

Supplementary Information

Identification and Characterization of New Proteins Crucial for Bacterial Spore Resistance and Germination

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Supplementary Table S1 Average parameters of the germination of multiple individual wt and *yetF* spores

Spores	PS832		PS4488	
	Valine	AGFK	Valine	AGFK
T_{lag}	20.3 ± 8.9	36.5 ± 16.6	44.6 ± 23.1	49.0 ± 20.5
$T_{release}$	24.0 ± 9.4	40.3 ± 16.9	48.2 ± 23.0	53.8 ± 20.9
T_{lys}	34.7 ± 9.2	52.0 ± 16.7	63.6 ± 17.6	74.5 ± 11.5
$\Delta T_{release}$	3.7 ± 1.4	3.8 ± 1.1	3.6 ± 1.2	4.8 ± 1.6
ΔT_{lys}	10.7 ± 2.8	11.7 ± 4.7	15.4 ± 8.0	20.7 ± 11.5
I_{lag}	0.88 ± 0.07	0.83 ± 0.06	0.77 ± 0.07	0.76 ± 0.09
$I_{release}$	0.21 ± 0.05	0.29 ± 0.07	0.29 ± 0.07	0.23 ± 0.07
ger/num†	97/139	80/104	44/133	14/40

Spores were germinated and individual germination parameters were measured as described in Methods. †Number of spores that germinated/number of spores examined.

Supplementary Table S2 Homologs of *B. subtilis yetF* or *2Duf* in completed genomes of *Bacilli*.

<i>Bacilli</i> spore forming species	Number of homologs to		Asporogenous <i>Bacilli</i> species	Number of homologs to	
	<i>yetF</i>	<i>2duf</i>		<i>yetF</i>	<i>2duf</i>
<i>Aeribacillus pallidus</i>	1	1	<i>Aerococcaceae bacterium</i>	1	0
<i>Alicyclobacillus acidocaldarius</i>	0	1	<i>Auricoccus indicus</i>	1	0
<i>Amphibacillus xylanus</i>	2	0	<i>Brochothrix thermosphacta</i>	1	0
<i>Aneurinibacillus soli</i>	0	1	<i>Carnobacterium maltaromaticum</i>	1	0
<i>Anoxyacillus flavithermus</i>	2	1	<i>Enterococcus faecalis</i>	1	0
<i>Bacillus amyloliquefaciens</i>	1	0	<i>Gemella haemolysans</i>	1	0
<i>Bacillus anthracis</i>	3	1	<i>Jeotgalibaca dankookensis</i>	2	0
<i>Bacillus atrophaeus</i>	1	0	<i>Lactobacillus acidophilus</i>	1	0
<i>Bacillus cereus</i>	5	1	<i>Lactobacillus plantarum</i>	1	0
<i>Bacillus firmus</i>	1	0	<i>Lactobacillus reuteri_</i>	1	0
<i>Bacillus halodurans</i>	8	2	<i>Lactobacillus rhamnosus</i>	1	0
<i>Bacillus licheniformis</i>	6	0	<i>Lactococcus lactis</i>	1	0
<i>Bacillus megaterium</i>	1	0	<i>Leuconostoc kimchii</i>	1	0
<i>Bacillus pumilus</i>	1	0	<i>Marinilactibacillus 15R</i>	1	0
<i>Bacillus subtilis</i>	5	0	<i>Melissococcus plutonius</i>	1	0
<i>Bacillus thuringiensis</i>	5	1	<i>Planococcus antarcticus</i>	1	0
<i>Bacillus weihenstephanensis</i>	1	0	<i>Salimicrobium jeotgali</i>	1	0
<i>Brevibacillus brevis</i>	4	1	<i>Salinicoccus halodurans</i>	2	0
<i>Cohnella candidum</i>	5	1	<i>Streptococcus mutans GS-5</i>	1	0
<i>Fictibacillus phosphorivorans</i>	6	0	<i>Streptococcus pneumoniae</i>	1	0
<i>Geobacillus kaustophilus</i>	0	1	<i>Vagococcus penaei</i>	1	0
<i>Geobacillus stearothermophilus</i>	1	0			
<i>Halobacillus halophilus</i>	6	1			
<i>Kyrpidia tusciae</i>	0	2			
<i>Laceyella sacchari</i>	1	1			
<i>Lentibacillus amyloliquefaciens</i>	3	1			
<i>Lysinibacillus sphaericus</i>	4	0			
<i>Novibacillus thermophilus</i>	3	0			
<i>Oceanobacillus iheyensis</i>	2	1			
<i>Paenibacillus polymyxa</i>	2	1			
<i>Paenisporosarcina cavernae</i>	3	0			
<i>Parageobacillus thermoglucosidasius</i>	1	1			
<i>Paraliobacillus zengyii</i>	8	0			
<i>Solibacillus silvestris</i>	4	0			
<i>Sporolactobacillus terrae</i>	5	0			
<i>Sporosarcina psychrophila</i>	3	0			
<i>Terribacillus goriensis</i>	4	0			
<i>Thermobacillus composti</i>	2	0			
<i>Virgibacillus halodenitrificans</i>	3	2			
Average number in ones with ≥ 1	3.2	1	Average number per species	1.1	0

