

# Arne Elofsson

## List of Publications by Year in descending order

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161  
papers

14,893  
citations

22099

59  
h-index

22764

112  
g-index

200  
all docs

200  
docs citations

200  
times ranked

15025  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | The TOPCONS web server for consensus prediction of membrane protein topology and signal peptides. <i>Nucleic Acids Research</i> , 2015, 43, W401-W407.                                     | 6.5  | 776       |
| 2  | 3D-Jury: a simple approach to improve protein structure predictions. <i>Bioinformatics</i> , 2003, 19, 1015-1018.  | 1.8  | 689       |
| 3  | Can correct protein models be identified?. <i>Protein Science</i> , 2003, 12, 1073-1086.   | 3.1  | 646       |
| 4  | Detecting sequence signals in targeting peptides using deep learning. <i>Life Science Alliance</i> , 2019, 2, e201900429.  | 1.3  | 561       |
| 5  | TOPCONS: consensus prediction of membrane protein topology. <i>Nucleic Acids Research</i> , 2009, 37, W465-W468.   | 6.5  | 487       |
| 6  | Structure is three to ten times more conserved than sequence—A study of structural response in protein cores. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 499-508. | 1.5  | 367       |
| 7  | OCTOPUS: improving topology prediction by two-track ANN-based preference scores and an extended topological grammar. <i>Bioinformatics</i> , 2008, 24, 1662-1668.                          | 1.8  | 349       |
| 8  | What properties characterize the hub proteins of the protein-protein interaction network of <i>Saccharomyces cerevisiae</i> ?. <i>Genome Biology</i> , 2006, 7, R45.                       | 13.9 | 337       |
| 9  | Improved prediction of protein-protein interactions using AlphaFold2. <i>Nature Communications</i> , 2022, 13, 1265.   | 5.8  | 331       |
| 10 | Molecular recognition of a single sphingolipid species by a protein's transmembrane domain. <i>Nature</i> , 2012, 481, 525-529.  | 13.7 | 330       |
| 11 | Prediction of membrane-protein topology from first principles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 7177-7181.              | 3.3  | 288       |
| 12 | Pcons: A neural-network-based consensus predictor that improves fold recognition. <i>Protein Science</i> , 2008, 10, 2354-2362.  | 3.1  | 285       |
| 13 | Prediction of MHC class I binding peptides, using SVMHC. <i>BMC Bioinformatics</i> , 2002, 3, 25.  | 1.2  | 271       |
| 14 | DisProt 7.0: a major update of the database of disordered proteins. <i>Nucleic Acids Research</i> , 2017, 45, D219-D227.   | 6.5  | 242       |
| 15 | Best $\alpha$ -helical transmembrane protein topology predictions are achieved using hidden Markov models and evolutionary information. <i>Protein Science</i> , 2004, 13, 1908-1917.      | 3.1  | 235       |
| 16 | Multi-domain Proteins in the Three Kingdoms of Life: Orphan Domains and Other Unassigned Regions. <i>Journal of Molecular Biology</i> , 2005, 348, 231-243.                                | 2.0  | 230       |
| 17 | Expansion of Protein Domain Repeats. <i>PLoS Computational Biology</i> , 2006, 2, e114.  | 1.5  | 225       |
| 18 | Membrane Protein Structure: Prediction versus Reality. <i>Annual Review of Biochemistry</i> , 2007, 76, 125-140.   | 5.0  | 220       |

