Curriculum Vitae

Possu Huang

Academic History

2004	Ph.D. in Biochemistry and Molecular Biophysics, California Institute of Technology, Pasadena, CA
1998	B.A. in Molecular and Cellular Biology, University of California, Berkeley, CA

Employment

Academic Positions

2016- (Oct. 1)	Assistant Professor Bioengineering Department, Stanford University, Stanford, CA
2011- 2016	Research Scientist Department of Biochemistry, University of Washington, Seattle, WA
2006-2011	Senior Fellow/Postdoctoral Scholar Department of Biochemistry, University of Washington, Seattle, WA Advisors: William Schief and David Baker
2004-2006	Research Associate Howard Hughes Medical Institute Advisor: Stephen L. Mayo
1998-2004	Graduate Research Fellow Advisor: Stephen L. Mayo
2003	Teaching Assistant, Biophysics of Macromolecules California Institute of Technology
2001-2002	Teaching Assistant, Biochemistry of the Cell California Institute of Technology
2000	Teaching Assistant, The Molecular Basis of Protein Function California Institute of Technology
1999	Teaching Assistant, Introduction to Biology California Institute of Technology

1997-1998	Undergraduate Honors Research University of California, Berkeley Advisor: Randy W. Schekman
1996-1997	Undergraduate Research Assistant Lawrence Berkeley National Laboratory Advisors: Thomas N. Earnest and Gerry McDermott
1995-1996	Undergraduate Research Assistant Fullerton College Advisor: Al Hermann

Non- Academic Positions

2012-	Associate Consultant Rosetta Design Group LLC

Professional Activities

Grants Review Panel

2017	National Science Foundation

Patent Applications

US 14/978,132	Engineered Outer Domain (eOD) of HIV gp120 and Mutants Thereof
US 62/268,320	Repeat Protein Architectures

Memberships

2006-	Developer: RosettaCommons (Primary developer for RosettaRemodel design suite)
2002, 2015-	Member: Protein Society
2005	Member: Biophysical Society

Consulting

2013	Sanofi-Pasteur, Boston, MA
2012	Crucell/Johnson&Johnson, San Diego, CA

Peer Reviewer

2018	Proceedings of the National Academy of Science, USA
2018	Nature Review Chemistry
2017	Proceedings of the National Academy of Science, USA

2016	Proceedings of the National Academy of Science, USA
2016	Journal of Structural Biology
2015	Proceedings of the National Academy of Science, USA
2006	Proceedings of the National Academy of Science, USA

University and Departmental Service

2016	Organizer/Instructor RosettaRemodel Workshop Stanford University
2016	Invited Instructor Workshop for Protein Modeling and Design Using Rosetta (Four day workshop by Huang P.-S. and Ovchinnikov S. for selected students) National Autonomous University of Mexico (Organizer: Prof. Alejandro Sosa)
2016	Presenter/Organizer Career workshop Institute for Protein Design, University of Washington
2016	Instructor Protein Design, Remodel 101 Institute for Protein Design, University of Washington
2014	Expert Panelist Protein Design Workshop Institute for Protein Design, University of Washington
2006-	Technical support for RosettaRemodel Protein Design software RosettaCommons

Awards and Honors

2016-2019	Frederick E. Terman Fellowship
2015	Best Poster Award. Proteins Gordon Research Conference
1998	Helen G. and Arthur McCallum Fellowship

BIBLIOGRAPHICAL INFORMATION

PUBLICATIONS

Customary practices in the field for order of authors on scholarly publications: Students and postdocs who primarily executed the research are listed as first authors. The principal investigator is listed last as corresponding author, otherwise noted.
† Co-corresponding authors.
* Equal-contributing first authors.
Supervised students in **boldface**; postdoc trainees in *italics*.

Refereed Journal Publications

1. Parmeggiani F.†, Huang P.-S.†, "Designing Repeat Proteins: A Modular Approach to Protein Design" *Current Opinions in Structure Biology*, 45:116-123, 2017

2. Ovchinnikov S., Park H, Varghese N., Huang P.-S., Pavlopoulos G.A., Kim D.E., Kamisetty H., Kyrpides N.C., Baker D., "Protein structure determination using metagenome sequence data" *Science* 355 (6322), 294-298, 2016.

