# Haim J Wolfson

List of Publications by Year
in descending order

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|---|---|---|---|
| 158 papers | 17,811 citations | 20759 60 h-index | 14702 127 g-index |
| 165 all docs | 165 docs citations | 165 times ranked | 15705 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | PatchDock and SymmDock: servers for rigid and symmetric docking. Nucleic Acids Research, 2005, 33, W363-W367. | 6.5 | 2,610 |
| 2 | Principles of docking: An overview of search algorithms and a guide to scoring functions. Proteins: Structure, Function and Bioinformatics, 2002, 47, 409-443. | 1.5 | 1,130 |
| 3 | Shape complementarity at protein-protein interfaces. Biopolymers, 1994, 34, 933-940. | 1.2 | 991 |
| 4 | FireDock: a web server for fast interaction refinement in molecular docking. Nucleic Acids Research, 2008, 36, W229-W232. | 6.5 | 657 |
| 5 | FireDock: Fast interaction refinement in molecular docking. Proteins: Structure, Function and Bioinformatics, 2007, 69, 139-159. | 1.5 | 607 |
| 6 | Protein-protein interactions: Structurally conserved residues distinguish between binding sites and exposed protein surfaces. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 5772-5777. | 3.3 | 553 |
| 7 | Efficient Unbound Docking of Rigid Molecules. Lecture Notes in Computer Science, 2002, , 185-200. | 1.0 | 481 |
| 8 | A method for simultaneous alignment of multiple protein structures. Proteins: Structure, Function and Bioinformatics, 2004, 56, 143-156. | 1.5 | 396 |
| 9 | Mechanism of Two Classes of Cancer Mutations in the Phosphoinositide 3-Kinase Catalytic Subunit. Science, 2007, 317, 239-242. | 6.0 | 364 |
| 10 | Multiple diverse ligands binding at a single protein site: A matter of pre-existing populations. Protein Science, 2009, 11, 184-197. | 3.1 | 364 |
| 11 | Context-free attentional operators: The generalized symmetry transform. International Journal of Computer Vision, 1995, 14, 119-130. | 10.9 | 361 |
| 12 | Studies of proteinâ€protein interfaces: A statistical analysis of the hydrophobic effect. Protein Science, 1997, 6, 53-64. | 3.1 | 361 |
| 13 | Protein Structure Fitting and Refinement Guided by Cryo-EM Density. Structure, 2008, 16, 295-307. | 1.6 | 334 |
| 14 | Affine invariant model-based object recognition. IEEE Transactions on Automation Science and Engineering, 1990, 6, 578-589. | 2.4 | 263 |
| 15 | Efficient detection of three-dimensional structural motifs in biological macromolecules by computer vision techniques.. Proceedings of the National Academy of Sciences of the United States of America, 1991, 88, 10495-10499. | 3.3 | 263 |
| 16 | Recognition of Functional Sites in Protein Structures. Journal of Molecular Biology, 2004, 339, 607-633. | 2.0 | 257 |
| 17 | Conservation of polar residues as hot spots at protein interfaces. , 2000, 39, 331-342. | | 253 |
| 18 | Taking geometry to its edge: Fast unbound rigid (and hinge-bent) docking. Proteins: Structure, Function and Bioinformatics, 2003, 52, 107-112. | 1.5 | 238 |

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| 19 | PharmaGist: a webserver for ligand-based pharmacophore detection. Nucleic Acids Research, 2008, 36, W223-W228. | 6.5 | 231 |
| 20 | HingeProt: Automated prediction of hinges in protein structures. Proteins: Structure, Function and Bioinformatics, 2008, 70, 1219-1227. | 1.5 | 195 |
| 21 | On curve matching. IEEE Transactions on Pattern Analysis and Machine Intelligence, 1990, 12, 483-489. | 9.7 | 192 |
| 22 | Principles of flexible proteinâ€“protein docking. Proteins: Structure, Function and Bioinformatics, 2008, 73, 271-289. | 1.5 | 186 |
