

1 **Table S6:** The interaction networks and the co-expression details of the SPI1 cluster proteins in *S. enterica* Typhimurium ms202.

node1	node2	node1 accession	node2 accession	node1 annotation	node2 annotation	score
sptP	sprB	CY43_15030	CY43_14970	<i>SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Transcriptional regulator SprB; Activates Salmonella pathogenicity island 4 genes and weakly represses Salmonella pathogenicity island 1 genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.440
sptP	spaO	CY43_15030	CY43_15095	<i>SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Involved in a secretory pathway responsible for the surface presentation of determinants needed for the entry of Salmonella species into mammalian cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.912
sptP	sipD	CY43_15030	CY43_15055	<i>SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Involved in the transport of effector protein by the type III secretion system of Salmonella pathogenicity island 1; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.956
sptP	sipC	CY43_15030	CY43_15060	<i>SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system needle tip complex protein SipC; Cell invasion protein C; required for entry of the bacteria into the host cell; binds to actin; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.980
sptP	sipB	CY43_15030	CY43_15065	<i>SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.987
sptP	sipA	CY43_15030	CY43_15050	<i>SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by</i>	<i>SPI-1 type III secretion system effector SipA; Cell invasion protein A; actin-binding; required for entry of the Salmonella into the host cell; Derived by</i>	0.988

				<i>automated computational analysis using gene prediction method: Protein Homology</i>	<i>automated computational analysis using gene prediction method: Protein Homology</i>	
sptP	sicP	CY43_15030	CY43_15035	<i>SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Chaperone protein SicP; Type III secretion system chaperone; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.998
sptP	prgK	CY43_15030	CY43_14995	<i>SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Lipoprotein; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.750
sptP	prgJ	CY43_15030	CY43_15000	<i>SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system needle complex protein PrgJ; May be involved in capping the needle substructure; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.460
sptP	prgI	CY43_15030	CY43_15005	<i>SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.757
sptP	prgH	CY43_15030	CY43_15010	<i>SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.938
sptP	invG	CY43_15030	CY43_15130	<i>SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system outer membrane ring protein InvG; May be involved in the export or assembly of proteins involved in the entry of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.840

sptP	iagB	CY43_15030	CY43_15025	<i>SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system invasion protein IagB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.495
sptP	hilA	CY43_15030	CY43_15020	<i>SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Invasion protein regulator; IagA; HilA; activates the expression of invasion genes and activates the expression of prgHIJK which is part of the pathogenicity island 1 type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.556
sptP	DD95_24045	CY43_15030	CY43_14490	<i>SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Flagellin FliC; Structural flagella protein; individual Salmonella serotypes usually alternate between the production of 2 antigenic forms of flagella, termed phase 1 and phase 2, each specified by separate structural genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.557
sptP	DD95_19955	CY43_15030	CY43_10320	<i>SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Flagellin; Structural flagella protein; individual Salmonella serotypes usually alternate between the production of 2 antigenic forms of flagella, termed phase 1 and phase 2, each specified by separate structural genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.558
sprB	sptP	CY43_14970	CY43_15030	<i>Transcriptional regulator SprB; Activates Salmonella pathogenicity island 4 genes and weakly represses Salmonella pathogenicity island 1 genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.440
sprB	spaO	CY43_14970	CY43_15095	<i>Transcriptional regulator SprB; Activates Salmonella pathogenicity island 4 genes and weakly represses Salmonella pathogenicity island 1 genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Involved in a secretory pathway responsible for the surface presentation of determinants needed for the entry of Salmonella species into mammalian cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.403

sprB	sitD	CY43_14970	CY43_14960	<i>Transcriptional regulator SprB; Activates Salmonella pathogenicity island 4 genes and weakly represses Salmonella pathogenicity island 1 genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Metal ABC transporter permease; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.599
sprB	sitC	CY43_14970	CY43_14955	<i>Transcriptional regulator SprB; Activates Salmonella pathogenicity island 4 genes and weakly represses Salmonella pathogenicity island 1 genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Metal ABC transporter permease; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.559
sprB	prgK	CY43_14970	CY43_14995	<i>Transcriptional regulator SprB; Activates Salmonella pathogenicity island 4 genes and weakly represses Salmonella pathogenicity island 1 genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Lipoprotein; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.434
sprB	prgI	CY43_14970	CY43_15005	<i>Transcriptional regulator SprB; Activates Salmonella pathogenicity island 4 genes and weakly represses Salmonella pathogenicity island 1 genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.494
sprB	prgH	CY43_14970	CY43_15010	<i>Transcriptional regulator SprB; Activates Salmonella pathogenicity island 4 genes and weakly represses Salmonella pathogenicity island 1 genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.483
sprB	iagB	CY43_14970	CY43_15025	<i>Transcriptional regulator SprB; Activates Salmonella pathogenicity island 4 genes and weakly represses Salmonella pathogenicity island 1 genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system invasion protein IagB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.639
spaQ	spaO	CY43_15085	CY43_15095	<i>SPI-1 type III secretion system export apparatus protein SpaQ; Involved in the surface</i>	<i>Involved in a secretory pathway responsible for the surface presentation of determinants needed for the</i>	0.987

				<i>presentation of antigens needed for the invasion of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>entry of Salmonella species into mammalian cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	
spaQ	sipD	CY43_15085	CY43_15055	<i>SPI-1 type III secretion system export apparatus protein SpaQ; Involved in the surface presentation of antigens needed for the invasion of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Involved in the transport of effector protein by the type III secretion system of Salmonella pathogenicity island 1; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.554
spaQ	sipC	CY43_15085	CY43_15060	<i>SPI-1 type III secretion system export apparatus protein SpaQ; Involved in the surface presentation of antigens needed for the invasion of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system needle tip complex protein SipC; Cell invasion protein C; required for entry of the bacteria into the host cell; binds to actin; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.574
spaQ	sipB	CY43_15085	CY43_15065	<i>SPI-1 type III secretion system export apparatus protein SpaQ; Involved in the surface presentation of antigens needed for the invasion of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.891
spaQ	sipA	CY43_15085	CY43_15050	<i>SPI-1 type III secretion system export apparatus protein SpaQ; Involved in the surface presentation of antigens needed for the invasion of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system effector SipA; Cell invasion protein A; actin-binding; required for entry of the Salmonella into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.433
spaQ	sicP	CY43_15085	CY43_15035	<i>SPI-1 type III secretion system export apparatus protein SpaQ; Involved in the surface presentation of antigens needed for the invasion of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Chaperone protein SicP; Type III secretion system chaperone; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.499
spaQ	prgK	CY43_15085	CY43_14995	<i>SPI-1 type III secretion system export apparatus protein SpaQ; Involved in the surface presentation of antigens needed for the invasion of Salmonella into host cells; Derived by</i>	<i>Lipoprotein; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.957

