Supplementary Information A1

Sequence Similarity of PurR from *E. faecalis*, *B. subtilis* and *L. lactis*

Score	Expect	Method	Identities	Positives	Gaps
329 bits(843)	5e-117	Compositional matrix adjust.	149/270(55%)	211/270(78%)	0/270(0%)

```
E.fa    MKIRRSERLIDMTQYLLDHPHTLVSLTYFADRYQSAKSSISEDLAIVKKTFKERGTGILE    60
        MK RRS RL+D+T YLL HPH L+ LT+F++RY+SAKSSISEDL I+K+TF+++G G L
B.sub   MKFRRSGRLVDLTNYLLTHPHELIPLTFFSERYESAKSSISEDLTIIKQTFEQQGIGTLL    60

E.fa    TIPGAAGGVRFIPEIPYEEAEQLIMDLCDRLSEQDRLLPGGYVYLSDLLGEPNLLRQVGR    120
        T+PGAAGGV++IP++   EAE+ + L   L+ +R+LPGGYVYL+D+LG+P++L +VG+
B.sub   TVPGAAGGVKYIPKMKQAEAEEFVQTLGQSLANPERILPGGYVYLTDILGKPSVLSKVGK    120

E.fa    IIASKYLGKQIDAVMTVATKGVPIAQAVSYYLNVPFVIVRRDSKITEGSTVSVNYVSGSS    180
        + AS +   ++ID VMTVATKG+P+A A + YLNVP VIVR+D+K+TEGSTVS+NYVSGSS
B.sub   LFASVFAEREIDVVMTVATKGIPLAYAAASYLNVPVVIVRKDNKVTEGSTVSINYVSGSS    180

E.fa    ERIEKMELSKRSLKRGSKVLVVDDFMKGGGTVNGMKSMIEEFEAELVGITVFAESKFNGR    240
         RI+ M L+KRS+K GS VL++DDFMK GGT+NGM ++++EF A + GI V  E++
B.sub   NRIQTMSLAKRSMKTGSNVLIIDDFMKAGGTINGMINLLDEFNANVAGIGVLVEAEGVDE    240

E.fa    RAIDDYTSLLYVEDVDTQTKTISVVPGNYF    270
        R +D+Y SLL + ++ + K+I +  GN+
B.sub   RLVDEYMSLLTLSTINMKEKSIEIQNGNFL    270
```

Score	Expect	Method	Identities	Positives	Gaps
318 bits(814)	9e-113	Compositional matrix adjust.	144/271(53%)	205/271(75%)	0/271(0%)

```
E.fa    IRRSERLIDMTQYLLDHPHTLVSLTYFADRYQSAKSSISEDLAIVKKTFKERGTGILETI    62
        ++R+ERL+D T +L++HP+ +++L   + Y+ AKSSISEDL +K+ F+ +G G++ET
L.lac   MKRNERLVDFTNFLINHPNQMLNLNELSKHYEVAKSSISEDLVFIKRVFENQGVGLVETF    60

E.fa    PGAAGGVRFIPEIPYEEAEQLIMDLCDRLSEQDRLLPGGYVYLSDLLGEPNLLRQVGRII    122
        PG+ GGVRF P I  E + ++  ++ + L E++R+LPGGY+YLSD+LG P+ LR++G+II
L.lac   PGSLGGVRFTPYITDERSLEMSQEIAELLREENRILPGGYIYLSDILGTPSNLRKIGQII    120

E.fa    ASKYLGKQIDAVMTVATKGVPIAQAVSYYLNVPFVIVRRDSKITEGSTVSVNYVSGSSER    182
        A +Y  KQ+D VMT+ATKG+PIAQ+V+  L+VPFVIVRRD K+TEG+T++VNY+SGSS R
L.lac   AHEYHEKQVDVVMTIATKGIPIAQSVAEILDVPFVIVRRDPKVTEGATLNVNYMSGSSSR    180

E.fa    IEKMELSKRSLKRGSKVLVVDDFMKGGGTVNGMKSMIEEFEAELVGITVFAESKFNGRRA    242
        +E M LSKRSL  G  VL+VDDFMKG GT+NGM+S++  EF+  L G+ VF E  F G R
L.lac   VENMTLSKRSLSIGQNVLIVDDFMKGAGTINGMRSLVHEFDCLLAGVAVFLEGPFKGERL    240

E.fa    IDDYTSLLYVEDVDTQTKTISVVPGNYFTEK    273
        IDDY S+L V+ +D   ++I V  GN F +K
L.lac   IDDYKSILKVDRIDIANRSIDVQLGNIFNDK    271
```

The pairwise sequence alignments were performed on the NCBI webserver with the blastp suite (http://blast.ncbi.nlm.nih.gov/Blast.cgi). All settings were kept as default.