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|----|---|-----|-----------|
| 19 | Structure prediction meta server. <i>Bioinformatics</i> , 2001, 17, 750-751.  | 1.8 | 219       |
| 20 | SPOCTOPUS: a combined predictor of signal peptides and membrane protein topology. <i>Bioinformatics</i> , 2008, 24, 2928-2929.  | 1.8 | 213       |
| 21 | Arrangements in the modular evolution of proteins. <i>Trends in Biochemical Sciences</i> , 2008, 33, 444-451.   | 3.7 | 193       |
| 22 | Domain Rearrangements in Protein Evolution. <i>Journal of Molecular Biology</i> , 2005, 353, 911-923.   | 2.0 | 190       |
| 23 | The interface of protein structure, protein biophysics, and molecular evolution. <i>Protein Science</i> , 2012, 21, 769-785.  | 3.1 | 188       |
| 24 | All are not equal: A benchmark of different homology modeling programs. <i>Protein Science</i> , 2005, 14, 1315-1327.   | 3.1 | 185       |
| 25 | Identification of correct regions in protein models using structural, alignment, and consensus information. <i>Protein Science</i> , 2006, 15, 900-913.               | 3.1 | 184       |
| 26 | Identification of related proteins on family, superfamily and fold level 1 1Edited by F. C. Cohen. <i>Journal of Molecular Biology</i> , 2000, 295, 613-625.          | 2.0 | 179       |
| 27 | A study of quality measures for protein threading models. <i>BMC Bioinformatics</i> , 2001, 2, 5.   | 1.2 | 174       |
| 28 | Molecular architecture of the active mitochondrial protein gate. <i>Science</i> , 2015, 349, 1544-1548.   | 6.0 | 169       |
| 29 | ProQ3D: improved model quality assessments using deep learning. <i>Bioinformatics</i> , 2017, 33, 1578-1580.  | 1.8 | 151       |
| 30 | Improved Contact Predictions Using the Recognition of Protein Like Contact Patterns. <i>PLoS Computational Biology</i> , 2014, 10, e1003889.                          | 1.5 | 142       |
| 31 | DisProt: intrinsic protein disorder annotation in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D269-D276.  | 6.5 | 141       |
| 32 | A Study of the Membraneâ€“Water Interface Region of Membrane Proteins. <i>Journal of Molecular Biology</i> , 2005, 346, 377-385.                                      | 2.0 | 140       |
| 33 | LiveBench-1: Continuous benchmarking of protein structure prediction servers. <i>Protein Science</i> , 2001, 10, 352-361.   | 3.1 | 135       |
| 34 | Architecture of helix bundle membrane proteins: An analysis of cytochrome c oxidase from bovine mitochondria. <i>Protein Science</i> , 1997, 6, 808-815.              | 3.1 | 134       |
| 35 | CAFASP2: The second critical assessment of fully automated structure prediction methods. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 171-183. | 1.5 | 130       |
| 36 | Using multiple templates to improve quality of homology models in automated homology modeling. <i>Protein Science</i> , 2008, 17, 990-1002.                           | 3.1 | 130       |

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|----|--|-----|-----------|
| 37 | DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. <i>Nucleic Acids Research</i> , 2022, 50, D480-D487.   | 6.5 | 117       |
| 38 | Automatic consensus-based fold recognition using Pcons, ProQ, and Pmodeller. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 534-541.  | 1.5 | 112       |
| 39 | CAFASP-1: Critical assessment of fully automated structure prediction methods. , 1999, 37, 209-217.  |     | 110       |
| 40 | CAFASP3: The third critical assessment of fully automated structure prediction methods. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 503-516.   | 1.5 | 108       |
| 41 | In Silico Prediction of the Peroxisomal Proteome in Fungi, Plants and Animals. <i>Journal of Molecular Biology</i> , 2003, 330, 443-456.   | 2.0 | 103       |
| 42 | Pcons5: combining consensus, structural evaluation and fold recognition scores. <i>Bioinformatics</i> , 2005, 21, 4248-4254.   | 1.8 | 103       |
| 43 | Prediction of global and local model quality in CASP7 using Pcons and ProQ. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 184-193.   | 1.5 | 97        |
| 44 | Quantification of the Elevated Rate of Domain Rearrangements in Metazoa. <i>Journal of Molecular Biology</i> , 2007, 372, 1337-1348.   | 2.0 | 96        |
| 45 | Turns in transmembrane helices: determination of the minimal length of a "helical hairpin" and derivation of a fine-grained turn propensity scale 1 1 Edited by F. E. Cohen. <i>Journal of Molecular Biology</i> , 1999, 293, 807-814. | 2.0 | 95        |
| 46 | PconsFold: improved contact predictions improve protein models. <i>Bioinformatics</i> , 2014, 30, i482-i488.   | 1.8 | 92        |
| 47 | ProQ3: Improved model quality assessments using Rosetta energy terms. <i>Scientific Reports</i> , 2016, 6, 33509.  | 1.6 | 92        |
| 48 | Profile-profile methods provide improved fold-recognition: A study of different profile-profile alignment methods. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 57, 188-197.  | 1.5 | 85        |
| 49 | How Consistent are Molecular Dynamics Simulations?. <i>Journal of Molecular Biology</i> , 1993, 233, 766-780.  | 2.0 | 84        |
| 50 | Structural Classification and Prediction of Reentrant Regions in $\alpha$ -Helical Transmembrane Proteins: Application to Complete Genomes. <i>Journal of Molecular Biology</i> , 2006, 361, 591-603.                                  | 2.0 | 83        |
| 51 | Membrane Insertion of Marginally Hydrophobic Transmembrane Helices Depends on Sequence Context. <i>Journal of Molecular Biology</i> , 2010, 396, 221-229.  | 2.0 | 82        |
| 52 | Estimation of model accuracy in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1361-1377.   | 1.5 | 78        |
| 53 | PRED-TMBB2: improved topology prediction and detection of beta-barrel outer membrane proteins. <i>Bioinformatics</i> , 2016, 32, i665-i671.  | 1.8 | 77        |
| 54 | Protein Expansion Is Primarily due to Indels in Intrinsically Disordered Regions. <i>Molecular Biology and Evolution</i> , 2013, 30, 2645-2653.  | 3.5 | 75        |

