ANEXOS/MATERIAL SUPLEMENTARIO

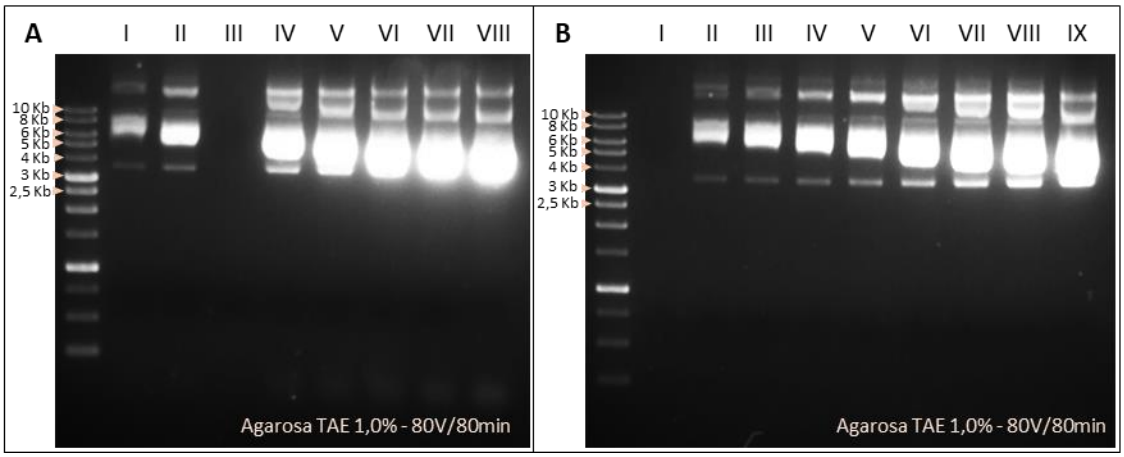

Figura S1. Ensayo diluciones de pDNA para su visualización mediante electroforesis en gel de agarosa TAE.
A) Visualización con luz UV de electroforesis en gel de agarosa TAE 1,0%, utilizando el marcador de peso molecular Ladder AccuRuler 1Kb DNA RTU de MAESTROGEN en el primer pocillo del gel (de izquierda a derecha). Se corrieron 157 ng, 314 ng, 0 ng, 628 ng, 942 ng, 1.256 ng, 1.570 ng y 2.198 ng de pFN18A $(L)_8$ en los pocillos A-I, A-II, A-III, A-IV, A-V, A-VI, A-VII y A-VIII, respectivamente.
B) Visualización con luz UV de electroforesis en gel de agarosa TAE 1,0%, utilizando el marcador de peso molecular Ladder AccuRuler 1Kb DNA RTU de MAESTROGEN en el primer pocillo del gel (de izquierda a derecha). Se corrieron 0 ng, 79 ng, 157 ng, 235 ng, 314 ng, 471 ng, 628 ng, 785 ng y 942 ng de pFN18A $(L)_8$ en los pocillos B-I, B-II, B-III, B-IV, B-V, B-VI, B-VII, B-VIII y B-IX, respectivamente.

Tabla S1. Resultados Blastp de WP_016210369.1 de *P. salmonis* contra toda la base de datos excluyendo *Proteobacteria*.

Blastp de WP_016210369.1 de *P. salmonis* contra toda la base de datos excluyendo *Proteobacteria*

Accesión	Nombre descriptivo (NCBI)	Especie	Puntaje máximo	Puntaje total	Cobertura	E-value	Porcentaje identidad	Longitud de accesión
MCF6354900.1	Molecular chaperone DnaK	*Candidatus Polarisedimenticolaceae Bacterium*	1000	1000	100%	0	77,09%	649
WP_198265375.1	Molecular chaperone DnaK	*Sulfur-oxidizing endosymbiont of Gigantopelta aegis*	997	997	100%	0	75,93%	639
EKD55342.1	Hypothetical protein ACD_60C00014G0016	*Uncultured bacterium*	995	995	99%	0	75,89%	652
VTS66348.1	Molecular chaperone DnaK	*Streptococcus dysgalactiae subsp. equisimilis*	986	986	100%	0	75,04%	637
EKD46075.1	Hypothetical protein ACD_69C00029G0008	*Uncultured bacterium*	983	983	100%	0	75,00%	648
MBE01732.1	Molecular chaperone DnaK	*Euryarchaeota archaeon*	978	978	99%	0	73,41%	641
NNJ93125.1	Molecular chaperone DnaK	*Halobacteria archaeon*	978	978	99%	0	74,18%	647
RLJ20055.1	Molecular chaperone DnaK	*Bacterium endosymbiont of Escarpia laminata*	976	976	100%	0	75,08%	647
RLJ22305.1	Molecular chaperone DnaK	*Bacterium endosymbiont of Escarpia laminata*	976	976	100%	0	74,92%	647
GBF29124.1	Chaperone protein DnaK	*Bacterium MnTg03*	973	973	100%	0	74,73%	642
NVN54353.1	Molecular chaperone DnaK	*Bacterium Scap17*	971	971	100%	0	74,26%	640
GGE53625.1	Chaperone protein DnaK	*Streptosporangium jomthongense*	970	970	99%	0	72,78%	639
MBD1589164.1	Molecular chaperone DnaK	*Pseudomonas typographi*	968	968	100%	0	72,40%	640
MBY6093926.1	Molecular chaperone DnaK	*Priestia flexa*	967	967	100%	0	73,76%	637
CDQ34587.1	Heat shock protein 70	*Virgibacillus halodenitrificans*	966	966	99%	0	73,72%	644
MBD1553775.1	Molecular chaperone DnaK	*Pseudomonas typographi*	966	966	100%	0	72,25%	640
EKE01821.1	Hypothetical protein ACD_21C00045G0001	*Uncultured bacterium*	965	965	99%	0	75,00%	651
VTQ30412.1	Molecular chaperone DnaK	*Streptococcus pneumoniae*	964	964	100%	0	74,26%	638
QEA06117.1	Chaperone protein DnaK	*uncultured organism*	964	964	99%	0	73,33%	647
MBR9812949.1	Molecular chaperone DnaK	*Bacterium*	963	963	100%	0	73,18%	641
UTW43316.1	Molecular chaperone DnaK	*Bacterium SCSIO 12844*	963	963	100%	0	73,35%	652
MCF6280601.1	Molecular chaperone DnaK	*Candidatus Polarisedimenticolaceae bacterium*	962	962	100%	0	75,70%	646
MPQ51091.1	Molecular chaperone DnaK	*Citrobacter telavivensis*	961	961	100%	0	73,33%	638
GFD71266.1	Chaperone protein DnaK	*Tenacibaculum sp. KUL113*	961	961	99%	0	74,49%	641
CJL34017.1	Molecular chaperone DnaK	*Streptococcus pneumoniae*	961	961	100%	0	73,80%	637
MBK5303641.1	Molecular chaperone DnaK	*Bacillus sp. TH86*	959	959	100%	0	72,09%	638
SCN47424.1	Chaperone protein DnaK	*Methanotrophic endosymbiont of Bathymodiolus azoricus (Menez Gwen)*	959	959	99%	0	73,09%	645
MZG79225.1	Molecular chaperone DnaK	*PhotoBacterium lucens*	956	956	100%	0	74,88%	637
QPN46160.1	Molecular chaperone DnaK	*Priestia aryabhattai*	956	956	100%	0	73,72%	641
MBW8054076.1	Molecular chaperone DnaK	*Nitrospira sp.*	956	956	100%	0	73,73%	647
CAG1022238.1	Heat shock 70kDa protein 1/2/6/8	*Patescibacteria group Bacterium*	956	956	99%	0	73,87%	639
GBF30606.1	Chaperone protein DnaK	*Bacterium MnTg04*	955	955	100%	0	72,25%	646
MPQ83844.1	Molecular chaperone DnaK	*Pseudomonas kitaguniensis*	955	955	100%	0	72,71%	638
XP_040091687.1	Chaperone protein DnaK	*Oryx dammah*	953	953	100%	0	72,40%	638
KJR43016.1	Molecular chaperone DnaK	*Candidatus Magnetoovum chiemensis*	952	952	100%	0	73,02%	638
MCG1033418.1	Molecular chaperone DnaK	*Bacillus amyloliquefaciens*	952	952	100%	0	73,64%	639
MBC7984233.1	Molecular chaperone DnaK	*Candidatus Obscuribacterales Bacterium*	952	952	100%	0	71,52%	643
KAH8298918.1	Hypothetical protein KR044_005073	*Drosophila immigrans*	952	952	100%	0	74,73%	637
RTZ64876.1	Molecular chaperone DnaK	*Aquificaceae Bacterium*	951	951	100%	0	74,07%	637
MBH30344.1	Molecular chaperone DnaK	*Actinomycetia Bacterium*	949	949	99%	0	72,54%	641
MBE2897558.1	Molecular chaperone DnaK	*SpirabilliBacterium mucosae*	949	949	99%	0	74,26%	639
EKD77462.1	Hypothetical protein ACD_42C00325G0003	*Uncultured bacterium*	949	949	93%	0	75,29%	607
ERL83342.1	Hypothetical protein D910_00242	*Dendroctonus ponderosae*	949	949	100%	0	73,18%	633
HAW93975.1	TPA: Molecular chaperone DnaK	*Candidatus Azambacteria Bacterium*	948	948	99%	0	73,87%	637
VTQ53453.1	Molecular chaperone DnaK	*Campylobacter jejuni*	948	948	100%	0	73,49%	633
UTW46531.1	Molecular chaperone DnaK	*Bacterium SCSIO 12696*	948	948	100%	0	74,81%	645
GBE07263.1	Chaperone protein DnaK	*Bacterium BMS3Abin11*	948	948	100%	0	71,89%	641
OOK70956.1	Molecular chaperone DnaK	*Pedobacter himalayensis*	947	947	100%	0	73,49%	637
MBF5055848.1	Molecular chaperone DnaK	*Alloalcanivorax profundimaris*	947	947	100%	0	73,80%	642
GFD91142.1	Chaperone protein DnaK	*Tenacibaculum sp. KUL152*	947	947	99%	0	74,03%	641
MBE2896389.1	Molecular chaperone DnaK	*SpirabilliBacterium pneumoniae*	947	947	99%	0	74,26%	639
WP_253379538.1	Molecular chaperone DnaK	*unidentified bacterial endosymbiont*	946	946	100%	0	73,02%	637
MBC2382586.1	Molecular chaperone DnaK	*Pseudomonas cremoris*	944	944	100%	0	73,18%	638
GEW75136.1	heat shock 70 kDa protein, mitochondrial	*Tanacetum cinerariifolium*	944	944	99%	0	72,52%	5141
SGD20470.1	Chaperone protein DnaK	*MycoBacterium tuberculosis*	942	942	100%	0	72,71%	640
NCA69965.1	Molecular chaperone DnaK	*Sphingobacteriia Bacterium*	941	941	100%	0	73,11%	648
MBE8602806.1	Molecular chaperone DnaK	*Pseudomonas cyclaminis*	940	940	100%	0	72,87%	638
MBE2293929.1	Molecular chaperone DnaK	*Phycisphaerales Bacterium*	939	939	99%	0	72,32%	643
CAE7822159.1	DnaK	*Symbiodinium microadriaticum*	937	937	99%	0	72,74%	1212
WP_008300614.1	Molecular chaperone DnaK	*Candidatus Nitrosopumilus salaria*	936	936	99%	0	71,43%	642
KAF5283794.1	Hypothetical protein FQR65_LT13710	*Abscondita terminalis*	936	936	98%	0	69,95%	1410
MBP77954.1	Molecular chaperone DnaK	*Deltaproteobacteria Bacterium*	934	934	99%	0	71,89%	644
HES76298.1	TPA: Molecular chaperone DnaK	*Bacterium*	934	934	99%	0	72,09%	638
NWH34401.1	HSP7J protein	*Chloropsis hardwickii*	934	934	95%	0	73,94%	624
MBM3203083.1	Molecular chaperone DnaK	*Candidatus Woesearchaeota archaeon*	934	934	100%	0	70,52%	649
MBP9899184.1	Molecular chaperone DnaK	*Gemmatimonadales Bacterium*	933	933	100%	0	71,91%	647
MBC7698767.1	Molecular chaperone DnaK	*Bacteroidia Bacterium*	932	932	99%	0	71,23%	641
KAG7531907.1	Heat shock protein 70kD peptide-binding domain superfamily	*Arabidopsis suecica*	931	931	100%	0	70,39%	637
MBC7755950.1	Molecular chaperone DnaK	*Bdellovibrio sp.*	931	931	99%	0	71,23%	641
CAE7932356.1	CarB	*Symbiodinium necroappetens*	930	930	99%	0	71,70%	3156
AAW50075.1	Hypothetical protein FTT1269	*synthetic construct*	928	928	100%	0	71,87%	677
GBE48965.1	Chaperone protein DnaK	*Bacterium BMS3Bbin12*	927	927	99%	0	72,24%	654
WP_139659733.1	Molecular chaperone DnaK	*Bacterium endosymbiont of Bathymodiolus sp. 5 South*	927	927	99%	0	69,57%	643
GBE10087.1	Chaperone protein DnaK	*Bacterium BMS3Abin12*	927	927	99%	0	72,02%	656
MZG81889.1	Molecular chaperone DnaK	*PhotoBacterium lucens*	926	926	99%	0	71,29%	631
SHR90360.1	Chaperone protein DnaK (Hsp 70)	*Mycobacteroides abscessus subsp. abscessus*	924	924	99%	0	70,92%	641
CAB3504733.1	Unnamed protein product	*Digitaria exilis*	923	923	97%	0	73,68%	619
RPG68515.1	Molecular chaperone DnaK	*Flavobacteriaceae Bacterium TMED42*	923	923	99%	0	71,88%	631
OUS29746.1	Molecular chaperone DnaK	*Osedax' symbiont Bacterium Rs2_46_30_T18*	922	922	93%	0	75,00%	645
URW69966.1	Heat shock protein	*Bemisia tabaci*	922	922	100%	0	70,46%	635
KAF0102539.1	Molecular chaperone DnaK	*Bacterium*	922	922	99%	0	71,89%	640
WP_138146938.1	Molecular chaperone DnaK	*Bathymodiolus heckerae thiotrophic gill symbiont*	922	922	100%	0	69,28%	645
KAG1716289.1	Hypothetical protein ID866_851	*Astraeus odoratus*	922	922	97%	0	73,52%	619
MBC7752269.1	Molecular chaperone DnaK	*Candidatus Saccharibacteria Bacterium*	917	917	100%	0	70,34%	639
KZV14856.1	Molecular chaperone DnaK	*Dorcoceras hygrometricum*	917	917	100%	0	72,14%	639
MCL2344275.1	Molecular chaperone DnaK	*Desulfobulbus sp.*	915	915	100%	0	71,10%	644
MBE28645.1	Molecular chaperone DnaK	*Bacterium*	915	915	100%	0	68,27%	636
NMI47668.1	Molecular chaperone DnaK	*Xanthomonas hortorum pv. gardneri*	912	912	100%	0	71,72%	641
WP_253305913.1	Molecular chaperone DnaK	*unidentified bacterial endosymbiont*	911	911	100%	0	69,61%	634
NEN74997.1	Molecular chaperone DnaK	*Pelistega ratti*	911	911	99%	0	70,50%	638
RAN81554.1	Molecular chaperone DnaK	*Bacillus sp. SRB_336*	910	910	100%	0	71,67%	639
KAF4516667.1	Hypothetical protein B566_EDAN003415	*Ephemera danica*	910	910	100%	0	70,02%	640
MCL5049412.1	Molecular chaperone DnaK	*Bacillota Bacterium*	909	909	99%	0	73,25%	643
WP_138118853.1	Molecular chaperone DnaK	*Bathymodiolus heckerae thiotrophic gill symbiont*	909	909	100%	0	69,66%	635
VDH01483.1	Molecular chaperone	*Helicobacter pametensis*	906	906	100%	0	70,11%	643
WP_072907800.1	Molecular chaperone DnaK	*Malonomonas rubra*	905	905	100%	0	68,53%	638
KAG9588654.1	Hypothetical protein KCV01_g12552	*Aureobasidium melanogenum*	904	904	100%	0	71,10%	641
MCL4157221.1	Hypothetical protein	*Idotea baltica*	903	903	100%	0	71,12%	614
KAF1852810.1	Hypothetical protein Lal_00008972	*Lupinus albus*	903	903	95%	0	73,34%	1008
EKE18045.1	Hypothetical protein ACD_10C00152G0002	*Uncultured bacterium*	902	902	99%	0	69,97%	648

Tabla S2. Resultados Blastp de WP_016210369.1 de *P. salmonis* contra organismos filogenéticamente cercanos a *P. salmonis*.