3. **Rose J.C.**, Huang P.-S., Camp N.D., Ye J., Leidal A.M., Goreshnik I, Trevillian B.M., Dickinson M.S., Cunningham-Bryant D., Debnath J., Baker D., Wolf-Yadlin A., Maly D.J., "A computationally engineered RAS rheostat reveals RAS-ERK signaling dynamics", *Nature Chemical Biology* 13 (1), 119-126, 2016

4. Huang P.-S.*, Boyken S.E.*, Baker D., "The Coming of Age of *de novo* Protein Design," *Nature*, 537 (7620), 320-327, 2016.

5. *Bhardwaj G.,* Mulligan V.K., Bahl C.D., Gilmore J.M., Harvey P.J., Cheneval O., Buchko G.W., Pulavarti S.V., Kaas Q., Eletsky A., Huang P.-S., Johnsen W.A., Rocklin G.J., Song Y., Linsky T.W., Watkins A., Rettie S.A., Xu X., Carter L.P., Bonneau R., Olson J.M., Coutsias E., Correnti C.E., Szyperski T., Craik, D.J., Baker D., "Accurate *De Novo* Design of Hyperstable Constrained Peptides," *Nature*, 538 (7625) 329-335, 2016.

6. **Hsia Y.**, Bale J.B., Gonen S., Shi D., Sheffler W., Fong K.K., Nattermann U., Xu C., Huang, P.-S., Ravichandran R., Yi S., David T.N., Gonen T., King N.P., Baker D., "Design of A Hyperstable 60-subunit Protein Icosahedron," *Nature*, 535 (7610), 136-139, 2016.

7. Huang P.-S.*†, Feldmeier K.*, Parmeggiani F., *Fernandez Velasco D.A.,* Höcker B.†, Baker D.†, "*De novo* Design of a Four-fold Symmetric TIM-barrel Protein with Atomic-level Accuracy" *Nature Chemical Biology*, 12(1): 29-34, 2016.

8. Huang P.-S.*, *Brunette TJ**, Parmeggiani F.*, Bhabha G., Ekiert D.C., Tsutakawa S.E., Hura G.L., Tainer J., Baker D., "Exploring the Repeat Protein Universe Through Computational Protein Design" *Nature*, 528 (7583):580-4, 2015.

9. **Mou Y.**, Huang P.-S., Thomas L.M., Mayo S.L., "Using Molecular Dynamics Simulations to Predict Domain Swapping of Computationally Designed Protein Variants," *J. Mol. Bio*, 427(16):2697-706, 2015.

10. Huang P.-S.*, **Mou Y.*,** Hsu F.-C., Huang S.-J., Mayo S.L., "Computational Design and Experimental Verification of a Symmetric Homodimer," *Proc. Natl. Acad. Sci. USA*, 112(34):10714-9, 2015.

11. Huang P.-S.*, Parmeggiani F.*, Vorobiev S., Xiao R., *Park K.*, Caprari S., Su M., Jayaraman S., Mao L., Janjua H., Montelione G., Hunt J., Baker D., "A General Computational Approach for Repeat Protein Design," *J. Mol. Bio*, 427(2):563-575, 2015.

12. Kaltofen S., Li C., Huang P.-S., Serpell L.C., Barth A., Ingemar A., "Computational De Novo Design of a Self-Assembling Peptide with Predefined Structure," *J. Mol. Bio*, 427(2):550-562, 2015.

13. *Park K.*, Shen B.W., Parmeggiani F., Huang P.-S., Stoddard B., Baker D., "Control of Repeat Protein Curvature by Computational Protein Design," *Nature Structure and Molecular Biology*, doi: 10.1038/nsmb.2938, 2015.

14. Huang P.-S.*, Oberdorfer G.*, *Xu C.**, Pei X.Y., Nannenga B.L., Rogers J.M., Dimaio F., Gonen T., Luisi B., Baker D.*, "High Thermodynamic Stability of Parametrically Designed Helical Bundles," *Science*, 346(6208), 2014.

15. Schiffner T., Kong L., Duncan C.J., Back J.W., Benschop J.J., Shen X., Huang P.-S., Stewart-Jones G.B., DeStefano J., Seaman M.S., Tomaras G.D., Montefiori D.C., Schief W.R., Sattentau Q.J., "Immune Focusing and Enhanced Neutralization Induced by HIV-1 gp140 Chemical Cross-linking," *J Virol.*, 87(18):10163-72, 2013.

16. **Jardine J.**, Julien J.P., **Menis S.**, Ota T., Kalyuzhniy O., McGuire A., Sok D., Huang P.-S., MacPherson S., Jones M., Nieusma T., Mathison J., Baker D., Ward A.B., Burton D.R., Stamatatos L., Nemazee D., Wilson I.A., Schief W.R., "Rational HIV Immunogen Design to Target Specific Germline B Cell Receptors," *Science*, 340(6133), 2013.

