

**Supplementary Table S2.** Sequence characteristics of proteins that are encoded by genes immediately downstream of the *atpase* gene in various T3SS gene clusters.

T3SS family	Organism	Gene / Locus	Entrez Protein ID	Number of residues	Predicted disordered segments <sup>‡</sup> %	Predicted $\alpha$ -helix %	Predicted heptad repeats %
Ysc	<i>Aeromonas salmonicida</i> subsp. <i>salmonicida</i> A449	<i>ascO</i>	YP_00114 4299	153	98.7	94.0	95
	<i>Photorhabdus luminescens</i>	<i>lscO</i>	AAO1804 3	153	100	94.0	79
	<i>Pseudomonas aeruginosa</i> PAO1	<i>pscO</i>	NP_25038 7	158	94.3	91.1	92
	<i>Yersinia pestis</i> CO92	<i>yscO</i>	NP_39517 5	154	100	94.8	90
	<i>Vibrio parahaemolyticus</i> RIMD 2210633	<i>yscO</i>	BAC5993 2	153	96.1	96.7	91
	<i>Bordetella pertussis</i> Tohama I	<i>bscO</i>	NP_88088 7	169	57.4	91	88
Hrc1	<i>Pseudomonas syringae</i> pv. <i>phaseolicola</i>	<i>hrpO</i>	AAC2506 5	148	72.3	93.2	77
	<i>Pantoea stewartii</i> subsp. <i>stewartii</i>	<i>hrpO</i>	ABB7741 3	146	100	95.2	76
	<i>Erwinia amylovora</i>	<i>hrpO</i>	AAB0600 2	148	100	95.9	76
Hrc2	<i>Ralstonia solanacearum</i> GMI1000	<i>hrpd</i>	CAD1802 2	166	71.7	92.2	83
	<i>Burkholderia pseudomallei</i>	<i>orf7</i>	AAK7323 2	168	54.7	92.9	75
	<i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> str. 85-10	<i>hrpB7</i>	CAJ22064	169	51.5	90.5	63
Ssa-Esc	<i>Salmonella typhimurium</i> LT2 (SPI-2)	<i>ssaO</i>	NP_46038 1	125	40.8	85.6	72

T3SS family	Organism	Gene / Locus	Entrez Protein ID	Number of residues	Predicted disordered segments <sup>‡</sup> %	Predicted $\alpha$ -helix %	Predicted heptad repeats %
	<i>Edwardsiella tarda</i>	<i>orf1B</i>	AAX7691 9	122	83.6	86.0	97
	<i>Yersinia pestis</i> CO92	<i>ypO0268</i>	NP_40391 9	133	100	91.0	85
	Enteropathogenic <i>Escherichia coli</i> E2348/69	<i>orf15</i>	AAK2671 6	125	77.6	88.8	83
	<i>Chromobacterium violaceum</i> ATCC 12472	<i>CV_2604</i>	AAQ6027 4	119	68.9	91.6	88
	<i>Salmonella enterica</i> subsp. enterica serovar Typhi str. CT18	<i>ssaO</i>	NP_45611 2	125	40.8	86.4	87
	<i>Salmonella enterica</i> (serovar typhimurium) LT2	<i>invI</i>	NP_46181 4	147	58.5	92.5	79
	<i>Burkholderia pseudomallei</i> K96243	<i>bsaT</i>	YP_11154 6	154	32.5	87.0	88
<i>Inv-Mxi-Spa</i>	<i>Escherichia coli</i> O157:H7 str. Sakai	<i>eivI</i>	BAB3715 2	111	63.9	89.1	77
	<i>Shigella flexneri</i>	<i>spa13</i>	CAC0582 5	112	59.8	89.3	43
	<i>Sodalis glossinidius</i>	<i>spaM-like</i>	AAG4860 3	154	27.3	77.3	33
	<i>Yersinia enterocolitica</i> A127	<i>orf8</i>	AAK8413 0	151	82.8	93.4	92
<i>Chlamydiales</i>	<i>Chlamydia trachomatis</i> D/UW-3/CX	<i>CT670</i>	NP_22018 9	168	89.3	91.7	92
	<i>Chlamydomphila pneumoniae</i> AR39 ( <i>Chlamydia pneumoniae</i> AR39)	<i>CP_0040</i>	AAF3793 5	168	82.7	91.6	89

<b>T3SS family</b>	<b>Organism</b>	<b>Gene / Locus</b>	<b>Entrez Protein ID</b>	<b>Number of residues</b>	<b>Predicted disordered segments<sup>‡</sup> %</b>	<b>Predicted <math>\alpha</math>-helix %</b>	<b>Predicted heptad repeats %</b>
<i>Rhizo- biales</i>	<i>Mesorhizobium loti</i>	<i>mlr634</i>	BAB5265	177	37.3	90.9	58
	MAFF303099	3	3				
	<i>Rhizobium</i> sp. NGR234	<i>y4yJ</i>	NP_44416 2	178	66.3	91.0	77
Flagella	<i>E. coli</i>	<i>fliJ</i>	P52613	147	100	91.2	86

<sup>‡</sup>The % ratio represents the percentage of amino acids assigned with negative score by FoldIndex.