Sergey Ovchinnikov

List of Publications by Year in Descending Order

52 papers	4,162 citations	27 h-index	56 g-index
56 ext. papers	8,392 ext. citations	15 avg, IF	5.91 L-index

#	Paper	IF	Citations
52	Interpreting Potts and Transformer Protein Models Through the Lens of Simplified Attention. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2022**, 27, 34-45	1.3	
51	Computed structures of core eukaryotic protein complexes. *Science*, **2021**, 374, eabm4805	33.3	51
50	De novo protein design by deep network hallucination. *Nature*, **2021**,	50.4	33
49	Protein sequence design by conformational landscape optimization. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	29
48	Accurate prediction of protein structures and interactions using a three-track neural network. *Science*, **2021**, 373, 871-876	33.3	522
47	Structure-based protein design with deep learning. *Current Opinion in Chemical Biology*, **2021**, 65, 136-144	9.7	3
46	Macromolecular modeling and design in Rosetta: recent methods and frameworks. *Nature Methods*, **2020**, 17, 665-680	21.6	165
45	Structure determination of the HgcAB complex using metagenome sequence data: insights into microbial mercury methylation. *Communications Biology*, **2020**, 3, 320	6.7	8
44	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	11.5	496
43	Structural basis of ER-associated protein degradation mediated by the Hrd1 ubiquitin ligase complex. *Science*, **2020**, 368,	33.3	60
42	Development of a dual-functional conjugate of antigenic peptide and Fc-III mimetics (DCAF) for targeted antibody blocking. *Chemical Science*, **2019**, 10, 3271-3280	9.4	7
41	A structural and data-driven approach to engineering a plant cytochrome P450 enzyme. *Science China Life Sciences*, **2019**, 62, 873-882	8.5	6
40	A demonstration of unsupervised machine learning in species delimitation. *Molecular Phylogenetics and Evolution*, **2019**, 139, 106562	4.1	36
39	Template-based modeling by ClusPro in CASP13 and the potential for using co-evolutionary information in docking. *Proteins: Structure, Function and Bioinformatics*, **2019**, 87, 1241-1248	4.2	7
38	Protein interaction networks revealed by proteome coevolution. *Science*, **2019**, 365, 185-189	33.3	112
37	Structurally Mapping Endogenous Heme in the CcmCDE Membrane Complex for Cytochrome c Biogenesis. *Journal of Molecular Biology*, **2018**, 430, 1065-1080	6.5	11
36	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	11.5	49

35	Protein structure prediction using Rosetta in CASP12. *Proteins: Structure, Function and Bioinformatics*, **2018**, 86 Suppl 1, 113-121	4.2	63
34	Automatic structure prediction of oligomeric assemblies using Robetta in CASP12. *Proteins: Structure, Function and Bioinformatics*, **2018**, 86 Suppl 1, 283-291	4.2	29
33	An analysis and evaluation of the WeFold collaborative for protein structure prediction and its pipelines in CASP11 and CASP12. *Scientific Reports*, **2018**, 8, 9939	4.9	16
32	De novo design of a fluorescence-activating β-barrel. *Nature*, **2018**, 561, 485-491	50.4	156
31	Protein structure determination using metagenome sequence data. *Science*, **2017**, 355, 294-298	33.3	346
30	Overcoming an optimization plateau in the directed evolution of highly efficient nerve agent bioscavengers. *Protein Engineering, Design and Selection*, **2017**, 30, 333-345	1.9	41
29	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	11.5	92
28	Cryo-EM structure of the protein-conducting ERAD channel Hrd1 in complex with Hrd3. *Nature*, **2017**, 548, 352-355	50.4	117
27	Applications of contact predictions to structural biology. *IUCrJ*, **2017**, 4, 291-300	4.7	30
26	New insights into substrate folding preference of plant OSCs. *Science Bulletin*, **2016**, 61, 1407-1412	10.6	8
25	Catalytic efficiencies of directly evolved phosphotriesterase variants with structurally different organophosphorus compounds in vitro. *Archives of Toxicology*, **2016**, 90, 2711-2724	5.8	35
24	Structure prediction using sparse simulated NOE restraints with Rosetta in CASP11. *Proteins: Structure, Function and Bioinformatics*, **2016**, 84 Suppl 1, 181-8	4.2	11
23	Structural insights into SAM domain-mediated tankyrase oligomerization. *Protein Science*, **2016**, 25, 1744-52	6.3	15
22	Improved de novo structure prediction in CASP11 by incorporating coevolution information into Rosetta. *Proteins: Structure, Function and Bioinformatics*, **2016**, 84 Suppl 1, 67-75	4.2	82
21	Structure of a bd oxidase indicates similar mechanisms for membrane-integrated oxygen reductases. *Science*, **2016**, 352, 583-6	33.3	101
20	Computation and Functional Studies Provide a Model for the Structure of the Zinc Transporter hZIP4. *Journal of Biological Chemistry*, **2015**, 290, 17796-17805	5.4	51
19	Large-scale determination of previously unsolved protein structures using evolutionary information. *ELife*, **2015**, 4, e09248	8.9	173
18	Robust and accurate prediction of residue-residue interactions across protein interfaces using evolutionary information. *ELife*, **2014**, 3, e02030	8.9	397

17	Author response: Robust and accurate prediction of residue□residue interactions across protein interfaces using evolutionary information **2014**,		3
16	Assessing the utility of coevolution-based residue-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, 15674-9	11.5	423
15	ColabFold - Making protein folding accessible to all		2
14	Deep learning methods for designing proteins scaffolding functional sites		4
13	Structures of core eukaryotic protein complexes		7
12	End-to-end learning of multiple sequence alignments with differentiable Smith-Waterman		2
11	De novo protein design by deep network hallucination		26
10	Protein sequence design by explicit energy landscape optimization		4
9	Design of proteins presenting discontinuous functional sites using deep learning		8
8	Transformer protein language models are unsupervised structure learners		26
7	Single Layers of Attention Suffice to Predict Protein Contacts		7
6	Improved protein structure prediction using predicted inter-residue orientations		17
5	Accurate prediction of protein structures and interactions using a 3-track network		9
4	ColabFold - Making protein folding accessible to all		114
3	A structural biology community assessment of AlphaFold 2 applications		19
2	State-of-the-Art Estimation of Protein Model Accuracy using AlphaFold		4
1	ColabFold: making protein folding accessible to all. *Nature Methods*,	21.6	129