

Janet M Thornton

List of Publications by Year in descending order

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Version: 2024-02-01

408
papers

63,035
citations

1461

110
h-index

1096

239
g-index

541
all docs

541
docs citations

541
times ranked

65406
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | PDBe-KB: collaboratively defining the biological context of structural data. <i>Nucleic Acids Research</i> , 2022, 50, D534-D542. | 6.5 | 46 |
| 2 | <scp>PDBsum</scp> extras: <scp>SARSâ€CoV</scp>â€2 and <scp>AlphaFold</scp> models. <i>Protein Science</i> , 2022, 31, 283-289. | 3.1 | 42 |
| 3 | The impact of AlphaFold2 one year on. <i>Nature Methods</i> , 2022, 19, 15-20. | 9.0 | 107 |
| 4 | Srinivasan (1962â€2021) in Bioinformatics and beyond. <i>Bioinformatics</i> , 2022, 38, 2377-2379. | 1.8 | 2 |
| 5 | Conformational Variation in Enzyme Catalysis: A Structural Study on Catalytic Residues. <i>Journal of Molecular Biology</i> , 2022, 434, 167517. | 2.0 | 17 |
| 6 | GRaSP-web: a machine learning strategy to predict binding sites based on residue neighborhood graphs. <i>Nucleic Acids Research</i> , 2022, 50, W392-W397. | 6.5 | 7 |
| 7 | Capturing the geometry, function, and evolution of enzymes with <scp>3D</scp> templates. <i>Protein Science</i> , 2022, 31, . | 3.1 | 5 |
| 8 | Transposable Element Landscape in <i>Drosophila</i> Populations Selected for Longevity. <i>Genome Biology and Evolution</i> , 2021, 13, . | 1.1 | 6 |
| 9 | Data-driven identification of ageing-related diseases from electronic health records. <i>Scientific Reports</i> , 2021, 11, 2938. | 1.6 | 17 |
| 10 | Cell type-specific modulation of healthspan by Forkhead family transcription factors in the nervous system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, . | 3.3 | 9 |
| 11 | Impact of Structural Observables From Simulations to Predict the Effect of Single-Point Mutations in MHC Class II Peptide Binders. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 636562. | 1.6 | 3 |
| 12 | Transcriptomic profiling of long- and short-lived mutant mice implicates mitochondrial metabolism in ageing and shows signatures of normal ageing in progeroid mice. <i>Mechanisms of Ageing and Development</i> , 2021, 194, 111437. | 2.2 | 6 |
| 13 | Activating transcription factor 4-dependent lactate dehydrogenase activation as a protective response to amyloid beta toxicity. <i>Brain Communications</i> , 2021, 3, fcab053. | 1.5 | 9 |
| 14 | Common genetic associations between age-related diseases. <i>Nature Aging</i> , 2021, 1, 400-412. | 5.3 | 55 |
| 15 | Functional conservation in genes and pathways linking ageing and immunity. <i>Immunity and Ageing</i> , 2021, 18, 23. | 1.8 | 38 |
| 16 | A computational and structural analysis of germline and somatic variants affecting the DDR mechanism, and their impact on human diseases. <i>Scientific Reports</i> , 2021, 11, 14268. | 1.6 | 4 |
| 17 | The Enzyme Portal: an integrative tool for enzyme information and analysis. <i>FEBS Journal</i> , 2021, , . | 2.2 | 2 |
| 18 | AlphaFold heralds a data-driven revolution in biology and medicine. <i>Nature Medicine</i> , 2021, 27, 1666-1669. | 15.2 | 108 |

