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	Native proline-rich motifs exploit sequence context to target actin-remodeling Ena/VASP protein ENAH. ELife, 2022, 11, .	2.8	10
2	Tertiary motifs as building blocks for the design of proteinâ€binding peptides. Protein Science, 2022, 31, .	3.1	8
3	Data-driven computational protein design. Current Opinion in Structural Biology, 2021, 69, 63-69.	2.6	28
4	A distributed residue network permits conformational binding specificity in a conserved family of actin remodelers. ELife, 2021, 10, .	2.8	5
5	Spatial Multiplexing of Fluorescent Reporters for Imaging Signaling Network Dynamics. Cell, 2020, 183, 1682-1698.e24.	13.5	38
6	Precision Calcium Imaging of Dense Neural Populations via a Cell-Body-Targeted Calcium Indicator. Neuron, 2020, 107, 470-486.e11.	3.8	87
7	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
8	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
9	PixelDB: Proteinâ€“peptide complexes annotated with structural conservation of the peptide binding mode. Protein Science, 2018, 27, 276-285.	3.1	31
10	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
11	Modular assembly of a protein nanotriangle using orthogonally interacting coiled coils. Scientific Reports, 2017, 7, 10577.	1.6	31
12	Enriching Peptide Libraries for Binding Affinity and Specificity Through Computationally Directed Library Design. Methods in Molecular Biology, 2017, 1561, 213-232.	0.4	6
13	Combinatorial bZIP dimers display complex DNA-binding specificity landscapes. ELife, 2017, 6, .	2.8	109
14	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
15	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
16	The Orientations of Large Aspectâ€Ratio Coiledâ€Coil Proteins Attached to Gold Nanostructures. Small, 2016, 12, 1498-1505.	5.2	2
17	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
18	Designing helical peptide inhibitors of proteinâ€“protein interactions. Current Opinion in Structural Biology, 2016, 39, 27-38.	2.6	57

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19	<scp>AB</scp> â€Bind: Antibody binding mutational database for computational affinity predictions. Protein Science, 2016, 25, 393-409.	3.1	110
20	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
21	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
22	Potent and Specific Peptide Inhibitors of Human Pro-Survival Protein Bcl-xL. Journal of Molecular Biology, 2015, 427, 1241-1253.	2.0	35
23	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
24	SORTCERYâ€”A Highâ€“Throughput Method to Affinity Rank Peptide Ligands. Journal of Molecular Biology, 2015, 427, 2135-2150.	2.0	58
25	Data-Driven Prediction and Design of bZIP Coiled-Coil Interactions. PLoS Computational Biology, 2015, 11, e1004046.	1.5	38
26	A Barcoding Strategy Enabling Higher-Throughput Library Screening by Microscopy. ACS Synthetic Biology, 2015, 4, 1205-1216.	1.9	17
27	Genome-Wide Prediction and Validation of Peptides That Bind Human Prosurvival Bcl-2 Proteins. PLoS Computational Biology, 2014, 10, e1003693.	1.5	35
28	Increasing the affinity of selective bZIPâ€binding peptides through surface residue redesign. Protein Science, 2014, 23, 940-953.	3.1	22
29	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
30	Designed BH3 Peptides with High Affinity and Specificity for Targeting Mcl-1 in Cells. ACS Chemical Biology, 2014, 9, 1962-1968.	1.6	91
31	Networks of bZIP Protein-Protein Interactions Diversified Over a Billion Years of Evolution. Science, 2013, 340, 730-734.	6.0	151
32	Multistate Protein Design Using CLEVER and CLASSY. Methods in Enzymology, 2013, 523, 171-190.	0.4	19
33	Structure-Based Redesign of the Binding Specificity of Anti-Apoptotic Bcl-xL. Journal of Molecular Biology, 2013, 425, 171-185.	2.0	31
34	Helix Bundle Loops Determine Whether Histidine Kinases Autophosphorylate in cis or in trans. Journal of Molecular Biology, 2013, 425, 1198-1209.	2.0	61
35	Peptide Ligands for Pro-survival Protein Bfl-1 from Computationally Guided Library Screening. ACS Chemical Biology, 2013, 8, 778-788.	1.6	34
36	bZIP transcription factors affecting secondary metabolism, sexual development and stress responses in Aspergillus nidulans. Microbiology (United Kingdom), 2013, 159, 77-88.	0.7	89

