Iris Antes

List of Publications by Year
in descending order

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49 papers	1,381 citations	394421 19 h-index	345221 36 g-index
54 all docs	54 docs citations	54 times ranked	2415 citing authors

#	Article	IF	Citations
1	Recognition of 5-Hydroxymethylcytosine by the Uhrf1 SRA Domain. PLoS ONE, 2011, 6, e21306.	2.5	159
2	DynaDock: A new molecular dynamicsâ€based algorithm for proteinâ€“peptide docking including receptor flexibility. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1084-1104.	2.6	147
3	Regulation of the hepatitis C virus RNA replicase by endogenous lipid peroxidation. Nature Medicine, 2014, 20, 927-935.	30.7	130
4	Phenyl Esters Are Potent Inhibitors of Caseinolytic Protease P and Reveal a Stereogenic Switch for Deoligomerization. Journal of the American Chemical Society, 2015, 137, 8475-8483.	13.7	89
5	Repurposing human kinase inhibitors to create an antibiotic active against drug-resistant Staphylococcus aureus, persisters and biofilms. Nature Chemistry, 2020, 12, 145-158.	13.6	78
6	DynaPred: A structure and sequence based method for the prediction of MHC class I binding peptide sequences and conformations. Bioinformatics, 2006, 22, e16-e24.	4.1	63
7	IRECS: A new algorithm for the selection of most probable ensembles of side-chain conformations in protein models. Protein Science, 2007, 16, 1294-1307.	7.6	50
8	Prediction of VHâ€“VL domain orientation for antibody variable domain modeling. Proteins: Structure, Function and Bioinformatics, 2015, 83, 681-695.	2.6	47
9	BiPPred: Combined sequenceâ€and structureâ€based prediction of peptide binding to the Hsp70 chaperone BiP. Proteins: Structure, Function and Bioinformatics, 2016, 84, 1390-1407.	2.6	46
10	Bap (Sil1) regulates the molecular chaperone BiP by coupling release of nucleotide and substrate. Nature Structural and Molecular Biology, 2018, 25, 90-100.	8.2	39
11	Docking and scoring with alternative sideâ€chain conformations. Proteins: Structure, Function and Bioinformatics, 2009, 74, 712-726.	2.6	38
12	Conformational Selection in Substrate Recognition by Hsp70 Chaperones. Journal of Molecular Biology, 2013, 425, 466-474.	4.2	38
13	Predicting MHC class I epitopes in large datasets. BMC Bioinformatics, 2010, 11, 90.	2.6	37
14	Actin stabilizing compounds show specific biological effects due to their binding mode. Scientific Reports, 2019, 9, 9731.	3.3	30
15	Thiazoline-Specific Amidohydrolase PurAH Is the Gatekeeper of Bottromycin Biosynthesis. Journal of the American Chemical Society, 2019, 141, 9748-9752.	13.7	26
16	Gliotoxin Biosynthesis: Structure, Mechanism, and Metal Promiscuity of Carboxypeptidase GliJ. ACS Chemical Biology, 2017, 12, 1874-1882.	3.4	24
17	A Small Molecule Inhibits Protein Disulfide Isomerase and Triggers the Chemosensitization of Cancer Cells. Angewandte Chemie - International Edition, 2014, 53, 12960-12965.	13.8	23
18	Sequential Inactivation of Gliotoxin by the S-Methyltransferase TmtA. ACS Chemical Biology, 2016, 11, 1082-1089.	3.4	22

