Supplementary Tables and Figure

Table S1. Concentration of free amino acids in E. coli BL21 cell extracts

Table S2. Results from search of bacterial VFT signature in the 500 hits of Blastp. Altered signatures identified in 33 proteins are shown in bold

<u>Fig. S1.</u> Effect of Tyr275 mutations on aggressiveness of *A. tumefaciens*. Virulence symptoms (number of emerging tumors) induced by the constructed strains *atu2422(atu2422), atu2422(6000), atu2422(atu2422-Y275K), atu2422(atu2422-Y275A)* and *atu2422(atu2422-Y275F)* were measured in tomato and tobacco plants. Bacterial strains showing statistical differences (Kruskal-wallis test; α =0.05) in their aggressiveness categories are noted by different letters.

Fig. S2. Extended relation tree of Atu2422 related proteins. Extended view of the relation tree of the analyzed 386 proteins from 155 different species retrieved after a Blastp Search using Atu2422 as query. The branches are collapsed when related proteins are from species of a same Genus (i.e. *Pseudomonas, Burkholderia, Agrobacterium*). The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (2000 replicates) is shown next to the branches. Note the particular case of *Rhodospirillum centenum* strain SW, in which two sequences showed Phe or Leu at position 77.

	Amino acids in cell extracts of <i>E.coli</i> BL21				
-	nmol/µL	%			
Leu	1.24	18.5			
Lys	1.04	15.6			
Val	0.75	11.3			
Ala	0.72	10.8			
Phe	0.55	8.2			
Arg	0.54	8			
Ile	0.49	7.3			
Gly	0.31	4.6			
Met	0.23	3.5			
His	0.17	2.5			
Asp	0.17	2.5			
Pro	0.14	2			
Glu	0.12	1.8			
Tyr	0.11	1.7			
Ser	0.05	0.8			
Thr	0.05	0.8			
Orn	0.03	0.45			
GABA	0.01	0.18			
Cys	-	-			
Gln	-	-			
Asn	-	-			
Trp	-	-			

Table	S1:	Conce	ntration	of free	amino	acids in	E.	coli BL21	cell	extracts
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Pattern	Nb of retrieved sequences
[S]-x(22)-[T]-x(13)-[R]-x(4)-[D]-x(2)-[Q]-x(25)-[YG]-x(74)-[D]	144
[S]-x(22)-[T]-x(13)-[R]-x(4)-[D]-x(2)-[Q]-x(25)-[YG]-x(74)-[E]	154
[S]-x(22)-[T]-x(14)-[R]-x(4)-[D]-x(2)-[Q]-x(25)-[YG]-x(74)-[D]	4
[S]-x(22)-[T]-x(14)-[R]-x(4)-[D]-x(2)-[Q]-x(25)-[YG]-x(74)-[E]	31
[T]-x(22)-[T]-x(13)-[R]-x(4)-[D]-x(2)-[Q]-x(25)-[YG]-x(74)-[D]	0
[T]-x(22)-[T]-x(13)-[R]-x(4)-[D]-x(2)-[Q]-x(25)-[YG]-x(74)-[E]	13
[S]-x(22)-[T]-x(13)-[R]-x(4)-[D]-x(2)-[Q]-x(24)-[YG]-x(74)-[D]	25
[S]-x(22)-[T]-x(13)-[R]-x(4)-[D]-x(2)-[Q]-x(24)-[YG]-x(74)-[E]	4
[S]-x(22)-[V]-x(13)-[R]-x(4)-[D]-x(2)-[Q]-x(24)-[AS]-x(74)-[S]	5
[S]-x(21)-[T]-x(13)-[R]-x(4)-[D]-x(2)-[Q]-x(25)-[YG]-x(74)-[E]	29
[S]-x(22)-[T]-x(13)-[M]-x(4)-[D]-x(2)-[N]-x(25)-[FG]-x(74)-[G]	28
Total	437

Table S2. Results from search of bacterial VFT signature in the 500 hits of Blastp. Altered signatures identified in 33 proteins are shown in bold.

Figure S1.



Figure S2.



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