

The Phage-shock-protein Envelope Stress Response: Discovery of Novel Partners & Evolutionary History

Janani Ravi^{1,2*}, Vivek Anantharaman³, Samuel Zorn Chen¹, Pratik Datta², L Aravind^{3*}, Maria Laura Gennaro^{2*}.

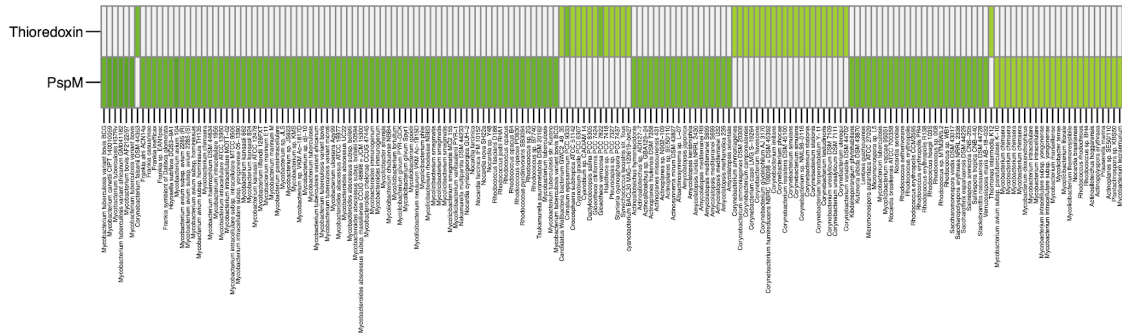
¹Pathobiology and Diagnostic Investigation, Michigan State University, East Lansing, MI, USA; ²Public Health Research Institute, Rutgers University, Newark, NJ, USA; ³National Center for Biotechnology Information, National Institutes of Health, Bethesda, MD, USA. *Corresponding authors. janani@msu.edu; aravind@nih.gov; marila.gennaro@rutgers.edu

Supplementary Figures and Tables

All PSP results (data summarizations and visualizations) can be accessed via our easy-to-use interactive webapp: <https://jrvilab.shinyapps.io/psp-evolution>.

Supplementary Figures

Figure S1. Mutual exclusion phyletic pattern of PspM, Thioredoxin.



Supplementary Tables

Table S1. Summary of Psp partner domains (query proteins)

| Domain Name | Old Name/Aliases | Pfam | COG | PDB |
|--------------|---|---|---|---|
| PspA | PspA_IM30 | PF04012 | COG1842 | 4WHE |
| Snf7 | | PF003357 | COG5491 | 5FD7 |
| PspA/Snf7 | PspA/ESCRT-III | CL0235 | | 3FRV |
| Toastrack | DUF4097/DUF2154/DUF2807 | PF13349/ PF09922/ PF10988 | COG3595/ COG4758 | 4QRK/ 3PET |
| Lial-LiaF-TM | DUF2157/Toast rack N | PF09925/ PF17115 | COG4872 | 4QRK |
| PspM | Rv2743c | | | |

| | | | | |
|---------|-----------------------|-------------------------|-------------------------|--|
| PspN | Rv2742c | | | |
| PspN_N | N-terminal part, PspN | | | |
| DUF3046 | C-terminal part, PspN | PF11248 | | |
| PspB | | PF06667 | | |
| PspC | | PF04024 | COG1983 | |

Table S2. Summary of novel Psp partner domains (companion table for final summary figure)

| Domain Name | Old Name/Aliases | Pfam | PDB |
|--|--|---|---|
| HAAS | DUF1700 alpha-helical/ DUF1129/Yip1/ DUF1048 | PF08006/PF06570/ PF04893/PF06304 | 2O3L |
| SHOCT-bihelical | DUF1707, SHOCT | PF08044/PF09851 | |
| PspAA | PspA-associated protein | | |
| PspAB | PspA-associated protein B | | |
| Vps4-AAA-ATPase/ Classical-AAA-ATPase | | PF08432/ PF00004 | 5FVK/ 3U5Z |
| MIT | | PF04212 | 5FVK |
| Thioredoxin | | PF00085 | 2OE3 |
| ClgR-HTH | XRE-HTH/HTH_3 | PF01381 | 6IRP |
| TM-Flotillin dyad | Flot | PF15975 | |
| Band-7 | Band_7 | PF01145 | 3BK6 |
| Spermine synthase | Spemine_synth | PF01564 | 6O63 |
| Yjfl-TM(s) | DUF350 | PF03994 | |
| CesT_Tir | CesT | PF05932 | 1TTW |
| CesT_Tir-DUF2170 | DUF2170 | PF09938 | |
| TPM_phosphatase | | PF04536 | 4OA3 |

