Christopher D. Snow, Ph.D.

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Education and Training

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

Research Experience

POSTDOCTORAL RESEARCH
- Cytochrome P450 structure determination (crystallography) with Professor Frances Arnold   Current
- 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   1998-2001
- Computational protein electrostatics with Professors Bruce Tidor and Dan Raleigh

INVITED TALKS
- 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-Current
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. Absolute comparison of simulated and experimental protein-folding dynamics
CD. Snow, H. Nguyen, VS. Pande, M. Gruebele. *Nature* (2002) 420(6911), 102-106

2. 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

3. 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

4. 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

5. 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

6. 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

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
CD. Snow, YM. Rhee, VS. 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. Meharenna, 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 Engineering Design & Selection. (2010) 24, 1-10.

22. Non-bulk-like Solvent Behavior in the Ribosome Exit Tunnel
D. Lucent, CD. Snow, C. Aitken, SE. Lee, VS. Pande. *PLoS Comp. Biol.* (2010) 6(10): e1000963.

23. Polarizable protein repacking.
AH. Ng & CD. Snow.   *Accepted: J. Comp. Chem*

24. Fatty acid binding in the heme domain of CYP102A2
CD. Snow, G. Bandara, M. Mazrooei, J. Paryani, FH. Arnold.   *In preparation*

25. Engineered Bacterial Mimics of Human Drug Metabolizing Enzyme CYP2C9
A. Rentmeister, TB. Brown, CD. Snow, M. Carbone, FH. Arnold.   *In preparation*

26. 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.   *In preparation*

27. Engineered ketol-acid reductoisomerase and alcohol dehydrogenase enable anaerobic isobutanaol production at theoretical yield in Escherichia coli.
S Bastian, X. Liu, JT. Meyerowitz, CD. Snow, P. Meinhold, T. Buelter, Chen, MMY, FH. Arnold.
In preparation