

Table S5: The interaction networks and the co-expression details of the SPI2 cluster proteins of *S. enterica* Typhimurium ms202.

node1	node2	node1 accession	node2 accession	node1 annotation	node2 annotation	score
ssrB	ssrA	CY43_07080	CY43_07085	Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology	Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology	0.999
ssrB	sseF	CY43_07080	CY43_07145	Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology	Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology	0.576
ssrB	sseD	CY43_07080	CY43_07130	Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology	SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	0.400
ssrB	sseB	CY43_07080	CY43_07115	Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology	SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology	0.777
ssrB	sscB	CY43_07080	CY43_07140	Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology	Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology	0.743
ssrB	sscA	CY43_07080	CY43_07120	Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the	CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the	0.804

				<i>expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	
ssrB	ssaV	CY43_07080	CY43_07195	<i>Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.474
ssrB	ssaU	CY43_07080	CY43_07235	<i>Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.519
ssrB	ssaS	CY43_07080	CY43_07225	<i>Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.493
ssrB	ssaR	CY43_07080	CY43_07220	<i>Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.779
ssrB	ssaQ	CY43_07080	CY43_07215	<i>Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.687

ssrB	ssaN	CY43_07080	CY43_07200	Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology	EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology	0.558
ssrB	ssaG	CY43_07080	CY43_07155	Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology	EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	0.919
ssrB	ssaE	CY43_07080	CY43_07105	Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology	Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology	0.674
ssrB	ssaD	CY43_07080	CY43_07100	Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology	Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	0.717
ssrB	spiC	CY43_07080	CY43_07090	Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology	SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology	0.856
ssrB	spiA	CY43_07080	CY43_07095	Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated	SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology	0.806

				<i>computational analysis using gene prediction method: Protein Homology</i>		
ssrB	DD95_20700	CY43_07080	CY43_07230	<i>Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.588
ssrA	ssrB	CY43_07085	CY43_07080	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.999
ssrA	sseF	CY43_07085	CY43_07145	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.510
ssrA	sseE	CY43_07085	CY43_07135	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.630
ssrA	sseD	CY43_07085	CY43_07130	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.579
ssrA	sseB	CY43_07085	CY43_07115	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.841

ssrA	sscB	CY43_07085	CY43_07140	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.924
ssrA	ssaA	CY43_07085	CY43_07120	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.924
ssrA	ssaV	CY43_07085	CY43_07195	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.469
ssrA	ssaU	CY43_07085	CY43_07235	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.698
ssrA	ssaS	CY43_07085	CY43_07225	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.439
ssrA	ssaR	CY43_07085	CY43_07220	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational</i>	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity</i>	0.747

				<i>analysis using gene prediction method: Protein Homology</i>	<i>response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	
ssrA	ssaQ	CY43_07085	CY43_07215	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.889
ssrA	ssaN	CY43_07085	CY43_07200	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.699
ssrA	ssaI	CY43_07085	CY43_07165	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.556
ssrA	ssaG	CY43_07085	CY43_07155	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.903
ssrA	ssaE	CY43_07085	CY43_07105	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.690
ssrA	ssaD	CY43_07085	CY43_07100	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved</i>	0.923

				<i>the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	
ssrA	spiC	CY43_07085	CY43_07090	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.902
ssrA	spiA	CY43_07085	CY43_07095	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.914
ssrA	DD95_20875	CY43_07085	CY43_07050	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Histidine kinase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.798
ssrA	DD95_20700	CY43_07085	CY43_07230	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.703
sseF	ssrB	CY43_07145	CY43_07080	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.576
sseF	ssrA	CY43_07145	CY43_07085	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated</i>	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational</i>	0.510

				<i>computational analysis using gene prediction method: Protein Homology</i>	<i>analysis using gene prediction method: Protein Homology</i>	
sseF	sseE	CY43_07145	CY43_07135	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.828
sseF	sseD	CY43_07145	CY43_07130	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.966
sseF	sseB	CY43_07145	CY43_07115	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.886
sseF	sscB	CY43_07145	CY43_07140	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.994
sseF	ssaA	CY43_07145	CY43_07120	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.855
sseF	ssaV	CY43_07145	CY43_07195	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III</i>	0.608

					<i>secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	
sseF	ssaU	CY43_07145	CY43_07235	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.671
sseF	ssaS	CY43_07145	CY43_07225	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.791
sseF	ssaR	CY43_07145	CY43_07220	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.587
sseF	ssaQ	CY43_07145	CY43_07215	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.730
sseF	ssaP	CY43_07145	CY43_07210	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.758
sseF	ssaO	CY43_07145	CY43_07205	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.726

sseF	ssaN	CY43_07145	CY43_07200	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.689
sseF	ssaI	CY43_07145	CY43_07165	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.894
sseF	ssaG	CY43_07145	CY43_07155	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.715
sseF	ssaE	CY43_07145	CY43_07105	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.576
sseF	ssaD	CY43_07145	CY43_07100	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.628
sseF	spiC	CY43_07145	CY43_07090	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.803

sseF	spiA	CY43_07145	CY43_07095	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.628
sseF	DD95_20700	CY43_07145	CY43_07230	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.544
sseE	ssrA	CY43_07135	CY43_07085	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.630
sseE	sseF	CY43_07135	CY43_07145	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.828
sseE	sseD	CY43_07135	CY43_07130	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.950
sseE	sseB	CY43_07135	CY43_07115	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.957
sseE	sscB	CY43_07135	CY43_07140	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the</i>	0.933

