**Table S2**. Characteristics of proteins encoded by different rhizobial T6SS genes (no *tss* or *tag* genes).

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Strain** | **NCBI ID** | **aa** | **Conserved domain1** | **Phyre22**  **Template information**  **Confidence3, identity, coverage (aa positions)** | **Signal**  **Peptide4** | **Bastion65** |
| *B. nanningense*  CCBAU 53390 | WP\_128917634.1 | 187 | No putative domain | Confidance <50% | No | No |
| WP\_164936006.1 | 528 | Methyltransferase PAM13847 (48-213) Methyltranserase regulatory PFAM10119 (222-306) | Lysine methyltransferase from *Rickettsia typhi*  100% , 28%, 94% (26-532) | No | No |
| *B.elkanii*  SEMIA 938 | WP\_137479828.1 | 187 | No putative domain | Confidance <50% | No | No |
| WP\_155262194.1 | 528 | Methyltransferase PAM13847 (53-225) Methyltranserase regulatory PFAM10119 (227-311) | Lysine methyltransferase from *Rickettsia typhi*  100%, 29%, 94% (26-532) | No | No |
| *B. pachyrhizi*  BR3262 | WP\_057019592 | 187 | No putative domain | Confidance <50% | No | No |
| WP\_057019682.1 | 528 | Methyltransferase PAM13847 (48-213) Methyltranserase regulatory PFAM10119 (222-306) | Lysine methyltransferase from *Rickettsia typhi*  100% , 28%, 94% (26-532) | No | No |
| *B. japonicum* SEMIA 5019 | WP\_016843428.1 | 187 | No putative domain | Confidance <50% | No | No |
| WP\_038380522.1 | 528 | Methyltransferase PAM13847 (48-213) Methyltranserase regulatory PFAM10119 (222-306) | Lysine methyltransferase from *Rickettsia typhi*  100% , 28%, 94% (26-532) | No | No |
| *B. japonicum* SEMIA 5079 | AHY53437.1 | 116 | No putative domain | Confidance <50% | No | No |
| AHY53447.1 | 533 | Methyltransferase PAM13847 (53-225) Methyltranserase regulatory PFAM10119 (227-311) | Lysine methyltransferase from *Rickettsia typhi*  100%, 29%, 94% (26-532) | No | No |
| *B. diazoefficiens* SEMIA 5080 | KGJ69127.1 | 187 | No putative domain | Confidance <50% | No | No |
| KGJ69117.1 | 533 | Methyltransferase PFAM13847 (53-225)  Methyltranserase regulatory PFAM10119 (227-311) | Lysine methyltransferase from *Rickettsia typhi*  100%, 29%, 94% (26-532) | No | No |
| *B. elkanii*  SEMIA 5019 | RYM19864.1. | 187 | No putative domain | Confidance <50% | No | No |
| RYM19874.1. | 533 | Methyltransferase PFAM13847 (53-217)  Methyltranserase regulatory PFAM10119 (227-311) | Lysine methyltransferase from *Rickettsia typhi*  100%, 29%, 94% (26-532) | No | No |
| *M. ciceri*  CC1192 | WP\_024504492.1 | 776 | M23 family metallopeptidase | Shya endopeptidase from *Vibrio cholerae* (open form) | No | Yes |
| WP\_081714360.1 | 131 | DUF1036 PFAM06282 | Confidance <50% | Yes | No |
| WP\_164752018.1 | 362 | No putative domain | De novo designed 16-helix transmembrane nanopore  99.9%, 15 %,67% (56-301) | No | No |
| WP\_013525293.1 | 265 | No putative domain | Confidance <50% | No | No |
| WP\_013525294.1 | 189 | SMI1/KNR4 PFAM09346 (26-148) | SMI1/KNR4-like  100%, 18%, 89% (1-171) | No | No |