| 23 | A new, structurally nonredundant, diverse data set of protein-protein interfaces and its implications. Protein Science, 2004, 13, 1043-1055. | 3.1 | 185 |
| 24 | Geometry-based flexible and symmetric protein docking. Proteins: Structure, Function and Bioinformatics, 2005, 60, 224-231. | 1.5 | 177 |
| 25 | FiberDock: Flexible inducedâ€fit backbone refinement in molecular docking. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1503-1519. | 1.5 | 162 |
| 26 | A Dataset of Proteinâ€“Protein Interfaces Generated with a Sequence-order-independent Comparison Technique. Journal of Molecular Biology, 1996, 260, 604-620. | 2.0 | 156 |
| 27 | Predicting Molecular Interactions in silico: I. A Guide to Pharmacophore Identification and its Applications to Drug Design. Current Medicinal Chemistry, 2004, 11, 71-90. | 1.2 | 142 |
| 28 | Protein-Protein Interactions. Structure, 2004, 12, 1027-1038. | 1.6 | 127 |
| 29 | A computer vision based technique for 3-D sequence-independent structural comparison of proteins. Protein Engineering, Design and Selection, 1993, 6, 279-287. | 1.0 | 125 |
| 30 | Examination of shape complementarity in docking ofUnbound proteins. , 1999, 36, 307-317. | | 118 |
| 31 | Inferential Optimization for Simultaneous Fitting of Multiple Components into a CryoEM Map of Their Assembly. Journal of Molecular Biology, 2009, 388, 180-194. | 2.0 | 117 |
| 32 | An integrated suite of fast docking algorithms. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3197-3204. | 1.5 | 117 |
| 33 | Protein functional epitopes: hot spots, dynamics and combinatorial libraries. Current Opinion in Structural Biology, 2001, 11, 364-369. | 2.6 | 114 |
| 34 | Molecular Surface Complementarity at Protein-Protein Interfaces: The Critical Role Played by Surface Normals at Well Placed, Sparse, Points in Docking. Journal of Molecular Biology, 1995, 252, 263-273. | 2.0 | 113 |
| 35 | Flexible protein alignment and hinge detection. Proteins: Structure, Function and Bioinformatics, 2002, 48, 242-256. | 1.5 | 113 |
| 36 | Interaction of C60-Fullerene and Carboxyfullerene with Proteins:Â Docking and Binding Site Alignment. Bioconjugate Chemistry, 2006, 17, 378-386. | 1.8 | 111 |

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| 37 | Novel Approach for Efficient Pharmacophore-Based Virtual Screening: Method and Applications. Journal of Chemical Information and Modeling, 2009, 49, 2333-2343. | 2.5 | 111 |
| 38 | Protein-Protein Interfaces: Architectures and Interactions in Protein-Protein Interfaces and in Protein Cores. Their Similarities and Differences. Critical Reviews in Biochemistry and Molecular Biology, 1996, 31, 127-152. | 2.3 | 110 |
| 39 | Flexible docking allowing induced fit in proteins: Insights from an open to closed conformational isomers. Proteins: Structure, Function and Bioinformatics, 1998, 32, 159-174. | 1.5 | 110 |
| 40 | Theoretical Characterization of Substrate Access/Exit Channels in the Human Cytochrome P450 3A4 Enzyme: Involvement of Phenylalanine Residues in the Gating Mechanism. Journal of Physical Chemistry B, 2009, 113, 13018-13025. | 1.2 | 105 |
| 41 | Molecular surface representations by sparse critical points. Proteins: Structure, Function and Bioinformatics, 1994, 18, 94-101. | 1.5 | 104 |
| 42 | Solving jigsaw puzzles by computer. Annals of Operations Research, 1988, 12, 51-64. | 2.6 | 102 |
| 43 | Molecular surface recognition by a computer vision-based technique. Protein Engineering, Design and Selection, 1994, 7, 39-46. | 1.0 | 102 |