					<i>efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	
sseE	sscA	CY43_07135	CY43_07120	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.951
sseE	ssaV	CY43_07135	CY43_07195	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.592
sseE	ssaU	CY43_07135	CY43_07235	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.682
sseE	ssaS	CY43_07135	CY43_07225	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.729
sseE	ssaR	CY43_07135	CY43_07220	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.838
sseE	ssaQ	CY43_07135	CY43_07215	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis</i>	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated</i>	0.871

				<i>using gene prediction method: Protein Homology</i>	<i>computational analysis using gene prediction method: Protein Homology</i>	
sseE	ssaP	CY43_07135	CY43_07210	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.837
sseE	ssaO	CY43_07135	CY43_07205	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.804
sseE	ssaN	CY43_07135	CY43_07200	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.669
sseE	ssaI	CY43_07135	CY43_07165	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.716
sseE	ssaG	CY43_07135	CY43_07155	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.656
sseE	ssaE	CY43_07135	CY43_07105	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis</i>	0.843

					<i>using gene prediction method: Protein Homology</i>	
sseE	ssaD	CY43_07135	CY43_07100	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.884
sseE	spiC	CY43_07135	CY43_07090	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.844
sseE	spiA	CY43_07135	CY43_07095	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.738
sseE	DD95_20700	CY43_07135	CY43_07230	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.556
sseD	ssrB	CY43_07130	CY43_07080	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.400
sseD	ssrA	CY43_07130	CY43_07085	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.579
sseD	sseF	CY43_07130	CY43_07145	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the</i>	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the</i>	0.966

				<i>translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	
sseD	sseE	CY43_07130	CY43_07135	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.950
sseD	sseB	CY43_07130	CY43_07115	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.987
sseD	sscB	CY43_07130	CY43_07140	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.926
sseD	ssaA	CY43_07130	CY43_07120	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.960
sseD	ssaV	CY43_07130	CY43_07195	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.672

sseD	ssaU	CY43_07130	CY43_07235	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.676
sseD	ssaS	CY43_07130	CY43_07225	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.868
sseD	ssaR	CY43_07130	CY43_07220	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.599
sseD	ssaQ	CY43_07130	CY43_07215	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.738
sseD	ssaP	CY43_07130	CY43_07210	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.691
sseD	ssaO	CY43_07130	CY43_07205	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.738

sseD	ssaN	CY43_07130	CY43_07200	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.726
sseD	ssaI	CY43_07130	CY43_07165	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.878
sseD	ssaG	CY43_07130	CY43_07155	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.888
sseD	ssaE	CY43_07130	CY43_07105	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.722
sseD	ssaD	CY43_07130	CY43_07100	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.792
sseD	spiC	CY43_07130	CY43_07090	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational</i>	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated</i>	0.863

				<i>analysis using gene prediction method: Protein Homology</i>	<i>computational analysis using gene prediction method: Protein Homology</i>	
sseD	spiA	CY43_07130	CY43_07095	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.849
sseD	DD95_20700	CY43_07130	CY43_07230	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.656
sseB	ssrB	CY43_07115	CY43_07080	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.777
sseB	ssrA	CY43_07115	CY43_07085	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.841
sseB	sseF	CY43_07115	CY43_07145	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.886
sseB	sseE	CY43_07115	CY43_07135	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.957

sseB	sseD	CY43_07115	CY43_07130	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.987
sseB	sscB	CY43_07115	CY43_07140	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.857
sseB	ssaA	CY43_07115	CY43_07120	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.976
sseB	ssaV	CY43_07115	CY43_07195	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.601
sseB	ssaU	CY43_07115	CY43_07235	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.644
sseB	ssaS	CY43_07115	CY43_07225	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated</i>	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.651

				<i>computational analysis using gene prediction method: Protein Homology</i>		
sseB	ssaR	CY43_07115	CY43_07220	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.633
sseB	ssaQ	CY43_07115	CY43_07215	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.821
sseB	ssaP	CY43_07115	CY43_07210	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.660
sseB	ssaO	CY43_07115	CY43_07205	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.586
sseB	ssaN	CY43_07115	CY43_07200	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.880
sseB	ssaI	CY43_07115	CY43_07165	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated</i>	0.764

				<i>computational analysis using gene prediction method: Protein Homology</i>	<i>computational analysis using gene prediction method: Protein Homology</i>	
sseB	ssaG	CY43_07115	CY43_07155	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.878
sseB	ssaE	CY43_07115	CY43_07105	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.923
sseB	ssaD	CY43_07115	CY43_07100	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.851
sseB	spiC	CY43_07115	CY43_07090	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.877
sseB	spiA	CY43_07115	CY43_07095	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.859
sseB	DD95_20700	CY43_07115	CY43_07230	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in</i>	0.651

				<i>cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	
sscB	ssrB	CY43_07140	CY43_07080	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.743
sscB	ssrA	CY43_07140	CY43_07085	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.924
sscB	sseF	CY43_07140	CY43_07145	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.994
sscB	sseE	CY43_07140	CY43_07135	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.933
sscB	sseD	CY43_07140	CY43_07130	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in</i>	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host</i>	0.926

