David Baker

List of Publications by Year
in descending order

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628	100,924	157 160	468 278
papers	citations	h-index	g-index

715	715	715	66699
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Accurate prediction of protein structures and interactions using a three-track neural network. Science, 2021, 373, 871-876.	6.0	2,843
2	Protein structure prediction and analysis using the Robetta server. Nucleic Acids Research, 2004, 32, W526-W531.	6.5	1,683
3	Rosetta3. Methods in Enzymology, 2011, 487, 545-574.	0.4	1,620
4	Design of a Novel Globular Protein Fold with Atomic-Level Accuracy. Science, 2003, 302, 1364-1368.	6.0	1,471
5	Contact order, transition state placement and the refolding rates of single domain proteins 1 1Edited by P. E. Wright. Journal of Molecular Biology, 1998, 277, 985-994.	2.0	1,449
6	Protein Structure Prediction and Structural Genomics. Science, 2001, 294, 93-96.	6.0	1,445
7	Protein Structure Prediction Using Rosetta. Methods in Enzymology, 2004, 383, 66-93.	0.4	1,445
8	Quantitative reactivity profiling predicts functional cysteines in proteomes. Nature, 2010, 468, 790-795.	13.7	1,359
9	Assembly of protein tertiary structures from fragments with similar local sequences using simulated annealing and bayesian scoring functions. Journal of Molecular Biology, 1997, 268, 209-225.	2.0	1,268
10	Improved protein structure prediction using predicted interresidue orientations. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 1496-1503.	3.3	1,135
11	Kemp elimination catalysts by computational enzyme design. Nature, 2008, 453, 190-195.	13.7	1,130
12	Improving physical realism, stereochemistry, and sideâ€chain accuracy in homology modeling: Four approaches that performed well in CASP8. Proteins: Structure, Function and Bioinformatics, 2009, 77, 114-122.	1.5	1,105
13	The coming of age of de novo protein design. Nature, 2016, 537, 320-327.	13.7	1,069
14	Predicting protein structures with a multiplayer online game. Nature, 2010, 466, 756-760.	13.7	1,062
15	The Rosetta All-Atom Energy Function for Macromolecular Modeling and Design. Journal of Chemical Theory and Computation, 2017, 13, 3031-3048.	2.3	1,032
16	De Novo Computational Design of Retro-Aldol Enzymes. Science, 2008, 319, 1387-1391.	6.0	1,031
17	Proteinâ€“Protein Docking with Simultaneous Optimization of Rigid-body Displacement and Side-chain Conformations. Journal of Molecular Biology, 2003, 331, 281-299.	2.0	1,017
18	High-Resolution Comparative Modeling with RosettaCM. Structure, 2013, 21, 1735-1742.	1.6	1,010

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19	Macromolecular Modeling with Rosetta. Annual Review of Biochemistry, 2008, 77, 363-382.	5.0	841
20	Toward High-Resolution de Novo Structure Prediction for Small Proteins. Science, 2005, 309, 1868-1871.	6.0	797
21	Consistent blind protein structure generation from NMR chemical shift data. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 4685-4690.	3.3	776
22	Computational Design of an Enzyme Catalyst for a Stereoselective Bimolecular Diels-Alder Reaction. Science, 2010, 329, 309-313.	6.0	776
23	A simple physical model for binding energy hot spots in protein-protein complexes. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 14116-14121.	3.3	754
24	Native protein sequences are close to optimal for their structures. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 10383-10388.	3.3	741
25	A surprising simplicity to protein folding. Nature, 2000, 405, 39-42.	13.7	711
26	Rational HIV Immunogen Design to Target Specific Germline B Cell Receptors. Science, 2013, 340, 711-716.	6.0	680
27	An Engineered Microbial Platform for Direct Biofuel Production from Brown Macroalgae. Science, 2012, 335, 308-313.	6.0	642
28	Assessing the utility of coevolution-based residueâ€“residue contact predictions in a sequence- and structure-rich era. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 15674-15679.	3.3	605
29	Computational Design of Self-Assembling Protein Nanomaterials with Atomic Level Accuracy. Science, 2012, 336, 1171-1174.	6.0	588
30	High-Resolution Microtubule Structures Reveal the Structural Transitions in Î±Î²-Tubulin upon GTP Hydrolysis. Cell, 2014, 157, 1117-1129.	13.5	582
31	Robust and accurate prediction of residueâ€“residue interactions across protein interfaces using evolutionary information. ELife, 2014, 3, e02030.	2.8	571
32	Role of conformational sampling in computing mutationâ€induced changes in protein structure and stability. Proteins: Structure, Function and Bioinformatics, 2011, 79, 830-838.	1.5	550
33	Computational Design of Proteins Targeting the Conserved Stem Region of Influenza Hemagglutinin. Science, 2011, 332, 816-821.	6.0	527
34	Principles for designing ideal protein structures. Nature, 2012, 491, 222-227.	13.7	522
35	Macromolecular modeling and design in Rosetta: recent methods and frameworks. Nature Methods, 2020, 17, 665-680.	9.0	513
36	RosettaScripts: A Scripting Language Interface to the Rosetta Macromolecular Modeling Suite. PLoS ONE, 2011, 6, e20161.	1.1	506

