

SUPPLEMENTAL MATERIAL

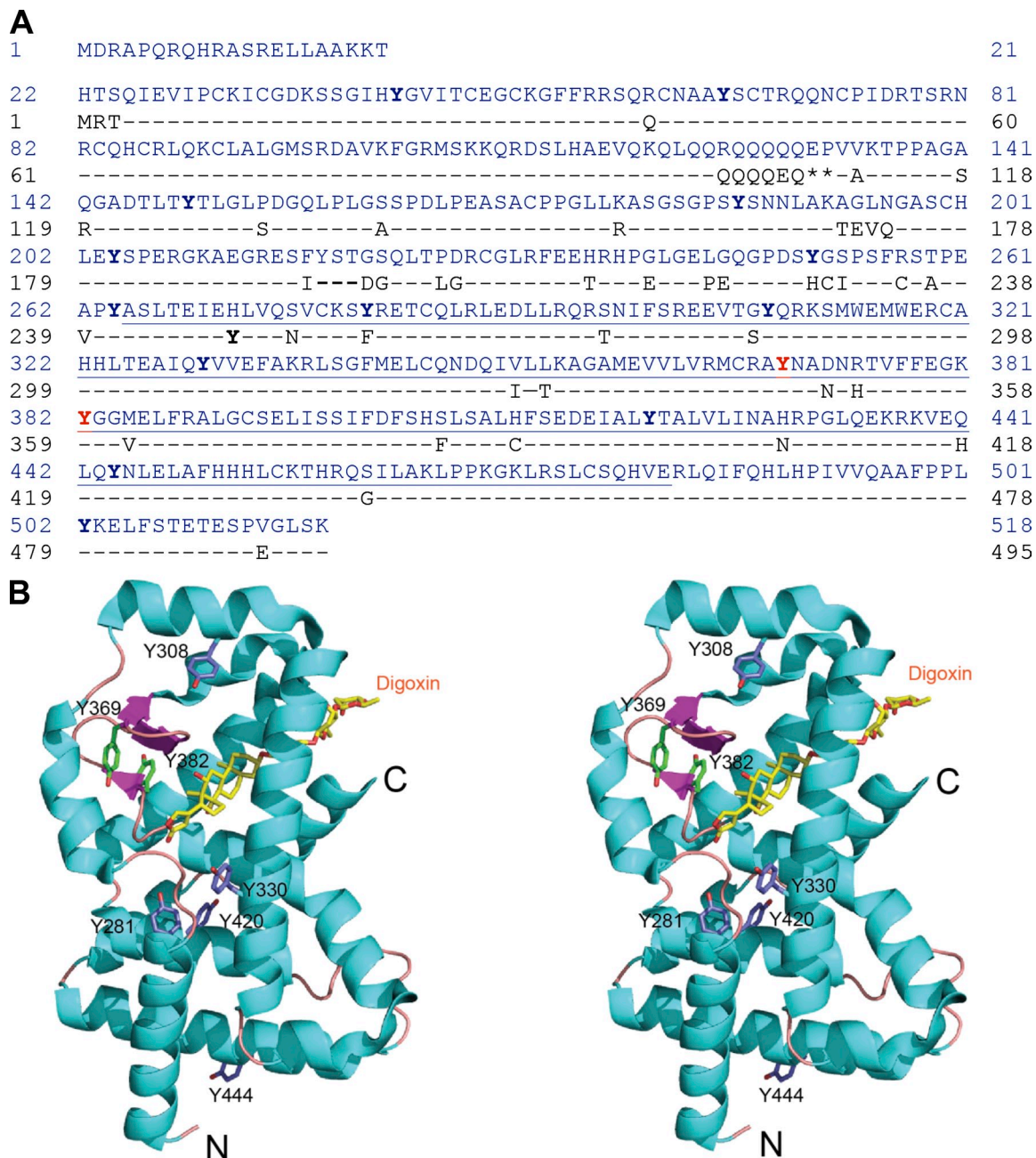
Yang et al., <http://www.jem.org/cgi/content/full/jem.20122494/DC1>

Figure S1. Structural analysis of the ligand-binding domain of ROR γ t. (A) Protein sequence alignment of human ROR γ t (blue) and mouse ROR γ t (black). The identical amino acid residues in the mouse ROR γ t to those in the human protein are indicated by a dash, whereas asterisk in the mouse protein denotes a short insertion in the protein sequence at the corresponding position in the human protein. The underlined segment in the ligand-binding domain of the human ROR γ t protein represents the fragment of the protein whose crystal structure is available. (B) Stereoview of the crystal structure of the human ROR γ t ligand binding domain in complex with digoxin (yellow). The side chains of all tyrosine residues in this region of the protein are color-coded by atom-type, of which Tyrosine369 and Tyrosine 382, located near the ligand binding pocket, are highlighted in green for carbon and red for oxygen atoms, respectively.