| WP\_082826755.1 | 253 | DUF 4150/PAAR (N-terminal)  DNase\_NucA\_NucB  (C-terminal 194-252) | *Enterobacteria phage* T4 gp5.4 PAAR repeat protein in complex with t42 gp5 beta-helix fragment 97%21%, 37% (27-121)  Endonuclease nucb  99.8%, 25%, 44% (140-252) | No | Yes |
| WP\_013525296.1 | 351 | Beta-ketoacyl synthase, N-terminal domain | Beta-ketoacyl-acp synthase II (fabf) from 2 *Staphylococcus aureus*  100%, 18%, 94%(4-350) | No | No |
| WP\_063170596.1 | 353 | DUF1036 PFAM09937 | Sulfite oxidase provides2 insight into sulfite oxidation in plants and animals  81.9%, 10%, 29% (62-166) | No | Yes |
| *M. mediterraneum*  USDA 3392 | PAQ00276.1 | 551 | Peptidase\_C14 PFAM00656  Caspase domain | Mucosa-associated lymphoid tissue lymphoma translocation  (MALT1) Paracaspase | Yes | No |
| PAQ00277.1 | 777 | M23 family metallopeptidase | Shya endopeptidase from *Vibrio cholerae* (open form) | No | Yes |
| PAQ00482.1 | 131 | DUF1036 PFAM06282 | c2ahnA. Thaumatin-like protein; cherry allergen pru av  72.1%, 7%, 40% (17-70) | Yes | No |
| PAQ00483.1 | 141 | No putative domain | Central spike of the type VI secretion system  99.9%, 31%, 95%, (6-141) | No | No |
| PAQ00284.1 | 387 | No putative domain | de novo designed 16-helix transmembrane nanopore  99.9%, 15 %,71% (12-290) | No | No |
| PAQ00285.1 | 347 | No putative domain | 3-oxoacyl-[acyl-carrier-protein] synthase from *Staphylococcus aureus* 100%, 13%, 95% (1-332)  Transferase, C-terminal part of rhie from *Burkholderia rhizoxinica* 100%, 13%, 95% (1-332) | Yes | No |
| PAQ00286.1 | 362 | DUF1036 PFAM09937 | Sulfite dehydrogenase from S*tarkeya novella*  79.3%, 15%, 27% (65-164) | No | Yes |
| PAQ00287.1 | 162 | No putative domain | N-terminal coiled coil domain of the 2 andes hantavirus nucleocapsid protein  50.5%, 27%, 35% (13-71) | No | No |
| PAQ00288.1. | 137 | No putative domain | Structure of a brca2-dss1 complex  51.5%, 43%, 23% (69-104) | No | No |
| PAQ00289.1. | 300 | DUF4150  PAAR | *Enterobacteria phage* t4 gp5.4 PAAR repeat protein in complex with t42 gp5 beta-helix fragment  97.6,19%,33%(26-125) | No | Yes |
| *Mesorhizobium* sp. 3007 | WP\_069092792.1 | 141 | DUF2345  PF10106 | Central spike of the type VI secretion system  99.9%, 32%, 95% (6-141) | No | No |
| WP\_069092799.1 | 441 | Peptidase\_C14 PFAM00656  Caspase domain | Mucosa-associated lymphoid tissue lymphoma translocation  (MALT1) Paracaspase  100%, 24%, 56% (27-277) | Yes | No |
| WP\_069092798.1 | 807 | M23 family metallopeptidase | Shya endopeptidase from *Vibrio cholerae* (open form)  100%, 22, 43%(244-593 | No | Yes |
| WP\_019859812.1 | 166 | DUF1036 PFAM06282 | Confidance <50% | Yes | No |
| WP\_141700965.1 | 115 | No putative domain | Confidance <50% | No | No |
| WP\_032931245.1 | 299 | No putative domain | Maltose binding protein fusion with rack1 from *A. thaliana*  100%, 11%, 91%(13-288) | No | Yes |
