Robert Preissner

List of Publications by Year
in descending order

135 papers	9,654 citations	46918 47 h-index	42291 92 g-index
141 all docs	141 docs citations	141 times ranked	13491 citing authors

#	Article	IF	Citations
1	ProTox-II: a webserver for the prediction of toxicity of chemicals. Nucleic Acids Research, 2018, 46, W257-W263.	6.5	1,328
2	The target landscape of clinical kinase drugs. Science, 2017, 358, .	6.0	609
3	SuperTarget and Matador: resources for exploring drug-target relationships. Nucleic Acids Research, 2007, 36, D919-D922.	6.5	518
4	SDM--a server for predicting effects of mutations on protein stability and malfunction. Nucleic Acids Research, 2011, 39, W215-W222.	6.5	453
5	ProTox: a web server for the in silico prediction of rodent oral toxicity. Nucleic Acids Research, 2014, 42, W53-W58.	6.5	400
6	mVOC: a database of microbial volatiles. Nucleic Acids Research, 2014, 42, D744-D748.	6.5	337
7	SuperPred: update on drug classification and target prediction. Nucleic Acids Research, 2014, 42, W26-W31.	6.5	288
8	mVOC 2.0: a database of microbial volatiles. Nucleic Acids Research, 2018, 46, D1261-D1265.	6.5	288
9	Super Natural IIâ€"a database of natural products. Nucleic Acids Research, 2015, 43, D935-D939.	6.5	279
10	SuperCYP: a comprehensive database on Cytochrome P450 enzymes including a tool for analysis of CYP-drug interactions. Nucleic Acids Research, 2010, 38, D237-D243.	6.5	215
11	WITHDRAWNâ€"a resource for withdrawn and discontinued drugs. Nucleic Acids Research, 2016, 44, D1080-D1086.	6.5	210
12	PROMISCUOUS: a database for network-based drug-repositioning. Nucleic Acids Research, 2011, 39, D1060-D1066.	6.5	203
13	Polymorphic Cytochrome P450 Enzymes (CYPs) and Their Role in Personalized Therapy. PLoS ONE, 2013, 8, e82562.	1.1	198
14	SuperTarget goes quantitative: update on drug-target interactions. Nucleic Acids Research, 2012, 40, D1113-D1117.	6.5	174
15	SuperPred: drug classification and target prediction. Nucleic Acids Research, 2008, 36, W55-W59.	6.5	144
16	Legionella pneumophila Induces IFNÎ² in Lung Epithelial Cells via IPS-1 and IRF3, Which Also Control Bacterial Replication. Journal of Biological Chemistry, 2006, 281, 36173-36179.	1.6	118
17	SuperScent--a database of flavors and scents. Nucleic Acids Research, 2009, 37, D291-D294.	6.5	106
18	Evidence for treatment with estradiol for women with SARS-CoV-2 infection. BMC Medicine, 2020, 18, 369.	2.3	106

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19	Prediction Is a Balancing Act: Importance of Sampling Methods to Balance Sensitivity and Specificity of Predictive Models Based on Imbalanced Chemical Data Sets. Frontiers in Chemistry, 2018, 6, 362.	1.8	97
20	A Comprehensive View on Proteasomal Sequences: Implications for the Evolution of the Proteasome. Journal of Molecular Biology, 2003, 326, 1437-1448.	2.0	96
21	TRPC6 G757D Loss-of-Function Mutation Associates with FSGS. Journal of the American Society of Nephrology: JASN, 2016, 27, 2771-2783.	3.0	94
22	SuperLooper--a prediction server for the modeling of loops in globular and membrane proteins. Nucleic Acids Research, 2009, 37, W571-W574.	6.5	85
23	SuperNatural: a searchable database of available natural compounds. Nucleic Acids Research, 2006, 34, D678-D683.	6.5	84
24	SuperSweet--a resource on natural and artificial sweetening agents. Nucleic Acids Research, 2011, 39, D377-D382.	6.5	84
