

Supplementary Information for

**Sucrose phosphorylase and related enzymes in glycoside hydrolase family 13:
discovery, application and engineering**

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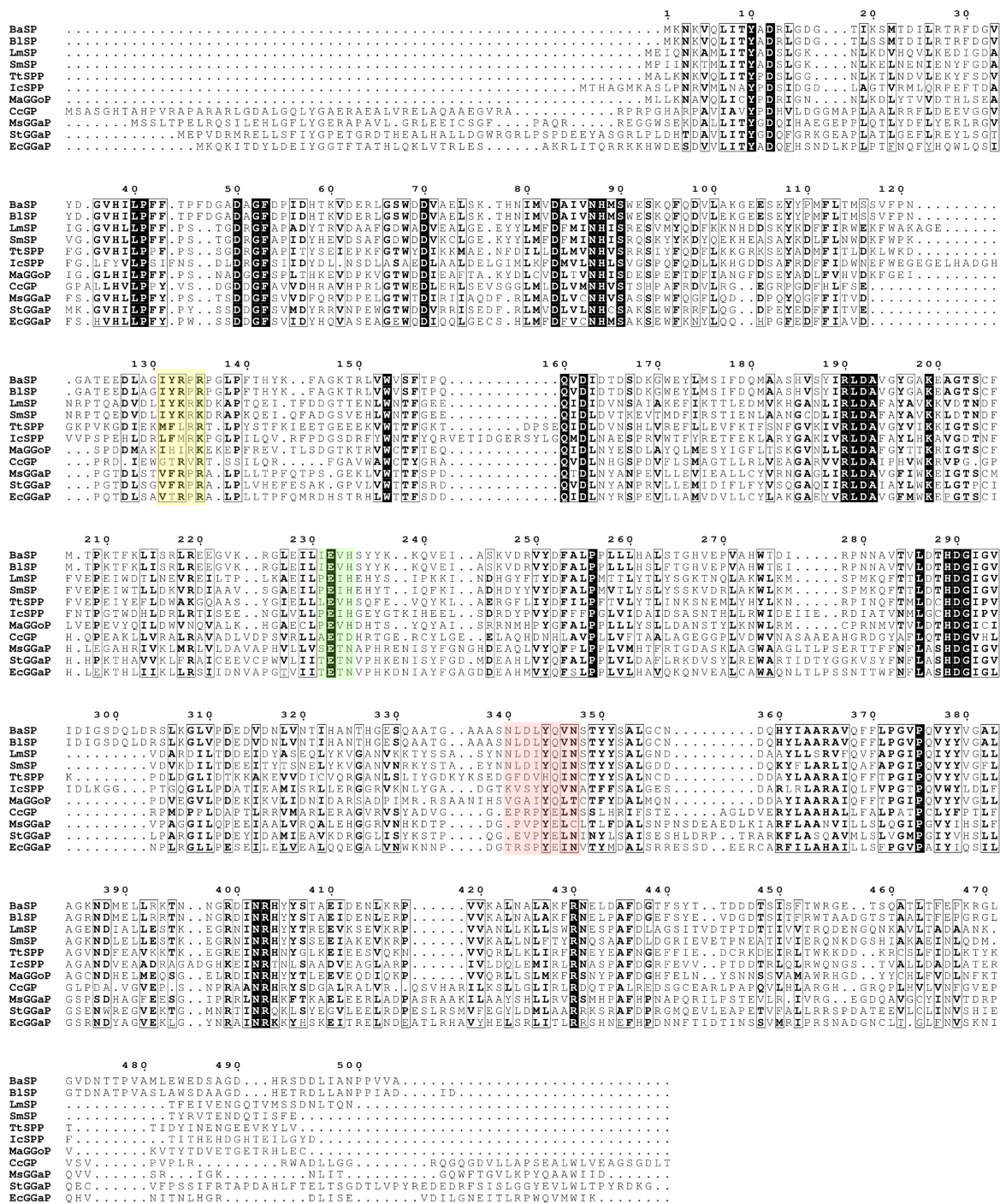


Figure S1 Multiple sequence alignment of characterised enzymes in subfamily GH13_18 (BaSP: *Bifidobacterium adolescentis* SP; B1SP: *B. longum* SP; LmSP: *Leuconostoc mesenteroides* SP; SmSP: *Streptococcus mutans* SP; TtSPP: *Thermoanaerobacterium thermosaccharolyticum* SPP; IcSPP: *Ilumatobacter coccineus* SPP; MaGGaP: *Marinobacter adhaerens* GGoP; CcGP: *Coralloccoccus coralloides* glycoside phosphorylase; MsGGaP: *Meiothermus silvanus* GGoP; StGGaP: *Spirochaeta thermophila* GGoP; EcGGaP: *Escherichia coli* GGoP). The alignment was visualised using ESPript 3.0 (<http://escript.ibcp.fr>). Important acceptor site loops were highlighted in yellow (loop B), green (catalytic acid/base residue loop) and red (loop A).