Blastp de WP_016210369.1 de *P. salmonis* contra *L. pneumophila*, *P. aeruginosa* y *C. burnetii*								
Accesión	Nombre descriptivo (NCBI)	Especie	Puntaje máximo	Puntaje total	Cobertura	E-value	Porcentaje identidad	Longitud de accesión
HBD7397718.1	TPA: Molecular chaperone DnaK	*Legionella pneumophila*	1002	1002	100%	0	75,77%	649
HBB6897971.1	TPA: Molecular chaperone DnaK	*Legionella pneumophila*	997	997	100%	0	75,69%	644
WP_061514385.1	Molecular chaperone DnaK	*Legionella*	996	996	100%	0	75,93%	644
AAU28094.1	Chaperone protein DnaK, heat shock protein Hsp70	*Legionella pneumophila subsp. pneumophila str. Philadelphia 1*	996	996	100%	0	75,93%	649
HAT1595824.1	TPA: Molecular chaperone DnaK	*Legionella pneumophila*	995	995	100%	0	75,93%	644
WP_062725547.1	Molecular chaperone DnaK	*Legionella pneumophila*	994	994	100%	0	75,93%	644
WP_011946925.1	Molecular chaperone DnaK	*Legionella pneumophila*	994	994	100%	0	75,93%	644
HAU0223363.1	TPA: Molecular chaperone DnaK	*Legionella pneumophila*	994	994	100%	0	75,77%	644
WP_015444335.1	Molecular chaperone DnaK	*Legionella pneumophila*	994	994	100%	0	75,93%	644
HAZ7572199.1	TPA: Molecular chaperone DnaK	*Legionella pneumophila*	994	994	100%	0	75,93%	644
HAT5934017.1	TPA: Molecular chaperone DnaK	*Legionella pneumophila*	994	994	100%	0	75,77%	644
WP_062726356.1	Molecular chaperone DnaK	*Legionella pneumophila*	994	994	100%	0	75,77%	644
WP_265677733.1	Molecular chaperone DnaK	*Legionella pneumophila*	994	994	100%	0	75,93%	644
WP_027219715.1	Molecular chaperone DnaK	*Legionella pneumophila*	994	994	100%	0	75,93%	644
HBD7143553.1	TPA: Molecular chaperone DnaK	*Legionella pneumophila*	994	994	100%	0	75,93%	644
HAU2264412.1	TPA: Molecular chaperone DnaK	*Legionella pneumophila*	994	994	100%	0	75,93%	644
WP_011214271.1	Molecular chaperone DnaK	*Legionella pneumophila*	993	993	100%	0	75,77%	644
WP_027222201.1	Molecular chaperone DnaK	*Legionella pneumophila*	993	993	100%	0	75,62%	644
WP_011215985.1	Molecular chaperone DnaK	*Legionella pneumophila*	993	993	100%	0	75,77%	644
HAU1327090.1	TPA: Molecular chaperone DnaK	*Legionella pneumophila*	992	992	100%	0	75,77%	644
WP_061483897.1	Molecular chaperone DnaK	*Legionella pneumophila*	992	992	100%	0	75,77%	644
WP_136690640.1	Molecular chaperone DnaK	*Legionella pneumophila*	991	991	100%	0	75,77%	644
WP_106225505.1	Molecular chaperone DnaK	*Legionella pneumophila*	991	991	100%	0	75,62%	644
HAT8179047.1	TPA: Molecular chaperone DnaK	*Legionella pneumophila*	991	991	100%	0	75,62%	644
HBD7053214.1	TPA: Molecular chaperone DnaK	*Legionella pneumophila*	991	991	100%	0	75,62%	644
WP_027229223.1	Molecular chaperone DnaK	*Legionella pneumophila*	991	991	100%	0	75,62%	644
HAU1150766.1	TPA: Molecular chaperone DnaK	*Legionella pneumophila*	990	990	100%	0	75,31%	644
WP_012077495.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa group*	986	986	100%	0	75,04%	637
MBG3902228.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	985	985	100%	0	74,88%	637
WP_005770882.1	Molecular chaperone DnaK	*Coxiella burnetii*	984	984	98%	0	76,60%	656
WP_058175394.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa group*	984	984	100%	0	74,88%	637
OYK79697.1	Molecular chaperone DnaK	*Coxiella burnetii*	984	984	98%	0	76,44%	656
WP_034082151.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	984	984	100%	0	74,88%	637
MBG7022588.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	983	983	100%	0	74,88%	637
WP_043081136.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	983	983	100%	0	74,88%	637
EIU3314617.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	982	982	100%	0	74,88%	637
WP_024916738.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	982	982	100%	0	74,73%	637
WP_272414034.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	982	982	100%	0	74,88%	637
HBN9875857.1	TPA: Molecular chaperone DnaK	*Pseudomonas aeruginosa*	982	982	100%	0	74,88%	637
WP_134301414.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	982	982	100%	0	74,88%	637
WP_040947915.1	Unnamed protein product	*Coxiella burnetii*	982	982	98%	0	76,44%	656
EIU7205545.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	982	982	100%	0	74,88%	637
WP_012569898.1	Unnamed protein product	*Coxiella burnetii*	982	982	98%	0	76,44%	656
WP_070338189.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	982	982	100%	0	74,88%	637
WP_023876021.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	981	981	100%	0	74,73%	637
WP_162288711.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	981	981	100%	0	74,73%	637
MBH9343429.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	981	981	100%	0	74,88%	637
HBO9661780.1	TPA: Molecular chaperone DnaK	*Pseudomonas aeruginosa*	981	981	100%	0	74,73%	637
WP_096081911.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	981	981	100%	0	74,73%	637
WP_039027895.1	Molecular chaperone DnaK	*Pseudomonas*	981	981	100%	0	74,73%	637
WP_012614574.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	981	981	100%	0	74,73%	637
WP_128458525.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	981	981	100%	0	74,73%	637
MCO4082697.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	981	981	100%	0	74,73%	637
WP_263473616.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	981	981	100%	0	74,73%	637
HBN7907100.1	TPA: Molecular chaperone DnaK	*Pseudomonas aeruginosa*	981	981	100%	0	74,73%	637
MBH9072134.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	981	981	100%	0	74,73%	637
WP_003095212.1	Molecular chaperone DnaK	*Pseudomonas*	981	981	100%	0	74,73%	637
MBG3935678.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	981	981	100%	0	74,73%	637
WP_132726422.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	981	981	100%	0	74,57%	637
MCO3847001.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	981	981	100%	0	74,73%	637
WP_132926101.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	981	981	100%	0	74,73%	637
HBO6334224.1	TPA: Molecular chaperone DnaK	*Pseudomonas aeruginosa*	981	981	100%	0	74,73%	637
WP_019726926.1	Molecular chaperone DnaK	*Pseudomonas*	981	981	100%	0	74,73%	637
WP_061195607.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	981	981	100%	0	74,73%	637
WP_116815500.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	981	981	100%	0	74,73%	637
WP_015503698.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	980	980	100%	0	74,73%	637
MBG7243746.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	980	980	100%	0	74,73%	637
WP_074227716.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	980	980	100%	0	74,73%	637
MBI7256831.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	980	980	100%	0	74,73%	637
HBO3267102.1	TPA: Molecular chaperone DnaK	*Pseudomonas aeruginosa*	980	980	100%	0	74,73%	637
WP_260573258.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	980	980	100%	0	74,73%	637
WP_174538517.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	980	980	100%	0	74,73%	637
WP_088376607.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	980	980	100%	0	74,73%	637
MBG4314412.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	980	980	100%	0	74,73%	637
WP_263962812.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	980	980	100%	0	74,73%	637
WP_033998982.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	980	980	100%	0	74,73%	637
MBN5478142.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	980	980	100%	0	74,73%	637
WP_134284467.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	980	980	100%	0	74,73%	637
WP_124204344.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	980	980	100%	0	74,73%	637
HBO3607191.1	TPA: Molecular chaperone DnaK	*Pseudomonas aeruginosa*	980	980	100%	0	74,73%	637
WP_270173152.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	980	980	100%	0	74,73%	637
WP_063456070.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	980	980	100%	0	74,73%	637
WP_134265354.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	980	980	100%	0	74,73%	637
WP_134596529.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	980	980	100%	0	74,57%	637
WP_059349771.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	980	980	100%	0	74,73%	637
WP_023102718.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	980	980	100%	0	74,73%	637
MBH9298385.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	980	980	100%	0	74,73%	637
MBI8152534.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	980	980	100%	0	74,73%	637
MBG5770115.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	980	980	100%	0	74,73%	637
HBO5710114.1	TPA: Molecular chaperone DnaK	*Pseudomonas aeruginosa*	980	980	100%	0	74,73%	637
MBG4532937.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	980	980	100%	0	74,57%	637
MBG3989232.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	979	979	100%	0	74,57%	637
HBO9468814.1	TPA: Molecular chaperone DnaK	*Pseudomonas aeruginosa*	979	979	100%	0	74,73%	637
MBG6541619.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	979	979	100%	0	74,57%	637
WP_132879783.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	979	979	100%	0	74,73%	637
MBG4108145.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	979	979	100%	0	74,57%	637
HBN9638955.1	TPA: Molecular chaperone DnaK	*Pseudomonas aeruginosa*	979	979	100%	0	74,73%	637
MBG6626402.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	979	979	100%	0	74,73%	637
HCD9060000.1	TPA: Molecular chaperone DnaK	*Pseudomonas aeruginosa*	979	979	100%	0	74,57%	637
WP_034015701.1	Molecular chaperone DnaK	*Pseudomonas aeruginosa*	979	979	100%	0	74,57%	637

Tabla S3. Resultados Blastp de WP_016209892.1 de *P. salmonis* contra toda la base de datos excluyendo *Proteobacteria* y contra organismos filogenéticamente cercanos a *P. salmonis*.

Blastp de WP_016209892.1 de *P. salmonis* contra toda la base de datos excepto *Proteobacteria*								
Accesión	**Nombre descriptivo (NCBI)**	**Especie**	**Puntaje máximo**	**Total Score**	**Cobertura**	**E-value**	**Porcentaje identidad**	**Longitud de accesión**
KAF5271492.1	Hypothetical protein FQR65_LT05112	*Abscondita terminalis*	68,2	129,0	100%	2,0E-09	29,74%	397
MCK5601640.1	Outer membrane beta-barrel protein	*Candidatus Pacearchaeota archaeon*	60,5	60,5	69%	3,0E-07	27,08%	202
GEU28528.1	Hypothetical protein	*Tanacetum cinerariifolium*	62,0	62,0	69%	3,0E-07	31,72%	1065
KAF5271491.1	Hypothetical protein FQR65_LT05111	*Abscondita terminalis*	59,3	59,3	69%	2,0E-06	28,00%	394
WP_257304054.1	Outer membrane protein transport protein	*Geothrix sp. SG10*	54,7	54,7	87%	9,0E-05	25,12%	499
GLH66671.1	Aromatic hydrocarbon degradation protein	*Geothrix sp. Red802*	53,5	53,5	87%	2,0E-04	23,38%	499
WP_243321249.1	Outer membrane protein transport protein	*Geothrix sp. SG200*	52,8	52,8	87%	3,0E-04	24,63%	499
MCF6206853.1	Porin family protein	*Sulfurovum sp.*	51,2	51,2	99%	6,0E-04	26,73%	199
WP_257308995.1	Outer membrane protein transport protein	*Geothrix fuzhouensis*	52,0	52,0	87%	7,0E-04	23,38%	499
WP_243293679.1	Outer membrane protein transport protein	*Geothrix sp. SG198*	51,6	51,6	87%	8,0E-04	24,63%	499
WP_243383394.1	Outer membrane protein transport protein	*Geothrix alkalitolerans*	51,6	51,6	87%	1,0E-03	24,63%	499
NTW99741.1	Hypothetical protein	*Geobacteraceae bacterium*	50,8	50,8	65%	1,0E-03	23,29%	267
WP_243301192.1	Outer membrane protein transport protein	*Geothrix oryzisoli*	48,9	48,9	87%	7,0E-03	23,27%	499
WP_243286189.1	Outer membrane protein transport protein	*Geothrix terrae*	47,8	47,8	87%	1,7E-02	23,65%	499
EKD73347.1	OmpA-like protein transmembrane protein	*uncultured bacterium*	46,6	46,6	86%	2,3E-02	27,04%	213
WP_069214270.1	Porin family protein	*Elizabethkingia meningoseptica*	46,2	46,2	76%	3,0E-02	26,19%	194
WP_089051724.1	Porin family protein	*Flavobacterium hercynium*	46,2	46,2	40%	3,1E-02	30,95%	190
WP_199906289.1	Hypothetical protein	*Mycobacterium tuberculosis*	43,9	43,9	41%	4,0E-02	32,98%	94
MBS6928868.1	Porin family protein	*Finegoldia magna*	45,4	45,4	47%	4,7E-02	30,77%	178

Blastp de WP_016209892.1 de *P. salmonis* contra *L. pneumophila*, *P. aeruginosa* y *C. burnetii*								
Accesión	**Nombre descriptivo (NCBI)**	**Especie**	**Puntaje máximo**	**Total Score**	**Cobertura**	**E-value**	**Porcentaje identidad**	**Longitud de accesión**
WP_040947705.1	Unnamed protein product	*Coxiella burnetii*	57,8	57,8	98%	3,0E-08	27,63%	231
WP_010957493.1	Outer membrane beta-barrel protein	*Coxiella burnetii*	57,0	57,0	98%	7,0E-08	27,63%	231
WP_012570389.1	Unnamed protein product	*Coxiella burnetii*	56,6	56,6	98%	8,0E-08	28,51%	231
WP_039669233.1	Outer membrane beta-barrel protein	*Coxiella burnetii*	55,8	55,8	98%	2,0E-07	28,07%	231
WP_005771408.1	Outer membrane beta-barrel protein	*Coxiella burnetii*	55,5	55,5	98%	2,0E-07	28,07%	231
WP_260511903.1	Outer membrane beta-barrel protein	*Coxiella burnetii*	54,7	54,7	98%	5,0E-07	27,19%	231
WP_061513559.1	Outer membrane beta-barrel protein	*Legionella pneumophila*	50,4	50,4	99%	1,0E-05	26,53%	243
HAT6977453.1	TPA: Outer membrane beta-barrel protein	*Legionella pneumophila*	49,7	49,7	99%	3,0E-05	25,31%	243
HAU1892339.1	TPA: Hypothetical protein	*Legionella pneumophila*	49,3	49,3	73%	3,0E-05	28,26%	243
WP_027227743.1	Outer membrane beta-barrel protein	*Legionella pneumophila*	49,3	49,3	99%	3,0E-05	26,12%	243
HAT1990808.1	TPA: Outer membrane beta-barrel protein	*Legionella pneumophila*	49,3	49,3	99%	3,0E-05	26,12%	243
HAT1917317.1	TPA: Outer membrane beta-barrel protein	*Legionella pneumophila*	49,3	49,3	99%	3,0E-05	26,12%	243
HAU1322178.1	TPA: Hypothetical protein	*Legionella pneumophila*	49,3	49,3	99%	3,0E-05	26,12%	243
WP_014841400.1	Outer membrane beta-barrel protein	*Legionella pneumophila*	49,3	49,3	99%	3,0E-05	26,12%	243
HAT1822502.1	TPA: Outer membrane beta-barrel protein	*Legionella pneumophila*	49,3	49,3	99%	3,0E-05	26,12%	243
HAT8859912.1	TPA: Hypothetical protein	*Legionella pneumophila subsp. pneumophila*	48,9	48,9	99%	4,0E-05	26,12%	243
HAT8179939.1	TPA: Hypothetical protein	*Legionella pneumophila*	48,9	48,9	99%	4,0E-05	26,12%	243
WP_010946896.1	Outer membrane beta-barrel protein	*Legionella pneumophila*	48,9	48,9	73%	5,0E-05	28,26%	243
HAT2099662.1	TPA: Outer membrane beta-barrel protein	*Legionella pneumophila*	48,5	48,5	73%	5,0E-05	28,26%	243
HAT1978464.1	TPA: Outer membrane beta-barrel protein	*Legionella pneumophila*	48,5	48,5	73%	6,0E-05	28,26%	243
HAT1596495.1	TPA: Outer membrane beta-barrel protein	*Legionella pneumophila*	48,5	48,5	73%	7,0E-05	28,26%	243
WP_027224139.1	Outer membrane beta-barrel protein	*Legionella pneumophila*	48,1	48,1	73%	7,0E-05	28,26%	243
HAT8173420.1	TPA: Hypothetical protein	*Legionella pneumophila*	48,1	48,1	73%	7,0E-05	28,26%	242
WP_011213518.1	Outer membrane beta-barrel protein	*Legionella pneumophila*	48,1	48,1	99%	8,0E-05	25,71%	243
HAT9858599.1	TPA: Hypothetical protein	*Legionella pneumophila subsp. pneumophila*	48,1	48,1	73%	8,0E-05	28,26%	243
HAT1802075.1	TPA: Outer membrane beta-barrel protein	*Legionella pneumophila*	47,4	47,4	73%	1,0E-04	27,72%	243
WP_061483188.1	Outer membrane beta-barrel protein	*Legionella pneumophila*	47,4	47,4	73%	2,0E-04	27,72%	243
WP_027221404.1	Outer membrane beta-barrel protein	*Legionella pneumophila*	47,4	47,4	73%	2,0E-04	28,26%	243
WP_011215267.1	Outer membrane beta-barrel protein	*Legionella pneumophila*	47,0	47,0	73%	2,0E-04	27,72%	243
WP_129904947.1	Outer membrane beta-barrel protein	*Legionella pneumophila*	46,2	46,2	73%	3,0E-04	27,72%	243
WP_010958108.1	Outer membrane beta-barrel protein	*Coxiella burnetii*	44,3	44,3	45%	2,0E-03	30,21%	248
WP_129890623.1	Outer membrane beta-barrel protein	*Legionella pneumophila*	43,5	43,5	86%	3,0E-03	26,92%	232
WP_005770828.1	Unnamed protein product	*Coxiella burnetii*	41,6	41,6	100%	1,5E-02	25,10%	248
WP_012569916.1	Unnamed protein product	*Coxiella burnetii*	41,2	41,2	100%	2,1E-02	25,10%	248
WP_011997045.1	Outer membrane beta-barrel protein	*Coxiella burnetii*	40,8	40,8	100%	2,6E-02	25,10%	248
PNT86367.1	Hypothetical protein C2L89_10175	*Coxiella burnetii*	40,8	40,8	100%	2,6E-02	23,32%	248

Tabla S4. Resultados Blastp de WP_016209681.1 de *P. salmonis* contra toda la base de datos excluyendo Proteobacteria y contra organismos filogenéticamente cercanos a *P. salmonis*.