25	Chemical Proteomics Reveals Ferrochelatase as a Common Off-target of Kinase Inhibitors. ACS Chemical Biology, 2016, 11, 1245-1254.	1.6	82
26	Evidence-Based Considerations Exploring Relations between SARS-CoV-2 Pandemic and Air Pollution: Involvement of PM2.5-Mediated Up-Regulation of the Viral Receptor ACE-2. International Journal of Environmental Research and Public Health, 2020, 17, 5573.	1.2	82
27	SuperDRUG2: a one stop resource for approved/marketed drugs. Nucleic Acids Research, 2018, 46, D1137-D1143.	6.5	81
28	SuperDrug: a conformational drug database. Bioinformatics, 2005, 21, 1751-1753.	1.8	80
29	IL-13 is a driver of COVID-19 severity. JCI Insight, 2021, 6, .	2.3	80
30	Voronoia: analyzing packing in protein structures. Nucleic Acids Research, 2009, 37, D393-D395.	6.5	78
31	CancerResource: a comprehensive database of cancer-relevant proteins and compound interactions supported by experimental knowledge. Nucleic Acids Research, 2011, 39, D960-D967.	6.5	70
32	Statin and rottlerin small-molecule inhibitors restrict colon cancer progression and metastasis via MACC1. PLoS Biology, 2017, 15, e2000784.	2.6	70
33	SuperToxic: a comprehensive database of toxic compounds. Nucleic Acids Research, 2009, 37, D295-D299.	6.5	69
34	Structural features of transmembrane helices. FEBS Letters, 2004, 559, 145-151.	1.3	63
35	Characterization of GD2 Peptide Mimotope DNA Vaccines Effective against Spontaneous Neuroblastoma Metastases. Cancer Research, 2006, 66, 10567-10575.	0.4	63
36	Survivin minigene DNA vaccination is effective against neuroblastoma. International Journal of Cancer, 2009, 125, 104-114.	2.3	63

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37	Natural products: sources and databases. Natural Product Reports, 2006, 23, 347-356.	5.2	62
38	Analysis of sex and gender-specific research reveals a common increase in publications and marked differences between disciplines. BMC Medicine, 2010, 8, 70.	2.3	60
39	Computational methods for prediction of in vitro effects of new chemical structures. Journal of Cheminformatics, 2016, 8, 51.	2.8	58
40	The Transformer database: biotransformation of xenobiotics. Nucleic Acids Research, 2014, 42, D1113-D1117.	6.5	57
41	The RTP Site Shared by the HIV-1 Tat Protein and the 11S Regulator Subunit Î± is Crucial for their Effects on Proteasome Function Including Antigen Processing. Journal of Molecular Biology, 2002, 323, 771-782.	2.0	56
42	SynSysNet: integration of experimental data on synaptic proteinâ€“protein interactions with drug-target relations. Nucleic Acids Research, 2012, 41, D834-D840.	6.5	54
43	Hydrogen-Bonding and Packing Features of Membrane Proteins: Functional Implications. Biophysical Journal, 2008, 94, 1945-1953.	0.2	52
44	Novel curcumin- and emodin-related compounds identified by in silico 2D/3D conformer screening induce apoptosis in tumor cells. BMC Cancer, 2005, 5, 97.	1.1	51
45	Photoactivation of an Inhibitor of the 12/15â€Lipoxygenase Pathway. ChemBioChem, 2006, 7, 1089-1095.	1.3	50
46	Docking without docking: ISEARCHâ€”prediction of interactions using known interfaces. Proteins: Structure, Function and Bioinformatics, 2007, 69, 839-844.	1.5	50
47	BitterSweetForest: A Random Forest Based Binary Classifier to Predict Bitterness and Sweetness of Chemical Compounds. Frontiers in Chemistry, 2018, 6, 93.	1.8	50
48	Comparison of 2DSimilarity and 3DSuperposition. Application to Searching a Conformational Drug Database. Journal of Chemical Information and Computer Sciences, 2004, 44, 1816-1822.	2.8	47
