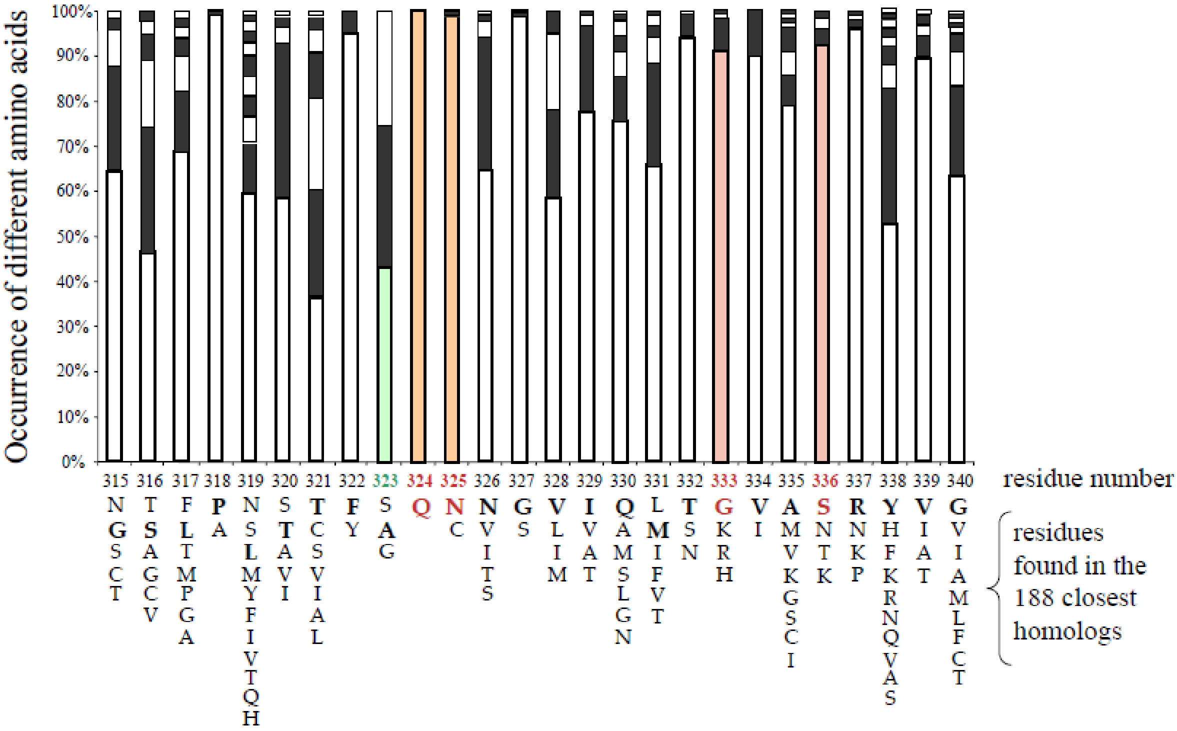
Supplemental Data

Table S3. Sequence deviations between homologues of YgfO (XanQ) at the NAT-motif region

Residues 315-340 (NAT motif and flanking TM9a and TM9b sequences)



ClustalW analysis (Larkin et al., 2007) was performed with the set of the 188 closest homologs of YgfO retrieved in the search presented in Table S2. Data from these sequence alignments, as well as from alignments between functionally known NAT homologs (Karena and Frillingos, 2009), are used in Figure 2. Raw data are presented in the table above: a histogram shows the number and relative abundance of different amino acids found at each position of the 188 closest homologues, with residues of YgfO shown in bold and corresponding variants listed in decreasing order of frequency. The positions of important residues analyzed in this study are highlighted in orange (Gln-324 and Asn-325), pink (Gly-333 and Ser-336), or green (Ala-323).

Reference used in Table S3

Larkin, M. A., Blackshields, G., Brown N. P., Chenna, R., McGettigan, P. A., McWilliam, H., Valentin, F., Wallace, I. M., Wilm, A., Lopez, R., Thompson, J. D., Gibson, T. J., and Higgins, D. G. (2007). *Bioinformatics* **23**, 2947-2948.

Karena, E., and Frillingos, S. (2009). *J. Biol. Chem.* **284**, 24257-24268.