| 44 | MolAxis: Efficient and accurate identification of channels in macromolecules. Proteins: Structure, Function and Bioinformatics, 2008, 73, 72-86. | 1.5 | 101 |
| 45 | SiteEngines: recognition and comparison of binding sites and protein-protein interfaces. Nucleic Acids Research, 2005, 33, W337-W341. | 6.5 | 99 |
| 46 | Correlated mutations: Advances and limitations. A study on fusion proteins and on the Cohesin-Dockerin families. Proteins: Structure, Function and Bioinformatics, 2006, 63, 832-845. | 1.5 | 95 |
| 47 | Model-based object recognition by geometric hashing. Lecture Notes in Computer Science, 1990, , 526-536. | 1.0 | 91 |
| 48 | Threeâ€dimensional, sequence orderâ€independent structural comparison of a serine protease against the crystallographic database reveals active site similarities: Potential implications to evolution and to protein folding. Protein Science, 1994, 3, 769-778. | 3.1 | 90 |
| 49 | FiberDock: a web server for flexible induced-fit backbone refinement in molecular docking. Nucleic Acids Research, 2010, 38, W457-W461. | 6.5 | 88 |
| 50 | Prediction of Multimolecular Assemblies by Multiple Docking. Journal of Molecular Biology, 2005, 349, 435-447. | 2.0 | 86 |
| 51 | MultiBind and MAPPIS: webservers for multiple alignment of protein 3D-binding sites and their interactions. Nucleic Acids Research, 2008, 36, W260-W264. | 6.5 | 86 |
| 52 | Folding funnels and conformational transitions via hinge-bending motions. Cell Biochemistry and Biophysics, 1999, 31, 141-164. | 0.9 | 85 |
| 53 | Predicting Molecular Interactions in silico: II. Protein-Protein and Protein- Drug Docking. Current Medicinal Chemistry, 2004, 11, 91-107. | 1.2 | 78 |
| 54 | PepCrawler: a fast RRT-based algorithm for high-resolution refinement and binding affinity estimation of peptide inhibitors. Bioinformatics, 2011, 27, 2836-2842. | 1.8 | 78 |

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| 55 | An Efficient Automated Computer Vision Based Technique for Detection of Three Dimensional Structural Motifs in Proteins. Journal of Biomolecular Structure and Dynamics, 1992, 9, 769-789. | 2.0 | 75 |
| 56 | Surface motifs by a computer vision technique: Searches, detection, and implications for protein-ligand recognition. Proteins: Structure, Function and Bioinformatics, 1993, 16, 278-292. | 1.5 | 72 |
| 57 | A Comparative Study of Amyloid Fibril Formation by Residues 15â€“19 of the Human Calcitonin Hormone: A Single Î²-Sheet Model with a Small Hydrophobic Core. Journal of Molecular Biology, 2005, 345, 1213-1227. | 2.0 | 71 |
| 58 | ScanNet: an interpretable geometric deep learning model for structure-based protein binding site prediction. Nature Methods, 2022, 19, 730-739. | 9.0 | 68 |
| 59 | The Multiple Common Point Set Problem and Its Application to Molecule Binding Pattern Detection. Journal of Computational Biology, 2006, 13, 407-428. | 0.8 | 67 |
| 60 | Deterministic Pharmacophore Detection via Multiple Flexible Alignment of Drug-Like Molecules. Journal of Computational Biology, 2008, 15, 737-754. | 0.8 | 67 |
| 61 | Spatial chemical conservation of hot spot interactions in protein-protein complexes. BMC Biology, 2007, 5, 43. | 1.7 | 65 |
| 62 | FlexProt: Alignment of Flexible Protein Structures Without a Predefinition of Hinge Regions. Journal of Computational Biology, 2004, 11, 83-106. | 0.8 | 64 |
| 63 | Determining macromolecular assembly structures by molecular docking and fitting into an electron density map. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3205-3211. | 1.5 | 63 |
| 64 | MUSTA - A General, Efficient, Automated Method for Multiple Structure Alignment and Detection of Common Motifs: Application to Proteins. Journal of Computational Biology, 2001, 8, 93-121. | 0.8 | 62 |