| | | | |
|-----------------------------|-------------------------|---|----------------------|
| SHOCT-like | DUF1707 | PF08044 | |
| Caspase | Peptidase_C14 | PF00656 | 3UO8 |
| PadR-like_wHTH PadR-wHTH | PadR-HTH/PadR | PF03551 | 1XMA |
| RHH | TraJ-RHH/RHH_1 | PF01402 | 3OD2 |
| SIGMA-HTH | | | |
| GerE-HTH/ DUF2089-HTH | GerE/ DUF2089 | PF00196 / PF09862 | 2JPC |
| GNTR-HTH | GntR | PF00392 | 4R1H |

Table S3. Domain architectures, genomic contexts, and lineages of representative PspA/Snf7 homologs. (next pages)

Table S4. Domain architectures, genomic contexts, and lineages of representative homologs of Psp cognate partner domains. (next pages)

| Table S3: Representative PspA/Snf7 homologs | | | | | |
|--|--------------------|--|--|---|--|
| Gene, Lineage information and Genomic Contexts grouped by Domain Architectures | | | | | |
| Gene Info | | Lineage Info | | GenContext | |
| AccNum | GeneName | Species | Lineage | | |
| MIT+Vps4-AAA-ATPase | | | | | |
| CKH37208.1 | ftsH_1 | Mycolicibacterium smegmatis | bacteria>actinobacteria | MIT+Vps4-AAA-ATPase-> | |
| ACB74714.1 | Oter_1429 | Oplutus terae PB901 | bacteria>PVC_group>vemucomicrobia | MIT+Vps4-AAA-ATPase->TPR+TM(s)-> | |
| NlpC+PspA | | | | | |
| AFZ52345.1 | Cyan10605_0189 | Cyanobacterium aponinum PCC 10605 | bacteria>cyanobacteria | NlpC+PspA-> | |
| PspA | | | | | |
| AKJ06548.1 | AA314_08174 | Archangium gephyra | bacteria>proteobacteria>delta | <-ABC-ATPase Glycos_trans_3N+Glycos_transf_3+PYNP_C->X(s)->PspA->SIG+PBPB->SIG+TM+Snf7-> <-X SIG+DUF3352->ABC-ATPase->SIG+TM(s)->SIG+TM(s)-> | |
| AEY64321.1 | Clo1100_0028 | Clostridium sp BNL1100 | bacteria>firmicutes | <-ParA-Soj-PloopNTPase X(s)->GNTR-HTH->Inactive-Classical-AAA+Classical-AAA->PspA->ACET-> | |
| ANQ40502.1 | BAR24_02900 | Gluconobacter oxydans | bacteria>proteobacteria>alpha | <-PspF-NtrC-AAA+FIS-HTH PspA->PspB->TM+Toastrack->TM+Toastrack->SIG+TM(s)->ABC-ATPase-> | |
| AOL22920.1 | Ga0102493_111899 | Erythrobacter litoralis | bacteria>proteobacteria>alpha | <-PspF-NtrC-AAA+FIS-HTH X->PspA->PspB->PspC+PspB->SIG+PspB->SIG+PspB->SIG+PspB->SIG+PspB->PspB-> | |
| BAB38581.1 | yjJ | Escherichia coli O157H7 str Sakai | bacteria>proteobacteria>gamma | CesT_Tir-DUF2170->PspA->DUF2491->YjJL-TM+TM(s)->LipoSIG+DUF1190->SpermGS-ATPgrasp-> | |
| AMJ95269.1 | AVL56_13815 | Alteromonas addita | bacteria>proteobacteria>gamma | CesT_Tir-DUF2170->PspA->Ion_trans_2+TrkA_N+TrkA_C->DUF2491->YjJL-TM+TM(s)->LipoSIG+DUF1190->SpermGS-ATPgrasp-> | |
| ABK71106.1 | MSMEG_2695 | Mycolicibacterium smegmatis MC2 155 | bacteria>actinobacteria | CigR-HTH->PspA->PspM-> <-X(s)->DUF3046-> | |
| CCP45543.1 | 35kd_ag | Mycobacterium tuberculosis H37Rv | bacteria>actinobacteria | CigR-HTH->PspA->PspM->PspN_N+DUF3046-> <-X(s)->DUF3046-> | |
| AOS62694.1 | TL08_09395 | Actinoalloteichus hymeniacidonis | bacteria>actinobacteria | CigR-HTH->UA74_09550-lowcomplexity->PspA->PspM-> | |
| ANX06812.1 | AS891_06225 | Bacillus subtilis subsp subtilis | bacteria>firmicutes | Lial-LiaF-TM->PspA->TM+Toastrack->Lial-LiaF-TM+Toastrack->SIG+TM+HAMP+HISKIN->REC+whTH-> | |
| AAN56746.1 | SO_3765 | Shewanella oneidensis MR1 | bacteria>proteobacteria>gamma | LipoSIG+Ctha_1186+Low-comp->YjJL-TM+TM(s)->SIG+TM(s)+Spermine_synth->CesT_Tir-DUF2170->PspA->DUF4178->RHH-> | |
