# Barry Honig

List of Publications by Year
in descending order

| 90 | 15,708 | 47006 47 | 45317 90 |
|---|---|---|---|
| papers | citations | h-index | g-index |

| 100 | 100 | 100 | 14898 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | ARTICLE | IF | CITATIONS |
|---|---------|-----|-----------|
| 1 | Protein folding and association: Insights from the interfacial and thermodynamic properties of hydrocarbons. Proteins: Structure, Function and Bioinformatics, 1991, 11, 281-296. | 2.6 | 5,360 |
| 2 | A rapid finite difference algorithm, utilizing successive over-relaxation to solve the Poisson-Boltzmann equation. Journal of Computational Chemistry, 1991, 12, 435-445. | 3.3 | 1,194 |
| 3 | Calculation of the total electrostatic energy of a macromolecular system: Solvation energies, binding energies, and conformational analysis. Proteins: Structure, Function and Bioinformatics, 1988, 4, 7-18. | 2.6 | 794 |
| 4 | Focusing of electric fields in the active site of Cu-Zn superoxide dismutase: Effects of ionic strength and amino-acid modification. Proteins: Structure, Function and Bioinformatics, 1986, 1, 47-59. | 2.6 | 730 |
| 5 | Structure-based prediction of protein–protein interactions on a genome-wide scale. Nature, 2012, 490, 556-560. | 27.8 | 652 |
| 6 | On the calculation of pKas in proteins. Proteins: Structure, Function and Bioinformatics, 1993, 15, 252-265. | 2.6 | 514 |
| 7 | Thinking outside the cell: how cadherins drive adhesion. Trends in Cell Biology, 2012, 22, 299-310. | 7.9 | 296 |
| 8 | Using multiple structure alignments, fast model building, and energetic analysis in fold recognition and homology modeling. Proteins: Structure, Function and Bioinformatics, 2003, 53, 430-435. | 2.6 | 290 |
| 9 | The electrostatic potential of B-DNA. Biopolymers, 1989, 28, 975-993. | 2.4 | 267 |
| 10 | Type II Cadherin Ectodomain Structures: Implications for Classical Cadherin Specificity. Cell, 2006, 124, 1255-1268. | 28.9 | 252 |
| 11 | Calculating the electrostatic properties of RNA provides new insights into molecular interactions and function. Nature Structural Biology, 1999, 6, 1055-1061. | 9.7 | 196 |
| 12 | Dclk1 Defines Quiescent Pancreatic Progenitors that Promote Injury-Induced Regeneration and Tumorigenesis. Cell Stem Cell, 2016, 18, 441-455. | 11.1 | 196 |
| 13 | An integrated approach to the analysis and modeling of protein sequences and structures. I. Protein structural alignment and a quantitative measure for protein structural distance 1 1Edited by F. E. Cohen. Journal of Molecular Biology, 2000, 301, 665-678. | 4.2 | 194 |
| 14 | Single-Cell Identity Generated by Combinatorial Homophilic Interactions between α, β, and γ Protocadherins. Cell, 2014, 158, 1045-1059. | 28.9 | 190 |
| 15 | Two-step adhesive binding by classical cadherins. Nature Structural and Molecular Biology, 2010, 17, 348-357. | 8.2 | 184 |
| 16 | On the calculation of binding free energies using continuum methods: Application to MHC class I protein–peptide interactions. Protein Science, 1997, 6, 1293-1301. | 7.6 | 179 |
| 17 | Acetylation-regulated interaction between p53 and SET reveals a widespread regulatory mode. Nature, 2016, 538, 118-122. | 27.8 | 160 |
| 18 | The fast multipole boundary element method for molecular electrostatics: An optimal approach for large systems. Journal of Computational Chemistry, 1995, 16, 898-913. | 3.3 | 147 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 19 | Molecular Logic of Neuronal Self-Recognition through Protocadherin Domain Interactions. Cell, 2015, 163, 629-642. | 28.9 | 141 |
| 20 | ON THE MECHANISM OF WAVELENGTH REGULATION IN VISUAL PIGMENTS. Photochemistry and Photobiology, 1985, 41, 471-479. | 2.5 | 137 |
