

SUPPORTING INFORMATIONStructure and Function of YghU, A *Nu*-class Glutathione TransferaseRelated to YfcG from *Escherichia coli*^{†,‡}Nina V. Stourman^{§,⊥}, Megan C. Branch[§], Matthew R. Schaab[§], Joel M. Harp[§], Jane E. Ladner^{||}, andRichard N. Armstrong^{§,*}

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CLUSTAL 2.0.12 multiple sequence alignment

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sp|P77526|YFCG_ECOLI          -----MIDLYFA 7
tr|Q4KED9|Q4KED9_PSEF5      -----MSDLSAFA-----VTQKWPAQFPEWIQLYSL 26
sp|Q46845|YGHU_ECOLI        MTDNTYQPAKVWTDKWSAGGAFANINRPVSGPTHEKTLFVKGKHPQLQLYSL 50
                               ::**

sp|P77526|YFCG_ECOLI        PTPNGHKITLFLEEA-----ELDYRLIKVDLGKGGQFRPEFLRISPNNK 51
tr|Q4KED9|Q4KED9_PSEF5      PTPNGVKVSIMLEEI-----GLPYEAHRVSFETQDQMTPEFLSVSPNNK 70
sp|Q46845|YGHU_ECOLI        GTPNGQKVTIMLEELLALGVTGAEYDAWLIRIGDGDQFSSGFVEVNPNSK 100
                               *** *:::***          *   : : .*: . *: :.***.*

sp|P77526|YFCG_ECOLI        IPAIVD-HSPADGGEPLSLFESGAILLYLAEKTGLFLSHETRERAATLQW 100
tr|Q4KED9|Q4KED9_PSEF5      IPAILDPHGPGD--QPLALFESGAILLYLADKSGQLLAQESAARYETIQW 118
sp|Q46845|YGHU_ECOLI        IPALRD-HTHNP---PIRVFESGSILLYLAEKFGYFLPQDLAKRTETMNW 146
                               ***: * *           *: :***:***:***:* * :*:: * *::*

sp|P77526|YFCG_ECOLI        LFWQVGLGPMLGQNHHFNHAAPQTIP--YAIERYQVETQRLYHVLNKRK 148
tr|Q4KED9|Q4KED9_PSEF5      LMFQMGIGGPMFGQVGFNFKFAGREYEDKRPLERYVNEAKRLLGVLDKHL 168
sp|Q46845|YGHU_ECOLI        LFWLQGAAPFLGGGFHFYHYAPVKIE--YAINRFTMEAKRLLDVLDKQL 194
                               *:: * . : * . * : *           .::*: *::** **::*

sp|P77526|YFCG_ECOLI        ENSPWLGGENYSIADIACWPVNAWT-----RQRIDLAMYPAVKNWHE 191
tr|Q4KED9|Q4KED9_PSEF5      GGREWIMGERYTIADIATFPWIRNLIG--FYEAGELVGIDNFPEVKRVL 216
sp|Q46845|YGHU_ECOLI        AQHKFVAGDEYTIADMAIWPWFVGNVVLGGVYDAAEFLDAGSYKHWQRWAK 244
                               :: *:.***:* :**          : : . : *:.

sp|P77526|YFCG_ECOLI        RIRSRPATGQALLKAQLG-----DERSDS----- 215
tr|Q4KED9|Q4KED9_PSEF5      KFVARPAVIRGLEIPKVS----- 234
sp|Q46845|YGHU_ECOLI        EVGERPAVKRGRIVNRTNGPLNEQLHERHDASDFETNTEDKRQG 288
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Figure S1: Sequence alignments between YfcG, YghU from *E. coli* and a similar enzyme from *Pseudomonas fluorescens*. The sequence identities of these proteins are between 38 and 42 %. The residues that are known to interact with GSH in the structures of YfcG and YghU are highlighted in red.