| 60 | Platelet glycoprotein Ib alpha receptor polymorphisms and recurrent ischaemic events in acute coronary syndrome patients. <i>Journal of Thrombosis and Thrombolysis</i> , 2002, 13, 13-19. | 2.1 | 33 |
| 61 | Predicting Binding within Disordered Protein Regions to Structurally Characterised Peptide-Binding Domains. <i>PLoS ONE</i> , 2013, 8, e72838. | 2.5 | 33 |
| 62 | Uroplakin III is not a major candidate gene for primary vesicoureteral reflux. <i>European Journal of Human Genetics</i> , 2005, 13, 500-502. | 2.8 | 32 |
| 63 | Genetic polymorphisms in platelet-related proteins and coronary artery disease: investigation of candidate genes, including N-acetylgalactosaminyltransferase 4 (GALNT4) and sulphotransferase 1A1/2 (SULT1A1/2). <i>Journal of Thrombosis and Thrombolysis</i> , 2009, 27, 175-184. | 2.1 | 32 |
| 64 | Interactome-wide prediction of short, disordered protein interaction motifs in humans. <i>Molecular BioSystems</i> , 2012, 8, 282-295. | 2.9 | 30 |
| 65 | Meta-analysis of genome-wide association studies of HDL cholesterol response to statins. <i>Journal of Medical Genetics</i> , 2016, 53, 835-845. | 3.2 | 28 |
| 66 | Casein Hydrolysate with Glycemic Control Properties: Evidence from Cells, Animal Models, and Humans. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 4352-4363. | 5.2 | 28 |
| 67 | Estimation and efficient computation of the true probability of recurrence of short linear protein sequence motifs in unrelated proteins. <i>BMC Bioinformatics</i> , 2010, 11, 14. | 2.6 | 27 |
| 68 | A polymorphism in <i>ACE2</i> is associated with a lower risk for fatal cardiovascular events in females: the MORGAM project. <i>JRAAS - Journal of the Renin-Angiotensin-Aldosterone System</i> , 2011, 12, 504-509. | 1.7 | 27 |
| 69 | Computational Approaches to Developing Short Cyclic Peptide Modulators of Protein-Protein Interactions. <i>Methods in Molecular Biology</i> , 2015, 1268, 241-271. | 0.9 | 27 |
| 70 | Acquisition of multiple virulence/avirulence determinants by potato virus X (PVX) has occurred through convergent evolution rather than through recombination. <i>Virus Genes</i> , 2000, 20, 165-172. | 1.6 | 26 |
| 71 | Discovery of Small Molecule Inhibitors of Protein-Protein Interactions Using Combined Ligand and Target Score Normalization. <i>Journal of Chemical Information and Modeling</i> , 2009, 49, 2708-2717. | 5.4 | 26 |
| 72 | Evidence that mutation patterns vary among <i>Drosophila</i> transposable elements. <i>Journal of Molecular Biology</i> , 1989, 207, 843-846. | 4.2 | 24 |

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|----|---|-----|-----------|
| 73 | Genetic variability in the extracellular matrix as a determinant of cardiovascular risk: association of type III collagen COL3A1 polymorphisms with coronary artery disease. <i>Blood</i> , 2002, 100, 1220-1223. | 1.4 | 24 |
| 74 | Protein Disorder and Short Conserved Motifs in Disordered Regions Are Enriched near the Cytoplasmic Side of Single-Pass Transmembrane Proteins. <i>PLoS ONE</i> , 2012, 7, e44389. | 2.5 | 21 |
| 75 | The evolution of haematopoietic cytokine /receptor complexes. <i>Cytokine</i> , 1995, 7, 679-688. | 3.2 | 20 |
| 76 | The Impact on Coronary Artery Disease of Common Polymorphisms Known to Modulate Responses to Pathogens. <i>Annals of Human Genetics</i> , 2006, 70, 934-945. | 0.8 | 19 |
| 77 | Meta-Analysis To Test the Association of HIV-1 <i>nef</i> Amino Acid Differences and Deletions with Disease Progression. <i>Journal of Virology</i> , 2010, 84, 3644-3653. | 3.4 | 19 |
| 78 | SLiMScape: a protein short linear motif analysis plugin for Cytoscape. <i>BMC Bioinformatics</i> , 2013, 14, 224. | 2.6 | 19 |
| 79 | Analysis with the exome array identifies multiple new independent variants in lipid loci. <i>Human Molecular Genetics</i> , 2016, 25, 4094-4106. | 2.9 | 19 |
| 80 | A method to predict residues conferring functional differences between related proteins: Application to MAP kinase pathways. <i>Protein Science</i> , 2000, 9, 655-670. | 7.6 | 18 |
| 81 | Potential of known and short prokaryotic protein motifs as a basis for novel peptide-based antibacterial therapeutics: a computational survey. <i>Frontiers in Microbiology</i> , 2014, 5, 4. | 3.5 | 18 |
| 82 | Functional characterisation of the YIPF protein family in mammalian cells. <i>Histochemistry and Cell Biology</i> , 2017, 147, 439-451. | 1.7 | 18 |
