PqqE from *Methylobacterium extorquens* AM1: a radical *S*-adenosyl-L-methionine enzyme with an unusual tolerance to oxygen

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Supplementary Data

Supplementary method

Construction of phylogenetic tree of PqqE homologs

A total of 141 amino acid sequences retrieved from the list of PqqE homologs in the structure-function linkage database (*1*) were subjected to multiple sequence alignment with a MEGA6 software (*2*) using the MUSCLE algorithm (*3*), and the alignment obtained was used for phylogenetic analysis in MEGA6 with the maximum-likelihood method using 100 bootstrap replications for branch support estimations. Phylogenetic distances for construction of the tree were evaluated using the substitution model reported by Le and Gascuel (*4*).

Supplementary references

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Acetobacter pasteurianus WP_014457300
80
Acidomonas methanolica WP_042060868
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Gluconobacter oxydans WP_011252550
Asaia platycodi WP_023978291
Gluconacetobacter diazotrophicus ACI51738
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Komagataeibacter xylinus WP_025439861
Novosphingobium nitrogenifigens WP_008067199
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Acidiphilium sp. JA12-A1 WP_035185346
Afipia broomeae WP_006020165
Bradyrhizobium diazoefficiens NP_773379
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Devosia sp. DBB001 WP_035027785
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Rhodobacter sphaeroides ABA79967
Loktanella cinnabarina WP_021694927
Granulibacter bethesdensis WP_011632626
Skermanella stibiiresistens WP_037458490
Azospirillum brasilense WP_014240195
Caenispirillum salinarum EKV28655
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Frateuria aurantia AFC84780
Xanthomonas citri AJY87648
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Lysobacter capsici WP_036111894
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Aurantimonas manganoxydans WP_009208582
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Fulvimarina pelagi EAU41523
Methylobacterium extorquens AAB58898
Chromohalobacter salexigens WP_011506151
Lutibaculum baratangense WP_023431289
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Bejierinkia indica WP_012386226
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Methylocella silvestris WP_012590190
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Actibacterium atlanticum WP_035248557
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Phaeobacter gallaeciensis WP_024099184
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Citreicella sp. SE45 WP_008887353
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Pelagibaca bermudensis WP_007802649
Dinoroseobacter shibae WP_012177132
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Paracoccus denitrificans ABL70449
Agrobacterium radiobacter ACM29924
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Ensifer sp. BR816 WP_018237697
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Sinorhizobium meliloti WP_015243470
Nitrobacter winogradskyi ABA03955
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Methylocystis parvus WP_016920980
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Methylosinus trichosporium WP_003610945
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Azotobacter vinelandii WP_012702666
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Klebsiella pneumoniae WP_004184158
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Pantoea ananatis WP_013025734
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Burkholderia glumae AJY62622
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Cystobacter fuscus EPX59561
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Halomonas campaniensis WP_038478879
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Advenella kashmirensis ETF00427
Ralstonia pickettii WP_004633348
Limnobacter sp. MED105 WP_008251406
Comamonas badia WP_024539395
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Hydrogenophaga sp. T4 EWS64823
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Polaromonas naphthalenivorans ABM36048
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Azoarcus toluclasticus WP_018991052
Derxia gummosa WP_034410041
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Azohydromonas australica WP_028996321
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Rubrivivax gelatinosus WP_014430241
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Variovorax paradoxus WP_018904576
Leptothrix cholodnii ACB32523
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Sphaerotilus natans WP_037476957
Thiomonas arsenitoxydans WP_041608865
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Alteromonas macleodii WP_014999503
Colvellia psychrerythraea WP_011041706
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Arcobacter nitrofigilis WP_013136573
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Pseudogulbenkiania ferrooxidans WP_008955408
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Thauera aminoaromatica WP_004326941
Hydrogenobacter thermophiles WP_012963847
Methylacidiphilum infernorum V4 ACD83291
Chthoniobacter flavus WP_006979472
0.2

Supplementary Fig. S1 Molecular phylogenetic analysis by the maximum likelihood method. The phylogenetic tree constructed for 141 PqqE sequences with the highest log likelihood (–41230.3329) is shown. The percentage of trees in which the associated PqqE homologs clustered together is shown next to the branches. Initial tree(s) for the heuristic search was obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with a superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites [5 categories (+*G*, parameter = 1.2410)]. The tree was drawn to scale with branch lengths measured in the number of substitutions per site. All positions containing gaps and missing data were eliminated. There were total of 315 positions in the final dataset. The branch support values which are less than 50% are not shown. The 26 PqqEs selected for multiple sequence alignment are marked in yellow.