Blastp de WP_016209681.1 de *P. salmonis* contra toda la base de datos excepto *Proteobacteria*								
Accesión	**Nombre descriptivo (NCBI)**	**Especie**	**Puntaje máximo**	**Total Score**	**Cobertura**	**E-value**	**Porcentaje identidad**	**Longitud de accesión**
UTW43560.1	Hypothetical protein KFE69_05580	Bacterium SCSIO 12844	82,0	82,0	39%	8,0E-14	34,85%	262

Blastp de WP_016209681.1 de *P. salmonis* contra *L. pneumophila* , *P. aeruginosa* y *C. burnetii*								
Accesión	**Nombre descriptivo (NCBI)**	**Especie**	**Puntaje máximo**	**Total Score**	**Cobertura**	**E-value**	**Porcentaje identidad**	**Longitud de accesión**
HAU1959604.1	TPA: Type IV secretion protein IcmG	*Legionella pneumophila*	63,5	63,5	48%	7,0E-10	30,57%	196
HAT8178648.1	TPA: Type IV secretion protein IcmG	*Legionella pneumophila*	64,3	64,3	46%	9,0E-10	31,79%	269
HAU1152143.1	TPA: Type IV secretion protein IcmG	*Legionella pneumophila*	64,3	64,3	48%	1,0E-09	31,21%	268
WP_027266641	Type IVB secretion system protein IcmG/DotF	*Legionella pneumophila*	64,3	64,3	38%	1,0E-09	29,22%	269
WP_110561174	Type IVB secretion system protein IcmG/DotF	*Legionella pneumophila*	64,3	64,3	44%	1,0E-09	30,61%	269
STX97929.1	Protein IcmG (DotF)	*Legionella pneumophila*	63,9	63,9	38%	1,0E-09	29,22%	268
HAT6978167.1	TPA: Type IV secretion protein IcmG	*Legionella pneumophila*	63,9	63,9	34%	1,0E-09	32,14%	269
WBV68745.1	Type IVB secretion system protein IcmG/DotF	*Legionella pneumophila*	61,2	61,2	30%	1,0E-09	31,67%	137
WP_080464004	Type IVB secretion system protein IcmG/DotF	*Legionella pneumophila*	63,9	63,9	48%	1,0E-09	30,57%	268
WP_027228891	Type IVB secretion system protein IcmG/DotF	*Legionella pneumophila*	63,9	63,9	46%	2,0E-09	30,46%	268
APF02302.1	Type IV secretion protein IcmG	*Legionella pneumophila subsp. fraseri*	63,9	63,9	46%	2,0E-09	30,46%	267
WBV70963.1	Type IVB secretion system protein IcmG/DotF	*Legionella pneumophila*	63,5	63,5	38%	2,0E-09	28,57%	269
WP_014841027	Type IVB secretion system protein IcmG/DotF	*Legionella pneumophila*	63,5	63,5	38%	2,0E-09	28,57%	269
CZG48411.1	Uncharacterised protein	*Legionella pneumophila*	63,5	63,5	38%	2,0E-09	28,57%	268
HAU1295616.1	TPA: Type IV secretion protein IcmG	*Legionella pneumophila*	63,5	63,5	46%	2,0E-09	30,46%	268
HAU2068045.1	TPA: Type IV secretion protein IcmG	*Legionella pneumophila*	61,2	61,2	44%	2,0E-09	31,03%	146
WP_010946201	Type IVB secretion system protein IcmG/DotF	*Legionella pneumophila*	63,5	63,5	38%	2,0E-09	29,87%	269
WP_028378015	Type IVB secretion system protein IcmG/DotF	*Legionella pneumophila*	63,2	63,2	46%	2,0E-09	30,46%	268
AAS91958.1	IcmG protein	*Legionella pneumophila*	63,2	63,2	46%	2,0E-09	30,46%	268
HAT9858426.1	TPA: Type IV secretion protein IcmG	*Legionella pneumophila subsp. pneumophila*	63,2	63,2	38%	2,0E-09	29,87%	269
AOU06002.1	Type IV secretion protein IcmG	*Legionella pneumophila*	63,2	63,2	38%	2,0E-09	29,87%	268
HAU1068788.1	TPA: Type IV secretion protein IcmG	*Legionella pneumophila*	63,2	63,2	46%	3,0E-09	29,41%	269
AOW52840.1	Type IV secretion protein IcmG	*Legionella pneumophila subsp. pneumophila*	63,2	63,2	41%	3,0E-09	28,08%	268
WP_027264789	Type IVB secretion system protein IcmG/DotF	*Legionella pneumophila*	63,2	63,2	46%	3,0E-09	29,41%	269
WP_011214705	Type IVB secretion system protein IcmG/DotF	*Legionella pneumophila*	62,8	62,8	41%	3,0E-09	28,08%	269
ABQ56792.1	IcmG (DotF)	*Legionella pneumophila str. Corby*	62,8	62,8	41%	3,0E-09	31,08%	268
HAT1966509.1	TPA: Type IV secretion protein IcmG	*Legionella pneumophila*	62,8	62,8	41%	3,0E-09	31,08%	269
CZG92221.1	Uncharacterised protein	*Legionella pneumophila*	62,8	62,8	46%	3,0E-09	29,41%	268
HAT9012065.1	TPA: Type IV secretion protein IcmG	*Legionella pneumophila subsp. pneumophila*	62,8	62,8	41%	3,0E-09	31,08%	269
WP_013101088	Type IVB secretion system protein IcmG/DotF	*Legionella pneumophila*	62,8	62,8	41%	3,0E-09	31,08%	269
HAT2039262.1	TPA: Type IV secretion protein IcmG	*Legionella pneumophila*	62,8	62,8	41%	3,0E-09	28,08%	269
HAT1726414.1	TPA: Type IV secretion protein IcmG	*Legionella pneumophila*	62,8	62,8	41%	3,0E-09	31,08%	269
HAT2139861.1	TPA: Type IV secretion protein IcmG	*Legionella pneumophila*	62,8	62,8	46%	4,0E-09	29,41%	269
HAT1595965.1	TPA: Type IV secretion protein IcmG	*Legionella pneumophila*	62,4	62,4	48%	4,0E-09	29,94%	268
AMQ29412.1	Type IV secretion protein IcmG	*Legionella pneumophila subsp. pneumophila*	62,4	62,4	41%	4,0E-09	28,08%	268
WP_027224227	Type IVB secretion system protein IcmG/DotF	*Legionella pneumophila*	62,4	62,4	41%	4,0E-09	28,08%	269
WP_161504490	Type IVB secretion system protein IcmG/DotF	*Legionella pneumophila*	62,4	62,4	46%	4,0E-09	29,41%	269
HAU0671027.1	TPA: Type IV secretion protein IcmG	*Legionella pneumophila*	62,4	62,4	41%	4,0E-09	28,08%	269
WP_011213093	Type IVB secretion system protein IcmG/DotF	*Legionella pneumophila*	62,4	62,4	41%	5,0E-09	28,08%	269
ANH11906.1	Type IV secretion protein IcmG	*Legionella pneumophila*	62,4	62,4	41%	5,0E-09	28,08%	268
HBD7429555.1	TPA: Type IVB secretion system protein IcmG/DotF	*Legionella pneumophila*	62,4	62,4	41%	5,0E-09	28,08%	269
WP_014843354	Type IVB secretion system protein IcmG/DotF	*Legionella pneumophila*	62,4	62,4	41%	5,0E-09	28,08%	269
CZG37146.1	Uncharacterised protein	*Legionella pneumophila*	62	62	41%	5,0E-09	28,08%	268
HAU2264623.1	TPA: Type IV secretion protein IcmG	*Legionella pneumophila*	62	62	46%	6,0E-09	30,07%	269
WP_027223525	Type IVB secretion system protein IcmG/DotF	*Legionella pneumophila*	62	62	34%	6,0E-09	30,00%	269
HAT9716961.1	TPA: Type IV secretion protein IcmG	*Legionella pneumophila subsp. pneumophila*	62	62	41%	7,0E-09	28,08%	269
HAU0827609.1	TPA: Type IV secretion protein IcmG	*Legionella pneumophila*	62	62	41%	7,0E-09	28,08%	269
AMP91511.1	Type IV secretion protein IcmG	*Legionella pneumophila subsp. pascullei*	62	62	34%	7,0E-09	30,00%	268
WP_080447277	Type IVB secretion system protein IcmG/DotF	*Legionella*	61,6	61,6	41%	7,0E-09	28,08%	269
HAZ7572009.1	TPA: Type IV secretion protein IcmG	*Legionella pneumophila*	61,6	61,6	46%	8,0E-09	30,46%	269
WP_033962433	Hypothetical protein	*Pseudomonas aeruginosa*	61,2	61,2	16%	1,0E-08	47,17%	304
HCL3851274.1	TPA: Hypothetical protein	*Pseudomonas aeruginosa*	59,7	59,7	16%	1,0E-08	47,17%	188
WP_080446195	Type IVB secretion system protein IcmG/DotF	*Legionella pneumophila*	60,8	60,8	41%	2,0E-08	28,08%	269
HBD7397473.1	TPA: Type IVB secretion system protein IcmG/DotF	*Legionella pneumophila*	60,8	60,8	28%	2,0E-08	34,86%	277
WP_070610851	Type IV secretion protein IcmG	*Pseudomonas aeruginosa*	60,5	60,5	16%	3,0E-08	47,17%	309
WP_270036767	Hypothetical protein	*Pseudomonas aeruginosa*	60,1	60,1	16%	4,0E-08	47,17%	311
WP_045666067	Hypothetical protein	*Pseudomonas aeruginosa*	60,1	60,1	16%	4,0E-08	47,17%	311
HBN8268356.1	TPA: Hypothetical protein	*Pseudomonas aeruginosa*	59,7	59,7	16%	5,0E-08	47,17%	306
WP_042923115	Hypothetical protein	*Pseudomonas aeruginosa*	59,3	59,3	16%	6,0E-08	47,17%	304
HBO9583045.1	TPA: Type IV secretion protein IcmG	*Pseudomonas aeruginosa*	58,2	58,2	16%	1,0E-07	45,28%	256
HBO9618321.1	TPA: Type IV secretion protein IcmG	*Pseudomonas aeruginosa*	55,5	55,5	16%	1,0E-07	45,28%	116
WP_269763219	Hypothetical protein	*Pseudomonas aeruginosa*	58,5	58,5	16%	1,0E-07	45,28%	309
HBO9536356.1	TPA: Type IV secretion protein IcmG	*Pseudomonas aeruginosa*	58,5	58,5	16%	1,0E-07	45,28%	309
WP_043094224	Hypothetical protein	*Pseudomonas aeruginosa*	58,2	58,2	16%	1,0E-07	45,28%	309
WP_209066293	Hypothetical protein	*Pseudomonas aeruginosa*	58,2	58,2	16%	1,0E-07	45,28%	309
WP_009684348	Hypothetical protein	*Pseudomonadaceae*	58,2	58,2	16%	1,0E-07	45,28%	309
WP_033955330	Hypothetical protein	*Pseudomonas aeruginosa*	58,2	58,2	16%	1,0E-07	45,28%	309
WP_034050799	Hypothetical protein	*Pseudomonas aeruginosa*	58,2	58,2	16%	2,0E-07	45,28%	309
MBG3954240.1	Hypothetical protein	*Pseudomonas aeruginosa*	58,2	58,2	16%	2,0E-07	45,28%	310
WP_023100628	Hypothetical protein	*Pseudomonas aeruginosa*	58,2	58,2	16%	2,0E-07	45,28%	310
MBH4098098.1	Hypothetical protein	*Pseudomonas aeruginosa*	57,8	57,8	16%	2,0E-07	45,28%	310
HCF3479681.1	TPA: Hypothetical protein	*Pseudomonas aeruginosa*	55,8	55,8	16%	3,0E-07	45,28%	188
HCE5933777.1	TPA: Hypothetical protein	*Pseudomonas aeruginosa*	57	57	16%	3,0E-07	45,28%	310
WP_132450824	Type IV secretion protein IcmG	*Pseudomonas aeruginosa*	57	57	16%	4,0E-07	45,28%	304
WP_270142499	Hypothetical protein	*Pseudomonas aeruginosa*	56,6	56,6	16%	5,0E-07	45,28%	304
WP_034022921	Type IV secretion protein IcmG	*Pseudomonas aeruginosa*	56,6	56,6	16%	5,0E-07	45,28%	304
WP_034026823	Type IV secretion protein IcmG	*Pseudomonas aeruginosa*	56,6	56,6	16%	5,0E-07	45,28%	304
WP_033945867	Type IV secretion protein IcmG	*Pseudomonas aeruginosa*	56,6	56,6	16%	5,0E-07	45,28%	304
MCT0357097.1	Hypothetical protein	*Pseudomonas aeruginosa*	56,6	56,6	16%	5,0E-07	45,28%	304
WP_005769611	Hypothetical protein	*Coxiella burnetii*	55,8	55,8	34%	6,0E-07	26,32%	244
WP_005772726	Type IVB secretion system protein IcmG/DotF	*Coxiella burnetii*	55,5	55,5	34%	8,0E-07	26,32%	244
WP_086230892	Type IV secretion protein IcmG	*Pseudomonas aeruginosa*	55,8	55,8	16%	9,0E-07	45,28%	304
WP_010958333	Type IVB secretion system protein IcmG/DotF	*Coxiella burnetii*	55,1	55,1	34%	1,0E-06	26,32%	244
WP_050465977	Hypothetical protein	*Pseudomonas aeruginosa*	51,2	51,2	16%	3,0E-06	45,28%	108
WP_228494806	Hypothetical protein	*Pseudomonas aeruginosa*	50,8	50,8	16%	4,0E-06	45,28%	107
RCI72009.1	Type IV secretion protein IcmG	*Pseudomonas aeruginosa*	45,1	45,1	14%	1,0E-04	44,68%	48

Tabla S5. Resultados Blastp de WP_017376766.1 de *P. salmonis* contra toda la base de datos excluyendo *Proteobacteria*.

Blastp de WP_017376766.1 de *P. salmonis* contra toda la base de datos excluyendo *Proteobacteria*								
Accesión	**Nombre descriptivo (NCBI)**	**Especie**	**Puntaje máximo**	**Puntaje total**	**Cobertura**	**E-value**	**Porcentaje identidad**	**Longitud de accesión**
MBI4691471.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Nitrospirota bacterium*	216	216	95%	1,0E-66	45,38%	231
MBI5409700.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Nitrospirota bacterium*	211	211	94%	2,0E-64	43,15%	249
MCK9418717.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Nitrospirota bacterium*	205	205	94%	4,0E-62	44,94%	232
OGP90583.1	Hypothetical protein A2156_09010	*Deltaproteobacteria bacterium RBG_16_48_10*	205	205	95%	5,0E-62	45,24%	234
OYV72648.1	Hypothetical protein B7Z74_05215	*Deltaproteobacteria bacterium 21-66-5*	203	203	94%	2,0E-61	43,95%	230
MBI3753937.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Deltaproteobacteria bacterium*	203	203	94%	3,0E-61	43,72%	232
KAF0145710.1	FKBP-type peptidyl-prolyl cis-trans isomerase FklB	*Nitrospirota bacterium*	201	201	94%	1,0E-60	44,76%	231
MBI5665642.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Nitrospirota bacterium*	201	201	93%	2,0E-60	43,09%	228
MBI5967497.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Deltaproteobacteria bacterium*	200	200	94%	4,0E-60	44,18%	234
MBI5047910.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Deltaproteobacteria bacterium*	200	200	94%	4,0E-60	43,37%	240
MBI5057987.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Nitrospirota bacterium*	199	199	98%	1,0E-59	42,25%	242
MBI5205135.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Nitrospirota bacterium*	199	199	94%	1,0E-59	43,95%	231
OGP19383.1	Hypothetical protein A2X90_04575	*Deltaproteobacteria bacterium GWA2_65_63*	199	199	94%	1,0E-59	43,15%	230
OGW55553.1	Hypothetical protein A2Z46_00040	*Nitrospirae bacterium RBG_19FT_COMBO_55_12*	199	199	97%	1,0E-59	44,15%	244
MBI5328030.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Deltaproteobacteria bacterium*	199	199	93%	1,0E-59	44,26%	238
OGW41090.1	Hypothetical protein A2Y97_12315	*Nitrospirae bacterium RBG_13_39_12*	198	198	95%	2,0E-59	44,40%	233
MBZ5572278.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Acidobacteriia bacterium*	199	199	89%	2,0E-59	46,98%	270
OGP49845.1	Hypothetical protein A2Y79_02555	*Deltaproteobacteria bacterium RBG_13_43_22*	198	198	85%	2,0E-59	45,95%	229
OGQ48498.1	Hypothetical protein A2W63_03380	*Deltaproteobacteria bacterium RIFCSPLOWO2_02_44_9*	198	198	94%	2,0E-59	43,90%	230
HBH61779.1	TPA: Hypothetical protein	*Nitrospiraceae bacterium*	197	197	94%	4,0E-59	42,68%	228
KPK89766.1	Hypothetical protein AMJ94_11255	*Deltaproteobacteria bacterium SM23_61*	197	197	92%	4,0E-59	41,63%	232
NWF56830.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Syntrophaceae bacterium*	197	197	91%	4,0E-59	41,98%	232
OGP63135.1	Hypothetical protein A2170_16300	*Deltaproteobacteria bacterium RBG_13_53_10*	197	197	87%	5,0E-59	44,74%	234
SPQ00288.1	Outer membrane protein MIP	*Candidatus Sulfobium mesophilum*	197	197	98%	6,0E-59	42,37%	234
OGW43478.1	Hypothetical protein A2Y66_02815	*Nitrospirae bacterium RBG_13_41_22*	197	197	95%	6,0E-59	41,77%	243
OGP78705.1	Hypothetical protein A2Z26_05155	*Deltaproteobacteria bacterium RBG_16_66_15*	196	196	94%	1,0E-58	42,74%	230
HAM50010.1	TPA: Hypothetical protein	*Nitrospiraceae bacterium*	196	196	92%	1,0E-58	45,27%	229
OGW60447.1	Hypothetical protein A2638_01495	*Nitrospirae bacterium RIFCSPHIGHO2_01_FULL_66_17*	196	196	91%	1,0E-58	43,21%	229
MBI4766958.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Deltaproteobacteria bacterium*	196	196	91%	2,0E-58	44,35%	229
MBI5098245.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Nitrospirota bacterium*	196	196	99%	2,0E-58	41,86%	239
MBS3906994.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Syntrophaceae bacterium*	196	196	89%	2,0E-58	44,21%	232
RPJ06443.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Deltaproteobacteria bacterium*	196	196	93%	2,0E-58	40,98%	234
UCH81588.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Nitrospiraceae bacterium*	195	195	93%	2,0E-58	41,87%	229
MBA4392315.1	Hypothetical protein	*Desulfobacca sp.*	194	194	85%	3,0E-58	44,59%	215
MBM4160332.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Ignavibacteria bacterium*	195	195	94%	3,0E-58	41,70%	229
MBF8260106.1	Peptidyl-prolyl cis-trans isomerase	*Actinomycetia bacterium*	195	195	94%	4,0E-58	41,53%	230
MCJ7704907.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Desulfobacterales bacterium*	194	194	84%	5,0E-58	45,70%	232
OGR15550.1	Hypothetical protein A2097_05220	*Desulfobacula sp. GWF2_41_7*	194	194	92%	6,0E-58	41,15%	230
OGP71795.1	Hypothetical protein A2W09_00260	*Deltaproteobacteria bacterium RBG_16_50_11*	194	194	96%	7,0E-58	41,34%	236
MBE0603138.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Deltaproteobacteria bacterium*	194	194	94%	7,0E-58	41,53%	230
MBI3995983.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Nitrospirota bacterium*	194	194	96%	1,0E-57	41,83%	237
RJQ23104.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Nitrospiraceae bacterium*	193	193	96%	2,0E-57	41,27%	234
MCP2502334.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Deltaproteobacteria bacterium*	192	192	94%	3,0E-57	41,13%	230
MBI4849070.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Nitrospirota bacterium*	193	193	98%	3,0E-57	41,86%	242
MBZ5630437.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Acidobacteriia bacterium*	192	192	93%	3,0E-57	41,98%	232
MBP1724297.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Deltaproteobacteria bacterium*	193	193	92%	4,0E-57	42,86%	264
MBE0605672.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Deltaproteobacteria bacterium*	192	192	94%	5,0E-57	40,73%	230
MBI5015533.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Deltaproteobacteria bacterium*	192	192	94%	5,0E-57	42,51%	251
MBE0426440.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Nitrospirota bacterium*	192	192	93%	5,0E-57	40,24%	243
MBS1244164.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Deltaproteobacteria bacterium*	192	192	94%	5,0E-57	41,13%	230
OGP11873.1	Hypothetical protein A2056_05475	*Deltaproteobacteria bacterium GWA2_42_85*	191	191	94%	7,0E-57	42,11%	230
MBV9479274.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Acidobacteriota bacterium*	191	191	92%	8,0E-57	44,58%	233
OGW52313.1	Peptidylprolyl isomerase	*Nitrospirae bacterium RBG_13_43_8*	192	192	99%	9,0E-57	40,77%	264
OGQ01281.1	Hypothetical protein A2Z51_08705	*Deltaproteobacteria bacterium RBG_19FT_COMBO_52_11*	191	191	94%	1,0E-56	40,73%	232
MBP2683053.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Deltaproteobacteria bacterium*	191	191	94%	1,0E-56	41,13%	230
MCL5024772.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Nitrospirota bacterium*	191	191	94%	1,0E-56	41,11%	241
KRT73743.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Deltaproteobacteria bacterium CSP1-8*	191	191	89%	1,0E-56	42,67%	245
MBI3811221.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Nitrospirota bacterium*	191	191	95%	2,0E-56	40,80%	237
MBI4685523.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Nitrospirota bacterium*	191	191	95%	2,0E-56	40,16%	230
MBI5774130.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Verrucomicrobiota bacterium*	191	191	93%	2,0E-56	41,30%	231
MBP2673455.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Deltaproteobacteria bacterium*	191	191	94%	2,0E-56	40,73%	230
OIP32833.1	Hypothetical protein AUK27_12205	*Deltaproteobacteria bacterium CG2_30_66_27*	191	191	94%	2,0E-56	41,94%	230
MBI3606564.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Nitrospirota bacterium*	191	191	88%	2,0E-56	43,78%	229
MBI4596185.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Candidatus Tectomicrobia bacterium*	190	190	93%	3,0E-56	42,62%	230
KPK29301.1	Hypothetical protein AMK70_16135	*Nitrospira bacterium SG8_35_1*	190	190	92%	3,0E-56	42,32%	228
RJR16931.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Nitrospiraceae bacterium*	190	190	93%	3,0E-56	39,84%	228
MBA2241996.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Chthoniobacterales bacterium*	191	191	94%	4,0E-56	42,68%	270
PYX57599.1	Hypothetical protein DMG76_11480	*Acidobacteriota bacterium*	191	191	88%	4,0E-56	43,91%	278
VTR68313.1	Outer membrane protein MIP	*Desulfosarcina cetonica*	189	189	86%	4,0E-56	44,89%	231
UCG78523.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Nitrospirota bacterium*	189	189	89%	6,0E-56	41,45%	229
MBI3621112.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Nitrospirota bacterium*	189	189	92%	6,0E-56	41,80%	233
MBI3397983.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Deltaproteobacteria bacterium*	189	189	93%	7,0E-56	41,32%	229
PYI91642.1	Hypothetical protein DMF03_03075	*Verrucomicrobiota bacterium*	189	189	94%	7,0E-56	41,46%	243
MBA3016509.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Desulfobulbaceae bacterium*	188	188	89%	8,0E-56	42,31%	219
UCF87269.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Nitrospiraceae bacterium*	189	189	94%	8,0E-56	41,06%	228
TAL25880.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Nitrospirota bacterium*	189	189	94%	9,0E-56	42,74%	231
MBP2685885.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Deltaproteobacteria bacterium*	189	189	94%	1,0E-55	40,73%	230
MBI5676491.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Nitrospirota bacterium*	189	189	88%	1,0E-55	44,59%	241
MBI3805213.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Nitrospirota bacterium*	189	189	95%	1,0E-55	42,00%	237
MBU2647265.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*bacterium*	188	188	92%	1,0E-55	42,74%	234
MBP2678428.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Deltaproteobacteria bacterium*	188	188	94%	1,0E-55	39,92%	230
OGP73670.1	Hypothetical protein A2V86_02595	*Deltaproteobacteria bacterium RBG_16_49_23*	188	188	85%	2,0E-55	44,14%	232
MCM2287107.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Desulfobacula sp.*	188	188	92%	2,0E-55	40,08%	230
MBP2677453.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Deltaproteobacteria bacterium*	188	188	94%	2,0E-55	40,73%	230
KPK02452.1	Hypothetical protein AMK71_02140	*Nitrospira bacterium SG8_35_4*	188	188	93%	2,0E-55	38,62%	229
HDL20673.1	TPA: FKBP-type peptidyl-prolyl cis-trans isomerase	*Nitrospirota bacterium*	187	187	86%	3,0E-55	42,41%	207
PAW89001.1	Hypothetical protein B9S33_04010	*Pedosphaera sp. Tous-C6FEB*	187	187	92%	3,0E-55	41,91%	233
MBF8250750.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Deltaproteobacteria bacterium*	187	187	92%	3,0E-55	40,98%	230
MBI3610708.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Nitrospirota bacterium*	187	187	92%	3,0E-55	41,49%	229
MBI4811413.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Ignavibacteriales bacterium*	187	187	93%	3,0E-55	41,80%	231
PYK91057.1	Hypothetical protein DME35_03710	*Verrucomicrobiota bacterium*	187	187	92%	4,0E-55	43,67%	238
NWF52079.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Nitrospirota bacterium*	187	187	94%	4,0E-55	40,32%	240
MBI5605479.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Deltaproteobacteria bacterium*	187	187	94%	4,0E-55	42,11%	229
MBM2837628.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Deltaproteobacteria bacterium*	187	187	92%	4,0E-55	40,98%	241
MCL2102864.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Syntrophorhabdaceae bacterium*	187	187	94%	5,0E-55	41,53%	245
OHB28748.1	Hypothetical protein A2X84_06590	*Desulfuromonadaceae bacterium GWC2_58_13*	187	187	91%	5,0E-55	42,45%	236
GBD98365.1	Outer membrane protein MIP precursor	*Bacterium BMS3Abin07*	187	187	86%	5,0E-55	42,41%	230
MBM4340656.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Deltaproteobacteria bacterium*	187	187	91%	6,0E-55	42,26%	231
RJP21497.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Deltaproteobacteria bacterium*	186	186	85%	7,0E-55	43,24%	230
MBM4324998.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Deltaproteobacteria bacterium*	186	186	91%	8,0E-55	42,26%	231