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|----|---|-----|-----------|
| 19 | PDBe-KB: a community-driven resource for structural and functional annotations. <i>Nucleic Acids Research</i> , 2020, 48, D344-D353. | 6.5 | 87 |
| 20 | VarSite: Disease variants and protein structure. <i>Protein Science</i> , 2020, 29, 111-119. | 3.1 | 77 |
| 21 | Identifying pseudoenzymes using functional annotation: pitfalls of common practice. <i>FEBS Journal</i> , 2020, 287, 4128-4140. | 2.2 | 19 |
| 22 | In conversation with Janet Thornton. <i>FEBS Journal</i> , 2020, 287, 4106-4113. | 2.2 | 5 |
| 23 | Temporal changes in the gene expression heterogeneity during brain development and aging. <i>Scientific Reports</i> , 2020, 10, 4080. | 1.6 | 34 |
| 24 | A global analysis of function and conservation of catalytic residues in enzymes. <i>Journal of Biological Chemistry</i> , 2020, 295, 314-324. | 1.6 | 68 |
| 25 | Structural analysis of pathogenic missense mutations in <i>GABRA2</i> and identification of a novel de novo variant in the desensitization gate. <i>Molecular Genetics & Genomic Medicine</i> , 2020, 8, e1106. | 0.6 | 9 |
| 26 | GRaSP: a graph-based residue neighborhood strategy to predict binding sites. <i>Bioinformatics</i> , 2020, 36, i726-i734. | 1.8 | 10 |
| 27 | An automated protocol for modelling peptide substrates to proteases. <i>BMC Bioinformatics</i> , 2020, 21, 586. | 1.2 | 7 |
| 28 | A community proposal to integrate structural bioinformatics activities in ELIXIR (3D-Bioinfo) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 382 T | 0.8 | 12 |
| 29 | Fine-tuning autophagy maximises lifespan and is associated with changes in mitochondrial gene expression in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2020, 16, e1009083. | 1.5 | 43 |
| 30 | A novel computational approach for predicting complex phenotypes in <i>Drosophila</i> (starvation-sensitive and sterile) by deriving their gene expression signatures from public data. <i>PLoS ONE</i> , 2020, 15, e0240824. | 1.1 | 0 |
| 31 | Title is missing!. , 2020, 15, e0240824. | | 0 |
| 32 | Title is missing!. , 2020, 15, e0240824. | | 0 |
| 33 | Title is missing!. , 2020, 15, e0240824. | | 0 |
| 34 | Title is missing!. , 2020, 15, e0240824. | | 0 |
| 35 | Emerging concepts in pseudoenzyme classification, evolution, and signaling. <i>Science Signaling</i> , 2019, 12, . | 1.6 | 80 |
| 36 | Screening for genes that accelerate the epigenetic aging clock in humans reveals a role for the H3K36 methyltransferase NSD1. <i>Genome Biology</i> , 2019, 20, 146. | 3.8 | 66 |

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|----|--|-----|-----------|
| 37 | Exploring Chemical Biosynthetic Design Space with Transform-MinER. ACS Synthetic Biology, 2019, 8, 2494-2506. | 1.9 | 16 |
| 38 | VarMap: a web tool for mapping genomic coordinates to protein sequence and structure and retrieving protein structural annotations. Bioinformatics, 2019, 35, 4854-4856. | 1.8 | 46 |
| 39 | Finding enzyme cofactors in Protein Data Bank. Bioinformatics, 2019, 35, 3510-3511. | 1.8 | 20 |
| 40 | Identifying Potential Ageing-Modulating Drugs In Silico. Trends in Endocrinology and Metabolism, 2019, 30, 118-131. | 3.1 | 15 |
| 41 | Using the drug-protein interactome to identify anti-ageing compounds for humans. PLoS Computational Biology, 2019, 15, e1006639. | 1.5 | 30 |
| 42 | CATH: expanding the horizons of structure-based functional annotations for genome sequences. Nucleic Acids Research, 2019, 47, D280-D284. | 6.5 | 131 |
| 43 | Exploring Enzyme Evolution from Changes in Sequence, Structure, and Function. Methods in Molecular Biology, 2019, 1851, 263-275. | 0.4 | 8 |
| 44 | The widespread increase in inter-individual variability of gene expression in the human brain with age. Aging, 2019, 11, 2253-2280. | 1.4 | 37 |
| 45 | Mechanism and Catalytic Site Atlas (M-CSA): a database of enzyme reaction mechanisms and active sites. Nucleic Acids Research, 2018, 46, D618-D623. | 6.5 | 151 |
| 46 | Ranking Enzyme Structures in the PDB by Bound Ligand Similarity to Biological Substrates. Structure, 2018, 26, 565-571.e3. | 1.6 | 23 |
| 47 | PDBsum: Structural summaries of PDB entries. Protein Science, 2018, 27, 129-134. | 3.1 | 910 |
| 48 | To what extent do structural changes in catalytic metal sites affect enzyme function?. Journal of Inorganic Biochemistry, 2018, 179, 40-53. | 1.5 | 55 |
| 49 | Transform-MinER: transforming molecules in enzyme reactions. Bioinformatics, 2018, 34, 3597-3599. | 1.8 | 10 |
| 50 | Gene expression-based drug repurposing to target aging. Aging Cell, 2018, 17, e12819. | 3.0 | 56 |
| 51 | Structural analysis of pathogenic mutations in the <i>DYRK1A</i> gene in patients with developmental disorders. Human Molecular Genetics, 2017, 26, ddw409. | 1.4 | 33 |
| 52 | Anna Tramontano 1957-2017. Nature Structural and Molecular Biology, 2017, 24, 431-432. | 3.6 | 2 |
| 53 | Drug repurposing for aging research using model organisms. Aging Cell, 2017, 16, 1006-1015. | 3.0 | 34 |
| 54 | Intestinal Fork Head Regulates Nutrient Absorption and Promotes Longevity. Cell Reports, 2017, 21, 641-653. | 2.9 | 41 |

