

Supplementary Table S3: Sequence characteristics of HrpE homologues in various T3SS

T3SS family	Organism	Gene / Locus	Entrez Protein ID	Number of residues	Predicted disordered segments [‡] %	Predicted α -helix %	Predicted heptad repeats %
Ysc	<i>Aeromonas salmonicida</i> subsp. <i>salmonicida</i> A449	<i>ascL</i>	YP_001144270	221	3.6	63.8	64
	<i>Photorhabdus luminescens</i>	<i>lscL</i>	AAO18079	205	29.8	67.3	56
	<i>Pseudomonas aeruginosa</i> PAO1	<i>pscL</i>	NP_250416	214	21	63.1	68
	<i>Yersinia pestis</i> CO92	<i>yscL</i>	NP_395195	221	17.2	65.2	50
	<i>Vibrio parahaemolyticus</i> RIMD 2210633	<i>vp1688</i>	NP_798067	212	14.6	65.1	60
	<i>Bordetella pertussis</i> Tohama I	<i>bscL</i>	NP_880889	212	25.5	67.9	58
Hrc1	<i>Pseudomonas syringae</i> pv. phaseolicola	<i>hrpE</i>	AAF99296	194	0	63.9	52
	<i>Pantoea stewartii</i> subsp. <i>stewartii</i>	<i>hrpE</i>	AAG01460	199	34.7	60.8	38
	<i>Erwinia amylovora</i>	<i>hrpE</i>	AAB49176	196	50	67.3	49
Hrc2	<i>Ralstonia solanacearum</i> GMI1000	<i>hrpF</i>	NP_522430	301	29.2	59	65
	<i>Burkholderia pseudomallei</i>	<i>sctL</i>	AAK73234	289	30.8	57.8	57
	<i>Xanthomonas campestris</i> pv. <i>Vesicatoria</i> str. 85-10	<i>hrcL</i>	YP_362162	233	17.6	70.8	54
Ssa-Esc	<i>Salmonella typhimurium</i> LT2	<i>ssaK</i>	NP_460376	224	34.8	69.6	26
	<i>Edwardsiella tarda</i>	<i>esaK</i>	AAX55260	271	18.1	55	43
	<i>Yersinia pestis</i> CO92	<i>ypo026</i> ₅	NP_403916	215	0	68.4	26
	Enteropathogenic <i>Escherichia coli</i> E2348/69	<i>orf5</i>	AAC38368	231	22.5	62.8	29
	<i>Chromobacterium violaceum</i> ATCC12472	<i>cv_259</i> ₄	NP_902264	268	19	65.3	50
	<i>Salmonella enterica</i> subsp. <i>Enterica</i> serovar Typhi str. CT18	<i>sty170</i> ₉	NP_456117	224	34.8	69.6	26
Inv-Mxi-Spa	<i>Salmonella typhimurium</i> LT2	<i>orgB</i>	NP_461790	226	37.2	71.3	28
	<i>Burkholderia pseudomallei</i> K96243	<i>sctL</i>	YP_111407	289	30.8	60.1	57

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	<i>Shigella flexneri</i> 2a str. 301	<i>mxiN</i>	NP_858274	231	26.9	73	70
	<i>Sodalis glossinidius</i> str. morsitans	<i>sg2074</i>	YP_455754	215	18.1	68.8	46
	<i>Yersinia enterocolitica</i> A127	<i>yscL</i>	AAN37554.1	223	17.1	64	59
<i>Chlamydiales</i>	<i>Chlamydia trachomatis</i> D/UW-3/CX	<i>yscL</i>	NP_220076	223	31.4	65	33
	<i>Chlamydomydia pneumoniae</i> AR39	<i>cp1045</i>	NP_445582	233	31.3	64.8	32
<i>Rhizobiales</i>	<i>Mesorhizobium loti</i> MAFF303099	<i>noIV</i>	NP_106865	207	0	66.7	21
	<i>Rhizobium</i> sp. NGR234	<i>noIV</i>	NP_444160	208	18.3	66.3	29
<i>Flagella</i>	<i>Escherichia coli</i> O157:H7 EDL933	<i>fliH</i>	NP_288401	235	40.9	63	48

[‡]The % ratio represents the percentage of amino acids assigned with negative score by FoldIndex.