| WP\_083246836.1 | 368 | DUF4150  PAAR | *Enterobacteria phage* t4 gp5.4 PAAR repeat protein in complex with t42 gp5 Beta-helix fragment 96.7%,19%, 27% (25-125)  Phycocyanin-like phycobilisome proteins 79.9%, 22%, 16% (245-305) | No | Yes |
| WP\_069092790.1 | 341 | Beta-ketoacyl synthase, N-terminal domain  PFAM00109 | Transferase, C-terminal part of rhie from *Burkholderiarhizoxinica*  100%, 14%, 98% (1-336)  Beta-ketoacyl-acp synthase II (fabf) from *Staphylococcus aureus* 100%, 16%, 97% (3-337) | Yes | No |
| WP\_069092789.1 | 367 | DUF2169  PFAM09937 | Molybdenum-containing oxidoreductases-like dimerisation domain  74.0%, 37%, 11% (62-103) | No | Yes |
| *S. fredii* HH103 (USDA 207) | WP\_153458313.1 | 172 | No putative domain | Glycosyl-asparaginase PHM/PNGase F 66.9%, 36%, 22% (3-41) | No | No |
| WP\_153458314.1 | 712 | Peptidase\_C14  PFAM00656  Caspase domain (35-253) | MALT1 paracaspase (p21 form), mucosa-associated lymphoid tissue lymphoma translocation 100%, 21%, 33% (31-269) | Yes | No |
| WP\_153458316.1 | 141 | DUF2345  PF10106 | Central spike of the type VI 2 secretion system  99.9%, 34%, 96% (5-141) | No | No |
| WP\_153458317.1 | 115 | No putative domain | Confidance <50% | No | No |
| WP\_153458318.1. | 324 | DUF4150  PAAR | *Enterobacteria* phage t4 gp5.4 PAAR repeat protein in complex with t42 gp5 beta-helix fragment 97.5%,22%, 30% (25-125) | No | Yes |
| WP\_153458319.1 | 343 | Beta-ketoacyl synthase, N-terminal domain  PFAM00109 | Transferase, C-terminal part of rhie from *Burkholderia rhizoxinica*  100%, 16%, 99% 1-343) | No | No |
| WP\_153458320.1 | 366 | DUF2169 PFAM09937 | Molybdenum-containing oxidoreductases-like dimerization 79.2%, 37%, 11% (62-103) | No | Yes |
| WP\_153458333.1 | 248 | OmpA family protein PFAM00691 | Maltose/Maltodextrin-binding periplasmic protein, *tssl*;  100%, 19%, 54% (111-246) | Yes | No |
| WP\_153458335.1 | 291 | M15 family metallopeptidase  PFAM13539 | L-Ala D-Glu endopeptidase2 chix of *Serratia marcescens*  99.6%, 23%, 21% (216-280) | No | No |
| WP\_153458336.1 | 1122 | AAA ATPase domain PFAM13191 | Bacteriophytochrome,adenylate cyclase  100%, 27%, 21% (26-264) | No | No |
| WP\_153458345.1 | 319 | No putative domain | Two-component system sensor histidine kinase/response; periplasmic domain  99.9, 7%, 97% (7-318) | No | Yes |
| *R. ruizarguesonis* UPM1132 | WP\_168250378.1 | 197 | No putative domain | Confidance <50% | No | No |
| WP\_130665622.1 | 369 | DUF1036 PFAM09937 | Sulfite dehydrogenase from *Starkeya novella*  67.7%, 18%, 34% (60-188) | No | Yes |
| WP\_168250373.1 | 508 | DUF4150  PAAR | *Enterobacteria phage* t4 gp5.4 PAAR repeat protein in complex with t42 gp5 beta-helix fragment  97.1 %, 29%, 18% (38-133) | No | Yes |
| WP\_130656480.1 | 349 | No putative domain | Maltose binding protein fusion with rack1 from *A. thaliana*  99%, 12%, 81% (8-294) | No | Yes |
