Supplemental Data for:

Biophysical and biochemical characterization of avian secretory component provides structural insights into the evolution of the polymeric Ig receptor

Running title: Biophysical characterization of avian secretory component

Beth M. Stadtmueller, Zhongyu Yang, Kathryn E. Huey-Tubman, Helena Roberts-Mataric, Wayne L. Hubbell, and Pamela J. Bjorkman

*Division of Biology and Biological Engineering, California Institute of Technology, Pasadena, CA 91125
†Department of Chemistry and Biochemistry, University of California, Los Angeles, Los Angeles, CA 90095
‡Jules Stein Eye Institute, University of California, Los Angeles, Los Angeles, CA 90095
§South Pasadena High School, South Pasadena, CA 91030
Figure S1. Spin-labeled ggSC binding to human dIgA and pIgM. Sensorgrams showing ggSC and nitroxide-labeled ggSC binding to dIgA (A-C) and pIgM (D-F). High concentrations shown are 1024uM and 512uM for dIgA and pIgM, respectively.
Figure S2. Human and avian IgA sequences. Sequence alignment of the IgA heavy chain constant regions from birds (ggIgA) and humans (hlgA1 and hlgA2). Residues implicated in mammalian SC binding to pIgA (1) are indicated by black ovals.
Figure S3. hSC and hSC D1-D3-D4-D5 binding to human dIgA and pIgM. (A-D) Sensorgrams showing the response (RU) of hSC and hSC D1-D3-D4-D5 binding to human dIgA and pIgM. High concentrations shown are 1024uM and 512uM for dIgA and pIgM, respectively.
SUPPLEMENTAL REFERENCES