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Summary

Biography

Degree in Biotechnology, University of Bologna

Ph.D. University of Zurich, with prof. Andreas Plückthun

Postdoctoral fellow and acting instructor, University of Washington, with prof. David Baker

I work on developing new hybrid computational and experimental methods for protein design. The focus is on modular systems based on designed repeat proteins for spatial control of protein structures and their applications as tools to study and influence cell behaviour.

Memberships

Organisations

[School of Chemistry](#)

Other sites

- [Brissynbio](#)
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School of Biochemistry staff

- [Biochemistry academic staff](#)

Recent publications

- Geiger-Schuller, K, Sforza, K, Yuhas, M, Parmeggiani, F, Baker, D & Barrick, D, 2018, '[Extreme stability in de novo-designed repeat arrays is determined by unusually stable short-range interactions](#)'. *Proceedings of the National Academy of Sciences of the United States of America*, vol 115., pp. 7539-7544
- Yeh, CT, Brunette, TJ, Baker, D, McIntosh-Smith, S & Parmeggiani, F, 2018, '[Elfin: an algorithm for the computational design of custom three-dimensional structures from modular repeat protein building blocks](#)'. *Journal of Structural Biology*, vol 201., pp. 100-107
- Parmeggiani, F & Huang, P-S, 2017, '[Designing repeat proteins: A modular approach to protein design](#)'. *Current Opinion in Structural Biology*, vol 45., pp. 116-123
- Fallas, JA, Ueda, G, Sheffler, W, Nguyen, V, McNamara, DE, Sankaran, B, Pereira, JH, Parmeggiani, F, Brunette, TJ, Cascio, D, Yeates, TR, Zwart, P & Baker, D, 2017, '[Computational design of self-assembling cyclic protein homo-oligomers](#)'. *Nature Chemistry*, vol 9., pp. 353-360
- Reichen, C, Hansen, S, Forzani, C, Honegger, A, Fleishman, SJ, Zhou, T, Parmeggiani, F, Ernst, P, Madhurantakam, C, Ewald, C, Mittl, PRE, Zerbe, O, Baker, D, Caflisch, A & Plückthun, A, 2016, '[Computationally Designed Armadillo Repeat Proteins for Modular Peptide Recognition](#)'. *Journal of Molecular Biology*, vol 428., pp. 4467-4489
- Huang, P-S, Feldmeier, K, Parmeggiani, F, Velasco, DAF, Höcker, B & Baker, D, 2016, '[De novo design of a four-fold symmetric TIM-barrel protein with atomic-level accuracy](#)'. *Nature Chemical Biology*, vol 12., pp. 29-34

- Mills, JH, Sheffler, W, Ener, ME, Almhjell, PJ, Oberdorfer, G, Pereira, JH, Parmeggiani, F, Sankaran, B, Zwart, PH & Baker, D, 2016, '[Computational design of a homotrimeric metalloprotein with a trisbipyridyl core](#)'. *Proceedings of the National Academy of Sciences of the United States of America*, vol 113., pp. 15012-15017
- Brunette, TJ, Parmeggiani, F, Huang, P-S, Bhabha, G, Ekiert, DC, Tsutakawa, SE, Hura, GL, Tainer, JA & Baker, D, 2015, '[Exploring the repeat protein universe through computational protein design](#)'. *Nature*, vol 528., pp. 580-4
- Doyle, L, Hallinan, J, Bolduc, J, Parmeggiani, F, Baker, D, Stoddard, BL & Bradley, P, 2015, '[Rational design of \$\alpha\$ -helical tandem repeat proteins with closed architectures](#)'. *Nature*, vol 528., pp. 585-8
- Parmeggiani, F, Huang, P-S, Vorobiev, S, Xiao, R, Park, K, Caprari, S, Su, M, Seetharaman, J, Mao, L, Janjua, H, Montelione, GT, Hunt, J & Baker, D, 2015, '[A general computational approach for repeat protein design](#)'. *Journal of Molecular Biology*, vol 427., pp. 563-75

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