49	SuperCYPsPredâ€”a web server for the prediction of cytochrome activity. Nucleic Acids Research, 2020, 48, W580-W585.	6.5	47
50	The Exponential Phase of the Covid-19 Pandemic in Central Italy: An Integrated Care Pathway. International Journal of Environmental Research and Public Health, 2020, 17, 3792.	1.2	46
51	SuperPred 3.0: drug classification and target predictionâ€”a machine learning approach. Nucleic Acids Research, 2022, 50, W726-W731.	6.5	46
52	Prediction of prolyl residues in cis -conformation in protein structures on the basis of the amino acid sequence. FEBS Letters, 1990, 277, 159-163.	1.3	45
53	Conservation of cis prolyl bonds in proteins during evolution. Proteins: Structure, Function and Bioinformatics, 2004, 58, 589-595.	1.5	43
54	Molecular similarity-based predictions of the Tox21 screening outcome. Frontiers in Environmental Science, 2015, 3, .	1.5	43

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55	Columba: an integrated database of proteins, structures, and annotations. BMC Bioinformatics, 2005, 6, 81.	1.2	40
56	Suppressive Effects of Clerodendrum volubile P Beauv. [Labiatae] Methanolic Extract and Its Fractions on Type 2 Diabetes and Its Complications. Frontiers in Pharmacology, 2018, 9, 8.	1.6	40
57	Molecular Packing and Packing Defects in Helical Membrane Proteins. Biophysical Journal, 2005, 88, 1970-1977.	0.2	39
58	The Catch-22 of Predicting hERG Blockade Using Publicly Accessible Bioactivity Data. Journal of Chemical Information and Modeling, 2018, 58, 1224-1233.	2.5	39
59	SuperLigands - a database of ligand structures derived from the Protein Data Bank. BMC Bioinformatics, 2005, 6, 122.	1.2	36
60	Anti-diabetic effect of the ethyl acetate fraction of Clerodendrum volubile: protocatechuic acid suppresses phagocytic oxidative burst and modulates inflammatory cytokines. Biomedicine and Pharmacotherapy, 2017, 86, 307-315.	2.5	36
61	Inhomogeneous molecular density: reference packing densities and distribution of cavities within proteins. Bioinformatics, 2003, 19, 2112-2121.	1.8	35
62	A rationally designed tyrosine hydroxylase DNA vaccine induces specific antineuroblastoma immunity. Molecular Cancer Therapeutics, 2008, 7, 2241-2251.	1.9	35
63	Sequence information within proteasomal prosequences mediates efficient integration of Î²-subunits into the 20 s proteasome complex. Journal of Molecular Biology, 1999, 288, 117-128.	2.0	34
64	CancerResourceâ€"updated database of cancer-relevant proteins, mutations and interacting drugs. Nucleic Acids Research, 2016, 44, D932-D937.	6.5	33
65	A New Algorithm for Integrated Analysis of miRNA-mRNA Interactions Based on Individual Classification Reveals Insights into Bladder Cancer. PLoS ONE, 2013, 8, e64543.	1.1	33
66	Superimpose: a 3D structural superposition server. Nucleic Acids Research, 2008, 36, W47-W54.	6.5	31
67	Representation of target-bound drugs by computed conformers: implications for conformational libraries. BMC Bioinformatics, 2006, 7, 293.	1.2	30
68	SuperSite: dictionary of metabolite and drug binding sites in proteins. Nucleic Acids Research, 2009, 37, D195-D200.	6.5	30
69	Analysis and prediction of helixâ€"helix interactions in membrane channels and transporters. Proteins: Structure, Function and Bioinformatics, 2006, 64, 253-262.	1.5	28
70	SuperMimic--fitting peptide mimetics into protein structures. BMC Bioinformatics, 2006, 7, 11.	1.2	28