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|----|---|-----|-----------|
| 55 | cuRRBS: simple and robust evaluation of enzyme combinations for reduced representation approaches. <i>Nucleic Acids Research</i> , 2017, 45, 11559-11569. | 6.5 | 14 |
| 56 | Understanding enzyme function evolution from a computational perspective. <i>Current Opinion in Structural Biology</i> , 2017, 47, 131-139. | 2.6 | 36 |
| 57 | Editorial overview: Catalysis and regulation. <i>Current Opinion in Structural Biology</i> , 2017, 47, vi-viii. | 2.6 | 0 |
| 58 | Protein structure and phenotypic analysis of pathogenic and population missense variants in <i>STXBP1</i> . <i>Molecular Genetics & Genomic Medicine</i> , 2017, 5, 495-507. | 0.6 | 29 |
| 59 | Direct Keap1-Nrf2 disruption as a potential therapeutic target for Alzheimer's disease. <i>PLoS Genetics</i> , 2017, 13, e1006593. | 1.5 | 102 |
| 60 | Reaction Decoder Tool (RDT): extracting features from chemical reactions. <i>Bioinformatics</i> , 2016, 32, 2065-2066. | 1.8 | 73 |
| 61 | Lithium Promotes Longevity through GSK3/NRF2-Dependent Hormesis. <i>Cell Reports</i> , 2016, 15, 638-650. | 2.9 | 163 |
| 62 | Chopping and Changing: the Evolution of the Flavin-dependent Monooxygenases. <i>Journal of Molecular Biology</i> , 2016, 428, 3131-3146. | 2.0 | 75 |
| 63 | Large-Scale Analysis Exploring Evolution of Catalytic Machineries and Mechanisms in Enzyme Superfamilies. <i>Journal of Molecular Biology</i> , 2016, 428, 253-267. | 2.0 | 55 |
| 64 | Integrating population variation and protein structural analysis to improve clinical interpretation of missense variation: application to the WD40 domain. <i>Human Molecular Genetics</i> , 2016, 25, 927-935. | 1.4 | 26 |
| 65 | Exploring the chemistry and evolution of the isomerases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 1796-1801. | 3.3 | 22 |
| 66 | Characterising Complex Enzyme Reaction Data. <i>PLoS ONE</i> , 2016, 11, e0147952. | 1.1 | 13 |
| 67 | The Evolution of Enzyme Mechanisms and Functional Diversity. <i>Biophysical Journal</i> , 2015, 108, 34a. | 0.2 | 0 |
| 68 | The Classification and Evolution of Enzyme Function. <i>Biophysical Journal</i> , 2015, 109, 1082-1086. | 0.2 | 95 |
| 69 | CATH: comprehensive structural and functional annotations for genome sequences. <i>Nucleic Acids Research</i> , 2015, 43, D376-D381. | 6.5 | 399 |
| 70 | Longevity GWAS Using the <i>Drosophila</i> Genetic Reference Panel. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2015, 70, 1470-1478. | 1.7 | 105 |
| 71 | The history of the CATH structural classification of protein domains. <i>Biochimie</i> , 2015, 119, 209-217. | 1.3 | 34 |
| 72 | SurvCurv database and online survival analysis platform update. <i>Bioinformatics</i> , 2015, 31, 3878-3880. | 1.8 | 13 |

