



WSM597



IPR011765: Pept_M16_N
PF00675: Insulinase (Peptidase family M16)

IPR007863: Peptidase_M16_C
PF05193: Peptidase M16 inactive domain

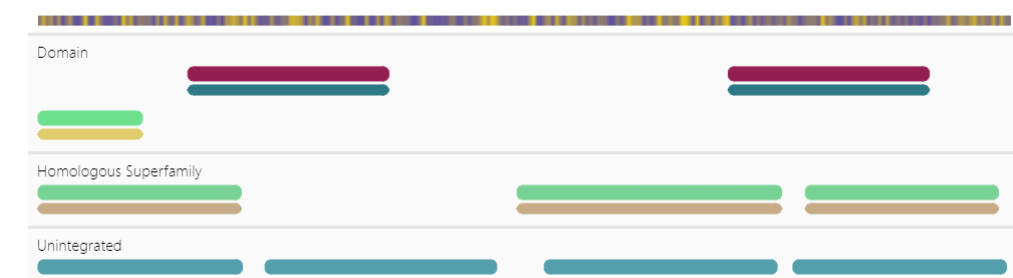
IPR011249: Metalloenz_LuxS/M16
SSF63411: LuxS/MPP-like metallohydrolase

IPR001431: Pept_M16_Zn_BS
PS00143: Insulinase family, Zinc-binding region si

PTHR43690: NARDILYSIN
G3DSA:3.30.830.10:



U268_1



IPR007863: Peptidase_M16_C
PF05193: Peptidase M16 inactive domain

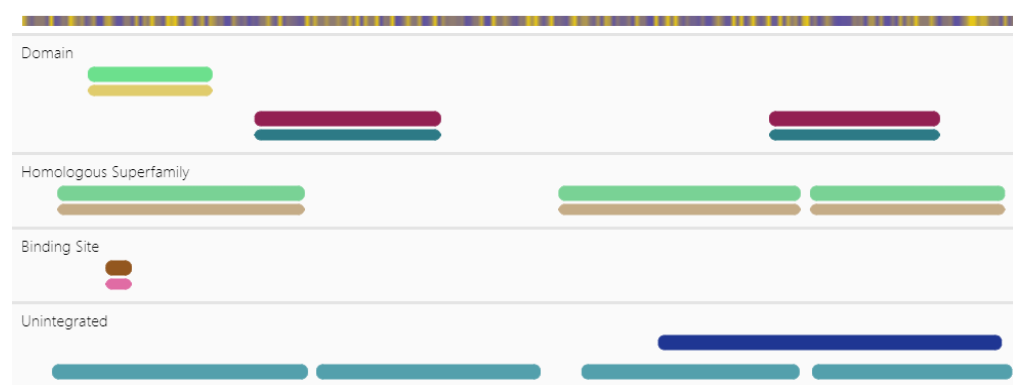
IPR011765: Pept_M16_N
PF00675: Insulinase (Peptidase family M16)

IPR011249: Metalloenz_LuxS/M16
SSF63411: LuxS/MPP-like metallohydrolase

G3DSA:3.30.830.10:



U268_2



IPR011765: Pept_M16_N
PF00675: Insulinase (Peptidase family M16)

IPR007863: Peptidase_M16_C
PF05193: Peptidase M16 inactive domain

IPR011249: Metalloenz_LuxS/M16
SSF63411: LuxS/MPP-like metallohydrolase

IPR001431: Pept_M16_Zn_BS
PS00143: Insulinase family, Zinc-binding region s

PTHR43690: NARDILYSIN
G3DSA:3.30.830.10:

