

Amino Acid Sequence Comparisons Among gp91phox Homologs. Sequences within the regions homologous to gp91phox for each predicted protein are aligned. Residues highlighted in red are absolutely conserved among all homologs, while those highlighted in blue match a majority consensus sequence. Superior bold hashed bars indicate transmembrane alpha helices that are strongly predicted, while the lighter hashed bar represents a transmembrane alpha helix that is more weakly predicted. Superior "Y" indicates glycosylation sites in gp91phox, while inferior filled circles indicate strictly conserved histidine residues that are candidates for liganding to heme iron. Yellow superior bars represent residues that are predicted to participate in FAD binding, while green superior bars are predicted to comprise the NADPH binding site. The most N terminal of these contains the indicated G-X-G-X-X-P canonical nucleotide binding motif.