				<i>a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	
sscB	sseB	CY43_07140	CY43_07115	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.857
sscB	ssaA	CY43_07140	CY43_07120	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.988
sscB	ssaV	CY43_07140	CY43_07195	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.773
sscB	ssaU	CY43_07140	CY43_07235	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.918

sscB	ssaS	CY43_07140	CY43_07225	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; chaperone for SseF; required for the efficient replication of <i>Salmonella</i> in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology	SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology	0.839
sscB	ssaR	CY43_07140	CY43_07220	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; chaperone for SseF; required for the efficient replication of <i>Salmonella</i> in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology	SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology	0.856
sscB	ssaQ	CY43_07140	CY43_07215	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; chaperone for SseF; required for the efficient replication of <i>Salmonella</i> in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology	SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology	0.960
sscB	ssaP	CY43_07140	CY43_07210	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; chaperone for SseF; required for the efficient replication of <i>Salmonella</i> in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	0.863
sscB	ssaO	CY43_07140	CY43_07205	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; chaperone for SseF; required for the efficient replication of <i>Salmonella</i> in host macrophages; Derived by automated	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	0.844

				<i>computational analysis using gene prediction method: Protein Homology</i>		
sscB	ssaN	CY43_07140	CY43_07200	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.884
sscB	ssaI	CY43_07140	CY43_07165	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.720
sscB	ssaG	CY43_07140	CY43_07155	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.717
sscB	ssaE	CY43_07140	CY43_07105	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.663
sscB	ssaD	CY43_07140	CY43_07100	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated</i>	0.955

				<i>efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>computational analysis using gene prediction method: Protein Homology</i>	
sscB	spiC	CY43_07140	CY43_07090	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.703
sscB	spiA	CY43_07140	CY43_07095	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.899
sscB	DD95_20700	CY43_07140	CY43_07230	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.883
ssaA	ssrB	CY43_07120	CY43_07080	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.804
ssaA	ssrA	CY43_07120	CY43_07085	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational</i>	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational</i>	0.924

				<i>analysis using gene prediction method: Protein Homology</i>	<i>analysis using gene prediction method: Protein Homology</i>	
sscA	sseF	CY43_07120	CY43_07145	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.855
sscA	sseE	CY43_07120	CY43_07135	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.951
sscA	sseD	CY43_07120	CY43_07130	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.960
sscA	sseB	CY43_07120	CY43_07115	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.976
sscA	ssCB	CY43_07120	CY43_07140	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.988
sscA	ssaV	CY43_07120	CY43_07195	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational</i>	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella</i>	0.788

				<i>analysis using gene prediction method: Protein Homology</i>	<i>pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	
sscA	ssaU	CY43_07120	CY43_07235	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.921
sscA	ssaS	CY43_07120	CY43_07225	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.929
sscA	ssaR	CY43_07120	CY43_07220	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.888
sscA	ssaQ	CY43_07120	CY43_07215	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.965
sscA	ssaP	CY43_07120	CY43_07210	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.821
sscA	ssaO	CY43_07120	CY43_07205	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in</i>	0.821

				<i>cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	
sscA	ssaN	CY43_07120	CY43_07200	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.926
sscA	ssaI	CY43_07120	CY43_07165	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.728
sscA	ssaG	CY43_07120	CY43_07155	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.862
sscA	ssaE	CY43_07120	CY43_07105	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.851
sscA	ssaD	CY43_07120	CY43_07100	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.975
sscA	spiC	CY43_07120	CY43_07090	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the</i>	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits</i>	0.876

				<i>translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	
sscA	spiA	CY43_07120	CY43_07095	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.976
sscA	DD95_20700	CY43_07120	CY43_07230	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.906
ssaV	ssrB	CY43_07195	CY43_07080	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.474
ssaV	ssrA	CY43_07195	CY43_07085	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.469
ssaV	sseF	CY43_07195	CY43_07145	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated</i>	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.608

				<i>computational analysis using gene prediction method: Protein Homology</i>		
ssaV	sseE	CY43_07195	CY43_07135	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.592
ssaV	sseD	CY43_07195	CY43_07130	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.672
ssaV	sseB	CY43_07195	CY43_07115	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.601
ssaV	sscB	CY43_07195	CY43_07140	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.773
ssaV	sscA	CY43_07195	CY43_07120	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella</i>	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational</i>	0.788

				<i>pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>analysis using gene prediction method: Protein Homology</i>	
ssaV	ssaU	CY43_07195	CY43_07235	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.960
ssaV	ssaS	CY43_07195	CY43_07225	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.959
ssaV	ssaR	CY43_07195	CY43_07220	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.966
ssaV	ssaQ	CY43_07195	CY43_07215	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.928
ssaV	ssaP	CY43_07195	CY43_07210	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved</i>	0.899

				<i>export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	
ssaV	ssaO	CY43_07195	CY43_07205	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.899
ssaV	ssaN	CY43_07195	CY43_07200	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.980
ssaV	ssaI	CY43_07195	CY43_07165	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.763
ssaV	ssaG	CY43_07195	CY43_07155	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.813

ssaV	ssaE	CY43_07195	CY43_07105	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.623
ssaV	ssaD	CY43_07195	CY43_07100	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.731
ssaV	spiC	CY43_07195	CY43_07090	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.607
ssaV	spiA	CY43_07195	CY43_07095	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.807
ssaV	DD95_20700	CY43_07195	CY43_07230	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.962