| 21 | Structural basis of adhesive binding by desmocollins and desmogleins. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 7160-7165. | 7.1 | 137 |
| 22 | Genetic Drivers of Kidney Defects in the DiGeorge Syndrome. New England Journal of Medicine, 2017, 376, 742-754. | 27.0 | 120 |
| 23 | Salt effects on polyelectrolyte-ligand binding: Comparison of Poisson-Boltzmann, and limiting law/counterion binding models. Biopolymers, 1995, 36, 245-262. | 2.4 | 116 |
| 24 | Evaluation of the conformational free energies of loops in proteins. Proteins: Structure, Function and Bioinformatics, 1994, 18, 119-132. | 2.6 | 113 |
| 25 | A Structure-Informed Atlas of Human-Virus Interactions. Cell, 2019, 178, 1526-1541.e16. | 28.9 | 108 |
| 26 | Adhesion Protein Structure, Molecular Affinities, and Principles of Cell-Cell Recognition. Cell, 2020, 181, 520-535. | 28.9 | 108 |
| 27 | Electrostatic contributions to protein-protein interactions: Fast energetic filters for docking and their physical basis. Protein Science, 2008, 10, 2147-2161. | 7.6 | 105 |
| 28 | Nectin ectodomain structures reveal a canonical adhesive interface. Nature Structural and Molecular Biology, 2012, 19, 906-915. | 8.2 | 104 |
| 29 | Molecular design principles underlying β-strand swapping in the adhesive dimerization of cadherins. Nature Structural and Molecular Biology, 2011, 18, 693-700. | 8.2 | 101 |
| 30 | PredUs: a web server for predicting protein interfaces using structural neighbors. Nucleic Acids Research, 2011, 39, W283-W287. | 14.5 | 101 |
| 31 | Free energy determinants of tertiary structure and the evaluation of protein models. Protein Science, 2000, 9, 2181-2191. | 7.6 | 96 |
| 32 | Silencing c-Myc translation as a therapeutic strategy through targeting PI3Kδ and CK1ε in hematological malignancies. Blood, 2017, 129, 88-99. | 1.4 | 92 |
| 33 | The electrostatic contribution to DNA base-stacking interactions. Biopolymers, 1992, 32, 145-159. | 2.4 | 89 |
| 34 | Splice Form Dependence of β-Neurexin/Neuroligin Binding Interactions. Neuron, 2010, 67, 61-74. | 8.1 | 89 |
| 35 | Structural Basis of Diverse Homophilic Recognition by Clustered α- and β-Protocadherins. Neuron, 2016, 90, 709-723. | 8.1 | 87 |
| 36 | Visualization of clustered protocadherin neuronal self-recognition complexes. Nature, 2019, 569, 280-283. | 27.8 | 86 |

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|---|---------|-----|-----------|
| 37 | E-cadherin junction formation involves an active kinetic nucleation process. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10932-10937. | 7.1 | 84 |
| 38 | Discovery of an O-mannosylation pathway selectively serving cadherins and protocadherins. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 11163-11168. | 7.1 | 83 |
| 39 | Free Energy Perturbation Calculation of Relative Binding Free Energy between Broadly Neutralizing Antibodies and the gp120 Glycoprotein of HIV-1. Journal of Molecular Biology, 2017, 429, 930-947. | 4.2 | 82 |
| 40 | Structural and energetic determinants of adhesive binding specificity in type I cadherins. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4175-84. | 7.1 | 78 |
| 41 | Mechanism of E-cadherin dimerization probed by NMR relaxation dispersion. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 16462-16467. | 7.1 | 70 |
| 42 | SH2 Domains Serve as Lipid-Binding Modules for pTyr-Signaling Proteins. Molecular Cell, 2016, 62, 7-20. | 9.7 | 69 |
| 43 | Neuron-Subtype-Specific Expression, Interaction Affinities, and Specificity Determinants of DIP/Dpr Cell Recognition Proteins. Neuron, 2018, 100, 1385-1400.e6. | 8.1 | 65 |