| AFZ14666.1 | Cr9333_3857 | Crinallium epipsammum PCC 9333 | bacteria>cyanobacteria | PspA->PspA->Thioredoxin-> | |
| AAM04874.1 | MA_1460 | Methanosarcina acetivorans C2A | archaea>euryarchaeota | PspA->PspAA-> | |
| CAB51252.1 | SCO2168 | Streptomyces coelicolor A32 | bacteria>actinobacteria | PspA->PspAA->SIG+TM(s)+HISKIN->REC+whTH-> | |
| ABW11964.1 | Franean1_2534 | Frankia sp EAN1pec | bacteria>actinobacteria | PspA->PspAA->TM(s)+Metallopeptidase+TM(s)->PspAB-> | |
| AEN5073.1 | Entas_2342 | Enterobacter soli | bacteria>proteobacteria>gamma | PspA->PspB->PspC+PspB->PspD->DO-GTPase2->TM(s)+IIGP1->PspF-NtrC-AAA+FIS-HTH-> | |
| ANW39986.1 | ASL45_10880 | Escherichia coli O157H7 | bacteria>proteobacteria>gamma | PspA->PspB->PspC+PspB->PspD->PspE-SIG+RHOD-CDC25-> | |
| ANX09535.1 | AS891_20665 | Bacillus subtilis subsp subtilis | bacteria>firmicutes | PspA->ZnR(s)+TM->SIG+TPM_phosphatase+TM->Band-7+ZnR-> | |
| CBH24266.1 | SRM_01345 | Salinibacter ruber M8 | bacteria>FCB_group>bacteroidetes | Ribosomal_L31->Glycos_trans_3N+Glycos_transf_3+PYNP_C->PspA->Rmar_0091-Coiled-coil->SIG+TM+Snf7-> <-X<-MoaC | |
| AKX93460.1 | MOTHE_c06560 | Moorella thermoacetica | bacteria>firmicutes | SIG+SHOCT-bihelical->TM(s)+Metallopeptidase+TM(s)->PspAB->PspA->PspAA-> | |
| APB74393.1 | PPYC2_05025 | Paenibacillus polymyxa | bacteria>firmicutes | SIG+TM(s)->Lial-LiaF-TM->PspA->PspC+Coiled-coil->PspA->SIG+TM+Toastrack->SIG+TM+HISKIN->REC+whTH-> | |
| AKK09942.1 | CTEST_12695 | Corynebacterium testudinoris | bacteria>actinobacteria | Thioredoxin->PspA-> | |
| ANH61663.1 | IS97_2772 | Dokdonia donghaensis DSW1 | bacteria>FCB_group>bacteroidetes | TM(s)->PadR-like-whTH->HAAS+PspC+Lial-LiaF-TM+Toastrack->SIG+NTF2->TM+Toastrack-> <-CHTH+Protease CesT_Tir->YqJ-YuaF-SIG+TM(s)->SIG+Band-7+Coiled-coil+TM-Flotillin->Betapropeller+Coiled-coil+AAA-ATPase-> | |
| AKB54760.1 | MSBRM_1762 | Methanosarcina barkeri M5 | archaea>euryarchaeota | TM(s)+Metallopeptidase+TM(s)->PspAB-> <-X(s)->PspA->PspAA-> | |
| PspA(s) | | | | | |
| BAG06017.1 | MAE_61950 | Microcystis aeruginosa NIES843 | bacteria>cyanobacteria | PspA->PspA->PspA(s)-> | |
| PspA+PspAA | | | | | |
| ACU53894.1 | Afer_0955 | Acidimicrobium ferrooxidans DSM 10331 | bacteria>actinobacteria | PspA+PspAA-> | |
| PspAB | | | | | |
| AAZ55047.1 | Tfu_1009 | Thermobifida fusca YX | bacteria>actinobacteria | <-TIMbarrel<-X PspA->PspAA->TM(s)+Metallopeptidase+TM(s)->PspAB-> | |
| SIG+MMPL+Snf7+MMPL | | | | | |
| CAM62382.1 | MAB_2301 | Mycobacteroides abscessus ATCC 19977 | bacteria>actinobacteria>actinobacteria | Mycobact_memb->SIG+MMPL+Snf7+MMPL-> | |
| SIG+TM+Snf7 | | | | | |
| OGG56892.1 | A3F84_10925 | Candidatus Handelsmanbacteria bacterium RIFCSLOWO2_12_FULL_64_10 | bacteria | FAD_binding_5+CO_deh_flav_C->X(s)->PspA->SIG+PBPB+OmpA->SIG+TM(s)->ABC-ATPase->SIG+TM+Snf7->Inactive-Classical-AAA+Classical-AAA-> | |
| Snf7 | | | | | |
| OLS27540.1 | HeimC3_03190 | Candidatus Heimdallarchaeota archaeon LC_3 | archaea>asgard_group | MIT+Vps4-AAA-ATPase-> <-X(s)->Snf7->Snf7->MIT+Vps4-AAA-ATPase->ESCRT-II-> | |
| CBY21170.1 | GSOID_T00008924001 | Oikopleura dioica | eukaryota>metazoa>chordata | Snf7->Snf7->Snf7-> | |
| More information available on our webapp . | | | | | |