| WP\_168250371.1 | 250 | GAD-like domain PFAM08887 | Type VI immunity protein atu4351 from *Agrobacterium tumefaciens*  100%, 21%, 98% (5-250) | No | No |
| WP\_168250559.1 | 132 | No putative domain | Two-component system sensor histidine kinase/response 99.6%, 10%, 93% (1-125) | No | No |
| WP\_168250369.1 | 391 | No putative domain | two-component system sensor histidine kinase/response  99.8%, 10%, 77% (85-387) | No | Yes |
| WP\_168250367.1 | 370 | No putative domain | two-component system sensor histidine kinase/response  100%, 9%, 93% (17-364) | No | Yes |
| *R. ruizarguesonis* UPM1133 | WP\_174827073.1 | 360 | No putative domain | Alkaline d-peptidase from *Bacillus cereus*  58.8%, 21%, 27% (232-331) | No | No |
| WP\_168575696.1 | 298 | No putative domain | Hypothetical protein pa0856 from *Pseudomonas aeruginosa* 68.6%, 28%, 17% (236-289) | Yes | No |
| WP\_168575683.1 | 369 | DUF1036 PFAM09937 | Molybdenum-containing oxidoreductases-like dimerisation domain 65.3%, 24%, 11% (60-101) | No | Yes |
| WP\_168575684.1 | 508 | DUF4150PAAR PFAM1366 | Hydrolase. *Enterobacteria phage* T4 gp5.4 PAAR repeat protein in complex with t42 gp5 beta-helix fragment  97.2%, 29%, 18% (38-132) | No | Yes |
| WP\_168575685.1 | 349 | No putative domain | Endo-1,4-Beta-glucanase/xyloglucanase, putative, gly74a; 99.9%, 16%, 96% (12-348) | No | Yes |
| *R. ruizarguesonis* UPM1134 | WP\_168250378.1 | 197 | No putative domain | Confidance <50% | No | No |
| WP\_130665622.1 | 369 | DUF1036 PFAM09937 | Sulfite dehydrogenase from *Starkeya novella*  67.7, 18%, 34% (60-188) | No | Yes |
| WP\_168250373.1 | 508 | DUF4150 PAAR PFAM1366 | *Enterobacteria phage* T4 gp5.4 PAAR repeat protein in complex with t42 gp5 beta-helix fragment  97.1 %, 29%, 18% (38-133) | No | Yes |
| WP\_130656480.1 | 349 | No putative domain | Maltose binding protein fusion with rack1 from A. thaliana  99%, 12%, 81% (8-294) | No | Yes |
| WP\_168250371.1 | 250 | Gad-like domain PFAM08887 | Type VI immunity protein atu4351 from *Agrobacterium tumefaciens*  100%, 21%, 98% (5-250) | No | No |
| WP\_174826651.1 | 114 | No putative domain | Two-component system sensor histidine kinase/ response; 89.4%, 16%, 58% (31-98) | No | Yes |
| WP\_168250369.1 | 391 | No putative domain | two-component system sensor histidine kinase/response;  99.8%, 10%, 77% (85-387) | No | Yes |
| WP\_168250367.1 | 370 | No putative domain | two-component system sensor histidine kinase/response  100%, 9%, 93% (17-364) | No | Yes |
| *R. laguerreae* OL29 | WP\_025397012.1 | 355 | DUF4123 domain PFAM13503 | 1-deoxy-d-xylulose 5-phosphate reductoisomerase; 79.1%, 16%, 16% (2-62)  NAD(P)-binding Rossmann-fold domains 78.6%, 11%, 32% (2-118) | No | No |
| WP\_025397013.1 | 274 | No putative domain | Confidance <50% | No | Yes |
| WP\_025397014.1 | 192 | SMI1/KNR4 PFAM09346 | Glucan synthesis regulator of SMI1/KNR4 family 99.9%, 16%, 79% (26-178) | No | Yes |
