Gevorg Grigoryan

List of Publications by Year in descending order

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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	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
2	Structureâ€conditioned aminoâ€acid couplings: How contact geometry affects pairwise sequence preferences. Protein Science, 2022, 31, 900-917.	7.6	3
3	Large-scale design and refinement of stable proteins using sequence-only models. PLoS ONE, 2022, 17, e0265020.	2.5	17
4	Tertiary motifs as building blocks for the design of proteinâ€binding peptides. Protein Science, 2022, 31, .	7.6	8
5	Structural analysis of cross Î±-helical nanotubes provides insight into the designability of filamentous peptide nanomaterials. Nature Communications, 2021, 12, 407.	12.8	35
6	Defining variant-resistant epitopes targeted by SARS-CoV-2 antibodies: A global consortium study. Science, 2021, 374, 472-478.	12.6	228
7	A general-purpose protein design framework based on mining sequenceâ€“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
8	Pareto Optimization of Combinatorial Mutagenesis Libraries. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1143-1153.	3.0	6
9	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
10	Dissociating STAT4 and STAT5 Signaling Inhibitory Functions of SOCS3: Effects on CD8 T Cell Responses. ImmunoHorizons, 2019, 3, 547-558.	1.8	1
11	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
12	Protein structural motifs in prediction and design. Current Opinion in Structural Biology, 2017, 44, 161-167.	5.7	41
13	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
14	The accommodation index measures the perturbation associated with insertions and deletions in coiledâ€coils: Application to understand signaling in histidine kinases. Protein Science, 2017, 26, 414-435.	7.6	26
15	Sequence statistics of tertiary structural motifs reflect protein stability. PLoS ONE, 2017, 12, e0178272.	2.5	26
16	Single methyl groups can act as toggle switches to specify transmembrane Protein-protein interactions. ELife, 2017, 6, .	6.0	14
17	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
18	Design of Specific Peptideâ€“Protein Recognition. Methods in Molecular Biology, 2016, 1414, 249-263.	0.9	1

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19	Protein-directed self-assembly of a fullerene crystal. Nature Communications, 2016, 7, 11429.	12.8	55
20	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
21	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
22	Graphene Symmetry Amplified by Designed Peptide Self-Assembly. Biophysical Journal, 2016, 110, 2507-2516.	0.5	31
23	Rapid search for tertiary fragments reveals protein sequenceâ€“structure relationships. Protein Science, 2015, 24, 508-524.	7.6	68
24	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
25	Structureâ€based design of combinatorial mutagenesis libraries. Protein Science, 2015, 24, 895-908.	7.6	15
26	Tertiary Structural Propensities Reveal Fundamental Sequence/Structure Relationships. Structure, 2015, 23, 961-971.	3.3	27
27	De novo design of a transmembrane Zn ²⁺ -transporting four-helix bundle. Science, 2014, 346, 1520-1524.	12.6	275
28	Design and designability of protein-based assemblies. Current Opinion in Structural Biology, 2014, 27, 79-86.	5.7	31
29	Absolute free energies of biomolecules from unperturbed ensembles. Journal of Computational Chemistry, 2013, 34, 2726-2741.	3.3	12
30	Mining Tertiary Structural Motifs for Assessment of Designability. Methods in Enzymology, 2013, 523, 21-40.	1.0	16
31	Structural informatics, modeling, and design with an openâ€source Molecular Software Library (MSL). Journal of Computational Chemistry, 2012, 33, 1645-1661.	3.3	23
32	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
33	Probing Designability via a Generalized Model of Helical Bundle Geometry. Journal of Molecular Biology, 2011, 405, 1079-1100.	4.2	203
34	Computational Design of Virus-Like Protein Assemblies on Carbon Nanotube Surfaces. Science, 2011, 332, 1071-1076.	12.6	196
35	Identifying and reducing error in clusterâ€expansion approximations of protein energies. Journal of Computational Chemistry, 2010, 31, 2900-2914.	3.3	14
36	Cluster expansion models for flexibleâ€backbone protein energetics. Journal of Computational Chemistry, 2009, 30, 2402-2413.	3.3	17

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37	Design of protein-interaction specificity gives selective bZIP-binding peptides. Nature, 2009, 458, 859-864.	27.8	317
38	Structural specificity in coiled-coil interactions. Current Opinion in Structural Biology, 2008, 18, 477-483.	5.7	252
39	Computing van der Waals energies in the context of the rotamer approximation. Proteins: Structure, Function and Bioinformatics, 2007, 68, 863-878.	2.6	23
40	Structure-based Prediction of bZIP Partnering Specificity. Journal of Molecular Biology, 2006, 355, 1125-1142.	4.2	62
41	Ultra-Fast Evaluation of Protein Energies Directly from Sequence. PLoS Computational Biology, 2006, 2, e63.	3.2	37
42	Coarse-Graining Protein Energetics in Sequence Variables. Physical Review Letters, 2005, 95, 148103.	7.8	19
43	Point-based probabilistic surfaces to show surface uncertainty. IEEE Transactions on Visualization and Computer Graphics, 2004, 10, 564-573.	4.4	92