| Table S4: Representative homologs of Psp cognate partner domains | | | | |
|--|---------------|--|---|---|
| Gene, Lineage information and Genomic Contexts grouped by Domain Architectures | | | | |
| Gene Info | | Lineage Info | | GenContext |
| AccNum | GeneName | Species | Lineage | |
| DUF4178 | | | | |
| AAN56747.1 | SO_3766 | Shewanella oneidensis MR1 | bacteria>proteobacteria>gammaproteobacteria | LipoSIG+Ctha_1186+Low-comp->YjL-TM+TM(s)->SIG+TM(s)+Spermine_synth->CesT_Ti-DUF2170->PspA->DUF4178->RHH-> |
| HAAS+FTSW_RODA_SPOVE | | | | |
| CAC98500.1 | lmo0421 | Listeria monocytogenes EGDe | bacteria>firmicutes | SIGMA-Factor->PadR-like-wHTH->HAAS+FTSW_RODA_SPOVE-> |
| HAAS+MacB_PCD+FtsX+MacB_PCD+FtsX | | | | |
| ACO32024.1 | ACP_2125 | Acidobacterium capsulatum ATCC 51196 | bacteria>acidobacteria | PadR-like-wHTH->HAAS+MacB_PCD+FtsX+MacB_PCD+FtsX-> |
| HAAS+Pentapeptide | | | | |
| AOH56696.1 | ABE28_020195 | Bacillus muralis | bacteria>firmicutes | PadR-like-wHTH->HAAS+Pentapeptide-> |
| Lial-LiaF-TM | | | | |
| APB74392.1 | PPYC2_05020 | Paenibacillus polymyxa | bacteria>firmicutes | SIG+TM(s)->Lial-LiaF-TM->PspA->PspC+Coiled-coil->PspA->SIG+TM+Toastrack->SIG+TM+HISKIN->REC+ wHTH-> |
| Lial-LiaF-TM+Toastrack | | | | |
| ABD83157.1 | Sde_3902 | Saccharophagus degradans 240 | bacteria>proteobacteria>gammaproteobacteria | Lial-LiaF-TM+Toastrack->SIG+TM(s)+HISKIN->REC+ wHTH-> |
| AFH48155.1 | IALB_0443 | Ignavibacterium album JCM 16511 | bacteria>ignavibacteriae | Lial-LiaF-TM+Toastrack->SIG+TM(s)+HISKIN->REC+ wHTH->X(s)->TM-> |
| AGK93623.1 | LA14_0400 | Lactobacillus acidophilus La14 | bacteria>firmicutes | LytTR->Lial-LiaF-TM+Toastrack-> |
| CAL82154.1 | CBO0601 | Clostridium botulinum A str ATCC 3502 | bacteria>firmicutes | LytTR->Lial-LiaF-TM+Toastrack-> |
| PspC | | | | |
| CAB15516.1 | yvIC | Bacillus subtilis subsp subtilis str 168 | bacteria>firmicutes | yvIA-SIG+TM(s)->SHOCT-like+Toastrack->PspC->SIG+TM(s)-> <-SIG+TM(s) |
| PspC+Lial-LiaF-TM | | | | |
| ABY34522.1 | Caur_1294 | Chloroflexus aurantiacus J108 | bacteria>chloroflexi | PspC+Lial-LiaF-TM-> |
| PspC+Lial-LiaF-TM+HISKIN | | | | |
| AU13865.1 | SLIV_14405 | Streptomyces lividans TK24 | bacteria>actinobacteria | <-PspC+TM(s)+Toastrack PspC+Lial-LiaF-TM+HISKIN->REC+ wHTH-> |
| PspC+Lial-LiaF-TM+TM(s)+Toastrack | | | | |
| ACV77657.1 | Namu_1253 | Nakamurella multipartita DSM 44233 | bacteria>actinobacteria | <-REC+ wHTH<-PspC+Lial-LiaF-TM+HISKIN PspC+Lial-LiaF-TM+TM(s)+Toastrack->X-> <-SIG+TM(s) |