| 65 | MolAxis: a server for identification of channels in macromolecules. Nucleic Acids Research, 2008, 36, W210-W215. | 6.5 | 62 |
| 66 | Identification of the N-terminal Peptide Binding Site of Glucose-regulated Protein 94. Journal of Biological Chemistry, 2004, 279, 16543-16552. | 1.6 | 61 |
| 67 | Automated multiple structure alignment and detection of a common substructural motif. Proteins: Structure, Function and Bioinformatics, 2001, 43, 235-245. | 1.5 | 60 |
| 68 | SiteLight: Binding-site prediction using phage display libraries. Protein Science, 2003, 12, 1344-1359. | 3.1 | 60 |
| 69 | Structure-based in silico identification of ubiquitin-binding domains provides insights into the ALIX-V:ubiquitin complex and retrovirus budding. EMBO Journal, 2013, 32, 538-551. | 3.5 | 59 |
| 70 | Multiple structural alignment by secondary structures: Algorithm and applications. Protein Science, 2009, 12, 2492-2507. | 3.1 | 58 |
| 71 | ARTS: alignment of RNA tertiary structures. Bioinformatics, 2005, 21, ii47-ii53. | 1.8 | 57 |
| 72 | A Method for Biomolecular Structural Recognition and Docking Allowing Conformational Flexibility. Journal of Computational Biology, 1998, 5, 631-654. | 0.8 | 56 |

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| 73 | How Does the Reductase Help To Regulate the Catalytic Cycle of Cytochrome P450 3A4 Using the Conserved Water Channel?. Journal of Physical Chemistry B, 2010, 114, 5964-5970. | 1.2 | 54 |
| 74 | Solving jigsaw puzzles by a robot. IEEE Transactions on Automation Science and Engineering, 1989, 5, 752-764. | 2.4 | 52 |
| 75 | Principles of nanostructure design with protein building blocks. Proteins: Structure, Function and Bioinformatics, 2007, 68, 1-12. | 1.5 | 51 |
| 76 | A 3D sequence-independent representation of the protein data bank. Protein Engineering, Design and Selection, 1995, 8, 981-997. | 1.0 | 49 |
| 77 | Reducing the computational complexity of protein folding via fragment folding and assembly. Protein Science, 2003, 12, 1177-1187. | 3.1 | 48 |
| 78 | Optimization of multiple-sequence alignment based on multiple-structure alignment. Proteins: Structure, Function and Bioinformatics, 2005, 62, 209-217. | 1.5 | 48 |
| 79 | Structural Dynamics of the Cooperative Binding of Organic Molecules in the Human Cytochrome P450 3A4. Journal of the American Chemical Society, 2007, 129, 1602-1611. | 6.6 | 48 |
| 80 | Automatic prediction of protein interactions with large scale motion. Proteins: Structure, Function and Bioinformatics, 2007, 69, 764-773. | 1.5 | 47 |
| 81 | Principles of docking: An overview of search algorithms and a guide to scoring functions. , 2002, 47, 409. | | 46 |
| 82 | Protein structure prediction via combinatorial assembly of sub-structural units. Bioinformatics, 2003, 19, i158-i168. | 1.8 | 44 |
| 83 | Generation and analysis of a protein-protein interface data set with similar chemical and spatial patterns of interactions. Proteins: Structure, Function and Bioinformatics, 2005, 61, 6-20. | 1.5 | 44 |
| 84 | Combinatorial docking approach for structure prediction of large proteins and multi-molecular assemblies. Physical Biology, 2005, 2, S156-S165. | 0.8 | 44 |
| 85 | MultiProt â€" A Multiple Protein Structural Alignment Algorithm. Lecture Notes in Computer Science, 2002, , 235-250. | 1.0 | 42 |
| 86 | Analysis and classification of RNA tertiary structures. Rna, 2008, 14, 2274-2289. | 1.6 | 42 |
| 87 | Memdock: an Î±-helical membrane protein docking algorithm. Bioinformatics, 2016, 32, 2444-2450. | 1.8 | 42 |