17. Yu Y., Zhu J., Huang P.-S., Wang J.H., Pullen N., Springer T.A., "Domain 1 of Mucosal Addressin Cell Adhesion Molecule Has an I1-set Fold and a Flexible Integrin-binding Loop," *J Biol. Chem.*, 288(9):6284-94, 2013.

18. **Azoitei M.L., Correia B.E.,** Ban Y.E., **Carrico C.**, Kalyuzhniy O., Chen L., Schroeter A., Huang P.-S., McLellan J.S., Kwong P.D., Baker D., Strong R.K., Schief W.R., "Computation-guided Backbone Grafting of a Discontinuous Motif onto a Protein Scaffold," *Science*, 334(6054), 2011.

19. Huang P.-S.*, Pejchal R.*, Doores K.J.*, Walker L.M.*, Khayat R.*, Wang S.K., Stanfield R.L., Julien J.P., Ramos A., Crispin M., Depetris R., Katpally U., Marozsan A., Cupo A., Maloveste S., Liu Y., McBride R., Ito Y., Sanders R.W., **Ogohara C.**, Paulson J.C., Feizi T.,

Scanlan C.N., Wong C.H., Moore J.P., Olson W.C., Ward A.B., Poignard P., Schief W.R., Burton D.R., Wilson I.A., "A Potent and Broad Neutralizing Antibody Recognizes and Penetrates The HIV Glycan Shield," *Science*, 334(6059), 2011.

20. Van Montfort T., Melchers M., Isik G., **Menis S.**, Huang P.-S., Matthews K., Michael E., Berkhout B, Schief WR, Moore JP, Sanders RW., "A Chimeric HIV-1 Envelope Glycoprotein Trimer with an Embedded Granulocyte-Macrophage Colony-stimulating Factor (GM-CSF) Domain Induces Enhanced Antibody and T Cell Responses," *J. Biol. Chem.*, 286 pp 22250-22261, 2011.

21. Huang P.-S., Ban A. Y.-E., Andre I, Richter F., Vernon R., Schief W.R., Baker D., "RosettaRemodel: A Generalized Framework for Flexible Backbone Protein Design," *PLoS One*. 6(8):e24109, 2011.

22. **Correia B.E.**, Holmes M.A., Huang P.-S., Strong R.K., Schief W.R., "High-resolution Structure Prediction of a Circular Permutation Loop," *Protein Sci.*, 20(11):1929-34, 2011.

23. Benoit S., Huang P.-S., Ban A. Y.-E., Baker D., Springer T.A., "Modulation of Integrin Activation by an Entropic Spring in The Beta-knee," *J. Bio. Chem.*, 285 pp 32954-32966, 2010.

24. Huang P.-S., Love J.J., Mayo S.L., "A De Novo Designed Protein/Protein Interface," *Protein Sci.* 16(12) pp 2770 – 2774, 2007.

25. Huang P.-S., Love J.J., Mayo S.L., "Adaptation of a Fast Fourier Transform-Based Docking Algorithm for Protein Design," *J. Comp. Chem.*, 26 (12) pp 1222 – 1232, 2005.

26. Shukla U., Marino H., Huang P.-S., Mayo S.L., Love, J.J., "A Designed Protein Interface that Blocks Fibril Formation," *J. Am. Chem. Soc.*, 126(43) pp 13914 – 13915, 2004.

Non-refereed Conference/Symposia Proceedings

1. Huang P.-S.*, Parmeggiani F.*, Brunette TJ*, Ekiert D., Bhabha G., Tsutakawa S., Hura G., Tainer J., Baker D., "The road not taken: Exploring the Repeat Protein architectures by Computational Design," *Protein Science*, 24, 194-195, 2015.

2. Huang P.-S.*†, Feldmeier K.*, Parmeggiani F., Fernandez Velasco D.A., Höcker B.†, Baker D.†, "De novo Design of an Ideal TIM-barrel scaffold," *Protein Science*, 24, 186-186, 2015.

3. Oberdorfer G., Huang P.-S., Xu C., Kohler V., Pei X.Y., Nannenga B.L., Rogers J.M., Gonen T., Gruber K., Baker D., "Parametric Design of Alpha-helical Barrels and Pore-like Assemblies with Very High Thermodynamic Stabilities," *Protein Science*, 24, 193-194, 2015.

