Supplementary Figure S1. Alignment of haem binding motifs 1 to 4 in the primary structures of NrfB and NrfH

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                        TM Helix in NrfH          --1--                       --2--
                        ________________________
NrfH_Dvul     MSEEKSRNGPARLKLVLGGATLGVVALATVAFG---MKYTDQR---PFCTSCHIMNPVGVTHKLSGHAN---------ISCNDCHAPHNLLAKLPFKAIAGARDVY
NrfB_Ecol     MSVLRSLLTAGVLASGLLWSLNGITATPAAQASDDRYEVTQQRNPDAACLDCHKPDTEGM-HGK--HASVINPNNKLPVTCTNCHGQPSPQHREGVKDVMRFNEP-
              **   *      *   *     *  *            * **     *  **     *   *     *        *  **           *
              ------------------------
              NrfB signal peptide                   --1--                       --2--

                              --3--                   --4--
NrfH_Dvul     MNTLGHPGDLILAGMETKEVVNANCKACHTMTNVEVASMEA-----KKYCTDCHRNVQHMRMKPISTREVADE*
NrfB_Ecol     --------------MYKVGEQNSVCMSCHLPEQLQKAFWPHDVHVTKVACASCH—-SLHPQQDTMQTLSDKGRIKICVDCHSDQRTNPNFNPASVPLLKEQP*
                           *  *  **                *  *  **    *
                              --3--                   --4--                   --5--
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Supplementary Figure S2. Model of the NrfA-NrfB ($\alpha_2\beta_2$) complex based on an alignment of NrfA and NrfB haems (red) with the haems of HAO oxidoreductase. The crystal structures of NrfA (PDB entry 1GU6) in green and NrfB (this study) in blue show that if a docking of the protein were to occur, movement of two NrfA surface α-helices would be necessary to allow NrfB to associate.