PNAS
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Supplementary Information for

Integrated structural and evolutionary analysis reveals common mechanisms underlying adaptive evolution in mammals

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Table S1

www.pnas.org/cgi/doi/10.1073/pnas.1916786117

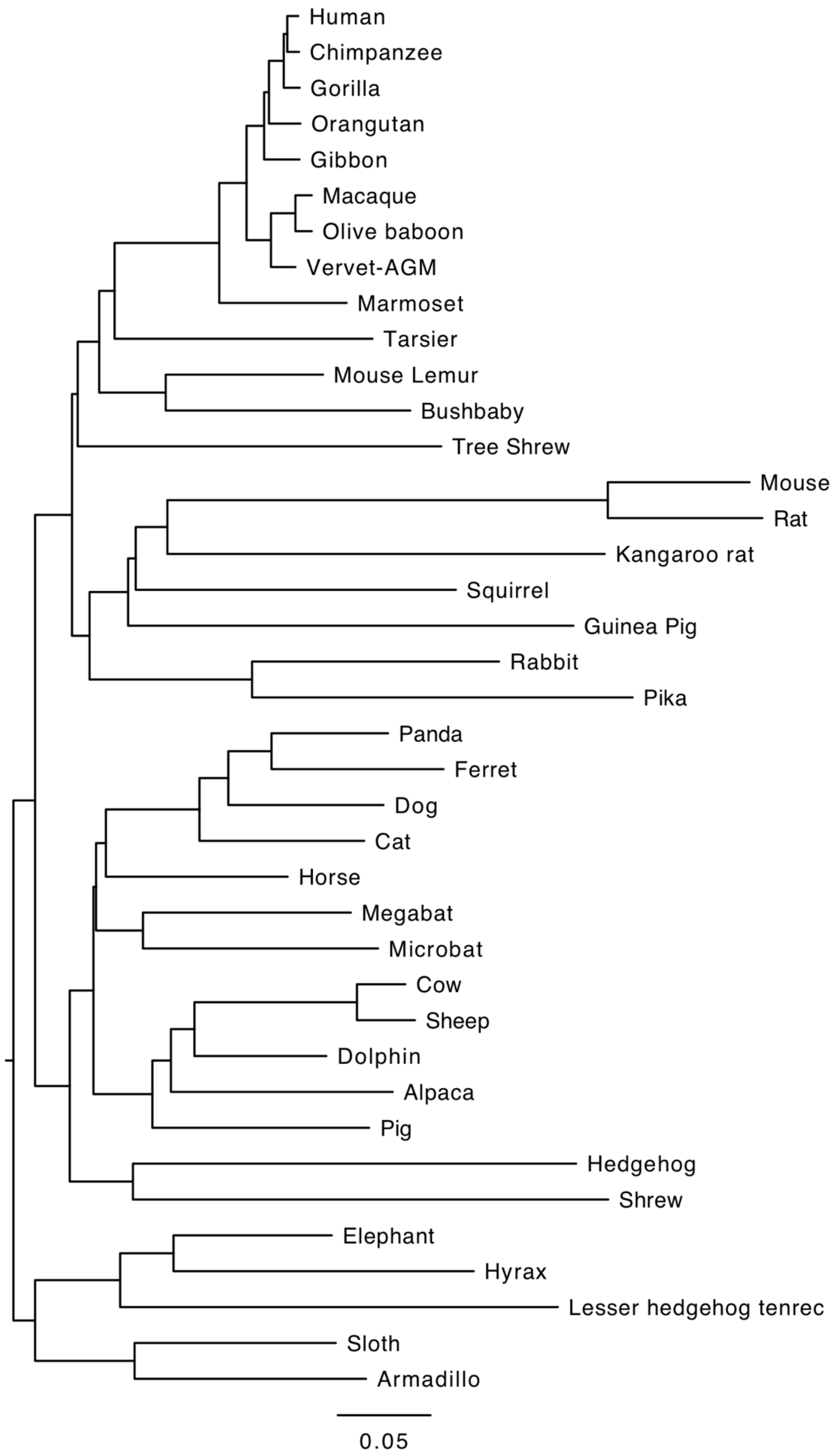

Fig. S1. Phylogenetic tree of species included in the analysis.

