

# Ronald V Swanson

## List of Publications by Year in descending order

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35  
papers

4,950  
citations

172457

29  
h-index

361022

35  
g-index

36  
all docs

36  
docs citations

36  
times ranked

5209  
citing authors

#	ARTICLE	IF	CITATIONS
1	T Cell Subset and Stimulation Strength-Dependent Modulation of T Cell Activation by Kv1.3 Blockers. PLoS ONE, 2017, 12, e0170102.	2.5	12
2	Targeting the Ion Channel Kv1.3 with Scorpion Venom Peptides Engineered for Potency, Selectivity, and Half-life. Journal of Biological Chemistry, 2014, 289, 22704-22714.	3.4	26
3	Genetic Construct Design and Recombinant Protein Expression for Structural Biology. Methods in Molecular Biology, 2012, 841, 29-47.	0.9	3
4	Characterization of a high-affinity human antibody with a disulfide bridge in the third complementarity-determining region of the heavy chain. Journal of Molecular Recognition, 2012, 25, 125-135.	2.1	31
5	Human Framework Adaptation of a Mouse Anti-Human IL-13 Antibody. Journal of Molecular Biology, 2010, 398, 214-231.	4.2	55
6	Mechanism of Inhibition of Novel Tryptophan Hydroxylase Inhibitors Revealed by Co-crystal Structures and Kinetic Analysis. Current Chemical Genomics, 2010, 4, 19-26.	2.0	28
7	Lead optimization and structure-based design of potent and bioavailable deoxycytidine kinase inhibitors. Bioorganic and Medicinal Chemistry Letters, 2009, 19, 6784-6787.	2.2	8
8	Structural basis for the inhibition of Aurora A kinase by a novel class of high affinity disubstituted pyrimidine inhibitors. Bioorganic and Medicinal Chemistry Letters, 2007, 17, 688-691.	2.2	36
9	Structural Snapshots of Human HDAC8 Provide Insights into the Class I Histone Deacetylases. Structure, 2004, 12, 1325-1334.	3.3	633
10	N-linked glycosylation of dipeptidyl peptidase IV (CD26): Effects on enzyme activity, homodimer formation, and adenosine deaminase binding. Protein Science, 2004, 13, 145-154.	7.6	59
11	Structural Basis for Bisphosphonate-mediated Inhibition of Isoprenoid Biosynthesis*. Journal of Biological Chemistry, 2004, 279, 8526-8529.	3.4	241
12	The Crystal Structure of Shikimate Dehydrogenase (AroE) Reveals a Unique NADPH Binding Mode. Journal of Bacteriology, 2003, 185, 4144-4151.	2.2	52
13	Crystal Structures of Active Fully Assembled Substrate- and Product-Bound Complexes of UDP- N -Acetylmuramic Acid: L -Alanine Ligase (MurC) from Haemophilus influenzae. Journal of Bacteriology, 2003, 185, 4152-4162.	2.2	61
14	Comparative Genomic Analysis of Archaeal Genotypic Variants in a Single Population and in Two Different Oceanic Provinces. Applied and Environmental Microbiology, 2002, 68, 335-345.	3.1	164
15	The Genome of <i>M. acetivorans</i> Reveals Extensive Metabolic and Physiological Diversity. Genome Research, 2002, 12, 532-542.	5.5	573
16	Structures of the Cancer-Related Aurora-A, FAK, and EphA2 Protein Kinases from Nanovolume Crystallography. Structure, 2002, 10, 1659-1667.	3.3	193
17	The solution structure and interactions of CheW from Thermotoga maritima. Nature Structural Biology, 2002, 9, 121-125.	9.7	82
18	Genome of Aquifex aeolicus. Methods in Enzymology, 2001, 330, 158-169.	1.0	15

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19	Crystal structure of the $\beta$ -glucosidase from the hyperthermophile <i>Thermosphaera aggregans</i> : insights into its activity and thermostability. <i>FEBS Letters</i> , 1999, 445, 375-383.	2.8	71
20	The complete genome of the hyperthermophilic bacterium <i>Aquifex aeolicus</i> . <i>Nature</i> , 1998, 392, 353-358.	27.8	1,120
21	Crystal structures of CheY from <i>Thermotoga maritima</i> do not support conventional explanations for the structural basis of enhanced thermostability. <i>Protein Science</i> , 1998, 7, 403-412.	7.6	71
22	Genomic Analysis Reveals Chromosomal Variation in Natural Populations of the Uncultured Psychrophilic Archaeon <i>Cenarchaeum symbiosum</i> . <i>Journal of Bacteriology</i> , 1998, 180, 5003-5009.	2.2	137
23	A fosmid-based genomic map and identification of 474 genes of the hyperthermophilic archaeon <i>Pyrobaculum aerophilum</i> . <i>Extremophiles</i> , 1997, 1, 36-52.	2.3	76
24	Phosphotransfer and CheY-Binding Domains of the Histidine Autokinase CheA Are Joined by a Flexible Linker. <i>Biochemistry</i> , 1996, 35, 433-443.	2.5	62
25	Comparison of a $\beta$ -Glucosidase and a $\beta$ -Mannosidase from the Hyperthermophilic Archaeon <i>Pyrococcus furiosus</i> . <i>Journal of Biological Chemistry</i> , 1996, 271, 23749-23755.	3.4	116
26	Mutations in the chemotactic response regulator, CheY, that confer resistance to the phosphatase activity of CheZ. <i>Molecular Microbiology</i> , 1995, 15, 1069-1079.	2.5	45
27	Localized perturbations in CheY structure monitored by NMR identify a CheA binding interface. <i>Nature Structural Biology</i> , 1995, 2, 906-910.	9.7	34
28	NMR studies of the phosphotransfer domain of the histidine kinase CheA from <i>Escherichia coli</i> : assignments, secondary structure, general fold, and backbone dynamics. <i>Biochemistry</i> , 1995, 34, 13858-13870.	2.5	84
29	Histidine and aspartate phosphorylation: two-component systems and the limits of homology. <i>Trends in Biochemical Sciences</i> , 1994, 19, 485-490.	7.5	198
30	Signal Transduction: Bringing the eukaryotes up to speed. <i>Current Biology</i> , 1994, 4, 234-237.	3.9	35
31	Assembly and function of a quaternary signal transduction complex monitored by surface plasmon resonance. <i>Nature</i> , 1993, 365, 343-347.	27.8	267
32	Intermolecular complementation of the kinase activity of CheA. <i>Molecular Microbiology</i> , 1993, 8, 435-441.	2.5	123
33	Expression of CheA fragments which define domains encoding kinase, phosphotransfer, and CheY binding activities. <i>Biochemistry</i> , 1993, 32, 7623-7629.	2.5	115
34	Separation of phycobiliprotein subunits by reverse-phase high-pressure liquid chromatography. <i>Analytical Biochemistry</i> , 1990, 188, 295-299.	2.4	66
35	Phycobiliprotein methylation. <i>Journal of Molecular Biology</i> , 1990, 214, 787-796.	4.2	56