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37	Accurate design of co-assembling multi-component protein nanomaterials. Nature, 2014, 510, 103-108.	13.7	504
38	High-resolution mapping of protein sequence-function relationships. Nature Methods, 2010, 7, 741-746.	9.0	482
39	Computational Alanine Scanning of Protein-Protein Interfaces. Science Signaling, 2004, 2004, pl2-pl2.	1.6	471
40	Accurate design of megadalton-scale two-component icosahedral protein complexes. Science, 2016, 353, 389-394.	6.0	466
41	De novo design of picomolar SARS-CoV-2 miniprotein inhibitors. Science, 2020, 370, 426-431.	6.0	464
42	Crystal structure of a monomeric retroviral protease solved by protein folding game players. Nature Structural and Molecular Biology, 2011, 18, 1175-1177.	3.6	463
43	An Orientation-dependent Hydrogen Bonding Potential Improves Prediction of Specificity and Structure for Proteins and Proteinâ€“Protein Complexes. Journal of Molecular Biology, 2003, 326, 1239-1259.	2.0	460
44	Protein structure determination using metagenome sequence data. Science, 2017, 355, 294-298.	6.0	456
45	Ca2+ Indicators Based on Computationally Redesigned Calmodulin-Peptide Pairs. Chemistry and Biology, 2006, 13, 521-530.	6.2	455
46	Proof of principle for epitope-focused vaccine design. Nature, 2014, 507, 201-206.	13.7	451
47	Algorithm discovery by protein folding game players. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 18949-18953.	3.3	450
48	Ab initio protein structure prediction of CASP III targets using ROSETTA. Proteins: Structure, Function and Bioinformatics, 1999, 37, 171-176.	1.5	435
49	Structure prediction for CASP8 with allâ€atom refinement using Rosetta. Proteins: Structure, Function and Bioinformatics, 2009, 77, 89-99.	1.5	425
50	ROSETTALIGAND: Protein-small molecule docking with full side-chain flexibility. Proteins: Structure, Function and Bioinformatics, 2006, 65, 538-548.	1.5	421
51	Computational Enzyme Design. Angewandte Chemie - International Edition, 2013, 52, 5700-5725.	7.2	413
52	Proteinâ€“Protein Docking with Backbone Flexibility. Journal of Molecular Biology, 2007, 373, 503-519.	2.0	401
53	Automated de novo prediction of native-like RNA tertiary structures. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 14664-14669.	3.3	397
54	Structure-based design of non-natural amino-acid inhibitors of amyloid fibril formation. Nature, 2011, 475, 96-100.	13.7	394

