

SI Guide: Myers *et al.* 'Structure of native lens connexin-46/50 intercellular channels by CryoEM'

Supplementary Table 1: Summary of molecular dynamics simulation setup and conditions for Cx50, Cx46, Cx26 and Cx46/50 heteromeric/heterotypic models. Asterisk indicate models that included modification by n-terminal acetylation. Connexin-26 models were derived from PDB 2ZW3¹⁰.

Supplementary Table 2: Local resolution assessment of a calculated map based on the Cx46 atomic model versus the 3.4 Å resolution CryoEM density map. Values indicated by each residue correspond to the range of resolutions (Å) reported for amino acid sidechain densities using BlocRes⁷⁰. Secondary structure and domain labels are indicated for the n-terminal helix (NTH), transmembrane helices (TM1-4) and extracellular domains (EC1-2) intracellular loop (ICL) and C-terminal domain (CTD).

Supplementary Table 3: Local resolution assessment of a calculated map based on the Cx50 atomic model versus the 3.4 Å resolution CryoEM density map. Values indicate by each residue correspond to the range of resolutions (Å) reported for amino acid sidechain densities using BlocRes⁷⁰. Secondary structure and domain labels are indicated for the n-terminal helix (NTH), transmembrane helices (TM1-4) and extracellular domains (EC1-2) intracellular loop (ICL) and C-terminal domain (CTD).