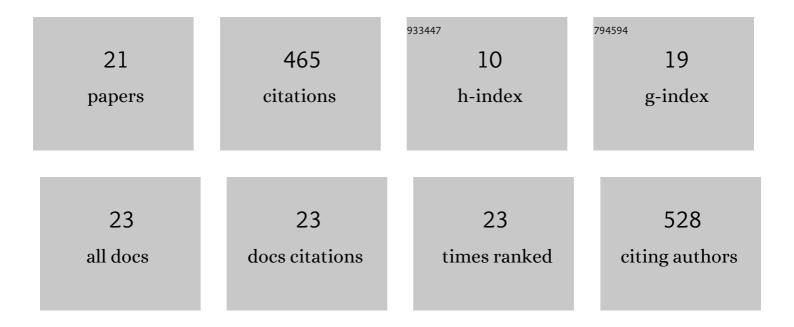
Gabriele Orlando

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	DEOGEN2: prediction and interactive visualization of single amino acid variant deleteriousness in human proteins. Nucleic Acids Research, 2017, 45, W201-W206.	14.5	114
2	Structure-based machine-guided mapping of amyloid sequence space reveals uncharted sequence clusters with higher solubilities. Nature Communications, 2020, 11, 3314.	12.8	54
3	Computational identification of prion-like RNA-binding proteins that form liquid phase-separated condensates. Bioinformatics, 2019, 35, 4617-4623.	4.1	45
4	Exploring the Sequence-based Prediction of Folding Initiation Sites in Proteins. Scientific Reports, 2017, 7, 8826.	3.3	39
5	Insight into the protein solubility driving forces with neural attention. PLoS Computational Biology, 2020, 16, e1007722.	3.2	25
6	Role and therapeutic potential of liquid–liquid phase separation in amyotrophic lateral sclerosis. Journal of Molecular Cell Biology, 2021, 13, 15-28.	3.3	23
7	Prediction of Disordered Regions in Proteins with Recurrent Neural Networks and Protein Dynamics. Journal of Molecular Biology, 2022, 434, 167579.	4.2	22
8	Accurate prediction of protein beta-aggregation with generalized statistical potentials. Bioinformatics, 2020, 36, 2076-2081.	4.1	20
9	Exploring the limitations of biophysical propensity scales coupled with machine learning for protein sequence analysis. Scientific Reports, 2019, 9, 16932.	3.3	19
10	<i>In silico</i> prediction of <i>in vitro</i> protein liquid–liquid phase separation experiments outcomes with multi-head neural attention. Bioinformatics, 2021, 37, 3473-3479.	4.1	14
11	Ultra-fast global homology detection with Discrete Cosine Transform and Dynamic Time Warping. Bioinformatics, 2018, 34, 3118-3125.	4.1	13
12	An Evolutionary View on Disulfide Bond Connectivities Prediction Using Phylogenetic Trees and a Simple Cysteine Mutation Model. PLoS ONE, 2015, 10, e0131792.	2.5	11
13	Clustering-based model of cysteine co-evolution improves disulfide bond connectivity prediction and reduces homologous sequence requirements. Bioinformatics, 2015, 31, 1219-1225.	4.1	10
14	PyUUL provides an interface between biological structures and deep learning algorithms. Nature Communications, 2022, 13, 961.	12.8	10
15	b2bTools: online predictions for protein biophysical features and their conservation. Nucleic Acids Research, 2021, 49, W52-W59.	14.5	9
16	SVM-dependent pairwise HMM: an application to protein pairwise alignments. Bioinformatics, 2017, 33, 3902-3908.	4.1	8
17	Large-scale in-silico statistical mutagenesis analysis sheds light on the deleteriousness landscape of the human proteome. Scientific Reports, 2018, 8, 16980.	3.3	7
18	Auto-encoding NMR chemical shifts from their native vector space to a residue-level biophysical index. Nature Communications, 2019, 10, 2511.	12.8	5

#	Article	IF	CITATIONS
19	Investigating the Molecular Mechanisms Behind Uncharacterized Cysteine Losses from Prediction of Their Oxidation State. Human Mutation, 2017, 38, 86-94.	2.5	4
20	ShiftCrypt: a web server to understand and biophysically align proteins through their NMR chemical shift values. Nucleic Acids Research, 2020, 48, W36-W40.	14.5	1
21	HPMPdb: a machine learning-ready database of protein molecular phenotypes associated to human missense variants. Current Research in Structural Biology, 2022, , .	2.2	1