| PspC+TM(s)+Toastrack | | | | |
| AU13866.1 | SLIV_14410 | Streptomyces lividans TK24 | bacteria>actinobacteria | <-REC+ wHTH<-PspC+Lial-LiaF-TM+HISKIN PspC+TM(s)+Toastrack-> |
| SHOCT-bihelical+Toastrack | | | | |
| CCP43715.1 | Rv0966c | Mycobacterium tuberculosis H37Rv | bacteria>actinobacteria | SHOCT-bihelical+Toastrack-> |
| CAB88834.1 | SCO2893 | Streptomyces coelicolor A32 | bacteria>actinobacteria | TM(s)->TM(s)->ABC-ATPase->SHOCT-bihelical+Toastrack-> |
| SHOCT-like+Toastrack | | | | |
| CAB15517.1 | yvIB | Bacillus subtilis subsp subtilis str 168 | bacteria>firmicutes | yvIA-SIG+TM(s)->SHOCT-like+Toastrack->PspC->SIG+TM(s)-> <-SIG+TM(s) |
| SIG+Lial-LiaF-TM+TM+Toastrack | | | | |
| AEU34960.1 | Acix8_0610 | Granulicella mallensis MP5ACTX8 | bacteria>acidobacteria | SIGMA-Factor->anti-sigma-ZF+TM->TM+Lial-LiaF-TM->SIG+Lial-LiaF-TM+TM+Toastrack-> |
| SIG+Lial-LiaF-TM+Toastrack | | | | |
| CAB15300.1 | liaF | Bacillus subtilis subsp subtilis str 168 | bacteria>firmicutes | Lial-LiaF-TM->PspA->TM+Toastrack->Lial-LiaF-TM+Toastrack->SIG+TM+HAMP+HISKIN->REC+ wHTH-> |
| SIG+TM(s)+Toastrack | | | | |
| ABD31150.1 | SAOUHSC_02100 | Staphylococcus aureus subsp aureus NCTC 8325 | bacteria>firmicutes | SIG+TM(s)+Toastrack->SIG+TM(s)+HISKIN->REC+ wHTH-> <-SIG+TM(s) |
| TM+DUF4178 | | | | |
| CCP45393.1 | Rv2597 | Mycobacterium tuberculosis H37Rv | bacteria>actinobacteria | TM+DUF4178->DUF2617->SIG+DUF4247->YjL-TM+TM(s)->SIG+TM(s)+Spermine_synth-> |
| TM+Toastrack | | | | |
| AUJ31452.1 | BF28_3762 | Bacillus cereus E33L | bacteria>firmicutes | ABC-ATPase->TM(s)->TM+Toastrack-> |
| AAM36414.1 | XAC1545 | Xanthomonas citri pv citri str 306 | bacteria>proteobacteria>gammaproteobacteria | GNTR-HTH->ABC-ATPase->TM(s)->TM+Toastrack->SIG+DUF2884-> |
| AFK03672.1 | Emtol_2536 | Emticicia oligotrophica DSM 17448 | bacteria>FCB_group>bacteroidetes | SIGMA-Factor->anti-sigma-ZF+TM+HEAT->TM+Toastrack->TM+Toastrack-> |
| TM+Toastrack+CASPASE | | | | |
| AFY83227.1 | OscI6304_3666 | Oscillatoria acuminata PCC 6304 | bacteria>cyanobacteria | TM+Toastrack+CASPASE-> |
| ZnR+DUF2089-HTH+SHOCT-like | | | | |
| ADE70705.1 | BMQ_3692 | Bacillus megaterium QM 81551 | bacteria>firmicutes | ZnR+DUF2089-HTH+SHOCT-like->SHOCT-like+X-> |
| ZnR+PspC | | | | |
| ABC83427.1 | Adeh_3661 | Anaeromyxobacter dehalogenans 2CPC | bacteria>proteobacteria>deltaproteobacteria | ZnR+PspC-> |
| More information available on our webapp . | | | | |