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55	Global analysis of protein folding using massively parallel design, synthesis, and testing. Science, 2017, 357, 168-175.	6.0	392
56	Improved recognition of native-like protein structures using a combination of sequence-dependent and sequence-independent features of proteins. , 1999, 34, 82-95.		389
57	Simultaneous Optimization of Biomolecular Energy Functions on Features from Small Molecules and Macromolecules. Journal of Chemical Theory and Computation, 2016, 12, 6201-6212.	2.3	382
58	RosettaLigand Docking with Full Ligand and Receptor Flexibility. Journal of Molecular Biology, 2009, 385, 381-392.	2.0	376
59	Role of neurogenic genes in establishment of follicle cell fate and oocyte polarity during oogenesis in Drosophila. Cell, 1991, 66, 433-449.	13.5	373
60	Design of a hyperstable 60-subunit protein icosahedron. Nature, 2016, 535, 136-139.	13.7	373
61	The 3D profile method for identifying fibril-forming segments of proteins. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 4074-4078.	3.3	372
62	Computational design of ligand-binding proteins with high affinity and selectivity. Nature, 2013, 501, 212-216.	13.7	370
63	De novo design of potent and selective mimics of IL-2 and IL-15. Nature, 2019, 565, 186-191.	13.7	362
64	Topology, Stability, Sequence, and Length:â€‰Defining the Determinants of Two-State Protein Folding Kinetics. Biochemistry, 2000, 39, 11177-11183.	1.2	360
65	Massively parallel de novo protein design for targeted therapeutics. Nature, 2017, 550, 74-79.	13.7	354
66	Experiment and theory highlight role of native state topology in SH3 folding. Nature Structural Biology, 1999, 6, 1016-1024.	9.7	349
67	Critical role of beta-hairpin formation in protein G folding. Nature Structural Biology, 2000, 7, 669-673.	9.7	345
68	Optimization of affinity, specificity and function of designed influenza inhibitors using deep sequencing. Nature Biotechnology, 2012, 30, 543-548.	9.4	342
69	Induction of Potent Neutralizing Antibody Responses by a Designed Protein Nanoparticle Vaccine for Respiratory Syncytial Virus. Cell, 2019, 176, 1420-1431.e17.	13.5	339
70	Computational Thermostabilization of an Enzyme. Science, 2005, 308, 857-860.	6.0	337
71	Reconstitution of SEC gene product-dependent intercompartmental protein transport. Cell, 1988, 54, 335-344.	13.5	336
72	Prediction of local structure in proteins using a library of sequence-structure motifs. Journal of Molecular Biology, 1998, 281, 565-577.	2.0	331

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73	Atomic accuracy in predicting and designing noncanonical RNA structure. Nature Methods, 2010, 7, 291-294.	9.0	328
74	Contact order revisited: Influence of protein size on the folding rate. Protein Science, 2003, 12, 2057-2062.	3.1	327
75	Accurate de novo design of hyperstable constrained peptides. Nature, 2016, 538, 329-335.	13.7	327
76	Alternate States of Proteins Revealed by Detailed Energy Landscape Mapping. Journal of Molecular Biology, 2011, 405, 607-618.	2.0	324
77	New algorithms and an in silico benchmark for computational enzyme design. Protein Science, 2006, 15, 2785-2794.	3.1	323
78	Relaxation of backbone bond geometry improves protein energy landscape modeling. Protein Science, 2014, 23, 47-55.	3.1	323
79	A protein-folding reaction under kinetic control. Nature, 1992, 356, 263-265.	13.7	318
80	Computed structures of core eukaryotic protein complexes. Science, 2021, 374, eabm4805.	6.0	316
81	Atomic-accuracy models from 4.5-Ã... cryo-electron microscopy data with density-guided iterative local refinement. Nature Methods, 2015, 12, 361-365.	9.0	313
82	RosettaRemodel: A Generalized Framework for Flexible Backbone Protein Design. PLoS ONE, 2011, 6, e24109.	1.1	310
83	Atomic model of the type III secretion system needle. Nature, 2012, 486, 276-279.	13.7	308
84	Multipass membrane protein structure prediction using Rosetta. Proteins: Structure, Function and Bioinformatics, 2005, 62, 1010-1025.	1.5	303
85	A synthetic homing endonuclease-based gene drive system in the human malaria mosquito. Nature, 2011, 473, 212-215.	13.7	303
86	Computational redesign of endonuclease DNA binding and cleavage specificity. Nature, 2006, 441, 656-659.	13.7	300
87	High-resolution structure prediction and the crystallographic phase problem. Nature, 2007, 450, 259-264.	13.7	296
88	A Large Scale Test of Computational Protein Design: Folding and Stability of Nine Completely Redesigned Globular Proteins. Journal of Molecular Biology, 2003, 332, 449-460.	2.0	293
89	Modeling structurally variable regions in homologous proteins with rosetta. Proteins: Structure, Function and Bioinformatics, 2004, 55, 656-677.	1.5	292
90	The trRosetta server for fast and accurate protein structure prediction. Nature Protocols, 2021, 16, 5634-5651.	5.5	290