				<i>automated computational analysis using gene prediction method: Protein Homology</i>		
spaQ	prgJ	CY43_15085	CY43_15000	<i>SPI-1 type III secretion system export apparatus protein SpaQ; Involved in the surface presentation of antigens needed for the invasion of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system needle complex protein PrgJ; May be involved in capping the needle substructure; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.775
spaQ	prgI	CY43_15085	CY43_15005	<i>SPI-1 type III secretion system export apparatus protein SpaQ; Involved in the surface presentation of antigens needed for the invasion of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.556
spaQ	prgH	CY43_15085	CY43_15010	<i>SPI-1 type III secretion system export apparatus protein SpaQ; Involved in the surface presentation of antigens needed for the invasion of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.863
spaQ	invG	CY43_15085	CY43_15130	<i>SPI-1 type III secretion system export apparatus protein SpaQ; Involved in the surface presentation of antigens needed for the invasion of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system outer membrane ring protein InvG; May be involved in the export or assembly of proteins involved in the entry of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.985
spaQ	iagB	CY43_15085	CY43_15025	<i>SPI-1 type III secretion system export apparatus protein SpaQ; Involved in the surface presentation of antigens needed for the invasion of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system invasion protein iagB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.650
spaO	sptP	CY43_15095	CY43_15030	<i>Involved in a secretory pathway responsible for the surface presentation of determinants needed for the entry of Salmonella species into mammalian cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.912

spaO	sprB	CY43_15095	CY43_14970	<i>Involved in a secretory pathway responsible for the surface presentation of determinants needed for the entry of Salmonella species into mammalian cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Transcriptional regulator SprB; Activates Salmonella pathogenicity island 4 genes and weakly represses Salmonella pathogenicity island 1 genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.403
spaO	spaQ	CY43_15095	CY43_15085	<i>Involved in a secretory pathway responsible for the surface presentation of determinants needed for the entry of Salmonella species into mammalian cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system export apparatus protein SpaQ; Involved in the surface presentation of antigens needed for the invasion of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.987
spaO	sipD	CY43_15095	CY43_15055	<i>Involved in a secretory pathway responsible for the surface presentation of determinants needed for the entry of Salmonella species into mammalian cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Involved in the transport of effector protein by the type III secretion system of Salmonella pathogenicity island 1; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.844
spaO	sipC	CY43_15095	CY43_15060	<i>Involved in a secretory pathway responsible for the surface presentation of determinants needed for the entry of Salmonella species into mammalian cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system needle tip complex protein SipC; Cell invasion protein C; required for entry of the bacteria into the host cell; binds to actin; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.860
spaO	sipB	CY43_15095	CY43_15065	<i>Involved in a secretory pathway responsible for the surface presentation of determinants needed for the entry of Salmonella species into mammalian cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.982
spaO	sipA	CY43_15095	CY43_15050	<i>Involved in a secretory pathway responsible for the surface presentation of determinants needed for the entry of Salmonella species into mammalian cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system effector SipA; Cell invasion protein A; actin-binding; required for entry of the Salmonella into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.803
spaO	sicP	CY43_15095	CY43_15035	<i>Involved in a secretory pathway responsible for the surface presentation of determinants needed</i>	<i>Chaperone protein SicP; Type III secretion system chaperone; Derived by automated computational</i>	0.752

				<i>for the entry of Salmonella species into mammalian cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>analysis using gene prediction method: Protein Homology</i>	
spaO	prgK	CY43_15095	CY43_14995	<i>Involved in a secretory pathway responsible for the surface presentation of determinants needed for the entry of Salmonella species into mammalian cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Lipoprotein; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.960
spaO	prgJ	CY43_15095	CY43_15000	<i>Involved in a secretory pathway responsible for the surface presentation of determinants needed for the entry of Salmonella species into mammalian cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system needle complex protein PrgJ; May be involved in capping the needle substructure; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.668
spaO	prgI	CY43_15095	CY43_15005	<i>Involved in a secretory pathway responsible for the surface presentation of determinants needed for the entry of Salmonella species into mammalian cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.810
spaO	prgH	CY43_15095	CY43_15010	<i>Involved in a secretory pathway responsible for the surface presentation of determinants needed for the entry of Salmonella species into mammalian cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.938
spaO	invG	CY43_15095	CY43_15130	<i>Involved in a secretory pathway responsible for the surface presentation of determinants needed for the entry of Salmonella species into mammalian cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system outer membrane ring protein InvG; May be involved in the export or assembly of proteins involved in the entry of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.974
paO	iagB	CY43_15095	CY43_15025	<i>Involved in a secretory pathway responsible for the surface presentation of determinants needed for the entry of Salmonella species into mammalian cells; Derived by automated</i>	<i>SPI-1 type III secretion system invasion protein IagB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.747

				<i>computational analysis using gene prediction method: Protein Homology</i>		
spaO	hilA	CY43_15095	CY43_15020	<i>Involved in a secretory pathway responsible for the surface presentation of determinants needed for the entry of Salmonella species into mammalian cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Invasion protein regulator; IagA; HilA; activates the expression of invasion genes and activates the expression of prgHIJK which is part of the pathogenicity island 1 type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.790
sitD	sprB	CY43_14960	CY43_14970	<i>Metal ABC transporter permease; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Transcriptional regulator SprB; Activates Salmonella pathogenicity island 4 genes and weakly represses Salmonella pathogenicity island 1 genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.599
sitD	sitC	CY43_14960	CY43_14955	<i>Metal ABC transporter permease; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Metal ABC transporter permease; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.987
sitD	sitB	CY43_14960	CY43_14950	<i>Metal ABC transporter permease; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Manganese/iron transporter ATP-binding protein; With SitACD is involved in the transport of manganese and iron; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.999
sitD	sitA	CY43_14960	CY43_14945	<i>Metal ABC transporter permease; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Metal ABC transporter substrate-binding protein; Derived by automated computational analysis using gene prediction method: Protein Homology; Belongs to the bacterial solute-binding protein 9 family</i>	0.999
sitC	sprB	CY43_14955	CY43_14970	<i>Metal ABC transporter permease; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Transcriptional regulator SprB; Activates Salmonella pathogenicity island 4 genes and weakly represses Salmonella pathogenicity island 1 genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.559
sitC	sitD	CY43_14955	CY43_14960	<i>Metal ABC transporter permease; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Metal ABC transporter permease; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.987
sitC	sitB	CY43_14955	CY43_14950	<i>Metal ABC transporter permease; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Manganese/iron transporter ATP-binding protein; With SitACD is involved in the transport of manganese and iron; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.999

sitC	sitA	CY43_14955	CY43_14945	<i>Metal ABC transporter permease; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Metal ABC transporter substrate-binding protein; Derived by automated computational analysis using gene prediction method: Protein Homology; Belongs to the bacterial solute-binding protein 9 family</i>	0.999
sitC	sipB	CY43_14955	CY43_15065	<i>Metal ABC transporter permease; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.596
sitC	prgH	CY43_14955	CY43_15010	<i>Metal ABC transporter permease; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.658
sitB	sitD	CY43_14950	CY43_14960	<i>Manganese/iron transporter ATP-binding protein; With SitACD is involved in the transport of manganese and iron; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Metal ABC transporter permease; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.999
sitB	sitC	CY43_14950	CY43_14955	<i>Manganese/iron transporter ATP-binding protein; With SitACD is involved in the transport of manganese and iron; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Metal ABC transporter permease; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.999
sitB	sitA	CY43_14950	CY43_14945	<i>Manganese/iron transporter ATP-binding protein; With SitACD is involved in the transport of manganese and iron; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Metal ABC transporter substrate-binding protein; Derived by automated computational analysis using gene prediction method: Protein Homology; Belongs to the bacterial solute-binding protein 9 family</i>	0.999
sitA	sitD	CY43_14945	CY43_14960	<i>Metal ABC transporter substrate-binding protein; Derived by automated computational analysis using gene prediction method: Protein Homology; Belongs to the bacterial solute-binding protein 9 family</i>	<i>Metal ABC transporter permease; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.999
sitA	sitC	CY43_14945	CY43_14955	<i>Metal ABC transporter substrate-binding protein; Derived by automated computational analysis using gene prediction method: Protein</i>	<i>Metal ABC transporter permease; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.999

