Wesley E Stites

List of Publications by Citations

44 papers	2,938 citations	24 h-index	44 g-index
44 ext. papers	3,051 ext. citations	5 avg, IF	4.82 L-index

#	Paper	IF	Citations
44	Proteinminus signProtein Interactions: Interface Structure, Binding Thermodynamics, and Mutational Analysis. *Chemical Reviews*, **1997**, 97, 1233-1250	68.1	431
43	Contributions of the large hydrophobic amino acids to the stability of staphylococcal nuclease. *Biochemistry*, **1990**, 29, 8033-41	3.2	370
42	High apparent dielectric constants in the interior of a protein reflect water penetration. *Biophysical Journal*, **2000**, 79, 1610-20	2.9	276
41	Experimental measurement of the effective dielectric in the hydrophobic core of a protein. *Biophysical Chemistry*, **1997**, 64, 211-24	3.5	215
40	Experimental pK(a) values of buried residues: analysis with continuum methods and role of water penetration. *Biophysical Journal*, **2002**, 82, 3289-304	2.9	180
39	In a staphylococcal nuclease mutant the side-chain of a lysine replacing valine 66 is fully buried in the hydrophobic core. *Journal of Molecular Biology*, **1991**, 221, 7-14	6.5	151
38	Protein surface hydration mapped by site-specific mutations. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 13979-84	11.5	139
37	High apparent dielectric constant inside a protein reflects structural reorganization coupled to the ionization of an internal Asp. *Biophysical Journal*, **2007**, 92, 2041-53	2.9	117
36	Increasing the thermostability of staphylococcal nuclease: implications for the origin of protein thermostability. *Journal of Molecular Biology*, **2000**, 303, 125-30	6.5	108
35	Comparing the effect on protein stability of methionine oxidation versus mutagenesis: steps toward engineering oxidative resistance in proteins. *Protein Engineering, Design and Selection*, **2001**, 14, 343-7	1.9	90
34	Energetic contribution of side chain hydrogen bonding to the stability of staphylococcal nuclease. *Biochemistry*, **1995**, 34, 13949-60	3.2	80
33	Packing is a key selection factor in the evolution of protein hydrophobic cores. *Biochemistry*, **2001**, 40, 15280-9	3.2	64
32	Evidence for strained interactions between side-chains and the polypeptide backbone. *Journal of Molecular Biology*, **1994**, 235, 27-32	6.5	57
31	The phase transition between a compact denatured state and a random coil state in staphylococcal nuclease is first-order. *Journal of Molecular Biology*, **1993**, 232, 718-24	6.5	56
30	Empirical evaluation of the influence of side chains on the conformational entropy of the polypeptide backbone. *Proteins: Structure, Function and Bioinformatics*, **1995**, 22, 132-40	4.2	55
29	A convenient preparation of derivatives of 3(s)-amino-10(r)-carboxy-1,6-diaza-cyclodeca-2,7-dione the dilactam of L-[illegible],[illegible]diaminobutyric acid and d-glutamic acid: A [illegible]turn template. *Tetrahedron Letters*, **1988**, 29, 5057-5060	2	55
28	Stability effects of increasing the hydrophobicity of solvent-exposed side chains in staphylococcal nuclease. *Biochemistry*, **1998**, 37, 6939-48	3.2	46