| 88 | De Novo Tubular Nanostructure Design Based on Self-Assembly of Î²-Helical Protein Motifs. Structure, 2006, 14, 1137-1148. | 1.6 | 41 |
| 89 | The ARTS web server for aligning RNA tertiary structures. Nucleic Acids Research, 2006, 34, W412-W415. | 6.5 | 40 |
| 90 | EMatch: Discovery of High Resolution Structural Homologues of Protein Domains in Intermediate Resolution Cryo-EM Maps. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 28-39. | 1.9 | 37 |

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| 91 | QM/MM Study of the Active Species of the Human Cytochrome P450 3A4, and the Influence Thereof of the Multiple Substrate Binding. Journal of Physical Chemistry B, 2007, 111, 13822-13832. | 1.2 | 36 |
| 92 | 3â€Ð curve matching using splines. Journal of Field Robotics, 1991, 8, 723-743. | 0.7 | 35 |
| 93 | Amino Acid Pair Interchanges at Spatially Conserved Locations. Journal of Molecular Biology, 1996, 256, 924-938. | 2.0 | 35 |
| 94 | Prediction of Interacting Single-Stranded RNA Bases by Protein-Binding Patterns. Journal of Molecular Biology, 2008, 379, 299-316. | 2.0 | 35 |
| 95 | 3-D curve matching using splines. Lecture Notes in Computer Science, 1990, , 589-591. | 1.0 | 32 |
| 96 | From Structure to Function: Methods and Applications. Current Protein and Peptide Science, 2005, 6, 171-183. | 0.7 | 32 |
| 97 | Detection of non-topological motifs in protein structures. Protein Engineering, Design and Selection, 1996, 9, 1103-1119. | 1.0 | 31 |
| 98 | Î²2-Microglobulin Amyloidosis: Insights from Conservation Analysis and Fibril Modelling by Protein Docking Techniques. Journal of Molecular Biology, 2003, 330, 159-174. | 2.0 | 31 |
| 99 | Flexible structural comparison allowing hinge-bending, swiveling motions. , 1999, 34, 232-254. | | 30 |
| 100 | Allosteric Regulation of Glycogen Synthase Kinase 3Î²: A Theoretical Study. Biochemistry, 2010, 49, 10890-10901. | 1.2 | 30 |
| 101 | Hierarchical protein folding pathways: A computational study of protein fragments. Proteins: Structure, Function and Bioinformatics, 2003, 51, 203-215. | 1.5 | 29 |
| 102 | RsiteDB: a database of protein binding pockets that interact with RNA nucleotide bases. Nucleic Acids Research, 2009, 37, D369-D373. | 6.5 | 27 |
| 103 | MultiFit: a web server for fitting multiple protein structures into their electron microscopy density map. Nucleic Acids Research, 2011, 39, W167-W170. | 6.5 | 27 |
| 104 | Minkowski spaces with extremal distance from the Euclidean space. Israel Journal of Mathematics, 1978, 29, 113-131. | 0.4 | 26 |
| 105 | Protein-Protein Interfaces: Recognition of Similar Spatial and Chemical Organizations. Lecture Notes in Computer Science, 2004, , 194-205. | 1.0 | 25 |
| 106 | PinaColada: peptideâ€“inhibitor ant colony ad-hoc design algorithm. Bioinformatics, 2016, 32, 2289-2296. | 1.8 | 24 |
| 107 | Generalizing the generalized hough transform. Pattern Recognition Letters, 1991, 12, 565-573. | 2.6 | 23 |
| 108 | BioInfo3D: a suite of tools for structural bioinformatics. Nucleic Acids Research, 2004, 32, W503-W507. | 6.5 | 23 |

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| 109 | Recognition of Binding Patterns Common to a Set of Protein Structures. Lecture Notes in Computer Science, 2005, , 440-455. | 1.0 | 23 |
| 110 | Metabolic stereoselectivity of cytochrome P450 3A4 towards deoxypodophyllotoxin: In silico predictions and experimental validation. European Journal of Medicinal Chemistry, 2008, 43, 1171-1179. | 2.6 | 21 |
| 111 | Approaching the CAPRI challenge with an efficient geometry-based docking. Proteins: Structure, Function and Bioinformatics, 2005, 60, 217-223. | 1.5 | 20 |