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|----|---|-----|-----------|
| 55 | Inclusion of dyad-repeat pattern improves topology prediction of transmembrane $\beta^2$ -barrel proteins. <i>Bioinformatics</i> , 2016, 32, 1571-1573.             | 1.8 | 75        |
| 56 | A study on protein sequence alignment quality. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 46, 330-339.   | 1.5 | 71        |
| 57 | BOCTOPUS: improved topology prediction of transmembrane $\beta^2$ barrel proteins. <i>Bioinformatics</i> , 2012, 28, 516-522.                                       | 1.8 | 71        |
| 58 | Why do eukaryotic proteins contain more intrinsically disordered regions?. <i>PLoS Computational Biology</i> , 2019, 15, e1007186.                                  | 1.5 | 70        |
| 59 | PconsC: combination of direct information methods and alignments improves contact prediction. <i>Bioinformatics</i> , 2013, 29, 1815-1816.                          | 1.8 | 69        |
| 60 | GraphQA: protein model quality assessment using graph convolutional networks. <i>Bioinformatics</i> , 2021, 37, 360-366.  | 1.8 | 68        |
| 61 | LiveBench-2: Large-scale automated evaluation of protein structure prediction servers. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 184-191. | 1.5 | 67        |
| 62 | Local moves: An efficient algorithm for simulation of protein folding. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 23, 73-82.                   | 1.5 | 64        |
| 63 | Hidden Markov models that use predicted secondary structures for fold recognition. , 1999, 36, 68-76.   |     | 63        |
| 64 | Assessment of global and local model quality in CASP8 using Pcons and ProQ. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 167-172.            | 1.5 | 62        |
| 65 | LiveBench-6: Large-scale automated evaluation of protein structure prediction servers. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 542-547. | 1.5 | 61        |
| 66 | Preferential attachment in the evolution of metabolic networks. <i>BMC Genomics</i> , 2005, 6, 159.   | 1.2 | 60        |
| 67 | An Introduction to Membrane Proteins. <i>Journal of Proteome Research</i> , 2011, 10, 3324-3331.  | 1.8 | 60        |
| 68 | CAFASP-1: critical assessment of fully automated structure prediction methods. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, Suppl 3, 209-17.     | 1.5 | 60        |
| 69 | Repositioning of Transmembrane $\beta$ -Helices during Membrane Protein Folding. <i>Journal of Molecular Biology</i> , 2010, 397, 190-201.                          | 2.0 | 59        |
| 70 | PconsC4: fast, accurate and hassle-free contact predictions. <i>Bioinformatics</i> , 2019, 35, 2677-2679.   | 1.8 | 59        |
| 71 | Identifying and Quantifying Orphan Protein Sequences in Fungi. <i>Journal of Molecular Biology</i> , 2010, 396, 396-405.  | 2.0 | 56        |
| 72 | Pcons.net: protein structure prediction meta server. <i>Nucleic Acids Research</i> , 2007, 35, W369-W374.   | 6.5 | 54        |