71	Oestrogen-mediated upregulation of the Mas receptor contributes to sex differences in acute lung injury and lung vascular barrier regulation. European Respiratory Journal, 2021, 57, 2000921.	3.1	28
72	SL2: an interactive webtool for modeling of missing segments in proteins. Nucleic Acids Research, 2016, 44, W390-W394.	6.5	26

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73	Enzymatic, expression and structural divergences among carboxyl O-methyltransferases after gene duplication and speciation in Nicotiana. Plant Molecular Biology, 2010, 72, 311-330.	2.0	25
74	Computational Prediction of Potential Inhibitors of the Main Protease of SARS-CoV-2. Frontiers in Chemistry, 2020, 8, 590263.	1.8	24
75	Reynoutria Rhizomes as a Natural Source of SARS-CoV-2 Mpro Inhibitorsâ€“Molecular Docking and In Vitro Study. Pharmaceuticals, 2021, 14, 742.	1.7	24
76	Volatile Organic Compounds in the Breath of Oral Squamous Cell Carcinoma Patients: A Pilot Study. Otolaryngology - Head and Neck Surgery, 2017, 157, 981-987.	1.1	23
77	Computational prediction of immune cell cytotoxicity. Food and Chemical Toxicology, 2017, 107, 150-166.	1.8	23
78	Identification of signature volatiles to discriminate <scp>C</scp>andida albicans, glabrata, krusei and tropicalis using gas chromatography and mass spectrometry. Mycoses, 2016, 59, 117-126.	1.8	22
79	Adjuvant antifungal therapy using tissue tolerable plasma on oral mucosa and removable dentures in oral candidiasis patients: a randomised doubleâ€blinded splitâ€mouth pilot study. Mycoses, 2016, 59, 467-475.	1.8	21
80	PROMISCUOUS 2.0: a resource for drug-repositioning. Nucleic Acids Research, 2021, 49, D1373-D1380.	6.5	21
81	VirtualTaste: a web server for the prediction of organoleptic properties of chemical compounds. Nucleic Acids Research, 2021, 49, W679-W684.	6.5	21
82	SuperHapten: a comprehensive database for small immunogenic compounds. Nucleic Acids Research, 2007, 35, D906-D910.	6.5	19
83	FragmentStore--a comprehensive database of fragments linking metabolites, toxic molecules and drugs. Nucleic Acids Research, 2011, 39, D1049-D1054.	6.5	19
84	GenderMedDB: an interactive database of sex and gender-specific medical literature. Biology of Sex Differences, 2014, 5, 7.	1.8	19
85	Computational and experimental validation of antioxidant properties of synthesized bioactive ferulic acid derivatives. International Journal of Food Properties, 2018, 21, 86-98.	1.3	19
86	Allosteric Modulation of the CB1 Cannabinoid Receptor by Cannabidiolâ€”A Molecular Modeling Study of the N-Terminal Domain and the Allosteric-Orthosteric Coupling. Molecules, 2021, 26, 2456.	1.7	19
87	Sixty-One Volatiles Have Phylogenetic Signals Across Bacterial Domain and Fungal Kingdom. Frontiers in Microbiology, 2020, 11, 557253.	1.5	17
88	Oxidative testicular injury: effect of l-leucine on redox, cholinergic and purinergic dysfunctions, and dysregulated metabolic pathways. Amino Acids, 2021, 53, 359-380.	1.2	17
89	Real-world evidence for improved outcomes with histamine antagonists and aspirin in 22,560 COVID-19 patients. Signal Transduction and Targeted Therapy, 2021, 6, 267.	7.1	17
90	SUPERFICIAL--surface mapping of proteins via structure-based peptide library design. BMC Bioinformatics, 2005, 6, 223.	1.2	15

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91	Theoretical Modeling Techniques and Their Impact on Tumor Immunology. Clinical and Developmental Immunology, 2010, 2010, 1-11.	3.3	15