| 112 | Concepts and schemes for the re-engineering of physical protein modules: generating nanodevices via targeted replacements with constrained amino acids. Physical Biology, 2006, 3, S54-S62. | 0.8 | 20 |
| 113 | EMatch: an efficient method for aligning atomic resolution subunits into intermediate-resolution cryo-EM maps of large macromolecular assemblies. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 42-49. | 2.5 | 20 |
| 114 | Side chain interactions determine the amyloid organization: a single layer Â-sheet molecular structure of the calcitonin peptide segment 15â€“19. Physical Biology, 2004, 1, 89-99. | 0.8 | 19 |
| 115 | Changing the Charge Distribution of Î²-Helical-Based Nanostructures Can Provide the Conditions for Charge Transfer. Biophysical Journal, 2007, 93, 245-253. | 0.2 | 18 |
| 116 | Deterministic Pharmacophore Detection Via Multiple Flexible Alignment of Drug-Like Molecules. Lecture Notes in Computer Science, 2007, , 412-429. | 1.0 | 17 |
| 117 | An automated computer vision and roboticsbased technique for 3-D flexible biomolecular docking and matching. Bioinformatics, 1995, 11, 87-99. | 1.8 | 16 |
| 118 | SymmRef: A flexible refinement method for symmetric multimers. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2607-2623. | 1.5 | 16 |
| 119 | Design of Disruptors of the Hsp90â€“Cdc37 Interface. Molecules, 2020, 25, 360. | 1.7 | 14 |
| 120 | Diameter-selective dispersion of carbon nanotubes by Î²-lactoglobulin whey protein. Colloids and Surfaces B: Biointerfaces, 2013, 112, 16-22. | 2.5 | 13 |
| 121 | Conservation and amyloid formation: A study of the gelsolin-like family. Proteins: Structure, Function and Bioinformatics, 2003, 51, 266-282. | 1.5 | 12 |
| 122 | DockStar: a novel ILP-based integrative method for structural modeling of multimolecular protein complexes. Bioinformatics, 2015, 31, 2801-2807. | 1.8 | 12 |
| 123 | Modeling of Multimolecular Complexes. Methods in Molecular Biology, 2020, 2112, 163-174. | 0.4 | 12 |
| 124 | Investigation of the enzymatic mechanism of the yeast chorismate mutase by docking a transition state analog. Journal of Molecular Biology, 1997, 271, 838-845. | 2.0 | 11 |
| 125 | Conformational transitions in human translin enable nucleic acid binding. Nucleic Acids Research, 2013, 41, 9956-9966. | 6.5 | 11 |
| 126 | SnapDockâ€”template-based docking by Geometric Hashing. Bioinformatics, 2017, 33, i30-i36. | 1.8 | 11 |

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| 127 | Geometric Hashing. IEEE Computational Science and Engineering, 1997, 4, 9-9. | 0.6 | 10 |
| 128 | Constructing templates for protein structure prediction by simulation of protein folding pathways. Proteins: Structure, Function and Bioinformatics, 2008, 73, 380-394. | 1.5 | 9 |
| 129 | 3-D substructure matching in protein Molecules. Lecture Notes in Computer Science, 1992, , 136-150. | 1.0 | 9 |
| 130 | 3-D docking of protein molecules. , 1993, , 20-34. | | 7 |
| 131 | Fibril modelling by sequence and structure conservation analysis combined with protein docking techniques: Î²2-microglobulin amyloidosis. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2005, 1753, 121-130. | 1.1 | 6 |
| 132 | Computational Validation of Protein Nanotubes. Nano Letters, 2009, 9, 1096-1102. | 4.5 | 6 |
| 133 | AAnchor: CNN guided detection of anchor amino acids in high resolution cryo-EM density maps. , 2018, , . | | 6 |
| 134 | Spatial, Sequence-Order-Independent Structural Comparison of Î±/Î² Proteins: Evolutionaiy Implications. Journal of Biomolecular Structure and Dynamics, 1993, 11, 367-380. | 2.0 | 5 |