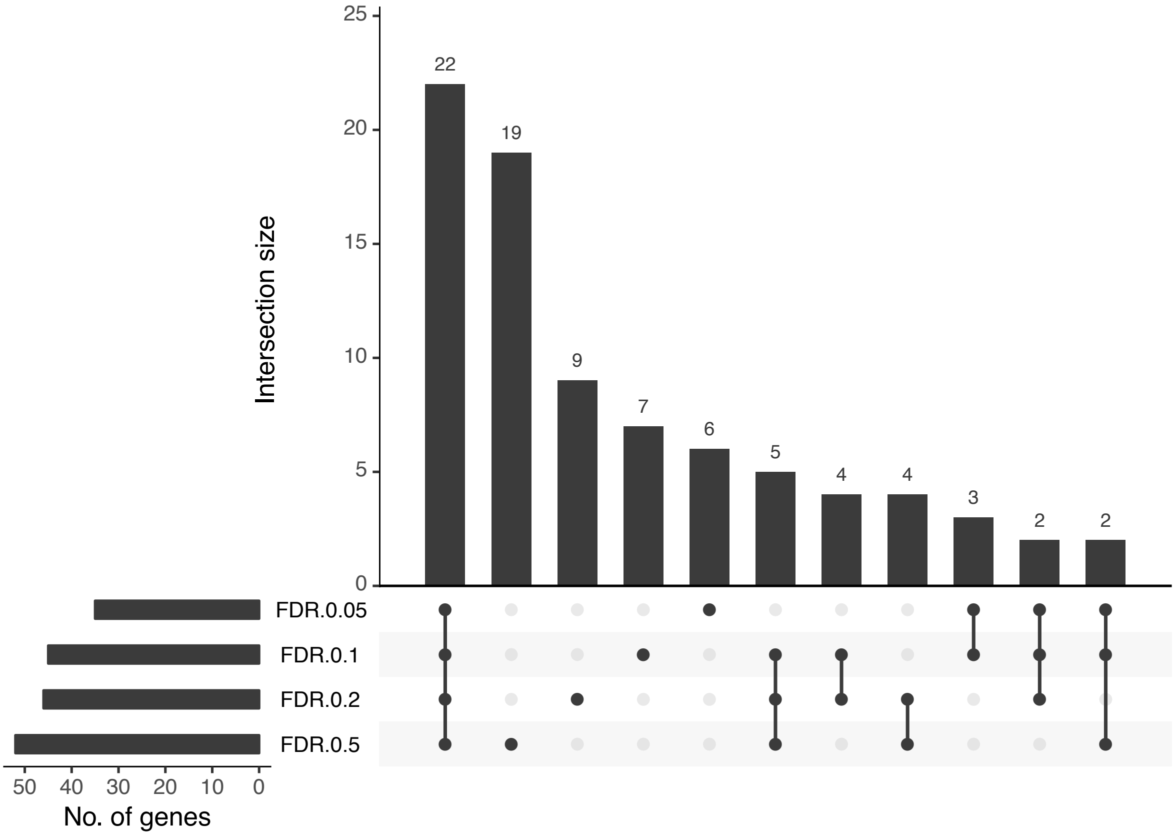

Fig. S2. Overlap between detected clusters of positively selected residues between four levels of stringency at which positively selected residues are identified.

