

Christopher D. Snow

Work:	Colorado State University, 1370 Campus Delivery, Fort Collins, CO 80523; 970.491.5276
Home:	105 Rachel Ct., Fort Collins, CO 80524; 650.387.2219
Online:	csnow@csnow.org http://www.engr.colostate.edu/~cdasnow/

Education and Training

Postdoc. Chem.E.	CALIFORNIA INSTITUTE OF TECHNOLOGY	2006-2011
Ph.D. Biophysics	STANFORD UNIVERSITY	2001-2006
Sc.B. Chemistry	MASSACHUSETTS INSTITUTE OF TECHNOLOGY	4.9/5.0 1997-2001

Research Experience

POSTDOCTORAL RESEARCH

- Cytochrome P450 structure determination and prediction with Professor Frances Arnold 2006-2011
- Computational protein structure prediction • Cellulase enzyme library design

GRADUATE RESEARCH

- Protein folding via distributed computing with Professor Vijay Pande 2001-2006
- RNA-antibiotic NMR with Professor Joseph Puglisi 2002
- Simulated annealing fragment MC with Professor Michael Levitt 2001

UNDERGRADUATE RESEARCH

- Computational protein electrostatics with Professors Bruce Tidor and Dan Raleigh 1998-2001

INVITED TALKS

- Society for Industrial Microbiology – Biocatalysts By Design 2011
- Keystone Drug Design 2008
- Protein Society 2004
- Xerox PARC 2003
- Biomedical Computation at Stanford 2002

TEACHING ASSISTANT

- Computational Structural Biology (Professor: M. Levitt) 2004-2006
- Biological Macromolecules (Lead Prof.: D. Herschlag) 2002-2003

Awards and Honors

KAUST Postdoctoral Fellowship	2008-2011
Jane Coffin Childs Postdoctoral Fellowship	2006
NSF Bioinformatics Postdoctoral Fellowship (declined)	2006
Protein Society Best Poster Awards	2004-2005
HHMI Predoctoral Fellowship	2001-2006
NSF Predoctoral Fellowship (declined)	2001
Phi Beta Kappa	2001
Outstanding Chemistry Research Achievement by a MIT Undergraduate	2001
Hypercube Computational Chemistry Award	2001
Pfizer Summer Undergraduate Research Fellow	2000
MIT Nominee for Goldwater Scholarship	2000
National Merit Scholar	1997

1. Surface Salt Bridges, Double-Mutant Cycles, and Protein Stability: an Experimental and Computational Analysis of the Interaction of the Asp 23 Side Chain with the N-Terminus of the N-Terminal Domain of the Ribosomal Protein L9

DL. Luisi, CD. Snow, J. Lin, ZS. Hendsch, B. Tidor, DP. Raleigh.
Biochemistry (2003) 42(23), 7050-7060

2. Atomistic protein folding simulations on the submillisecond time scale using worldwide distributed computing

VS. Pande, I. Baker, J. Chapman, S. Elmer, SM. Larson, YM. Rhee, MR. Shirts, CD. Snow, EJ. Sorin, B. Zagrovic. *Biopolymers* (2002) 68(1): 91-109

3. Simulation of folding of a small alpha-helical protein in atomistic detail using worldwide-distributed computing

B Zagrovic, CD. Snow, MR. Shirts, VS. Pande.
J. Mol. Biol. (2002) 323(5), 927-937

4. Native-like Mean Structure in the Unfolded Ensemble of Small Proteins

B. Zagrovic, CD. Snow, S. Khaliq, MR. Shirts, VS. Pande.
J. Mol. Biol. (2002) 323(1), 153-164

5. The Trp Cage: Folding Kinetics and Unfolded State Topology via Molecular Dynamics Simulations

CD. Snow, B. Zagrovic, VS. Pande. *J. Am. Chem. Soc.* (2002) 124(49), 14548-14549

6. Absolute comparison of simulated and experimental protein-folding dynamics

CD. Snow, H. Nguyen, VS. Pande, M. Gruebele. *Nature* (2002) 420(6911), 102-106

7. Using path sampling to build better Markovian state models: Predicting the folding rate and mechanism of a tryptophan zipper beta hairpin

N. Singhal, CD. Snow, VS. Pande. *J. Chem. Phys.* (2004) 121(1) 415-425

8. Trp zipper folding kinetics by molecular dynamics and T-jump spectroscopy

CD. Snow, L. Qiu, D. Du, F. Gai, SJ. Hagen, VS. Pande.
Proc. Natl. Acad. Sci. USA (2004) 101(12), 4077-4082

