Barry Honig

List of Publications by Year
in descending order

90 papers	15,708 citations	53939 47 h-index	51423 90 g-index
100 all docs	100 docs citations	100 times ranked	16909 citing authors

#	Article	IF	Citations
1	Affinity requirements for control of synaptic targeting and neuronal cell survival by heterophilic IgSF cell adhesion molecules. Cell Reports, 2022, 39, 110618.	2.9	9
2	A Sweep of Earthâ€™s Virome Reveals Host-Guided Viral Protein Structural Mimicry and Points to Determinants of Human Disease. Cell Systems, 2021, 12, 82-91.e3.	2.9	24
3	Oncoprotein-specific molecular interaction maps (SigMaps) for cancer network analyses. Nature Biotechnology, 2021, 39, 215-224.	9.4	21
4	Integrating 3D structural information into systems biology. Journal of Biological Chemistry, 2021, 296, 100562.	1.6	18
5	Dimerization of Cadherin-11 involves multi-site coupled unfolding and strand swapping. Structure, 2021, 29, 1105-1115.e6.	1.6	3
6	Sorting of cadherinâ€"catenin-associated proteins into individual clusters. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	14
7	Synaptogenic activity of the axon guidance molecule Robo2 underlies hippocampal circuit function. Cell Reports, 2021, 37, 109828.	2.9	18
8	Histone Acetyltransferase (HAT) Activator, YF2, Modulates the p53:BCL6 Axis and Antigen Presentation in Diffuse Large B-Cell Lymphomas. Blood, 2021, 138, 2254-2254.	0.6	0
9	DIP/Dpr interactions and the evolutionary design of specificity in protein families. Nature Communications, 2020, 11, 2125.	5.8	26
10	Bi-allelic missense disease-causing variants in RPL3L associate neonatal dilated cardiomyopathy with muscle-specific ribosome biogenesis. Human Genetics, 2020, 139, 1443-1454.	1.8	20
11	Sensing Actin Dynamics through Adherens Junctions. Cell Reports, 2020, 30, 2820-2833.e3.	2.9	22
12	Family-wide Structural and Biophysical Analysis of Binding Interactions among Non-clustered Î´-Protocadherins. Cell Reports, 2020, 30, 2655-2671.e7.	2.9	35
13	Adhesion Protein Structure, Molecular Affinities, and Principles of Cell-Cell Recognition. Cell, 2020, 181, 520-535.	13.5	108
14	Trans-endocytosis elicited by nectins transfers cytoplasmic cargo including infectious material between cells. Journal of Cell Science, 2019, 132, .	1.2	25
15	A Structure-Informed Atlas of Human-Virus Interactions. Cell, 2019, 178, 1526-1541.e16.	13.5	108
16	Visualization of clustered protocadherin neuronal self-recognition complexes. Nature, 2019, 569, 280-283.	13.7	86
17	Strategy for Overcoming Crebbp and EP300 Mutations in Lymphoma: Development of First-in-Class HAT Activators. Blood, 2019, 134, 4068-4068.	0.6	3
18	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.	3.3	46