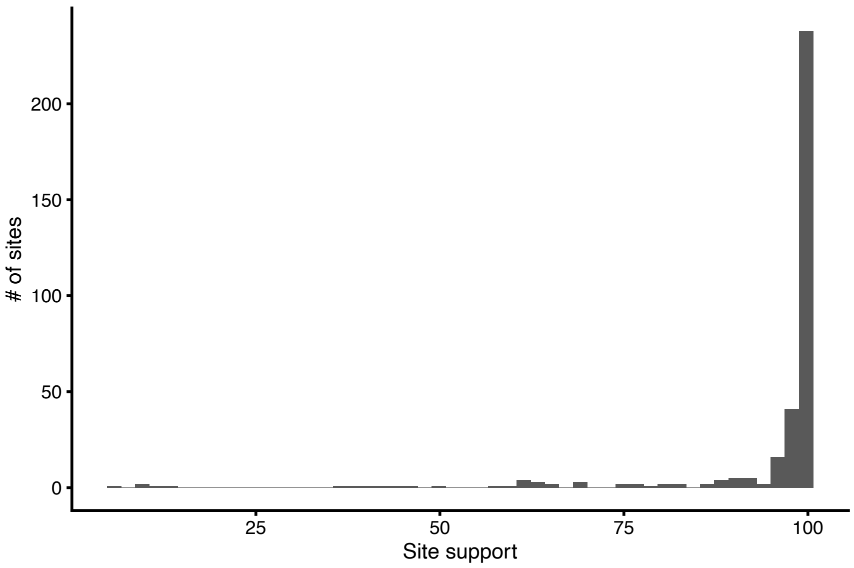

Fig. S3. Distribution of support values for positively selected sites upon perturbing the underlying tree topology. Most sites (84.7%) have support values of above 0.95, with the mean support of 0.944.

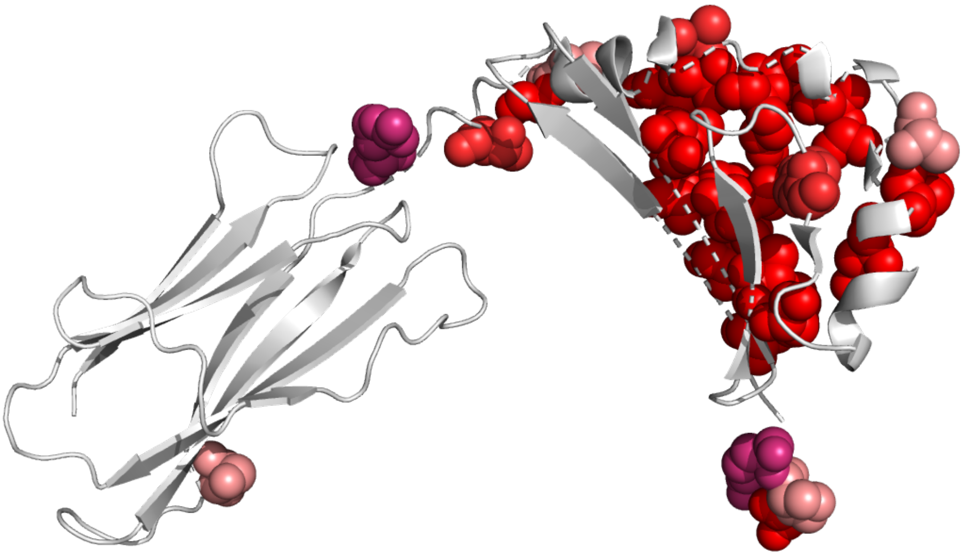

Fig. S4. Positively selected sites in major histocompatibility complex class II (PDB: 1aqd).