				<i>computational analysis using gene prediction method: Protein Homology</i>		
ssaU	ssrB	CY43_07235	CY43_07080	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.519
ssaU	ssrA	CY43_07235	CY43_07085	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.698
ssaU	sseF	CY43_07235	CY43_07145	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.671
ssaU	sseE	CY43_07235	CY43_07135	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.682
ssaU	sseD	CY43_07235	CY43_07130	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.676
ssaU	sseB	CY43_07235	CY43_07115	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.644

ssaU	sscB	CY43_07235	CY43_07140	Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology	Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology	0.918
ssaU	ssaA	CY43_07235	CY43_07120	Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology	CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	0.921
ssaU	ssaV	CY43_07235	CY43_07195	Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology	SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology	0.960
ssaU	ssaS	CY43_07235	CY43_07225	Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology	SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology	0.997
ssaU	ssaR	CY43_07235	CY43_07220	Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology	SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology	0.994
ssaU	ssaQ	CY43_07235	CY43_07215	Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli;	SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated	0.948

				<i>Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>computational analysis using gene prediction method: Protein Homology</i>	
ssaU	ssaP	CY43_07235	CY43_07210	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.918
ssaU	ssaO	CY43_07235	CY43_07205	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.964
ssaU	ssaN	CY43_07235	CY43_07200	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.989
ssaU	ssaI	CY43_07235	CY43_07165	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.702
ssaU	ssaG	CY43_07235	CY43_07155	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.790
ssaU	ssaE	CY43_07235	CY43_07105	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli;</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in</i>	0.492

				<i>Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	
ssaU	ssaD	CY43_07235	CY43_07100	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.902
ssaU	spiC	CY43_07235	CY43_07090	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.662
ssaU	spiA	CY43_07235	CY43_07095	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.815
ssaU	DD95_20700	CY43_07235	CY43_07230	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.991
ssaS	ssrB	CY43_07225	CY43_07080	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.493
ssaS	ssrA	CY43_07225	CY43_07085	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational</i>	0.439

					<i>analysis using gene prediction method: Protein Homology</i>	
ssaS	sseF	CY43_07225	CY43_07145	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.791
ssaS	sseE	CY43_07225	CY43_07135	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.729
ssaS	sseD	CY43_07225	CY43_07130	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.868
ssaS	sseB	CY43_07225	CY43_07115	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.651
ssaS	sscB	CY43_07225	CY43_07140	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.839
ssaS	ssaA	CY43_07225	CY43_07120	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.929

ssaS	ssaV	CY43_07225	CY43_07195	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.959
ssaS	ssaU	CY43_07225	CY43_07235	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.997
ssaS	ssaR	CY43_07225	CY43_07220	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.996
ssaS	ssaQ	CY43_07225	CY43_07215	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.939
ssaS	ssaP	CY43_07225	CY43_07210	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.928
ssaS	ssaO	CY43_07225	CY43_07205	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.968

ssaS	ssaN	CY43_07225	CY43_07200	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.986
ssaS	ssaI	CY43_07225	CY43_07165	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.841
ssaS	ssaG	CY43_07225	CY43_07155	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.735
ssaS	ssaE	CY43_07225	CY43_07105	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.598
ssaS	ssaD	CY43_07225	CY43_07100	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.860
ssaS	spiC	CY43_07225	CY43_07090	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.691

ssaS	spiA	CY43_07225	CY43_07095	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.807
ssaS	DD95_20700	CY43_07225	CY43_07230	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.983
ssaR	ssrB	CY43_07220	CY43_07080	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.779
ssaR	ssrA	CY43_07220	CY43_07085	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.747
ssaR	sseF	CY43_07220	CY43_07145	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.587
ssaR	sseE	CY43_07220	CY43_07135	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.838

ssaR	sseD	CY43_07220	CY43_07130	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.599
ssaR	sseB	CY43_07220	CY43_07115	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.633
ssaR	sscB	CY43_07220	CY43_07140	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.856
ssaR	ssaA	CY43_07220	CY43_07120	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.888
ssaR	ssaV	CY43_07220	CY43_07195	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.966

ssaR	ssaU	CY43_07220	CY43_07235	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.994
ssaR	ssaS	CY43_07220	CY43_07225	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.996
ssaR	ssaQ	CY43_07220	CY43_07215	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.935
ssaR	ssaP	CY43_07220	CY43_07210	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.922
ssaR	ssaO	CY43_07220	CY43_07205	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.922
ssaR	ssaN	CY43_07220	CY43_07200	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant</i>	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated</i>	0.986

				<i>pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>computational analysis using gene prediction method: Protein Homology</i>	
ssaR	ssaI	CY43_07220	CY43_07165	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.751
ssaR	ssaG	CY43_07220	CY43_07155	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.893
ssaR	ssaE	CY43_07220	CY43_07105	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.710
ssaR	ssaD	CY43_07220	CY43_07100	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.888
ssaR	spiC	CY43_07220	CY43_07090	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational</i>	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated</i>	0.841

				<i>analysis using gene prediction method: Protein Homology</i>	<i>computational analysis using gene prediction method: Protein Homology</i>	
ssaR	spiA	CY43_07220	CY43_07095	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.839
ssaR	DD95_20700	CY43_07220	CY43_07230	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.990
ssaQ	ssrB	CY43_07215	CY43_07080	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.687
ssaQ	ssrA	CY43_07215	CY43_07085	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.889
ssaQ	sseF	CY43_07215	CY43_07145	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.730
ssaQ	sseE	CY43_07215	CY43_07135	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.871

ssaQ	sseD	CY43_07215	CY43_07130	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.738
ssaQ	sseB	CY43_07215	CY43_07115	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.821
ssaQ	sscB	CY43_07215	CY43_07140	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.960
ssaQ	ssaA	CY43_07215	CY43_07120	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.965
ssaQ	ssaV	CY43_07215	CY43_07195	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.928
ssaQ	ssaU	CY43_07215	CY43_07235	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis</i>	0.948

