

# Susanna Repo

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8850861/publications.pdf>

Version: 2024-02-01

15  
papers

1,417  
citations

840776

11  
h-index

996975

15  
g-index

15  
all docs

15  
docs citations

15  
times ranked

2705  
citing authors

#	ARTICLE	IF	CITATIONS
1	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013, 10, 221-227.	19.0	789
2	BODIL: a molecular modeling environment for structure-function analysis and drug design. <i>Journal of Computer-Aided Molecular Design</i> , 2004, 18, 401-419.	2.9	200
3	Association of gut microbiota with post-operative clinical course in Crohn's disease. <i>BMC Gastroenterology</i> , 2013, 13, 131.	2.0	95
4	Somatic Mutations of ErbB4. <i>Journal of Biological Chemistry</i> , 2009, 284, 5582-5591.	3.4	55
5	Construction of Hevein (Hev b 6.02) with Reduced Allergenicity for Immunotherapy of Latex Allergy by Computation of Six Amino Acid Residues on the Conformational IgE Epitopes. <i>Journal of Immunology</i> , 2004, 172, 2621-2628.	0.8	47
6	Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. <i>Human Mutation</i> , 2017, 38, 1182-1192.	2.5	39
7	Reports from CAGI: The Critical Assessment of Genome Interpretation. <i>Human Mutation</i> , 2017, 38, 1039-1041.	2.5	38
8	The Major Conformational IgE-binding Epitopes of Hevein (Hev b6.02) Are Identified by a Novel Chimera-based Allergen Epitope Mapping Strategy. <i>Journal of Biological Chemistry</i> , 2002, 277, 22656-22661.	3.4	37
9	Binding Properties of HABA-Type Azo Derivatives to Avidin and Avidin-Related Protein 4. <i>Chemistry and Biology</i> , 2006, 13, 1029-1039.	6.0	36
10	Functional Classification of Amino Acid Decarboxylases from the Alanine Racemase Structural Family by Phylogenetic Studies. <i>Molecular Biology and Evolution</i> , 2006, 24, 79-89.	8.9	29
11	Ligand Specificity of Constitutive Androstane Receptor as Probed by Induced-Fit Docking and Mutagenesis. <i>Journal of Medicinal Chemistry</i> , 2008, 51, 7119-7131.	6.4	14
12	Matching phenotypes to whole genomes: Lessons learned from four iterations of the personal genome project community challenges. <i>Human Mutation</i> , 2017, 38, 1266-1276.	2.5	14
13	Performance of in silico tools for the evaluation of p16INK4a (CDKN2A) variants in CAGI. <i>Human Mutation</i> , 2017, 38, 1042-1050.	2.5	13
14	Demonstrating public value to funders and other stakeholders—the journey of ELIXIR, a virtual and distributed research infrastructure for life science data. <i>Annals of Public and Cooperative Economics</i> , 2021, 92, 497-510.	2.4	6
15	Assessing computational predictions of the phenotypic effect of cystathionine- $\beta$ -synthase variants. <i>Human Mutation</i> , 2019, 40, 1530-1545.	2.5	5