# David R Hall

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/11939908/publications.pdf

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|---|---|---|---|
| 31 papers | 5,640 citations | 218677 26 h-index | 434195 31 g-index |
| 32 all docs | 32 docs citations | 32 times ranked | 8265 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | The ClusPro web server for proteinâ€“protein docking. Nature Protocols, 2017, 12, 255-278. | 12.0 | 1,959 |
| 2 | How good is automated protein docking?. Proteins: Structure, Function and Bioinformatics, 2013, 81, 2159-2166. | 2.6 | 570 |
| 3 | The FTMap family of web servers for determining and characterizing ligand-binding hot spots of proteins. Nature Protocols, 2015, 10, 733-755. | 12.0 | 496 |
| 4 | New additions to the <scp>C</scp>lus<scp>P</scp>ro server motivated by <scp>CAPRI</scp>. Proteins: Structure, Function and Bioinformatics, 2017, 85, 435-444. | 2.6 | 395 |
| 5 | Structural conservation of druggable hot spots in proteinâ€“protein interfaces. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 13528-13533. | 7.1 | 220 |
| 6 | Achieving reliability and high accuracy in automated protein docking: Cluspro, PIPER, SDU, and stability analysis in CAPRI rounds 13â€“19. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3124-3130. | 2.6 | 211 |
| 7 | FTSite: high accuracy detection of ligand binding sites on unbound protein structures. Bioinformatics, 2012, 28, 286-287. | 4.1 | 189 |
| 8 | Application of asymmetric statistical potentials to antibodyâ€“protein docking. Bioinformatics, 2012, 28, 2608-2614. | 4.1 | 156 |
| 9 | Reversing chemoresistance by small molecule inhibition of the translation initiation complex eIF4F. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1046-1051. | 7.1 | 153 |
| 10 | Prediction of homoprotein and heteroprotein complexes by protein docking and templateâ€based modeling: A CASPâ€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2016, 84, 323-348. | 2.6 | 148 |
| 11 | FTMAP: extended protein mapping with user-selected probe molecules. Nucleic Acids Research, 2012, 40, W271-W275. | 14.5 | 130 |
| 12 | Relationship between Hot Spot Residues and Ligand Binding Hot Spots in Proteinâ€“Protein Interfaces. Journal of Chemical Information and Modeling, 2012, 52, 2236-2244. | 5.4 | 99 |
| 13 | Exploring the structural origins of cryptic sites on proteins. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E3416-E3425. | 7.1 | 96 |
| 14 | Blocking eIF4E-eIF4G Interaction as a Strategy To Impair Coronavirus Replication. Journal of Virology, 2011, 85, 6381-6389. | 3.4 | 93 |
| 15 | New Frontiers in Druggability. Journal of Medicinal Chemistry, 2015, 58, 9063-9088. | 6.4 | 93 |
| 16 | Community-wide evaluation of methods for predicting the effect of mutations on protein-protein interactions. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1980-1987. | 2.6 | 87 |
| 17 | Ligand deconstruction: Why some fragment binding positions are conserved and others are not. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E2585-94. | 7.1 | 61 |
| 18 | Encounter complexes and dimensionality reduction in proteinâ€“protein association. ELife, 2014, 3, e01370. | 6.0 | 61 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Sampling and scoring: A marriage made in heaven. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1874-1884. | 2.6 | 58 |
| 20 | Lessons from Hot Spot Analysis for Fragment-Based Drug Discovery. Trends in Pharmacological Sciences, 2015, 36, 724-736. | 8.7 | 58 |
| 21 | Hot Spot Analysis for Driving the Development of Hits into Leads in Fragment-Based Drug Discovery. Journal of Chemical Information and Modeling, 2012, 52, 199-209. | 5.4 | 52 |
| 22 | Kinase Atlas: Druggability Analysis of Potential Allosteric Sites in Kinases. Journal of Medicinal Chemistry, 2019, 62, 6512-6524. | 6.4 | 52 |
| 23 | Computational mapping reveals dramatic effect of Hoogsteen breathing on duplex DNA reactivity with formaldehyde. Nucleic Acids Research, 2012, 40, 7644-7652. | 14.5 | 37 |
| 24 | ClusPro-DC: Dimer Classification by the Cluspro Server for Proteinâ€“Protein Docking. Journal of Molecular Biology, 2017, 429, 372-381. | 4.2 | 36 |
| 25 | FTFlex: accounting for binding site flexibility to improve fragment-based identification of druggable hot spots. Bioinformatics, 2013, 29, 1218-1219. | 4.1 | 30 |
| 26 | Interaction Energetics and Druggability of the Proteinâ€“Protein Interaction between Kelch-like ECH-Associated Protein 1 (KEAP1) and Nuclear Factor Erythroid 2 Like 2 (Nrf2). Biochemistry, 2020, 59, 563-581. | 2.5 | 28 |
| 27 | Minimal ensembles of side chain conformers for modeling proteinâ€“protein interactions. Proteins: Structure, Function and Bioinformatics, 2012, 80, 591-601. | 2.6 | 26 |
| 28 | Analysis of Protein Binding Sites by Computational Solvent Mapping. Methods in Molecular Biology, 2012, 819, 13-27. | 0.9 | 19 |
| 29 | Computational solvent mapping in structure-based drug design. Future Medicinal Chemistry, 2015, 7, 337-353. | 2.3 | 14 |
| 30 | Proteinâ€“ligand docking using FFT based sampling: D3R case study. Journal of Computer-Aided Molecular Design, 2018, 32, 225-230. | 2.9 | 9 |
| 31 | Stimulators of translation identified during a small molecule screening campaign. Analytical Biochemistry, 2014, 447, 6-14. | 2.4 | 4 |