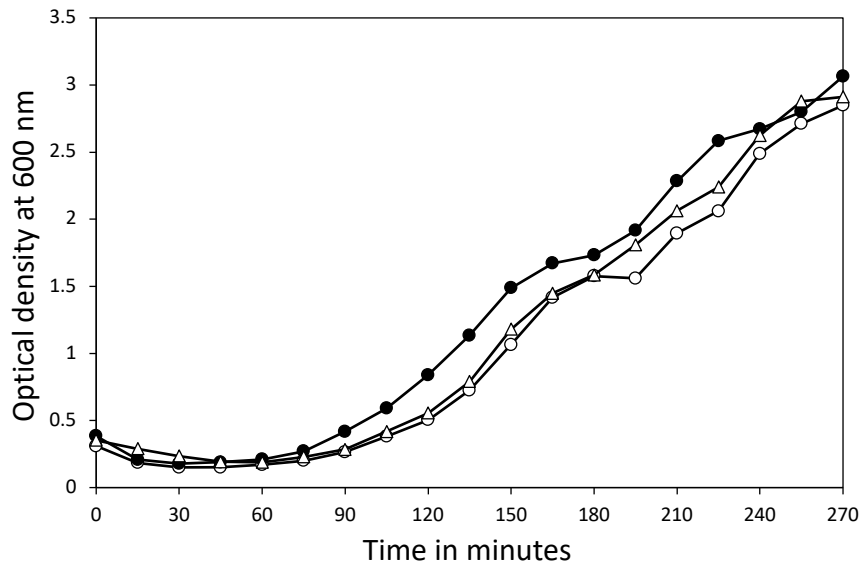
Supplementary Table S3 Homologs of *B. subtilis* yetF/2Duf in *Clostridia* genomes.

<i>Clostridia</i> spore formers	Number of homologs to		Likely <i>Clostridia</i> spore formers (have <i>gpr</i> , <i>spoVFA</i> , <i>spoVFB</i>)	Number of homologs to	
	<i>yetF</i>	<i>2duf</i>		<i>yetF</i>	<i>2duf</i>
<i>Alkaliphilus metalliredigens</i>	3	1	<i>Acetohalobium arabaticum</i>	5	0
<i>Ammonifex degensii</i>	2	0	<i>Anoxybacter fermentans</i>	2	0
<i>Caldanaerobacter subterraneus</i>	1	0	<i>Caldicellulosiruptor saccharolyticus</i>	1	0
<i>Candidatus Arthromitus</i> sp. <i>SFB-mouse</i>	1	0	<i>Carboxydocella thermautotrophica</i>	2	0
<i>Candidatus Desulforudis audaxviator</i>	1	0	<i>Ethanoligenens harbinense</i>	4	0
<i>Caproiciproducens</i> sp. <i>NJN-50</i>	2	0	<i>Faecalibacterium prausnitzii</i>	1	0
<i>Cellulosilyticum lentocellum</i>	1	0	<i>Flavonifractor plautii</i>	1	0
<i>Clostridioides difficile</i> _	1	0	<i>Halobacteroides halobius</i>	6	0
<i>Clostridium acetobutylicum</i>	5	0	<i>Halocella</i> sp. <i>SP3-1</i>	5	0
<i>Clostridium botulinum</i>	2	0	<i>Halothermothrix orenii</i>	6	0
<i>Clostridium perfringens</i>	1	0	<i>Herbinix luporum</i>	2	0
<i>Clostridium tetani</i>	2	0	<i>Natranaerobius thermophilus</i>	2	0
<i>Dehalobacterium formicoaceticum</i>	1	1	<i>Pelotomaculum thermopropionicum</i>	2	0
<i>Desulfallas gibsoniae</i>	2	1	<i>Ruminococcus albus</i>	1	0
<i>Desulfitobacterium hafniense</i>	3	0	<i>Syntrophomonas wolfei</i>	3	0
<i>Desulfofarcimen acetoxidans</i>	3	0	<i>Syntrophothermus lipocalidus</i>	2	0
<i>Desulfofundulus kuznetsovii</i>	2	0	<i>Thermincola potens</i>	3	0
<i>Desulfosporosinus orientis</i>	2	1	Average number in ones with ≥ 1	2.8	0
<i>Desulfotomaculum ruminis</i>	3	1			
<i>Hungateiclostridium thermocellum</i>	1	0	<i>Asporogenous Clostridia species</i>		
<i>Intestinimonas butyriciproducens</i>	1	0	<i>Aminipila</i> sp. <i>JN-39</i>	1	0
<i>Lachnoanaerobaculum umeaense</i>	2	0	<i>Carboxydotherrmus hydrogenoformans</i>	1	0
<i>Lachnoclostridium phytofermentans</i>	1	0	<i>Dehalobacter</i> sp. <i>CF</i>	1	0
<i>Mahella australiensis</i>	1	0	<i>Thermosediminibacter oceani</i>	1	0
<i>Moorella thermoacetica</i>	1	0	Average number per species	1	0
<i>Paeniclostridium sordellii</i>	2	0			
<i>Pseudoclostridium thermosuccinogenes</i>	1	1			
<i>Ruminiclostridium cellulolyticum</i>	3	0			
<i>Symbiobacterium thermophilum</i>	2	0			
<i>Syntrophobotulus glycolicus</i>	1	0			
<i>Tepidanaerobacter acetatoxydans</i>	1	0			
<i>Thermacetogenium phaeum</i>	2	0			
<i>Thermoanaerobacter italicus</i>	1	0			
<i>Thermoclostridium stercorarium</i>	1	0			
Average number in ones with ≥ 1	1.6	1			