				<i>Homology; Belongs to the bacterial solute-binding protein 9 family</i>		
sitA	sitB	CY43_14945	CY43_14950	<i>Metal ABC transporter substrate-binding protein; Derived by automated computational analysis using gene prediction method: Protein Homology; Belongs to the bacterial solute-binding protein 9 family</i>	<i>Manganese/iron transporter ATP-binding protein; With SitACD is involved in the transport of manganese and iron; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.999
sipD	sptP	CY43_15055	CY43_15030	<i>Involved in the transport of effector protein by the type III secretion system of Salmonella pathogenicity island 1; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.956
sipD	spaQ	CY43_15055	CY43_15085	<i>Involved in the transport of effector protein by the type III secretion system of Salmonella pathogenicity island 1; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system export apparatus protein SpaQ; Involved in the surface presentation of antigens needed for the invasion of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.554
sipD	spaO	CY43_15055	CY43_15095	<i>Involved in the transport of effector protein by the type III secretion system of Salmonella pathogenicity island 1; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Involved in a secretory pathway responsible for the surface presentation of determinants needed for the entry of Salmonella species into mammalian cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.844
sipD	sipC	CY43_15055	CY43_15060	<i>Involved in the transport of effector protein by the type III secretion system of Salmonella pathogenicity island 1; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system needle tip complex protein SipC; Cell invasion protein C; required for entry of the bacteria into the host cell; binds to actin; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.993
sipD	sipB	CY43_15055	CY43_15065	<i>Involved in the transport of effector protein by the type III secretion system of Salmonella pathogenicity island 1; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.994
sipD	sipA	CY43_15055	CY43_15050	<i>Involved in the transport of effector protein by the type III secretion system of Salmonella pathogenicity island 1; Derived by automated</i>	<i>SPI-1 type III secretion system effector SipA; Cell invasion protein A; actin-binding; required for entry of the Salmonella into the host cell; Derived by</i>	0.993

				<i>computational analysis using gene prediction method: Protein Homology</i>	<i>automated computational analysis using gene prediction method: Protein Homology</i>	
sipD	sicP	CY43_15055	CY43_15035	<i>Involved in the transport of effector protein by the type III secretion system of Salmonella pathogenicity island 1; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Chaperone protein SicP; Type III secretion system chaperone; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.888
sipD	prgK	CY43_15055	CY43_14995	<i>Involved in the transport of effector protein by the type III secretion system of Salmonella pathogenicity island 1; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Lipoprotein; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.758
sipD	prgJ	CY43_15055	CY43_15000	<i>Involved in the transport of effector protein by the type III secretion system of Salmonella pathogenicity island 1; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system needle complex protein PrgJ; May be involved in capping the needle substructure; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.586
sipD	prgI	CY43_15055	CY43_15005	<i>Involved in the transport of effector protein by the type III secretion system of Salmonella pathogenicity island 1; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.953
sipD	prgH	CY43_15055	CY43_15010	<i>Involved in the transport of effector protein by the type III secretion system of Salmonella pathogenicity island 1; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.780
sipD	invG	CY43_15055	CY43_15130	<i>Involved in the transport of effector protein by the type III secretion system of Salmonella pathogenicity island 1; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system outer membrane ring protein InvG; May be involved in the export or assembly of proteins involved in the entry of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.823
sipD	iagB	CY43_15055	CY43_15025	<i>Involved in the transport of effector protein by the type III secretion system of Salmonella pathogenicity island 1; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system invasion protein IagB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.587

sipC	sptP	CY43_15060	CY43_15030	<i>SPI-1 type III secretion system needle tip complex protein SipC; Cell invasion protein C; required for entry of the bacteria into the host cell; binds to actin; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.980
sipC	spaQ	CY43_15060	CY43_15085	<i>SPI-1 type III secretion system needle tip complex protein SipC; Cell invasion protein C; required for entry of the bacteria into the host cell; binds to actin; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system export apparatus protein SpaQ; Involved in the surface presentation of antigens needed for the invasion of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.574
sipC	spaO	CY43_15060	CY43_15095	<i>SPI-1 type III secretion system needle tip complex protein SipC; Cell invasion protein C; required for entry of the bacteria into the host cell; binds to actin; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Involved in a secretory pathway responsible for the surface presentation of determinants needed for the entry of Salmonella species into mammalian cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.860
sipC	sipD	CY43_15060	CY43_15055	<i>SPI-1 type III secretion system needle tip complex protein SipC; Cell invasion protein C; required for entry of the bacteria into the host cell; binds to actin; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Involved in the transport of effector protein by the type III secretion system of Salmonella pathogenicity island 1; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.993
sipC	sipB	CY43_15060	CY43_15065	<i>SPI-1 type III secretion system needle tip complex protein SipC; Cell invasion protein C; required for entry of the bacteria into the host cell; binds to actin; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.997
sipC	sipA	CY43_15060	CY43_15050	<i>SPI-1 type III secretion system needle tip complex protein SipC; Cell invasion protein C; required for entry of the bacteria into the host cell; binds to actin; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system effector SipA; Cell invasion protein A; actin-binding; required for entry of the Salmonella into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.992
sipC	sicP	CY43_15060	CY43_15035	<i>SPI-1 type III secretion system needle tip complex protein SipC; Cell invasion protein C; required</i>	<i>Chaperone protein SicP; Type III secretion system chaperone; Derived by automated computational</i>	0.823