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|----|---|------|-----------|
| 73 | All-atom 3D structure prediction of transmembrane $\beta$ -barrel proteins from sequences. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 5413-5418. | 3.3  | 53        |
| 74 | Rapid membrane protein topology prediction. Bioinformatics, 2011, 27, 1322-1323.  | 1.8  | 51        |
| 75 | ZPRED: Predicting the distance to the membrane center for residues in $\alpha$ -helical membrane proteins. Bioinformatics, 2006, 22, e191-e196.   | 1.8  | 50        |
| 76 | High GC content causes orphan proteins to be intrinsically disordered. PLoS Computational Biology, 2017, 13, e1005375.  | 1.5  | 50        |
| 77 | Nebulin: A Study of Protein Repeat Evolution. Journal of Molecular Biology, 2010, 402, 38-51.   | 2.0  | 47        |
| 78 | Architecture of $\beta$ -barrel membrane proteins: Analysis of trimeric porins. Protein Science, 1998, 7, 2026-2032.  | 3.1  | 46        |
| 79 | Enhanced Protein Production in <i>Escherichia coli</i> by Optimization of Cloning Scars at the Vector-Coding Sequence Junction. ACS Synthetic Biology, 2015, 4, 959-965.                          | 1.9  | 46        |
| 80 | A New Census of Protein Tandem Repeats and Their Relationship with Intrinsic Disorder. Genes, 2020, 11, 407.  | 1.0  | 45        |
| 81 | Why are polar residues within the membrane core evolutionary conserved?. Proteins: Structure, Function and Bioinformatics, 2011, 79, 79-91.   | 1.5  | 43        |
| 82 | A study of combined structure/sequence profiles. Folding & Design, 1996, 1, 451-461.  | 4.5  | 42        |
| 83 | Estimating the impact of mobility patterns on COVID-19 infection rates in 11 European countries. PeerJ, 2020, 8, e9879.   | 0.9  | 42        |
| 84 | Helix-helix packing in a membrane-like environment. Journal of Molecular Biology, 1997, 272, 633-641.   | 2.0  | 40        |
| 85 | Evaluating dosage compensation as a cause of duplicate gene retention in <i>Paramecium tetraurelia</i> . Genome Biology, 2007, 8, 213.  | 13.9 | 40        |
| 86 | Improved topology prediction using the terminal hydrophobic helices rule. Bioinformatics, 2016, 32, 1158-1162.  | 1.8  | 40        |
| 87 | Predicting accurate contacts in thousands of Pfam domain families using PconsC3. Bioinformatics, 2017, 33, 2859-2866.   | 1.8  | 40        |
| 88 | Tertiary Windowing to Detect Positive Diversifying Selection. Journal of Molecular Evolution, 2005, 60, 499-504.  | 0.8  | 37        |
| 89 | PONGO: a web server for multiple predictions of all-alpha transmembrane proteins. Nucleic Acids Research, 2006, 34, W169-W172.  | 6.5  | 37        |
| 90 | The impact of splicing on protein domain architecture. Current Opinion in Structural Biology, 2013, 23, 451-458.  | 2.6  | 37        |

