



Supplementary Figure 1: sequence alignment of bacterial azoreductases.

Sequence alignment were carried out using ClustalW (Thompson, *et al.*, 1994) and the figure was generated using Bioedit version 7.0.9 (Hall, 1999). All Sequences were identified from a BLAST (Altschul, *et al.*, 1997) search based upon the sequence of paAzoR1 (GI:49079048). The identifiers for each of the sequences were as follows: *Pseudomonas fluorescens* (GI:77456797), *Plantomyces maris* (GI:149178908), *Pseudomonas mendocina* (GI:146308180), *Anabaena variabilis* (GI:75907285), *Marinobacter algicola* (GI:149377215) and *Variovorax paradoxus* (GI:239815888). The sequence identities for the azoreductases are as follows: *P. flu* 77.4%, *P. mar* 46.0%, *P. men* 43.1%, *A. var*

38.2% *M. alg* 37.7% and *V. par* 36.2%. Positions of identity among the six sequences are highlighted in red while Tyr131 is boxed in blue.

Numbering is based upon numbering in paAzoRI.

References

Altschul, S. F., Madden, T. L., Schaffer, A. A., Zhang, J., Zhang, Z., Miller, W. and Lipman, D. J. (1997). *Nucleic Acids Res.* 25, 3389-402.

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Thompson, J. D., Higgins, D. G. and Gibson, T. J. (1994). *Nucleic Acids Res.* 22, 4673-80.