

# Adam Godzik

## List of Publications by Year in descending order

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Version: 2024-02-01

377  
papers

42,279  
citations

5574

82  
h-index

3034

188  
g-index

404  
all docs

404  
docs citations

404  
times ranked

57850  
citing authors

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 1  | Cd-hit: a fast program for clustering and comparing large sets of protein or nucleotide sequences. <i>Bioinformatics</i> , 2006, 22, 1658-1659.   | 4.1  | 8,965     |
| 2  | Protein Tyrosine Phosphatases in the Human Genome. <i>Cell</i> , 2004, 117, 699-711.  | 28.9 | 1,697     |
| 3  | Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018, 173, 371-385.e18.  | 28.9 | 1,670     |
| 4  | Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. <i>Nature</i> , 2002, 420, 563-573.   | 27.8 | 1,548     |
| 5  | Detection of a SARS-CoV-2 variant of concern in South Africa. <i>Nature</i> , 2021, 592, 438-443.   | 27.8 | 1,381     |
| 6  | S-Nitrosylation of Drp1 Mediates $\beta$ -Amyloid-Related Mitochondrial Fission and Neuronal Injury. <i>Science</i> , 2009, 324, 102-105.   | 12.6 | 957       |
| 7  | Clustering of highly homologous sequences to reduce the size of large protein databases. <i>Bioinformatics</i> , 2001, 17, 282-283.   | 4.1  | 895       |
| 8  | The NLR Gene Family: A Standard Nomenclature. <i>Immunity</i> , 2008, 28, 285-287.  | 14.3 | 761       |
| 9  | The Sorcerer II Global Ocean Sampling Expedition: Expanding the Universe of Protein Families. <i>PLoS Biology</i> , 2007, 5, e16.   | 5.6  | 736       |
| 10 | Flexible structure alignment by chaining aligned fragment pairs allowing twists. <i>Bioinformatics</i> , 2003, 19, ii246-ii255.   | 4.1  | 524       |
| 11 | A Primer on Metagenomics. <i>PLoS Computational Biology</i> , 2010, 6, e1000667.  | 3.2  | 523       |
| 12 | FFAS03: a server for profile-profile sequence alignments. <i>Nucleic Acids Research</i> , 2005, 33, W284-W288.  | 14.5 | 522       |
| 13 | The Functional Impact of Alternative Splicing in Cancer. <i>Cell Reports</i> , 2017, 20, 2215-2226.   | 6.4  | 517       |
| 14 | Shotgun metaproteomics of the human distal gut microbiota. <i>ISME Journal</i> , 2009, 3, 179-189.  | 9.8  | 484       |
| 15 | Tolerating some redundancy significantly speeds up clustering of large protein databases. <i>Bioinformatics</i> , 2002, 18, 77-82.  | 4.1  | 475       |
| 16 | The amphioxus genome illuminates vertebrate origins and cephalochordate biology. <i>Genome Research</i> , 2008, 18, 1100-1111.  | 5.5  | 456       |
| 17 | Comparison of sequence profiles. Strategies for structural predictions using sequence information. <i>Protein Science</i> , 2000, 9, 232-241.   | 7.6  | 431       |
| 18 | Structural genomics of the <i>Thermotoga maritima</i> proteome implemented in a high-throughput structure determination pipeline. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 11664-11669. | 7.1  | 397       |