					<i>using gene prediction method: Protein Homology</i>	
ssaQ	ssaS	CY43_07215	CY43_07225	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.939
ssaQ	ssaR	CY43_07215	CY43_07220	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.935
ssaQ	ssaP	CY43_07215	CY43_07210	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.978
ssaQ	ssaO	CY43_07215	CY43_07205	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.977
ssaQ	ssaN	CY43_07215	CY43_07200	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.979
ssaQ	ssaI	CY43_07215	CY43_07165	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.821
ssaQ	ssaG	CY43_07215	CY43_07155	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated</i>	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a</i>	0.754

				<i>computational analysis using gene prediction method: Protein Homology</i>	<i>type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	
ssaQ	ssaE	CY43_07215	CY43_07105	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.767
ssaQ	ssaD	CY43_07215	CY43_07100	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.964
ssaQ	spiC	CY43_07215	CY43_07090	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.651
ssaQ	spiA	CY43_07215	CY43_07095	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.948
ssaQ	DD95_20700	CY43_07215	CY43_07230	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.919
ssaP	sseF	CY43_07210	CY43_07145	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated</i>	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated</i>	0.758

				<i>computational analysis using gene prediction method: Protein Homology</i>	<i>computational analysis using gene prediction method: Protein Homology</i>	
ssaP	sseE	CY43_07210	CY43_07135	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.837
ssaP	sseD	CY43_07210	CY43_07130	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.691
ssaP	sseB	CY43_07210	CY43_07115	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.660
ssaP	sscB	CY43_07210	CY43_07140	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.863
ssaP	ssaA	CY43_07210	CY43_07120	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.821
ssaP	ssaV	CY43_07210	CY43_07195	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated</i>	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella</i>	0.899

				<i>computational analysis using gene prediction method: Protein Homology</i>	<i>pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	
ssaP	ssaU	CY43_07210	CY43_07235	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.918
ssaP	ssaS	CY43_07210	CY43_07225	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.928
ssaP	ssaR	CY43_07210	CY43_07220	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.922
ssaP	ssaQ	CY43_07210	CY43_07215	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.978
ssaP	ssaO	CY43_07210	CY43_07205	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.983
ssaP	ssaN	CY43_07210	CY43_07200	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in</i>	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated</i>	0.969

				<i>a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>computational analysis using gene prediction method: Protein Homology</i>	
ssaP	ssaI	CY43_07210	CY43_07165	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.757
ssaP	ssaG	CY43_07210	CY43_07155	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.747
ssaP	ssaE	CY43_07210	CY43_07105	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.478
ssaP	ssaD	CY43_07210	CY43_07100	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.840
ssaP	spiC	CY43_07210	CY43_07090	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.683
ssaP	spiA	CY43_07210	CY43_07095	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved</i>	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis</i>	0.626

				<i>in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>using gene prediction method: Protein Homology</i>	
ssaP	DD95_20700	CY43_07210	CY43_07230	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.762
ssaO	sseF	CY43_07205	CY43_07145	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.726
ssaO	sseE	CY43_07205	CY43_07135	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.804
ssaO	sseD	CY43_07205	CY43_07130	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.738
ssaO	sseB	CY43_07205	CY43_07115	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.586
ssaO	sscB	CY43_07205	CY43_07140	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in</i>	0.844

				<i>a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	
ssaO	ssaA	CY43_07205	CY43_07120	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.821
ssaO	ssaV	CY43_07205	CY43_07195	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.899
ssaO	ssaU	CY43_07205	CY43_07235	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.964
ssaO	ssaS	CY43_07205	CY43_07225	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.968
ssaO	ssaR	CY43_07205	CY43_07220	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.922

ssaO	ssaQ	CY43_07205	CY43_07215	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology	0.977
ssaO	ssaP	CY43_07205	CY43_07210	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	0.983
ssaO	ssaN	CY43_07205	CY43_07200	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology	0.969
ssaO	ssaI	CY43_07205	CY43_07165	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	0.759
ssaO	ssaG	CY43_07205	CY43_07155	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	EscF/YscF/HrpA family type III secretion system needle major subunit; <i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	0.750
ssaO	ssaE	CY43_07205	CY43_07105	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; involved in the secretion of SseB; Derived by automated computational analysis	0.494

					<i>using gene prediction method: Protein Homology</i>	
ssaO	ssaD	CY43_07205	CY43_07100	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.839
ssaO	spiC	CY43_07205	CY43_07090	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.642
ssaO	spiA	CY43_07205	CY43_07095	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.486
ssaO	DD95_20700	CY43_07205	CY43_07230	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.763
ssaN	ssrB	CY43_07200	CY43_07080	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.558
ssaN	ssrA	CY43_07200	CY43_07085	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.699

ssaN	sseF	CY43_07200	CY43_07145	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.689
ssaN	sseE	CY43_07200	CY43_07135	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.669
ssaN	sseD	CY43_07200	CY43_07130	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.726
ssaN	sseB	CY43_07200	CY43_07115	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.880
ssaN	sscB	CY43_07200	CY43_07140	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.884
ssaN	ssaA	CY43_07200	CY43_07120	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.926
ssaN	ssaV	CY43_07200	CY43_07195	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated</i>	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell</i>	0.980