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|----|--|-----|-----------|
| 73 | Proteins: interaction at a distance. IUCrJ, 2015, 2, 609-610. | 1.0 | 2 |
| 74 | Comparisons of Allergenic and Metazoan Parasite Proteins: Allergy the Price of Immunity. PLoS Computational Biology, 2015, 11, e1004546. | 1.5 | 43 |
| 75 | DAF-16/FoxO Directly Regulates an Atypical AMP-Activated Protein Kinase Gamma Isoform to Mediate the Effects of Insulin/IGF-1 Signaling on Aging in Caenorhabditis elegans. PLoS Genetics, 2014, 10, e1004109. | 1.5 | 55 |
| 76 | Comparison of the mammalian insulin signalling pathway to invertebrates in the context of FOXO-mediated ageing. Bioinformatics, 2014, 30, 2999-3003. | 1.8 | 15 |
| 77 | Molecular Basis for DPY-30 Association to COMPASS-like and NURF Complexes. Structure, 2014, 22, 1821-1830. | 1.6 | 40 |
| 78 | The Catalytic Site Atlas 2.0: cataloging catalytic sites and residues identified in enzymes. Nucleic Acids Research, 2014, 42, D485-D489. | 6.5 | 168 |
| 79 | The evolution of enzyme function in the isomerases. Current Opinion in Structural Biology, 2014, 26, 121-130. | 2.6 | 33 |
| 80 | PDBsum additions. Nucleic Acids Research, 2014, 42, D292-D296. | 6.5 | 279 |
| 81 | EC-BLAST: a tool to automatically search and compare enzyme reactions. Nature Methods, 2014, 11, 171-174. | 9.0 | 112 |
| 82 | Exploring the Biological and Chemical Complexity of the Ligases. Journal of Molecular Biology, 2014, 426, 2098-2111. | 2.0 | 11 |
| 83 | The European Bioinformatics Institute's data resources 2014. Nucleic Acids Research, 2014, 42, D18-D25. | 6.5 | 71 |
| 84 | MDL-1, a growth- and tumor-suppressor, slows aging and prevents germline hyperplasia and hypertrophy in C. elegans. Aging, 2014, 6, 98-117. | 1.4 | 27 |
| 85 | Analysing variation in <i>Drosophila</i> aging across independent experimental studies: a meta-analysis of survival data. Aging Cell, 2013, 12, 917-922. | 3.0 | 27 |
| 86 | Abstracting knowledge from the protein data bank. Biopolymers, 2013, 99, 183-188. | 1.2 | 6 |
| 87 | Transcriptional feedback in the insulin signalling pathway modulates ageing in both Caenorhabditis elegans and Drosophila melanogaster. Molecular BioSystems, 2013, 9, 1756. | 2.9 | 4 |
| 88 | Elucidating Human Phosphatase-Substrate Networks. Science Signaling, 2013, 6, rs10. | 1.6 | 145 |
| 89 | The EBI enzyme portal. Nucleic Acids Research, 2013, 41, D773-D780. | 6.5 | 19 |
| 90 | Amino Acid Changes in Disease-Associated Variants Differ Radically from Variants Observed in the 1000 Genomes Project Dataset. PLoS Computational Biology, 2013, 9, e1003382. | 1.5 | 54 |