Tabla S6. Resultados Blastp de WP_017376766.1 de *P. salmonis* contra organismos filogenéticamente cercanos a *P. salmonis*.

Blastp de WP_017376766.1 de *P. salmonis* contra *L. pneumophila*, *P. aeruginosa* y *C. burnetii*								
Accesión	Nombre descriptivo (NCBI)	Especie	Puntaje máximo	Puntaje total	Cobertura	E-value	Porcentaje identidad	Longitud de accesión
WP_011996666.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Coxiella burnetii*	192	192	95%	4,0E-59	40,56%	230
WP_005771923.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Coxiella burnetii*	191	191	95%	7,0E-59	40,56%	230
WP_039669542.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Coxiella burnetii*	191	191	95%	1,0E-58	40,56%	230
WP_043902321.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Coxiella burnetii*	191	191	94%	1,0E-58	40,65%	227
WP_010957701.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Coxiella burnetii*	191	191	95%	2,0E-58	40,16%	230
WP_040947768.1	Unnamed protein product	*Coxiella burnetii*	190	190	95%	2,0E-58	40,16%	230
AAA92352.1	Peptidyl propyl cis/trans isomerase	*Coxiella burnetii*	190	190	95%	4,0E-58	40,16%	230
HBD7398638.1	TPA: FKBP-type peptidyl-prolyl cis-trans isomerase	*Legionella pneumophila*	182	182	95%	4,0E-55	40,40%	233
WP_059427894.1	Macrophage infectivity potentiator Mip	*Legionella pneumophila*	175	175	95%	2,0E-52	38,80%	233
HAT8264969.1	TPA: hypothetical protein	*Legionella pneumophila*	174	174	95%	3,0E-52	38,80%	235
WP_027221154.1	Macrophage infectivity potentiator Mip	*Legionella pneumophila*	173	173	95%	1,0E-51	38,80%	233
HAT1798020.1	TPA: FKBP-type peptidyl-prolyl cis-trans isomerase	*Legionella pneumophila*	173	173	95%	1,0E-51	38,40%	233
HAT6978448.1	TPA: hypothetical protein	*Legionella pneumophila*	173	173	95%	1,0E-51	38,40%	235
HAT8595325.1	TPA: hypothetical protein	*Legionella pneumophila*	173	173	95%	1,0E-51	38,80%	235
BCL64321.1	Outer membrane protein MIP	*Legionella pneumophila serogroup 3*	173	173	95%	1,0E-51	38,71%	231
HBI2945245.1	TPA: Macrophage infectivity potentiator Mip	*Legionella pneumophila*	173	173	95%	1,0E-51	38,40%	233
HAU1319624.1	TPA: FKBP-type peptidyl-prolyl cis-trans isomerase	*Legionella pneumophila*	173	173	95%	1,0E-51	38,40%	235
HBD7144128.1	TPA: Macrophage infectivity potentiator Mip	*Legionella pneumophila*	172	172	95%	2,0E-51	38,40%	233
HCD9490600.1	TPA: Macrophage infectivity potentiator Mip	*Legionella pneumophila*	172	172	95%	2,0E-51	38,40%	233
HAT7953900.1	TPA: hypothetical protein	*Legionella pneumophila*	172	172	95%	2,0E-51	38,40%	235
CAD42887.1	Macrophage infectivity potentiator	*Legionella pneumophila serogroup 1*	172	172	95%	2,0E-51	38,40%	233
HAT9076908.1	TPA: hypothetical protein	*Legionella pneumophila subsp. pneumophila*	172	172	95%	3,0E-51	38,40%	235
WP_061504390.1	Macrophage infectivity potentiator Mip	*Legionella*	172	172	95%	3,0E-51	38,40%	233
HAU1152645.1	TPA: FKBP-type peptidyl-prolyl cis-trans isomerase	*Legionella pneumophila*	172	172	95%	3,0E-51	38,40%	235
HAT8180409.1	TPA: hypothetical protein	*Legionella pneumophila*	172	172	95%	4,0E-51	38,40%	233
WP_040184983.1	Macrophage infectivity potentiator Mip	*Legionella pneumophila*	172	172	95%	4,0E-51	38,40%	233
WP_061512860.1	Macrophage infectivity potentiator Mip	*Legionella*	172	172	95%	4,0E-51	38,40%	233
HAT6809143.1	TPA: hypothetical protein	*Legionella pneumophila*	172	172	95%	4,0E-51	38,40%	235
WP_011213317.1	Macrophage infectivity potentiator Mip	*Legionella pneumophila*	172	172	95%	4,0E-51	38,40%	233
WP_011214989.1	Macrophage infectivity potentiator Mip	*Legionella pneumophila*	172	172	95%	5,0E-51	38,40%	233
HAT8907207.1	TPA: hypothetical protein	*Legionella pneumophila subsp. pneumophila*	171	171	95%	5,0E-51	38,40%	235
CAD42890.1	Macrophage infectivity potentiator	*Legionella pneumophila serogroup 8*	171	171	95%	5,0E-51	38,40%	236
HAT7072221.1	TPA: hypothetical protein	*Legionella pneumophila*	171	171	95%	5,0E-51	38,40%	235
AAU26880.1	Macrophage infectivity potentiator (Mip)	*Legionella pneumophila subsp. pneumophila str. Philadelphia 1*	171	171	95%	6,0E-51	38,40%	235
AEW51083.1	Macrophage infectivity potentiator (Mip)	*Legionella pneumophila subsp. pneumophila ATCC 43290*	171	171	95%	7,0E-51	38,40%	235
BCL64447.1	Outer membrane protein MIP	*Legionella pneumophila serogroup 7*	170	170	95%	2,0E-50	38,31%	231
BCL64252.1	Outer membrane protein MIP	*Legionella pneumophila serogroup 9*	170	170	95%	2,0E-50	38,31%	231
BCL64738.1	Outer membrane protein MIP	*Legionella pneumophila serogroup 14*	170	170	95%	2,0E-50	38,31%	231
AEY75264.1	Macrophage infectivity potentiator	*Legionella pneumophila*	170	170	94%	3,0E-50	39,44%	235
HAT5044632.1	TPA: FKBP-type peptidyl-prolyl cis-trans isomerase	*Legionella pneumophila*	160	160	91%	7,0E-47	38,49%	220
UTH72215.1	Macrophage infectivity potentiator	*Legionella pneumophila*	149	149	85%	9,0E-43	39,19%	199
UTH72214.1	Macrophage infectivity potentiator	*Legionella pneumophila*	148	148	76%	3,0E-42	40,00%	194
ADR82274.1	Macrophage infectivity potentiator	*Legionella pneumophila*	148	148	87%	4,0E-42	36,96%	214
ADR82273.1	Macrophage infectivity potentiator	*Legionella pneumophila*	147	147	88%	6,0E-42	36,91%	214
ALK24285.1	Mip	*Legionella pneumophila*	145	145	88%	3,0E-41	37,39%	207
ADR82275.1	Macrophage infectivity potentiator	*Legionella pneumophila*	145	145	88%	4,0E-41	36,80%	213
AAB81367.1	Macrophage infectivity potentiator protein	*Legionella pneumophila serogroup 5*	143	143	84%	2,0E-40	37,56%	204
AFX72766.1	Macrophage infectivity potentiator	*Legionella pneumophila*	142	142	85%	4,0E-40	37,22%	202
AAB86706.1	Macrophage infectivity potentiator protein	*Legionella pneumophila*	142	142	86%	5,0E-40	36,61%	204
CAH17708.2	Macrophage infectivity potentiator	*Legionella pneumophila*	142	142	81%	7,0E-40	39,44%	202
AAB81381.1	Macrophage infectivity potentiator protein	*Legionella pneumophila serogroup 1*	142	142	86%	7,0E-40	36,61%	202
AAB81365.1	Macrophage infectivity potentiator protein	*Legionella pneumophila serogroup 3*	142	142	84%	7,0E-40	37,10%	199
AFP92004.1	Macrophage infectivity potentiator	*Legionella pneumophila serogroup 8*	142	142	85%	7,0E-40	36,94%	200
CAH17706.1	Macrophage infectivity potentiator	*Legionella pneumophila*	142	142	86%	9,0E-40	36,61%	202
AAB81369.1	Macrophage infectivity potentiator protein	*Legionella pneumophila serogroup 7*	142	142	86%	9,0E-40	36,61%	204
CAH17718.1	Macrophage infectivity potentiator	*Legionella pneumophila*	142	142	84%	9,0E-40	37,10%	202
CAH17720.1	Macrophage infectivity potentiator	*Legionella pneumophila*	142	142	84%	1,0E-39	37,10%	202
AAB81366.1	Macrophage infectivity potentiator protein	*Legionella pneumophila serogroup 4*	142	142	86%	1,0E-39	36,61%	204
CAH17704.1	Macrophage infectivity potentiator	*Legionella pneumophila*	141	141	86%	1,0E-39	36,61%	202
AAB81379.1	Macrophage infectivity potentiator protein	*Legionella pneumophila serogroup 1*	141	141	84%	1,0E-39	37,27%	201
AAX85461.1	Macrophage infectivity potentiator	*Legionella pneumophila*	141	141	84%	2,0E-39	37,27%	200
AAB81370.1	Macrophage infectivity potentiator protein	*Legionella pneumophila serogroup 8*	141	141	84%	2,0E-39	37,27%	202
CAH17707.1	Macrophage infectivity potentiator	*Legionella pneumophila*	141	141	84%	2,0E-39	37,27%	201
AAB81364.1	Macrophage infectivity potentiator protein	*Legionella pneumophila serogroup 2*	141	141	84%	2,0E-39	37,27%	202
AAV97866.1	Macrophage infectivity potentiator	*Legionella pneumophila*	140	140	84%	2,0E-39	37,27%	200
CAH17705.1	Macrophage infectivity potentiator	*Legionella pneumophila*	140	140	84%	2,0E-39	37,27%	201
UTH72213.1	Macrophage infectivity potentiator	*Legionella pneumophila*	139	139	82%	6,0E-39	37,67%	197
CAH17832.1	Macrophage infectivity potentiator	*Legionella pneumophila*	139	139	84%	7,0E-39	36,20%	202
CAH17719.1	Macrophage infectivity potentiator	*Legionella pneumophila*	139	139	86%	8,0E-39	36,16%	202
CAI53728.1	Mip protein	*Legionella pneumophila subsp. pneumophila str. Philadelphia 1*	135	135	79%	1,0E-37	37,98%	186
CAI53736.1	Mip protein	*Legionella pneumophila subsp. pneumophila str. Philadelphia 1*	134	134	76%	3,0E-37	37,69%	183
CRR57457.1	Peptidyl-prolyl cis-trans isomerase Mip precursor	*Pseudomonas aeruginosa*	139	139	72%	3,0E-37	39,68%	325
CAI53731.1	Mip protein	*Legionella pneumophila subsp. pneumophila str. Philadelphia 1*	134	134	76%	4,0E-37	37,69%	186
AAB81384.1	Macrophage infectivity potentiator protein	*Legionella pneumophila serogroup 1*	133	133	82%	1,0E-36	36,28%	196
CAD42886.1	Macrophage infectivity potentiator	*Legionella pneumophila serogroup 1*	134	134	95%	2,0E-36	33,20%	232
CAI53734.1	Mip protein	*Legionella pneumophila subsp. pneumophila str. Philadelphia 1*	131	131	79%	6,0E-36	37,38%	186
CAI53727.1	Mip protein	*Legionella pneumophila subsp. pneumophila str. Philadelphia 1*	129	129	74%	4,0E-35	36,92%	180
CAI53737.1	Mip protein	*Legionella pneumophila subsp. pneumophila str. Philadelphia 1*	129	129	74%	4,0E-35	36,92%	179
AHI88013.1	Macrophage infectivity potentiator	*Legionella pneumophila*	126	126	71%	5,0E-34	37,97%	174
EIU2598685.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Pseudomonas aeruginosa*	128	128	98%	6,0E-34	34,35%	253
AHI88045.1	Macrophage infectivity potentiator	*Legionella pneumophila*	125	125	71%	7,0E-34	37,97%	174
AHI87995.1	Macrophage infectivity potentiator	*Legionella pneumophila*	125	125	71%	7,0E-34	37,97%	174
AHI87997.1	Macrophage infectivity potentiator	*Legionella pneumophila*	125	125	71%	9,0E-34	37,97%	174
HBP5807692.1	TPA: FKBP-type peptidyl-prolyl cis-trans isomerase	*Pseudomonas aeruginosa*	127	127	98%	1,0E-33	34,35%	253
WP_196732902.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Pseudomonas aeruginosa*	127	127	98%	2,0E-33	34,35%	253
ABK30067.1	Macrophage infectivity potentiator	*Legionella pneumophila*	124	124	71%	3,0E-33	37,84%	173
WP_174215295.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Pseudomonas aeruginosa*	126	126	98%	3,0E-33	34,35%	253
ABK30090.1	Macrophage infectivity potentiator	*Legionella pneumophila*	124	124	71%	3,0E-33	37,84%	173
ABK30061.1	Macrophage infectivity potentiator	*Legionella pneumophila*	124	124	71%	3,0E-33	37,84%	173
WP_023129599.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Pseudomonas aeruginosa*	126	126	98%	4,0E-33	33,97%	253
WP_034021053.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Pseudomonas aeruginosa*	125	125	98%	5,0E-33	33,97%	253
WP_134313069.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Pseudomonas aeruginosa*	125	125	98%	5,0E-33	33,97%	253
WP_124783419.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Pseudomonas aeruginosa*	125	125	98%	6,0E-33	33,97%	253
MCO2610411.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Pseudomonas aeruginosa*	125	125	97%	6,0E-33	34,23%	237
WP_179118900.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Pseudomonas aeruginosa*	125	125	98%	7,0E-33	33,97%	253
MBG7008153.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Pseudomonas aeruginosa*	125	125	98%	8,0E-33	33,97%	253
WP_043082757.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Pseudomonas aeruginosa*	125	125	98%	8,0E-33	33,97%	253
WP_125028177.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Pseudomonas aeruginosa*	125	125	98%	8,0E-33	33,97%	253
WP_015502605.1	FKBP-type peptidyl-prolyl cis-trans isomerase	*Pseudomonas aeruginosa*	125	125	100%	8,0E-33	33,71%	253

Tabla S7. Resultados Blastp de WP_016210800.1 de *P. salmonis* contra toda la base de datos excluyendo *Proteobacteria*.

