

A

DNase_B	MNLLGSRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKY	60
GP_01207	MNLLGSRVFSKKCRLVKFSMVALVSATMAVTTVTLENTALARQTQVSNDVVLNDGASKY	60

DNase_B	LNEALAWTFNDSPNYKTLGTSQITPALFPKAGDILYSKLDLGRTTARGTLTYANVEG	120
GP_01207	LNEALAWTFNDSPNYKTLGTSQITPALFPKAGDILYSKLDLGRTTARGTLTYANVEG	120

DNase_B	SYGVRQSFQKQNPAGWTGNPNHVKYIEWNLGLSYVGFWNRSHLIADSLGGDALRVNA	180
GP_01207	SYGVRQSFQKQNPAGWTGNPNHVKYIEWNLGLSYVGFWNRSHLIADSLGGDALRVNA	180

DNase_B	VTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYEAAPIYNADELIPRAVVSMQ	240
GP_01207	VTGTRTQNVGGRDQKGGMRYTEQRAQEWLEANRDGYLYEVAPIYNADELIPRAVVSMQ	240

DNase_B	SSDNTINEKVLVYNTANGYTINYHNGTPTQK	271
GP_01207	SSDNTINEKVLVYNTANGYTINYHNGTPTQK	271

B

SpdB	MKLSKQKASLLTAVLLLLSLSITTTITVDAARVRTYPNVSHANTHYKNTVSSKLLPFTANY	60
GP_01309	MKLSKQKASLLTAVLLLLSLSITTTITVDAAKVRTYPNVSHANTHYKNTASSKLLPFTANY	60

SpdB	QLQLGELDNLRATFSHIQLQDRHETKDVRTKINYDPVGVHNYQFPYGDGSKSSWVMNRG	120
GP_01309	QLQLGELDNLRATFSHIQLQDRHETKDVRTKINYDPVGVHNYQFPYGDGSKSSWVMNRG	120

SpdB	HLVGYQFCGLNDEPRNLVAMTAWLNTGAYSGANDSNPEGMLYYENRLDSWLALHPDFWLD	180
GP_01309	HLVGYQFCGLNDEPRNLVTMTAWLNTGAYSGANDSNPEGMLYYENRLDSWLALHPDFWLD	180

SpdB	YKVTPIYSGNEVVPRIELQYVGIDSSGELLTIRLNSNKESIDENGVTTVILENSAPNIN	240
GP_01309	YKVTPIYSGNEVVPRIELQYVGIDSSGELLTIRLNSNKESIDENGVTTVILENSAPNIN	240

SpdB	LDYLNGTATPKN	252
GP_01309	LDYLNGTATPKN	252

Figure S3. Alignments of DNase B (SpeF) and SpdB with amino acid sequences in proteome encoded by M3.11 genomic DNA. Alignment of amino acid sequence of DNase B (NCBI Reference Sequence: WP_010922721.1) with GP_01207 (amino acid sequence from GAS M3.11 proteome) A); and SpdB (NCBI Reference Sequence: WP_002985324.1) with GP_01309 (amino acid sequence from GAS M3.11 proteome) (B) by Clustal Omega (<https://www.ebi.ac.uk/Tools/msa/clustalo/>). Amino acid color

code obtained from Clustal Omega is as follows: red, small; blue, acidic; magenta, basic; green, hydroxyl or sulfhydryl or amine.