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91	HMMSTR: a hidden Markov model for local sequence-structure correlations in proteins 1 1Edited by J. Thornton. Journal of Molecular Biology, 2000, 301, 173-190.	2.0	286
92	Computational protein design enables a novel one-carbon assimilation pathway. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3704-3709.	3.3	286
93	De novo protein design by deep network hallucination. Nature, 2021, 600, 547-552.	13.7	280
94	Functional rapidly folding proteins from simplified amino acid sequences. Nature Structural Biology, 1997, 4, 805-809.	9.7	279
95	Computational redesign of protein-protein interaction specificity. Nature Structural and Molecular Biology, 2004, 11, 371-379.	3.6	279
96	Ab Initio Protein Structure Prediction: Progress and Prospects. Annual Review of Biophysics and Biomolecular Structure, 2001, 30, 173-189.	18.3	278
97	Important role of hydrogen bonds in the structurally polarized transition state for folding of the src SH3 domain. Nature Structural and Molecular Biology, 1998, 5, 714-720.	3.6	277
98	De Novo Enzyme Design Using Rosetta3. PLoS ONE, 2011, 6, e19230.	1.1	274
99	Engineering an allosteric transcription factor to respond to new ligands. Nature Methods, 2016, 13, 177-183.	9.0	274
100	Refinement of Protein Structures into Low-Resolution Density Maps Using Rosetta. Journal of Molecular Biology, 2009, 392, 181-190.	2.0	272
101	Progress in Modeling of Protein Structures and Interactions. Science, 2005, 310, 638-642.	6.0	271
102	De novo design of a fluorescence-activating Î²-barrel. Nature, 2018, 561, 485-491.	13.7	269
103	Solution structure of a minor and transiently formed state of a T4 lysozyme mutant. Nature, 2011, 477, 111-114.	13.7	265
104	High thermodynamic stability of parametrically designed helical bundles. Science, 2014, 346, 481-485.	6.0	264
105	Surrogate Wnt agonists that phenocopy canonical Wnt and Î²-catenin signalling. Nature, 2017, 545, 234-237.	13.7	264
106	De novo design of protein homo-oligomers with modular hydrogen-bond networkâ€“mediated specificity. Science, 2016, 352, 680-687.	6.0	262
107	Automated prediction of CASP-5 structures using the Robetta server. Proteins: Structure, Function and Bioinformatics, 2003, 53, 524-533.	1.5	261
108	Elicitation of structure-specific antibodies by epitope scaffolds. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 17880-17887.	3.3	261