Blastp de WP_016210800.1 de *P. salmonis* contra toda la base de datos excluyendo *Proteobacteria*								
Accesión	**Nombre descriptivo (NCBI)**	**Especie**	**Puntaje máximo**	**Puntaje total**	**Cobertura**	**E-value**	**Porcentaje identidad**	**Longitud de accesión**
PRP61050.1	Disulfide bond formation protein DsbA	Bacillus halotolerans	243	243	43%	1,0E-78	100,00%	120
MBS7036608.1	Thioredoxin domain-containing protein	Bifidobacterium sp.	231	231	100%	7,0E-72	43,97%	262
VTQ56480.1	Protein-disulfide isomerase	Campylobacter jejuni	230	230	88%	3,0E-71	49,80%	264
KAI3492047.1	Hypothetical protein L1887_43593	Cichorium endivia	230	230	99%	3,0E-71	45,04%	262
ALJ52217.1	DSBA oxidoreductase	Uncultured bacterium	219	219	89%	7,0E-67	47,20%	263
MZG82426.1	DsbA family protein	Photobacterium lucens	217	217	90%	5,0E-66	45,38%	259
WP_129710690.1	DsbA family protein	Priestia megaterium	188	188	88%	5,0E-55	42,98%	265
KAH8361279.1	Hypothetical protein KR084_009366	Drosophila pseudotakahashii	187	187	84%	2,0E-51	40,00%	532
AEP14554.1	His-Flag-Francisella lipoprotein	Synthetic construct	173	173	69%	5,0E-48	46,88%	352
AAX77909.1	Unknown protein	Synthetic construct	173	173	69%	2,0E-47	46,88%	400
NVJ11123.1	DsbA family protein	Myxococcus sp. AM001	150	150	56%	1,0E-41	49,04%	159
MBS6124126.1	DsbA family protein	Veillonella sp.	135	135	89%	6,0E-34	34,12%	314
MBX4425979.1	Hypothetical protein	Mycobacterium tuberculosis	125	125	33%	2,0E-32	55,91%	93
NUB10178.1	DsbA family protein	Azospirillum baldaniorum	129	129	74%	3,0E-32	37,25%	251
MBX4293342.1	Hypothetical protein	Mycobacterium tuberculosis	125	125	48%	5,0E-32	47,37%	141
THJ12125.1	DsbA family protein	Nitrospira sp. CG24C	127	127	83%	2,0E-31	33,33%	247
MBV8552641.1	Thioredoxin domain-containing protein	Acidobacteriaceae bacterium	127	127	72%	2,0E-31	35,78%	263
AAW50001.1	Hypothetical protein FTT0507	Synthetic construct	128	128	67%	2,0E-31	36,84%	290
MCG3773779.1	Hypothetical protein	Nitrospira sp.	127	127	81%	3,0E-31	33,63%	247
ULA63884.1	DsbA family protein	Nitrospira sp.	124	124	85%	4,0E-30	33,33%	248
MBK8377946.1	DsbA family protein	Nitrospira sp.	124	124	72%	5,0E-30	35,15%	259
UTW53597.1	DsbA family protein	Bacterium SCSIO 12827	124	124	76%	5,0E-30	33,81%	259
MBI3807892.1	DsbA family protein	Nitrospirota bacterium	123	123	70%	9,0E-30	36,22%	247
MBP6261903.1	DsbA family protein	Nitrospira sp.	123	123	75%	9,0E-30	34,12%	253
MBK9998451.1	DsbA family protein	Nitrospira sp.	122	122	72%	1,0E-29	32,50%	253
MCS6317396.1	DsbA family protein	Nitrospira sp.	122	122	75%	2,0E-29	35,55%	253
HAN93679.1	TPA: Hypothetical protein	Nitrospira sp.	121	121	72%	2,0E-29	34,17%	232
TSD84983.1	DsbA family protein	Mycobacterium sp. KBS0706	122	122	76%	2,0E-29	33,49%	250
TKB76053.1	DsbA family protein	Nitrospira sp.	122	122	74%	3,0E-29	34,95%	247
NYZ21610.1	DsbA family protein	Azospirillum oleiclasticum	121	121	73%	3,0E-29	32,67%	245
TKB52271.1	DsbA family protein	Nitrospira sp.	123	123	70%	4,0E-29	36,79%	335
WP_080880231.1	DsbA family protein	Nitrospira sp. ND1	121	121	72%	5,0E-29	34,17%	253
NOS80731.1	DsbA family protein	Nitrospira sp.	123	123	74%	5,0E-29	34,95%	315
CBK43203.1	putative Oxidoreductase, DsbA-like	Nitrospira defluvii	119	119	73%	2,0E-28	33,66%	253
MCS6288083.1	DsbA family protein	Nitrospira sp.	119	119	73%	4,0E-28	34,15%	253
MCG8468789.1	DsbA family protein	Gemmatimonadota bacterium	119	119	81%	5,0E-28	33,19%	267
MCI1279017.1	DsbA family protein	Nitrospira sp.	118	118	80%	5,0E-28	32,14%	253
MBX3302440.1	DsbA family protein	Nitrospira sp.	119	119	84%	5,0E-28	30,96%	258
TKB86284.1	DsbA family protein	Nitrospira sp.	117	117	70%	6,0E-28	34,72%	209
WHZ24667.1	27kDa Outer membrane protein	Nitrospira sp.	118	118	85%	7,0E-28	31,22%	253
OAI49833.1	Hypothetical protein AYO43_00200	Nitrospira sp. SCGC AG-212-E16	118	118	70%	9,0E-28	38,19%	257
EKD91984.1	Outer membrane protein	Uncultured bacterium	118	118	75%	2,0E-27	38,28%	304
MBI1964184.1	DsbA family protein	Candidatus Rokubacteria bacterium	116	116	73%	2,0E-27	31,53%	240
WP_213042437.1	DsbA family protein	Nitrospira defluvii	117	117	84%	2,0E-27	32,19%	253
MBH0208670.1	DsbA family protein	Nitrospira sp.	117	117	77%	3,0E-27	32,41%	257
MCS6265169.1	DsbA family protein	Nitrospira sp.	116	116	73%	5,0E-27	32,68%	253
KOX44642.1	DSBA oxidoreductase	Streptomyces purpurogeneiscleroticus	115	115	83%	7,0E-27	31,33%	260
MBS0169490.1	DsbA family protein	Nitrospira sp.	115	115	83%	7,0E-27	31,49%	253
MBU6481728.1	DsbA family protein	Nitrospirota bacterium	115	115	90%	7,0E-27	32,06%	257
MBU6434051.1	DsbA family protein	Nitrospirota bacterium	115	115	83%	8,0E-27	33,48%	231
MBI2155362.1	DsbA family protein	Candidatus Rokubacteria bacterium	115	115	72%	9,0E-27	31,66%	240
MBI2492712.1	DsbA family protein	Candidatus Rokubacteria bacterium	115	115	72%	1,0E-26	31,66%	240
MBS0155392.1	DsbA family protein	Nitrospira sp.	115	115	70%	1,0E-26	33,67%	257
MBE7245846.1	Thioredoxin domain-containing protein	Actinomycetospora chiangmaiensis	115	115	80%	1,0E-26	31,70%	261
WHZ16120.1	27kDa Outer membrane protein	Nitrospira sp.	114	114	77%	1,0E-26	33,18%	233
MBL8043714.1	DsbA family protein	Nitrospira sp.	114	114	72%	2,0E-26	31,68%	253
MCG3777540.1	Disulfide bond formation protein D	Nitrospira sp.	114	114	70%	2,0E-26	35,90%	258
MBP6200597.1	DsbA family protein	Nitrospira sp.	113	113	60%	2,0E-26	34,52%	215
TKB65457.1	DsbA family protein	Nitrospira sp.	114	114	70%	2,0E-26	35,20%	257
MBD24503.1	Hypothetical protein	Candidatus Marinimicrobia bacterium	114	114	84%	2,0E-26	30,77%	255
MBA5865961.1	Thioredoxin domain-containing protein	Nitrospira sp. CR1.3	114	114	85%	2,0E-26	30,77%	264
MCK6493046.1	DsbA family protein	Nitrospira sp.	114	114	74%	3,0E-26	32,21%	246
MBA5871703.1	Thioredoxin domain-containing protein	Nitrospira sp. CR2.1	114	114	83%	3,0E-26	32,34%	253
NJL08029.1	DsbA family protein	Methylacidiphilales bacterium	114	114	73%	3,0E-26	35,12%	270
MBA5863078.1	Thioredoxin domain-containing protein	Nitrospira sp. CR1.1	114	114	72%	3,0E-26	31,68%	273
MBV6470602.1	Hypothetical protein	Nitrospirota bacterium	114	114	74%	3,0E-26	32,21%	253
MBX3327954.1	DsbA family protein	Nitrospira sp.	114	114	84%	3,0E-26	32,33%	257
MBL8071680.1	DsbA family protein	Nitrospira sp.	114	114	73%	4,0E-26	32,68%	253
MBS0165419.1	DsbA family protein	Nitrospira sp.	114	114	70%	4,0E-26	33,16%	257
MBX3120872.1	DsbA family protein	Fimbriimonadaceae bacterium	113	113	72%	5,0E-26	31,66%	255
CAE7594645.1	NhaA2	Symbiodinium microadriaticum	113	113	77%	5,0E-26	32,57%	239
MBI4537564.1	DsbA family protein	Candidate division NC10 bacterium	113	113	74%	5,0E-26	32,69%	254
MBX3120844.1	DsbA family protein	Fimbriimonadaceae bacterium	113	113	72%	5,0E-26	32,18%	255
MBI2215682.1	DsbA family protein	Candidatus Rokubacteria bacterium	113	113	72%	5,0E-26	33,50%	249
MCH2314703.1	DsbA family protein	SAR202 cluster bacterium	113	113	84%	6,0E-26	28,76%	254
MBM4440574.1	DsbA family protein	Candidatus Rokubacteria bacterium	112	112	80%	8,0E-26	33,18%	246
WP_173044195.1	DsbA family protein	Nitrospira sp. KM1	113	113	70%	8,0E-26	34,18%	257
HAP40767.1	TPA: Hypothetical protein	Nitrospira sp.	113	113	72%	1,0E-25	32,18%	275
MCC6862737.1	Thioredoxin domain-containing protein	Bryobacterales bacterium	112	112	81%	1,0E-25	28,25%	267
TGS95856.1	DsbA family protein	Bacterium M00.F.Ca.ET.177.01.1.1	112	112	82%	1,0E-25	34,47%	263
EKD77533.1	Outer membrane protein	Uncultured bacterium	112	112	76%	2,0E-25	35,81%	284
MCC6967099.1	DsbA family protein	Nitrospira sp.	112	112	78%	2,0E-25	32,42%	253
MCA9451731.1	Thioredoxin domain-containing protein	Nitrospira sp.	112	112	79%	2,0E-25	32,29%	259
MCA9500813.1	DsbA family protein	Nitrospira sp.	112	112	81%	2,0E-25	32,60%	270
GBE42393.1	Disulfide bond formation protein D precursor	Bacterium BMS3Bbin10	111	111	83%	4,0E-25	32,62%	268
PYN46495.1	Hypothetical protein DME00_18805	Candidatus Rokubacteria bacterium	110	110	73%	4,0E-25	35,64%	250
WP_143838713.1	DsbA family protein	Nitrospira cf. moscoviensis SBR1015	110	110	63%	4,0E-25	32,76%	218
MYH22497.1	DsbA family protein	Acidobacteriota bacterium	110	110	73%	5,0E-25	31,25%	249
NWF74060.1	DsbA family protein	Nitrospirota bacterium	110	110	78%	5,0E-25	34,09%	257
MYA97510.1	DsbA family protein	Nitrospinota bacterium	111	111	73%	5,0E-25	33,82%	275
PYN10701.1	Hypothetical protein DME05_26550	Candidatus Rokubacteria bacterium	110	110	73%	6,0E-25	35,64%	250
MBS1117329.1	Putative Oxidoreductase, DsbA-like	Candidate division NC10 bacterium	110	110	74%	7,0E-25	32,21%	249
MYE43090.1	DsbA family protein	Acidobacteriota bacterium	110	110	73%	8,0E-25	31,25%	249
WP_172834348.1	DsbA family protein	Nitrospira japonica	110	110	74%	8,0E-25	34,31%	256
MBP1778935.1	Putative Oxidoreductase, DsbA-like	Candidate division NC10 bacterium	109	109	73%	9,0E-25	31,55%	216
MCL6645840.1	DsbA family protein	Dehalococcoidia bacterium	109	109	75%	9,0E-25	31,10%	232
MBE7202276.1	Thioredoxin domain-containing protein	Parafilimonas terrae	110	110	75%	9,0E-25	31,43%	260
MXW72027.1	DsbA family protein	Acidobacteriota bacterium	109	109	73%	1,0E-24	31,25%	249
NJO54140.1	DsbA family protein	Bacteroidales bacterium	110	110	73%	1,0E-24	34,15%	275
TFG64069.1	DsbA family protein	Nitrospirales bacterium	110	110	79%	1,0E-24	33,93%	260

Tabla S8. Resultados Blastp de WP_016210800.1 de *P. salmonis* contra organismos filogenéticamente cercanos a *P. salmonis*.

