Gevorg Grigoryan

List of Publications by Year
in descending order

43 papers	2,475 citations	304743 22 h-index	254184 43 g-index
48 all docs	48 docs citations	48 times ranked	3584 citing authors

#	Article	IF	Citations
1	Design of protein-interaction specificity gives selective bZIP-binding peptides. Nature, 2009, 458, 859-864.	27.8	317
2	De novo design of a transmembrane Zn^{2+}-transporting four-helix bundle. Science, 2014, 346, 1520-1524.	12.6	275
3	Structural specificity in coiled-coil interactions. Current Opinion in Structural Biology, 2008, 18, 477-483.	5.7	252
4	Defining variant-resistant epitopes targeted by SARS-CoV-2 antibodies: A global consortium study. Science, 2021, 374, 472-478.	12.6	228
5	Probing Designability via a Generalized Model of Helical Bundle Geometry. Journal of Molecular Biology, 2011, 405, 1079-1100.	4.2	203
6	Computational Design of Virus-Like Protein Assemblies on Carbon Nanotube Surfaces. Science, 2011, 332, 1071-1076.	12.6	196
7	Point-based probabilistic surfaces to show surface uncertainty. IEEE Transactions on Visualization and Computer Graphics, 2004, 10, 564-573.	4.4	92
8	A general-purpose protein design framework based on mining sequence–structure relationships in known protein structures. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 1059-1068.	7.1	78
9	Rapid search for tertiary fragments reveals protein sequence–structure relationships. Protein Science, 2015, 24, 508-524.	7.6	68
10	Structure-based Prediction of bZIP Partnering Specificity. Journal of Molecular Biology, 2006, 355, 1125-1142.	4.2	62
11	Tertiary alphabet for the observable protein structural universe. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E7438-E7447.	7.1	60
12	Protein-directed self-assembly of a fullerene crystal. Nature Communications, 2016, 7, 11429.	12.8	55
13	Protein structural motifs in prediction and design. Current Opinion in Structural Biology, 2017, 44, 161-167.	5.7	41
14	Ultra-Fast Evaluation of Protein Energies Directly from Sequence. PLoS Computational Biology, 2006, 2, e63.	3.2	37
15	Structural analysis of cross α-helical nanotubes provides insight into the designability of filamentous peptide nanomaterials. Nature Communications, 2021, 12, 407.	12.8	35
16	Transmembrane Communication: General Principles and Lessons from the Structure and Function of the M2 Proton Channel, K+Channels, and Integrin Receptors. Annual Review of Biochemistry, 2011, 80, 211-237.	11.1	33
17	Design and designability of protein-based assemblies. Current Opinion in Structural Biology, 2014, 27, 79-86.	5.7	31
18	Graphene Symmetry Amplified by Designed Peptide Self-Assembly. Biophysical Journal, 2016, 110, 2507-2516.	0.5	31

#	Article	IF	Citations
19	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.	3.3	29
20	Tertiary Structural Propensities Reveal Fundamental Sequence/Structure Relationships. Structure, 2015, 23, 961-971.	3.3	27
21	The accommodation index measures the perturbation associated with insertions and deletions in coiled-coils: Application to understand signaling in histidine kinases. Protein Science, 2017, 26, 414-435.	7.6	26
22	Sequence statistics of tertiary structural motifs reflect protein stability. PLoS ONE, 2017, 12, e0178272.	2.5	26
23	Design of self-assembling transmembrane helical bundles to elucidate principles required for membrane protein folding and ion transport. Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20160214.	4.0	24
24	Computing van der Waals energies in the context of the rotamer approximation. Proteins: Structure, Function and Bioinformatics, 2007, 68, 863-878.	2.6	23
25	Structural informatics, modeling, and design with an open-source Molecular Software Library (MSL). Journal of Computational Chemistry, 2012, 33, 1645-1661.	3.3	23
26	Computational Design of Selective Peptides to Discriminate between Similar PDZ Domains in an Oncogenic Pathway. Journal of Molecular Biology, 2015, 427, 491-510.	4.2	23
27	Coarse-Graining Protein Energetics in Sequence Variables. Physical Review Letters, 2005, 95, 148103.	7.8	19
28	Cluster expansion models for flexible-backbone protein energetics. Journal of Computational Chemistry, 2009, 30, 2402-2413.	3.3	17
29	Large-scale design and refinement of stable proteins using sequence-only models. PLoS ONE, 2022, 17, e0265020.	2.5	17
30	Mining Tertiary Structural Motifs for Assessment of Designability. Methods in Enzymology, 2013, 523, 21-40.	1.0	16
31	Structure-based design of combinatorial mutagenesis libraries. Protein Science, 2015, 24, 895-908.	7.6	15
32	Identifying and reducing error in cluster-expansion approximations of protein energies. Journal of Computational Chemistry, 2010, 31, 2900-2914.	3.3	14
33	Single methyl groups can act as toggle switches to specify transmembrane Protein-protein interactions. ELife, 2017, 6, .	6.0	14
34	Absolute free energies of biomolecules from unperturbed ensembles. Journal of Computational Chemistry, 2013, 34, 2726-2741.	3.3	12
35	Deletion of Na^+/H^+ exchanger regulatory factor 2 represses colon cancer progress by suppression of Stat3 and CD24. American Journal of Physiology - Renal Physiology, 2016, 310, G586-G598.	3.4	12
36	Tertiary motifs as building blocks for the design of protein-binding peptides. Protein Science, 2022, 31, .	7.6	8

#	ARTICLE	IF	CITATIONS
37	Pareto Optimization of Combinatorial Mutagenesis Libraries. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1143-1153.	3.0	6
38	Contact prediction is hardest for the most informative contacts, but improves with the incorporation of contact potentials. PLoS ONE, 2018, 13, e0199585.	2.5	5
39	Structure-conditioned amino-acid couplings: How contact geometry affects pairwise sequence preferences. Protein Science, 2022, 31, 900-917.	7.6	3
40	Simplifying the Design of Protein-Peptide Interaction Specificity with Sequence-Based Representations of Atomistic Models. Methods in Molecular Biology, 2017, 1561, 189-200.	0.9	2
41	Gap detection responses modelled using the Hill equation in adults with well-controlled HIV. International Journal of Audiology, 2023, 62, 383-392.	1.7	2
42	Design of Specific Peptide–Protein Recognition. Methods in Molecular Biology, 2016, 1414, 249-263.	0.9	1
43	Dissociating STAT4 and STAT5 Signaling Inhibitory Functions of SOCS3: Effects on CD8 T Cell Responses. ImmunoHorizons, 2019, 3, 547-558.	1.8	1