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|----|--|------|-----------|
| 19 | Mitochondrial fission in apoptosis, neurodegeneration and aging. <i>Current Opinion in Cell Biology</i> , 2003, 15, 706-716.   | 5.4  | 390       |
| 20 | Cysteine regulation of protein function as exemplified by NMDA-receptor modulation. <i>Trends in Neurosciences</i> , 2002, 25, 474-480.  | 8.6  | 349       |
| 21 | A Blueprint for HIV Vaccine Discovery. <i>Cell Host and Microbe</i> , 2012, 12, 396-407.   | 11.0 | 348       |
| 22 | Topology fingerprint approach to the inverse protein folding problem. <i>Journal of Molecular Biology</i> , 1992, 227, 227-238.  | 4.2  | 341       |
| 23 | Crystal structure of Nsp15 endoribonuclease from SARS-CoV-2. <i>Protein Science</i> , 2020, 29, 1596-1605.   | 7.6  | 294       |
| 24 | FATCAT: a web server for flexible structure comparison and structure similarity searching. <i>Nucleic Acids Research</i> , 2004, 32, W582-W585.  | 14.5 | 291       |
| 25 | XtalPred: a web server for prediction of protein crystallizability. <i>Bioinformatics</i> , 2007, 23, 3403-3405.   | 4.1  | 269       |
| 26 | Broadly Neutralizing Antibody Responses in a Large Longitudinal Sub-Saharan HIV Primary Infection Cohort. <i>PLoS Pathogens</i> , 2016, 12, e1005369.  | 4.7  | 241       |
| 27 | Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. <i>Nature Communications</i> , 2019, 10, 2674.   | 12.8 | 240       |
| 28 | The structural alignment between two proteins: Is there a unique answer?. <i>Protein Science</i> , 1996, 5, 1325-1338.   | 7.6  | 219       |
| 29 | The retinitis pigmentosa GTPase regulator (RPGR)- interacting protein: Sub-serving RPGR function and participating in disk morphogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 3965-3970. | 7.1  | 205       |
| 30 | Identification and Functional Characterization of the BAG Protein Family in <i>Arabidopsis thaliana</i> . <i>Journal of Biological Chemistry</i> , 2006, 281, 18793-18801.   | 3.4  | 200       |
| 31 | A general method for the prediction of the three dimensional structure and folding pathway of globular proteins: Application to designed helical proteins. <i>Journal of Chemical Physics</i> , 1993, 98, 7420-7433.                                     | 3.0  | 192       |
| 32 | A Diverse Family of Proteins Containing Tumor Necrosis Factor Receptor-associated Factor Domains. <i>Journal of Biological Chemistry</i> , 2001, 276, 24242-24252.   | 3.4  | 192       |
| 33 | Pre-calculated protein structure alignments at the RCSB PDB website. <i>Bioinformatics</i> , 2010, 26, 2983-2985.  | 4.1  | 183       |
| 34 | Derivation and testing of pair potentials for protein folding. When is the quasichemical approximation correct?. <i>Protein Science</i> , 1997, 6, 676-688.  | 7.6  | 182       |
| 35 | Evolutionarily conserved cytoprotection provided by Bax Inhibitor-1 homologs from animals, plants, and yeast. <i>Gene</i> , 2003, 323, 101-113.  | 2.2  | 181       |
| 36 | Three-Dimensional Structural View of the Central Metabolic Network of <i>Thermotoga maritima</i> . <i>Science</i> , 2009, 325, 1544-1549.  | 12.6 | 176       |