				<i>computational analysis using gene prediction method: Protein Homology</i>	<i>membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	
ssaN	ssaU	CY43_07200	CY43_07235	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.989
ssaN	ssaS	CY43_07200	CY43_07225	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.986
ssaN	ssaR	CY43_07200	CY43_07220	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.986
ssaN	ssaQ	CY43_07200	CY43_07215	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.979
ssaN	ssaP	CY43_07200	CY43_07210	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.969
ssaN	ssaO	CY43_07200	CY43_07205	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.969

ssaN	ssaI	CY43_07200	CY43_07165	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.817
ssaN	ssaG	CY43_07200	CY43_07155	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.764
ssaN	ssaE	CY43_07200	CY43_07105	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.687
ssaN	ssaD	CY43_07200	CY43_07100	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.830
ssaN	spiC	CY43_07200	CY43_07090	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.607
ssaN	spiA	CY43_07200	CY43_07095	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.789

ssaN	DD95_20700	CY43_07200	CY43_07230	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.945
ssaI	ssrA	CY43_07165	CY43_07085	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.556
ssaI	sseF	CY43_07165	CY43_07145	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.894
ssaI	sseE	CY43_07165	CY43_07135	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.716
ssaI	sseD	CY43_07165	CY43_07130	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.878
ssaI	sseB	CY43_07165	CY43_07115	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.764
ssaI	sscB	CY43_07165	CY43_07140	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved</i>	0.720

				<i>in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	
ssaI	ssaA	CY43_07165	CY43_07120	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.728
ssaI	ssaV	CY43_07165	CY43_07195	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.763
ssaI	ssaU	CY43_07165	CY43_07235	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.702
ssaI	ssaS	CY43_07165	CY43_07225	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.841
ssaI	ssaR	CY43_07165	CY43_07220	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational</i>	0.751

					<i>analysis using gene prediction method: Protein Homology</i>	
ssaI	ssaQ	CY43_07165	CY43_07215	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.821
ssaI	ssaP	CY43_07165	CY43_07210	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.757
ssaI	ssaO	CY43_07165	CY43_07205	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.759
ssaI	ssaN	CY43_07165	CY43_07200	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.817
ssaI	ssaG	CY43_07165	CY43_07155	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.939
ssaI	ssaE	CY43_07165	CY43_07105	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB;</i>	0.537

				<i>computational analysis using gene prediction method: Protein Homology</i>	<i>Derived by automated computational analysis using gene prediction method: Protein Homology</i>	
ssaI	ssaD	CY43_07165	CY43_07100	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.535
ssaI	spiC	CY43_07165	CY43_07090	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.538
ssaI	spiA	CY43_07165	CY43_07095	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.537
ssaI	DD95_20700	CY43_07165	CY43_07230	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.746
ssaG	ssrB	CY43_07155	CY43_07080	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.919
ssaG	ssrA	CY43_07155	CY43_07085	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a</i>	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity</i>	0.903

				<i>type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	
ssaG	sseF	CY43_07155	CY43_07145	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.715
ssaG	sseE	CY43_07155	CY43_07135	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.656
ssaG	sseD	CY43_07155	CY43_07130	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.888
ssaG	sseB	CY43_07155	CY43_07115	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.878

ssaG	sscB	CY43_07155	CY43_07140	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.717
ssaG	ssaA	CY43_07155	CY43_07120	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.862
ssaG	ssaV	CY43_07155	CY43_07195	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.813
ssaG	ssaU	CY43_07155	CY43_07235	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.790
ssaG	ssaS	CY43_07155	CY43_07225	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis</i>	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.735

				<i>using gene prediction method: Protein Homology</i>		
ssaG	ssaR	CY43_07155	CY43_07220	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.893
ssaG	ssaQ	CY43_07155	CY43_07215	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.754
ssaG	ssaP	CY43_07155	CY43_07210	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.747
ssaG	ssaO	CY43_07155	CY43_07205	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.750
ssaG	ssaN	CY43_07155	CY43_07200	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival</i>	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.764

				<i>and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>		
ssaG	ssaI	CY43_07155	CY43_07165	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.939
ssaG	ssaE	CY43_07155	CY43_07105	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.716
ssaG	ssaD	CY43_07155	CY43_07100	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.642
ssaG	spiC	CY43_07155	CY43_07090	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.937
ssaG	spiA	CY43_07155	CY43_07095	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella</i>	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis</i>	0.775

				<i>pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>using gene prediction method: Protein Homology</i>	
ssaG	DD95_20700	CY43_07155	CY43_07230	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.746
ssaE	ssrB	CY43_07105	CY43_07080	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.674
ssaE	ssrA	CY43_07105	CY43_07085	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.690
ssaE	sseF	CY43_07105	CY43_07145	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.576
ssaE	sseE	CY43_07105	CY43_07135	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in</i>	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis</i>	0.843

				<i>a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>using gene prediction method: Protein Homology</i>	
ssaE	sseD	CY43_07105	CY43_07130	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.722
ssaE	sseB	CY43_07105	CY43_07115	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.923
ssaE	sscB	CY43_07105	CY43_07140	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.663
ssaE	ssaA	CY43_07105	CY43_07120	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.851
ssaE	ssaV	CY43_07105	CY43_07195	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis</i>	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III</i>	0.623

				<i>using gene prediction method: Protein Homology</i>	<i>secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	
ssaE	ssaU	CY43_07105	CY43_07235	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.492
ssaE	ssaS	CY43_07105	CY43_07225	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.598
ssaE	ssaR	CY43_07105	CY43_07220	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.710
ssaE	ssaQ	CY43_07105	CY43_07215	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.767
ssaE	ssaP	CY43_07105	CY43_07210	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.478

ssaE	ssaO	CY43_07105	CY43_07205	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	0.494
ssaE	ssaN	CY43_07105	CY43_07200	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology	EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology	0.687
ssaE	ssaI	CY43_07105	CY43_07165	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	0.537
ssaE	ssaG	CY43_07105	CY43_07155	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology	EscF/YscF/HrpA family type III secretion system needle major subunit; <i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	0.716
ssaE	ssaD	CY43_07105	CY43_07100	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	0.926
ssaE	spiC	CY43_07105	CY43_07090	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved	SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits	0.930