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19	MoFvAb: Modeling the Fv region of antibodies. MAbs, 2015, 7, 838-852.	5.2	21
20	1,5â€Disubstituted 1,2,3â€Triazoleâ€Containing Peptidotriazolamers: Design Principles for a Class of Versatile Peptidomimetics. Chemistry - A European Journal, 2018, 24, 953-961.	3.3	21
21	Broad spectrum antibiotic-degrading metallo-Î²-lactamases are phylogenetically diverse. Protein and Cell, 2020, 11, 613-617.	11.0	21
22	Amythiamicinâ€…D and Related Thiopeptides as Inhibitors of the Bacterial Elongation Factor EFâ€Tu: Modification of the Amino Acid at Carbon Atom C2 of Ringâ€…C Dramatically Influences Activity. ChemMedChem, 2013, 8, 1954-1962.	3.2	18
23	A modular approach to the bisbenzylisoquinoline alkaloids tetrandrine and isotetrandrine. Organic and Biomolecular Chemistry, 2020, 18, 3047-3068.	2.8	17
24	DynaDom: structure-based prediction of T cell receptor inter-domain and T cell receptor-peptide-MHC (class I) association angles. BMC Structural Biology, 2018, 17, 2.	2.3	16
25	1,4-Disubstituted 1H-1,2,3-Triazole Containing Peptidotriazolamers: A New Class of Peptidomimetics With Interesting Foldamer Properties. Frontiers in Chemistry, 2019, 7, 155.	3.6	16
26	Improvement of the fungal enzyme pyranose 2-oxidase using protein engineering. Journal of Biotechnology, 2006, 124, 26-40.	3.8	14
27	Naturalâ€Productâ€Inspired Aminoepoxybenzoquinones Kill Members of the Gramâ€Negative Pathogen Salmonella by Attenuating Cellular Stress Response. Angewandte Chemie - International Edition, 2016, 55, 14852-14857.	13.8	14
28	Predicting the bioactive conformations of macrocycles: a molecular dynamics-based docking procedure with DynaDock. Journal of Molecular Modeling, 2019, 25, 197.	1.8	13
29	Identification of essential amino acids for glucose transporter 5 (GLUT5)-mediated fructose transport. Journal of Biological Chemistry, 2018, 293, 2115-2124.	3.4	11
30	Amber-Compatible Parametrization Procedure for Peptide-like Compounds: Application to 1,4- and 1,5-Substituted Triazole-Based Peptidomimetics. Journal of Chemical Information and Modeling, 2018, 58, 90-110.	5.4	11
31	Systematic analysis of the binding behaviour of UHRF1 towards different methyl- and carboxylcytosine modification patterns at CpG dyads. PLoS ONE, 2020, 15, e0229144.	2.5	11
32	Quantitative Analysis of the Association Angle between T-cell Receptor Vα/Vβ Domains Reveals Important Features for Epitope Recognition. PLoS Computational Biology, 2015, 11, e1004244.	3.2	10
33	Extended interaction networks with HCV protease NS3-4A substrates explain the lack of adaptive capability against protease inhibitors. Journal of Biological Chemistry, 2020, 295, 13862-13874.	3.4	10
34	Multiple sclerosis. Neurology: Neuroimmunology and NeuroInflammation, 2016, 3, e241.	6.0	9
35	Key Features Relevant to Select Antigens and TCR From the MHC-Mismatched Repertoire to Treat Cancer. Frontiers in Immunology, 2019, 10, 1485.	4.8	8
36	Ca2+ binding induced sequential allosteric activation of sortase A: An example for ion-triggered conformational selection. PLoS ONE, 2018, 13, e0205057.	2.5	7

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37	Functional analysis of peripheral and intratumoral neoantigen-specific TCRs identified in a patient with melanoma. , 2021, 9, e002754.		7
38	Structureâ€Guided Modulation of the Catalytic Properties of [2Feâ^'2S]â€Dependent Dehydratases. ChemBioChem, 2022, 23, .	2.6	6
39	Eine niedermolekulare Verbindung inhibiert die Proteindisulfidisomerase und sensibilisiert Krebszellen fÃ¼r die Chemotherapie. Angewandte Chemie, 2014, 126, 13174-13179.	2.0	5
40	Acyldepsipeptide Probes Facilitate Specific Detection of Caseinolytic Proteaseâ€...P Independent of Its Oligomeric and Activity State. ChemBioChem, 2020, 21, 235-240.	2.6	5
41	Turning the Actin Nucleating Compound Miuraenamide into Nucleation Inhibitors. ACS Omega, 2021, 6, 22165-22172.	3.5	5
42	Investigation of the pH-dependent aggregation mechanisms of GCSF using low resolution protein characterization techniques and advanced molecular dynamics simulations. Computational and Structural Biotechnology Journal, 2022, 20, 1439-1455.	4.1	4
43	Naturstoffbasierte Aminoepoxybenzochinone inhibieren das Wachstum verschiedener Serovare des Gramâ€negativen Krankheitserregers Salmonella durch AbschwÃ¤chen der bakteriellen Stressabwehr. Angewandte Chemie, 2016, 128, 15074-15079.	2.0	3
44	<scp>DynaBiS</scp>: A hierarchical sampling algorithm to identify flexible binding sites for large ligands and peptides. Proteins: Structure, Function and Bioinformatics, 2022, 90, 18-32.	2.6	3
45	A combined in silico and in vitro study on mouse Serpina1a antitrypsin-deficiency mutants. Scientific Reports, 2019, 9, 7486.	3.3	2
46	SenseNet, a tool for analysis of protein structure networks obtained from molecular dynamics simulations. PLoS ONE, 2022, 17, e0265194.	2.5	2
47	Parameterization of the Hamiltonian Dielectric Solvent (HADES) Reactionâ€Field Method for the Solvation Free Energies of Amino Acid Sideâ€Chain Analogs. ChemPhysChem, 2015, 16, 1739-1749.	2.1	1
48	The Q41R mutation in the HCV-protease enhances the reactivity towards MAVS by suppressing non-reactive pathways. Physical Chemistry Chemical Physics, 2022, 24, 2126-2138.	2.8	1
49	Dynamic Docking of Macrocycles in Bound and Unbound Protein Structures with DynaDock. Journal of Chemical Information and Modeling, 2022, 62, 3426-3441.	5.4	0