Supplementary Information A2

The *glyA* gene of *Enterococcus faecalis* V583 represented starting 200 bp upstream of the start codon.

```
>gi|29374661:c2465545-2464007 Enterococcus faecalis V583 chromosome,
complete genome
AGTGATGAACAGGCAGCACAACTAGATACAGAAAATGCGTTTGTTTATTCTTATGGTGCAGAAACGGTTG
AAAATGCCACAAAAGAACTATTTGCAGGGTTAAGAGCGTTAGATGAGCAAGGAGCTACCACGATTTTTGC
GCAAGGATTTGCAGAAACTGGTTTAGGCACTGCTTACATGAATCGCTTGAAAAAATCAGCCAATCAAAAA
TTTTTTGAAAAATAAGAGGTAT TTGTAA CGAAGCTGACACAGAAGTA TGATACAAT CAGACAAAAGAAAA
CAAAATGGAGTGTTGTTTGA ATG GATTACAAAACGTATGACCCAGATTTATGGAATGCAATTGCAAGAGA
AGAAGAGCGCCAAGAAAATAACTTGGAACTAATCGCATCTGAGAATGTCGTGTCAAAAGCAGTTATGGCT
GCCCAAGGAAGTATTTTAACGAATAAATACGCAGAAGGTTACCCTGGCAAACGGTACTATGGTGGTTGTG
AATTTATCGATATCGTAGAAAATTTAGCTATCGATCGTGCCAAAGAATTATTTGGTGCAAAATTCGCGAA
TGTACAAGCCCATTCAGGTTCTCAAGCCAATACAGCGGCATACCTTTCATTGGTTGAACCAGGTGATACC
ATTTTGGGGATGGATTTATCAGCTGGTGGTCACTTAACACATGGTTCGCCCGTTAACTTTAGTGGAAAAA
CCTATAATTTTGTCAGTTATGGAGTGGATCCTTCAACAGAAGTAATCGATTACGATGTCGTGCGAATTTT
AGCAAGAGAACATCGTCCAAAACTAATCGTTGCAGGCGCAAGTGCGTATTCACGAACGATTGACTTCAAA
CGTTTCCGTGAAATCGCTGATGAAGTAGATGCCAAGTTAATGGTTGATATGGCGCATATTGCAGGCTTGG
TAGCTTCAGGGTTGCACCCAAATCCAGTTCCGTATGCTGATATCGTAACAAGTACGACCCATAAAACATT
GCGTGGTCCTCGTGGCGGTTTAATTTTGACAAATAGCGAAGAATTGGCGAAAAAAGTAAATAGTAGTATT
TTCCCAGGCATTCAAGGTGGCCCATTGGAACATGTGATTGCCGGAAAAGCCGCAGCTTTTAAAGAAGCAT
TGGATCCAAGTTTTGCTGAATATAGTCAGCAAGTGATTGCAAATGCGCAAGCGATGACGAAAGTTTTCAA
TCAAGCGCCAGAAGCTCGTTTAATTAGTGGGGCAACAGATAACCACTTATTACTGATTGAAGTGACAGGT
TTTGGTTTAAATGGAAAAGAAGCAGAAGCTATTTTAGATAGTGTAAATATTACTGTCAATAAAAATTCAA
TTCCGTTTGAACAATTAAGTCCATTTAAAACAAGTGGTATCCGTATTGGAACGCCTGCAATTACTTCACG
TGGTTTTAAAGAAGAAGATGCGGTAGAAGTTGCTAAATTAATCGTTCAAGTCTTAAAAGATCCAGAAAAT
ACAGCAGTTCATGATGAAGTCAAAGCAGCTGTAGCAGCGCTAACTAAAAAATATCCATTATATAACTAA
```

The start codon of the *glyA* (NC_004668.1) is highlighted in blue and the -10 and -35 elements in the promotor region in green respectively.

The -10 and -35 elements were both predicted with the programs "BPROM" (http://linux1.softberry.com/) and "PromoterHunter" (http://phisite.org/main/index.php?nav=tools&nav_sel=hunter).

The consensus PurR binding motif in *L. lactis*:   5'AWWWCCGAACWWT 3' (W=A or T)

Double binding motif at reasonable distance from the -10 element:

```
consensus motif:                        TWWCAAGCCWWWA
glyA double strand:  5'  TGAATCGCTTGAAAAAATCAGCCAATCAAAAA  3'
                     3'  ACTTAGCGAACTTTTTTAGTCGGTTAGTTTTT  5'
consensus motif:          AWWWCCGAACWWT
```

Overlapping with the -35 element:

```
glyA:          5' TGTAA CGAAGCTG 3'   →   3' TGTAA CGAAGCTGACA 5'
consensus motif:  5'AWWWCCGAACWWT 3'        3'TWWCAAGCCWWWA 5'
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