

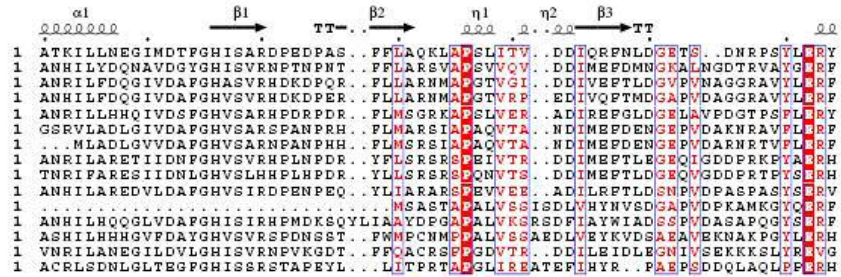
SUPPORTING INFORMATION

Supplemental Figure 1. Sequence alignment of proteins identified through BLAST to be similar to *M/HMPDdc*. Strictly conserved residues are highlighted in red while less strictly conserved residues are shown in red font. The secondary structure for HMPDdc is shown above the alignment.

Supplemental Figure 2. Sequence alignment of decarboxylase proteins identified through BLAST with HMPDdc and the aldolase submitted to BLAST. Strictly conserved residues are highlighted in red and less strictly conserved residues are shown in red font. The secondary structure of HMPDdc is shown above the alignment.

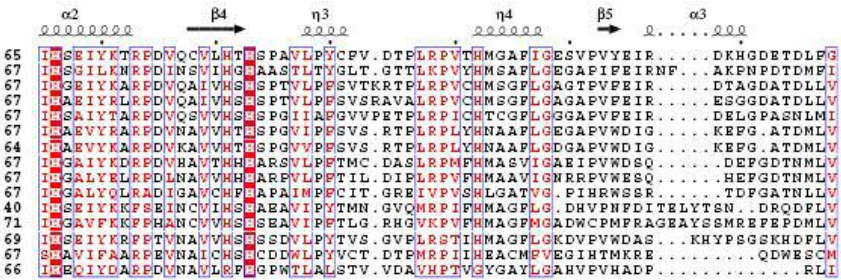
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aldolase/adducin [Polynucleobac
aldolase/adducin-like [Burkhold
aldolase/Pseudomonas entomophi
aldolase/adducin [Hypocmonas ne
aldolase/adducin [Bradyrhizobi
putative aldolase [Bradyrhizobi
possible ribulose-5-phosphate
N-methylhydantoinaseB/acetone
possible aldolase [Aurantimonas
hypBC1G 11697 [Botryotinia fuck
hypSNOG 06501 [Phaeosphaeria no
SNOG 00416 [Phaeosphaeria nodor
aldolase/adducin [Desulfitobact
aldolase/adducin [Nocardioide