				<i>for entry of the bacteria into the host cell; binds to actin; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>analysis using gene prediction method: Protein Homology</i>	
sipC	prgK	CY43_15060	CY43_14995	<i>SPI-1 type III secretion system needle tip complex protein SipC; Cell invasion protein C; required for entry of the bacteria into the host cell; binds to actin; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Lipoprotein; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.728
sipC	prgJ	CY43_15060	CY43_15000	<i>SPI-1 type III secretion system needle tip complex protein SipC; Cell invasion protein C; required for entry of the bacteria into the host cell; binds to actin; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system needle complex protein PrgJ; May be involved in capping the needle substructure; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.576
sipC	prgI	CY43_15060	CY43_15005	<i>SPI-1 type III secretion system needle tip complex protein SipC; Cell invasion protein C; required for entry of the bacteria into the host cell; binds to actin; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<u>0.849</u>
sipC	prgH	CY43_15060	CY43_15010	<i>SPI-1 type III secretion system needle tip complex protein SipC; Cell invasion protein C; required for entry of the bacteria into the host cell; binds to actin; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.860
sipC	invG	CY43_15060	CY43_15130	<i>SPI-1 type III secretion system needle tip complex protein SipC; Cell invasion protein C; required for entry of the bacteria into the host cell; binds to actin; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system outer membrane ring protein InvG; May be involved in the export or assembly of proteins involved in the entry of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.842
sipC	DD95_24045	CY43_15060	CY43_14490	<i>SPI-1 type III secretion system needle tip complex protein SipC; Cell invasion protein C; required for entry of the bacteria into the host cell; binds to actin; Derived by automated computational</i>	<i>Flagellin FliC; Structural flagella protein; individual Salmonella serotypes usually alternate between the production of 2 antigenic forms of flagella, termed phase 1 and phase 2, each specified</i>	0.559

				<i>analysis using gene prediction method: Protein Homology</i>	<i>by separate structural genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	
sipC	DD95_19955	CY43_15060	CY43_10320	<i>SPI-1 type III secretion system needle tip complex protein SipC; Cell invasion protein C; required for entry of the bacteria into the host cell; binds to actin; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Flagellin; Structural flagella protein; individual Salmonella serotypes usually alternate between the production of 2 antigenic forms of flagella, termed phase 1 and phase 2, each specified by separate structural genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.558
sipB	sptP	CY43_15065	CY43_15030	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.987
sipB	spaQ	CY43_15065	CY43_15085	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system export apparatus protein SpaQ; Involved in the surface presentation of antigens needed for the invasion of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.891
sipB	spaO	CY43_15065	CY43_15095	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Involved in a secretory pathway responsible for the surface presentation of determinants needed for the entry of Salmonella species into mammalian cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.982
sipB	sitC	CY43_15065	CY43_14955	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Metal ABC transporter permease; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.596
sipB	sipD	CY43_15065	CY43_15055	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated</i>	<i>Involved in the transport of effector protein by the type III secretion system of Salmonella pathogenicity island 1; Derived by automated computational</i>	0.994

				<i>computational analysis using gene prediction method: Protein Homology</i>	<i>analysis using gene prediction method: Protein Homology</i>	
sipB	sipC	CY43_15065	CY43_15060	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system needle tip complex protein SipC; Cell invasion protein C; required for entry of the bacteria into the host cell; binds to actin; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.997
sipB	sipA	CY43_15065	CY43_15050	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system effector SipA; Cell invasion protein A; actin-binding; required for entry of the Salmonella into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.991
sipB	sicP	CY43_15065	CY43_15035	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Chaperone protein SicP; Type III secretion system chaperone; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.828
sipB	prgK	CY43_15065	CY43_14995	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Lipoprotein; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.951
sipB	prgJ	CY43_15065	CY43_15000	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system needle complex protein PrgJ; May be involved in capping the needle substructure; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.847
sipB	prgI	CY43_15065	CY43_15005	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.852

sipB	prgH	CY43_15065	CY43_15010	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.969
sipB	invG	CY43_15065	CY43_15130	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system outer membrane ring protein InvG; May be involved in the export or assembly of proteins involved in the entry of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.971
sipB	iagB	CY43_15065	CY43_15025	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system invasion protein IagB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.718
sipB	hilA	CY43_15065	CY43_15020	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Invasion protein regulator; IagA; HilA; activates the expression of invasion genes and activates the expression of prgHIJK which is part of the pathogenicity island 1 type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.876
sipB	DD95_24045	CY43_15065	CY43_14490	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Flagellin FliC; Structural flagella protein; individual Salmonella serotypes usually alternate between the production of 2 antigenic forms of flagella, termed phase 1 and phase 2, each specified by separate structural genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.663
sipB	DD95_19955	CY43_15065	CY43_10320	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Flagellin; Structural flagella protein; individual Salmonella serotypes usually alternate between the production of 2 antigenic forms of flagella, termed phase 1 and phase 2, each specified by separate structural genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.658

sipA	sptP	CY43_15050	CY43_15030	<i>SPI-1 type III secretion system effector SipA; Cell invasion protein A; actin-binding; required for entry of the Salmonella into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.988
sipA	spaQ	CY43_15050	CY43_15085	<i>SPI-1 type III secretion system effector SipA; Cell invasion protein A; actin-binding; required for entry of the Salmonella into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system export apparatus protein SpaQ; Involved in the surface presentation of antigens needed for the invasion of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.433
sipA	spaO	CY43_15050	CY43_15095	<i>SPI-1 type III secretion system effector SipA; Cell invasion protein A; actin-binding; required for entry of the Salmonella into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Involved in a secretory pathway responsible for the surface presentation of determinants needed for the entry of Salmonella species into mammalian cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.803
sipA	sipD	CY43_15050	CY43_15055	<i>SPI-1 type III secretion system effector SipA; Cell invasion protein A; actin-binding; required for entry of the Salmonella into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Involved in the transport of effector protein by the type III secretion system of Salmonella pathogenicity island 1; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.993
sipA	sipC	CY43_15050	CY43_15060	<i>SPI-1 type III secretion system effector SipA; Cell invasion protein A; actin-binding; required for entry of the Salmonella into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system needle tip complex protein SipC; Cell invasion protein C; required for entry of the bacteria into the host cell; binds to actin; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.992
sipA	sipB	CY43_15050	CY43_15065	<i>SPI-1 type III secretion system effector SipA; Cell invasion protein A; actin-binding; required for entry of the Salmonella into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.991
sipA	sicP	CY43_15050	CY43_15035	<i>SPI-1 type III secretion system effector SipA; Cell invasion protein A; actin-binding; required for entry of the Salmonella into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Chaperone protein SicP; Type III secretion system chaperone; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.812

sipA	prgK	CY43_15050	CY43_14995	<i>SPI-1 type III secretion system effector SipA; Cell invasion protein A; actin-binding; required for entry of the Salmonella into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Lipoprotein; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.716
sipA	prgJ	CY43_15050	CY43_15000	<i>SPI-1 type III secretion system effector SipA; Cell invasion protein A; actin-binding; required for entry of the Salmonella into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system needle complex protein PrgJ; May be involved in capping the needle substructure; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.717
sipA	prgI	CY43_15050	CY43_15005	<i>SPI-1 type III secretion system effector SipA; Cell invasion protein A; actin-binding; required for entry of the Salmonella into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.755
sipA	prgH	CY43_15050	CY43_15010	<i>SPI-1 type III secretion system effector SipA; Cell invasion protein A; actin-binding; required for entry of the Salmonella into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.811
sipA	invG	CY43_15050	CY43_15130	<i>SPI-1 type III secretion system effector SipA; Cell invasion protein A; actin-binding; required for entry of the Salmonella into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system outer membrane ring protein InvG; May be involved in the export or assembly of proteins involved in the entry of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.850
sipA	iagB	CY43_15050	CY43_15025	<i>SPI-1 type III secretion system effector SipA; Cell invasion protein A; actin-binding; required for entry of the Salmonella into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system invasion protein iagB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.407
sipA	DD95_24045	CY43_15050	CY43_14490	<i>SPI-1 type III secretion system effector SipA; Cell invasion protein A; actin-binding; required for entry of the Salmonella into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Flagellin FliC; Structural flagella protein; individual Salmonella serotypes usually alternate between the production of 2 antigenic forms of flagella, termed phase 1 and phase 2, each specified by separate structural genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.705