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|-----|--|------|-----------|
| 91 | LigSearch: a knowledge-based web server to identify likely ligands for a protein target. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2395-2402. | 2.5 | 2 |
| 92 | Unlocking the potential of survival data for model organisms through a new database and online analysis platform: <sc>S</sc>urv<sc>C</sc>urv. <i>Aging Cell</i> , 2013, 12, 910-916. | 3.0 | 24 |
| 93 | Adenosine Triphosphate (ATP) Is a Candidate Signaling Molecule in the Mitochondria-to-Nucleus Retrograde Response Pathway. <i>Genes</i> , 2013, 4, 86-100. | 1.0 | 42 |
| 94 | Exploring the Evolution of Novel Enzyme Functions within Structurally Defined Protein Superfamilies. <i>PLoS Computational Biology</i> , 2012, 8, e1002403. | 1.5 | 80 |
| 95 | TORC2 Signaling Is Antagonized by Protein Phosphatase 2A and the Far Complex in <i>Saccharomyces cerevisiae</i>. <i>Genetics</i> , 2012, 190, 1325-1339. | 1.2 | 39 |
| 96 | FunTree: a resource for exploring the functional evolution of structurally defined enzyme superfamilies. <i>Nucleic Acids Research</i> , 2012, 40, D776-D782. | 6.5 | 44 |
| 97 | New functional families (FunFams) in CATH to improve the mapping of conserved functional sites to 3D structures. <i>Nucleic Acids Research</i> , 2012, 41, D490-D498. | 6.5 | 188 |
| 98 | Shouldn't enantiomeric purity be included in the 'minimum information about a bioactive entity? Response from the MIABE group. <i>Nature Reviews Drug Discovery</i> , 2012, 11, 730-730. | 21.5 | 0 |
| 99 | Current challenges in genome annotation through structural biology and bioinformatics. <i>Current Opinion in Structural Biology</i> , 2012, 22, 594-601. | 2.6 | 14 |
| 100 | Cell Proliferation and Migration Are Modulated by Cdk-1-Phosphorylated Endothelial-Monocyte Activating Polypeptide II. <i>PLoS ONE</i> , 2012, 7, e33101. | 1.1 | 4 |
| 101 | ELIXIR: a distributed infrastructure for European biological data. <i>Trends in Biotechnology</i> , 2012, 30, 241-242. | 4.9 | 78 |
| 102 | Endothelial-monocyte activating polypeptide II disrupts alveolar epithelial type II to type I cell transdifferentiation. <i>Respiratory Research</i> , 2012, 13, 1. | 1.4 | 53 |
| 103 | Using Answer Set Programming to Integrate RNA Expression with Signalling Pathway Information to Infer How Mutations Affect Ageing. <i>PLoS ONE</i> , 2012, 7, e50881. | 1.1 | 13 |
| 104 | The Metastasis-Promoting Phosphatase PRL-3 Shows Activity toward Phosphoinositides. <i>Biochemistry</i> , 2011, 50, 7579-7590. | 1.2 | 59 |
| 105 | Genome-wide dFOXO targets and topology of the transcriptomic response to stress and insulin signalling. <i>Molecular Systems Biology</i> , 2011, 7, 502. | 3.2 | 112 |
| 106 | Minimum information about a bioactive entity (MIABE). <i>Nature Reviews Drug Discovery</i> , 2011, 10, 661-669. | 21.5 | 80 |
| 107 | Characterizing the complexity of enzymes on the basis of their mechanisms and structures with a bio-computational analysis. <i>FEBS Journal</i> , 2011, 278, 3835-3845. | 2.2 | 30 |
| 108 | 1,000 structures and more from the MCSG. <i>BMC Structural Biology</i> , 2011, 11, 2. | 2.3 | 14 |