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109	Increased Diels-Alderase activity through backbone remodeling guided by Foldit players. Nature Biotechnology, 2012, 30, 190-192.	9.4	259
110	Mechanisms of protein folding. Current Opinion in Structural Biology, 2001, 11, 70-82.	2.6	258
111	Clustering of low-energy conformations near the native structures of small proteins. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 11158-11162.	3.3	255
112	Selective targeting of engineered T cells using orthogonal IL-2 cytokine-receptor complexes. Science, 2018, 359, 1037-1042.	6.0	254
113	Assigning Function to Yeast Proteins by Integration of Technologies. Molecular Cell, 2003, 12, 1353-1365.	4.5	248
114	Emergence of a catalytic tetrad during evolution of a highly active artificial aldolase. Nature Chemistry, 2017, 9, 50-56.	6.6	248
115	Kinetics versus Thermodynamics in Protein Folding. Biochemistry, 1994, 33, 7505-7509.	1.2	245
116	NMR Structure Determination for Larger Proteins Using Backbone-Only Data. Science, 2010, 327, 1014-1018.	6.0	245
117	Rosetta in CASP4: Progress in ab initio protein structure prediction. Proteins: Structure, Function and Bioinformatics, 2001, 45, 119-126.	1.5	242
118	Intratumoral activation of the necroptotic pathway components RIPK1 and RIPK3 potentiates antitumor immunity. Science Immunology, 2019, 4, .	5.6	242
119	De Novo Prediction of Three-dimensional Structures for Major Protein Families. Journal of Molecular Biology, 2002, 322, 65-78.	2.0	237
120	De novo protein structure generation from incomplete chemical shift assignments. Journal of Biomolecular NMR, 2009, 43, 63-78.	1.6	234
121	A Pareto-Optimal Refinement Method for Protein Design Scaffolds. PLoS ONE, 2013, 8, e59004.	1.1	233
122	Large-scale determination of previously unsolved protein structures using evolutionary information. ELife, 2015, 4, e09248.	2.8	229
123	Close agreement between the orientation dependence of hydrogen bonds observed in protein structures and quantum mechanical calculations. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 6946-6951.	3.3	227
124	Exploring the repeat protein universe through computational protein design. Nature, 2015, 528, 580-584.	13.7	227
125	Improved molecular replacement by density- and energy-guided protein structure optimization. Nature, 2011, 473, 540-543.	13.7	226
126	Structural basis for gating charge movement in the voltage sensor of a sodium channel. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E93-102.	3.3	223

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127	A breakdown of symmetry in the folding transition state of protein L. Journal of Molecular Biology, 2000, 298, 971-984.	2.0	222
128	Toward high-resolution prediction and design of transmembrane helical protein structures. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 15682-15687.	3.3	221
129	Evolution of a designed retro-aldolase leads to complete active site remodeling. Nature Chemical Biology, 2013, 9, 494-498.	3.9	220
130	Voltage sensor conformations in the open and closed states in ROSETTA structural models of K+ channels. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 7292-7297.	3.3	219
131	Design of ordered two-dimensional arrays mediated by noncovalent protein-protein interfaces. Science, 2015, 348, 1365-1368.	6.0	219
132	Design, Activity, and Structure of a Highly Specific Artificial Endonuclease. Molecular Cell, 2002, 10, 895-905.	4.5	218
133	Structure of the Type VI Secretion System Contractile Sheath. Cell, 2015, 160, 952-962.	13.5	216
134	Improved side-chain modeling for protein-protein docking. Protein Science, 2005, 14, 1328-1339.	3.1	215
135	De novo design of a four-fold symmetric TIM-barrel protein with atomic-level accuracy. Nature Chemical Biology, 2016, 12, 29-34.	3.9	214
136	Computational design of proteinâ€“protein interactions. Current Opinion in Chemical Biology, 2004, 8, 91-97.	2.8	213
137	Computation-Guided Backbone Grafting of a Discontinuous Motif onto a Protein Scaffold. Science, 2011, 334, 373-376.	6.0	212
138	A Vast Repertoire of Dscam Binding Specificities Arises from Modular Interactions of Variable Ig Domains. Cell, 2007, 130, 1134-1145.	13.5	210
139	Protein interaction networks revealed by proteome coevolution. Science, 2019, 365, 185-189.	6.0	208
140	Computer-based redesign of a protein folding pathway. Nature Structural Biology, 2001, 8, 602-605.	9.7	206
141	Computational redesign of a mononuclear zinc metalloenzyme for organophosphate hydrolysis. Nature Chemical Biology, 2012, 8, 294-300.	3.9	205
142	Bridging the gaps in design methodologies by evolutionary optimization of the stability and proficiency of designed Kemp eliminase KE59. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 10358-10363.	3.3	205
143	Computationally designed libraries for rapid enzyme stabilization. Protein Engineering, Design and Selection, 2014, 27, 49-58.	1.0	205
144	Combined Covalent-Electrostatic Model of Hydrogen Bonding Improves Structure Prediction with Rosetta. Journal of Chemical Theory and Computation, 2015, 11, 609-622.	2.3	204