Blastp de WP_016210800.1 de *P. salmonis* contra *L. pneumophila*, *P. aeruginosa* y *C. burnetii*								
Accesión	Nombre descriptivo (NCBI)	Especie	Puntaje máximo	Puntaje total	Cobertura	E-value	Porcentaje identidad	Longitud de accesión
MXH37503.1	Thioredoxin domain-containing protein	Pseudomonas aeruginosa	233,0	233,0	90%	2,0E-74	48,61%	261
MXH38692.1	Thioredoxin domain-containing protein	Pseudomonas aeruginosa	197,0	197,0	95%	1,0E-60	39,25%	262
WP_000031378.1	DsbA family protein	Gammaproteobacteria	151,0	151,0	88%	1,0E-42	35,34%	269
MBN0668848.1	DsbA family protein	Pseudomonas aeruginosa	142,0	142,0	42%	2,0E-40	54,24%	141
MBN0009376.1	Thioredoxin domain-containing protein	Pseudomonas aeruginosa	133,0	133,0	37%	3,0E-37	55,88%	110
OYK83150.1	Hypothetical protein CbuD7D7780_01075	Coxiella burnetii	129,0	129,0	77%	4,0E-34	36,41%	252
BAA20508.1	27kDa outer membrane protein	Coxiella burnetii	129,0	129,0	75%	5,0E-34	37,26%	252
WP_284185834.1	DsbA family protein	Coxiella burnetii	128,0	128,0	77%	6,0E-34	36,41%	248
WP_005769970.1	DsbA family protein	Coxiella burnetii	128,0	128,0	77%	7,0E-34	36,41%	252
AAG41984.1	27kDa outer membrane protein	Coxiella burnetii	127,0	127,0	75%	1,0E-33	36,79%	245
WP_268828498.1	DsbA family protein	Coxiella burnetii	127,0	127,0	75%	1,0E-33	36,79%	248
AAG41986.1	27kDa outer membrane protein	Coxiella burnetii	127,0	127,0	77%	2,0E-33	35,94%	245
WP_010958530.1	DsbA family protein	Coxiella burnetii	127,0	127,0	75%	2,0E-33	36,79%	252
PNT87582.1	Hypothetical protein C2L89_08700	Coxiella burnetii	127,0	127,0	75%	2,0E-33	36,79%	252
WP_238024501.1	DsbA family protein	Coxiella burnetii	127,0	127,0	77%	3,0E-33	35,94%	252
ADJ96886.1	27 kDa outer membrane protein	Coxiella burnetii	125,0	125,0	77%	3,0E-33	35,68%	207
WP_284185806.1	DsbA family protein	Coxiella burnetii	126,0	126,0	75%	6,0E-33	36,32%	248
BAA20493.1	27kDa outer membrane protein	Coxiella burnetii	126,0	126,0	75%	6,0E-33	36,32%	252
WP_040953438.1	DsbA family protein	Coxiella burnetii	126,0	126,0	75%	6,0E-33	36,32%	252
WP_005772802.1	DsbA family protein	Coxiella burnetii	125,0	125,0	77%	1,0E-32	35,94%	252
BAA20496.1	27kDa outer membrane protein	Coxiella burnetii	125,0	125,0	77%	1,0E-32	35,94%	252
WP_012569542.1	Unnamed protein product	Coxiella burnetii	125,0	125,0	77%	1,0E-32	35,94%	252
BAA20499.1	27kDa outer membrane protein	Coxiella burnetii	124,0	124,0	77%	2,0E-32	35,94%	252
MBN0530862.1	DsbA family protein	Pseudomonas aeruginosa	119,0	119,0	45%	5,0E-32	48,39%	116
BAA20498.1	27kDa outer membrane protein	Coxiella burnetii	123,0	123,0	77%	9,0E-32	36,24%	252
QOC63421.1	Outer membrane protein	Coxiella burnetii	115,0	115,0	63%	1,0E-29	36,21%	192
AIQ80295.1	Outer membrane protein	Coxiella burnetii	112,0	112,0	60%	9,0E-29	37,13%	162
HAT1767894.1	TPA: DsbA family protein	Legionella pneumophila	115,0	115,0	82%	1,0E-28	36,40%	261
MBN0772888.1	DsbA family protein	Pseudomonas aeruginosa	110,0	110,0	32%	2,0E-28	53,41%	101
WP_044497326.1	DsbA family protein	Legionella pneumophila	112,0	112,0	84%	1,0E-27	37,02%	261
MBN0379196.1	DsbA family protein	Pseudomonas aeruginosa	108,0	108,0	42%	1,0E-27	50,00%	120
WP_027222026.1	DsbA family protein	Legionella pneumophila	112,0	112,0	82%	1,0E-27	37,72%	261
HAT6979195.1	TPA: thioredoxin domain-containing protein	Legionella pneumophila	112,0	112,0	82%	2,0E-27	36,84%	261
HCC0304814.1	TPA: DsbA family protein	Legionella pneumophila	112,0	112,0	82%	2,0E-27	36,40%	261
HBD7396830.1	TPA: DsbA family protein	Legionella pneumophila	112,0	112,0	80%	2,0E-27	35,87%	262
HAZ7571760.1	TPA: DsbA family protein	Legionella pneumophila	111,0	111,0	84%	3,0E-27	36,17%	261
HAU1150576.1	TPA: DsbA family protein	Legionella pneumophila	111,0	111,0	82%	3,0E-27	36,40%	261
HAU0224829.1	TPA: DsbA family protein	Legionella pneumophila	111,0	111,0	82%	4,0E-27	36,40%	261
WP_061512522.1	DsbA family protein	Legionella	111,0	111,0	84%	4,0E-27	36,60%	261
WP_061637949.1	DsbA family protein	Legionella pneumophila	111,0	111,0	82%	4,0E-27	36,40%	261
WP_061483997.1	DsbA family protein	Legionella pneumophila	111,0	111,0	82%	4,0E-27	37,28%	261
WP_014841915.1	DsbA family protein	Legionella pneumophila	110,0	110,0	82%	5,0E-27	36,40%	261
WP_010947567.1	DsbA family protein	Legionella pneumophila	110,0	110,0	82%	5,0E-27	36,40%	261
HAT8179441.1	TPA: thioredoxin domain-containing protein	Legionella pneumophila	110,0	110,0	84%	5,0E-27	36,17%	261
WP_042237127.1	DsbA family protein	Legionella pneumophila	110,0	110,0	82%	5,0E-27	36,40%	261
WP_061636434.1	DsbA family protein	Legionella pneumophila	110,0	110,0	82%	5,0E-27	36,40%	261
HAU1248840.1	TPA: DsbA family protein	Legionella pneumophila	110,0	110,0	82%	5,0E-27	36,40%	261
WP_027264694.1	DsbA family protein	Legionella pneumophila	110,0	110,0	82%	5,0E-27	36,40%	261
WP_028378051.1	DsbA family protein	Legionella pneumophila	110,0	110,0	82%	1,0E-26	36,40%	261
WP_062727944.1	DsbA family protein	Legionella pneumophila	109,0	109,0	82%	1,0E-26	36,40%	260
WP_061691747.1	DsbA family protein	Legionella pneumophila	109,0	109,0	82%	1,0E-26	35,96%	261
HAT1594942.1	TPA: DsbA family protein	Legionella pneumophila	109,0	109,0	82%	1,0E-26	36,96%	261
HBD7071603.1	TPA: DsbA family protein	Legionella pneumophila	109,0	109,0	82%	1,0E-26	35,96%	261
WP_241010372.1	DsbA family protein	Legionella pneumophila	108,0	108,0	78%	2,0E-26	37,44%	240
AVB77357.1	Outer membrane protein	Coxiella burnetii	103,0	103,0	48%	1,0E-25	40,15%	134
WP_038838744.1	DsbA family protein	Legionella pneumophila	95,9	95,9	69%	8,0E-22	38,54%	213
MBN0839176.1	DsbA family protein	Pseudomonas aeruginosa	92,8	92,8	37%	1,0E-21	49,04%	112
QHB12871.1	Capsular outer membrane protein	Coxiella burnetii	92,8	92,8	54%	2,0E-21	35,33%	146
WAQ69489.1	Outer membrane protein	Coxiella burnetii	93,2	93,2	63%	3,0E-21	34,64%	164
QHB12872.1	Capsular outer membrane protein	Coxiella burnetii	92,8	92,8	54%	3,0E-21	35,33%	147
QHB12870.1	Capsular outer membrane protein	Coxiella burnetii	92,8	92,8	54%	3,0E-21	35,33%	145
HAT8971524.1	TPA: thioredoxin domain-containing protein	Legionella pneumophila subsp. pneumophila	93,6	93,6	55%	3,0E-21	39,47%	186
WAQ69494.1	Outer membrane protein	Coxiella burnetii	92,8	92,8	61%	3,0E-21	34,30%	161
WBV64161.1	DsbA family protein	Legionella pneumophila 130b	93,6	93,6	55%	5,0E-21	39,47%	207
QGY72265.1	Capsular outer membrane protein	Coxiella burnetii	91,3	91,3	53%	8,0E-21	34,69%	139
WAQ69492.1	Outer membrane protein	Coxiella burnetii	92,0	92,0	64%	9,0E-21	34,44%	165
WAQ69482.1	Outer membrane protein	Coxiella burnetii	91,3	91,3	60%	1,0E-20	34,50%	160
WAQ69493.1	Outer membrane protein	Coxiella burnetii	91,3	91,3	60%	1,0E-20	34,50%	160
MBN0763568.1	DsbA family protein	Pseudomonas aeruginosa	89,7	89,7	36%	1,0E-20	49,00%	109
QGY72266.1	Capsular outer membrane protein	Coxiella burnetii	90,9	90,9	54%	1,0E-20	34,90%	147
QGY72269.1	Capsular outer membrane protein	Coxiella burnetii	90,9	90,9	54%	1,0E-20	34,90%	145
WAQ69483.1	Outer membrane protein	Coxiella burnetii	91,3	91,3	60%	1,0E-20	34,50%	163
WAQ69486.1	Outer membrane protein	Coxiella burnetii	91,3	91,3	60%	1,0E-20	34,50%	161
WAQ69488.1	Outer membrane protein	Coxiella burnetii	90,1	90,1	60%	3,0E-20	34,12%	156
WAQ69490.1	Outer membrane protein	Coxiella burnetii	89,7	89,7	60%	5,0E-20	34,12%	162
WAQ69480.1	Outer membrane protein	Coxiella burnetii	89,7	89,7	60%	5,0E-20	34,32%	158
WAQ69481.1	Outer membrane protein	Coxiella burnetii	89,7	89,7	60%	5,0E-20	34,32%	157
QGY72271.1	Capsular outer membrane protein	Coxiella burnetii	89,0	89,0	53%	6,0E-20	34,69%	145
UZS59090.1	DsbA family protein	Coxiella burnetii	89,0	89,0	53%	7,0E-20	34,69%	149
WGU43377.1	Capsular outer membrane protein	Coxiella burnetii	88,6	88,6	56%	9,0E-20	35,22%	149
WAQ69487.1	Outer membrane protein	Coxiella burnetii	89,0	89,0	59%	1,0E-19	33,93%	155
WAQ69485.1	Outer membrane protein	Coxiella burnetii	87,8	87,8	53%	2,0E-19	34,69%	149
QBP37231.1	Capsular outer membrane protein	Coxiella burnetii	87,4	87,4	56%	3,0E-19	35,62%	146
QBP37232.1	Capsular outer membrane protein	Coxiella burnetii	87,4	87,4	54%	3,0E-19	35,71%	146
QGY72267.1	Capsular outer membrane protein	Coxiella burnetii	86,7	86,7	48%	3,0E-19	36,36%	130
WAQ69491.1	Outer membrane protein	Coxiella burnetii	87,4	87,4	56%	4,0E-19	34,59%	153
QGY72268.1	Capsular outer membrane protein	Coxiella burnetii	85,9	85,9	43%	4,0E-19	38,66%	115
WAQ69495.1	Outer membrane protein	Coxiella burnetii	86,7	86,7	52%	6,0E-19	34,48%	148
QBA88954.1	Outer membrane protein	Coxiella burnetii	85,5	85,5	55%	2,0E-18	34,39%	146
UPQ46238.1	Outer membrane protein	Coxiella burnetii	85,1	85,1	49%	2,0E-18	35,56%	141
UPQ46240.1	Outer membrane protein	Coxiella burnetii	85,1	85,1	49%	2,0E-18	35,56%	140
AYA62479.1	Outer membrane protein	Coxiella burnetii	84,3	84,3	46%	3,0E-18	36,72%	133
AYA62471.1	Outer membrane protein	Coxiella burnetii	84,3	84,3	46%	3,0E-18	36,72%	135
QGY72270.1	Capsular outer membrane protein	Coxiella burnetii	84,3	84,3	54%	3,0E-18	35,71%	141
UPQ46241.1	Outer membrane protein	Coxiella burnetii	83,6	83,6	46%	6,0E-18	35,94%	134
UPQ46239.1	Outer membrane protein	Coxiella burnetii	83,6	83,6	48%	6,0E-18	35,07%	138
UPQ46242.1	Outer membrane protein	Coxiella burnetii	83,2	83,2	44%	7,0E-18	36,89%	136
WAQ69484.1	Outer membrane protein	Coxiella burnetii	83,6	83,6	49%	7,0E-18	34,81%	144
QID05198.1	Outer membrane protein	Coxiella burnetii	83,2	83,2	46%	7,0E-18	35,94%	132
QID05199.1	Outer membrane protein	Coxiella burnetii	82,8	82,8	46%	9,0E-18	35,94%	132

Tabla S9. Resultados Blastp de WP_017376173.1 de *P. salmonis* contra toda la base de datos excluyendo *Proteobacteria*.

Blastp de WP_017376173.1 de *P. salmonis* contra toda la base de datos excluyendo *Proteobacteria*								
Accesión	Nombre descriptivo (NCBI)	Especie	Puntaje máximo	Puntaje total	Cobertura	E-value	Porcentaje identidad	Longitud de accesión
MBI5675186.1	OmpA family protein	*Nitrospirota bacterium*	156	156	98%	6,0E-41	31,14%	344
MBS1112070.1	Peptidoglycan-binding outer membrane protein	*Nitrospirota bacterium*	141	141	90%	2,0E-35	29,25%	329
PLX77249.1	Hypothetical protein C0615_05710	*Desulfuromonas sp.*	141	141	98%	3,0E-35	29,91%	324
WP_214299400.1	OmpA family protein	*Geobacter chapellei*	144	209	94%	4,0E-35	32,94%	477
OGP89592.1	Hypothetical protein A2031_04590	*Deltaproteobacteria bacterium*	140	140	99%	8,0E-35	30,11%	337
MCR5219892.1	OmpA family protein	*Bacterium*	138	138	98%	4,0E-34	28,95%	343
WP_225072957.1	OmpA family protein	*Desulfuromonas sp. CSMB_57*	138	138	99%	8,0E-34	28,85%	365
WP_012529806.1	OmpA family protein	*Citrifermentans bemidjiense*	140	140	98%	1,0E-33	30,29%	468
WP_026840066.1	OmpA family protein	*Citrifermentans bremense*	140	140	98%	1,0E-33	30,09%	468
PIP42605.1	Hypothetical protein COX19_00475	*Desulfobacterales bacterium*	136	136	99%	2,0E-33	29,97%	338
HBA87664.1	TPA: Hypothetical protein	*Geobacter sp.*	136	199	98%	2,0E-32	33,04%	464
OGP67307.1	Hypothetical protein A2W27_07365	*Deltaproteobacteria bacterium RBG_16_44_11*	133	133	97%	3,0E-32	29,53%	332
RII27159.1	Hypothetical protein CXR31_07860	*Geobacter sp.*	134	134	97%	2,0E-31	30,12%	461
WP_121764593.1	OmpA family protein	*Helicobacter burdigaliensis*	129	129	94%	4,0E-31	29,75%	309
NTW77141.1	Outer membrane beta-barrel domain-containing protein	*Syntrophaceae bacterium*	129	129	98%	7,0E-31	29,82%	335
WP_060663014.1	OmpA family protein	*Helicobacter pullorum*	129	129	94%	8,0E-31	30,06%	307
MBP6914897.1	OmpA family protein	*Syntrophaceae bacterium*	129	129	97%	1,0E-30	29,55%	329
SPD74082.1	Conserved exported hypothetical protein	*uncultured Desulfobacterium sp.*	129	129	97%	2,0E-30	30,84%	343
MBV1711425.1	OmpA family protein	*Desulfomicrobium sp.*	128	128	92%	3,0E-30	31,06%	338
PIP04950.1	Hypothetical protein COX52_14625	*Syntrophobacterales bacterium*	127	127	89%	6,0E-30	29,90%	349
HAO22398.1	TPA: Hypothetical protein	*Desulfobacteraceae bacterium*	127	127	99%	9,0E-30	29,58%	353
MBN1472400.1	Outer membrane beta-barrel domain-containing protein	*Syntrophaceae bacterium*	126	126	95%	9,0E-30	30,40%	330
OQX02940.1	Hypothetical protein BWK80_56800	*Desulfobacteraceae bacterium IS3*	127	127	99%	1,0E-29	29,30%	353
OGU08609.1	Hypothetical protein A2075_17540	*Geobacteraceae bacterium GWC2_58_44*	128	200	92%	2,0E-29	31,78%	464
NIO15887.1	OmpA family protein	*Deltaproteobacteria bacterium*	126	126	98%	2,0E-29	29,25%	366
HIS08703.1	TPA: OmpA family protein	*Candidatus Scatomorpha intestinipullorum*	125	125	94%	3,0E-29	29,11%	309
WP_054198121.1	OmpA family protein	*Helicobacter pullorum*	124	124	94%	3,0E-29	29,11%	308
WP_005021991.1	OmpA family protein	*Helicobacter pullorum*	124	124	94%	4,0E-29	29,97%	308
PID73976.1	Hypothetical protein CSB33_00935	*Desulfobacterales bacterium*	127	127	93%	4,0E-29	31,33%	474
HAL85705.1	TPA: Hypothetical protein	*Deferribacteraceae bacterium*	125	125	99%	5,0E-29	28,89%	360
WP_054195392.1	OmpA family protein	*Helicobacter pullorum*	123	123	94%	1,0E-28	28,80%	308
WP_006655115.1	OmpA family protein	*Helicobacter canadensis*	122	122	94%	1,0E-28	28,16%	306
OGU12128.1	Hypothetical protein A2075_09780	*Geobacteraceae bacterium GWC2_58_44*	125	125	95%	1,0E-28	30,61%	466
OGU10085.1	Hypothetical protein A2075_12360	*Geobacteraceae bacterium GWC2_58_44*	125	196	90%	2,0E-28	30,03%	449
WP_065827670.1	OmpA family protein	*Helicobacter pullorum*	122	122	94%	2,0E-28	28,80%	308
WP_278347641.1	OmpA family protein	*Helicobacter pullorum*	122	122	94%	2,0E-28	28,80%	308
WP_060661498.1	OmpA family protein	*Helicobacter pullorum*	122	122	94%	2,0E-28	29,65%	308
MCI5633780.1	OmpA family protein	*Helicobacter sp.*	122	122	94%	3,0E-28	26,81%	306
BEH11188.1	OmpA family protein	*Geobacter sulfurreducens subsp. ethanolicus*	125	201	98%	3,0E-28	31,04%	466
WP_111229557.1	OmpA family protein	*Helicobacter valdiviensis*	122	122	94%	3,0E-28	29,43%	307
MBP7015712.1	Outer membrane beta-barrel domain-containing protein	*Smithella sp.*	122	122	97%	3,0E-28	27,76%	326
UQZ89780.1	Porin	*Deltaproteobacteria bacterium Smac51*	122	122	98%	4,0E-28	27,46%	340
WP_183354351.1	OmpA family protein	*Geomonas silvestris*	124	201	96%	4,0E-28	29,39%	475
WP_136514170.1	OmpA family protein	*Geomonas edaphica*	124	202	98%	5,0E-28	29,03%	468
MBD5166092.1	OmpA family protein	*Helicobacter sp.*	120	120	95%	6,0E-28	27,50%	297
RQW85838.1	OmpA family protein	*Geobacter sp.*	122	122	97%	7,0E-28	29,48%	354
RJP86591.1	Outer membrane beta-barrel domain-containing protein	*Desulfobacteraceae bacterium*	121	121	97%	8,0E-28	30,03%	336
MCK9197372.1	OmpA family protein	*Syntrophales bacterium*	121	121	92%	9,0E-28	30,70%	346
WP_085812090.1	OmpA family protein	*Geoanaerobacter pelophilus*	123	123	98%	1,0E-27	30,18%	468
OGT96813.1	Hypothetical protein A2X80_09950	*Geobacteraceae bacterium GWB2_52_12*	123	192	92%	1,0E-27	29,43%	471
WP_185242817.1	OmpA family protein	*Citrifermentans bremense*	123	123	98%	1,0E-27	30,18%	468
HIJ95613.1	TPA: outer membrane beta-barrel domain-containing protein	*Desulfuromonadales bacterium*	121	121	90%	2,0E-27	28,49%	367
SPD72785.1	Conserved exported Hypothetical protein	*uncultured Desulfobacterium sp.*	120	120	100%	2,0E-27	28,23%	348
MBN1548165.1	OmpA family protein	*Syntrophaceae bacterium*	120	120	96%	2,0E-27	29,38%	330
WP_242099100.1	OmpA family protein	*Helicobacter sp. CaF467b*	119	119	89%	3,0E-27	28,15%	308
WP_250604272.1	OmpA family protein	*Helicobacter colisuis*	119	119	89%	3,0E-27	28,15%	314
WP_183362945.1	OmpA family protein	*Geomonas limicola*	122	196	96%	3,0E-27	29,43%	478
WP_250644545.1	OmpA family protein	*Helicobacter colisuis*	118	118	89%	8,0E-27	27,81%	308
WP_010941476.1	OmpA family protein	*Geobacter sulfurreducens*	121	198	98%	8,0E-27	32,24%	466
WP_112057123.1	OmpA family protein	*Helicobacter*	118	118	89%	9,0E-27	27,81%	308
MRR53616.1	OmpA family protein	*Deltaproteobacteria bacterium*	119	119	94%	1,0E-26	32,85%	356
MCE5264542.1	OmpA family protein	*Deltaproteobacteria bacterium*	119	119	97%	1,0E-26	28,85%	361
MBP6938560.1	Outer membrane beta-barrel domain-containing protein	*Deltaproteobacteria bacterium*	118	118	93%	2,0E-26	31,55%	348
WP_129127576.1	OmpA family protein	*Geomonas oryzae*	119	197	98%	3,0E-26	28,05%	470
WP_119331970.1	OmpA family protein	*Geobacter sulfurreducens*	119	199	98%	4,0E-26	31,94%	466
NCC84702.1	OmpA family protein	*Clostridia bacterium*	116	116	89%	5,0E-26	29,68%	329
NOX15385.1	TonB-dependent receptor	*Campylobacterota bacterium*	117	117	94%	5,0E-26	27,12%	354
PKN33547.1	Hypothetical protein CVU61_12690	*Deltaproteobacteria bacterium HGW-Deltaproteobacteria-19*	117	117	97%	7,0E-26	26,42%	364
MSM38153.1	OmpA family protein	*Geobacter sp.*	118	118	98%	8,0E-26	28,87%	459
WP_011941106.1	OmpA family protein	*Geotalea uraniireducens*	118	118	97%	9,0E-26	28,92%	454
WP_224981566.1	OmpA family protein	*Geomonas agri*	118	181	98%	1,0E-25	28,74%	475
KAF0156668.1	OmpA-OmpF porin OOP family	*Syntrophaceae bacterium*	116	116	92%	1,0E-25	28,99%	361
WP_108911183.1	OmpA family protein	*Helicobacter apodemus*	115	115	95%	1,0E-25	27,41%	308
WP_026944407.1	OmpA family protein	*Helicobacter rodentium*	114	114	94%	1,0E-25	28,39%	297
NMC75504.1	OmpA family protein	*Geobacteraceae bacterium*	116	116	91%	1,0E-25	29,04%	360
PKN67424.1	Hypothetical protein CVU54_16915	*Deltaproteobacteria bacterium HGW-Deltaproteobacteria-12*	115	115	92%	2,0E-25	27,94%	367
WP_273212697.1	OmpA family protein	*Helicobacter rodentium*	114	114	94%	2,0E-25	28,39%	297
WP_282000119.1	OmpA family protein	*Geotalea uraniireducens*	117	117	96%	2,0E-25	29,23%	467
VTS62409.1	Outer membrane porin F precursor	*Streptococcus dysgalactiae subsp. equisimilis*	115	115	97%	2,0E-25	29,21%	350
WP_215734045.1	OmpA family protein	*Geobacter grbiciae*	117	117	95%	2,0E-25	28,21%	456
WP_199387944.1	OmpA family protein	*Geomonas anaerohicana*	117	186	98%	3,0E-25	28,00%	477
WP_138121419.1	OmpA family protein	*Helicobacter sp. MIT 05-5294*	114	114	95%	3,0E-25	28,12%	298
WP_216499367.1	OmpA family protein	*Geomonas*	116	186	98%	4,0E-25	28,37%	474
MBN1473738.1	OmpA family protein	*Syntrophaceae bacterium*	114	114	100%	4,0E-25	29,97%	326
TLE16992.1	OmpA family protein	*Helicobacter apodemus*	113	113	95%	4,0E-25	26,79%	308
GAW65667.1	Membrane protein	*Geoanaerobacter pelophilus*	116	116	95%	5,0E-25	30,00%	459
MCK9336671.1	OmpA family protein	*Arcobacteraceae bacterium*	114	114	98%	5,0E-25	26,44%	341
WP_216511810.1	OmpA family protein	*Geomonas azotofigens*	116	184	98%	6,0E-25	28,29%	475
NPU82905.1	OmpA family protein	*Syntrophaceae bacterium*	114	114	97%	6,0E-25	26,76%	358
WP_238700652.1	OmpA family protein	*Helicobacter apodemus*	113	113	88%	6,0E-25	27,76%	297
WP_217299645.1	OmpA family protein	*Geomonas nitrogenifigens*	115	186	98%	6,0E-25	28,37%	474
MCK4536285.1	OmpA family protein	*Desulfuromonadales bacterium*	114	114	98%	9,0E-25	26,79%	395
WP_034290355.1	OmpA family protein	*Helicobacter sp. MIT 11-5569*	112	112	94%	9,0E-25	26,58%	308
WP_183361369.1	OmpA family protein	*Geomonas limicola*	115	190	96%	1,0E-24	30,89%	461
WP_039646234.1	OmpA family protein	*Geobacter*	115	192	98%	1,0E-24	31,33%	464
MBW2560933.1	Outer membrane beta-barrel domain-containing protein	*Deltaproteobacteria bacterium*	113	113	98%	1,0E-24	27,22%	348
WP_092188711.1	OmpA family protein	*Desulfomicrobium norvegicum*	112	112	84%	2,0E-24	29,41%	336
WP_115551424.1	OmpA family protein	*Helicobacter ganmani*	111	111	95%	2,0E-24	26,56%	294
WP_267524160.1	OmpA family protein	*Campylobacter sp. MG1*	112	112	83%	2,0E-24	29,68%	321
NLA40910.1	OmpA family protein	*Smithella sp.*	112	112	90%	2,0E-24	26,18%	363