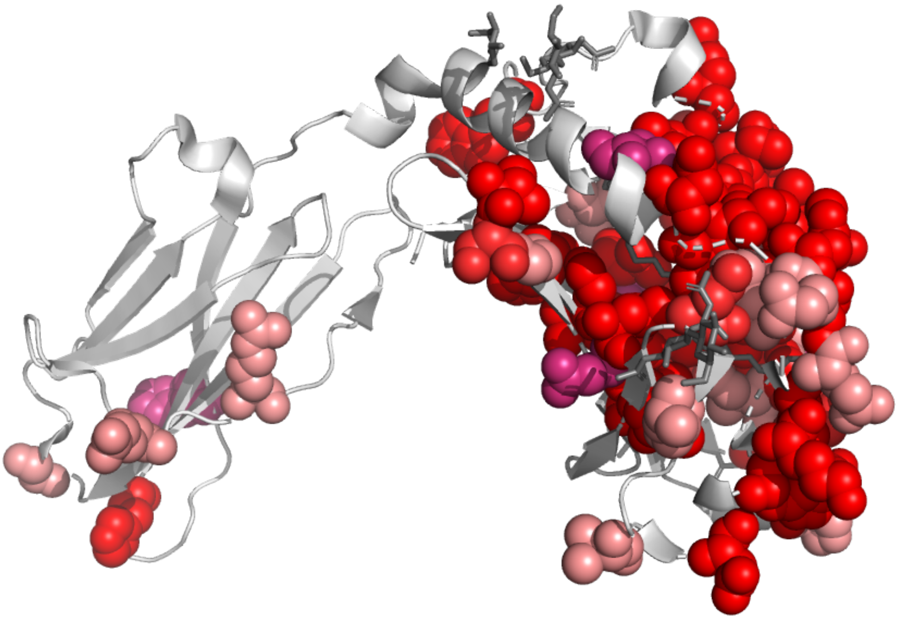

Fig. S5. Positively selected sites in CD1a molecule (PDB: 1onq).

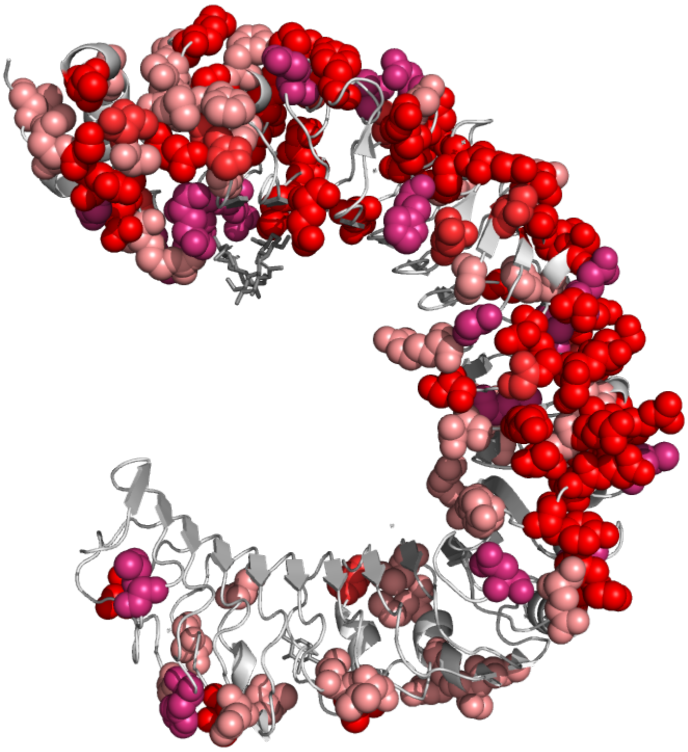

Fig. S6. Positively selected sites in toll-like receptor 4 (PDB: 4g8a).

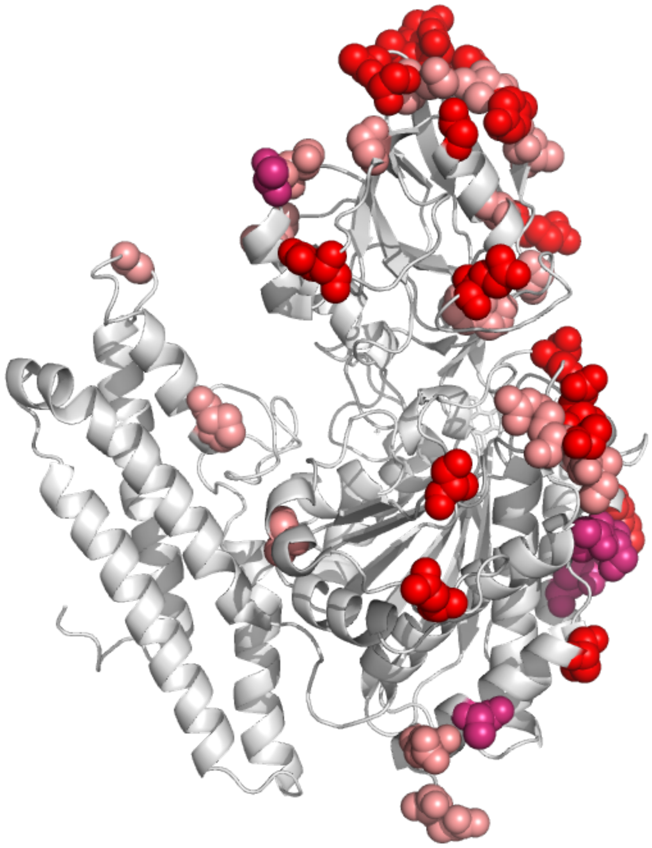

Fig. S7. Positively selected sites in transferrin receptor 1 (PDB: 3s9l).