| 44 | Interactions between the Ig-Superfamily Proteins DIP-Î± and Dpr6/10 Regulate Assembly of Neural Circuits. Neuron, 2018, 100, 1369-1384.e6. | 8.1 | 64 |
| 45 | Genome-wide prediction of minor-groove electrostatic potential enables biophysical modeling of proteinâ€"DNA binding. Nucleic Acids Research, 2017, 45, 12565-12576. | 14.5 | 63 |
| 46 | Monovalent and Divalent Salt Effects on Electrostatic Free Energies Defined by the Nonlinear Poissonâ^Boltzmann Equation:Â Application to DNA Binding Reactions. Journal of Physical Chemistry B, 1997, 101, 9113-9118. | 2.6 | 60 |
| 47 | A computational interactome and functional annotation for the human proteome. ELife, 2016, 5, . | 6.0 | 58 |
| 48 | Dynamic Properties of a Type II Cadherin Adhesive Domain: Implications for the Mechanism of Strand-Swapping of Classical Cadherins. Structure, 2008, 16, 1195-1205. | 3.3 | 55 |
| 49 | Protocadherin *cis* -dimer architecture and recognition unit diversity. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9829-E9837. | 7.1 | 55 |
| 50 | Homophilic and Heterophilic Interactions of Type II Cadherins Identify Specificity Groups Underlying Cell-Adhesive Behavior. Cell Reports, 2018, 23, 1840-1852. | 6.4 | 54 |
| 51 | Î³-Protocadherin structural diversity and functional implications. ELife, 2016, 5, . | 6.0 | 54 |
| 52 | An Ankyrin Repeat Domain of AKR2 Drives Chloroplast Targeting through Coincident Binding of Two Chloroplast Lipids. Developmental Cell, 2014, 30, 598-609. | 7.0 | 49 |
| 53 | Sequence to structure alignment in comparative modeling using PrISM. Proteins: Structure, Function and Bioinformatics, 1999, 37, 66-72. | 2.6 | 48 |
| 54 | Spatial and temporal organization of cadherin in punctate adherens junctions. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E4406-E4415. | 7.1 | 46 |

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|---|---------|-----|-----------|
| 55 | Structure-based prediction of ligand–protein interactions on a genome-wide scale. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 13685-13690. | 7.1 | 44 |
| 56 | Mechanotransduction by PCDH15 Relies on a Novel cis-Dimeric Architecture. Neuron, 2018, 99, 480-492.e5. | 8.1 | 43 |
| 57 | α-Catenin–mediated cadherin clustering couples cadherin and actin dynamics. Journal of Cell Biology, 2015, 210, 647-661. | 5.2 | 42 |
| 58 | Lipids Regulate Lck Protein Activity through Their Interactions with the Lck Src Homology 2 Domain. Journal of Biological Chemistry, 2016, 291, 17639-17650. | 3.4 | 42 |
| 59 | Theory and Simulations of Adhesion Receptor Dimerization on Membrane Surfaces. Biophysical Journal, 2013, 104, 1221-1229. | 0.5 | 40 |
| 60 | Template-based prediction of protein function. Current Opinion in Structural Biology, 2015, 32, 33-38. | 5.7 | 39 |
| 61 | A hybrid method for protein–protein interface prediction. Protein Science, 2016, 25, 159-165. | 7.6 | 37 |
| 62 | Structural origins of clustered protocadherin-mediated neuronal barcoding. Seminars in Cell and Developmental Biology, 2017, 69, 140-150. | 5.0 | 36 |
| 63 | Molecular basis of sidekick-mediated cell-cell adhesion and specificity. ELife, 2016, 5, . | 6.0 | 36 |
| 64 | Family-wide Structural and Biophysical Analysis of Binding Interactions among Non-clustered γ-Protocadherins. Cell Reports, 2020, 30, 2655-2671.e7. | 6.4 | 35 |
| 65 | Crystal Structures of β-Neurexin 1 and β-Neurexin 2 Ectodomains and Dynamics of Splice Insertion Sequence 4. Structure, 2008, 16, 410-421. | 3.3 | 33 |
| 66 | Grass: A server for the graphical representation and analysis of structures. Protein Science, 1999, 8, 676-679. | 7.6 | 32 |
| 67 | Intrinsic DNA Shape Accounts for Affinity Differences between Hox-Cofactor Binding Sites. Cell Reports, 2018, 24, 2221-2230. | 6.4 | 31 |