Tabla S10. Resultados Blastp de WP_017376173.1 de *P. salmonis* contra organismos filogenéticamente cercanos a *P. salmonis*.

Blastp de WP_017376173.1 de *P. salmonis* contra *L. pneumophila*, *P. aeruginosa* y *C. burnetii*								
Accesión	**Nombre descriptivo (NCBI)**	**Especie**	**Puntaje máximo**	**Puntaje total**	**Cobertura**	**E-value**	**Porcentaje identidad**	**Longitud de accesión**
WP_070338528.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	118	118	97%	1,0E-28	30,06%	350
WP_227328239.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	118	118	97%	2,0E-28	29,49%	350
WP_112302711.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	117	117	97%	5,0E-28	29,49%	350
WP_231280432.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	117	117	97%	5,0E-28	29,21%	350
MBG4764837.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	116	116	97%	6,0E-28	29,21%	350
HBO2801504.1	TPA: outer membrane porin OprF	*Pseudomonas aeruginosa*	116	116	97%	7,0E-28	29,21%	350
WP_243260390.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	116	116	98%	9,0E-28	29,33%	349
WP_134315076.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	116	116	97%	9,0E-28	29,21%	350
WP_128677620.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	116	116	97%	9,0E-28	29,21%	350
MBH9311100.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	116	116	97%	9,0E-28	29,49%	350
HCK4843865.1	TPA: outer membrane porin OprF	*Pseudomonas aeruginosa*	116	116	97%	9,0E-28	29,49%	350
WP_034002471.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	116	116	97%	1,0E-27	29,21%	350
WP_132687599.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	116	116	97%	1,0E-27	29,78%	350
MBV6150621.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	116	116	97%	1,0E-27	29,21%	350
WP_070331993.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	116	116	97%	1,0E-27	29,78%	350
WP_132764427.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	116	116	97%	1,0E-27	29,21%	350
WP_116814306.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	1,0E-27	29,21%	350
WP_134286465.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	1,0E-27	29,21%	350
WP_122338775.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	1,0E-27	29,21%	350
HBO1566131.1	TPA: outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	1,0E-27	29,78%	350
HBN9932436.1	TPA: outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	1,0E-27	29,49%	350
WP_132585590.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	1,0E-27	29,21%	350
WP_124132211.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	1,0E-27	29,21%	350
HCE7278531.1	TPA: outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	1,0E-27	29,21%	350
WP_257359952.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	1,0E-27	29,78%	350
EIU2745708.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,78%	350
WP_219832405.1	OmpA family protein	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,78%	350
WCX37983.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,21%	345
MBG6664507.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,49%	350
MBG6553408.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,21%	350
WP_132737712.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,21%	350
WP_124199761.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,78%	350
WP_124984679.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,78%	350
WP_136200974.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,21%	350
MCO3805664.1	OmpA family protein	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,78%	350
WP_128668008.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,21%	350
MCO3433192.1	OmpA family protein	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,21%	350
WP_124124036.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,78%	350
WP_003087843.1	Outer membrane porin OprF	*Pseudomonas*	115	115	97%	2,0E-27	29,21%	350
WP_132893135.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,21%	350
HCG0906243.1	TPA: outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,21%	350
WP_129592549.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,21%	350
WP_039843162.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,21%	350
WP_128537535.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,21%	350
WP_128664175.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,21%	350
WP_134304455.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,21%	350
WP_124186845.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,21%	350
WP_132642916.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,21%	350
WP_128666243.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,21%	350
HBP1035254.1	TPA: OmpA family protein	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,21%	350
WP_235575026.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,21%	350
MBG6519767.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,21%	350
HBO6042264.1	TPA: OmpA family protein	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,21%	350
WP_134282053.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,21%	350
WP_134312624.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	98%	2,0E-27	29,05%	350
WP_126867486.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,21%	350
MBG4560762.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,21%	350
WP_134483298.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,78%	350
HCG1011491.1	TPA: outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,21%	350
WP_134277007.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,21%	350
HBO5768941.1	TPA: OmpA family protein	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,21%	350
HCF5437220.1	TPA: outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,21%	350
MBG6536906.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	2,0E-27	29,21%	350
WP_100882816.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	3,0E-27	29,21%	350
WP_093945253.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	3,0E-27	29,21%	350
WP_033973003.1	Outer membrane porin OprF	*Pseudomonas*	115	115	97%	3,0E-27	28,81%	350
WP_086353283.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	96%	3,0E-27	29,30%	350
WP_126675958.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	3,0E-27	29,21%	350
EJD6743210.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	115	115	97%	3,0E-27	29,25%	350
HCH6837143.1	TPA: outer membrane porin OprF	*Pseudomonas aeruginosa*	114	114	97%	3,0E-27	29,21%	350
WP_160939807.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	114	114	97%	3,0E-27	28,69%	350
HCF0005749.1	TPA: outer membrane porin OprF	*Pseudomonas aeruginosa*	114	114	97%	3,0E-27	29,21%	350
HBO2181831.1	TPA: outer membrane porin OprF	*Pseudomonas aeruginosa*	114	114	97%	3,0E-27	28,93%	350
WP_148711207.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	114	114	97%	3,0E-27	29,21%	350
WP_181858766.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	114	114	97%	3,0E-27	29,21%	350
WP_136310541.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	114	114	97%	4,0E-27	29,21%	350
WP_226021066.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	114	114	97%	4,0E-27	29,21%	350
WP_272413678.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	114	114	97%	4,0E-27	29,33%	350
WP_219788516.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	114	114	97%	4,0E-27	29,78%	350
WP_124168677.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	114	114	97%	4,0E-27	28,93%	350
WP_124089853.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	114	114	96%	4,0E-27	29,30%	350
WCX92980.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	114	114	97%	5,0E-27	28,65%	352
WP_282393411.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	114	114	97%	5,0E-27	28,69%	350
HCI3991090.1	TPA: outer membrane porin OprF	*Pseudomonas aeruginosa*	114	114	96%	5,0E-27	29,26%	350
WP_126644241.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	114	114	97%	5,0E-27	29,33%	350
HCK5043905.1	TPA: outer membrane porin OprF	*Pseudomonas aeruginosa*	114	114	97%	5,0E-27	29,78%	350
MBG6431981.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	114	114	97%	5,0E-27	28,93%	350
WP_128711317.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	114	114	97%	5,0E-27	29,21%	350
WP_124142147.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	114	114	97%	5,0E-27	29,21%	350
WP_134320359.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	114	114	97%	5,0E-27	29,21%	350
HCF3889405.1	TPA: outer membrane porin OprF	*Pseudomonas aeruginosa*	114	114	97%	6,0E-27	28,73%	350
WP_132808892.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	114	114	97%	6,0E-27	29,21%	349
MBH9335341.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	114	114	97%	6,0E-27	28,93%	350
WP_096246116.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	114	114	97%	6,0E-27	29,30%	350
WP_070331590.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	114	114	97%	7,0E-27	29,21%	350
WP_128667907.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	114	114	97%	7,0E-27	28,93%	350
WP_132571790.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	114	114	97%	7,0E-27	28,93%	350
WP_124132453.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	114	114	97%	7,0E-27	28,93%	350
MBG4553890.1	Outer membrane porin OprF	*Pseudomonas aeruginosa*	114	114	97%	7,0E-27	29,21%	350
HBO3195089.1	TPA: outer membrane porin OprF	*Pseudomonas aeruginosa*	113	113	97%	8,0E-27	29,49%	350

Tabla S11. Resultados Blastp de WP_027242773.1 de *P. salmonis* contra toda la base de datos excluyendo *Proteobacteria*.