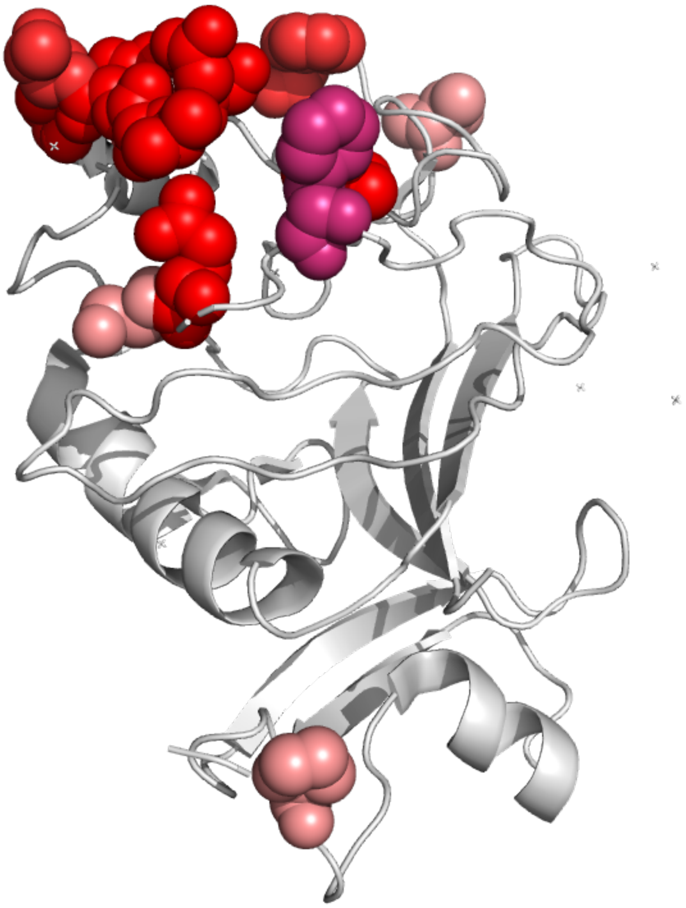

Fig. S8. Positively selected sites in ficolin 2 (PDB: 2j3f).