| 68 | Size Dependence of Transfer Free Energies. 2. Hard Sphere Models. The Journal of Physical Chemistry, 1996, 100, 14166-14177. | 2.9 | 27 |
| 69 | Structural determinants of trypsin affinity and specificity for cationic inhibitors. Protein Science, 1999, 8, 2621-2629. | 7.6 | 27 |
| 70 | DIP/Dpr interactions and the evolutionary design of specificity in protein families. Nature Communications, 2020, 11, 2125. | 12.8 | 26 |
| 71 | Trans-endocytosis elicited by nectins transfers cytoplasmic cargo including infectious material between cells. Journal of Cell Science, 2019, 132, . | 2.0 | 25 |
| 72 | A Sweep of Earth's Virome Reveals Host-Guided Viral Protein Structural Mimicry and Points to Determinants of Human Disease. Cell Systems, 2021, 12, 82-91.e3. | 6.2 | 24 |

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|---|---------|-----|-----------|
| 73 | Toward a "Structural BLAST" Using structural relationships to infer function. Protein Science, 2013, 22, 359-366. | 7.6 | 23 |
| 74 | Sensing Actin Dynamics through Adherens Junctions. Cell Reports, 2020, 30, 2820-2833.e3. | 6.4 | 22 |
| 75 | Oncoprotein-specific molecular interaction maps (SigMaps) for cancer network analyses. Nature Biotechnology, 2021, 39, 215-224. | 17.5 | 21 |
| 76 | Bi-allelic missense disease-causing variants in RPL3L associate neonatal dilated cardiomyopathy with muscle-specific ribosome biogenesis. Human Genetics, 2020, 139, 1443-1454. | 3.8 | 20 |
| 77 | Pathogenic IgG4 autoantibodies from endemic pemphigus foliaceus recognize a desmoglein-1 conformational epitope. Journal of Autoimmunity, 2018, 89, 171-185. | 6.5 | 19 |
| 78 | Integrating 3D structural information into systems biology. Journal of Biological Chemistry, 2021, 296, 100562. | 3.4 | 18 |
| 79 | Synaptogenic activity of the axon guidance molecule Robo2 underlies hippocampal circuit function. Cell Reports, 2021, 37, 109828. | 6.4 | 18 |
| 80 | Sequence to structure alignment in comparative modeling using PrISM. Proteins: Structure, Function and Bioinformatics, 1999, 37, 66-72. | 2.6 | 17 |
| 81 | Predicting Peptide-Mediated Interactions on a Genome-Wide Scale. PLoS Computational Biology, 2015, 11, e1004248. | 3.2 | 16 |
| 82 | p21-activated Kinases (PAKs) Mediate the Phosphorylation of PREX2 Protein to Initiate Feedback Inhibition of Rac1 GTPase. Journal of Biological Chemistry, 2015, 290, 28915-28931. | 3.4 | 14 |
| 83 | Sorting of cadherin–catenin-associated proteins into individual clusters. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, . | 7.1 | 14 |
| 84 | Affinity requirements for control of synaptic targeting and neuronal cell survival by heterophilic IgSF cell adhesion molecules. Cell Reports, 2022, 39, 110618. | 6.4 | 9 |
| 85 | A High-Throughput Strategy for Dissecting Mammalian Genetic Interactions. PLoS ONE, 2016, 11, e0167617. | 2.5 | 4 |
| 86 | Dimerization of Cadherin-11 involves multi-site coupled unfolding and strand swapping. Structure, 2021, 29, 1105-1115.e6. | 3.3 | 3 |
| 87 | Strategy for Overcoming Crebbp and EP300 Mutations in Lymphoma: Development of First-in-Class HAT Activators. Blood, 2019, 134, 4068-4068. | 1.4 | 3 |
| 88 | Combining Bioinformatics and Biophysics to Understand Protein-Protein and Protein-Ligand Interactions. Scientific World Journal, The, 2002, 2, 43-44. | 2.1 | 1 |
| 89 | Macroscopic Treatments of Electrostatic and Hydrophobic Free Energies. AIP Conference Proceedings, 1991, , . | 0.4 | 0 |
| 90 | Histone Acetyltransferase (HAT) Activator, YF2, Modulates the p53:BCL6 Axis and Antigen Presentation in Diffuse Large B-Cell Lymphomas. Blood, 2021, 138, 2254-2254. | 1.4 | 0 |