# Research at the Systems Immunology/Genome Informatics Lab

Overview

The Systems Immunology/Genome Informatics lab has increased its focus on immunology since moving to RIMD. Although we still develop general bioinformatics methods, our emphasis on immunology research has increased with time. Concomitantly, our yearly citations have grown from less than 100 in 2009 to nearly 1800 in 2016 (Figure 1). This increase is due largely to intensive collaboration with immunology groups at IFReC and the popularity of several software tools, including the *MAFFT* multiple sequence alignment software. Below, we describe specific projects that have contributed to this success.

We are an international research laboratory and we welcome both Japanese and international students. Our former lab members have gone on to become scientists, entrepreneurs and software developers. Please come visit us or get in touch by mail at standley@biken.osaka-u.ac.jp.
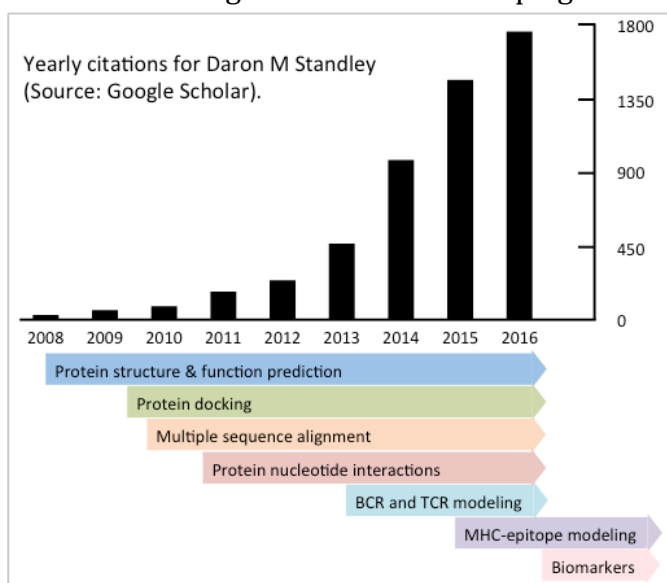
B and T cell receptor modeling

In 2014, our lab was invited to join the AMA-II antibody structural modeling contest sponsored by Pfizer, Johnson and Johnson and the Scripps Research Institute. Our team included researchers from Astellas Pharma and the Institute for Protein Research at Osaka University. In spite of stiff competition, our team won the AMA-II contest (Shirai et al., 2014). We subsequently developed *KOTAI Antibody Builder*, a fully automated server that can model B cell receptor sequences in a short amount of time with no loss in accuracy. This new technology has opened new doors for both biomarker and therapeutic discovery.

Multiple sequence alignment

We are continuously developing the popular multiple sequence alignment (MSA) program, *MAFFT*. Along with advances in sequencing technologies, the need for handling larger data is increasing. The number of citations per year for *MAFFT* has increased from 228 in 2007 to 2558 in 2015. The cumulative number of citations is about 14,000 as of Nov. 2016. The *MAFFT* web server is also very popular: The number of unique users is approaching 3000 per week