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|----|--|------|-----------|
| 37 | Ion Channel Activity of the BH3 Only Bcl-2 Family Member, BID. <i>Journal of Biological Chemistry</i> , 1999, 274, 21932-21936.  | 3.4  | 174       |
| 38 | BAR: An apoptosis regulator at the intersection of caspases and Bcl-2 family proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 2597-2602.   | 7.1  | 172       |
| 39 | The Domains of Apoptosis: A Genomics Perspective. <i>Science Signaling</i> , 2004, 2004, re9-re9.  | 3.6  | 169       |
| 40 | CARD8 and NLRP1 Undergo Autoproteolytic Processing through a ZU5-Like Domain. <i>PLoS ONE</i> , 2011, 6, e27396.   | 2.5  | 168       |
| 41 | The PAAD/PYRIN-only protein POP1/ASC2 is a modulator of ASC-mediated nuclear-factor-kappaB and pro-caspase-1 regulation. <i>Biochemical Journal</i> , 2003, 373, 101-113.  | 3.7  | 156       |
| 42 | A Novel Enhancer of the Apaf1 Apoptosome Involved in Cytochrome c-dependent Caspase Activation and Apoptosis. <i>Journal of Biological Chemistry</i> , 2001, 276, 9239-9245.   | 3.4  | 154       |
| 43 | Divergent evolution of protein conformational dynamics in dihydrofolate reductase. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1243-1249.   | 8.2  | 153       |
| 44 | Identification and Characterization of a Novel Bacterial Virulence Factor That Shares Homology with Mammalian Toll/Interleukin-1 Receptor Family Proteins. <i>Infection and Immunity</i> , 2006, 74, 594-601.  | 2.2  | 150       |
| 45 | The importance of alignment accuracy for molecular replacement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1229-1236.   | 2.5  | 149       |
| 46 | Are proteins ideal mixtures of amino acids? Analysis of energy parameter sets. <i>Protein Science</i> , 1995, 4, 2107-2117.  | 7.6  | 146       |
| 47 | Bcl-G, a Novel Pro-apoptotic Member of the Bcl-2 Family. <i>Journal of Biological Chemistry</i> , 2001, 276, 2780-2785.  | 3.4  | 146       |
| 48 | The challenge of protein structure determination—lessons from structural genomics. <i>Protein Science</i> , 2007, 16, 2472-2482.   | 7.6  | 135       |
| 49 | <i>Salmonella</i> Secreted Factor L Deubiquitinase of <i>Salmonella typhimurium</i> Inhibits NF- $\kappa$ B, Suppresses I $\kappa$ B $\alpha$ Ubiquitination and Modulates Innate Immune Responses. <i>Journal of Immunology</i> , 2008, 180, 5045-5056. | 0.8  | 135       |
| 50 | Sequence-structure matching in globular proteins: application to supersecondary and tertiary structure determination.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1992, 89, 12098-12102.                   | 7.1  | 134       |
| 51 | FATCAT 2.0: towards a better understanding of the structural diversity of proteins. <i>Nucleic Acids Research</i> , 2020, 48, W60-W64.   | 14.5 | 134       |
| 52 | Contribution of Electrostatic Interactions, Compactness and Quaternary Structure to Protein Thermostability: Lessons from Structural Genomics of <i>Thermotoga maritima</i> . <i>Journal of Molecular Biology</i> , 2006, 356, 547-557.                  | 4.2  | 132       |
| 53 | FFAS server: novel features and applications. <i>Nucleic Acids Research</i> , 2011, 39, W38-W44.   | 14.5 | 130       |
| 54 | PAAD—a new protein domain associated with apoptosis, cancer and autoimmune diseases. <i>Trends in Biochemical Sciences</i> , 2001, 26, 85-87.  | 7.5  | 129       |

