

Table S2. Organisms with proposed homologues of both NExo and NApe.

The residue equivalent to His¹⁶⁷ in NExo in sequence alignments is shown for both enzymes, with the percentage identity to the more closely related enzyme.

Organism	NExo paralogue	% amino acid identity with NExo	His ¹⁶⁷ equiv.	NApe paralogue	% amino acid identity with NApe	His ¹⁶⁷ equiv.
Actinobacteria						
Corynebacterium diphtheriae	Q6NF54	35.9	H	Q6NIY3	36.8	G
<i>Corynebacterium efficiens</i>	Q8FMC8	36.6	H	Q8FRS0	35.7	G
<i>Corynebacterium glutamicum</i>	Q8NM39	36.6	H	Q6M7A1	35.6	G
<i>Corynebacterium jeikeium</i>	Q4JXP6	33.5	H	Q4JT19	35.0	G
<i>Leifsonia xyli</i> subsp. Xyli	Q6ACA2	37.6	H	Q6AGQ6	37.1	G
<i>Nocardia</i>	Q5YNT6	39.9	H	Q5Z1B5	45.4	G

farcinica

Streptomyces Q82LP4 38.5 H Q82H83 49.6 G
avermitilis

Streptomyces O86610 37.8 H Q9RKB3 49.2 G
coelicolor

Thermobifida Q47TC1 38.3 H Q47PP2 50.8 G
fusca YX

Betaproteobacteria

Azoarcus sp. Q5P7J4 53.3 H Q5P3W6 61.4 G
EbN1

Bordetella Q7WJJ8 50.0 L Q7WEU8 57.1 G
bronchiseptica

Bordetella Q7WAF5 50.0 L Q7W3H4 57.1 G
parapertussis

Bordetella Q7VWT3 50.0 L Q7VSN5 57.1 G
pertussis

Burkholderia Q62IW2 49.2 L Q62MR1 57.8 G

<i>mallei</i>						
<i>Burkholderia</i>	Q63SK5	49.2	L	Q63YJ6	57.8	G
<i>pseudomallei</i>						
<i>Chromobacteriu</i>	Q7NZP5	54.0	L	Q7NQ93	67.7	G
<i>m violaceum</i>						
<i>Dechloromonas</i>	Q479V4	48.6	L	Q47JU9	62.0	G
<i>aromatica</i> RCB						
<i>Neisseria</i>	Q5F6J3	95.7	H	Q5F5D5	98.8	G
<i>gonorrhoeae</i>						
<i>N. meningitidis</i>	Q9JSY0	96.9	H	Q9JR99	100.0	G
Z2491						
<i>N. meningitidis</i>	Q9K100	100.0	H	Q7DD47	100.0	G
MC58						
<i>Nitrosomonas</i>	Q820S9	51.0	L	Q820I5	56.1	G
<i>europaea</i>						
<i>Ralstonia</i>	Q8XZ13	47.2	L	Q8Y341	57.0	G
<i>solanacearum</i>						

Gammaproteobacteria

<i>L.pneumophila</i>	Q5WYQ1	46.9	L	Q5WYQ2	50.0	G
str. Lens						
<i>L.pneumophila</i>	Q5X7A2	46.9	L	Q5X7A3	50.0	G
str. Paris						
<i>L. pneumophila.</i>	Q5ZXT2	48.0	L	Q5ZXT3	49.2	G
Philadelphia 1						
<i>Methylococcus</i>	Q602J3	53.1	L	Q60BZ2	54.7	G
<i>capsulatus</i>						
<i>Pseudomonas</i>	Q9HWK9	42.4	L	Q51380	37.3	G
<i>aeruginosa</i>						
<i>Pseudomonas</i>	Q88JE2	40.1	L	Q88C91	35.3	G
<i>putida</i> KT2440						
<i>Xanthomonas</i>	Q8P3M5	52.0	L	Q8P470	48.9	G
<i>campestris</i> pv. <i>campestris</i>						
<i>Xanthomonas</i>	Q4UP49	52.0	L	Q4UPQ4	48.9	G
<i>campestris</i> pv. <i>campestris</i> str.						

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<i>Xanthomonas</i>	Q8PF17	51.6	L	Q8PFS6	48.5	G
<i>axonopodis</i> pv.						
<i>citri</i>						
<i>Xylella</i>	Q9PC52	49.2	L	Q9PGY2	47.0	G
<i>fastidiosa</i>						
<i>Xylella fastidiosa</i>	Q87D22	49.2	L	Q87F10	46.6	G
Temecula1						
<i>Xanthomonas</i>	Q5GU19	49.6	L	Q5H5K7	47.7	G
<i>oryzae</i> pv.						
<i>oryzae</i>						