| WP\_131661147.1 | 229 | No putative domain | Glutathione biosynthetic ligase from *Escherichia coli* 83%, 20%, 41% (121-216) | No | No |
| WP\_165503763.1 | 89 | PAARmotif domain PFAM05488 | *Enterobacteria phage* T4 gp5.4 PAAR repeat protein in complex with t42 gp5 beta-helix fragment  99%, 20%, 95% (3-88) | No | No |
| WP\_025397017.1 | 224 | GAD like domain PFAM0887 | Type VI immunity protein atu4351 from *Agrobacterium tumefaciens* 100%, 57% 96% (8-224) | No | No |
| WP\_080685848.1 | 100 | PAAR motif domain PFAM05488 | PAAR-repeat protein from *Escherichia coli* in complex with a2 *vgrG*-like beta-helix that is based on a fragment of t4 gp5 100%, 25%, 94% (5-99) | No | No |
| WP\_025397019.1 | 221 | GAD like domain PFAM08887 (6-109), DUF1851 PFAM08906 (133-201) | Type VI immunity protein atu4351, tdi1  100%, 33%, 95% (9-221)  SMI1/KNR4-like, 93.2%, 15%, 39% (7-95) | No | No |
| WP\_025397020.1 | 199 | No putative domain | P-loop containing nucleoside triphosphate hydrolases 62.8%, 22%, 29% (99-158) | No | No |
| WP\_168339500.1 | 242 | GAD like domain PFAM08887 (13-116), DUF1851 PFAM08906 (151-213) | Type VI immunity protein atu4351 from *Agrobacterium tumefaciens* 100%, 29%, 93% (15-241) | No | No |
| WP\_131661145.1 | 392 | No putative domain | Type malate/lactate dehydrogenase from *Thermus thermophilus* HB8 63.4%, 25%, 14% (219-275) | No | No |
| *R. leguminosarum* bv. *viciae* L145 | WP\_128403421.1 | 358 | No putative domain | Alpha/beta hydrolase 58.6%, 23%, 20% (227-301); Alkaline D-peptidase from *Bacillus cereus* 50.3%, 21%, 27% (230-329) | No | Yes |
| WP\_128403450.1 | 298 | No putative domain | Confidance <50% | Yes | No |
| WP\_130809847.1 | 369 | DUF1036 PFAM09937 | Molybdenum-containing oxidoreductases-like dimerization 66.1%, 20% 11% (60-101) | No | Yes |
| WP\_168325346.1 | 499 | DUF4150 PFAM13665 | *Enterobacteria phage* t4 gp5.4 PAAR repeat protein in complex with t42 gp5 beta-helix fragment  97 %, 23%, 18% (32-132) | No | Yes |
| WP\_128403418.1 | 330 | DUF3396 PFAM11876 | Confidance <50% | No | No |
| WP\_128403417.1 | 128 | tusA domain PFAM01206 | SirA functions as a response regulator as part of a two-component system  99.8%, 32%, 54% (48-118) | No | No |
| WP\_168325337.1 | 500 | DUF4150 PF13665  PAAR repeat | *Enterobacteria phage* t4 gp5.4 PAAR repeat protein in complex with t42 gp5 beta-helix fragment  97.2%, 17%, 18% (41-133) | No | Yes |
| WP\_128403415.1 | 370 | No putative domain | two-component system sensor histidine kinase/response;  99.9%, 8%, 97% (2-364) | No | Yes |
| WP\_128403414.1 | 221 | GAD like domain PFAM08887 (6-109) DUF1851 PFAM (133-201) | Type VI immunity protein atu4351 from *Agrobacterium tumefaciens* 100%, 33%, 96% (8-221) | No | No |
| WP\_128403413.1 | 150 | No putative domain | Myosin chaperone unc-45 from *C.elegans* in2 complex with a hsp70 peptide  99.8%, 14%, 75% (15-128) | No | No |
| WP\_168325336.1 | 101 | No putative domain | 99.4%, 21%, 70% (12-83) | No | No |