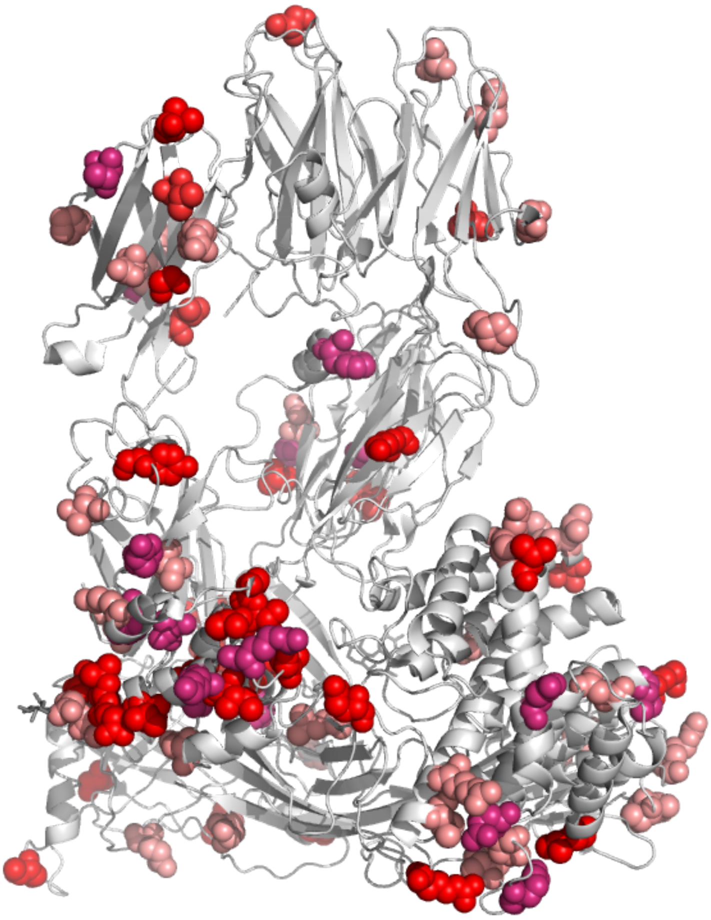

Fig. S9. Positively selected sites in complement component C5 (PDB: 3cu7).

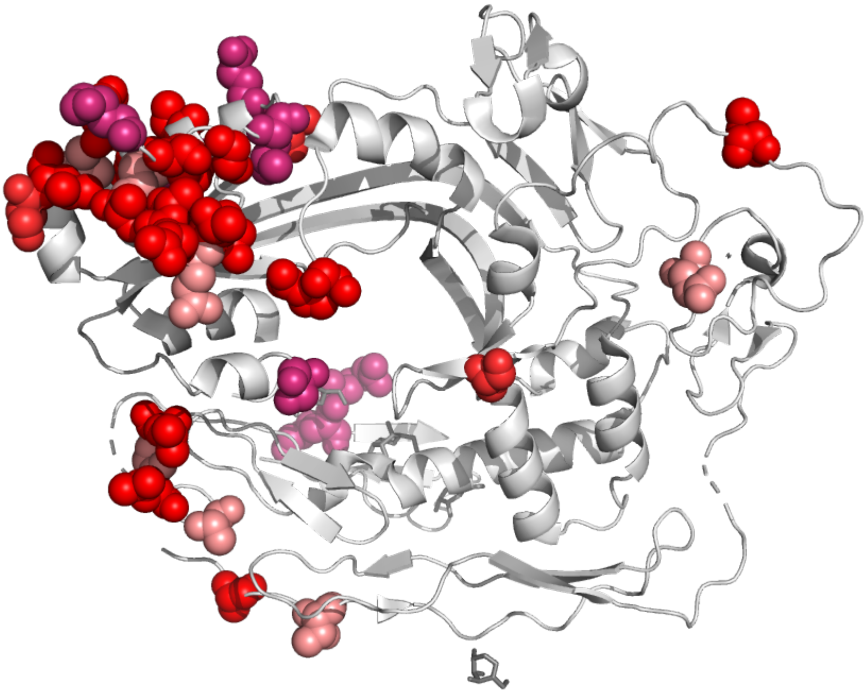

Fig. S10. Positively selected sites in complement component C8 (PDB: 3ojy).

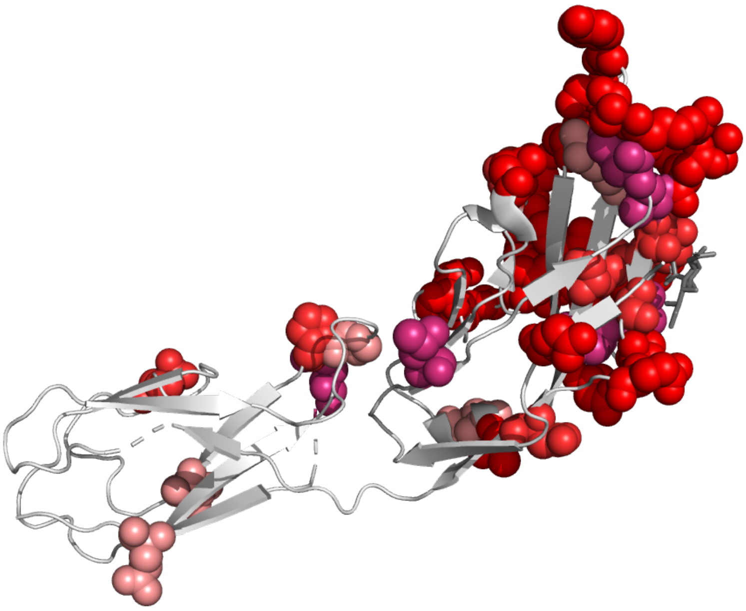

Fig. S11. Positively selected sites in siglec-5 (PDB: 2zg1).