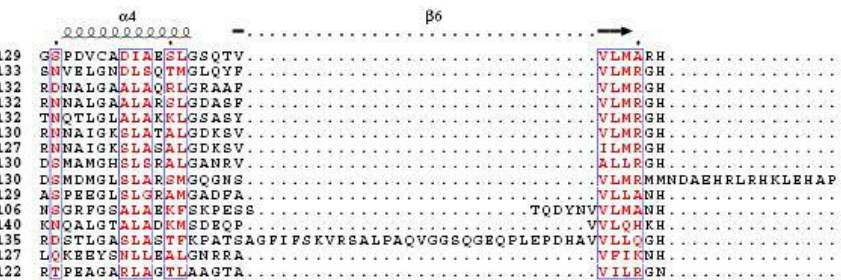
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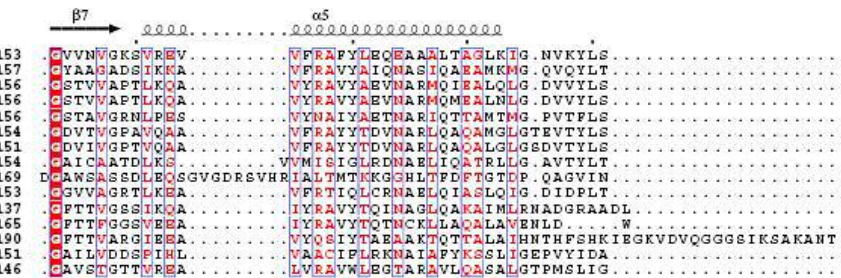
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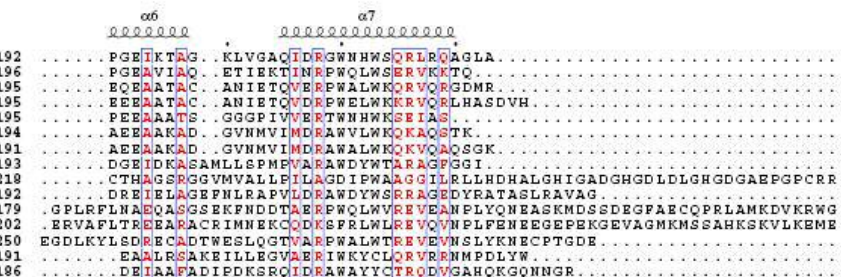
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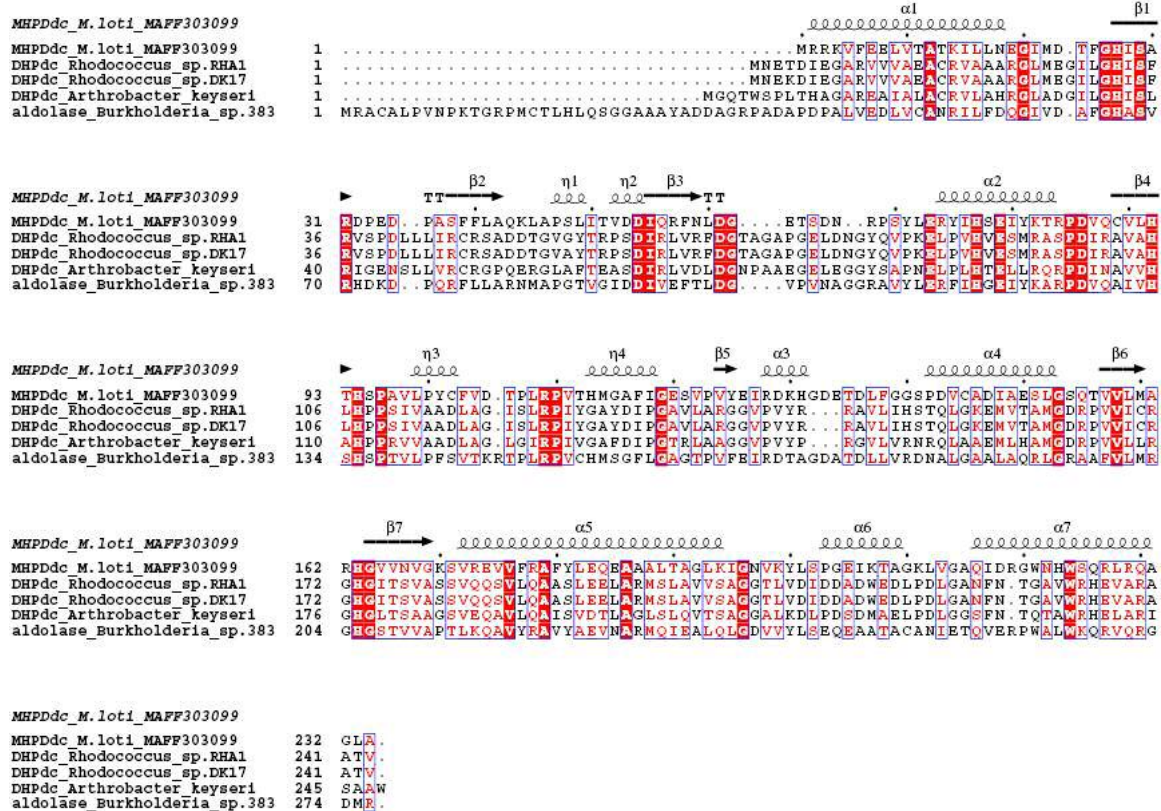


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Supplemental Figure 1



Supplemental Figure 2