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|----|--|------|-----------|
| 55 | Numerous proteins with unique characteristics are degraded by the 26S proteasome following monoubiquitination. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E4639-47. | 7.1  | 127       |
| 56 | Multiple flexible structure alignment using partial order graphs. Bioinformatics, 2005, 21, 2362-2369.   | 4.1  | 125       |
| 57 | Exploration of Uncharted Regions of the Protein Universe. PLoS Biology, 2009, 7, e1000205.   | 5.6  | 123       |
| 58 | Polysaccharides utilization in human gut bacterium Bacteroides thetaiotaomicron: comparative genomics reconstruction of metabolic and regulatory networks. BMC Genomics, 2013, 14, 873.                              | 2.8  | 122       |
| 59 | A Pan-Cancer Catalogue of Cancer Driver Protein Interaction Interfaces. PLoS Computational Biology, 2015, 11, e1004518.  | 3.2  | 122       |
| 60 | Improving the quality of twilight-zone alignments. Protein Science, 2000, 9, 1487-1496.  | 7.6  | 120       |
| 61 | PSI-2: Structural Genomics to Cover Protein Domain Family Space. Structure, 2009, 17, 869-881.   | 3.3  | 120       |
| 62 | S-Nitrosylation of Drp1 links excessive mitochondrial fission to neuronal injury in neurodegeneration. Mitochondrion, 2010, 10, 573-578.   | 3.4  | 120       |
| 63 | CutDB: a proteolytic event database. Nucleic Acids Research, 2007, 35, D546-D549.  | 14.5 | 119       |
| 64 | Defining the risk of SARS-CoV-2 variants on immune protection. Nature, 2022, 605, 640-652.   | 27.8 | 117       |
| 65 | e-Driver: a novel method to identify protein regions driving cancer. Bioinformatics, 2014, 30, 3109-3114.  | 4.1  | 116       |
| 66 | Structural Systems Biology Evaluation of Metabolic Thermotolerance in <i>Escherichia coli</i> . Science, 2013, 340, 1220-1223.   | 12.6 | 111       |
| 67 | CAFASP-1: Critical assessment of fully automated structure prediction methods. , 1999, 37, 209-217.  |      | 110       |
| 68 | Bcl-B, a Novel Bcl-2 Family Member That Differentially Binds and Regulates Bax and Bak. Journal of Biological Chemistry, 2001, 276, 12481-12484.   | 3.4  | 109       |
| 69 | Practical lessons from protein structure prediction. Nucleic Acids Research, 2005, 33, 1874-1891.  | 14.5 | 109       |
| 70 | <i>Chla</i> Dub1 of <i>Chlamydia trachomatis</i> suppresses NF- $\kappa$ B activation and inhibits I $\kappa$ B $\alpha$ ubiquitination and degradation. Cellular Microbiology, 2008, 10, 1879-1892.                 | 2.1  | 107       |
| 71 | Comparative Analysis of Apoptosis and Inflammation Genes of Mice and Humans. Genome Research, 2003, 13, 1376-1388.   | 5.5  | 104       |
| 72 | A Unique Substrate Recognition Profile for Matrix Metalloproteinase-2. Journal of Biological Chemistry, 2002, 277, 4485-4491.  | 3.4  | 103       |

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|----|--|------|-----------|
| 73 | The JCSG high-throughput structural biology pipeline. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1137-1142.  | 0.7  | 99        |
| 74 | Functional analysis of the Escherichia coli genome using the sequence-to-structure-to-function paradigm: identification of proteins exhibiting the Glutaredoxin/Thioredoxin disulfide oxidoreductase activity 1 Edited by F. E. Cohen. <i>Journal of Molecular Biology</i> , 1998, 282, 703-711. | 4.2  | 97        |
| 75 | FFAS-3D: improving fold recognition by including optimized structural features and template re-ranking. <i>Bioinformatics</i> , 2014, 30, 660-667.   | 4.1  | 97        |
| 76 | Fold and function predictions for Mycoplasma genitalium proteins. <i>Folding &amp; Design</i> , 1998, 3, 229-238.  | 4.5  | 94        |
| 77 | TUCAN, an Antiapoptotic Caspase-associated Recruitment Domain Family Protein Overexpressed in Cancer. <i>Journal of Biological Chemistry</i> , 2001, 276, 32220-32229.   | 3.4  | 94        |
| 78 | Tyrosine phosphorylation of VHR phosphatase by ZAP-70. <i>Nature Immunology</i> , 2003, 4, 44-48.  | 14.5 | 94        |
| 79 | Cleavage targets and the D-arginine-based inhibitors of the West Nile virus NS3 processing proteinase. <i>Biochemical Journal</i> , 2006, 393, 503-511.  | 3.7  | 94        |
| 80 | A Novel PAAD-containing Protein That Modulates NF- $\kappa$ B Induction by Cytokines Tumor Necrosis Factor- $\alpha$ and Interleukin-1 $\beta$ . <i>Journal of Biological Chemistry</i> , 2002, 277, 35333-35340.  | 3.4  | 93        |
| 81 | Fold prediction by a hierarchy of sequence, threading, and modeling methods. <i>Protein Science</i> , 1998, 7, 1431-1440.  | 7.6  | 91        |
| 82 | Lattice representations of globular proteins: How good are they?. <i>Journal of Computational Chemistry</i> , 1993, 14, 1194-1202.   | 3.3  | 89        |
| 83 | De novo and inverse folding predictions of protein structure and dynamics. <i>Journal of Computer-Aided Molecular Design</i> , 1993, 7, 397-438.   | 2.9  | 84        |
| 84 | CADD, a Chlamydia Protein That Interacts with Death Receptors. <i>Journal of Biological Chemistry</i> , 2002, 277, 9633-9636.  | 3.4  | 84        |
| 85 | A Unique Substrate Binding Mode Discriminates Membrane Type-1 Matrix Metalloproteinase from Other Matrix Metalloproteinases. <i>Journal of Biological Chemistry</i> , 2002, 277, 23788-23793.  | 3.4  | 84        |
| 86 | Strong functional patterns in the evolution of eukaryotic genomes revealed by the reconstruction of ancestral protein domain repertoires. <i>Genome Biology</i> , 2011, 12, R4.  | 9.6  | 84        |
| 87 | Crystal structures of two novel dye-decolorizing peroxidases reveal a $\beta$ -barrel fold with a conserved heme-binding motif. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 223-233.   | 2.6  | 81        |
| 88 | A method for predicting protein structure from sequence. <i>Current Biology</i> , 1993, 3, 414-423.  | 3.9  | 80        |
| 89 | Comparative Analysis of Protein Domain Organization. <i>Genome Research</i> , 2004, 14, 343-353.   | 5.5  | 80        |
| 90 | Characterization of matrix metalloproteinase-26, a novel metalloproteinase widely expressed in cancer cells of epithelial origin. <i>Biochemical Journal</i> , 2001, 356, 705.   | 3.7  | 79        |