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|-----|---|-----|-----------|
| 109 | Extending CATH: increasing coverage of the protein structure universe and linking structure with function. <i>Nucleic Acids Research</i> , 2011, 39, D420-D426. | 6.5 | 126 |
| 110 | Computational biology for ageing. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2011, 366, 51-63. | 1.8 | 35 |
| 111 | The new science of ageing. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2011, 366, 6-8. | 1.8 | 24 |
| 112 | Domainâ€“ligand mapping for enzymes. <i>Journal of Molecular Recognition</i> , 2010, 23, 194-208. | 1.1 | 6 |
| 113 | The (non)malignancy of cancerous amino acidic substitutions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 518-529. | 1.5 | 15 |
| 114 | On the diversity of physicochemical environments experienced by identical ligands in binding pockets of unrelated proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 1120-1136. | 1.5 | 59 |
| 115 | Heme proteinsâ€“Diversity in structural characteristics, function, and folding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2349-2368. | 1.5 | 147 |
| 116 | <i>Molecular Sociology</i> . , 2010, , 23-28. | | 0 |
| 117 | The European Bioinformatics Institute's data resources. <i>Nucleic Acids Research</i> , 2010, 38, D17-D25. | 6.5 | 90 |
| 118 | Electrostatics of aquaporin and aquaglyceroporin channels correlates with their transport selectivity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 4135-4140. | 3.3 | 47 |
| 119 | Regulation of Lifespan, Metabolism, and Stress Responses by the <i>Drosophila</i> SH2B Protein, Lnk. <i>PLoS Genetics</i> , 2010, 6, e1000881. | 1.5 | 75 |
| 120 | The CoFactor database: organic cofactors in enzyme catalysis. <i>Bioinformatics</i> , 2010, 26, 2496-2497. | 1.8 | 57 |
| 121 | DamID in <i>C. elegans</i> reveals longevityâ€“associated targets of DAFâ€“16/FoxO. <i>Molecular Systems Biology</i> , 2010, 6, 399. | 3.2 | 122 |
| 122 | The Structures and Physicochemical Properties of Organic Cofactors in Biocatalysis. <i>Journal of Molecular Biology</i> , 2010, 403, 803-824. | 2.0 | 63 |
| 123 | PoreLogo: a new tool to analyse, visualize and compare channels in transmembrane proteins. <i>Bioinformatics</i> , 2009, 25, 3183-3184. | 1.8 | 11 |
| 124 | WSsas: a web service for the annotation of functional residues through structural homologues. <i>Bioinformatics</i> , 2009, 25, 1192-1194. | 1.8 | 17 |
| 125 | Predicting Protein Ligand Binding Sites by Combining Evolutionary Sequence Conservation and 3D Structure. <i>PLoS Computational Biology</i> , 2009, 5, e1000585. | 1.5 | 356 |
| 126 | PoreWalker: A Novel Tool for the Identification and Characterization of Channels in Transmembrane Proteins from Their Three-Dimensional Structure. <i>PLoS Computational Biology</i> , 2009, 5, e1000440. | 1.5 | 146 |

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|-----|---|------|-----------|
| 127 | Metal-MACiE: a database of metals involved in biological catalysis. <i>Bioinformatics</i> , 2009, 25, 2088-2089. | 1.8 | 73 |
| 128 | The CATH classification revisited--architectures reviewed and new ways to characterize structural divergence in superfamilies. <i>Nucleic Acids Research</i> , 2009, 37, D310-D314. | 6.5 | 174 |
| 129 | The CATH Hierarchy Revisited--Structural Divergence in Domain Superfamilies and the Continuity of Fold Space. <i>Structure</i> , 2009, 17, 1051-1062. | 1.6 | 58 |
| 130 | The structural basis of allosteric regulation in proteins. <i>FEBS Letters</i> , 2009, 583, 1692-1698. | 1.3 | 187 |
| 131 | The SDR (short-chain dehydrogenase/reductase and related enzymes) nomenclature initiative. <i>Chemico-Biological Interactions</i> , 2009, 178, 94-98. | 1.7 | 329 |
| 132 | Small Molecule Subgraph Detector (SMSD) toolkit. <i>Journal of Cheminformatics</i> , 2009, 1, 12. | 2.8 | 117 |
| 133 | Prepublication data sharing. <i>Nature</i> , 2009, 461, 168-170. | 13.7 | 243 |
| 134 | Protein promiscuity and its implications for biotechnology. <i>Nature Biotechnology</i> , 2009, 27, 157-167. | 9.4 | 434 |
| 135 | Missing in action: enzyme functional annotations in biological databases. <i>Nature Chemical Biology</i> , 2009, 5, 521-525. | 3.9 | 53 |
| 136 | Structural Analysis of Metal Sites in Proteins: Non-heme Iron Sites as a Case Study. <i>Journal of Molecular Biology</i> , 2009, 388, 356-380. | 2.0 | 48 |
| 137 | Understanding the Functional Roles of Amino Acid Residues in Enzyme Catalysis. <i>Journal of Molecular Biology</i> , 2009, 390, 560-577. | 2.0 | 117 |
| 138 | Ribosomal Protein S6 Kinase 1 Signaling Regulates Mammalian Life Span. <i>Science</i> , 2009, 326, 140-144. | 6.0 | 1,009 |
| 139 | Genome and proteome annotation: organization, interpretation and integration. <i>Journal of the Royal Society Interface</i> , 2009, 6, 129-147. | 1.5 | 45 |
| 140 | Annotations for all by all - the BioSapiens network. <i>Genome Biology</i> , 2009, 10, 401. | 13.9 | 9 |
| 141 | Protein function annotation by homology-based inference. <i>Genome Biology</i> , 2009, 10, 207. | 13.9 | 182 |
| 142 | Mapping Human Metabolic Pathways in the Small Molecule Chemical Space. <i>Journal of Chemical Information and Modeling</i> , 2009, 49, 2272-2289. | 2.5 | 14 |
| 143 | Data Curation in Biology - Past, Present and Future. <i>Nature Precedings</i> , 2009, , . | 0.1 | 2 |
| 144 | The fine details of evolution. <i>Biochemical Society Transactions</i> , 2009, 37, 723-726. | 1.6 | 3 |