| 135 | Docking of conformationally flexible proteins. Lecture Notes in Computer Science, 1996, , 271-287. | 1.0 | 5 |
| 136 | Structural similarity of genetically interacting proteins. BMC Systems Biology, 2008, 2, 69. | 3.0 | 5 |
| 137 | Efficient Computational Algorithms for Docking and for Generating and Matching a Library of Functional Epitopes I. Rigid and Flexible Hinge-Bending Docking Algorithms. Combinatorial Chemistry and High Throughput Screening, 1999, 2, 249-259. | 0.6 | 5 |
| 138 | Geometrical Docking Algorithms A Practical Approach. , 2000, 143, 377-397. | | 4 |
| 139 | Potential folding-function interrelationship in proteins. Proteins: Structure, Function and Bioinformatics, 2004, 56, 635-649. | 1.5 | 4 |
| 140 | A permissive secondary structure-guided superposition tool for clustering of protein fragments toward protein structure prediction via fragment assembly. Bioinformatics, 2006, 22, 1343-1352. | 1.8 | 4 |
| 141 | Memdock: An Î±-Helical Membrane Protein Docking Algorithm. Methods in Molecular Biology, 2021, 2315, 111-117. | 0.4 | 4 |
| 142 | Discovery of Protein Substructures in EM Maps. Lecture Notes in Computer Science, 2005, , 423-434. | 1.0 | 4 |
| 143 | MAPPIS: Multiple 3D Alignment of Protein-Protein Interfaces. Lecture Notes in Computer Science, 2005, , 91-103. | 1.0 | 4 |
| 144 | Algorithms for Multiple Protein Structure Alignment and Structure-Derived Multiple Sequence Alignment. , 2008, 413, 125-146. | | 3 |

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| 145 | Protein structure prediction using a dockingâ€based hierarchical folding scheme. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1759-1773. | 1.5 | 3 |
| 146 | Conservation of polar residues as hot spots at protein interfaces. , 2000, 39, 331. | | 3 |
| 147 | Efficient Computational Algorithms for Docking and for Generating and Matching a Library of Functional Epitopes II. Computer Vision-Based Techniques for the Generation and Utilization of Functional Epitopes. Combinatorial Chemistry and High Throughput Screening, 1999, 2, 261-269. | 0.6 | 3 |
| 148 | Pepâ€“Whisperer: Inhibitory peptide design. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1886-1895. | 1.5 | 3 |
| 149 | Techniques for searching for structural similarities between protein cores, protein surfaces and between protein-protein interfaces. Techniques in Protein Chemistry, 1996, , 419-429. | 0.3 | 2 |
| 150 | A Hierarchical Protein Folding Scheme Based on the Building Block Folding Model. , 2007, 350, 189-204. | | 2 |
| 151 | Protein-Peptide Interaction Design: PepCrawler and PinaColada. Methods in Molecular Biology, 2017, 1561, 279-290. | 0.4 | 2 |
| 152 | From computer vision to protein structure and association. New Comprehensive Biochemistry, 1998, , 313-334. | 0.1 | 1 |
| 153 | Symmetry-Based Self-Assembled Nanotubes Constructed Using Native Protein Structures: The Key Role of Flexible Linkers. Protein and Peptide Letters, 2011, 18, 362-372. | 0.4 | 1 |
| 154 | Spatial Pattern Detection in Structural Bionformatics. Lecture Notes in Computer Science, 2003, , 35-56. | 1.0 | 0 |
| 155 | Gelsolin. , 0, , 625-634. | | 0 |
| 156 | Proteinâ€Protein Interaction Modeling and Inhibition: The TAU Bioinfo3D Perspective. Israel Journal of Chemistry, 2013, 53, 180-184. | 1.0 | 0 |
| 157 | Accelerating protein-protein complex validation by GPU based funnel generation. , 2016, , . | | 0 |
| 158 | Self-Assembly of Fused Homo-Oligomers to Create Nanotubes. Methods in Molecular Biology, 2008, 474, 117-131. | 0.4 | 0 |