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145	Computational Design of Epitope-Scaffolds Allows Induction of Antibodies Specific for a Poorly Immunogenic HIV Vaccine Epitope. Structure, 2010, 18, 1116-1126.	1.6	203
146	Modeling Symmetric Macromolecular Structures in Rosetta3. PLoS ONE, 2011, 6, e20450.	1.1	197
147	GTP-binding Ypt1 protein and Ca2+ function independently in a cell-free protein transport reaction.. Proceedings of the National Academy of Sciences of the United States of America, 1990, 87, 355-359.	3.3	195
148	Scientific Benchmarks for Guiding Macromolecular Energy Function Improvement. Methods in Enzymology, 2013, 523, 109-143.	0.4	195
149	Evaluation of Structural and Evolutionary Contributions to Deleterious Mutation Prediction. Journal of Molecular Biology, 2002, 322, 891-901.	2.0	193
150	Structural basis for scaffolding-mediated assembly and maturation of a dsDNA virus. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1355-1360.	3.3	191
151	Ab initio protein structure prediction of CASP III targets using ROSETTA. Proteins: Structure, Function and Bioinformatics, 1999, Suppl 3, 171-6.	1.5	191
152	De novo design of bioactive protein switches. Nature, 2019, 572, 205-210.	13.7	190
153	Determination of solution structures of proteins up to 40ÂkDa using CS-Rosetta with sparse NMR data from deuterated samples. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 10873-10878.	3.3	188
154	Folding Dynamics of the src SH3 Domainâ€. Biochemistry, 1997, 36, 15685-15692.	1.2	186
155	A Novel Semi-biosynthetic Route for Artemisinin Production Using Engineered Substrate-Promiscuous P450_{BM3}. ACS Chemical Biology, 2009, 4, 261-267.	1.6	184
156	Realistic protein-protein association rates from a simple diffusional model neglecting long-range interactions, free energy barriers, and landscape ruggedness. Protein Science, 2004, 13, 1660-1669.	3.1	181
157	Quadrivalent influenza nanoparticle vaccines induce broad protection. Nature, 2021, 592, 623-628.	13.7	180
158	Structure prediction for CASP7 targets using extensive all-atom refinement with Rosetta@home. Proteins: Structure, Function and Bioinformatics, 2007, 69, 118-128.	1.5	178
159	De Novo Determination of Protein Backbone Structure from Residual Dipolar Couplings Using Rosetta. Journal of the American Chemical Society, 2002, 124, 2723-2729.	6.6	177
160	Improved low-resolution crystallographic refinement with Phenix and Rosetta. Nature Methods, 2013, 10, 1102-1104.	9.0	175
161	Evolution of a designed protein assembly encapsulating its own RNA genome. Nature, 2017, 552, 415-420.	13.7	174
162	The role of pro regions in protein folding. Current Opinion in Cell Biology, 1993, 5, 966-970.	2.6	172

