



Figure S1. WebLogo of the RS_TY motif. The MEME motif search was performed on the upstream regions (-300) of known Type IV effectors encoding genes in α -proteobacteria. The motif logo was generated by WebLogo (61).

```

# S4TE 1.0
# Use of compilation.pl program version 1.0
# File list: /Users/pathway_to_S4TE/S4TE/Jobs/jobLegionellapneumophila2013541428/
FileList.txt
# threshold : 5
# Weighting code : 1311111111111
# The code corresponds to the boolean result in the following software sequence :
# RS_TY.pl blastcut.pl PfamManager.pl NLS.pl Mitocut.pl CaaX.pl pepcoilcut.pl charge.pl
hydro.pl E-block.pl
# Compilation on 4/5/2013 at 15h41
//
Number of proteins with a score of 9 : 4
Number of proteins with a score of 8 : 16
Number of proteins with a score of 7 : 63
Number of proteins with a score of 6 : 108
Number of proteins with a score of 5 : 123
Number of proteins with a score of 4 : 229
Number of proteins with a score of 3 : 554
Number of proteins with a score of 2 : 955
Number of proteins with a score of 1 : 712
//
lpg0695 : ankyrin repeat-containing protein [Legionella pneumophila pneumophila
Philadelphia-1]
Score : 9
number of hits : 7
Code : 0110000111110    SIL : 1 PIL : 0

//
lpg2490 : LepB [Legionella pneumophila pneumophila Philadelphia-1]
Score : 9
number of hits : 7
Code : 1100100101110    SIL : 1 PIL : 0

//
lpg1701 : kinectin 1 (kinesin receptor) [Legionella pneumophila pneumophila
Philadelphia-1]
Score : 9
number of hits : 7
Code : 1100100100111    SIL : 1 PIL : 0

//
lpg1227 : hypothetical protein [Legionella pneumophila pneumophila Philadelphia-1]
Score : 9
number of hits : 7
Code : 1110000100111    SIL : 1 PIL : 0

//
lpg1953 : coiled-coil-containing protein [Legionella pneumophila pneumophila
Philadelphia-1]
Score : 8
number of hits : 6
Code : 1100100100110    SIL : 1 PIL : 0

//
lpg1890 : leucine-rich repeat- and coiled coil-containing protein [Legionella pneumophila
pneumophila Philadelphia-1]
Score : 8
number of hits : 6
Code : 0110000101110    SIL : 1 PIL : 0

```

Figure S2. Example of S4TE output file (*CompilationFile.txt*)

```
# S4TE 1.0 summary results
# Genome : jobLegionellapneumophila201353137
# Threshold : 5
# Weighting code : 13111111111111
```

Results:

```
Number of proteins with a score of 9 : 4
Number of proteins with a score of 8 : 16
Number of proteins with a score of 7 : 63
Number of proteins with a score of 6 : 108
Number of proteins with a score of 5 : 123
Number of proteins with a score of 4 : 229
Number of proteins with a score of 3 : 554
Number of proteins with a score of 2 : 955
Number of proteins with a score of 1 : 712
```