Supplementary Table S4 Sequence identity between 2Duf homologs in *Bacilli* and *Clostridia* and 2Duf encoded in *spoVA*^{2mob}.

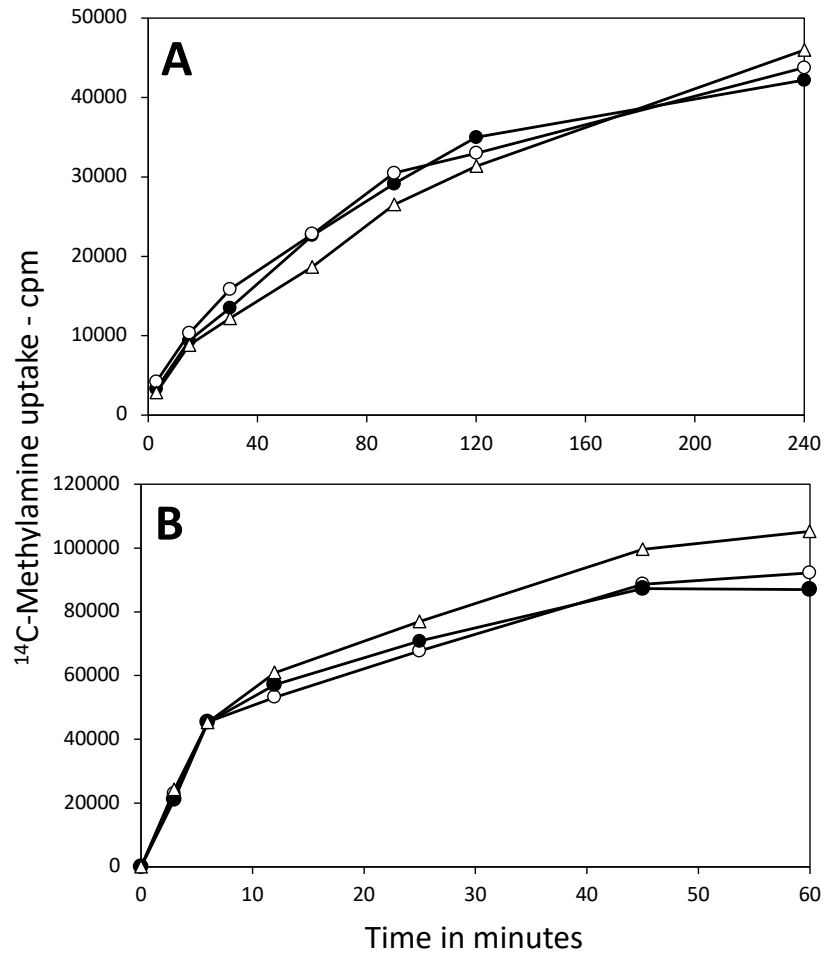
<i>Bacilli</i>	NCBI ID	Identity to 2Duf (%)
Group 1		
<i>Aeribacillus pallidus</i>	WP_066246610.1	55.2
<i>Aneurinibacillus soli</i>	WP_096463052.1	50.9
<i>Anoxyacillus flavithermus</i>	WP_012575624.	55.1
<i>Bacillus anthracis</i>	WP_000018934	59.1
<i>Bacillus cereus</i>	WP_000018922.1	60.5
<i>Bacillus halodurans</i>	WP_010897735.1	30.5
<i>Bacillus thuringiensis</i>	WP_000018924.1	60.8
<i>Brevibacillus brevis</i>	WP_015892354.1	52.4
<i>Cohnella candidum</i>	WP_123042938.1	53.1
<i>Geobacillus kaustophilus</i>	WP_011230358	54.5
<i>Halobacillus halophilus</i>	WP_014642772.1	57.3
<i>Lentibacillus amyloliquefaciens</i>	WP_068440573.1	55.1
<i>Oceanobacillus iheyensis</i>	WP_011065783.1	50.9
<i>Parageobacillus thermoglucosidasius</i>	WP_003252282.1	55.6
<i>Virgibacillus halodenitrificans</i>	WP_019376107.1	59.6
Group 2		
<i>Alicyclobacillus acidocaldarius</i>	WP_041694969	48.6
<i>Kyrpidia tusciae</i>	WP_013075904.1	38.1
<i>Laceyella sacchari</i>	WP_102991708.1	47.9
Group 3		
<i>Paenibacillus polymyxa</i>	WP_013370894.1	39.9
<i>Clostridia</i>		
<i>Alkaliphilus metalliredigens</i>	WP_012065254.1	42.0
<i>Dehalobacterium formicoaceticum</i>	WP_089611718.1	54.0
<i>Desulfallas gibsoniae</i>	WP_006522674.1	46.5
<i>Desulfosporosinus orientis</i>	WP_014185970.1	38.6
<i>Desulfotomaculum ruminis</i>	WP_013842559.1	44.8
<i>Pseudoclostridium thermosuccinogenes</i>	WP_103081847.1	39.9

