Amy E Keating

List of Publications by Year
in descending order

78 papers	4,830 citations	109137 35 h-index	102304 66 g-index
88 all docs	88 docs citations	88 times ranked	5841 citing authors

#	Article	IF	Citations
1	Comprehensive Identification of Human bZIP Interactions with Coiled-Coil Arrays. Science, 2003, 300, 2097-2101.	6.0	435
2	The MCL-1 BH3 helix is an exclusive MCL-1 inhibitor and apoptosis sensitizer. Nature Chemical Biology, 2010, 6, 595-601.	3.9	374
3	Design of protein-interaction specificity gives selective bZIP-binding peptides. Nature, 2009, 458, 859-864.	13.7	317
4	Structural specificity in coiled-coil interactions. Current Opinion in Structural Biology, 2008, 18, 477-483.	2.6	252
5	Protein binding specificity versus promiscuity. Current Opinion in Structural Biology, 2011, 21, 50-61.	2.6	209
6	SYNZIP Protein Interaction Toolbox: in Vitro and in Vivo Specifications of Heterospecific Coiled-Coil Interaction Domains. ACS Synthetic Biology, 2012, 1, 118-129.	1.9	178
7	A Synthetic Coiled-Coil Interactome Provides Heterospecific Modules for Molecular Engineering. Journal of the American Chemical Society, 2010, 132, 6025-6031.	6.6	170
8	Networks of bZIP Protein-Protein Interactions Diversified Over a Billion Years of Evolution. Science, 2013, 340, 730-734.	6.0	151
9	Determinants of BH3 Binding Specificity for Mcl-1 versus Bcl-xL. Journal of Molecular Biology, 2010, 398, 747-762.	2.0	113
10	<scp>AB</scp> â€Bind: Antibody binding mutational database for computational affinity predictions. Protein Science, 2016, 25, 393-409.	3.1	110
11	Combinatorial bZIP dimers display complex DNA-binding specificity landscapes. ELife, 2017, 6, .	2.8	109
12	Predicting specificity in bZIP coiled-coil protein interactions. Genome Biology, 2004, 5, R11.	13.9	105
13	Designed BH3 Peptides with High Affinity and Specificity for Targeting Mcl-1 in Cells. ACS Chemical Biology, 2014, 9, 1962-1968.	1.6	91
14	bZIP transcription factors affecting secondary metabolism, sexual development and stress responses in Aspergillus nidulans. Microbiology (United Kingdom), 2013, 159, 77-88.	0.7	89
15	Mclâ€‰â€“Bim complexes accommodate surprising point mutations via minor structural changes. Protein Science, 2010, 19, 507-519.	3.1	88
16	Precision Calcium Imaging of Dense Neural Populations via a Cell-Body-Targeted Calcium Indicator. Neuron, 2020, 107, 470-486.e11.	3.8	87
17	Experimental Proof of the Non-Least-Motion Cycloadditions of Dichlorocarbene to Alkenes:Â Kinetic Isotope Effects and Quantum Mechanical Transition States. Journal of the American Chemical Society, 1999, 121, 3933-3938.	6.6	77
18	Modeling Backbone Flexibility to Achieve Sequence Diversity: The Design of Novel Î±-Helical Ligands for Bcl-xL. Journal of Molecular Biology, 2007, 371, 1099-1117.	2.0	73

