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Shuguang Zhang is at Center for Bits & Atoms, Massachusetts Institute of Technology. He received his B.S from Sichuan University, China and Ph.D. in Biochemistry & Molecular Biology from University of California at Santa Barbara, USA. He was an American Cancer Society Postdoctoral Fellow and a Whitaker Foundation Investigator at MIT. He was a 2003 Fellow of Japan Society for Promotion of Science (JSPS fellow). His work of designer self-assembling peptide scaffold won 2004 R&D100 award. His and his colleagues' work for direct harvesting biosolar energy was selected one of the 10 finalists of the 2005 Saatchi & Saatchi Award for World Changing Ideas. He won 2006 Wilhelm Exner Medal of Austria. He is a Fellow of American Institute of Medical and Biological Engineering and Fellow of US National Academy of Inventors. He is a Foreign Corresponding Member of Austrian Academy of Sciences. He published >160 scientific papers that have so far been cited >27,700 times, with h-index 80. He is also a co-founder and board member of Molecular Frontiers Foundation that encourages young people to ask big and good questions in order to win Molecular Frontiers Inquiry Prize.

Shuguang Zhang made a serendipitous discovery of a repetitious and ionic self-complementary peptide segment in yeast protein Zuotin in 1990. This is discovery of the first self-assembling peptides that eventually led to the development of a new field of peptide nanobiotecnology. Furthermore, his discovery inspired numerous people around the world to design a variety of self-assembling peptides for wide spread uses including peptide hydrogels in materials science, 3D tissue cell culture and tissue engineering, nanomedicine, sustained molecular releases, clinical and surgical applications. He co-founded a startup company 3DMatrix that brings the self-assembling peptide materials to human clinical and surgical uses.

Shuguang Zhang in 2011 invented a simple molecular QTY code (glutamine, threonine and tyrosine) to systematically replace the hydrophobic amino acids leucine, valine, isoleucine and phenylalanine in the 7 transmembrane α-helices of CCR5, CXCR4, CCR10 and CXCR7. Using a yeast 2-hybrid system, we showed that variants with QTY changes still retain their α-helical structure and their ligand-binding activities in buffer and human serum. $CCR5^{QTY}$, $CXCR4^{QTY}$ and $CXCR7^{QTY}$ also bind to HIV coat protein gp41-120. Our results suggest that despite 46%-56% transmembrane changes, the detergent-free QTY variants still maintain stable structures and ligand-binding activities. Our simple QTY code is a likely useful tool and has implications for engineering water-soluble variants of previously water-insoluble and perhaps aggregated proteins, including amyloids.