Hits Results :

```
GeneNumber;CDS_name;start;end;3'FIR;5'FIR;Nb Hits
637131911;lpg1972;2212015;2212392;223;463;3
637131296;lpg1356;1501020;1502150;138;486;3
637131465;lpg1525;1688628;1689866;13;74;5
637131085;lpg1144;1258828;1259334;346;258;4
637130562;lpg0621;654121;655545;89;160;3
637132655;lpg2718;3069837;3071399;709;280;5
637131167;lpg1227;1353613;1355409;392;194;7
637131479;lpg1539;1704272;1704697;54;0;3
637130839;lpg0898;972975;973706;272;211;3
637131606;lpg1666;1849247;1850650;264;161;4
637132237;lpg2298;2596514;2597791;362;593;4
637132493;lpg2555;2888571;2889425;476;587;3
637131737;lpg1798;2005655;2006851;184;524;4
637132155;lpg2216;2500553;2502325;20;249;4
637131050;lpg1109;1212967;1215027;238;504;5
637132891;lpg2959;3348048;3349640;206;296;3
637131042;lpg1101;1204272;1205240;281;488;6
637132624;lpg2687;3037576;3038031;0;112;5
637131887;lpg1948;2175670;2176677;11;308;4
637131627;lpg1687;1877800;1879002;50;36;5
637130133;lpg0190;220962;221183;102;52;5
637130379;lpg0437;474811;476811;284;262;5
637130103;lpg0160;192160;193137;253;220;4
637132111;lpg2172;2437187;2438290;121;170;4
637132465;lpg2527;2856264;2857940;306;166;5
637132210;lpg2271;2574377;2575027;174;151;3
637131424;lpg1484;1639917;1640726;53;198;4
637132339;lpg2400;2711277;2712341;208;292;3
637132094;lpg2155;2407667;2410288;265;52;3
637131181;lpg1241;1368713;1371382;164;67;6
637132107;lpg2168;2433697;2434470;0;189;3
637132528;lpg2591;2924663;2925160;116;172;3
637131062;lpg1121;1231463;1232233;627;581;4
637130228;lpg0285;339639;340322;32;236;3
637130464;lpg0522;564885;565352;0;151;4
637130382;lpg0440;478631;478843;170;91;3
637131088;lpg1147;1263574;1264077;289;60;4
637131925;lpg1986;2226164;2229016;168;176;5
637132764;lpg2830;3201113;3201853;120;251;4
637131915;lpg1976;2215443;2216303;177;0;5
637130347;lpg0405;446478;447068;199;0;3
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637132382;lpg2443;2757867;2758424;123;226;3
637131457;lpg1517;1678858;1679994;86;3;5
637132261;lpg2322;2623900;2625825;92;86;3
637130345;lpg0403;443204;444748;336;179;5
637132313;lpg2374;2680222;2680533;347;447;3
637131945;lpg2006;2245044;2246900;81;57;6
637129958;lpg0015;19643;20716;0;100;4
637130033;lpg0090;99689;103663;214;110;4
637132070;lpg2131;2374714;2375256;16;18;4
637131658;lpg1718;1914091;1915728;390;143;3
637132115;lpg2176;2440714;2442540;3;216;4
637131790;lpg1851;2072773;2073435;23;345;4
637130674;lpg0733;799869;801317;51;165;4
637131582;lpg1642;1815442;1816695;200;255;5
637132479;lpg2541;2872931;2873764;114;285;5
637130069;lpg0126;143588;146896;96;113;4
637131601;lpg1661;1838135;1839253;93;160;6
637131423;lpg1483;1638274;1639863;53;145;5
637131864;lpg1925;2149854;2152499;69;316;5
637131070;lpg1129;1243201;1244760;128;427;4
637131561;lpg1621;1789603;1790922;169;119;4
637132283;lpg2344;2647010;2647636;727;110;3
637130837;lpg0896;971284;971661;81;5;3
637130881;lpg0940;1017170;1019359;179;241;5
637132707;lpg2772;3121904;3124510;3;88;5
637132310;lpg2371;2675881;2676495;698;542;3
637132271;lpg2332;2635647;2636246;28;0;4
637132058;lpg2119;2363881;2364906;667;158;5
637132098;lpg2159;2422285;2423406;28;292;5
637131632;lpg1692;1885806;1887116;0;293;3
637131898;lpg1959;2191518;2193512;184;252;3
637132765;lpg2831;3202105;3203970;54;251;5
637131172;lpg1232;1359759;1361036;613;0;5
637130138;lpg0195;225828;226832;131;201;3
637132821;lpg2888;3268809;3270722;130;227;3
637130164;lpg0221;251956;254244;13;14;5
637132932;lpg3000;3391800;3393638;0;295;5
```

FIR Results:

	639(21.7 %)	835(28.4 %)	
Genome	-----	-----	total :2941
	825(28.1 %)	642(21.8 %)	

	71(22.8 %)	164(52.7 %)	
Hits	-----	-----	total :311
	24(7.7 %)	52(16.7 %)	

Figure S3. Example of S4TE summary of results (*Results.txt*)

Domain name	Pfam ID number	Description
Sec7	PF01369.15	Sec7 domain
Ank	PF00023.25	Ankyrin repeat
Ank_3	PF13606.1	Ankyrin repeat
Ank_4	PF13637.1	Ankyrin repeat (many copies)
Ank_5	PF13857.1	Ankyrin repeat (many copies)
SET	PF00856.23	SET domain
F-box	PF00646.28	F-box domain
F-box-like	PF12937.2	F-box-like
F-box-like_2	PF13013.1	F-box-like domain
LRR	PF13855.1	Leucine rich repeat
Pkinase	PF00069.20	Protein kinase domain
Metallophos_2	PF12850.2	Calcineurin-like phosphoesterase superfamily domain
Pyridoxal_deC	PF00282.14	Pyridoxal-dependent decarboxylase conserved domain
RCC1	PF00415.13	Regulator of chromosome condensation (RCC1) repeat
RCC1_2	PF13540.1	Regulator of chromosome condensation (RCC1) repeat
RasGEF	PF00617.14	RasGEF domain
RasGEF_N	PF00618.15	RasGEF N-terminal motif
U-box	PF04564.10	U-box domain
cNMP_binding	PF00027.24	Cyclic nucleotide binding domain
Glycohydro_11	PF00457.12	Glycosyl hydrolases family 11
Glycohydro_12	PF01670.11	Glycosyl hydrolases family 12
Glycohydro_14	PF01373.12	Glycosyl hydrolases family 14
Glycohydro_15	PF00723.16	Glycosyl hydrolases family 15
Glycohydro_16	PF00722.16	Glycosyl hydrolases family 16
Glycohydro_17	PF00332.13	Glycosyl hydrolases family 17
Glycohydro_18	PF00704.23	Glycosyl hydrolases family 18
PhyH	PF05721.8	Pytanoyl-CoA dioxygenase (PhyH)
Astacin	PF01400.19	Astacin (Peptidase family M12A)
Thaumat	PF00314.12	Thaumat family