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|-----|---|-----|-----------|
| 91  | MPRAP: An accessibility predictor for $\alpha$ -helical transmembrane proteins that performs well inside and outside the membrane. BMC Bioinformatics, 2010, 11, 333.                 | 1.2 | 36        |
| 92  | Large-scale structure prediction by improved contact predictions and model quality assessment. Bioinformatics, 2017, 33, i23-i29.   | 1.8 | 35        |
| 93  | Coils in the Membrane Core Are Conserved and Functionally Important. Journal of Molecular Biology, 2008, 380, 170-180.  | 2.0 | 34        |
| 94  | Topology of membrane proteins $\alpha$ predictions, limitations and variations. Current Opinion in Structural Biology, 2018, 50, 9-17.  | 2.6 | 31        |
| 95  | Genomic evolution and complexity of the Anaphase-promoting Complex (APC) in land plants. BMC Plant Biology, 2010, 10, 254.  | 1.6 | 30        |
| 96  | PconsD: ultra rapid, accurate model quality assessment for protein structure prediction. Bioinformatics, 2013, 29, 1817-1818.   | 1.8 | 30        |
| 97  | Long indels are disordered: A study of disorder and indels in homologous eukaryotic proteins. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 890-897.           | 1.1 | 30        |
| 98  | Charge Pair Interactions in Transmembrane Helices and Turn Propensity of the Connecting Sequence Promote Helical Hairpin Insertion. Journal of Molecular Biology, 2013, 425, 830-840. | 2.0 | 30        |
| 99  | Protein sequence $\rightarrow$ structure learning: Is this the end(revolution)? Proteins: Structure, Function and Bioinformatics, 2021, 89, 1770-1786.                                | 1.5 | 30        |
| 100 | Using evolutionary information for the query and target improves fold recognition. Proteins: Structure, Function and Bioinformatics, 2003, 54, 342-350.                               | 1.5 | 29        |
| 101 | A guideline to proteome-wide $\alpha$ -helical membrane protein topology predictions. Proteomics, 2012, 12, 2282-2294.  | 1.3 | 29        |
| 102 | Interaction of mitochondrial presequences with DnaK and mitochondrial hsp70. Journal of Molecular Biology, 1999, 288, 177-190.  | 2.0 | 28        |
| 103 | The Use of Phylogenetic Profiles for Gene Predictions. Current Genomics, 2002, 3, 131-137.  | 0.7 | 28        |
| 104 | Estimating the length of transmembrane helices using Z-coordinate predictions. Protein Science, 2008, 17, 271-278.  | 3.1 | 27        |
| 105 | Orphans and new gene origination, a structural and evolutionary perspective. Current Opinion in Structural Biology, 2014, 26, 73-83.  | 2.6 | 27        |
| 106 | Methods for estimation of model accuracy in CASP12. Proteins: Structure, Function and Bioinformatics, 2018, 86, 361-373.  | 1.5 | 27        |
| 107 | Protein design on computers. Five new proteins: Shpilka, grendel, fingerclasp, leather, and aida. Proteins: Structure, Function and Bioinformatics, 1992, 12, 105-110.                | 1.5 | 26        |
| 108 | Marginally hydrophobic transmembrane $\alpha$ -helices shaping membrane protein folding. Protein Science, 2015, 24, 1057-1074.  | 3.1 | 25        |

