

Molecular Pharmacology

Supplemental Information for:

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Substrate and inhibitor specificity of the *Plasmodium berghei* Equilibrative Nucleoside Transporter Type 1 (PbENT1)

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1      10      20      30      40      50      60
ATGAGTAAGA TTAAGGAATCA TC TTC TGGAA TTC TAGGC GCAAGTAA TAA CACAAACAAA
70      80      90      100     110     120
GAGTCCAGCCAGAAATC TGCCAGATCAAT TGC TTTACCAA TGACC TACGC TTTAATCGGT
130     140     150     160     170     180
GTTAGCTGCC TGAATGTAT TGGAACTCAGCAC TTGGTTTGAAATA TCAAGA TCAC TTACAAC
190     200     210     220     230     240
ATCTTTCAAATGGCTGGTC TGTAAACATC TTC TGTTC TAGCAC TATTTG TTAATTACCC T
250     260     270     280     290     300
CGTGTGTTG TTGCC TACATCCC TTGGTGTCTTACC TTGTTATGTGCTGGATTTCAAAT T
310     320     330     340     350     360
GCGCATCAGACATTC TCCGATTC TGCATTCGATACTTAT TGT TTTGGCTGCCTTTATAAC A
370     380     390     400     410     420
ATCGGTC TGA TGGCTGGAA TTGCCCAAACAATTGCC TTTGCCA TTGGTAC TACTAAAGAG
430     440     450     460     470     480
TCTAATA TGTCTGGGTA TATTTCCGCTGGTATCGGCATG TCTGGAGTTC TAAATCTCTGC
490     500     510     520     530     540
ATAAACC TCA TACTAGACTACAT TGT TTTCTGATGAGAAGA TCTACGAAA TCAA TAAGTC T
550     560     570     580     590     600
AAAC TAT TGTGCTTGTTC TCAATCAGCGAAA TCTTTCTAA TCA TTACAA TCGTC TGT TGC
610     620     630     640     650     660
GTC TTATAC A TTGATCTCT TTTCCAAAGAA TGACAACAACA AAGACTCAACAGATA TAGAG
670     680     690     700     710     720
AAAGCTGAAGAGAAGGAAGGAAGATTGCC A TTGATTGAAA TTA TCAAAGA TGGTTACAAA
730     740     750     760     770     780
GCAATAC TTTCTATCT TTTCTCGTAAAC TGGTTGTCA TTACAAC TCTTTCTGGAA TAGGC
790     800     810     820     830     840
CATAAGAAA TGGCAAGAGAAACACGGTATGACAGACAATAATGTTACTA TTATAGTAGGC
850     860     870     880     890     900
ATGTTTCAAGTATTCGACTTTATCTCAAGA TACCCACCAAATTTACCCACATCAAGATC
910     920     930     940     950     960
TTTAAGTACTTTACTTTTCA GTTTGAA TACC TTACTGATCGGTAAC TTTCTAAGGCTGTTA
970     980     990     1,000  1,010  1,020
TTCA TCCCA TGGTTTGTACTGAA TGCAGTGA TTAGTTCC TCA TTTCTTACGAA TATAGTG
1,030  1,040  1,050  1,060  1,070  1,080
CAACAATGTG TCTGTATTGCTGCAC TCGCTTTTCACTAATGGGTGGTTTAA TACTGTACCA
1,090  1,100  1,110  1,120  1,130  1,140
TTCA TTGTC TTTGTTAAGGAAC TCAAGAAAGTGA AACATCAGAAAGATA TTGAAACTATA
1,150  1,160  1,170  1,180  1,190  1,200
TCTAGAA TTA TGGTCGTTTCA TTGTTCTTTGGCTTATTC TTTGGCATGTTGACAACA TGT
1,210  1,220  1,230  1,240  1,250  1,260
TTATATGAT TACTTTTCAA TTGGGATCTTGAATAACTACC TTTATGATGTTCC TGATTA T
1,269
GCGTAA TGA

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Supplemental Fig. 2. Nucleotide sequence for *pbent1-HA-CO*, codon-optimized for *S. cerevisiae*. Nucleotide sequence designed by DNA2.0 (Newark, CA) software

<https://www.dna20.com/>