9. Dimerization of the p53 oligomerization domain: Identification of a folding nucleus by molecular dynamics simulations

LT. Chong, CD. Snow, YM. Rhee, VS. Pande. *J. Mol. Biol.* (2005) 345(4), 869-878

10. How well can simulation predict kinetics and thermodynamics of protein folding?

CD. Snow, E. Sorin, YM. Rhee, VS. Pande.
Annu. Rev. Biophys. and Biomol. Struct. (2005) 34, 43-69

11. Direct calculation of the binding free energies of FKBP ligands using the Fujitsu BioServer massively parallel computer

H. Fujitani, Y. Tanida, M. Ito, G. Jayachandran, CD. Snow, MR. Shirts, EJ. Sorin, VS. Pande.
J. Chem. Phys., (2005) 123, 084108

12. Kinetic definition of protein folding transition state ensembles and reaction coordinates

Christopher D. Snow, Young Min Rhee, Vijay S. Pande. *Biophys. J.* (2006) 91, 14-24.

13. Electric fields at the active site of an enzyme: direct comparison of experiment with theory

IT. Suydam, CD. Snow, VS. Pande, SG. Boxer. *Science* (2006) 313, 200-204.

14. A diverse family of thermostable cytochrome P450s created by recombination of stabilizing fragments

Y. Li, DA. Drummond, AM. Sawayama, CD. Snow, JD. Bloom, FH. Arnold
Nature Biotechnology (2007) 25(9), 1051-1056

15. Hunting for predictive computational drug-discovery models

CD. Snow. *Expert Reviews in Anti-Infective Therapy* (2008) 6(3), 291-3

16. Evolutionary History of a Specialized P450 Propane Monooxygenase

R. Fasan, Y. Meharena, CD. Snow, T. Poulos, FH. Arnold
J. Mol. Biol. (2008) 383(5), 1069-80

17. Side-chain recognition and gating in the ribosome exit tunnel

P. Petrone, CD. Snow, D. Lucent, VS. Pande. *PNAS* (2008) 105(43), 16549-16554

18. SHARPEN: Systematic Hierarchical Algorithms for Rotamers and Proteins on an Expansive Network

IV. Loksha, J. Maiolo, C. Hong, A. Ng, CD. Snow. *J Comp Chem* (2009) 30(6), 999-1005

19. A family of thermostable fungal cellulases created by structure-guided recombination

P. Heinzelman, CD. Snow, I. Wu, C. Nguyen, A. Villalobos, S. Govindarajan, J. Minshull, FH. Arnold. *PNAS* (2009) 106(14), 5610-5615

20. SCHEMA recombination of a fungal cellulose uncovers a single mutation that contributes markedly to stability

P. Heinzelman, CD. Snow, MA. Smith, X. Yu, A. Kannan, A. Villalobos, S. Govindarajan, J. Minshull, Frances H. Arnold. *J. Biol. Chem.* (2009) 284(39), 26229-26233

21. Efficient Screening of Fungal Cellobiohydrolase Class I Enzymes for Thermostabilizing Sequence Blocks by SCHEMA Structure-Guided Recombination

P. Heinzelman, R. Komor, A. Kannan, PA. Romero, L. Yu, S. Mohler, CD. Snow, FH. Arnold
Protein Eng. Des. Sel. (2010) 23(11): 871-880

22. Non-bulk-like solvent behavior in the ribosome exit tunnel

D. Lucent, CD. Snow, C. Aitken, SE. Lee, VS. Pande. *PLoS Comput. Biol.* (2010) 6(10): e1000963

23. Combinatorial alanine substitution enables rapid optimization of cytochrome P450BM3 for selective hydroxylation of large substrates

JC. Lewis, SM. Mantovani, Y. Fu, CD. Snow, RS. Komor, CH. Wong, FH. Arnold.
Chem. Bio. Chem. (2010) 11(18): 2502-2505

24. Polarizable protein repacking

AH. Ng & CD. Snow. *J. Comp. Chem* (2011) 32(7): 1334-1344

25. Engineered ketol-acid reductoisomerase and alcohol dehydrogenase enable anaerobic 2-methylpropan-1-ol production at theoretical yield in Escherichia coli

S. Bastian, X. Liu, JT. Meyerowitz, CD. Snow, MM. Chen, FH. Arnold
Metab. Eng. (2011) 13(3): 345-52

26. Engineered Bacterial Mimics of Human Drug Metabolizing Enzyme CYP2C9

A. Rentmeister, TB. Brown, CD. Snow, M. Carbone, FH. Arnold. *In preparation*

27. Crystallographic Structure Determination via Recombination

EM. Brustad, M. Mazrooei, G. Bandara, JT. Kaiser, FH. Arnold, CD. Snow. *In preparation*