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19	Pathogenic IgG4 autoantibodies from endemic pemphigus foliaceus recognize a desmoglein-1 conformational epitope. Journal of Autoimmunity, 2018, 89, 171-185.	3.0	19
20	Neuron-Subtype-Specific Expression, Interaction Affinities, and Specificity Determinants of DIP/Dpr Cell Recognition Proteins. Neuron, 2018, 100, 1385-1400.e6.	3.8	65
21	Interactions between the Ig-Superfamily Proteins DIP-Î± and Dpr6/10 Regulate Assembly of Neural Circuits. Neuron, 2018, 100, 1369-1384.e6.	3.8	64
22	Intrinsic DNA Shape Accounts for Affinity Differences between Hox-Cofactor Binding Sites. Cell Reports, 2018, 24, 2221-2230.	2.9	31
23	Mechanotransduction by PCDH15 Relies on a Novel cis-Dimeric Architecture. Neuron, 2018, 99, 480-492.e5.	3.8	43
24	Homophilic and Heterophilic Interactions of Type II Cadherins Identify Specificity Groups Underlying Cell-Adhesive Behavior. Cell Reports, 2018, 23, 1840-1852.	2.9	54
25	Genetic Drivers of Kidney Defects in the DiGeorge Syndrome. New England Journal of Medicine, 2017, 376, 742-754.	13.9	120
26	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.	2.0	82
27	Silencing c-Myc translation as a therapeutic strategy through targeting PI3KÎ´ and CK1Îµ in hematological malignancies. Blood, 2017, 129, 88-99.	0.6	92
28	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.	3.3	83
29	Protocadherin <i>cis</i> -dimer architecture and recognition unit diversity. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9829-E9837.	3.3	55
30	Genome-wide prediction of minor-groove electrostatic potential enables biophysical modeling of proteinâ€“DNA binding. Nucleic Acids Research, 2017, 45, 12565-12576.	6.5	63
31	Structural origins of clustered protocadherin-mediated neuronal barcoding. Seminars in Cell and Developmental Biology, 2017, 69, 140-150.	2.3	36
32	Structure-based prediction of ligandâ€“protein interactions on a genome-wide scale. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 13685-13690.	3.3	44
33	A hybrid method for proteinâ€“protein interface prediction. Protein Science, 2016, 25, 159-165.	3.1	37
34	Structural Basis of Diverse Homophilic Recognition by Clustered Î±- and Î²-Protocadherins. Neuron, 2016, 90, 709-723.	3.8	87
35	Dclk1 Defines Quiescent Pancreatic Progenitors that Promote Injury-Induced Regeneration and Tumorigenesis. Cell Stem Cell, 2016, 18, 441-455.	5.2	196
36	Acetylation-regulated interaction between p53 and SET reveals a widespread regulatory mode. Nature, 2016, 538, 118-122.	13.7	160

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37	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.	3.3	137
38	Lipids Regulate Lck Protein Activity through Their Interactions with the Lck Src Homology 2 Domain. Journal of Biological Chemistry, 2016, 291, 17639-17650.	1.6	42
39	SH2 Domains Serve as Lipid-Binding Modules for pTyr-Signaling Proteins. Molecular Cell, 2016, 62, 7-20.	4.5	69
40	A High-Throughput Strategy for Dissecting Mammalian Genetic Interactions. PLoS ONE, 2016, 11, e0167617.	1.1	4
41	A computational interactome and functional annotation for the human proteome. ELife, 2016, 5, .	2.8	58
42	Molecular basis of sidekick-mediated cell-cell adhesion and specificity. ELife, 2016, 5, .	2.8	36
43	Î³-Protocadherin structural diversity and functional implications. ELife, 2016, 5, .	2.8	54
44	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.	3.3	84
45	Template-based prediction of protein function. Current Opinion in Structural Biology, 2015, 32, 33-38.	2.6	39
46	Predicting Peptide-Mediated Interactions on a Genome-Wide Scale. PLoS Computational Biology, 2015, 11, e1004248.	1.5	16
47	Î±-Cateninâ€"mediated cadherin clustering couples cadherin and actin dynamics. Journal of Cell Biology, 2015, 210, 647-661.	2.3	42
48	Molecular Logic of Neuronal Self-Recognition through Protocadherin Domain Interactions. Cell, 2015, 163, 629-642.	13.5	141
49	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.	1.6	14
50	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.	3.3	78
51	Single-Cell Identity Generated by Combinatorial Homophilic Interactions between Î±, Î², and Î³ Protocadherins. Cell, 2014, 158, 1045-1059.	13.5	190
52	An Ankyrin Repeat Domain of AKR2 Drives Chloroplast Targeting through Coincident Binding of Two Chloroplast Lipids. Developmental Cell, 2014, 30, 598-609.	3.1	49
53	Theory and Simulations of Adhesion Receptor Dimerization on Membrane Surfaces. Biophysical Journal, 2013, 104, 1221-1229.	0.2	40
54	Toward a â€œStructural BLASTâ€: Using structural relationships to infer function. Protein Science, 2013, 22, 359-366.	3.1	23