| 83 | Enriching antimicrobial peptides from milk hydrolysates using pectin/alginate food-gels. <i>Food Chemistry</i> , 2021, 352, 129220. | 8.2 | 18 |
| 84 | Identification of Potential Small Molecule Peptidomimetics Similar to Motifs in Proteins. <i>Journal of Chemical Information and Modeling</i> , 2007, 47, 464-474. | 5.4 | 17 |
| 85 | Platelet signalling networks: Pathway perturbation demonstrates differential sensitivity of ADP secretion and fibrinogen binding. <i>Platelets</i> , 2012, 23, 17-25. | 2.3 | 17 |
| 86 | Genome-Wide Analysis of Blood Pressure Variability and Ischemic Stroke. <i>Stroke</i> , 2013, 44, 2703-2709. | 2.0 | 17 |
| 87 | Lack of evidence for a major locus for bipolar disorder in the pericentromeric region of chromosome 18 in Irish pedigrees. <i>Biological Psychiatry</i> , 1997, 42, 486-494. | 1.3 | 14 |
| 88 | Evaluation of Whether Accelerated Protein Evolution in Chordates Has Occurred before, after, or Simultaneously with Gene Duplication. <i>Molecular Biology and Evolution</i> , 2006, 24, 315-323. | 8.9 | 14 |
| 89 | Profile-based short linear protein motif discovery. <i>BMC Bioinformatics</i> , 2012, 13, 104. | 2.6 | 14 |
| 90 | Virtual Screening Using Combinatorial Cyclic Peptide Libraries Reveals Protein Interfaces Readily Targetable by Cyclic Peptides. <i>Journal of Chemical Information and Modeling</i> , 2015, 55, 600-613. | 5.4 | 14 |

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|-----|---|-----|-----------|
| 91 | Genetic stratification of pathogen-response-related and other variants within a homogeneous Caucasian Irish population. <i>European Journal of Human Genetics</i> , 2005, 13, 798-806. | 2.8 | 13 |
| 92 | Evolution of the isoelectric point of mammalian proteins as a consequence of indels and adaptive evolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 1635-1648. | 2.6 | 13 |
| 93 | Haplotypic analysis of tag SNPs of the interleukin-18 gene in relation to cardiovascular disease events: the MORGAM Project. <i>European Journal of Human Genetics</i> , 2008, 16, 1512-1520. | 2.8 | 12 |
| 94 | Peptide-Binding Domains: Are Limp Handshakes Safest?. <i>Science Signaling</i> , 2012, 5, pe40. | 3.6 | 12 |
| 95 | Implications of kappa-casein evolutionary diversity for the self-assembly and aggregation of casein micelles. <i>Royal Society Open Science</i> , 2019, 6, 190939. | 2.4 | 12 |
| 96 | Prediction of polyproline II secondary structure propensity in proteins. <i>Royal Society Open Science</i> , 2020, 7, 191239. | 2.4 | 12 |
| 97 | Differences in the Number of Intrinsically Disordered Regions between Yeast Duplicated Proteins, and Their Relationship with Functional Divergence. <i>PLoS ONE</i> , 2011, 6, e24989. | 2.5 | 12 |
| 98 | The CEPH consortium linkage map of human chromosome 2. <i>Genomics</i> , 1992, 14, 1055-1063. | 2.9 | 10 |
| 99 | The impact of genetic variation in the region of the GPIIIa gene, on PIA2 expression bias and GPIIb/IIIa receptor density in platelets. <i>British Journal of Haematology</i> , 2005, 132, 051220022257002. | 2.5 | 10 |
| 100 | Ligand Switching in Cell-Permeable Peptides: Manipulation of the α -Integrin Signature Motif. <i>ACS Chemical Biology</i> , 2009, 4, 457-471. | 3.4 | 9 |
| 101 | SCL-Epred: a generalised de novo eukaryotic protein subcellular localisation predictor. <i>Amino Acids</i> , 2013, 45, 291-299. | 2.7 | 9 |
| 102 | SLIMSearch: A Webserver for Finding Novel Occurrences of Short Linear Motifs in Proteins, Incorporating Sequence Context. <i>Lecture Notes in Computer Science</i> , 2010, , 50-61. | 1.3 | 9 |
| 103 | Amino acid enrichment and compositional changes among mammalian milk proteins and the resulting nutritional consequences. <i>Journal of Dairy Science</i> , 2014, 97, 1248-1258. | 3.4 | 8 |
| 104 | Peptides derived from cadherin juxtamembrane region inhibit platelet function. <i>Royal Society Open Science</i> , 2018, 5, 172347. | 2.4 | 8 |
| 105 | Web Server To Identify Similarity of Amino Acid Motifs to Compounds (SAAMCO). <i>Journal of Chemical Information and Modeling</i> , 2008, 48, 1524-1529. | 5.4 | 7 |
| 106 | Angiotensin converting enzyme and nitric oxide inhibitory activities of novel milk derived peptides. <i>International Dairy Journal</i> , 2014, 35, 38-42. | 3.0 | 7 |