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|-----|---|------|-----------|
| 91  | Fold Recognition Methods. <i>Methods of Biochemical Analysis</i> , 2005, 44, 525-546.   | 0.2  | 78        |
| 92  | A Distinct Type of Pilus from the Human Microbiome. <i>Cell</i> , 2016, 165, 690-703.   | 28.9 | 78        |
| 93  | Surprising complexity of the ancestral apoptosis network. <i>Genome Biology</i> , 2007, 8, R226.  | 9.6  | 77        |
| 94  | Drosophila Pro-apoptotic Bcl-2/Bax Homologue Reveals Evolutionary Conservation of Cell Death Mechanisms. <i>Journal of Biological Chemistry</i> , 2000, 275, 27303-27306.   | 3.4  | 76        |
| 95  | Basis for substrate recognition and distinction by matrix metalloproteinases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4148-55.   | 7.1  | 75        |
| 96  | Drosophila pro-apoptotic Bcl-2/Bax homologue reveals evolutionary conservation of cell death mechanisms. <i>Journal of Biological Chemistry</i> , 2000, 275, 27303-6.   | 3.4  | 74        |
| 97  | Inhibition of T Cell Antigen Receptor Signaling by VHR-related MKPX (VHX), a New Dual Specificity Phosphatase Related to VH1 Related (VHR). <i>Journal of Biological Chemistry</i> , 2002, 277, 5524-5528.  | 3.4  | 73        |
| 98  | Global distribution of conformational states derived from redundant models in the PDB points to non-uniqueness of the protein structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 10505-10510. | 7.1  | 73        |
| 99  | Structural Basis of Murein Peptide Specificity of a $\hat{3}$ -D-Glutamyl-L-Diamino Acid Endopeptidase. <i>Structure</i> , 2009, 17, 303-313.   | 3.3  | 73        |
| 100 | HIV-1 and SARS-CoV-2: Patterns in the evolution of two pandemic pathogens. <i>Cell Host and Microbe</i> , 2021, 29, 1093-1110.  | 11.0 | 73        |
| 101 | Between Order and Disorder in Protein Structures: Analysis of "Dual Personality" Fragments in Proteins. <i>Structure</i> , 2007, 15, 1141-1147.   | 3.3  | 72        |
| 102 | In search for more accurate alignments in the twilight zone. <i>Protein Science</i> , 2009, 11, 1702-1713.  | 7.6  | 72        |
| 103 | Comparison of algorithms for the detection of cancer drivers at subgene resolution. <i>Nature Methods</i> , 2017, 14, 782-788.  | 19.0 | 72        |
| 104 | AhpF Can Be Dissected into Two Functional Units: A Tandem Repeats of Two Thioredoxin-like Folds in the N-Terminus Mediate Electron Transfer from the Thioredoxin Reductase-like C-Terminus to AhpC. <i>Biochemistry</i> , 2000, 39, 6602-6615.            | 2.5  | 71        |
| 105 | CLAN, a Novel Human CED-4-like Gene. <i>Genomics</i> , 2001, 75, 77-83.   | 2.9  | 70        |
| 106 | PDBFlex: exploring flexibility in protein structures. <i>Nucleic Acids Research</i> , 2016, 44, D423-D428.  | 14.5 | 70        |
| 107 | Saturated BLAST: an automated multiple intermediate sequence search used to detect distant homology. <i>Bioinformatics</i> , 2000, 16, 1105-1110.   | 4.1  | 69        |
| 108 | Crystal structure of the global regulatory protein CsrA from <i>Pseudomonas putida</i> at 2.05 Å... resolution reveals a new fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 449-453.   | 2.6  | 69        |

