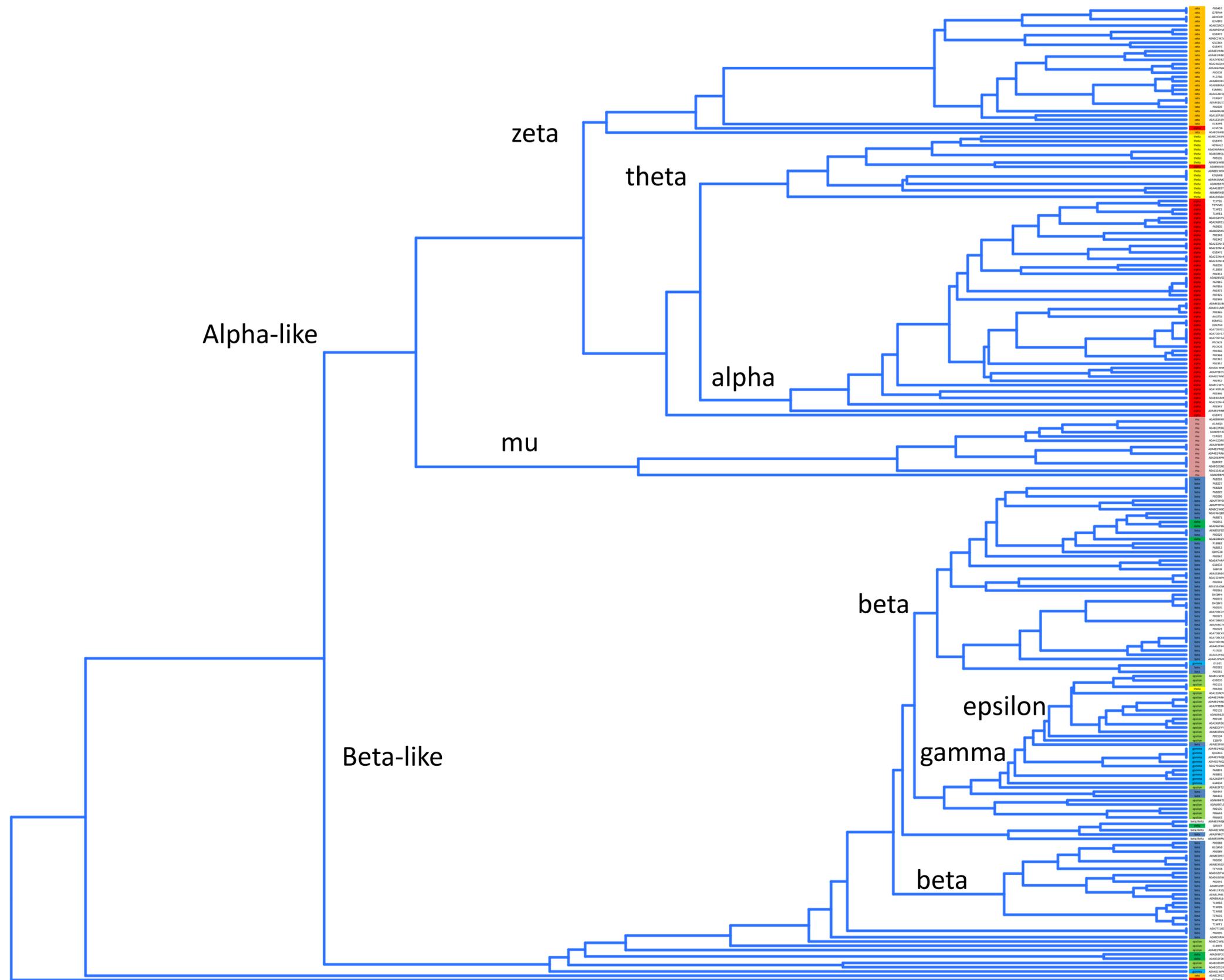


Figure S1. Phylogenetic reconstruction of hemoglobin protein sequences by similarity using BLOSUM62 matrix UPGMA clustering.