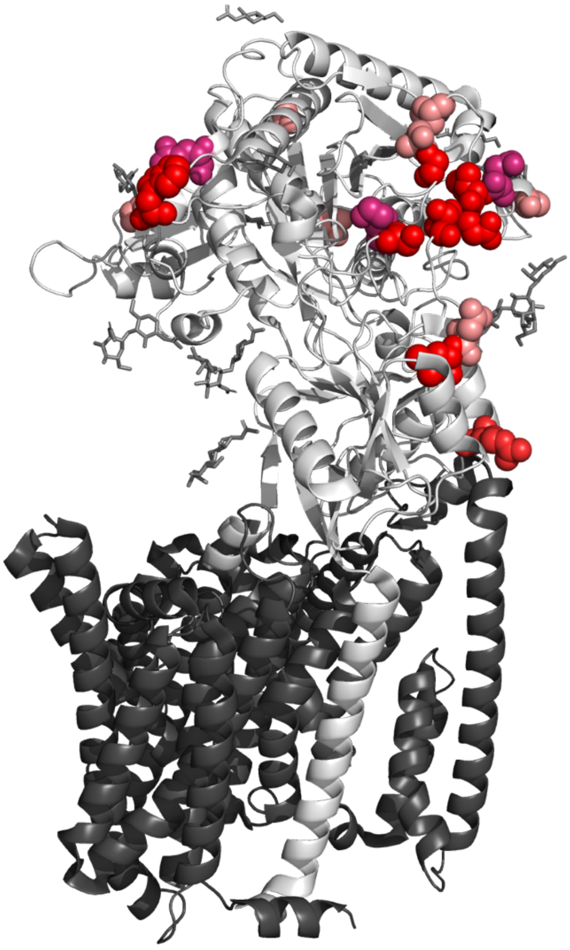

Fig. S12. Positively selected sites in nicastrin (PDB: 5a63).

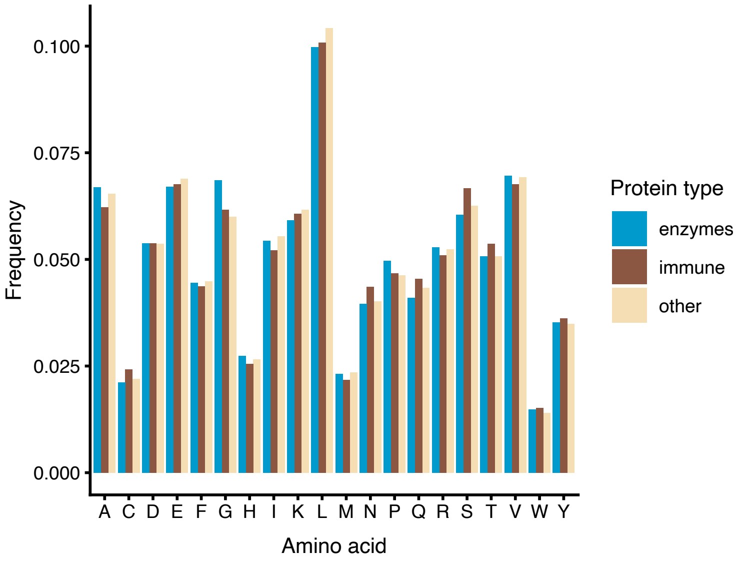

Fig. S13. Amino acid frequencies in enzymes, immune-related proteins and remaining proteins.

Property	Pearson’s r	P-value	Adj. p-value
Size (Dawson, 1972)	0.211	0.373	0.932
Hydrophobicity (Levitt, 1976)	0.067	0.780	0.941
Net charge (Klein et al., 1984)	0.460	0.042	0.207
Polarity (Zimmerman et al., 1968)	-0.018	0.942	0.941

Table S1. Correlations between amino-acid physicochemical properties and frequency changes at positively selected residues.