

Figure. S1 Comparison of amino acid sequences of H chain and L chain of HoSF and H-1 chain and H-2 chain of SSF. Conserved residues in the alignment are highlighted in red. Hyphens indicate gaps in the sequences to allow the best alignment. The amino acid residues of EP are boxed in purple and marked "EP" at the top. The three-fold channels are boxed in blue and marked "TF" at the top. The four-fold channels are boxed in black and marked "FF" at the top. This alignment was analyzed by Clustal W. H and L chains of HoSF share ~54% identity, while H-1 and H-2 subunits of SSF share ~75% identity. Specifically, SSF and HoSF share 40-52% sequence homology