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|-----|--|------|-----------|
| 109 | Structural genomics is the largest contributor of novel structural leverage. <i>Journal of Structural and Functional Genomics</i> , 2009, 10, 181-191.   | 1.2  | 69        |
| 110 | bNAber: database of broadly neutralizing HIV antibodies. <i>Nucleic Acids Research</i> , 2014, 42, D1133-D1139.  | 14.5 | 69        |
| 111 | Domain architecture evolution of pattern-recognition receptors. <i>Immunogenetics</i> , 2010, 62, 263-272.   | 2.4  | 68        |
| 112 | Structural Determinants of Limited Proteolysis. <i>Journal of Proteome Research</i> , 2011, 10, 3642-3651.   | 3.7  | 68        |
| 113 | Identification and structural characterization of heme binding in a novel dye-decolorizing peroxidase, TyrA. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 234-243.  | 2.6  | 67        |
| 114 | TIR domain-containing adaptor SARM is a late addition to the ongoing microbe-host dialog. <i>Developmental and Comparative Immunology</i> , 2011, 35, 461-468.   | 2.3  | 66        |
| 115 | Structure of the $\beta$ -glutamyl-L-diamino acid endopeptidase YkfC from <i>Bacillus cereus</i> in complex with L-Ala- $\beta$ -D-Glu: insights into substrate recognition by NlpC/P60 cysteine peptidases. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1354-1364. | 0.7  | 64        |
| 116 | Regularities in interaction patterns of globular proteins. <i>Protein Engineering, Design and Selection</i> , 1993, 6, 801-810.  | 2.1  | 63        |
| 117 | CARD6 Is a Modulator of NF- $\kappa$ B Activation by Nod1- and Cardiak-mediated Pathways. <i>Journal of Biological Chemistry</i> , 2003, 278, 31941-31949.   | 3.4  | 63        |
| 118 | Evolution of the Animal Apoptosis Network. <i>Cold Spring Harbor Perspectives in Biology</i> , 2013, 5, a008649-a008649.   | 5.5  | 63        |
| 119 | Metagenomics and the protein universe. <i>Current Opinion in Structural Biology</i> , 2011, 21, 398-403.   | 5.7  | 62        |
| 120 | Connecting the Protein Structure Universe by Using Sparse Recurring Fragments. <i>Structure</i> , 2005, 13, 1213-1224.   | 3.3  | 61        |
| 121 | Outcome of a Workshop on Archiving Structural Models of Biological Macromolecules. <i>Structure</i> , 2006, 14, 1211-1217.   | 3.3  | 60        |
| 122 | CAFASP-1: Critical assessment of fully automated structure prediction methods. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 37, 209-217.  | 2.6  | 60        |
| 123 | From fold predictions to function predictions: Automation of functional site conservation analysis for functional genome predictions. <i>Protein Science</i> , 1999, 8, 1104-1115.   | 7.6  | 59        |
| 124 | HEPN: a common domain in bacterial drug resistance and human neurodegenerative proteins. <i>Trends in Biochemical Sciences</i> , 2003, 28, 224-226.  | 7.5  | 59        |
| 125 | Automatic detection of subsystem/pathway variants in genome analysis. <i>Bioinformatics</i> , 2005, 21, i478-i486.   | 4.1  | 59        |
| 126 | AIDA: <i>ab initio</i> domain assembly for automated multi-domain protein structure prediction and domain-domain interaction prediction. <i>Bioinformatics</i> , 2015, 31, 2098-2105.  | 4.1  | 59        |