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37	Preface. Methods in Enzymology, 2013, 523, xvii-xviii.	0.4	1
38	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
39	In Silico and in Vitro Elucidation of BH3 Binding Specificity toward Bcl-2. Biochemistry, 2012, 51, 5841-5850.	1.2	35
40	Predictive Bcl-2 Family Binding Models Rooted in Experiment or Structure. Journal of Molecular Biology, 2012, 422, 124-144.	2.0	50
41	Designing specific proteinâ€“protein interactions using computation, experimental library screening, or integrated methods. Protein Science, 2012, 21, 949-963.	3.1	43
42	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
43	Determinants of Homodimerization Specificity in Histidine Kinases. Journal of Molecular Biology, 2011, 413, 222-235.	2.0	38
44	Multicoil2: Predicting Coiled Coils and Their Oligomerization States from Sequence in the Twilight Zone. PLoS ONE, 2011, 6, e23519.	1.1	72
45	Protein binding specificity versus promiscuity. Current Opinion in Structural Biology, 2011, 21, 50-61.	2.6	209
46	Identifying and reducing error in clusterâ€expansion approximations of protein energies. Journal of Computational Chemistry, 2010, 31, 2900-2914.	1.5	14
47	Mclâ€1â€“Bim complexes accommodate surprising point mutations via minor structural changes. Protein Science, 2010, 19, 507-519.	3.1	88
48	The MCL-1 BH3 helix is an exclusive MCL-1 inhibitor and apoptosis sensitizer. Nature Chemical Biology, 2010, 6, 595-601.	3.9	374
49	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
50	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
51	Determinants of BH3 Binding Specificity for Mcl-1 versus Bcl-xL. Journal of Molecular Biology, 2010, 398, 747-762.	2.0	113
52	A Synthetic Coiled-Coil Interactome Provides Heterospecific Modules for Molecular Engineering. Journal of the American Chemical Society, 2010, 132, 6025-6031.	6.6	170
53	Cluster expansion models for flexibleâ€backbone protein energetics. Journal of Computational Chemistry, 2009, 30, 2402-2413.	1.5	17
54	Xâ€ray vs. NMR structures as templates for computational protein design. Proteins: Structure, Function and Bioinformatics, 2009, 77, 97-110.	1.5	43

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55	Design of protein-interaction specificity gives selective bZIP-binding peptides. Nature, 2009, 458, 859-864.	13.7	317
56	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
57	Predicting helix orientation for coiledâ€coil dimers. Proteins: Structure, Function and Bioinformatics, 2008, 72, 1048-1065.	1.5	34
58	Structural specificity in coiled-coil interactions. Current Opinion in Structural Biology, 2008, 18, 477-483.	2.6	252
59	Analysis of Coiled-Coil Interactions between Core Proteins of the Spindle Pole Body. Biochemistry, 2008, 47, 11858-11868.	1.2	19
60	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
61	A rational route to probing membrane proteins. Genome Biology, 2007, 8, 214.	13.9	5
62	Computing van der Waals energies in the context of the rotamer approximation. Proteins: Structure, Function and Bioinformatics, 2007, 68, 863-878.	1.5	23
63	Structure-based Prediction of bZIP Partnering Specificity. Journal of Molecular Biology, 2006, 355, 1125-1142.	2.0	62
64	Ultra-Fast Evaluation of Protein Energies Directly from Sequence. PLoS Computational Biology, 2006, 2, e63.	1.5	37
65	Design of a Heterospecific, Tetrameric, 21-Residue Miniprotein with Mixed Î±/Î² Structure. Structure, 2005, 13, 225-234.	1.6	33
66	Coarse-Graining Protein Energetics in Sequence Variables. Physical Review Letters, 2005, 95, 148103.	2.9	19
67	Orientation and Oligomerization Specificity of the Bcr Coiled-Coil Oligomerization Domainâ€. Biochemistry, 2005, 44, 16246-16256.	1.2	31
68	Predicting specificity in bZIP coiled-coil protein interactions. Genome Biology, 2004, 5, R11.	13.9	105
69	Comprehensive Identification of Human bZIP Interactions with Coiled-Coil Arrays. Science, 2003, 300, 2097-2101.	6.0	435
70	Experimental and computational modeling of biphenyl twisting in a solid-to-solid carbene reaction. Tetrahedron Letters, 1999, 40, 261-264.	0.7	10
71	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
72	Computational Prediction of the Enantioselectivity of a Solid-State Photoreaction. Organic Letters, 1999, 1, 1279-1281.	2.4	11

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73	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
74	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
75	Self-Assembling Ternary Complex Stabilities and Template Ratios in Carceplex Formation. Journal of the American Chemical Society, 1997, 119, 4321-4322.	6.6	37
76	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
77	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
78	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