Groups 1, 2 and 3 have the genomic arrangements around *2dof* in *B. cereus*, *A. acidocaldarius* and *D. gibsoniae*, respectively, in Figure 11A.



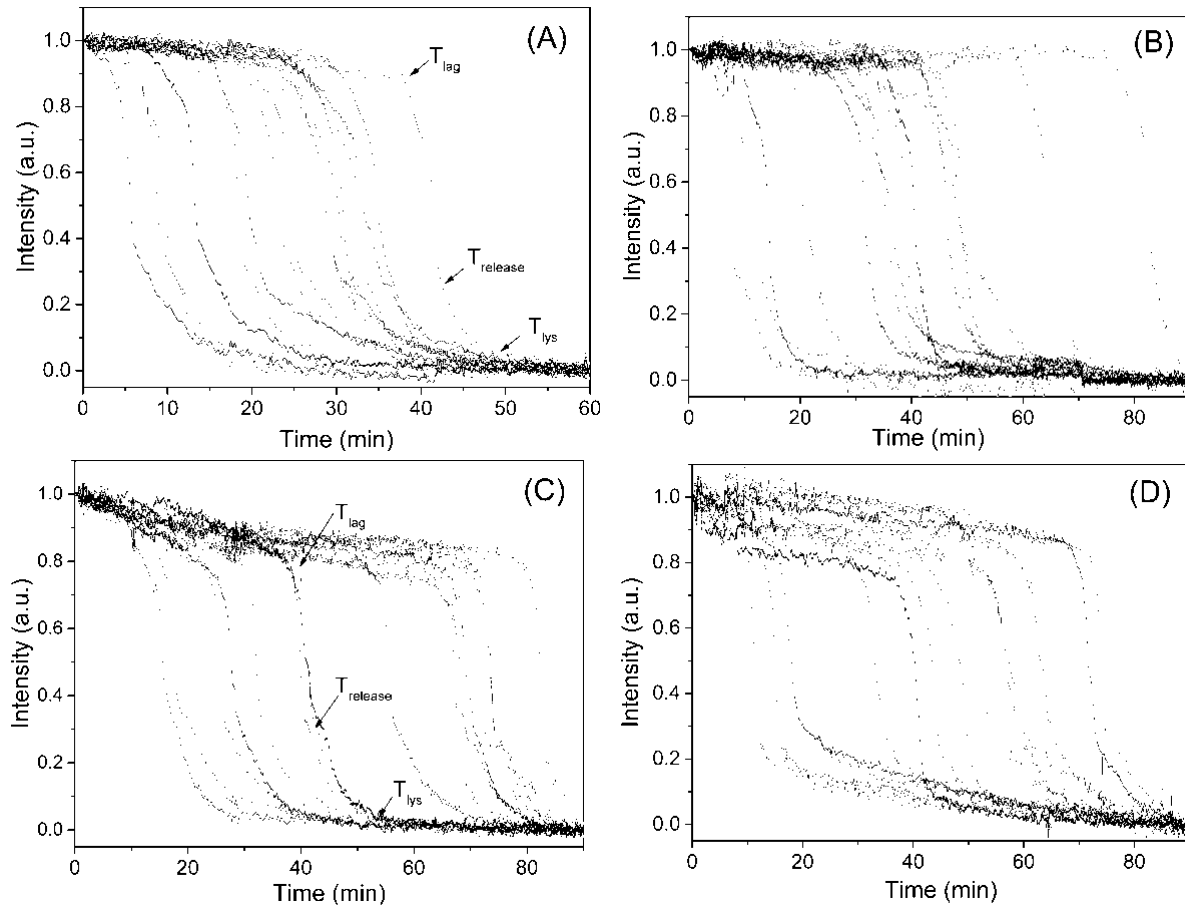
Supplementary Figure S1

Germination, outgrowth, and vegetative growth from dormant spores of various strains inoculated at $\sim 10^8/\text{ml}$ in LB medium, incubated at 37°C and the culture's OD_{600} measured. The symbols used are: ○ – PS832; ● – PS4487; and △ – PS4488. A duplicate experiment found that all three strains again gave similar results.



