Sergey Ovchinnikov

List of Publications by Year
in descending order

37	13,104	201674	345221
papers	citations	27 h-index	36 g-index

56	56	56	9300
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	ColabFold: making protein folding accessible to all. Nature Methods, 2022, 19, 679-682.	19.0	3,242
2	Accurate prediction of protein structures and interactions using a three-track neural network. Science, 2021, 373, 871-876.	12.6	2,843
3	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.	7.1	1,135
4	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.	7.1	605
5	Robust and accurate prediction of residueâ€“residue interactions across protein interfaces using evolutionary information. ELife, 2014, 3, e02030.	6.0	571
6	Macromolecular modeling and design in Rosetta: recent methods and frameworks. Nature Methods, 2020, 17, 665-680.	19.0	513
7	Protein structure determination using metagenome sequence data. Science, 2017, 355, 294-298.	12.6	456
8	Computed structures of core eukaryotic protein complexes. Science, 2021, 374, eabm4805.	12.6	316
9	De novo protein design by deep network hallucination. Nature, 2021, 600, 547-552.	27.8	280
10	De novo design of a fluorescence-activating Î²-barrel. Nature, 2018, 561, 485-491.	27.8	269
11	Large-scale determination of previously unsolved protein structures using evolutionary information. ELife, 2015, 4, e09248.	6.0	229
12	Protein interaction networks revealed by proteome coevolution. Science, 2019, 365, 185-189.	12.6	208
13	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.	7.1	167
14	Cryo-EM structure of the protein-conducting ERAD channel Hrd1 in complex with Hrd3. Nature, 2017, 548, 352-355.	27.8	160
15	Structure of a bd oxidase indicates similar mechanisms for membrane-integrated oxygen reductases. Science, 2016, 352, 583-586.	12.6	143
16	Structural basis of ER-associated protein degradation mediated by the Hrd1 ubiquitin ligase complex. Science, 2020, 368, .	12.6	143
17	Protein sequence design by conformational landscape optimization. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	97
18	Improved de novo structure prediction in <scp>CASP</scp>11 by incorporating coevolution information into Rosetta. Proteins: Structure, Function and Bioinformatics, 2016, 84, 67-75.	2.6	96

#	Article	IF	Citations
19	Protein structure prediction using Rosetta in CASP12. Proteins: Structure, Function and Bioinformatics, 2018, 86, 113-121.	2.6	85
20	A demonstration of unsupervised machine learning in species delimitation. Molecular Phylogenetics and Evolution, 2019, 139, 106562.	2.7	67
21	Computation and Functional Studies Provide a Model for the Structure of the Zinc Transporter hZIP4. Journal of Biological Chemistry, 2015, 290, 17796-17805.	3.4	63
22	Protein homology model refinement by large-scale energy optimization. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 3054-3059.	7.1	62
23	Overcoming an optimization plateau in the directed evolution of highly efficient nerve agent bioscavengers. Protein Engineering, Design and Selection, 2017, 30, 333-345.	2.1	57
24	Structure-based protein design with deep learning. Current Opinion in Chemical Biology, 2021, 65, 136-144.	6.1	53
25	Automatic structure prediction of oligomeric assemblies using Robetta in CASP12. Proteins: Structure, Function and Bioinformatics, 2018, 86, 283-291.	2.6	49
26	Catalytic efficiencies of directly evolved phosphotriesterase variants with structurally different organophosphorus compounds in vitro. Archives of Toxicology, 2016, 90, 2711-2724.	4.2	42
27	Applications of contact predictions to structural biology. IUCrJ, 2017, 4, 291-300.	2.2	39
28	Structure determination of the HgcAB complex using metagenome sequence data: insights into microbial mercury methylation. Communications Biology, 2020, 3, 320.	4.4	30
29	Structural insights into SAM domainâ€mediated tankyrase oligomerization. Protein Science, 2016, 25, 1744-1752.	7.6	25
30	An analysis and evaluation of the WeFold collaborative for protein structure prediction and its pipelines in CASP11 and CASP12. Scientific Reports, 2018, 8, 9939.	3.3	19
31	A structural and data-driven approach to engineering a plant cytochrome P450 enzyme. Science China Life Sciences, 2019, 62, 873-882.	4.9	18
32	Structure prediction using sparse simulated <scp>NOE</scp> restraints with Rosetta in <scp>CASP</scp>11. Proteins: Structure, Function and Bioinformatics, 2016, 84, 181-188.	2.6	16
33	Structurally Mapping Endogenous Heme in the CcmCDE Membrane Complex for Cytochrome c Biogenesis. Journal of Molecular Biology, 2018, 430, 1065-1080.	4.2	16
34	Templateâ€based modeling by ClusPro in CASP13 and the potential for using coâ€evolutionary information in docking. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1241-1248.	2.6	15
35	New insights into substrate folding preference of plant OSCs. Science Bulletin, 2016, 61, 1407-1412.	9.0	14
36	Development of a dual-functional conjugate of antigenic peptide and Fc-III mimetics (DCAF) for targeted antibody blocking. Chemical Science, 2019, 10, 3271-3280.	7.4	12

#	Article	IF	Citations
37	Interpreting Potts and Transformer Protein Models Through the Lens of Simplified Attention. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2022, 27, 34-45.	0.7	0