| WP\_128403421.1 | 358 | No putative domain | Alpha/beta hydrolase  58.6%, 23%, 20% (227-301) | No | Yes |
| WP\_128403411.1 | 199 | No putative domain | Confidance <50% | No | No |
| WP\_168325335.1 | 303 | No putative domain | Confidance <50% | No | No |
| WP\_128403409.1 | 329 | DUF3396 PFAM11876 | Confidance <50% | No | No |
| WP\_130809850.1 | 250 | GAD like domain PFAM08887 | Type VI immunity protein atu4351, tdi1  100%, 18%, 97% (2-246) | No | Yes |
| WP\_128411129.1 | 198 | No putative domain | Two-component system sensor histidine kinase/response;  99.12%, 8%, 94% (2-189) | No | Yes |
| *Rhizobium* sp. SEMIA 4032 | TGE87375.1 | 129 | Tai4, Ssp | Type VI immunity tai4 from *Agrobacterium tumefaciens*  100%, 97%, 76%(26-125) | Yes | No |
| TGE87376.1 | 166 | Tae4, Rap | Type VI immunity tae4 from *Agrobacterium tumefaciens*  100%, 95%, 97%(1-163) | No | Yes |
| TGE87378.1 | 371 | DUF2169 PFAM09937 | Molybdenum-containing oxidoreductases-like dimerization 70.3%, 27%, 11% (60-101) | No | Yes |
| TGE87379.1 | 366 | No putative domain | Ycf48-like protein from *Thermosynechococcus elongates* 99.3%, 12%, 85% (44-357) | No | Yes |
| TGE86662.1 | 402 | DUF1036 PFAM09937 | Molybdenum-containing oxidoreductases-like dimerization 68%, 20%, 10% (61-102) | No | Yes |
| TGE86661.1 | 195 | DUF4150PAARPFAM13665 | *Enterobacteria phage* T4 gp5.4 PAAR repeat protein in complex with t42 gp5 beta-helix fragment 97.6%, 21%, 47% (21-113) | No | Yes |
| TGE86660.1 | 169 | No putative domain | Ribonuclease H-like motif  63.6%, 33%, 8% (42-56) | No | No |
| TGE86659.1 | 1458 | RHS repeat domain PFAM05593 | Teneurin 2 partial extracellular domain, transmembrane glycoproteins, The C-terminal teneurin scaffold shows a strong similarity to the TcB-TcC subcomplex of bacterial ABC insecticidal toxin complexes (Tc)  100%,15%,73% (257-1335), | No | Yes |
| TGE86658.1 | 283 | No putative domain | Internalin B (inlb), a *Listeriamonocytogenes* virulence protein containing sh3-like3 domains  73.5%, 24%,44%( 91-217) | No | No |
| *Rhizobium* sp. SEMIA 439 | TGE77457.1 | 129 | Tai4, Ssp | Type VI effector-immunity complex (tae4-tai4)2 from *Agrobacterium tumefaciens* 100%, 94%, 76% (26-125) | Yes | No |
| TGE77456.1 | 166 | Tae4, Rap | Type vi effector-immunity complex (tae4-tai4)2 from *Agrobacterium tumefaciens* 100%, 94%, 97% (1-163) | No | Yes |
| TGE77454.1 | 371 | DUF2169 PFAM09937 | Molybdenum-containing oxidoreductases-like dimerization 72.5%, 27%, 11% (60-101) | No | Yes |
| TGE77453.1 | 366 | No putative domain | Ycf48-like protein from *Thermosynechococcus elongates* 99.2%, 10%, 87% (44-365) | No | Yes |
| TGE78293.1 | 354 | DUF4123 PFAM13503 | Barwin-like endoglucanases MLTA-like 57%, 19%, 33% (126-245) | No | No |
| TGE78292.1 | 282 | No putative domain | Confidance <50% | No | Yes |
| TGE78291.1 | 175 | SMI1/KNR4 family PFAM09346 | Cell wall assembly regulator SMI1/KNR4-like  99.9%, 16%, 97% (2-173) | No | Yes |