Supplementary Figure S2

^{14}C -Methylamine uptake by (A) intact and (B) decoated spores of PS832 (wt), PS4487 (*ydfS*) and PS4488 (*yetF*) spores. ^{14}C -Methylamine uptake by spores of various strains, either intact or decoated, was as described in Methods. Symbols used are: ○ – PS832; ● – PS4487; and △ – PS4488. These results were from single measurements in one experiment.



Supplementary Figure S3

Germination of multiple individual (A,B) PS832 (wt) and (C,D) PS4488 (*yetF*) spores germinating with (A,C) L-valine or (B,D) AGFK. Spores were heat-activated and germinated with L-valine or AGFK and the germination of 16 individual spores of each strain and with each germinant were followed as described in Methods. Arrows on one trace in panels (A) and (C) denote the times of T_{lag} , $T_{release}$ and T_{lys} and I_{lag} and I_{lys} were measured at T_{lag} and T_{lys} , respectively.

sspA

-35 σ^G -10

CAATTTTCAGCTCCTGTATACAATTACCAAAGTTTTTCT**GAATGA**AGCCATGTGTTTTGACAC**CATTCTA**TACTC

RBS **TSC**

AC**AAGGAGGTG**AGACAC**ATG**GCTAACA

ykjA

-35 σ^F -10

TGTT**CAGGCG**ATATGCACGTTTCGCCTAGACACTGAT**GCATAG**AGGGCCTGCCACG**GGGCACAAT**AGGCTC

RBS **TSC**

AATATGACCAGCGG**ATGGAGGTA**AAGATCG**GTG**TTATGGA

yrbG

-35 σ^G -10

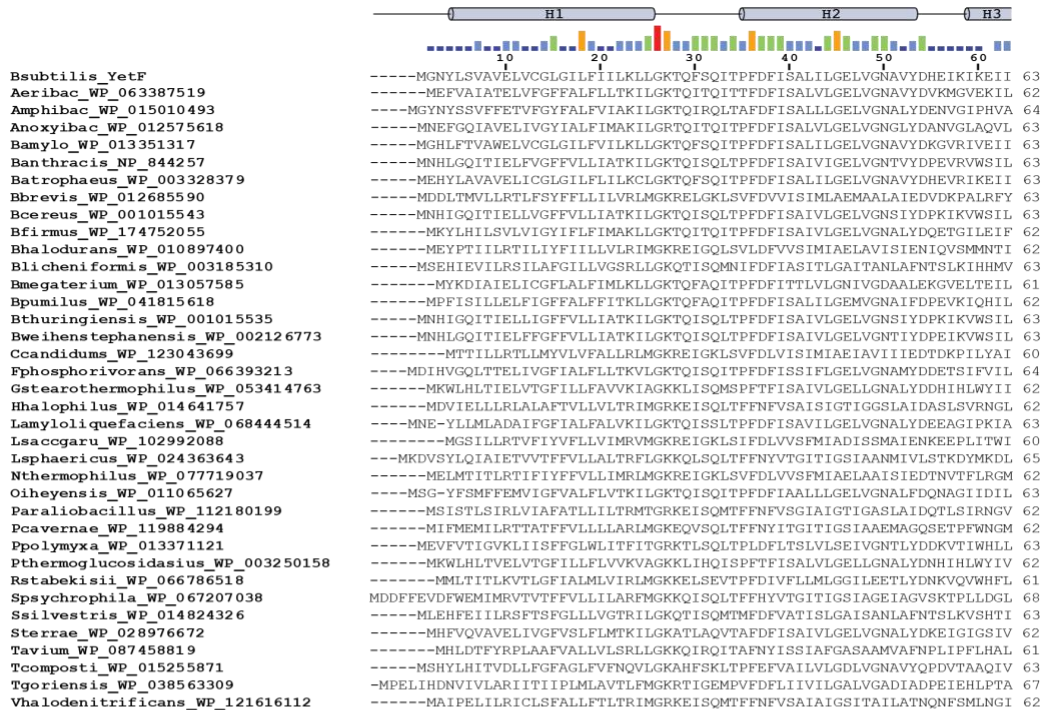
GACGTAAAAGCTTTGT**GAAAT**GCAATCGGTTTTTCTTA**CATAAAT**TGATCATTTTTGTTGCAACCTATAAT

RBS **TSC**

GAG**TTGGAGGTG**CATA**ATG**GAAGAGC

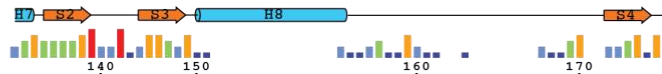
Supplementary Figure S4

Likely promoter sequences for the *ykjA* and *yrbG* genes and comparison with the very strong σ^G -dependent promoter sequence of *sspA*. The *sspA*, *ykjA* and *yrbG* upstream sequences include: -35 and -10 promoter sequences; a GG sequence just upstream of the putative -10 promoter sequence for *ykjA* indicative of a σ^F promoter; the ribosome binding sites (RBS) that were identified based on the optimal *B. subtilis* RBS sequence (AAGGAGGTG) and the translation start codon (TSC). The *sspA* promoter sequences were experimentally determined, and the promoter sequences for *ykjA* and *yrbG* were chosen to give the best matches to consensus σ^F and σ^G promoter sequences, respectively (Wang et al., 2006).