sipA	DD95_19955	CY43_15050	CY43_10320	<i>SPI-1 type III secretion system effector SipA; Cell invasion protein A; actin-binding; required for entry of the Salmonella into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Flagellin; Structural flagella protein; individual Salmonella serotypes usually alternate between the production of 2 antigenic forms of flagella, termed phase 1 and phase 2, each specified by separate structural genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.700
sicP	sptP	CY43_15035	CY43_15030	<i>Chaperone protein SicP; Type III secretion system chaperone; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.998
sicP	spaQ	CY43_15035	CY43_15085	<i>Chaperone protein SicP; Type III secretion system chaperone; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system export apparatus protein SpaQ; Involved in the surface presentation of antigens needed for the invasion of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.499
sicP	spaO	CY43_15035	CY43_15095	<i>Chaperone protein SicP; Type III secretion system chaperone; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Involved in a secretory pathway responsible for the surface presentation of determinants needed for the entry of Salmonella species into mammalian cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.752
sicP	sipD	CY43_15035	CY43_15055	<i>Chaperone protein SicP; Type III secretion system chaperone; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Involved in the transport of effector protein by the type III secretion system of Salmonella pathogenicity island 1; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.888
sicP	sipC	CY43_15035	CY43_15060	<i>Chaperone protein SicP; Type III secretion system chaperone; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system needle tip complex protein SipC; Cell invasion protein C; required for entry of the bacteria into the host cell; binds to actin; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.823
sicP	sipB	CY43_15035	CY43_15065	<i>Chaperone protein SicP; Type III secretion system chaperone; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated</i>	0.828

					<i>computational analysis using gene prediction method: Protein Homology</i>	
sicP	sipA	CY43_15035	CY43_15050	<i>Chaperone protein SicP; Type III secretion system chaperone; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system effector SipA; Cell invasion protein A; actin-binding; required for entry of the Salmonella into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.812
sicP	prgJ	CY43_15035	CY43_15000	<i>Chaperone protein SicP; Type III secretion system chaperone; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system needle complex protein PrgJ; May be involved in capping the needle substructure; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.682
sicP	prgI	CY43_15035	CY43_15005	<i>Chaperone protein SicP; Type III secretion system chaperone; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.521
sicP	prgH	CY43_15035	CY43_15010	<i>Chaperone protein SicP; Type III secretion system chaperone; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.739
sicP	iagB	CY43_15035	CY43_15025	<i>Chaperone protein SicP; Type III secretion system chaperone; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system invasion protein IagB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.607
prgK	sptP	CY43_14995	CY43_15030	<i>Lipoprotein; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.750
prgK	sprB	CY43_14995	CY43_14970	<i>Lipoprotein; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Transcriptional regulator SprB; Activates Salmonella pathogenicity island 4 genes and weakly represses Salmonella pathogenicity island 1 genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.434

prgK	spaQ	CY43_14995	CY43_15085	<i>Lipoprotein; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system export apparatus protein SpaQ; Involved in the surface presentation of antigens needed for the invasion of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.957
prgK	spaO	CY43_14995	CY43_15095	<i>Lipoprotein; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Involved in a secretory pathway responsible for the surface presentation of determinants needed for the entry of Salmonella species into mammalian cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.960
prgK	sipD	CY43_14995	CY43_15055	<i>Lipoprotein; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Involved in the transport of effector protein by the type III secretion system of Salmonella pathogenicity island 1; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.758
prgK	sipC	CY43_14995	CY43_15060	<i>Lipoprotein; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system needle tip complex protein SipC; Cell invasion protein C; required for entry of the bacteria into the host cell; binds to actin; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.728
prgK	sipB	CY43_14995	CY43_15065	<i>Lipoprotein; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.951
prgK	sipA	CY43_14995	CY43_15050	<i>Lipoprotein; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system effector SipA; Cell invasion protein A; actin-binding; required for entry of the Salmonella into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.716
prgK	prgJ	CY43_14995	CY43_15000	<i>Lipoprotein; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system needle complex protein PrgJ; May be involved in capping the needle substructure; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.990

prgK	prgI	CY43_14995	CY43_15005	<i>Lipoprotein; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.991
prgK	prgH	CY43_14995	CY43_15010	<i>Lipoprotein; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.999
prgK	invG	CY43_14995	CY43_15130	<i>Lipoprotein; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system outer membrane ring protein InvG; May be involved in the export or assembly of proteins involved in the entry of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.998
prgK	iagB	CY43_14995	CY43_15025	<i>Lipoprotein; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system invasion protein IagB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.858
prgK	hilA	CY43_14995	CY43_15020	<i>Lipoprotein; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Invasion protein regulator; IagA; HilA; activates the expression of invasion genes and activates the expression of prgHIJK which is part of the pathogenicity island 1 type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.680
prgJ	sptP	CY43_15000	CY43_15030	<i>Type III secretion system needle complex protein PrgJ; May be involved in capping the needle substructure; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.460
prgJ	spaQ	CY43_15000	CY43_15085	<i>Type III secretion system needle complex protein PrgJ; May be involved in capping the needle substructure; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system export apparatus protein SpaQ; Involved in the surface presentation of antigens needed for the invasion of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.775

prgJ	spaO	CY43_15000	CY43_15095	Type III secretion system needle complex protein PrgJ; May be involved in capping the needle substructure; Derived by automated computational analysis using gene prediction method: Protein Homology	Involved in a secretory pathway responsible for the surface presentation of determinants needed for the entry of Salmonella species into mammalian cells; Derived by automated computational analysis using gene prediction method: Protein Homology	0.668
prgJ	sipD	CY43_15000	CY43_15055	Type III secretion system needle complex protein PrgJ; May be involved in capping the needle substructure; Derived by automated computational analysis using gene prediction method: Protein Homology	Involved in the transport of effector protein by the type III secretion system of Salmonella pathogenicity island 1; Derived by automated computational analysis using gene prediction method: Protein Homology	0.586
prgJ	sipC	CY43_15000	CY43_15060	Type III secretion system needle complex protein PrgJ; May be involved in capping the needle substructure; Derived by automated computational analysis using gene prediction method: Protein Homology	SPI-1 type III secretion system needle tip complex protein SipC; Cell invasion protein C; required for entry of the bacteria into the host cell; binds to actin; Derived by automated computational analysis using gene prediction method: Protein Homology	0.576
prgJ	sipB	CY43_15000	CY43_15065	Type III secretion system needle complex protein PrgJ; May be involved in capping the needle substructure; Derived by automated computational analysis using gene prediction method: Protein Homology	SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology	0.847
prgJ	sipA	CY43_15000	CY43_15050	Type III secretion system needle complex protein PrgJ; May be involved in capping the needle substructure; Derived by automated computational analysis using gene prediction method: Protein Homology	SPI-1 type III secretion system effector SipA; Cell invasion protein A; actin-binding; required for entry of the Salmonella into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	0.717
prgJ	sicP	CY43_15000	CY43_15035	Type III secretion system needle complex protein PrgJ; May be involved in capping the needle substructure; Derived by automated computational analysis using gene prediction method: Protein Homology	Chaperone protein SicP; Type III secretion system chaperone; Derived by automated computational analysis using gene prediction method: Protein Homology	0.682
prgJ	prgK	CY43_15000	CY43_14995	Type III secretion system needle complex protein PrgJ; May be involved in capping the needle substructure; Derived by automated computational analysis using gene prediction method: Protein Homology	Lipoprotein; Derived by automated computational analysis using gene prediction method: Protein Homology	0.990
prgJ	prgI	CY43_15000	CY43_15005	Type III secretion system needle complex protein PrgJ; May be involved in capping the needle	Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the	0.996