| TGE78290.1 | 202 | SMI1-KNR4 cell wall PFAM14568 | SMI1/KNR4-like 97.1%, 16%, 70% (43-186) | No | Yes |
| TGE78289.1 | 176 | SMI1-NR4 PFAM09346 | SMI1/KNR4-like 95.9%, 21%, 95% (3-171) | No | Yes |
| TGE78288.1 | 238 | No putative domain | Cell division cycle protein 123 complexed with the C-terminal domain of eukaryote initiation factor gamma  96%, 21%, 86% (18-223) | No | No |
| TGE78287.1 | 101 | PAAR motif PFAM05488 | c1882 PAAR-repeat protein from *Escherichia coli* in complex with a2 *vgrG*-like beta-helix that is based on a fragment of t4 gp5  99.9%,24%, 94% (5-100) | No | No |
| *R. leguminosarum* CCBAU 30058 | WP\_168252851.1 | 358 | No putative domain | Confidance <50% | No | Yes |
| WP\_168252901.1 | 298 | No putative domain | Confidance <50% | Yes | No |
| WP\_168252846.1 | 250 | GAD like PFAM08887 | Type VI immunity protein atu4351 from *Agrobacterium tumefaciens* 100% 21%, 76% (5-195) | No | Yes |
| WP\_168252845.1 | 392 | No putative domain | type 2 malate/lactate dehydrogenase from *Thermus thermophilus* HB8, 75.3%, 23%, 14% (219-275) | No | No |
| WP\_168252849.1 | 369 | DUF1036 PFAM09937 | Molybdenum-containing oxidoreductases-like dimerization 70.3%, 24%, 11% (60-101) | No | Yes |
| WP\_168252848.1 | 508 | DUF4150 PAAR | *Enterobacteria phage* t4 gp5.4 PAAR repeat protein in complex with t42 gp5 beta-helix fragment  97.1 %, 29%, 18% (38-133) | No | Yes |
| WP\_168252695.1 | 305 | No putative domain | Two-component system sensor histidine kinase/response 100%, 11%, 97% (6-304) | No | No |
| WP\_168252847.1 | 349 | No putative domain | two-component system sensor histidine kinase/response 100%, 10%, 98% (2-345) | No | Yes |

1: Pfam protein families database (El-Gebali et al., 2019)

2: Phyre2 web portal (Kelley et al., 2015)

3: Only confidence higher than 50 % are detailed.

4: SignalP-5.0 Server: “Yes” score higher than 50%, (Armenteros et al., 2019)

5: Bastion6 Server predicting T6SS effectors: “Yes” score higher than 50%, (Wang et al., 2018)

**REFERENCES**

Armenteros, J. J. A., Tsirigos, K. D., Sønderby, C. K., Petersen, T. N., Winther, O., Brunak, S., et al. (2019). SignalP 5.0 improves signal peptide predictions using deep neural networks. *Nat. Biotechnol*. 37, 420-423. doi: 10.1038/s41587-019-0036-z

El-Gebali, S., Mistry, J., Bateman, A., Eddy, S. R., Luciani, A., Potter, S. C., et al. (2019). The Pfam protein families database in 2019. *Nucleic Acids Res*. 47, D427-D432. doi:10.1093/nar/gky995

Kelley, L. A., Mezulis, S., Yates, C. M., Wass, M. N. and Sternberg, M. J. E. (2015). The Phyre2 web portal for protein modeling, prediction and analysis. *Nat. Protoc*. 10, 845–858.doi:10.1038/nprot.2015.053

Wang, J., Yang, B., Leier, A., Marquez-Lago, T. T., Hayashida, M., Rocker, A et al. (2018). Bastion6: a bioinformatics approach for accurate prediction of type VI secreted effectors. *Bioinformatics*, 34, 2546–2555. https://doi.org/10.1093/bioinformatics/bty155