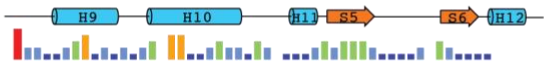
Conservation 30% -100%

Bsubtilis YetF
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Amphibac_WP_015010493
Anoxyibac_WP_012575618
Bamylo_WP_013351317
Banthracis NP_844257
Batrophaeus_WP_003328379
Bbrevis_WP_012685590
Bcereus_WP_001015543
Bfirmus_WP_174752055
Bhalodurans_WP_010897400
Blicheniformis_WP_003185310
Bmegaterium_WP_013057585
Bpumilus_WP_041815618
Bthuringiensis_WP_001015535
Bweihenstephanensis_WP_002126773
Ccandidums_WP_123043699
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Lsaccgaru_WP_102992088
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Pthermoglucoisidiasius_WP_003250158
Rstabekisii_WP_066786518
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Ssilvestris_WP_014824326
Sterrae_WP_028976672
Tavium_WP_087458819
Tcomposti_WP_015255871
Tgoriensis_WP_038563309
Vhalodenitrificans_WP_121616112



QEVEYAILETNGMVSVLKPSD-----FDKPTNKDLQIPSK-----SVSLP--ITLIID 176
 REVEYAVLETGTISVLKKS-----FDKPTRNDLNLSS-----PATIP--YTIIVD 175
 RDVEYAILENDGTISVLNNTS-----SQTPTKDLKLQDE-----KVYLP--VTLIND 177
 REVEYAILETGTYSVMKAP-----YEQPTRQDHNISAS-----EAVLP--VTVIID 176
 QEAEYAILETNGMVSVLKFP-----YDTTKNGDMQIKPK-----QVSLP--VTLIID 176
 REVEYMILEPNNGISVLKKS-----YESPTINDLSLKHK-----PVYLP--ISLISD 177
 KEAEYAILETNGMISVLKKS-----YDTPKMDVDELAPK-----QVYLP--ITLIID 176
 ADVEFALLEPTGQMSVFLKEQ---KE-----KVTREDLALMKKLQVGPVSYKGLP--IPLIID 183
 REVEYMILEPNNGISVLKKS-----YESPTINDLSLKHK-----PVYLP--ISLISD 177
 REVEYAILETGTYSVAFKKPL-----YATPTIQDLNLPY-----NAELP--VTLIID 175
 SDVEFAILEPFGKLSVLEKR-----PFSGKSSS-----YLP--LPLIID 166
 EEVLYAIVETNGTLTVLKKPQ-----FRNVTKKDLVWATTPEG-----KLP--TELIMD 177
 YEAEYVILETNGEVSVPKHE-----FGPPTKNDLNI PYS-----QTNLP--IALIMD 174
 NEIEYAILETGDSVSVLPKMK-----YATAEDVNVKKG-----EVKLP--RTFIID 175
 REVEYMILEPNNGISVLKKS-----YESPTVNDLSLKHK-----PVYLP--ISLISD 177
 REVEYMILEPNNGISVLKKS-----YESPTINDLSLKHK-----PVYLP--ISLISD 177
 EDVELAVLEANGKLSVVPKTRNSKETGITQRNVSAAPSQKSETPPKIRYE-----LLP--LPLIID 187
 REVEYAILESNGSLSILPKYQ-----YGPNNRQDLNLQSQ-----EQPELP--ITLIID 178
 REVAFCLEADGEISVLKKAH-----YQKTTREDFQLPPH-----PVYVP--VTLIID 175
 SEVSYAIFETDGLSVMKKTG-----EQPFTKKGDNVVSN-----SPAVYPIPTTVSD 178
 EEVEYAILEADGEVSVLKKPE-----YQPTIADLNLAPK-----PVKIG--RVLISD 176
 SDVEFAVLETTGKLSVFPKKE---KR-----PAFKEDVRRDLK-QF-----RMP--IPVIID 173
 DEIDFAILEPNTLSLILKPP-----FQGTQKIDINISPE-----NPPFLP--IEIISD 179
 TDVEHAILETSGKLSVILKEG---KQ-----PVTKEEAGVELRGQH-----HLP--VPLIID 176
 QEVEFAVLEANGKLSVLPKKS-----YQIPTRKDLKMTT-----EVDLS--TTLIND 176
 NDVDYAI FETDGLSVDKKEK-----VKPLAKT-LQIQN-----KANVEPTPTMIVSD 177
 QEVYAVLETNGKLSIMKTEE-----AKNPTKSDGLGVAKK-----TPKIP--AAVID 176
 REVLYATLETNGSLSVMKKE-----YEPAAQDMGIDAQ-----PDLFS--VTVIDK 176
 REVAFCYLETNGTISVLKKA-----YQKTTREDFQLPPH-----PVHVP--VTLIID 175
 REVKYVILEPQGQISVMKR-----DSS-DQIT-----TDTLN--RLIIDE 165
 KDHYAILETNGKLSVILKAG-----LEAATKVDNAAIQ-----VPKYP--TEVIAE 182
 EEVLFYAIETNGTLTVLKKPQ-----FRNVNKQDLMI PITPEF-----NLP--TELIMD 177
 REVAFAILETNGSISVKQKQ-----YATPTMEDLQKQK-----PVYLP--ITIIED 175
 TDVDYAILEPQGQISLILKTK-----HLPASKHVDVETGRA-----NTAPFG--VQIVSD 175
 REIEYAVLETNGMISVLKRP-----YGPPTRADLGLHG-----GGRVP--ITLIID 176
 RDVETAI VEPNGALSVLKQK-----KMPATREDLQIQKQ-----PSAIA--FPVIVSD 180
 KEVDYAI FETSGKLSVMKKN-----KQPATKSDIHQLTTY-----SPKIFP--TEIISD 177