				substructure; Derived by automated computational analysis using gene prediction method: Protein Homology	membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology	
prgJ	prgH	CY43_15000	CY43_15010	Type III secretion system needle complex protein PrgJ; May be involved in capping the needle substructure; Derived by automated computational analysis using gene prediction method: Protein Homology	Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology	0.977
prgJ	invG	CY43_15000	CY43_15130	Type III secretion system needle complex protein PrgJ; May be involved in capping the needle substructure; Derived by automated computational analysis using gene prediction method: Protein Homology	Type III secretion system outer membrane ring protein InvG; May be involved in the export or assembly of proteins involved in the entry of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology	0.858
prgJ	DD95_24045	CY43_15000	CY43_14490	Type III secretion system needle complex protein PrgJ; May be involved in capping the needle substructure; Derived by automated computational analysis using gene prediction method: Protein Homology	Flagellin FliC; Structural flagella protein; individual Salmonella serotypes usually alternate between the production of 2 antigenic forms of flagella, termed phase 1 and phase 2, each specified by separate structural genes; Derived by automated computational analysis using gene prediction method: Protein Homology	0.963
prgJ	DD95_19955	CY43_15000	CY43_10320	Type III secretion system needle complex protein PrgJ; May be involved in capping the needle substructure; Derived by automated computational analysis using gene prediction method: Protein Homology	Flagellin; Structural flagella protein; individual Salmonella serotypes usually alternate between the production of 2 antigenic forms of flagella, termed phase 1 and phase 2, each specified by separate structural genes; Derived by automated computational analysis using gene prediction method: Protein Homology	0.963
prgI	sptP	CY43_15005	CY43_15030	Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology	SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by automated computational analysis using gene prediction method: Protein Homology	0.757
prgI	sprB	CY43_15005	CY43_14970	Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the membrane spanning needle complex; Derived by	Transcriptional regulator SprB; Activates Salmonella pathogenicity island 4 genes and weakly represses Salmonella pathogenicity island 1 genes;	0.494

				<i>automated computational analysis using gene prediction method: Protein Homology</i>	<i>Derived by automated computational analysis using gene prediction method: Protein Homology</i>	
prgI	spaQ	CY43_15005	CY43_15085	<i>Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system export apparatus protein SpaQ; Involved in the surface presentation of antigens needed for the invasion of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.556
prgI	spaO	CY43_15005	CY43_15095	<i>Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Involved in a secretory pathway responsible for the surface presentation of determinants needed for the entry of Salmonella species into mammalian cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.810
prgI	sipD	CY43_15005	CY43_15055	<i>Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Involved in the transport of effector protein by the type III secretion system of Salmonella pathogenicity island 1; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.953
prgI	sipC	CY43_15005	CY43_15060	<i>Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system needle tip complex protein SipC; Cell invasion protein C; required for entry of the bacteria into the host cell; binds to actin; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.849
prgI	sipB	CY43_15005	CY43_15065	<i>Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.852
prgI	sipA	CY43_15005	CY43_15050	<i>Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system effector SipA; Cell invasion protein A; actin-binding; required for entry of the Salmonella into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.755
prgI	sicP	CY43_15005	CY43_15035	<i>Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the membrane spanning needle complex; Derived by</i>	<i>Chaperone protein SicP; Type III secretion system chaperone; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.521

				<i>automated computational analysis using gene prediction method: Protein Homology</i>		
prgI	prgK	CY43_15005	CY43_14995	<i>Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Lipoprotein; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.991
prgI	prgJ	CY43_15005	CY43_15000	<i>Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system needle complex protein PrgJ; May be involved in capping the needle substructure; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.996
prgI	prgH	CY43_15005	CY43_15010	<i>Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.984
prgI	invG	CY43_15005	CY43_15130	<i>Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system outer membrane ring protein InvG; May be involved in the export or assembly of proteins involved in the entry of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.919
prgI	iagB	CY43_15005	CY43_15025	<i>Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system invasion protein IagB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.662
prgI	DD95_24045	CY43_15005	CY43_14490	<i>Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Flagellin FliC; Structural flagella protein; individual Salmonella serotypes usually alternate between the production of 2 antigenic forms of flagella, termed phase 1 and phase 2, each specified by separate structural genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.656
gI	DD95_19955	CY43_15005	CY43_10320	<i>Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the membrane spanning needle complex; Derived by</i>	<i>Flagellin; Structural flagella protein; individual Salmonella serotypes usually alternate between the production of 2 antigenic forms of flagella, termed</i>	0.596

				<i>automated computational analysis using gene prediction method: Protein Homology</i>	<i>phase 1 and phase 2, each specified by separate structural genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	
prgH	sptP	CY43_15010	CY43_15030	<i>Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.938
prgH	sprB	CY43_15010	CY43_14970	<i>Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Transcriptional regulator SprB; Activates Salmonella pathogenicity island 4 genes and weakly represses Salmonella pathogenicity island 1 genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.483
prgH	spaQ	CY43_15010	CY43_15085	<i>Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system export apparatus protein SpaQ; Involved in the surface presentation of antigens needed for the invasion of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.863
prgH	spaO	CY43_15010	CY43_15095	<i>Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Involved in a secretory pathway responsible for the surface presentation of determinants needed for the entry of Salmonella species into mammalian cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.938
prgH	sitC	CY43_15010	CY43_14955	<i>Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Metal ABC transporter permease; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.658
prgH	sipD	CY43_15010	CY43_15055	<i>Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Involved in the transport of effector protein by the type III secretion system of Salmonella pathogenicity island 1; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.780
prgH	sipC	CY43_15010	CY43_15060	<i>Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes</i>	<i>SPI-1 type III secretion system needle tip complex protein SipC; Cell invasion protein C; required for</i>	0.860