92	Outcome of revascularization therapy in traumatized immature incisors. BMC Oral Health, 2020, 20, 207.	0.8	15
93	Onset of Oral Lichenoid Lesions and Oral Lichen Planus Following COVID-19 Vaccination: A Retrospective Analysis of about 300,000 Vaccinated Patients. Vaccines, 2022, 10, 480.	2.1	15
94	Accelerating screening of 3D protein data with a graph theoretical approach. Bioinformatics, 2003, 19, 2442-2447.	1.8	14
95	Sensitive to Infection but Strong in Defenseâ€"Female Sex and the Power of Oestradiol in the COVID-19 Pandemic. Frontiers in Global Women S Health, 2021, 2, 651752.	1.1	14
96	Inverse sequence similarity of proteins does not imply structural similarity. FEBS Letters, 2003, 545, 105-109.	1.3	13
97	Exploring Activity Profiles of PAINS and Their Structural Context in Targetâ€"Ligand Complexes. Journal of Chemical Information and Modeling, 2018, 58, 1847-1857.	2.5	13
98	Norditerpenoids with Selective Anti-Cholinesterase Activity from the Roots of Perovskia atriplicifolia Benth.. International Journal of Molecular Sciences, 2020, 21, 4475.	1.8	13
99	VaccImm: simulating peptide vaccination in cancer therapy. BMC Bioinformatics, 2013, 14, 127.	1.2	12
100	Development of Immune-Specific Interaction Potentials and Their Application in the Multi-Agent-System VaccImm. PLoS ONE, 2011, 6, e23257.	1.1	12
101	DNA Vaccination: Using the Patient's Immune System to Overcome Cancer. Clinical and Developmental Immunology, 2010, 2010, 1-14.	3.3	11
102	Acyclovir Has Low but Detectable Influence on HLA-B*57:01 Specificity without Inducing Hypersensitivity. PLoS ONE, 2015, 10, e0124878.	1.1	11
103	Drugs as habitable planets in the space of dark chemical matter. Drug Discovery Today, 2018, 23, 481-486.	3.2	11
104	Cytotoxic Effect of Vanicosides A and B from Reynoutria sachalinensis against Melanotic and Amelanotic Melanoma Cell Lines and in silico Evaluation for Inhibition of BRAFV600E and MEK1. International Journal of Molecular Sciences, 2020, 21, 4611.	1.8	11
105	Cellular Fingerprints: A Novel Approach Using Largeâ€Scale Cancer Cell Line Data for the Identification of Potential Anticancer Agents. Chemical Biology and Drug Design, 2009, 74, 439-448.	1.5	10
106	Inhibiting the inhibitors: Retro-inverso Smac peptides. Peptides, 2009, 30, 2374-2379.	1.2	10
107	Inhibition of DNAâ€"Topoisomerase I by Acylated Triterpene Saponins from Pittosporum angustifolium Lodd.. Natural Products and Bioprospecting, 2016, 6, 141-147.	2.0	10
108	Personalized Cancer Therapy Considering Cytochrome P450 Variability. Advances in Pharmacology, 2015, 74, 113-130.	1.2	9

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109	2D and 3D similarity landscape analysis identifies PARP as a novel off-target for the drug Vatalanib. BMC Bioinformatics, 2015, 16, 308.	1.2	9
110	A Comparative Analysis of COVID-19 Vaccines Based on over 580,000 Cases from the Vaccination Adverse Event Reporting System. Vaccines, 2022, 10, 408.	2.1	9
111	Cobweb: a Java applet for network exploration and visualisation. Bioinformatics, 2011, 27, 1725-1726.	1.8	8
112	L-leucine stimulation of glucose uptake and utilization involves modulation of glucose â€“ lipid metabolic switch and improved bioenergetic homeostasis in isolated rat psoas muscle ex vivo. Amino Acids, 2021, 53, 1135-1151.	1.2	8
113	A minigene DNA vaccine encoding peptide epitopes derived from Galectin-1 has protective antitumoral effects in a model of neuroblastoma. Cancer Letters, 2021, 509, 105-114.	3.2	8
