

## DYLAN CHIVIAN

Dept. of Biochemistry, U. of Washington, Seattle, WA 98102 USA  
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### EDUCATION

**University of Washington**, Seattle, WA, 1999-Present  
Dept. of Biochemistry and Biomolecular Structure and Design Program  
Laboratory of Dr. David Baker  
Project: Automated Homology Modeling

**University of California**, Berkeley, CA, 1989-1994  
B.S. 1994 Bioengineering  
Emphasis: Computer Science and Molecular Biology

### EMPLOYMENT

**Andromedia** (Macromedia), San Francisco, CA, 1998-1999  
Software Engineer

**Novo Group** (Semaphore Partners), San Francisco, CA, 1996-1998  
Software Engineer

**University of California**, San Francisco, CA, 1993  
Summer Internship  
Laboratory of Dr. John Sedat

### AWARDS

**PMMB National Fellowship**, 2001-2003  
Program in Mathematics and Molecular Biology (Burroughs-Wellcome)

### INVITED PRESENTATIONS

“Automated prediction of CASP-5 structures using the Robetta server” (with Rohl CA)  
Fifth Meeting on the Critical Assessment of Techniques for Protein Structure Prediction.  
Monterey, CA, 2002

### SOFTWARE AUTHORED

**K\*Sync** Protein sequence to structure alignment  
**Ginzu** Protein homolog identification and domain parsing  
**Robetta** Protein tertiary structure prediction web server

### REFERENCES

**Dr. David Baker**, Thesis Advisor, UW, 206-543-1295, dabaker@u.washington.edu  
**Dr. Rachel Klevit**, Committee Member, UW, 206-543-5891 (telephone only)  
**Dr. Charles Strauss**, Collaborator, Los Alamos Natl Lab, 505-665-4838, cems@lanl.gov

## PEER REVIEWED PUBLICATIONS

Kim DE\*, **Chivian D\***, Baker D. (2004) "Protein structure prediction and analysis using the Robetta server" *Nucleic Acids Res* 32(Web Server issue):W526-31

Rohl CA, Strauss CE, **Chivian D**, Baker D. (2004) "Modeling structurally variable regions in homologous proteins with rosetta" *Proteins* 55:656-77

**Chivian D**, Kim DE, Malmstrom L, Bradley P, Robertson T, Murphy P, Strauss CE, Bonneau R, Rohl CA, Baker D. (2003) "Automated prediction of CASP-5 structures using the Robetta server" *Proteins* 53 Suppl 6:524-33

Bradley P\*, **Chivian D\***, Meiler J\*, Misura KM\*, Rohl CA\*, Schief WR\*, Wedemeyer WJ\*, Schueler-Furman O, Murphy P, Schonbrun J, Strauss CE, Baker D. (2003) "Rosetta predictions in CASP5: successes, failures, and prospects for complete automation" *Proteins* 53 Suppl 6:457-68

Bonneau R, Strauss CE, Rohl CA, **Chivian D**, Bradley P, Malmstrom L, Robertson T, Baker D. (2002) "De novo prediction of three-dimensional structures for major protein families" *J Mol Biol* 322:65-78

Bonneau R, Tsai J, Ruczinski I, **Chivian D**, Rohl CA, Strauss CE, Baker D. (2001) "Rosetta in CASP4: progress in ab initio protein structure prediction" *Proteins Suppl* 5:119-26

## BOOK CHAPTERS

**Chivian D**, Robertson T, Bonneau R, Baker D. (2003) "Ab initio methods" Chapter 27 of "Structural Bioinformatics" (ed: Bourne & Weissig), John Wiley & Sons, Inc.

## POSTERS

**Chivian D**, Kim DE, Rohl CA, Malmstrom L, Meiler J, Robertson T, Baker D. "Automated method for full chain structure prediction using Rosetta" Fifth Meeting on the Critical Assessment of Techniques for Protein Structure Prediction. Monterey, CA, 2002

**Chivian D\***, Rohl CA\*, Strauss CE, Murphy P, Baker D. "Comparative modeling using Rosetta" Fifth Meeting on the Critical Assessment of Techniques for Protein Structure Prediction. Monterey, CA, 2002

**Chivian D**, Baker D. "K\*SYNC: throwing everything at protein sequence to structure alignment" Mathematics and Molecular Biology VII: Modeling Across the Scales - Atoms to Organisms. Santa Fe, NM, 2002

**Chivian D**, Rohl CA, Strauss CE, Baker D. "Comparative modeling using Rosetta" Fourth Meeting on the Critical Assessment of Techniques for Protein Structure Prediction. Monterey, CA, 2000

\* contributed equally