				<i>up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>entry of the bacteria into the host cell; binds to actin; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	
prgH	sipB	CY43_15010	CY43_15065	<i>Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.969
prgH	sipA	CY43_15010	CY43_15050	<i>Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system effector SipA; Cell invasion protein A; actin-binding; required for entry of the Salmonella into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.811
prgH	sicP	CY43_15010	CY43_15035	<i>Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Chaperone protein SicP; Type III secretion system chaperone; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.739
prgH	prgK	CY43_15010	CY43_14995	<i>Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Lipoprotein; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<u>0.999</u>
prgH	prgJ	CY43_15010	CY43_15000	<i>Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system needle complex protein PrgJ; May be involved in capping the needle substructure; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.977
prgH	prgI	CY43_15010	CY43_15005	<i>Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.984
prgH	invG	CY43_15010	CY43_15130	<i>Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes up the membrane spanning needle complex;</i>	<i>Type III secretion system outer membrane ring protein InvG; May be involved in the export or assembly of proteins involved in the entry of Salmonella into host cells; Derived by automated</i>	0.998

				<i>Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>computational analysis using gene prediction method: Protein Homology</i>	
prgH	iagB	CY43_15010	CY43_15025	<i>Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system invasion protein IagB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.858
prgH	hilA	CY43_15010	CY43_15020	<i>Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Invasion protein regulator; IagA; HilA; activates the expression of invasion genes and activates the expression of prgHIJK which is part of the pathogenicity island 1 type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.816
invG	sptP	CY43_15130	CY43_15030	<i>Type III secretion system outer membrane ring protein InvG; May be involved in the export or assembly of proteins involved in the entry of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.840
invG	spaQ	CY43_15130	CY43_15085	<i>Type III secretion system outer membrane ring protein InvG; May be involved in the export or assembly of proteins involved in the entry of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system export apparatus protein SpaQ; Involved in the surface presentation of antigens needed for the invasion of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.985
invG	spaO	CY43_15130	CY43_15095	<i>Type III secretion system outer membrane ring protein InvG; May be involved in the export or assembly of proteins involved in the entry of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Involved in a secretory pathway responsible for the surface presentation of determinants needed for the entry of Salmonella species into mammalian cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.974
invG	sipD	CY43_15130	CY43_15055	<i>Type III secretion system outer membrane ring protein InvG; May be involved in the export or assembly of proteins involved in the entry of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Involved in the transport of effector protein by the type III secretion system of Salmonella pathogenicity island 1; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.823

invG	sipC	CY43_15130	CY43_15060	Type III secretion system outer membrane ring protein InvG; May be involved in the export or assembly of proteins involved in the entry of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology	SPI-1 type III secretion system needle tip complex protein SipC; Cell invasion protein C; required for entry of the bacteria into the host cell; binds to actin; Derived by automated computational analysis using gene prediction method: Protein Homology	0.842
invG	sipB	CY43_15130	CY43_15065	Type III secretion system outer membrane ring protein InvG; May be involved in the export or assembly of proteins involved in the entry of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology	SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology	0.971
invG	sipA	CY43_15130	CY43_15050	Type III secretion system outer membrane ring protein InvG; May be involved in the export or assembly of proteins involved in the entry of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology	SPI-1 type III secretion system effector SipA; Cell invasion protein A; actin-binding; required for entry of the Salmonella into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology	0.850
invG	prgK	CY43_15130	CY43_14995	Type III secretion system outer membrane ring protein InvG; May be involved in the export or assembly of proteins involved in the entry of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology	Lipoprotein; Derived by automated computational analysis using gene prediction method: Protein Homology	0.998
invG	prgJ	CY43_15130	CY43_15000	Type III secretion system outer membrane ring protein InvG; May be involved in the export or assembly of proteins involved in the entry of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology	Type III secretion system needle complex protein PrgJ; May be involved in capping the needle substructure; Derived by automated computational analysis using gene prediction method: Protein Homology	0.858
invG	prgI	CY43_15130	CY43_15005	Type III secretion system outer membrane ring protein InvG; May be involved in the export or assembly of proteins involved in the entry of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology	Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology	0.919
invG	prgH	CY43_15130	CY43_15010	Type III secretion system outer membrane ring protein InvG; May be involved in the export or	Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes up	0.998

				<i>assembly of proteins involved in the entry of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	
invG	iagB	CY43_15130	CY43_15025	<i>Type III secretion system outer membrane ring protein InvG; May be involved in the export or assembly of proteins involved in the entry of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system invasion protein IagB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.882
invG	hilA	CY43_15130	CY43_15020	<i>Type III secretion system outer membrane ring protein InvG; May be involved in the export or assembly of proteins involved in the entry of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Invasion protein regulator; IagA; HilA; activates the expression of invasion genes and activates the expression of prgHIJK which is part of the pathogenicity island 1 type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.701
iagB	sptP	CY43_15025	CY43_15030	<i>SPI-1 type III secretion system invasion protein IagB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.495
iagB	sprB	CY43_15025	CY43_14970	<i>SPI-1 type III secretion system invasion protein IagB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Transcriptional regulator SprB; Activates Salmonella pathogenicity island 4 genes and weakly represses Salmonella pathogenicity island 1 genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.639
iagB	spaQ	CY43_15025	CY43_15085	<i>SPI-1 type III secretion system invasion protein IagB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system export apparatus protein SpaQ; Involved in the surface presentation of antigens needed for the invasion of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.650
iagB	spaO	CY43_15025	CY43_15095	<i>SPI-1 type III secretion system invasion protein IagB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Involved in a secretory pathway responsible for the surface presentation of determinants needed for the entry of Salmonella species into mammalian cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.747

iagB	sipD	CY43_15025	CY43_15055	<i>SPI-1 type III secretion system invasion protein IagB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Involved in the transport of effector protein by the type III secretion system of Salmonella pathogenicity island 1; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.587
iagB	sipB	CY43_15025	CY43_15065	<i>SPI-1 type III secretion system invasion protein IagB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.718
iagB	sipA	CY43_15025	CY43_15050	<i>SPI-1 type III secretion system invasion protein IagB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system effector SipA; Cell invasion protein A; actin-binding; required for entry of the Salmonella into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.407
iagB	sicP	CY43_15025	CY43_15035	<i>SPI-1 type III secretion system invasion protein IagB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Chaperone protein SicP; Type III secretion system chaperone; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.607
iagB	prgK	CY43_15025	CY43_14995	<i>SPI-1 type III secretion system invasion protein IagB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Lipoprotein; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.858
iagB	prgI	CY43_15025	CY43_15005	<i>SPI-1 type III secretion system invasion protein IagB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.662
iagB	prgH	CY43_15025	CY43_15010	<i>SPI-1 type III secretion system invasion protein IagB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.858
iagB	invG	CY43_15025	CY43_15130	<i>SPI-1 type III secretion system invasion protein IagB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system outer membrane ring protein InvG; May be involved in the export or assembly of proteins involved in the entry of Salmonella into host cells; Derived by automated</i>	0.882

