

Table S1: Representative PspA/Snf7 homologs					
Gene, Lineage info and Genomic Contexts grouped by Domain Architectures					
Gene Info		Lineage Info		GenContext	
AccNum	GeneName	Species	Lineage		
NLPC+PspA					
AFZ52345.1	Cyan10605_0189	Cyanobacterium aponinum PCC 10605	bacteria>cyanobacteria	NLPC+PspA->	
PspA					
ANQ40502.1	BAR24_02900	Gluconobacter oxydans	bacteria>proteobacteria>alphaproteobacteria	<-pspF-NtrC-AAA+FIS-HTH PspA->PspB->SIG+Toast-rack->SIG+Toast-rack->SIG+ATPase->	
AOL22920.1	Ga0102493_111899	Erythrobacter litoralis	bacteria>proteobacteria>alphaproteobacteria	<-PspF-NtrC-AAA+FIS-HTH X->PspA->PspB->PspC+PspB->SIG+PspB->SIG+PspB->SIG+PspB->SIG+PspB->SIG+PspB->PspB->	
ANL88610.1	AMC81_PE00364	Rhizobium phaseoli	bacteria>proteobacteria>alphaproteobacteria	<-SpermGS-ATPgrasp<-SIG+DUF1190<-yjfl-TM(s)<-DUF2491<-lon_trans_2 CesT_Tir-DUF2170->PspA->	
BAB38581.1	yjfl	Escherichia coli O157:H7 str Sakai	bacteria>proteobacteria>gammaproteobacteria	CesT_Tir-DUF2170->PspA->DUF2491->yjfl-TM(s)->SIG+DUF1190->SpermGS-ATPgrasp->Acyl-CoA_dh_M+Acyl-CoA_dh_1->	
AEF02306.1	ambt_03780	Alteromonas naphthalenivorans	bacteria>proteobacteria>gammaproteobacteria	CesT_Tir-DUF2170->PspA->lon+trans_2->DUF2491->yjfl-TM(s)->SIG+DUF1190->SpermGS-ATPgrasp->	
AAK24333.1	CC_2362	Caulobacter vibrioides CB15	bacteria>proteobacteria>alphaproteobacteria	CesT_Tir-DUF2170->PspA->SpermGS-ATPgrasp->	
AKK09009.1	CTEST_07895	Corynebacterium testudinoris	bacteria>actinobacteria	clgR-HTH->PspA->	
CCP45543.1	35kd_ag	Mycobacterium tuberculosis H37Rv	bacteria>actinobacteria	clgR-HTH->PspA->PspM->PspN_N+DUF3046-> <-X(s)->DUF3046->	
AO562694.1	TL08_09395	Actinoaloteichus hymeniacidonis	bacteria>actinobacteria	clgR-HTH->UA74_09550-lowcomplexity->PspA->PspM->	
ANX06812.1	AS891_06225	Bacillus subtilis subsp subtilis	bacteria>firmicutes	Lial-LiaF-TM->PspA->SIG+Toast-rack->Lial-LiaF-TM+Toast-rack->SIG+TM+HAM+HISKIN->REC+GerE-HTH->	
AAM04874.1	MA_1460	Methanosarcina acetivorans C2A	archaea>euryarchaeota	PspA->Psp-AA->	
CAB51252.1	SCO2168	Streptomyces coelicolor A32	bacteria>actinobacteria	>SIG+TM(s)+HISKIN->REC+GerE-HTH->	
ABW11964.1	Franean1_2534	Frankia sp EAN1pec	bacteria>actinobacteria	PspA->Psp-AA->TM(s)+Metallopeptidase+TM(s)->Tfu_1009->	
AHA65439.1	Asd1617_02612	Shigella dysenteriae 1617	bacteria>proteobacteria>gammaproteobacteria	PspA->PspA->PspB->PspC+PspB->Phageshock_PspD->PspE-SIG+RHOD-CDC25->	
AFZ14666.1	Cn9333_3857	Crinalium epipsammum PCC 9333	bacteria>cyanobacteria	PspA->PspA->Thioredoxin->	
AEN65073.1	Entas_2342	Enterobacter soli	bacteria>proteobacteria>gammaproteobacteria	PspA->PspB->PspC+PspB->Phageshock_PspD->DO-GTPase2->TM(s)+IIGP1->pspF-NtrC-AAA+FIS-HTH->	
ANW39986.1	A9L45_10880	Escherichia coli O157:H7	bacteria>proteobacteria>gammaproteobacteria	PspA->PspB->PspC+PspB->Phageshock_PspD->PspE-SIG+RHOD-CDC25->	