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|-----|--|------|-----------|
| 127 | Structural Genomics of <i>Thermotoga maritima</i> Proteins Shows that Contact Order Is a Major Determinant of Protein Thermostability. <i>Structure</i> , 2005, 13, 857-860.                                     | 3.3  | 58        |
| 128 | S-Nitrosylation-Mediated Redox Transcriptional Switch Modulates Neurogenesis and Neuronal Cell Death. <i>Cell Reports</i> , 2014, 8, 217-228.  | 6.4  | 58        |
| 129 | Sequence clustering strategies improve remote homology recognitions while reducing search times. <i>Protein Engineering, Design and Selection</i> , 2002, 15, 643-649.   | 2.1  | 57        |
| 130 | PMAP: databases for analyzing proteolytic events and pathways. <i>Nucleic Acids Research</i> , 2009, 37, D611-D618.  | 14.5 | 57        |
| 131 | The <i>Drosophila</i> Tumor Necrosis Factor Receptor-associated Factor-1 (DTRAF1) Interacts with Pelle and Regulates NF $\kappa$ B Activity. <i>Journal of Biological Chemistry</i> , 2000, 275, 12102-12107.    | 3.4  | 53        |
| 132 | Expansion of the Protein Repertoire in Newly Explored Environments: Human Gut Microbiome Specific Protein Families. <i>PLoS Computational Biology</i> , 2010, 6, e1000798.                                       | 3.2  | 52        |
| 133 | Aggregate formation and synaptic abnormality induced by DSCR1. <i>Journal of Neurochemistry</i> , 2004, 88, 1485-1496.   | 3.9  | 51        |
| 134 | Crystal Structure of the Actin Binding Domain of the Cyclase-Associated Protein. <i>Biochemistry</i> , 2004, 43, 10628-10641.  | 2.5  | 51        |
| 135 | Subunit-Specific Roles of Glycine-Binding Domains in Activation of NR1/NR3 N-Methyl-d-aspartate Receptors. <i>Molecular Pharmacology</i> , 2007, 71, 112-122.  | 2.3  | 51        |
| 136 | Crystal structure of thy1, a thymidylate synthase complementing protein from <i>Thermotoga maritima</i> at 2.25 Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 49, 142-145.    | 2.6  | 50        |
| 137 | POSA: a user-driven, interactive multiple protein structure alignment server. <i>Nucleic Acids Research</i> , 2014, 42, W240-W245.   | 14.5 | 50        |
| 138 | The FGGY Carbohydrate Kinase Family: Insights into the Evolution of Functional Specificities. <i>PLoS Computational Biology</i> , 2011, 7, e1002318.   | 3.2  | 48        |
| 139 | AIDA: ab initio domain assembly server. <i>Nucleic Acids Research</i> , 2014, 42, W308-W313.   | 14.5 | 47        |
| 140 | Neutralizing antibody affords comparable protection against vaginal and rectal simian/human immunodeficiency virus challenge in macaques. <i>Aids</i> , 2016, 30, 1543-1551.                                     | 2.2  | 47        |
| 141 | Mapping genetic variations to three-dimensional protein structures to enhance variant interpretation: a proposed framework. <i>Genome Medicine</i> , 2017, 9, 113.   | 8.2  | 47        |
| 142 | Simulations of the folding pathway of triose phosphate isomerase-type alpha/beta barrel proteins.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1992, 89, 2629-2633. | 7.1  | 46        |
| 143 | Database searching by flexible protein structure alignment. <i>Protein Science</i> , 2004, 13, 1841-1850.  | 7.6  | 46        |
| 144 | Computational protein function prediction: Are we making progress?. <i>Cellular and Molecular Life Sciences</i> , 2007, 64, 2505-2511.   | 5.4  | 46        |

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