				<i>in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	
ssaE	spiA	CY43_07105	CY43_07095	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.927
ssaE	DD95_20700	CY43_07105	CY43_07230	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.610
ssaD	ssrB	CY43_07100	CY43_07080	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.717
ssaD	ssrA	CY43_07100	CY43_07085	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.923
ssaD	sseF	CY43_07100	CY43_07145	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.628

ssaD	sseE	CY43_07100	CY43_07135	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology	0.884
ssaD	sseD	CY43_07100	CY43_07130	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	0.792
ssaD	sseB	CY43_07100	CY43_07115	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology	0.851
ssaD	sscB	CY43_07100	CY43_07140	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; chaperone for SseF; required for the efficient replication of <i>Salmonella</i> in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology	0.955
ssaD	ssaA	CY43_07100	CY43_07120	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	0.975
ssaD	ssaV	CY43_07100	CY43_07195	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the <i>Salmonella</i> pathogenicity island 2; part of the type III secretion system; Derived by automated	0.731

					<i>computational analysis using gene prediction method: Protein Homology</i>	
ssaD	ssaU	CY43_07100	CY43_07235	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.902
ssaD	ssaS	CY43_07100	CY43_07225	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.860
ssaD	ssaR	CY43_07100	CY43_07220	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.888
ssaD	ssaQ	CY43_07100	CY43_07215	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.964
ssaD	ssaP	CY43_07100	CY43_07210	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.840
ssaD	ssaO	CY43_07100	CY43_07205	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated</i>	0.839

				<i>computational analysis using gene prediction method: Protein Homology</i>	<i>computational analysis using gene prediction method: Protein Homology</i>	
ssaD	ssaN	CY43_07100	CY43_07200	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.830
ssaD	ssaI	CY43_07100	CY43_07165	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.535
ssaD	ssaG	CY43_07100	CY43_07155	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.642
ssaD	ssaE	CY43_07100	CY43_07105	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.926
ssaD	spiC	CY43_07100	CY43_07090	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.955
ssaD	spiA	CY43_07100	CY43_07095	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in</i>	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis</i>	0.988

				<i>a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>using gene prediction method: Protein Homology</i>	
ssaD	DD95_20700	CY43_07100	CY43_07230	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.892
spiC	ssrB	CY43_07090	CY43_07080	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.856
spiC	ssrA	CY43_07090	CY43_07085	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.902
spiC	sseF	CY43_07090	CY43_07145	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.803
spiC	sseE	CY43_07090	CY43_07135	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.844
spiC	sseD	CY43_07090	CY43_07130	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated</i>	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational</i>	0.863

				<i>computational analysis using gene prediction method: Protein Homology</i>	<i>analysis using gene prediction method: Protein Homology</i>	
spiC	sseB	CY43_07090	CY43_07115	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.877
spiC	sscB	CY43_07090	CY43_07140	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.703
spiC	ssaA	CY43_07090	CY43_07120	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.876
spiC	ssaV	CY43_07090	CY43_07195	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.607
spiC	ssaU	CY43_07090	CY43_07235	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.662
spiC	ssaS	CY43_07090	CY43_07225	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits</i>	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated</i>	0.691

				<i>phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>computational analysis using gene prediction method: Protein Homology</i>	
spiC	ssaR	CY43_07090	CY43_07220	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.841
spiC	ssaQ	CY43_07090	CY43_07215	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.651
spiC	ssaP	CY43_07090	CY43_07210	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.683
spiC	ssaO	CY43_07090	CY43_07205	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.642
spiC	ssaN	CY43_07090	CY43_07200	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.607
spiC	ssaI	CY43_07090	CY43_07165	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved</i>	0.538

				<i>phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	
spiC	ssaG	CY43_07090	CY43_07155	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.937
spiC	ssaE	CY43_07090	CY43_07105	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.930
spiC	ssaD	CY43_07090	CY43_07100	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.955
spiC	spiA	CY43_07090	CY43_07095	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.959
spiC	DD95_20700	CY43_07090	CY43_07230	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.569

spiA	ssrB	CY43_07095	CY43_07080	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.806
spiA	ssrA	CY43_07095	CY43_07085	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.914
spiA	sseF	CY43_07095	CY43_07145	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.628
spiA	sseE	CY43_07095	CY43_07135	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.738
spiA	sseD	CY43_07095	CY43_07130	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.849
spiA	sseB	CY43_07095	CY43_07115	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.859
spiA	sscB	CY43_07095	CY43_07140	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; chaperone for SseF; required for the efficient replication of Salmonella in host</i>	0.899