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19	Multicoil2: Predicting Coiled Coils and Their Oligomerization States from Sequence in the Twilight Zone. PLoS ONE, 2011, 6, e23519.	1.1	72
20	Iterative optimization yields Mcl-1â€“targeting stapled peptides with selective cytotoxicity to Mcl-1â€“dependent cancer cells. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E886-E895.	3.3	69
21	Structure-based Prediction of bZIP Partnering Specificity. Journal of Molecular Biology, 2006, 355, 1125-1142.	2.0	62
22	Helix Bundle Loops Determine Whether Histidine Kinases Autophosphorylate in cis or in trans. Journal of Molecular Biology, 2013, 425, 1198-1209.	2.0	61
23	SORTCERYâ€”A Highâ€“Throughput Method to Affinity Rank Peptide Ligands. Journal of Molecular Biology, 2015, 427, 2135-2150.	2.0	58
24	Designing helical peptide inhibitors of proteinâ€“protein interactions. Current Opinion in Structural Biology, 2016, 39, 27-38.	2.6	57
25	A Set of Computationally Designed Orthogonal Antiparallel Homodimers that Expands the Synthetic Coiled-Coil Toolkit. Journal of the American Chemical Society, 2014, 136, 16544-16556.	6.6	54
26	Identification of bZIP Interaction Partners of Viral Proteins HBZ, MEQ, BZLF1, and K-bZIP Using Coiled-Coil Arrays. Biochemistry, 2010, 49, 1985-1997.	1.2	53
27	Origins of Stereoselective Carbene 1,2-Shifts and Cycloadditions of 1,2-Dichloroethylidene:â€‰ A Theoretical Model Based on CBS-Q and B3LYP Calculations. Journal of the American Chemical Society, 1997, 119, 10805-10809.	6.6	51
28	Predictive Bcl-2 Family Binding Models Rooted in Experiment or Structure. Journal of Molecular Biology, 2012, 422, 124-144.	2.0	50
29	Peptide design by optimization on a data-parameterized protein interaction landscape. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E10342-E10351.	3.3	47
30	Xâ€ray vs. NMR structures as templates for computational protein design. Proteins: Structure, Function and Bioinformatics, 2009, 77, 97-110.	1.5	43
31	Designing specific proteinâ€“protein interactions using computation, experimental library screening, or integrated methods. Protein Science, 2012, 21, 949-963.	3.1	43
32	Influence of Bystander Substituents on the Rates of 1,2-H and 1,2-Ph Shifts in Singlet and Triplet Carbenes. Journal of Physical Chemistry A, 1998, 102, 8467-8476.	1.1	41
33	Determinants of Homodimerization Specificity in Histidine Kinases. Journal of Molecular Biology, 2011, 413, 222-235.	2.0	38
34	Data-Driven Prediction and Design of bZIP Coiled-Coil Interactions. PLoS Computational Biology, 2015, 11, e1004046.	1.5	38
35	Rapid Optimization of Mcl-1 Inhibitors using Stapled Peptide Libraries Including Non-Natural Side Chains. ACS Chemical Biology, 2016, 11, 1238-1244.	1.6	38
36	Spatial Multiplexing of Fluorescent Reporters for Imaging Signaling Network Dynamics. Cell, 2020, 183, 1682-1698.e24.	13.5	38

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37	Self-Assembling Ternary Complex Stabilities and Template Ratios in Carceplex Formation. Journal of the American Chemical Society, 1997, 119, 4321-4322.	6.6	37
38	Ultra-Fast Evaluation of Protein Energies Directly from Sequence. PLoS Computational Biology, 2006, 2, e63.	1.5	37
39	In Silico and in Vitro Elucidation of BH3 Binding Specificity toward Bcl-2. Biochemistry, 2012, 51, 5841-5850.	1.2	35
40	Genome-Wide Prediction and Validation of Peptides That Bind Human Prosurvival Bcl-2 Proteins. PLoS Computational Biology, 2014, 10, e1003693.	1.5	35
41	Potent and Specific Peptide Inhibitors of Human Pro-Survival Protein Bcl-xL. Journal of Molecular Biology, 2015, 427, 1241-1253.	2.0	35
42	Predicting helix orientation for coiledâ€coil dimers. Proteins: Structure, Function and Bioinformatics, 2008, 72, 1048-1065.	1.5	34
43	Peptide Ligands for Pro-survival Protein Bfl-1 from Computationally Guided Library Screening. ACS Chemical Biology, 2013, 8, 778-788.	1.6	34
44	Design of a Heterospecific, Tetrameric, 21-Residue Miniprotein with Mixed Î±/Î² Structure. Structure, 2005, 13, 225-234.	1.6	33
45	Epistatic mutations in PUMA BH3 drive an alternate binding mode to potently and selectively inhibit anti-apoptotic Bfl-1. ELife, 2017, 6, .	2.8	33
46	Orientation and Oligomerization Specificity of the Bcr Coiled-Coil Oligomerization Domainâ€. Biochemistry, 2005, 44, 16246-16256.	1.2	31
47	Structure-Based Redesign of the Binding Specificity of Anti-Apoptotic Bcl-xL. Journal of Molecular Biology, 2013, 425, 171-185.	2.0	31
48	Modular assembly of a protein nanotriangle using orthogonally interacting coiled coils. Scientific Reports, 2017, 7, 10577.	1.6	31
49	PixelDB: Proteinâ€“peptide complexes annotated with structural conservation of the peptide binding mode. Protein Science, 2018, 27, 276-285.	3.1	31
50	Control of Carbene Reactivity by Crystals. A Highly Selective 1,2-H Shift in the Solid-to-Solid Reaction of 1-(4â€˜-Biphenylyl)-2-phenyldiazopropane to (Z)-1-(4â€˜-Biphenylyl)-2-phenylpropene. Journal of the American Chemical Society, 1997, 119, 1859-1868.	6.6	30
51	Tertiary Structural Motif Sequence Statistics Enable Facile Prediction and Design of Peptides that Bind Anti-apoptotic Bfl-1 and Mcl-1. Structure, 2019, 27, 606-617.e5.	1.6	29
52	Data-driven computational protein design. Current Opinion in Structural Biology, 2021, 69, 63-69.	2.6	28
53	Transforming a Nonselective Carbene Rearrangement into a Highly Selective Process by Using Crystalline Media. Journal of the American Chemical Society, 1996, 118, 7626-7627.	6.6	27
54	Comparison of the peptide binding preferences of three closely related TRAF paralogs: TRAF2, TRAF3, and TRAF5. Protein Science, 2016, 25, 1273-1289.	3.1	25