Table S1. List of the 58 eukaryotic domains searched by S4TE (*PfamManager.pl*)

Domain name	Pfam ID number	Description
Acetyltransf_1	PF00583.19	Acetyltransferase (GNAT) family
Acetyltransf_10	PF13673.1	Acetyltransferase (GNAT) family
Patatin	PF01734.17	Patatin-like phospholipase
TRP_1	PF00515.23	Tetratricopeptide repeat
TRP_10	PF13374.1	Tetratricopeptide repeat
TRP_11	PF13414.1	Tetratricopeptide repeat
TRP_12	PF13424.1	Tetratricopeptide repeat
TRP_14	PF13428.1	Tetratricopeptide repeat
TRP-15	PF13429.1	Tetratricopeptide repeat
TRP-16	PF13432.1	Tetratricopeptide repeat
TRP-17	PF13431.1	Tetratricopeptide repeat
TRP-18	PF13512.1	Tetratricopeptide repeat
TRP-2	PF07719.12	Tetratricopeptide repeat
TRP-3	PF07720.7	Tetratricopeptide repeat
TRP-4	PF07721.9	Tetratricopeptide repeat
TRP-5	PF12688.2	Tetratricopeptide repeat
TRP-6	PF13174.1	Tetratricopeptide repeat
TRP-7	PF13176.1	Tetratricopeptide repeat
TRP-8	PF13181.1	Tetratricopeptide repeat
TRP-9	PF13371.1	Tetratricopeptide repeat
SNARE	PF05739.14	SNARE domain
SNARE assoc	PF09335.6	SNARE associated Golgi protein
HIT	PF01230.18	HIT domain
PD40	PF07676.7	WD40-like Beta Propeller Repeat
Band_7	PF01145.20	SPFH domain / Band 7 family
Band_7_1	PF00533.21	SPFH domain-Band 7 family
BRCT	PF02661.13	BRCA1 C Terminus (BRCT) domain
Fic	PF13784.1	Fic/DOC family
Fic_N	PF06207.6	Fic/DOC family N-terminal

Table S1 (cont.). List of the 58 eukaryotic domains searched by S4TE (*PfamManager.pl*)