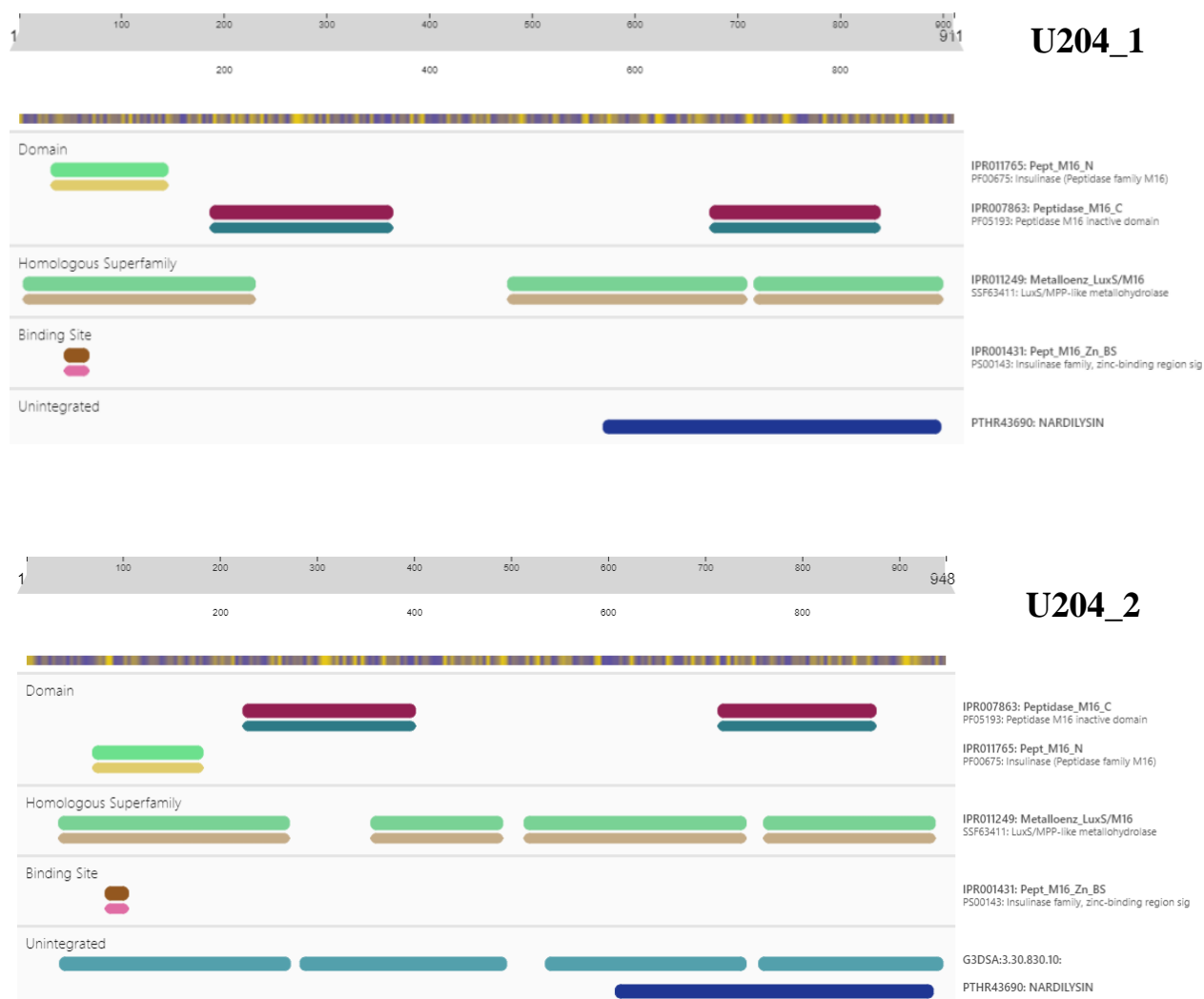


Figure S5. Graphical view of The InterPro search and protein classification of M16 peptidase sequences found in the genome of strains U268, U204 and WSM 597 using InterPro database. The InterPro entry was the aminoacidic sequence for the putative M16 peptidases. In the graphical view, matches to the InterPro databases and the relevant positions of these matches on the query sequence are displayed.