| 107 | Design and Evaluation of Antimalarial Peptides Derived from Prediction of Short Linear Motifs in Proteins Related to Erythrocyte Invasion. <i>PLoS ONE</i> , 2015, 10, e0127383. | 2.5 | 7 |
| 108 | Impact of genetic variation in the 5-HT transporter and receptor on platelet function in patients with stable CAD taking aspirin. <i>Thrombosis Research</i> , 2016, 146, 51-55. | 1.7 | 7 |

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|-----|--|------|-----------|
| 109 | Genetic variants in PPARGC1B and CNTN4 are associated with thromboxane A2 formation and with cardiovascular event free survival in the Anglo-Scandinavian Cardiac Outcomes Trial (ASCOT). <i>Atherosclerosis</i> , 2018, 269, 42-49. | 0.8 | 7 |
| 110 | Computational Opportunities and Challenges in Finding Cyclic Peptide Modulators of Protein-Protein Interactions. <i>Methods in Molecular Biology</i> , 2019, 2001, 73-95. | 0.9 | 7 |
| 111 | Integrating Genotypic Data with Transcriptomic and Proteomic Data. <i>Comparative and Functional Genomics</i> , 2002, 3, 22-27. | 2.0 | 6 |
| 112 | Absolute Net Charge and the Biological Activity of Oligopeptides. <i>Journal of Chemical Information and Modeling</i> , 2006, 46, 2183-2190. | 5.4 | 5 |
| 113 | Lack of association between NFKBIL1/LTA polymorphisms and hypertension, myocardial infarct, unstable angina and stable angina in a large Irish population sample. <i>Atherosclerosis</i> , 2008, 197, 465-466. | 0.8 | 5 |
| 114 | Genome-wide epistatic expression quantitative trait loci discovery in four human tissues reveals the importance of local chromosomal interactions governing gene expression. <i>BMC Genomics</i> , 2015, 16, 109. | 2.8 | 5 |
| 115 | Optimal computational comparison of mass spectrometric peptide profiles of alternative hydrolysates from the same starting material. <i>LWT - Food Science and Technology</i> , 2016, 73, 296-302. | 5.2 | 5 |
| 116 | Computational and experimental analysis of bioactive peptide linear motifs in the integrin adhesome. <i>PLoS ONE</i> , 2019, 14, e0210337. | 2.5 | 5 |
| 117 | Prediction of Genetic Risks from Segregation Analyses of Morbid Risks. <i>Human Heredity</i> , 1994, 44, 52-55. | 0.8 | 4 |
| 118 | Cadherin juxtamembrane region derived peptides inhibit TGF β 1 induced gene expression. <i>Bioarchitecture</i> , 2014, 4, 103-110. | 1.5 | 4 |
| 119 | Discovering Anti-platelet Drug Combinations with an Integrated Model of Activator-Inhibitor Relationships, Activator-Activator Synergies and Inhibitor-Inhibitor Synergies. <i>PLoS Computational Biology</i> , 2015, 11, e1004119. | 3.2 | 4 |
| 120 | Resolving the Interactome of the Human Macrophage Immunometabolism Regulator (MACIR) with Enhanced Membrane Protein Preparation and Affinity Proteomics. <i>Proteomics</i> , 2020, 20, e2000062. | 2.2 | 4 |
| 121 | Coding of pointers in the segregation analysis program POINTER. <i>Genetic Epidemiology</i> , 1994, 11, 385-387. | 1.3 | 3 |
| 122 | Computational survey of peptides derived from disulphide-bonded protein loops that may serve as mediators of protein-protein interactions. <i>BMC Bioinformatics</i> , 2014, 15, 305. | 2.6 | 3 |
| 123 | Overdispersion of allele frequency differences between populations: implications for meta-analyses of genotypic disease associations. <i>European Journal of Human Genetics</i> , 2005, 13, 79-85. | 2.8 | 2 |
| 124 | Mapping Genes Within a YAC by Computer-Assisted Interpretation of Partial Restriction Digestions. <i>Nucleic Acids Research</i> , 1996, 24, 4495-4500. | 14.5 | 1 |
| 125 | A sequence sub-sampling algorithm increases the power to detect distant homologues. <i>Nucleic Acids Research</i> , 2005, 33, 3772-3778. | 14.5 | 1 |
| 126 | Correlation of disorder between <i>S. cerevisiae</i> interacting proteins. <i>Molecular BioSystems</i> , 2012, 8, 417-425. | 2.9 | 1 |

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|-----|--|-----|-----------|
| 127 | Coarse Master Equation-Based Analysis of N-Methylation and Temperature Effects on the Dynamics of Cyclic Peptides. <i>Biophysical Journal</i> , 2016, 110, 379a. | 0.5 | 1 |
| 128 | SLiMScape 3.x: a Cytoscape 3 app for discovery of Short Linear Motifs in protein interaction networks. <i>F1000Research</i> , 2015, 4, 477. | 1.6 | 1 |
| 129 | Computational modelling of chromosomally clustering protein domains in bacteria. <i>BMC Bioinformatics</i> , 2021, 22, 593. | 2.6 | 1 |