Bsubtilis YetF
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Amphibac_WP_015010493
Anoxyibac_WP_012575618
Bamylo_WP_013351317
Banthracis NP_844257
Batrophaeus_WP_003328379
Bbrevis_WP_012685590
Bcereus_WP_001015543
Bfirmus_WP_174752055
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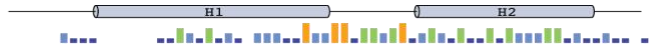


GEIVRDLNKEAGVDEQWLKQELKKNIDKTEDVLF AEWHKKNP-LYTVTYEQSRST 231
 GEVSENLEKAGFDEKWLQQLLAYSVEDAKDVFYAEWQNNNG-LFVQKY 224
 GEI EDNLAEINKDKWLYDQIKKQKISSIEEIFYAEYLEDEP-LFIQYM 226
 GEVIWDLNRENGWDEQWLKKHIRHAGFENYSIDILYAEWQDGGK-MHVQPY 225
 GEVLYENLEKAGVKEQLIQDLKKNIKRTEDEVFYAEWKHKDP-LFVLPYEEKK 229
 GKVVKDNLEAGFDEGWLYKQIKKKGITKFEDEVLYAEWKTDDG-FFCQEMDR 228
 GEVVDNLQEAQVDEWLEWQLQASQVNECKDVLFAEWHAGQP-LFFIKYDSGSDK 231
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 GEVVDNLKSNWDETLLKNEIKKYGASGVKDVLYAEWKKGAE-LHVQTY 224
 GKVQEKHLEKINKTSLWLKQRLKLYRDIKISYCAIKE-DGTFDIDKDEK 218
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Conservation 30% - 100%

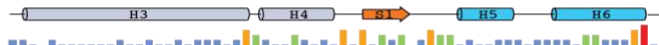
Supplementary Figure S5

Sequence alignment of *B. subtilis* YetF with the best YetF match in other *Bacilli*. Sequence conservation is shown as a bar graph, with red bars indicating identity among YetF homologs. Secondary-structure assignments of YetF from the crystal structure (PDB ID: 3C6F) are shown as blue cylinders (helices) and orange arrows (β strands). Predicted secondary-structure elements by AlphaFold for the N-terminal TM region are shown as gray cylinders (α helices).



