

Supplementary Figure S1: Evolutionary conservation of amino acids in human CRY2 protein as predicted by ConSurf tool. The colour code below shows the conservation scale which depicts the extent of conservation of each amino acid in hCRY2.



The conservation scale:

? 1 2 3 4 5 6 7 8 9

Variable Average Conserved

- e** - An exposed residue according to the neural-network algorithm.
- b** - A buried residue according to the neural-network algorithm.
- f** - A predicted functional residue (highly conserved and exposed).
- s** - A predicted structural residue (highly conserved and buried).
- *** - Insufficient data - the calculation for this site was performed on less than 10% of the sequences.