27	Compact denatured state of a staphylococcal nuclease mutant by guanidinium as determined by resonance energy transfer. *Biochemistry*, **1992**, 31, 10217-25	3.2	42
26	Energetics of side chain packing in staphylococcal nuclease assessed by systematic double mutant cycles. *Biochemistry*, **2001**, 40, 14004-11	3.2	38
25	Higher-order packing interactions in triple and quadruple mutants of staphylococcal nuclease. *Biochemistry*, **2001**, 40, 14012-9	3.2	37
24	Changes in stability upon charge reversal and neutralization substitution in staphylococcal nuclease are dominated by favorable electrostatic effects. *Biochemistry*, **2003**, 42, 1118-28	3.2	34
23	Energetics of side chain packing in staphylococcal nuclease assessed by exchange of valines, isoleucines, and leucines. *Biochemistry*, **2001**, 40, 13998-4003	3.2	32
22	Instrumentation for automated determination of protein stability. *Analytical Biochemistry*, **1995**, 227, 112-22	3.1	32
21	Mustard gas crosslinking of proteins through preferential alkylation of cysteines. *The Protein Journal*, **1996**, 15, 131-6		28
20	The M32L substitution of staphylococcal nuclease: disagreement between theoretical prediction and experimental protein stability. *Journal of Molecular Biology*, **1996**, 257, 497-9	6.5	24
19	Effects of excluded volume upon protein stability in covalently cross-linked proteins with variable linker lengths. *Biochemistry*, **2008**, 47, 8804-14	3.2	23
18	Replacement of staphylococcal nuclease hydrophobic core residues with those from thermophilic homologues indicates packing is improved in some thermostable proteins. *Journal of Molecular Biology*, **2004**, 344, 271-80	6.5	22
17	Refinement of noncalorimetric determination of the change in heat capacity, DeltaC(p), of protein unfolding and validation across a wide temperature range. *Proteins: Structure, Function and Bioinformatics*, **2008**, 71, 1607-16	4.2	16
16	Chemically crosslinked protein dimers: stability and denaturation effects. *Protein Science*, **1995**, 4, 2545-58	6.3	16
15	Inactivation of thrombomodulin by ionizing radiation in a cell-free system: possible implications for radiation responses in vascular endothelium. *Radiation Research*, **2008**, 169, 408-16	3.1	15
14	Investigation of biological, chemical and physical processes on and in planetary surfaces by laboratory simulation. *Planetary and Space Science*, **2002**, 50, 821-828	2	13
13	Application of automated methods for determination of protein conformational stability. *Methods in Enzymology*, **1998**, 295, 150-70	1.7	13
12	Thermodynamic principles for the engineering of pH-driven conformational switches and acid insensitive proteins. *Biophysical Chemistry*, **2011**, 159, 217-26	3.5	12
11	Does the oxidation of methionine in thrombomodulin contribute to the hypercoaguable state of smokers and diabetics?. *Medical Hypotheses*, **2007**, 68, 811-21	3.8	11
10	Thermal denaturations of staphylococcal nuclease wild-type and mutants monitored by fluorescence and circular dichroism are similar: lack of evidence for other than a two state thermal denaturation. *Biophysical Chemistry*, **2007**, 125, 490-6	3.5	8

9	Theory of the Protein Equilibrium Population Snapshot by H/D Exchange Electrospray Ionization Mass Spectrometry (PEPS-HDX-ESI-MS) Method used to obtain Protein Folding Energies/Rates and Selected Supporting Experimental Evidence. *International Journal of Mass Spectrometry*, **2012**, 330-332, 63-70	1.9	7
8	An electrophoretic mobility shift assay for methionine sulfoxide in proteins. *Analytical Biochemistry*, **2012**, 421, 767-9	3.1	7
7	Comparison of Two ESI MS Based H/D Exchange Methods for Extracting Protein Folding Energies. *International Journal of Mass Spectrometry*, **2009**, 287, 96-104	1.9	7
6	Proteins with simplified hydrophobic cores compared to other packing mutants. *Biophysical Chemistry*, **2004**, 110, 239-48	3.5	7
5	Oxidation of buried cysteines is slow and an insignificant factor in the structural destabilization of staphylococcal nuclease caused by H2O2 exposure. *Amino Acids*, **2004**, 27, 175-81	3.5	2
4	The fluorescence detected guanidine hydrochloride equilibrium denaturation of wild-type staphylococcal nuclease does not fit a three-state unfolding model. *Biochimie*, **2013**, 95, 1386-93	4.6	1
3	The pH dependence of staphylococcal nuclease stability is incompatible with a three-state denaturation model. *Biophysical Chemistry*, **2013**, 180-181, 86-94	3.5	1
2	Development of an immunoassay for oxidized or unoxidized forms of thrombomodulin. *FASEB Journal*, **2006**, 20, A1452	0.9	
1	A First-Order Phase Transition Between a Compact Denatured State and a Random Coil State in Staphylococcal Nuclease. *NATO ASI Series Series B: Physics*, **1994**, 39-47		