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|-----|--|-----|-----------|
| 109 | Ten simple rules on how to create open access and reproducible molecular simulations of biological systems. <i>PLoS Computational Biology</i> , 2019, 15, e1006649.  | 1.5 | 25        |
| 110 | Manipulating the genetic code for membrane protein production: What have we learnt so far?. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012, 1818, 1091-1096.   | 1.4 | 24        |
| 111 | Study of the electrostatics treatment in molecular dynamics simulations. , 1999, 37, 417-428.  |     | 23        |
| 112 | Improved detection of homologous membrane proteins by inclusion of information from topology predictions. <i>Protein Science</i> , 2009, 11, 652-658.  | 3.1 | 23        |
| 113 | Ligand binding properties of human galanin receptors. <i>Molecular Membrane Biology</i> , 2013, 30, 206-216.   | 2.0 | 23        |
| 114 | Quantitative assessment of the structural bias in protein-protein interaction assays. <i>Proteomics</i> , 2008, 8, 4657-4667.  | 1.3 | 22        |
| 115 | The evolution of filamin - A protein domain repeat perspective. <i>Journal of Structural Biology</i> , 2012, 179, 289-298.   | 1.3 | 22        |
| 116 | Protein Contact Map Prediction Based on ResNet and DenseNet. <i>BioMed Research International</i> , 2020, 2020, 1-12.  | 0.9 | 20        |
| 117 | Folding of Aquaporin 1: Multiple evidence that helix 3 can shift out of the membrane core. <i>Protein Science</i> , 2014, 23, 981-992.   | 3.1 | 18        |
| 118 | The 2000 Olympic Games of protein structure prediction; fully automated programs are being evaluated vis-à-vis human teams in the protein structure prediction experiment CAFASP2. <i>Protein Engineering, Design and Selection</i> , 2000, 13, 667-670. | 1.0 | 17        |
| 119 | ProfNet, a method to derive profile-profile alignment scoring functions that improves the alignments of distantly related proteins. <i>BMC Bioinformatics</i> , 2005, 6, 253.  | 1.2 | 17        |
| 120 | Internal duplications in $\alpha$ -helical membrane protein topologies are common but the nonduplicated forms are rare. <i>Protein Science</i> , 2010, 19, 2305-2318.  | 3.1 | 17        |
| 121 | Why is the biological hydrophobicity scale more accurate than earlier experimental hydrophobicity scales?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 2190-2198.  | 1.5 | 16        |
| 122 | Ranking models of transmembrane $\alpha$ -barrel proteins using Z-coordinate predictions. <i>Bioinformatics</i> , 2012, 28, i90-i96.   | 1.8 | 15        |
| 123 | A Bi-LSTM Based Ensemble Algorithm for Prediction of Protein Secondary Structure. <i>Applied Sciences (Switzerland)</i> , 2019, 9, 3538.   | 1.3 | 14        |
| 124 | PconsFam: An Interactive Database of Structure Predictions of Pfam Families. <i>Journal of Molecular Biology</i> , 2019, 431, 2442-2448.   | 2.0 | 14        |
| 125 | Limits and potential of combined folding and docking. <i>Bioinformatics</i> , 2022, 38, 954-961.   | 1.8 | 14        |
| 126 | Determining receptor-ligand interaction of human galanin receptor type 3. <i>Neurochemistry International</i> , 2010, 57, 804-811.   | 1.9 | 13        |



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|-----|---|-----|-----------|
| 127 | Complementing machine learning-based structure predictions with native mass spectrometry. <i>Protein Science</i> , 2022, 31, .  | 3.1 | 13        |
| 128 | Improved alignment quality by combining evolutionary information, predicted secondary structure and self-organizing maps. <i>BMC Bioinformatics</i> , 2006, 7, 357.   | 1.2 | 12        |
| 129 | Improved predictions by Pcons.net using multiple templates. <i>Bioinformatics</i> , 2011, 27, 426-427.  | 1.8 | 12        |
| 130 | The SubCons webserver: A user friendly web interface for state-of-the-art subcellular localization prediction. <i>Protein Science</i> , 2018, 27, 195-201.  | 3.1 | 12        |
| 131 | GCSENet: A GCN, CNN and SENet ensemble model for microRNA-disease association prediction. <i>PLoS Computational Biology</i> , 2021, 17, e1009048.   | 1.5 | 12        |
| 132 | An intrinsically disordered proteins community for ELIXIR. <i>F1000Research</i> , 2019, 8, 1753.  | 0.8 | 12        |
| 133 | A community proposal to integrate structural bioinformatics activities in ELIXIR (3D-Bioinfo) <a href="#">Tj ETQq1 1 0.784314</a> <a href="#">rgBT /Overlock 10</a> <a href="#">TF</a>  | 0.8 | 12        |
| 134 | The Positive Inside Rule Is Stronger When Followed by a Transmembrane Helix. <i>Journal of Molecular Biology</i> , 2014, 426, 2982-2991.  | 2.0 | 11        |
| 135 | Improved protein model quality assessments by changing the target function. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 654-663.  | 1.5 | 11        |
| 136 | Site specific point mutation changes specificity: A molecular modeling study by free energy simulations and enzyme kinetics of the thermodynamics in ribonuclease T1 substrate interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 17, 161-175. | 1.5 | 10        |
| 137 | Membrane protein shaving with thermolysin can be used to evaluate topology predictors. <i>Proteomics</i> , 2013, 13, 1467-1480.   | 1.3 | 10        |
| 138 | Remote homology detection of integral membrane proteins using conserved sequence features. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 1387-1399.   | 1.5 | 9         |
| 139 | The Complement Regulator CD46 Is Bactericidal to <i>Helicobacter pylori</i> and Blocks Urease Activity. <i>Gastroenterology</i> , 2011, 141, 918-928.   | 0.6 | 9         |
| 140 | Free Energy Perturbations in Ribonuclease T <sub>1</sub> Substrate Binding. A Study of the Influence of Simulation Length, Internal Degrees of Freedom and Structure in Free Energy Perturbations. <i>Molecular Simulation</i> , 1993, 10, 255-276.                       | 0.9 | 8         |
| 141 | GWAR: robust analysis and meta-analysis of genome-wide association studies. <i>Bioinformatics</i> , 2017, 33, 1521-1527.  | 1.8 | 8         |
| 142 | Accurate contact-based modelling of repeat proteins predicts the structure of new repeats protein families. <i>PLoS Computational Biology</i> , 2021, 17, e1008798.   | 1.5 | 8         |
| 143 | pyconsFold: a fast and easy tool for modeling and docking using distance predictions. <i>Bioinformatics</i> , 2021, 37, 3959-3960.  | 1.8 | 8         |
| 144 | Hidden Markov models that use predicted secondary structures for fold recognition. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 36, 68-76.   | 1.5 | 8         |