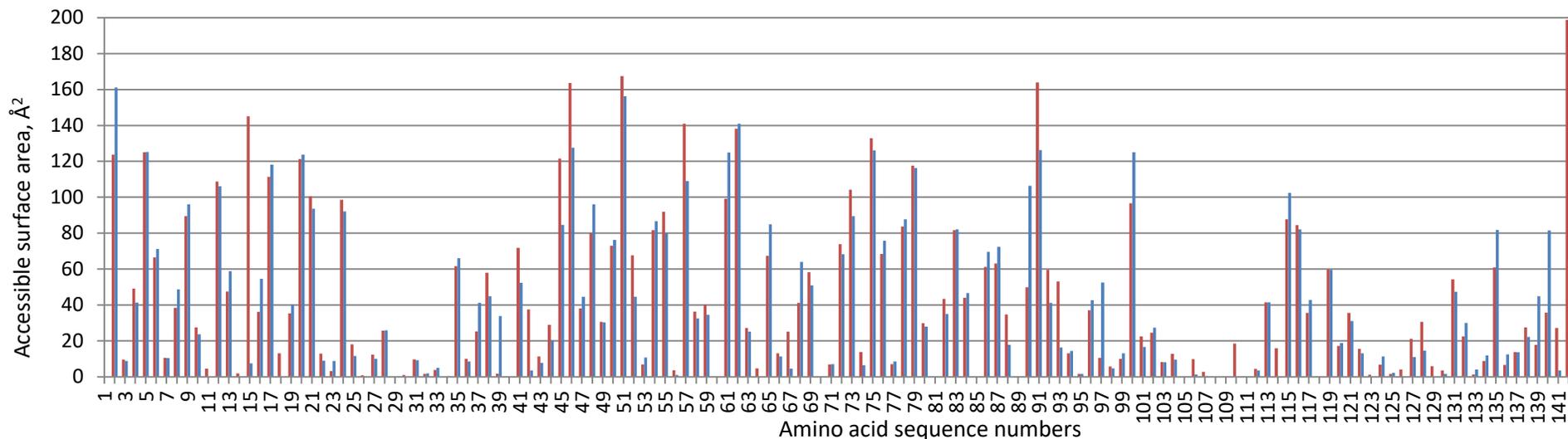


Figure S2. Accessible surface area of amino acid residues of the alpha-subunit of human hemoglobin in the oxy-form (based on the oxy 1r1x(red) and deoxy 1a3n(blue) structures).

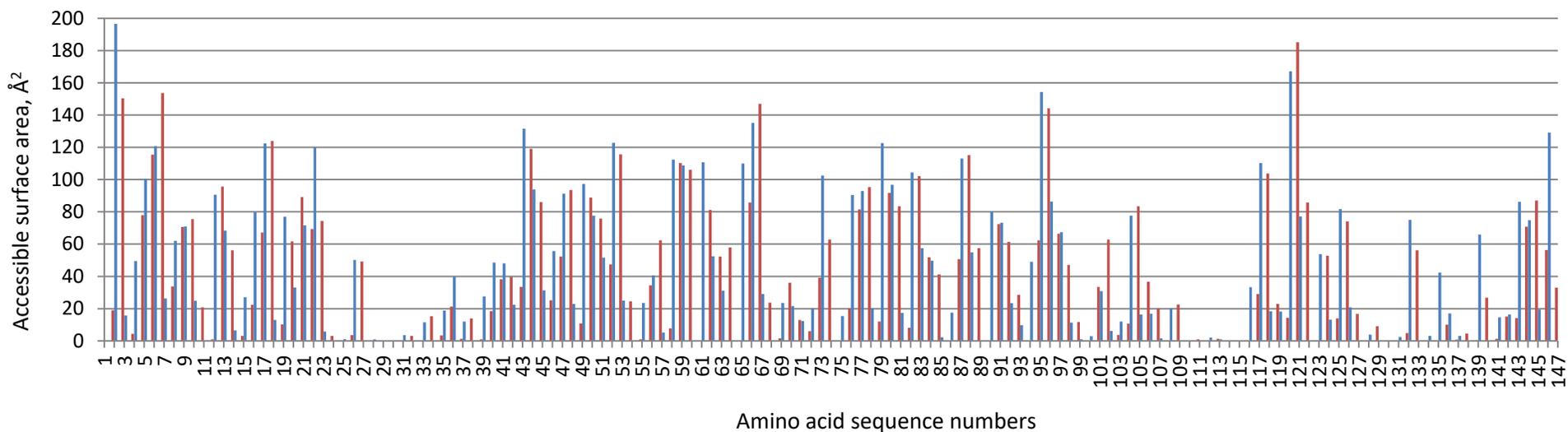


Figure S3. Accessible surface area of amino acid residues of the beta-subunit of human hemoglobin in the oxy-form (based on the oxy 1r1x(red) and deoxy 1a3n(blue) structures).

Figure S4. Sequence alignment of hemoglobin alpha-subunit both hypoxia-tolerant and hypoxia-sensitive species.