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163	The Acidic Transcription Activator Gcn4 Binds the Mediator Subunit Gal11/Med15ÂUsing a Simple Protein Interface Forming a Fuzzy Complex. Molecular Cell, 2011, 44, 942-953.	4.5	172
164	De novo protein structure determination from near-atomic-resolution cryo-EM maps. Nature Methods, 2015, 12, 335-338.	9.0	172
165	Generalized Fragment Picking in Rosetta: Design, Protocols and Applications. PLoS ONE, 2011, 6, e23294.	1.1	172
166	Coupled prediction of protein secondary and tertiary structure. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 12105-12110.	3.3	170
167	A conserved structural motif mediates formation of the periplasmic rings in the type III secretion system. Nature Structural and Molecular Biology, 2009, 16, 468-476.	3.6	170
168	Prospects for ab initio protein structural genomics. Journal of Molecular Biology, 2001, 306, 1191-1199.	2.0	168
169	Chain collapse can occur concomitantly with the rate-limiting step in protein folding. Nature Structural Biology, 1999, 6, 554-556.	9.7	167
170	Protein-DNA binding specificity predictions with structural models. Nucleic Acids Research, 2005, 33, 5781-5798.	6.5	167
171	Origins of coevolution between residues distant in protein 3D structures. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 9122-9127.	3.3	167
172	Prediction of the structure of symmetrical protein assemblies. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 17656-17661.	3.3	164
173	Design of protein-binding proteins from the target structure alone. Nature, 2022, 605, 551-560.	13.7	164
174	De novo protein structure determination using sparse NMR data. Journal of Biomolecular NMR, 2000, 18, 311-318.	1.6	162
175	Rosetta predictions in CASP5: Successes, failures, and prospects for complete automation. Proteins: Structure, Function and Bioinformatics, 2003, 53, 457-468.	1.5	162
176	Bioluminescent sensor proteins for point-of-care therapeutic drug monitoring. Nature Chemical Biology, 2014, 10, 598-603.	3.9	161
177	Cryo-EM structure of the protein-conducting ERAD channel Hrd1 in complex with Hrd3. Nature, 2017, 548, 352-355.	13.7	160
178	Improved protein structure refinement guided by deep learning based accuracy estimation. Nature Communications, 2021, 12, 1340.	5.8	160
179	A De Novo Protein Binding Pair By Computational Design and Directed Evolution. Molecular Cell, 2011, 42, 250-260.	4.5	159
180	Evolutionary Optimization of Computationally Designed Enzymes: Kemp Eliminases of the KE07 Series. Journal of Molecular Biology, 2010, 396, 1025-1042.	2.0	154

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181	Kinetics of Folding of the IgG Binding Domain of Peptostreptoccocal Protein L. Biochemistry, 1997, 36, 3373-3382.	1.2	153
182	Emergence of symmetry in homooligomeric biological assemblies. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 16148-16152.	3.3	153
183	An exciting but challenging road ahead for computational enzyme design. Protein Science, 2010, 19, 1817-1819.	3.1	153
184	De novo design of modular and tunable protein biosensors. Nature, 2021, 591, 482-487.	13.7	153
185	Optimization of the In-Silico-Designed Kemp Eliminase KE70 by Computational Design and Directed Evolution. Journal of Molecular Biology, 2011, 407, 391-412.	2.0	152
186	Matching theory and experiment in protein folding. Current Opinion in Structural Biology, 1999, 9, 189-196.	2.6	151
187	megaTALs: a rare-cleaving nuclease architecture for therapeutic genome engineering. Nucleic Acids Research, 2014, 42, 2591-2601.	6.5	151
188	De novo design of protein logic gates. Science, 2020, 368, 78-84.	6.0	151
189	An improved protein decoy set for testing energy functions for protein structure prediction. Proteins: Structure, Function and Bioinformatics, 2003, 53, 76-87.	1.5	150
190	Physically realistic homology models built with ROSETTA can be more accurate than their templates. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 5361-5366.	3.3	149
191	Accurate computational design of multipass transmembrane proteins. Science, 2018, 359, 1042-1046.	6.0	149
192	Enhancing and shaping the immunogenicity of native-like HIV-1 envelope trimers with a two-component protein nanoparticle. Nature Communications, 2019, 10, 4272.	5.8	149
193	Protein transport to the vacuole and receptor-mediated endocytosis by clathrin heavy chain-deficient yeast.. Journal of Cell Biology, 1988, 106, 1453-1461.	2.3	148
194	Comprehensive computational design of ordered peptide macrocycles. Science, 2017, 358, 1461-1466.	6.0	146
195	Spatially localized rhomboid is required for establishment of the dorsal-ventral axis in Drosophila oogenesis. Cell, 1993, 73, 953-965.	13.5	145
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