114	Pain-Prescription Differences - An Analysis of 500,000 Discharge Summaries. Current Drug Research Reviews, 2019, 11, 58-66.	0.7	8
115	Prediction of oral squamous cell carcinoma based on machine learning of breath samples: a prospective controlled study. BMC Oral Health, 2021, 21, 500.	0.8	8
116	Comparison of five-year survival rates among patients with oral squamous cell carcinoma with and without association with syphilis: a retrospective case-control study. BMC Cancer, 2022, 22, 454.	1.1	8
117	JAIL: a structure-based interface library for macromolecules. Nucleic Acids Research, 2009, 37, D338-D341.	6.5	7
118	Binding sites in membrane proteins â€“ Diversity, druggability and prospects. European Journal of Cell Biology, 2012, 91, 326-339.	1.6	7
119	Voronoia 4-ever. Nucleic Acids Research, 2021, 49, W685-W690.	6.5	7
120	Non-Psychotropic Cannabinoids as Inhibitors of TET1 Protein. Bioorganic Chemistry, 2022, 124, 105793.	2.0	7
121	Residues of a proposed gate region in type I ATP-binding cassette import systems are crucial for function as revealed by mutational analysis. Biochimica Et Biophysica Acta - Biomembranes, 2013, 1828, 2164-2172.	1.4	6
122	CardioScape mapping the cardiovascular funding landscape in Europe. European Heart Journal, 2018, 39, 2423-2430.	1.0	6
123	Evaluation of Drugâ€”Drug Interactions in EGFR-Mutated Non-Small-Cell Lung Cancer Patients during Treatment with Tyrosine-Kinase Inhibitors. Journal of Personalized Medicine, 2021, 11, 424.	1.1	6
124	The druggability of bitter taste receptors for the treatment of neurodegenerative disorders. Biochemical Pharmacology, 2022, 197, 114915.	2.0	6
125	A Birds-Eye (Re)View of Acid-Suppression Drugs, COVID-19, and the Highly Variable Literature. Frontiers in Pharmacology, 2021, 12, 700703.	1.6	5
126	In silico screening of drug databases for TSE inhibitors. BioSystems, 2005, 80, 117-122.	0.9	4

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127	Mapping discontinuous proteinâ€binding sites via structureâ€based peptide libraries: combining in silico and in vitro approaches. Journal of Molecular Recognition, 2013, 26, 23-31.	1.1	4
128	Volatile organic compounds in the breath of oral candidiasis patients: a pilot study. Clinical Oral Investigations, 2018, 22, 721-731.	1.4	4
129	Individualized Drugsâ€™ Selection by Evaluation of Drug Properties, Pharmacogenomics and Clinical Parameters: Performance of a Bioinformatic Tool Compared to a Clinically Established Counselling Process. Pharmacogenomics and Personalized Medicine, 2021, Volume 14, 955-962.	0.4	3
130	Man vs. machine: comparison of pharmacogenetic expert counselling with a clinical medication support system in a study with 200 genotyped patients. European Journal of Clinical Pharmacology, 2022, 78, 579-587.	0.8	2
131	Computer-assisted identification of small-molecule Bcl-2 modulators. Computational Biology and Chemistry, 2009, 33, 451-456.	1.1	1
132	Molecular basis for the sensitivity of TRP channels to polyunsaturated fatty acids. Naunyn-Schmiedeberg's Archives of Pharmacology, 2018, 391, 833-846.	1.4	1
133	Comparison of Computerized Prescription Support Systems in COVID-19 Patients: INTERCheck and Drug-PIN. SN Comprehensive Clinical Medicine, 2021, 4, 3.	0.3	1
134	DBEndo: a web-based endodontic case management tool. BMC Research Notes, 2015, 8, 685.	0.6	0
135	CardioScape-II: the need to map cardiovascular funding patterns in Europe. Cardiovascular Research, 2020, 116, 879-881.	1.8	0