					<i>computational analysis using gene prediction method: Protein Homology</i>	
iagB	hilA	CY43_15025	CY43_15020	<i>SPI-1 type III secretion system invasion protein IagB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Invasion protein regulator; IagA; HilA; activates the expression of invasion genes and activates the expression of prgHIJK which is part of the pathogenicity island 1 type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.915
hilA	sptP	CY43_15020	CY43_15030	<i>Invasion protein regulator; IagA; HilA; activates the expression of invasion genes and activates the expression of prgHIJK which is part of the pathogenicity island 1 type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.556
hilA	spaO	CY43_15020	CY43_15095	<i>Invasion protein regulator; IagA; HilA; activates the expression of invasion genes and activates the expression of prgHIJK which is part of the pathogenicity island 1 type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Involved in a secretory pathway responsible for the surface presentation of determinants needed for the entry of Salmonella species into mammalian cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.790
hilA	sipB	CY43_15020	CY43_15065	<i>Invasion protein regulator; IagA; HilA; activates the expression of invasion genes and activates the expression of prgHIJK which is part of the pathogenicity island 1 type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.876
hilA	prgK	CY43_15020	CY43_14995	<i>Invasion protein regulator; IagA; HilA; activates the expression of invasion genes and activates the expression of prgHIJK which is part of the pathogenicity island 1 type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Lipoprotein; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.680
hilA	prgH	CY43_15020	CY43_15010	<i>Invasion protein regulator; IagA; HilA; activates the expression of invasion genes and activates the expression of prgHIJK which is part of the pathogenicity island 1 type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system inner membrane ring protein PrgH; With InvG, PrgI, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.816

hilA	invG	CY43_15020	CY43_15130	<i>Invasion protein regulator; IagA; HilA; activates the expression of invasion genes and activates the expression of prgHIJK which is part of the pathogenicity island 1 type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system outer membrane ring protein InvG; May be involved in the export or assembly of proteins involved in the entry of Salmonella into host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.701
hilA	iagB	CY43_15020	CY43_15025	<i>Invasion protein regulator; IagA; HilA; activates the expression of invasion genes and activates the expression of prgHIJK which is part of the pathogenicity island 1 type III secretion system; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system invasion protein IagB; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.915
DD95_24045	sptP	CY43_14490	CY43_15030	<i>Flagellin FliC; Structural flagella protein; individual Salmonella serotypes usually alternate between the production of 2 antigenic forms of flagella, termed phase 1 and phase 2, each specified by separate structural genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.557
DD95_24045	sipC	CY43_14490	CY43_15060	<i>Flagellin FliC; Structural flagella protein; individual Salmonella serotypes usually alternate between the production of 2 antigenic forms of flagella, termed phase 1 and phase 2, each specified by separate structural genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system needle tip complex protein SipC; Cell invasion protein C; required for entry of the bacteria into the host cell; binds to actin; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.559
DD95_24045	sipB	CY43_14490	CY43_15065	<i>Flagellin FliC; Structural flagella protein; individual Salmonella serotypes usually alternate between the production of 2 antigenic forms of flagella, termed phase 1 and phase 2, each specified by separate structural genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.663
DD95_24045	sipA	CY43_14490	CY43_15050	<i>Flagellin FliC; Structural flagella protein; individual Salmonella serotypes usually alternate between the production of 2 antigenic forms of flagella, termed phase 1 and phase 2, each specified by separate structural genes; Derived by</i>	<i>SPI-1 type III secretion system effector SipA; Cell invasion protein A; actin-binding; required for entry of the Salmonella into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.705

				<i>automated computational analysis using gene prediction method: Protein Homology</i>		
DD95_24045	prgJ	CY43_14490	CY43_15000	<i>Flagellin FliC; Structural flagella protein; individual Salmonella serotypes usually alternate between the production of 2 antigenic forms of flagella, termed phase 1 and phase 2, each specified by separate structural genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system needle complex protein PrgJ; May be involved in capping the needle substructure; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.963
DD95_24045	prgI	CY43_14490	CY43_15005	<i>Flagellin FliC; Structural flagella protein; individual Salmonella serotypes usually alternate between the production of 2 antigenic forms of flagella, termed phase 1 and phase 2, each specified by separate structural genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.656
DD95_24045	DD95_19955	CY43_14490	CY43_10320	<i>Flagellin FliC; Structural flagella protein; individual Salmonella serotypes usually alternate between the production of 2 antigenic forms of flagella, termed phase 1 and phase 2, each specified by separate structural genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Flagellin; Structural flagella protein; individual Salmonella serotypes usually alternate between the production of 2 antigenic forms of flagella, termed phase 1 and phase 2, each specified by separate structural genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.803
DD95_19955	sptP	CY43_10320	CY43_15030	<i>Flagellin; Structural flagella protein; individual Salmonella serotypes usually alternate between the production of 2 antigenic forms of flagella, termed phase 1 and phase 2, each specified by separate structural genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system effector GTPase-activating protein SptP; GTP-activating protein/tyrosine phosphatase; facilitates bacterial survival in host cells; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.558
DD95_19955	sipC	CY43_10320	CY43_15060	<i>Flagellin; Structural flagella protein; individual Salmonella serotypes usually alternate between the production of 2 antigenic forms of flagella, termed phase 1 and phase 2, each specified by separate structural genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system needle tip complex protein SipC; Cell invasion protein C; required for entry of the bacteria into the host cell; binds to actin; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.558

DD95_19955	sipB	CY43_10320	CY43_15065	<i>Flagellin; Structural flagella protein; individual Salmonella serotypes usually alternate between the production of 2 antigenic forms of flagella, termed phase 1 and phase 2, each specified by separate structural genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system needle tip complex protein SipB; Cell invasion protein B; required for entry of the bacteria into the host cell; induces apoptosis in macrophages; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.658
DD95_19955	sipA	CY43_10320	CY43_15050	<i>Flagellin; Structural flagella protein; individual Salmonella serotypes usually alternate between the production of 2 antigenic forms of flagella, termed phase 1 and phase 2, each specified by separate structural genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>SPI-1 type III secretion system effector SipA; Cell invasion protein A; actin-binding; required for entry of the Salmonella into the host cell; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.700
DD95_19955	prgJ	CY43_10320	CY43_15000	<i>Flagellin; Structural flagella protein; individual Salmonella serotypes usually alternate between the production of 2 antigenic forms of flagella, termed phase 1 and phase 2, each specified by separate structural genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system needle complex protein PrgJ; May be involved in capping the needle substructure; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.963
DD95_19955	prgI	CY43_10320	CY43_15005	<i>Flagellin; Structural flagella protein; individual Salmonella serotypes usually alternate between the production of 2 antigenic forms of flagella, termed phase 1 and phase 2, each specified by separate structural genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Type III secretion system needle complex protein PrgI; With InvG, PrgH, and Prg K makes up the membrane spanning needle complex; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.596
DD95_19955	DD95_24045	CY43_10320	CY43_14490	<i>Flagellin; Structural flagella protein; individual Salmonella serotypes usually alternate between the production of 2 antigenic forms of flagella, termed phase 1 and phase 2, each specified by separate structural genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	<i>Flagellin FliC; Structural flagella protein; individual Salmonella serotypes usually alternate between the production of 2 antigenic forms of flagella, termed phase 1 and phase 2, each specified by separate structural genes; Derived by automated computational analysis using gene prediction method: Protein Homology</i>	0.803

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