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|-----|---|------|-----------|
| 145 | A 1.2 ns Molecular Dynamics Simulation of the Ribonuclease T1 <sup>3</sup> -Guanosine Monophosphate Complex. <i>The Journal of Physical Chemistry</i> , 1996, 100, 2480-2488.   | 2.9  | 7         |
| 146 | KalignP: Improved multiple sequence alignments using position specific gap penalties in Kalign2. <i>Bioinformatics</i> , 2011, 27, 1702-1703.   | 1.8  | 6         |
| 147 | Structural basis for the interaction of the chaperone Cbp3 with newly synthesized cytochrome b during mitochondrial respiratory chain assembly. <i>Journal of Biological Chemistry</i> , 2019, 294, 16663-16671.  | 1.6  | 6         |
| 148 | Large Tilts in Transmembrane Helices Can Be Induced during Tertiary Structure Formation. <i>Journal of Molecular Biology</i> , 2014, 426, 2529-2538.  | 2.0  | 5         |
| 149 | Using PconsC4 and PconsFold2 to Predict Protein Structure. <i>Current Protocols in Bioinformatics</i> , 2019, 66, e75.  | 25.8 | 5         |
| 150 | Scoring of protein-protein docking models utilizing predicted interface residues. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 1493-1505.  | 1.5  | 4         |
| 151 | Localization Prediction and Structure-Based In Silico Analysis of Bacterial Proteins: With Emphasis on Outer Membrane Proteins. <i>Methods in Molecular Biology</i> , 2013, 939, 115-140.   | 0.4  | 3         |
| 152 | Toward Characterising the Cellular 3D-Proteome. <i>Frontiers in Bioinformatics</i> , 2021, 1, .   | 1.0  | 3         |
| 153 | The evolutionary history of topological variations in the CPA/AT transporters. <i>PLoS Computational Biology</i> , 2021, 17, e1009278.  | 1.5  | 3         |
| 154 | Intra-Helical Salt Bridge Contribution to Membrane Protein Insertion. <i>Journal of Molecular Biology</i> , 2022, 434, 167467.  | 2.0  | 3         |
| 155 | Using Micro- and Macro-Level Network Metrics Unveils Top Communicative Gene Modules in Psoriasis. <i>Genes</i> , 2020, 11, 914.   | 1.0  | 2         |
| 156 | The relationship between ageing and changes in the human blood and brain methylomes. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqac001.   | 1.5  | 2         |
| 157 | The Use of Phylogenetic Profiles for Gene Predictions Revisited. <i>Current Genomics</i> , 2006, 7, 79-86.  | 0.7  | 1         |
| 158 | Decomposing Structural Response Due to Sequence Changes in Protein Domains with Machine Learning. <i>Journal of Molecular Biology</i> , 2020, 432, 4435-4446.   | 2.0  | 1         |
| 159 | Study of the distribution function of the three-dimensional structures of rat galanin determined by two-dimensional <sup>1</sup> H NMR, distance geometry calculations, molecular dynamics and energy transfer measurements. <i>Regulatory Peptides</i> , 1992, 37, S175. | 1.9  | 0         |
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