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|-----|--|-----|-----------|
| 145 | Protein Function Prediction from Structure in Structural Genomics and its Contribution to the Study of Health and Disease. NATO Science for Peace and Security Series A: Chemistry and Biology, 2009, , 201-215. | 0.5 | 0 |
| 146 | Case Studies: Function Predictions of Structural Genomics Results. , 2009, , 273-291. | | 0 |
| 147 | Metal ions in biological catalysis: from enzyme databases to general principles. Journal of Biological Inorganic Chemistry, 2008, 13, 1205-1218. | 1.1 | 868 |
| 148 | Evolution of binding sites for zinc and calcium ions playing structural roles. Proteins: Structure, Function and Bioinformatics, 2008, 71, 813-830. | 1.5 | 48 |
| 149 | Understanding the molecular machinery of genetics through 3D structures. Nature Reviews Genetics, 2008, 9, 141-151. | 7.7 | 69 |
| 150 | Metabolic innovations towards the human lineage. BMC Evolutionary Biology, 2008, 8, 247. | 3.2 | 14 |
| 151 | Evidence for lifespan extension and delayed age-related biomarkers in insulin receptor substrate 1 null mice. FASEB Journal, 2008, 22, 807-818. | 0.2 | 487 |
| 152 | Molecular Docking for Substrate Identification: The Short-Chain Dehydrogenases/Reductases. Journal of Molecular Biology, 2008, 375, 855-874. | 2.0 | 60 |
| 153 | Detection of 3D atomic similarities and their use in the discrimination of small molecule protein-binding sites. Bioinformatics, 2008, 24, i105-i111. | 1.8 | 89 |
| 154 | The Protein Feature Ontology: a tool for the unification of protein feature annotations. Bioinformatics, 2008, 24, 2767-2772. | 1.8 | 19 |
| 155 | The Impact of Structural Proteomics on Macromolecular Structure Databases. , 2008, , 29-49. | | 0 |
| 156 | MACIE (Mechanism, Annotation and Classification in Enzymes): novel tools for searching catalytic mechanisms. Nucleic Acids Research, 2007, 35, D515-D520. | 6.5 | 64 |
| 157 | Analysis of binding site similarity, small-molecule similarity and experimental binding profiles in the human cytosolic sulfotransferase family. Bioinformatics, 2007, 23, e104-e109. | 1.8 | 33 |
| 158 | Construction, Visualisation, and Clustering of Transcription Networks from Microarray Expression Data. PLoS Computational Biology, 2007, 3, e206. | 1.5 | 261 |
| 159 | Evolutionary Models for Formation of Network Motifs and Modularity in the Saccharomyces Transcription Factor Network. PLoS Computational Biology, 2007, 3, e198. | 1.5 | 38 |
| 160 | Structural and Chemical Profiling of the Human Cytosolic Sulfotransferases. PLoS Biology, 2007, 5, e97. | 2.6 | 187 |
| 161 | PROCOGNATE: a cognate ligand domain mapping for enzymes. Nucleic Acids Research, 2007, 36, D618-D622. | 6.5 | 42 |
| 162 | The implications of alternative splicing in the ENCODE protein complement. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 5495-5500. | 3.3 | 206 |

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|-----|---|------|-----------|
| 163 | The CATH domain structure database: new protocols and classification levels give a more comprehensive resource for exploring evolution. <i>Nucleic Acids Research</i> , 2007, 35, D291-D297. | 6.5 | 274 |
| 164 | Towards Fully Automated Structure-based Function Prediction in Structural Genomics: A Case Study. <i>Journal of Molecular Biology</i> , 2007, 367, 1511-1522. | 2.0 | 79 |
| 165 | Shape Variation in Protein Binding Pockets and their Ligands. <i>Journal of Molecular Biology</i> , 2007, 368, 283-301. | 2.0 | 188 |
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