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55	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.	3.3	70
56	Nectin ectodomain structures reveal a canonical adhesive interface. Nature Structural and Molecular Biology, 2012, 19, 906-915.	3.6	104
57	Structure-based prediction of proteinâ€"protein interactions on a genome-wide scale. Nature, 2012, 490, 556-560.	13.7	652
58	Thinking outside the cell: how cadherins drive adhesion. Trends in Cell Biology, 2012, 22, 299-310.	3.6	296
59	Molecular design principles underlying Î²-strand swapping in the adhesive dimerization of cadherins. Nature Structural and Molecular Biology, 2011, 18, 693-700.	3.6	101
60	PredUs: a web server for predicting protein interfaces using structural neighbors. Nucleic Acids Research, 2011, 39, W283-W287.	6.5	101
61	Two-step adhesive binding by classical cadherins. Nature Structural and Molecular Biology, 2010, 17, 348-357.	3.6	184
62	Splice Form Dependence of Î²-Neurexin/Neuroligin Binding Interactions. Neuron, 2010, 67, 61-74.	3.8	89
63	Electrostatic contributions to protein-protein interactions: Fast energetic filters for docking and their physical basis. Protein Science, 2008, 10, 2147-2161.	3.1	105
64	Crystal Structures of Î²-Neurexin 1 and Î²-Neurexin 2 Ectodomains and Dynamics of Splice Insertion Sequence 4. Structure, 2008, 16, 410-421.	1.6	33
65	Dynamic Properties of a Type II Cadherin Adhesive Domain: Implications for the Mechanism of Strand-Swapping of Classical Cadherins. Structure, 2008, 16, 1195-1205.	1.6	55
66	Type II Cadherin Ectodomain Structures: Implications for Classical Cadherin Specificity. Cell, 2006, 124, 1255-1268.	13.5	252
67	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.	1.5	290
68	Combining Bioinformatics and Biophysics to Understand Protein-Protein and Protein-Ligand Interactions. Scientific World Journal, The, 2002, 2, 43-44.	0.8	1
69	Free energy determinants of tertiary structure and the evaluation of protein models. Protein Science, 2000, 9, 2181-2191.	3.1	96
70	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.	2.0	194
71	Calculating the electrostatic properties of RNA provides new insights into molecular interactions and function. Nature Structural Biology, 1999, 6, 1055-1061.	9.7	196
72	Sequence to structure alignment in comparative modeling using PrISM. Proteins: Structure, Function and Bioinformatics, 1999, 37, 66-72.	1.5	48

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73	Structural determinants of trypsin affinity and specificity for cationic inhibitors. Protein Science, 1999, 8, 2621-2629.	3.1	27
74	Grass: A server for the graphical representation and analysis of structures. Protein Science, 1999, 8, 676-679.	3.1	32
75	Sequence to structure alignment in comparative modeling using PrISM. Proteins: Structure, Function and Bioinformatics, 1999, Suppl 3, 66-72.	1.5	17
76	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.	1.2	60
77	On the calculation of binding free energies using continuum methods: Application to MHC class I proteinâ€peptide interactions. Protein Science, 1997, 6, 1293-1301.	3.1	179
78	Size Dependence of Transfer Free Energies. 2. Hard Sphere Models. The Journal of Physical Chemistry, 1996, 100, 14166-14177.	2.9	27
79	Salt effects on polyelectrolyte-ligand binding: Comparison of Poisson-Boltzmann, and limiting law/counterion binding models. Biopolymers, 1995, 36, 245-262.	1.2	116
80	The fast multipole boundary element method for molecular electrostatics: An optimal approach for large systems. Journal of Computational Chemistry, 1995, 16, 898-913.	1.5	147
81	Evaluation of the conformational free energies of loops in proteins. Proteins: Structure, Function and Bioinformatics, 1994, 18, 119-132.	1.5	113
82	On the calculation of pKas in proteins. Proteins: Structure, Function and Bioinformatics, 1993, 15, 252-265.	1.5	514
83	The electrostatic contribution to DNA base-stacking interactions. Biopolymers, 1992, 32, 145-159.	1.2	89
84	Macroscopic Treatments of Electrostatic and Hydrophobic Free Energies. AIP Conference Proceedings, 1991, , .	0.3	0
85	A rapid finite difference algorithm, utilizing successive over-relaxation to solve the Poisson-Boltzmann equation. Journal of Computational Chemistry, 1991, 12, 435-445.	1.5	1,194
86	Protein folding and association: Insights from the interfacial and thermodynamic properties of hydrocarbons. Proteins: Structure, Function and Bioinformatics, 1991, 11, 281-296.	1.5	5,360
87	The electrostatic potential of B-DNA. Biopolymers, 1989, 28, 975-993.	1.2	267
88	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.	1.5	794
89	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.	1.5	730
90	ON THE MECHANISM OF WAVELENGTH REGULATION IN VISUAL PIGMENTS. Photochemistry and Photobiology, 1985, 41, 471-479.	1.3	137