AEC01378.1	Spico_0140	Sphaerochaeta coccoides DSM 17374	bacteria>spirochaetes	PspA->PspC-> <-pspF-NtrC-AAA+FIS-HTH PspA->PspB-like->PspC+PspB->SIG+Toast-rack->	
AMQ41621.1	AMS64_04095	Aeromonas veronii	bacteria>proteobacteria>gammaproteobacteria	PspA->PspC->Phageshock_PspG->	
BAG04642.1	MAE_48200	Microcystis aeruginosa NIES843	bacteria>cyanobacteria	PspA->SIG+TPR+PBP1->	
AIK12556.1	GZ59_06830	Pectobacterium atrosepticum	bacteria>proteobacteria>gammaproteobacteria	PspA->SIG+TPR+TM+DUF5401->	
ANL45788.1	AMC87_CH01062	Rhizobium phaseoli	bacteria>proteobacteria>alphaproteobacteria	PspA->YiaAB->X(s)-> <-SIG+TM(s)	
AAS43862.1	BCE_4961	Bacillus cereus ATCC 10987	bacteria>firmicutes	PspA->yjfl-TM(s)->SIG+DUF4178->SIG+DUF4247->	
ANX09535.1	AS891_20665	Bacillus subtilis subsp subtilis	bacteria>firmicutes	PspA->ZNR(s)+TM->SIG+TPM_phosphatase+TM->Band_7+ZNR->	
AAN56746.1	SO_3765	Shewanella oneidensis MR1	bacteria>proteobacteria>gammaproteobacteria	SIG+Ctha_1186+Low-comp->DUF350-TM(s)->SIG+TM(s)+Spermine_synth->CesT_Tir-DUF2170->PspA->DUF4178->RHH->	
AKX93460.1	MOTHE_c06560	Moorella thermoacetica	bacteria>firmicutes	SIG+DUF1707-SHOCT->TM(s)+Metallopeptidase+TM(s)->Tfu_1009->PspA->Psp-AA->	
CCG46123.1	pspA	Halobacillus halophilus DSM 2266	bacteria>firmicutes	SIG+DUF4178->PspA->SIG+DUF4247->yjfl-TM(s)->SIG+TM(s)+Spermine_synth->	
APB74393.1	PPYC2_05025	Paenibacillus polymyxa	bacteria>firmicutes	SIG+TM(s)->Lial-LiaF-TM->PspA->PspC+Coiled-coil->PspA->SIG+TM+Toast-rack->SIG+TM+HISKIN->REC+GerE-HTH->	
AKL67689.1	M444_22280	Streptomyces sp Mg1	bacteria>actinobacteria	SIG+TPM_phosphatase+TM+Coiled-coil->PspA->	
ALD73647.1	AN946_04100	Trueperella pyogenes	bacteria>actinobacteria	SIG+TPM_phosphatase+TM+Coiled-coil->PspA->NVN->REC+GerE-HTH->SIG+TM+HAM+HISKIN-> <-Acyltransferase	
AKK09942.1	CTEST_12695	Corynebacterium testudinoris	bacteria>actinobacteria	Thioredoxin->PspA->	
ANH61663.1	I597_2772	Dokdonia donghaensis DSW1	bacteria>bacteroidetes	TM(s)->PADR-HTH->DUF1700-ahelical+PspC+Lial-LiaF-TM+Toast-rack->SIG+NTF2->TM+Toast-rack-> <-CHTH+Proteas CesT_Tir->PspA->SIG+TM(s)->SIG+Band_7+coiled-coil+Flot->Beta-Propeller+AAA-ATPase->	
AKB54760.1	MSBRM_1762	Methanosarcina barkeri MS	archaea>euryarchaeota	TM(s)+Metallopeptidase+TM(s)->Tfu_1009-> <-X(s)->PspA->Psp-AA->	
PspA(s)					
BAG06017.1	MAE_61950	Microcystis aeruginosa NIES843	bacteria>cyanobacteria	PspA->PspA->PspA(s)->	
PspA+Psp-AA					
ACU53894.1	Afer_0955	Acidimicrobium ferrooxidans DSM 10331	bacteria>actinobacteria	PspA+Psp-AA->	
Snf7					
OLB70630.1	AUI06_06150	archaeon 13_2_20CM_2_52_21	archaea	Snf7->DUF5401-coiled-coil->Snf7+ZDNA-HTH->MIT+Classical-AAA->HTH->SIG+TM(s)->ABC-ATPase->Snf7->DUF5401-coiled-coil->Creatinase_N+Peptidase_M24->	
OLS27540.1	HeimC3_03190	Candidatus Heimdallarchaeota archaeon LC_3	archaea>asgard group	Snf7->Snf7->MIT+Classical-AAA->ESCRT-II->	
CBY21170.1	GSOID_T00008924001	Oikopleura dioica	eukaryota>metazoa>chordata	Snf7->Snf7->Snf7->	
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