					<i>macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	
spiA	ssaA	CY43_07095	CY43_07120	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>CesD/SycD/LcrH family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.976
spiA	ssaV	CY43_07095	CY43_07195	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the Salmonella pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.807
spiA	ssaU	CY43_07095	CY43_07235	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Member of a type III secretion system which is part of a pathogenicity island in Salmonella, Yersinia and pathogenic Escherichia coli; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.815
spiA	ssaS	CY43_07095	CY43_07225	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.807
spiA	ssaR	CY43_07095	CY43_07220	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.839
spiA	ssaQ	CY43_07095	CY43_07215	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.948

spiA	ssaP	CY43_07095	CY43_07210	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.626
spiA	ssaO	CY43_07095	CY43_07205	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.486
spiA	ssaN	CY43_07095	CY43_07200	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.789
spiA	ssaI	CY43_07095	CY43_07165	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.537
spiA	ssaG	CY43_07095	CY43_07155	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.775
spiA	ssaE	CY43_07095	CY43_07105	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.927

spiA	ssaD	CY43_07095	CY43_07100	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.988
spiA	spiC	CY43_07095	CY43_07090	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.959
spiA	DD95_20700	CY43_07095	CY43_07230	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.905
DD95_20875	ssrA	CY43_07050	CY43_07085	<i>Histidine kinase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.798
DD95_20875	DD95_20870	CY43_07050	CY43_07055	<i>Histidine kinase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Tetrathionate response regulatory protein TtrR; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.997
DD95_20870	DD95_20875	CY43_07055	CY43_07050	<i>Tetrathionate response regulatory protein TtrR; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Histidine kinase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.997
DD95_20700	ssrB	CY43_07230	CY43_07080	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system regulator; Is phosphorylated by SsrA; is involved in the expression of the virulence genes of Salmonella pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.588

DD95_20700	ssrA	CY43_07230	CY43_07085	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	Histidine kinase; Phosphorylates the response regulator SsrB; is involved in the expression of the virulence genes of <i>Salmonella</i> pathogenicity island-2; Derived by automated computational analysis using gene prediction method: Protein Homology	0.703
DD95_20700	sseF	CY43_07230	CY43_07145	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	Pathogenicity island 2 effector protein SseF; With SseG is involved in the aggregation of the host endosomes; Derived by automated computational analysis using gene prediction method: Protein Homology	0.544
DD95_20700	sseE	CY43_07230	CY43_07135	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	Pathogenicity island 2 effector protein SseE; Derived by automated computational analysis using gene prediction method: Protein Homology	0.556
DD95_20700	sseD	CY43_07230	CY43_07130	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	SPI-2 type III secretion system translocon protein SseD; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	0.656
DD95_20700	sseB	CY43_07230	CY43_07115	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	SPI-2 type III secretion system translocon protein SseB; Necessary for the correct localization of SseC and SseD on the bacterial cell surface; Derived by automated computational analysis using gene prediction method: Protein Homology	0.651
DD95_20700	sscB	CY43_07230	CY43_07140	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; chaperone for SseF; required for the efficient replication of <i>Salmonella</i> in host macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology	0.883

DD95_20700	ssaA	CY43_07230	CY43_07120	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	<i>CesD/SycD/LcrH</i> family type III secretion system chaperone; May be involved in the translocation of effector proteins into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	0.906
DD95_20700	ssaV	CY43_07230	CY43_07195	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	SPI-2 type III secretion system apparatus protein SsaV; With SsaC forms part of a protein export system across the inner and outer cell membranes; part of the <i>Salmonella</i> pathogenicity island 2; part of the type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology	0.962
DD95_20700	ssaU	CY43_07230	CY43_07235	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	Member of a type III secretion system which is part of a pathogenicity island in <i>Salmonella</i> , <i>Yersinia</i> and pathogenic <i>Escherichia coli</i> ; Derived by automated computational analysis using gene prediction method: Protein Homology	0.991
DD95_20700	ssaS	CY43_07230	CY43_07225	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	SPI-2 type III secretion system apparatus protein SsaS; Derived by automated computational analysis using gene prediction method: Protein Homology	0.983
DD95_20700	ssaR	CY43_07230	CY43_07220	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	SPI-2 type III secretion system export apparatus protein SsaR; Part of a set of proteins involved in the infection of eukaryotic cells; in plant pathogens involved in the hypersensitivity response; Derived by automated computational analysis using gene prediction method: Protein Homology	0.990
DD95_20700	ssaQ	CY43_07230	CY43_07215	<i>Salmonella</i> pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of <i>Salmonella</i> in a host cell; Derived by automated	SPI-2 type III secretion system apparatus protein SsaQ; Derived by automated computational analysis using gene prediction method: Protein Homology	0.919

				<i>computational analysis using gene prediction method: Protein Homology</i>		
DD95_20700	ssaP	CY43_07230	CY43_07210	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.762
DD95_20700	ssaO	CY43_07230	CY43_07205	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.763
DD95_20700	ssaN	CY43_07230	CY43_07200	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscN/YscN/HrcN family type III secretion system ATPase; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.945
DD95_20700	ssaI	CY43_07230	CY43_07165	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.746
DD95_20700	ssaG	CY43_07230	CY43_07155	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>EscF/YscF/HrpA family type III secretion system needle major subunit; Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.746
DD95_20700	ssaE	CY43_07230	CY43_07105	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; involved in the secretion of SseB;</i>	0.610

				<i>computational analysis using gene prediction method: Protein Homology</i>	<i>Derived by automated computational analysis using gene prediction method: Protein Homology</i>	
DD95_20700	ssaD	CY43_07230	CY43_07100	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.892
DD95_20700	spiC	CY43_07230	CY43_07090	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiC; Involved in macrophage infection; inhibits phagosome-lysosome fusion and cellular trafficking; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.569
DD95_20700	spiA	CY43_07230	CY43_07095	<i>Salmonella pathogenicity island 2 protein; member of a type III secretion system involved in the survival and replication of Salmonella in a host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-2 type III secretion system protein SpiA; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.905