Number of features	Code	1	2	3	4	5	6	7	8	9	10	11	12	13	TP	%TP	FP	%FP	SI _L	PI _L
3	010000001100														12	5.38	0	0.00	1.00	0
3	010000100100														5	2.24	0	0.00	1.00	0
3	110000000100														2	0.90	0	0.00	1.00	0
3	010000000110														2	0.90	0	0.00	1.00	0
3	110000000010														2	0.90	0	0.00	1.00	0
3	010001000100														2	0.90	0	0.00	1.00	0
3	010000000011														1	0.45	0	0.00	1.00	0
3	110000010000														1	0.45	0	0.00	1.00	0
3	010010000010														1	0.45	0	0.00	1.00	0
3	110000000100														1	0.45	0	0.00	1.00	0
3	0110000000100														1	0.45	0	0.00	1.00	0
3	010000010100														6	2.69	1	1.20	0.86	5.00
3	0110000001000														3	1.35	1	1.20	0.75	2.00
3	0110000000010														3	1.35	1	1.20	0.75	2.00
3	0100000001010														25	11.21	9	10.84	0.74	1.78
3	010000011000														2	0.90	3	3.61	0.40	-0.33
3	0101000001000														0	0.00	1	1.20	0.00	-1.00
3	0100000100010														0	0.00	1	1.20	0.00	-1.00
4	0100000101100														9	4.04	0	0.00	1.00	0
4	0100000100110														7	3.14	0	0.00	1.00	0
4	11000000011000														3	1.35	0	0.00	1.00	0
4	0100100001100														2	0.90	0	0.00	1.00	0
4	01000000011100														2	0.90	0	0.00	1.00	0
4	1110000000010														2	0.90	0	0.00	1.00	0
4	0110000100100														1	0.45	0	0.00	1.00	0
4	0101000001001														1	0.45	0	0.00	1.00	0
4	01100000101000														1	0.45	0	0.00	1.00	0
4	0101000001010														1	0.45	0	0.00	1.00	0
4	010000010000110														1	0.45	0	0.00	1.00	0
4	01000000001011														1	0.45	0	0.00	1.00	0
4	1100000100001														1	0.45	0	0.00	1.00	0
4	0100110000010														1	0.45	0	0.00	1.00	0
4	11000000001100														1	0.45	0	0.00	1.00	0
4	0100000101001														1	0.45	0	0.00	1.00	0
4	01100000001001														1	0.45	0	0.00	1.00	0
4	01000000001110														11	4.93	1	1.20	0.92	10.00
4	11000000001010														8	3.59	2	2.41	0.80	3.00
4	0100000101010														14	6.28	4	4.82	0.78	2.50
4	0100000011010														8	3.59	4	4.82	0.67	1.00
4	01100000011000														2	0.90	1	1.20	0.67	1.00
4	01100000001010														3	1.35	3	3.61	0.50	0.00
4	0100000110000														0	0.00	1	1.20	0.00	-1.00
5	1100000101010														2	0.90	0	0.00	1.00	0
5	0100000111000														2	0.90	0	0.00	1.00	0
5	01100000001110														2	0.90	0	0.00	1.00	0
5	01001000011010														1	0.45	0	0.00	1.00	0
5	0100000101011														1	0.45	0	0.00	1.00	0
5	01001000011100														1	0.45	0	0.00	1.00	0
5	01010000101010														1	0.45	0	0.00	1.00	0
5	1100000100110														1	0.45	0	0.00	1.00	0
5	0100100101001														1	0.45	0	0.00	1.00	0
5	0100100100110														1	0.45	0	0.00	1.00	0
5	0100100001110														1	0.45	0	0.00	1.00	0
5	11100000001100														1	0.45	0	0.00	1.00	0
5	0100000101110														22	9.87	3	3.61	0.88	6.33
5	11000000011010														2	0.90	1	1.20	0.67	1.00
5	11000000001110														2	0.90	2	2.41	0.50	0.00
5	0100100101100														2	0.90	2	2.41	0.50	0.00
5	0100000111010														1	0.45	1	1.20	0.50	0.00
5	01100000011010														2	0.90	3	3.61	0.40	-0.33
5	10001000001110														0	0.00	2	2.41	0.00	-1.00
5	10100000011010														0	0.00	1	1.20	0.00	-1.00
5	10010000011010														0	0.00	2	2.41	0.00	-1.00
5	1000010011010														0	0.00	1	1.20	0.00	-1.00
5	1000000101110														0	0.00	1	1.20	0.00	-1.00
5	0000000111110														0	0.00	2	2.41	0.00	-1.00
5	00010000011110														0	0.00	1	1.20	0.00	-1.00
5	0001000011010														0	0.00	2	2.41	0.00	-1.00
5	10001000011100														0	0.00	1	1.20	0.00	-1.00
5	0000000101111														0	0.00	2	2.41	0.00	-1.00
5	00001000011110														0	0.00	1	1.20	0.00	-1.00
5	0000100111010														0	0.00	2	2.41	0.00	-1.00
5	1000000001011														0	0.00	1	1.20	0.00	-1.00
5	0101100001000														0	0.00	1	1.20	0.00	-1.00
5	1000000111010														0	0.00	1	1.20	0.00	-1.00
5	00010000011110														0	0.00	1	1.20	0.00	-1.00
5	00001001011000														0	0.00	2	2.41	0.00	-1.00
5	0001100110000														0	0.00	1	1.20	0.00	-1.00
5	10001000011010														0	0.00	2	2.41	0.00	-1.00
5	0000100101010														0	0.00	2	2.41	0.00	-1.00
5	10010000001011														0	0.00	1	1.20	0.00	-1.00
5	01000000011110														0	0.00	1	1.20	0.00	-1.00
6	0100100101110														4	1.79	0	0.00	1.00	0
6	1100000101110														2	0.90	0	0.00	1.00	0
6	11000000011110														1	0.45	0	0.00	1.00	0
6	11100000010100														1	0.45	0	0.00	1.00	0
6	01001000001011														1	0.45	0	0.00	1.00	0
6	01100001011010														1	0.45	0	0.00	1.00	0
6	01100000111010														1	0.45	0	0.00	1.00	0
6	011000000101110														1	0.45	0	0.00	1.00	0
6	011000000011110														1	0.45	0	0.00	1.00	0
6	11010000011010														1	0.45	0	0.00	1.00	0
6	11001001000110														1	0.45	0	0.00	1.00	0
6	01000000010111														1	0.45	0	0.00	1.00	0
6	00011001011110														0	0.00	1	1.20	0.00	-1.00
6	10001001011110	</																		