4. Schiffner T., Leonavicius K., Schuster H., Kim H.J., Kong L,. Saliba R., Brod F., Wegmann F., Huang P.-S., Stewart-Jones G.B., Schief W.R., Ward A.B., Moore J.P., Sanders R.W.,

Davis B.G., Sattentau Q.J., "Refocussing Antibody Responses by Chemical Modification of Vaccine Antigens," *AIDS research and Human Retroviruses,* 2014.

5. Huang P.-S., Love J.J., Mayo S.L., "Computational Design and Experimental Characterization of De Novo Protein Oligomers," *Biophysical Journal* 88(1), 333A, 2005

PRESENTATIONS

Invited Plenary Talks and Distinguished Lectures

1. Plenary Speaker, Simposio de la Licenciatura en Biología Molecular, "*De Novo* Protein Design" Metropolitan Autonomous University, Mexico City, Mexico, 2016

2. Plenary Speaker, International Workshop on Frontiers in Protein Folding, Evolution and Function. "Exploring the Repeat Protein Universe by Computational Protein Design." Oaxaca, Mexico, 2015

3. Plenary Speaker, Defense Threat Reduction Agency, Computational Chemistry Workshop. "Prediction and Design of Macromolecular Structures and Interactions." Maui, HI, 2007

Other Invited Presentations

1. California Institute of Technology, special lecture on Protein Design, March 2018

2. Agilent Technology, Jan. 2018

3. Alpbach workshop on Coiled coils and Repeat Proteins, Alpbach, Austria, 2017

4. VIB conference Next Generation Antibodies and Protein Analysis,
   Ghent, Belgium, Oct. 2017

5. NovoNordisk, Denmark, Oct. 2017

6. Technical Univeristy of Munich, Munich, Germany, Sept. 2017

7. Amgen, San Francisco, June, 2017

8. Stanford Student in Biodesign, Stanford, Jan, 2017

9. Seminar Speaker, Joint Genome Institute, Department of Energy, USA, Jan. 2017

10. Guest lecturer, CS279, Stanford University, Nov 2016

11. Guest instructor, Bio495, University of Washington, Bothell, 2016

12. Speaker, Rising Stars in Chemical Biology Symposium. University of Utah, 2015.

13. Invited attendee and presented on “Self-evolving materials” for Atomic Precision for Medical Applications workshop
Foresight Institute, Palo Alto, CA, 2015.

14. Speaker, “RosettaRemodel” Pfizer Inc., Boston, MA, 2010.

Department Seminars

1. Invited Speaker, Biological Sciences Division, Stanford Linear Accelerator Center, 2016

2. BIOE 393, “The Advent of Functional Engineered Molecular Platforms” Bioengineering Department, Stanford Univeristy, 2016.

3. Students’ choice speaker, “Creating a New Molecular Sensor Platform by *De Novo* Protein Design” Biophysics Retreat, Stanford University, 2016.

4. Invited Speaker, Bioengineering Department, Stanford University, 2016.

5. Invited Speaker, Department of Bioengineering, University of California, Berkeley, 2016.

6. Invited Speaker, Department of Biochemistry, University of Utah, 2016.

7. Invited Speaker, Department of Biomedical Engineering, Duke University, 2015.

8. Invited Speaker, Institute for Bioscience & Biotechnology Research, Univ. of Maryland, College Park, 2015.

9. Invited Speaker, European Molecular Biology Laboratory, Heidelberg, Germany, 2008.

Contributed Conference Presentations

1. “Design of a chemically synthesized disulfide bonded mini-protein: de novo TIM barrel from parts” RosettaCon2016, Leavenworth, WA 2016.

2. “De Novo Design of Repeat Proteins” RosettaCon2012, Leavenworth, WA, 2012.

3. “RosettaRemodel” RosettaCon2010, Leavenworth, WA, 2010.

4. “Template Problems and Conformer Libraries” RosettaCon2006, Leavenworth, WA, 2006.

STUDENTS

My primary job as a Research Scientist at the University of Washington includes teaching and direct student and junior postdoc research at an extensive level in a lab with 70+ members. Listed here is a subset of students and postdocs who have published a paper with me in a refereed venue.

Students Supervised with Joint Publications: (alpha order)
Azoitei, Mihai
Carrico, Christopher
Correia, Bruno
Hsia, Yang
Jardine, Joseph
Menis, Sergey
Mou, Yun
Ogohara, Cassandra
Rose, Jack

Postdocs Supervised with Joint Publications: (alpha order)
Brunette, TJ, PhD
Bhardwaj, Gaurav, PhD
Fernandez Velasco, D. Alejandro, PhD
Greisen Per, PhD
Park, Keunwan, PhD
Xu, Chunfu, PhD