Ivan Anishchenko

List of Publications by Citations

38 papers	1,871 citations	17 h-index	41 g-index
41 ext. papers	4,268 ext. citations	10.9 avg, IF	5.48 L-index

#	Paper	IF	Citations
38	Accurate prediction of protein structures and interactions using a three-track neural network. *Science*, **2021**, 373, 871-876	33.3	522
37	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
36	Protein interaction networks revealed by proteome coevolution. *Science*, **2019**, 365, 185-189	33.3	112
35	Prediction of homoprotein and heteroprotein complexes by protein docking and template-based modeling: A CASP-CAPRI experiment. *Proteins: Structure, Function and Bioinformatics*, **2016**, 84 Suppl 1, 323-48	4.2	111
34	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
33	Computed structures of core eukaryotic protein complexes. *Science*, **2021**, 374, eabm4805	33.3	51
32	Improved protein structure refinement guided by deep learning based accuracy estimation. *Nature Communications*, **2021**, 12, 1340	17.4	50
31	Protein contact prediction using metagenome sequence data and residual neural networks. *Bioinformatics*, **2020**, 36, 41-48	7.2	43
30	The trRosetta server for fast and accurate protein structure prediction. *Nature Protocols*, **2021**, 16, 5634-5651	13.8	36
29	De novo protein design by deep network hallucination. *Nature*, **2021**,	50.4	33
28	Dockground: A comprehensive data resource for modeling of protein complexes. *Protein Science*, **2018**, 27, 172-181	6.3	32
27	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
26	High-accuracy refinement using Rosetta in CASP13. *Proteins: Structure, Function and Bioinformatics*, **2019**, 87, 1276-1282	4.2	26
25	De novo protein design by deep network hallucination		26
24	Structural templates for comparative protein docking. *Proteins: Structure, Function and Bioinformatics*, **2015**, 83, 1563-70	4.2	19
23	Modeling complexes of modeled proteins. *Proteins: Structure, Function and Bioinformatics*, **2017**, 85, 470-478	4.2	18
22	Protein models: the Grand Challenge of protein docking. *Proteins: Structure, Function and Bioinformatics*, **2014**, 82, 278-87	4.2	18

21	Protein models docking benchmark 2. *Proteins: Structure, Function and Bioinformatics*, **2015**, 83, 891-7	4.2	17
20	Improved protein structure prediction using predicted inter-residue orientations		17
19	Modeling CAPRI targets 110-120 by template-based and free docking using contact potential and combined scoring function. *Proteins: Structure, Function and Bioinformatics*, **2018**, 86 Suppl 1, 302-310	4.2	13
18	Contact Potential for Structure Prediction of Proteins and Protein Complexes from Potts Model. *Biophysical Journal*, **2018**, 115, 809-821	2.9	12
17	Improved protein structure refinement guided by deep learning based accuracy estimation		10
16	Structural basis for autophagy inhibition by the human Rubicon-Rab7 complex. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 17003-17010	11.5	9
15	Accurate prediction of protein structures and interactions using a 3-track network		9
14	In silico detection of SARS-CoV-2 specific B-cell epitopes and validation in ELISA for serological diagnosis of COVID-19. *Scientific Reports*, **2021**, 11, 4290	4.9	9
13	Protein tertiary structure prediction and refinement using deep learning and Rosetta in CASP14. *Proteins: Structure, Function and Bioinformatics*, **2021**, 89, 1722-1733	4.2	9
12	Design of proteins presenting discontinuous functional sites using deep learning		8
11	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
10	Structures of core eukaryotic protein complexes		7
9	Deep learning enables the atomic structure determination of the Fanconi Anemia core complex from cryoEM. *IUCrJ*, **2020**, 7, 881-892	4.7	5
8	Structural quality of unrefined models in protein docking. *Proteins: Structure, Function and Bioinformatics*, **2017**, 85, 39-45	4.2	4
7	Deep learning methods for designing proteins scaffolding functional sites		4
6	In silico detection of SARS-CoV-2 specific B-cell epitopes and validation in ELISA for serological diagnosis of COVID-19		4
5	Protein sequence design by explicit energy landscape optimization		4
4	Protein oligomer modeling guided by predicted interchain contacts in CASP14. *Proteins: Structure, Function and Bioinformatics*, **2021**, 89, 1824-1833	4.2	4

3	Gene ontology improves template selection in comparative protein docking. *Proteins: Structure, Function and Bioinformatics*, **2019**, 87, 245-253	4.2	2
2	Structural basis for autophagy inhibition by the human Rubicon-Rab7 complex		1
1	Deep learning enables the atomic structure determination of the Fanconi Anemia core complex from cryoEM		1