Bsubtilis_YetF
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 Sglycolicus_WP_013625014
 Sthermophilum_WP_011197382
 Tacetatoxydans_WP_013778043
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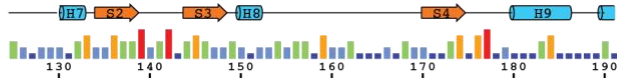
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 -----MNAFL---VAIKLLIGFPAIVIIINSIGKGNLAPSASDQIVNYVVLGGIIGGVYINSS-V 57
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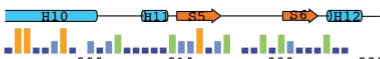
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Tthermosaccharolyticum_WP_015312322	MGYPNIADVEYAILLETNGLSVLPKSKDRPVTNDLMLTPQYEGPLPIIIDGKIHKNMKMANVDM	188
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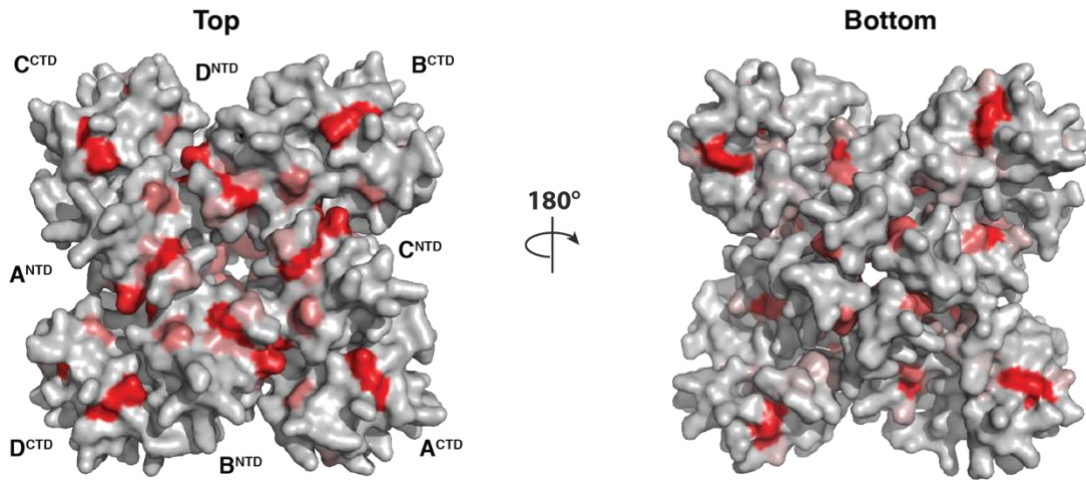
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Caproiciproducens_WP_128742257	DWLQGVLN-GQHLQAG-EIFLMTAN-TKGDFFIVKREAPK	225
Carthromitus_WP_005805303	DWLMKQLK-ENKIKSPKDVLYAYTD-SNGTFKYQLETK	213
Cbotulinum_WP_011948896	EWLKAEK-KRNKDSSDVFLATIN-ENNQIYIDTYKDLKRR--IIDIGDY-KG----PY	242
Cdesulforudis_WP_012303154	EWLYRELE-KQGVRSSEVMYASLD-SEGKLYVDLKEDAIEH--YTDITDKVPD--KIQ	245
Cdifficile_WP_009889750	NWLMGILK-SNHIEYFKDVLICVLD-ENDKIFIQNKGD	219
Clentocellum_WP_013658886	KWLTQQLR-IHDVSDIEVFLATCD-RNNKLCVYKLLTEKMTADLLE	235
Cperfringens_WP_003472738	KWLDEKLR-SLNYSPRDKLFLVMD-SNGKLFYQKRNKQDKEDIIL	232
Csubterraneus_WP_009611278	AWLDEQLK-IWNIKSVEVLFASLD-SNKVLTVYKKEG	224
Ctsetani_WP_035111051	KWLKELK-KRNINDPSEVFLATMD-TNGFYADKYNDLMMKENVTDKGTY-KG----PL	244
Dacetoxidans_WP_015757363	NWLERELA-KFGIDSHQVLFASLD-TNGKLFQWLKSD	224
Dformicoaceticum_WP_089609402	AELAEILE-SFHIDDLNQLSIVIT-PDGHIALTKKQQ	218
Dgibsoniae_WP_006522671	DWLLKQLQTEHGVEISQVIAQLD-TSGNLYVDLKNANPEN--KPH	237
Dhafniense_WP_011459753	KWLQKELQ-KQGIKDVSEVFFASLD-PAGSLYIDLKDRQLN--PVDIGDY-KG----PY	242
Dkuznetsovii_AEG16849	DWLYRELE-KQGIKSVKDVYASLD-AEGKLYVDRKEDTMQH--VTDITDKLPD--KMPQ	245
Dorientis_WP_014187430	QWLKELK-KQKIQIEVDVFIASLD-SSGNLFAQEKQPKKQKNNKKNPDR	240
Druminis_WP_041275606	AWLKEKLA-ERGFH-PKVVLLATLN-TNGQLLIDCQNDDRQK	228
Ibutyriciproducens_WP_058117823	GWLNKRLK-EHGVRAVDFVLLSVD-EQNRVYFVPEVGVK	227
Lphytofermentans_WP_012198749	DWLIKQLK-SQGVNDYHELLVTCN-HKHEITAYKRYKKNHAS	230
Lumeaense_WP_111524166	DWLEELK-KQGIKYSVDFLGEYV-NNSLILITDK	210
Maustraliensis_WP_013780881	KWLMMLA-AHDHISKEVAYASIDPLTKFVYDVTYKDSVPK--NIDISVYK--KLE	245
Mtermoacetica_WP_011391764	KWLIQQLQ-AQGIQIDVQVAVLR-SNGTLYNVTKEDDIIN--PVDITDAPESPVTKEEQDRP	253
Psordellii_WP_055331643	KWLNSELD-KKGIKNTSDILLAYMD-SSKLNLYKNDIPITPTL	236
Pthermosuccinogenes_WP_103079909	NWLKSELA-KHGISDARDVLFASLD-SSGNLFLQKREK	224

Conservation 30% -100%

Supplementary Figure S6

Sequence alignment of *B. subtilis* YetF with the best YetF match in *Clostridia* species. Sequence conservation is shown as a bar graph, with red bars indicating identity among YetF homologs. Secondary-structure assignments of YetF from the crystal structure (PDB ID: 3C6F) are shown as blue cylinders (helices) and orange arrows (β strands). Predicted secondary-structure elements by AlphaFold for the N-terminal TM region are shown as gray cylinders (α helices).

Clostridia



Supplementary Figure S7

Surface representation of a tetrameric YetF, showing conservation among best matched YetF homologs identified in *Clostridia* species.