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55	Computing van der Waals energies in the context of the rotamer approximation. Proteins: Structure, Function and Bioinformatics, 2007, 68, 863-878.	1.5	23
56	Increasing the affinity of selective bZIPâ€binding peptides through surface residue redesign. Protein Science, 2014, 23, 940-953.	3.1	22
57	Combining Quantum Mechanical Reaction Pathways with Force Field Lattice Interactions To Model a Solid-State Phototransformation. Journal of the American Chemical Society, 1997, 119, 1474-1475.	6.6	20
58	Coarse-Graining Protein Energetics in Sequence Variables. Physical Review Letters, 2005, 95, 148103.	2.9	19
59	Analysis of Coiled-Coil Interactions between Core Proteins of the Spindle Pole Body. Biochemistry, 2008, 47, 11858-11868.	1.2	19
60	Multistate Protein Design Using CLEVER and CLASSY. Methods in Enzymology, 2013, 523, 171-190.	0.4	19
61	Cluster expansion models for flexibleâ€backbone protein energetics. Journal of Computational Chemistry, 2009, 30, 2402-2413.	1.5	17
62	A Barcoding Strategy Enabling Higher-Throughput Library Screening by Microscopy. ACS Synthetic Biology, 2015, 4, 1205-1216.	1.9	17
63	A Computationally Guided Protein-Interaction Screen Uncovers Coiled-Coil Interactions Involved in Vesicular Trafficking. Journal of Molecular Biology, 2009, 392, 228-241.	2.0	16
64	Locating Herpesvirus Bcl-2 Homologs in the Specificity Landscape of Anti-Apoptotic Bcl-2 Proteins. Journal of Molecular Biology, 2015, 427, 2468-2490.	2.0	16
65	Identifying and reducing error in clusterâ€expansion approximations of protein energies. Journal of Computational Chemistry, 2010, 31, 2900-2914.	1.5	14
66	Design of Peptide Inhibitors That Bind the bZIP Domain of Epsteinâ€“Barr Virus Protein BZLF1. Journal of Molecular Biology, 2011, 408, 304-320.	2.0	14
67	Generating High-Accuracy Peptide-Binding Data in High Throughput with Yeast Surface Display and SORTCERY. Methods in Molecular Biology, 2016, 1414, 233-247.	0.4	13
68	Computational Prediction of the Enantioselectivity of a Solid-State Photoreaction. Organic Letters, 1999, 1, 1279-1281.	2.4	11
69	Experimental and computational modeling of biphenyl twisting in a solid-to-solid carbene reaction. Tetrahedron Letters, 1999, 40, 261-264.	0.7	10
70	Native proline-rich motifs exploit sequence context to target actin-remodeling Ena/VASP protein ENAH. ELife, 2022, 11, .	2.8	10
71	Selective peptide inhibitors of antiapoptotic cellular and viral Bcl-2 proteins lead to cytochrome c release during latent Kaposiâ€™s sarcoma-associated herpesvirus infection. Virus Research, 2016, 211, 86-88.	1.1	8
72	Tertiary motifs as building blocks for the design of proteinâ€binding peptides. Protein Science, 2022, 31, .	3.1	8

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73	Specific coiled-coil interactions contribute to a global model of the structure of the spindle pole body. Journal of Structural Biology, 2010, 170, 246-256.	1.3	6
74	Enriching Peptide Libraries for Binding Affinity and Specificity Through Computationally Directed Library Design. Methods in Molecular Biology, 2017, 1561, 213-232.	0.4	6
75	A rational route to probing membrane proteins. Genome Biology, 2007, 8, 214.	13.9	5
76	A distributed residue network permits conformational binding specificity in a conserved family of actin remodelers. ELife, 2021, 10, .	2.8	5
77	The Orientations of Large Aspectâ€Ratio Coiledâ€Coil Proteins Attached to Gold Nanostructures. Small, 2016, 12, 1498-1505.	5.2	2
78	Preface. Methods in Enzymology, 2013, 523, xvii-xviii.	0.4	1