Blastp de WP_027242773.1 de *P. salmonis* contra toda la base de datos excluyendo *Proteobacteria*								
Accesión	**Nombre descriptivo (NCBI)**	**Especie**	**Puntaje máximo**	**Puntaje total**	**Cobertura**	**E-value**	**Porcentaje identidad**	**Longitud de accesión**
MCS5643047.1	RT0821/Lpp0805 family surface protein	*Dehalococcoidia bacterium*	137	137	95%	5,0E-38	43,48%	157
WP_029914123.1	RT0821/Lpp0805 family surface protein	*Pelobacter seleniigenes*	136	136	91%	1,0E-37	46,10%	156
MBE18141.1	Hypothetical protein	*Nitrospinota bacterium*	136	136	91%	2,0E-37	41,40%	166
EKD70871.1	17 kDa surface antigen	*Uncultured bacterium*	133	133	92%	2,0E-36	44,00%	152
NNJ94719.1	Glycine zipper 2TM domain-containing protein	*Halobacteria archaeon*	130	130	82%	3,0E-35	43,28%	150
EKD53725.1	OspA	*Uncultured bacterium*	130	130	91%	4,0E-35	47,30%	152
NOY13527.1	Glycine zipper 2TM domain-containing protein	*Deltaproteobacteria bacterium*	129	129	90%	6,0E-35	43,42%	155
MAG12709.1	Hypothetical protein	*Bacterium*	127	127	92%	4,0E-34	39,61%	156
MCL5966824.1	RT0821/Lpp0805 family surface protein	*Deltaproteobacteria bacterium*	126	126	91%	2,0E-33	41,18%	156
EKD72583.1	Hypothetical protein ACD_45C00633G0010	*Uncultured bacterium*	125	125	91%	3,0E-33	45,27%	153
QQG37137.1	Glycine zipper 2TM domain-containing protein	*Micavibrio aeruginosavorus*	125	125	91%	4,0E-33	38,99%	158
MBT8370027.1	Glycine zipper 2TM domain-containing protein	*Deltaproteobacteria bacterium*	125	125	91%	4,0E-33	43,31%	156
WP_253959779.1	RT0821/Lpp0805 family surface protein	*Desulfuromonas sp. KJ2020*	124	124	91%	9,0E-33	41,18%	156
NJD62231.1	Glycine zipper 2TM domain-containing protein	*Deltaproteobacteria bacterium*	124	124	90%	1,0E-32	42,95%	156
PWB62480.1	Hypothetical protein C3F14_09865	*Deltaproteobacteria bacterium*	122	122	90%	4,0E-32	42,48%	156
WP_053549150.1	RT0821/Lpp0805 family surface protein	*Desulfuromonas soudanensis*	122	122	91%	4,0E-32	40,91%	156
MCL4150145.1	Hypothetical protein	*Idotea baltica*	122	122	93%	5,0E-32	42,58%	155
GBE07542.1	Hypothetical protein BMS3Abin11_00650	*Bacterium BMS3Abin11*	121	121	91%	7,0E-32	44,30%	151
NJC88214.1	Glycine zipper 2TM domain-containing protein	*Desulfuromonas sp.*	120	120	92%	2,0E-31	41,94%	156
WP_020677620.1	RT0821/Lpp0805 family surface protein	*Geopsychrobacter electrodiphilus*	120	120	91%	3,0E-31	38,85%	156
RQD59328.1	Glycine zipper 2TM domain-containing protein	*Desulfonatronovibrio sp. MSAO_Bac4*	119	119	91%	7,0E-31	44,08%	154
WP_155874625.1	RT0821/Lpp0805 family surface protein	*Desulfuromonas sp. AOP6*	119	119	81%	8,0E-31	43,38%	156
KAJ6645118.1	17 kDa surface antigen	*Pseudolycoriella hygida*	118	118	91%	1,0E-30	40,13%	149
MBI5576982.1	Glycine zipper 2TM domain-containing protein	*Deltaproteobacteria bacterium*	117	117	90%	4,0E-30	38,71%	158
WP_107737537.1	RT0821/Lpp0805 family surface protein	*Desulfonatronum sp. SC1*	117	117	67%	5,0E-30	50,00%	161
WP_148896032.1	RT0821/Lpp0805 family surface protein	*Geothermobacter ehrlichii*	117	117	96%	6,0E-30	37,65%	160
OHB25896.1	Hypothetical protein A2X84_05275	*Desulfuromonadaceae bacterium GWC2_58_13*	117	117	91%	6,0E-30	40,76%	156
WP_066722481.1	RT0821/Lpp0805 family surface protein	*Desulfuromonas sp. DDH964*	115	115	91%	3,0E-29	41,18%	156
WP_028573332.1	RT0821/Lpp0805 family surface protein	*Desulfonatronum lacustre*	114	114	66%	5,0E-29	48,15%	158
SMP49349.1	Surface antigen	*Desulfonatronum zhilinae*	114	114	66%	5,0E-29	48,15%	158
MCB9984949.1	Glycine zipper 2TM domain-containing protein	*Micavibrio sp.*	114	114	87%	5,0E-29	41,10%	157
TVQ98632.1	Hypothetical protein EA399_10510	*Desulfovibrionales bacterium*	114	114	66%	5,0E-29	48,15%	157
MCD4688375.1	Glycine zipper 2TM domain-containing protein	*Desulfuromonadaceae bacterium*	114	114	91%	7,0E-29	42,04%	156
MAE05686.1	Hypothetical protein	*Nitrospinota bacterium*	114	114	91%	8,0E-29	36,31%	162
MBI5440898.1	Glycine zipper 2TM domain-containing protein	*Deltaproteobacteria bacterium*	116	116	80%	1,0E-28	41,22%	247
MBI1275785.1	Glycine zipper 2TM domain-containing protein	*Bacterium*	113	113	91%	2,0E-28	42,14%	160
WP_020676175.1	RT0821/Lpp0805 family surface protein	*Geopsychrobacter electrodiphilus*	115	115	91%	2,0E-28	42,48%	221
WP_072286866.1	RT0821/Lpp0805 family surface protein	*Syntrophotalea acetylenica*	113	113	92%	2,0E-28	38,71%	156
MBE0568301.1	Glycine zipper 2TM domain-containing protein	*Deltaproteobacteria bacterium*	112	112	90%	3,0E-28	41,06%	155
GBF27178.1	Hypothetical protein MnTg02_02224	*Bacterium MnTg02*	112	112	91%	6,0E-28	37,91%	156
WP_011342527.1	RT0821/Lpp0805 family surface protein	*Syntrophotalea carbinolica*	112	112	79%	6,0E-28	42,86%	156
WP_244148831.1	RT0821/Lpp0805 family surface protein	*Desulfonatronum thioautotrophicum*	112	112	66%	6,0E-28	47,22%	162
WP_235185504.1	RT0821/Lpp0805 family surface protein	*Desulfonatronum thiodismutans*	112	112	66%	7,0E-28	46,30%	160
MBI5017025.1	Glycine zipper 2TM domain-containing protein	*Deltaproteobacteria bacterium*	111	111	92%	8,0E-28	37,33%	150
HDQ41257.1	TPA: Hypothetical protein	*Desulfonatronum sp.*	111	111	67%	9,0E-28	47,71%	159
WP_208596562.1	RT0821/Lpp0805 family surface protein	*Desulfonatronum thiosulfatophilum*	111	111	66%	9,0E-28	47,22%	157
MCF6354390.1	Glycine zipper 2TM domain-containing protein	*Candidatus Polarisedimenticolaceae bacterium*	111	111	70%	9,0E-28	44,35%	149
WP_085010263.1	RT0821/Lpp0805 family surface protein	*Geothermobacter hydrogeniphilus*	111	111	91%	1,0E-27	38,61%	156
MBG0777225.1	Glycine zipper 2TM domain-containing protein	*Desulfovibrionaceae bacterium*	111	111	91%	2,0E-27	44,94%	175
WP_260749799.1	RT0821/Lpp0805 family surface protein	*Geoalkalibacter halelectricus*	110	110	91%	2,0E-27	40,52%	156
MBI3126730.1	Glycine zipper 2TM domain-containing protein	*Candidatus Tectomicrobia bacterium*	110	110	93%	2,0E-27	40,88%	161
MCA1743696.1	Glycine zipper 2TM domain-containing protein	*Desulfovibrionales bacterium*	110	110	92%	2,0E-27	40,26%	154
MCM2265851.1	RT0821/Lpp0805 family surface protein	*Desulfuromonadales bacterium*	109	109	71%	4,0E-27	44,17%	156
CAF2028599.1	Unnamed protein product	*Rotaria magnacalcarata*	109	109	91%	4,0E-27	39,22%	157
MCF6178189.1	Glycine zipper 2TM domain-containing protein	*Geopsychrobacter sp.*	109	109	91%	5,0E-27	37,25%	156
WP_103116029.1	RT0821/Lpp0805 family surface protein	*Geothermobacter hydrogeniphilus*	109	109	91%	6,0E-27	37,97%	156
WP_072284009.1	RT0821/Lpp0805 family surface protein	*Syntrophotalea acetylenivorans*	109	109	90%	6,0E-27	39,47%	156
WP_082820256.1	RT0821/Lpp0805 family surface protein	*Desulfuromonas sp. DDH964*	111	111	69%	6,0E-27	44,44%	217
PHR90641.1	Hypothetical protein COA78_34855	*Blastopirellula sp.*	108	108	91%	2,0E-26	37,18%	164
OUT42685.1	Hypothetical protein CBB62_06905	*Micavibrio sp. TMED2*	108	108	96%	2,0E-26	41,10%	161
OGQ01088.1	Hypothetical protein A2Z40_01565	*Deltaproteobacteria bacterium RBG_19FT_COMBO_60_16*	107	107	70%	3,0E-26	42,86%	158
MBI5018544.1	Glycine zipper 2TM domain-containing protein	*Deltaproteobacteria bacterium*	107	107	69%	4,0E-26	43,75%	146
MCF6179718.1	Glycine zipper 2TM domain-containing protein	*Geopsychrobacter sp.*	107	107	70%	5,0E-26	41,53%	156
MAZ00024.1	Hypothetical protein	*Micavibrio sp.*	107	107	93%	5,0E-26	41,03%	157
MAI62958.1	Hypothetical protein	*Micavibrio sp.*	106	106	90%	6,0E-26	32,47%	157
OYV96718.1	Hypothetical protein B7Z62_07700	*Deltaproteobacteria bacterium 37-65-8*	106	106	61%	1,0E-25	47,12%	155
OGL59254.1	Hypothetical protein A3J27_01295	*Candidatus Tectomicrobia bacterium*	105	105	79%	1,0E-25	43,18%	147
OGP20430.1	Hypothetical protein A2X90_06170	*Deltaproteobacteria bacterium GWA2_65_63*	105	105	91%	2,0E-25	41,45%	155
MBK7361798.1	Glycine zipper 2TM domain-containing protein	*Micavibrio sp.*	105	105	91%	2,0E-25	35,26%	161
WP_221250396.1	RT0821/Lpp0805 family surface protein	*Desulfuromonas versatilis*	105	105	67%	2,0E-25	47,01%	156
NBT89127.1	Hypothetical protein	*Flavobacteriaceae bacterium*	105	105	82%	2,0E-25	41,30%	162
WP_008871141.1	RT0821/Lpp0805 family surface protein	*Desulfonatronospira thiodismutans*	105	105	70%	2,0E-25	40,68%	152
WP_020677970.1	RT0821/Lpp0805 family surface protein	*Geopsychrobacter electrodiphilus*	105	105	90%	2,0E-25	34,21%	156
RQD77936.1	Glycine zipper 2TM domain-containing protein	*Desulfonatronospira sp. MSAO_Bac3*	105	105	70%	3,0E-25	40,68%	152
WP_040100315.1	RT0821/Lpp0805 family surface protein	*Geoalkalibacter ferrihydriticus*	105	105	91%	3,0E-25	38,31%	156
OGZ05783.1	Hypothetical protein A2762_03640	*Candidatus Lloydbacteria bacterium*	105	105	95%	3,0E-25	34,84%	151
MCP3677419.1	Glycine zipper 2TM domain-containing protein	*Deltaproteobacteria bacterium*	105	105	90%	3,0E-25	40,14%	161
MCH7775367.1	Hypothetical protein	*Gemmatimonadota bacterium*	107	107	72%	5,0E-25	44,44%	244
WP_020676581.1	RT0821/Lpp0805 family surface protein	*Geopsychrobacter electrodiphilus*	104	104	90%	6,0E-25	35,29%	156
MBI5904059.1	Glycine zipper 2TM domain-containing protein	*Deltaproteobacteria bacterium*	104	104	90%	7,0E-25	42,38%	155
WP_225072430.1	RT0821/Lpp0805 family surface protein	*Desulfuromonas sp. CSMB_57*	103	103	71%	7,0E-25	42,50%	155
MBI2233621.1	Glycine zipper 2TM domain-containing protein	*Micavibrio aeruginosavorus*	103	103	86%	8,0E-25	35,66%	162
MBI1724855.1	Glycine zipper 2TM domain-containing protein	*Candidatus Tectomicrobia bacterium*	103	103	67%	9,0E-25	43,36%	160
MCH7776930.1	Hypothetical protein	*Gemmatimonadota bacterium*	104	104	70%	9,0E-25	43,86%	169
WP_027714599.1	RT0821/Lpp0805 family surface protein	*Desulfuromonas sp. TF*	103	103	67%	9,0E-25	46,15%	156
MBI2178810.1	Glycine zipper 2TM domain-containing protein	*Candidatus Tectomicrobia bacterium*	105	105	79%	9,0E-25	43,18%	206
MCP4934314.1	Glycine zipper 2TM domain-containing protein	*Bacterium*	103	103	89%	1,0E-24	36,91%	156
KAJ6644815.1	Zinc import ATP-binding protein ZnuC	*Pseudolycoriella hygida*	108	108	75%	1,0E-24	44,62%	335
MBI5419046.1	Glycine zipper 2TM domain-containing protein	*Deltaproteobacteria bacterium*	103	103	90%	1,0E-24	36,42%	155
MBI5443540.1	Glycine zipper 2TM domain-containing protein	*Deltaproteobacteria bacterium*	103	103	74%	1,0E-24	44,17%	153
WP_028575076.1	RT0821/Lpp0805 family surface protein	*Desulfonatronovibrio hydrogenovorans*	103	103	91%	1,0E-24	36,42%	153
MBD24271.1	Hypothetical protein	*Candidatus Marinimicrobia bacterium*	103	103	92%	2,0E-24	37,42%	162
QEA06901.1	Hypothetical protein KBTEX_03243	*Uncultured organism*	103	103	70%	2,0E-24	42,98%	153
MCA8967081.1	Glycine zipper 2TM domain-containing protein	*Planctomycetota bacterium*	102	102	82%	2,0E-24	41,01%	137
MBF8257724.1	Hypothetical protein	*Actinomycetia bacterium*	102	102	90%	2,0E-24	38,56%	152
RJP25529.1	Glycine zipper 2TM domain-containing protein	*Deltaproteobacteria bacterium*	102	102	90%	4,0E-24	42,38%	155
WP_045215243.1	RT0821/Lpp0805 family surface protein	*Desulfonatronovibrio magnus*	102	102	70%	5,0E-24	42,37%	154
MBX2834008.1	Glycine zipper 2TM domain-containing protein	*Micavibrio sp.*	102	102	86%	5,0E-24	39,16%	158
MBK7973923.1	Glycine zipper 2TM domain-containing protein	*Deltaproteobacteria bacterium*	102	102	93%	6,0E-24	33,75%	160
OYV97949.1	Hypothetical protein B7Z62_04900	*Deltaproteobacteria bacterium 37-65-8*	101	101	91%	6,0E-24	36,36%	158

Tabla S12. Resultados Blastp de WP_027242773.1 de *P. salmonis* contra organismos filogenéticamente cercanos a *P. salmonis*.

Blastp de WP_027242773.1 de *P. salmonis* contra *L. pneumophila*, *P. aeruginosa* y *C. burnetii*								
Accesión	**Nombre descriptivo (NCBI)**	**Especie**	**Puntaje máximo**	**Puntaje total**	**Cobertura**	**E-value**	**Porcentaje identidad**	**Longitud de accesión**
HAT6362931.1	TPA: glycine zipper 2TM domain-containing protein	*Legionella pneumophila*	120,0	120,0	91%	2,0E-33	46,71%	149
HBD7396457.1	TPA: glycine zipper 2TM domain-containing protein	*Legionella pneumophila*	109,0	109,0	90%	3,0E-29	43,54%	148
WP_027228358.1	RT0821/Lpp0805 family surface protein	*Legionella pneumophila*	104,0	104,0	91%	5,0E-27	46,71%	149
HAT1752277.1	TPA: glycine zipper 2TM domain-containing protein	*Legionella pneumophila*	99,4	99,4	91%	4,0E-25	44,08%	147
HAU1151861.1	TPA: glycine zipper 2TM domain-containing protein	*Legionella pneumophila*	96,3	96,3	56%	6,0E-24	48,35%	149
WP_010946477.1	RT0821/Lpp0805 family surface protein	*Legionella*	96,3	96,3	56%	7,0E-24	48,35%	149
WP_027223780.1	RT0821/Lpp0805 family surface protein	*Legionella*	96,3	96,3	56%	7,0E-24	48,35%	149
WP_238501471.1	RT0821/Lpp0805 family surface protein	*Legionella pneumophila*	96,3	96,3	56%	7,0E-24	48,35%	149
HAT7072451.1	TPA: glycine zipper 2TM domain-containing protein	*Legionella pneumophila*	94,7	94,7	56%	2,0E-23	47,25%	149
HAU2083503.1	TPA: glycine zipper 2TM domain-containing protein	*Legionella pneumophila*	89,4	89,4	52%	3,0E-21	49,41%	144
WP_005773063.1	Dot/Icm type IV secretion system effector CoxDFB4	*Coxiella burnetii*	89,0	89,0	91%	4,0E-21	35,10%	142
WP_040947937.1	Unnamed protein product	*Coxiella burnetii*	88,6	88,6	90%	8,0E-21	35,14%	150
WP_005771746.1	Dot/Icm type IV secretion system effector CoxDFB4	*Coxiella burnetii*	87,8	87,8	90%	1,0E-20	35,14%	150
WP_040933640.1	Dot/Icm type IV secretion system effector CoxDFB4	*Coxiella burnetii*	87,4	87,4	90%	2,0E-20	35,14%	150
HAU2049754.1	TPA: glycine zipper 2TM domain-containing protein	*Legionella pneumophila*	56,6	56,6	32%	5,0E-09	43,40%	116
WP_009681801.1	SH3 domain-containing protein	*Pseudomonas*	48,5	48,5	71%	3,0E-05	24,00%	286
WP_088177408.1	Glycine zipper 2TM domain-containing protein	*Pseudomonas aeruginosa*	43,5	43,5	45%	1,0E-03	34,41%	182
WP_134593327.1	SH3 domain-containing protein	*Pseudomonas aeruginosa*	42,0	42,0	69%	5,0E-03	29,17%	261
WP_127005463.1	Glycine zipper 2TM domain-containing protein	*Pseudomonas aeruginosa*	40,4	40,4	45%	1,2E-02	33,33%	182

Tabla S13. Resultados Blastp de WP_032126547.1 de *P. salmonis* contra toda la base de datos excluyendo *Proteobacteria*.

Blastp de WP_032126547.1 de *P. salmonis* contra toda la base de datos excluyendo *Proteobacteria*								
Accesión	**Nombre descriptivo (NCBI)**	**Especie**	**Puntaje máximo**	**Puntaje total**	**Cobertura**	**E-value**	**Porcentaje identidad**	**Longitud de accesión**
UTW43205.1	TolC family outer membrane protein	*Bacterium SCSIO 12844*	286	286	85%	2,0E-87	41,12%	482
EKE02001.1	Hypothetical protein ACD_21C00003G0004	*Uncultured bacterium*	273	273	87%	2,0E-81	39,16%	557
QWT20064.1	TolC family outer membrane protein	*Bacillus sp. NP157*	250	250	86%	7,0E-74	36,18%	461
UTW43766.1	TolC family outer membrane protein	*Bacterium SCSIO 12844*	243	243	86%	3,0E-71	35,76%	444
NNJ93384.1	TolC family outer membrane protein	*Halobacteria archaeon*	242	242	85%	6,0E-71	37,20%	426
EKD71569.1	Hypothetical protein ACD_46C00159G0005	*Uncultured bacterium*	241	241	85%	5,0E-70	37,91%	479
MCB0256359.1	TolC family outer membrane protein	*Anaerolineae bacterium*	233	233	86%	2,0E-67	36,43%	440
KAG9611597.1	Hypothetical protein KCV01_g2422	*Aureobasidium melanogenum*	240	240	86%	8,0E-66	36,10%	1055
ELU09021.1	Hypothetical protein CAPTEDRAFT_50201	*Capitella teleta*	228	228	83%	9,0E-66	36,30%	416
MBN67831.1	Hypothetical protein	*Gimesia sp.*	228	228	85%	2,0E-65	37,59%	458
NNF95986.1	TolC family outer membrane protein	*Halobacteria archaeon*	226	226	80%	3,0E-65	35,20%	410
EKD73899.1	Hypothetical protein ACD_45C00151G0003	*Uncultured bacterium*	227	227	86%	3,0E-65	36,05%	443
MCK5539166.1	TolC family outer membrane protein	*Bacteroidales bacterium*	226	226	85%	1,0E-64	34,45%	446
MCF6354315.1	TolC family outer membrane protein	*Candidatus Polarisedimenticolaceae bacterium*	225	225	85%	2,0E-64	33,33%	442
CDQ35084.1	Outer membrane protein TolC precursor	*Virgibacillus halodenitrificans*	226	226	86%	3,0E-64	34,03%	490
MBR9814243.1	TolC family outer membrane protein	*Bacterium*	224	224	84%	7,0E-64	34,63%	468
MCH2695764.1	TolC family outer membrane protein	*Acidobacteriia bacterium*	220	220	85%	3,0E-62	33,26%	461
KGQ13479.1	Outer membrane protein tolC	*Beauveria bassiana D1-5*	220	220	85%	4,0E-62	35,93%	476
MCF6281813.1	TolC family outer membrane protein	*Candidatus Polarisedimenticolaceae bacterium*	219	219	85%	5,0E-62	33,41%	438
VTQ26017.1	Outer membrane protein tolC precursor	*Streptococcus pneumoniae*	220	220	85%	7,0E-62	36,26%	493
CDW60244.1	OEP domain containing protein	*Trichuris trichiura*	220	220	85%	7,0E-62	36,26%	495
CAG8948198.1	Unnamed protein product	*Penicillium salamii*	218	218	85%	1,0E-61	36,45%	455
MBI4666436.1	TolC family outer membrane protein	*Nitrospinota bacterium*	218	218	88%	2,0E-61	32,65%	465
WP_198262725.1	TolC family outer membrane protein	*Sulfur-oxidizing endosymbiont of Gigantopelta aegis*	217	217	85%	2,0E-61	33,01%	425
GGE74583.1	Hypothetical protein GCM10011533_28790	*Streptosporangium jomthongense*	218	218	86%	3,0E-61	34,19%	460
MCL4133337.1	Hypothetical protein	*Idotea baltica*	217	217	85%	3,0E-61	34,53%	442
MBG7610078.1	TolC family outer membrane protein	*Anaerolineae bacterium*	217	217	85%	3,0E-61	36,17%	452
KAH8256734.1	Hypothetical protein KR044_000243	*Drosophila immigrans*	218	218	83%	5,0E-61	35,68%	503
WP_253381938.1	Outer membrane channel protein TolC	*unidentified bacterial endosymbiont*	218	218	85%	5,0E-61	35,78%	494
OAB57077.1	Hypothetical protein AY599_21075	*Leptolyngbya valderiana BDU 20041*	216	216	86%	7,0E-61	32,64%	447
NCA68826.1	Type I secretion protein TolC	*Sphingobacteriia bacterium*	216	216	85%	1,0E-60	34,84%	449
GBE11182.1	Outer membrane protein TolC precursor	*Bacterium BMS3Abin12*	215	215	85%	1,0E-60	32,86%	447
RAN75125.1	Type I secretion protein TolC	*Bacillus sp. SRB_336*	215	215	85%	2,0E-60	34,57%	453
DAL08934.1	TPA: outer membrane channel protein	*Caudoviricetes sp.*	215	215	85%	3,0E-60	36,19%	489
EKD53994.1	Hypothetical protein ACD_60C00133G0014	*Uncultured bacterium*	212	212	86%	3,0E-59	34,18%	448
KAF5282958.1	Hypothetical protein FQR65_LT14158	*Abscondita terminalis*	211	211	77%	3,0E-59	34,29%	423
MCI0627965.1	TolC family outer membrane protein	*Acidobacteriota bacterium*	210	210	85%	2,0E-58	33,02%	462
MPQ53758.1	Outer membrane channel protein TolC	*Citrobacter telavivensis*	211	211	85%	2,0E-58	34,52%	495
MCG1034399.1	Outer membrane channel protein TolC	*Bacillus amyloliquefaciens*	211	211	85%	2,0E-58	35,05%	476
KAG6333391.1	Hypothetical protein ID866_5692	*Astraeus odoratus*	211	211	85%	2,0E-58	34,75%	495
VTQ57279.1	Protein SapF	*Campylobacter jejuni*	210	210	85%	3,0E-58	34,67%	495
MBW8053988.1	TolC family outer membrane protein	*Nitrospira sp.*	209	209	86%	4,0E-58	32,94%	448
GFD74699.1	Outer membrane channel protein TolC	*Tenacibaculum sp. KUL113*	207	207	86%	2,0E-57	30,54%	449
MBE2295716.1	TolC family outer membrane protein	*Phycisphaerales bacterium*	208	208	85%	2,0E-57	34,46%	497
MBV8445605.1	TolC family outer membrane protein	*Candidatus Dormibacteraeota bacterium*	206	206	76%	2,0E-57	35,38%	421
QPN44996.1	TolC family outer membrane protein	*Priestia aryabhattai*	207	207	86%	3,0E-57	32,55%	477
MBW2471369.1	TolC family outer membrane protein	*Deltaproteobacteria bacterium*	204	204	85%	7,0E-57	31,88%	417
OOK72523.1	Outer membrane channel protein TolC	*Pedobacter himalayensis*	206	206	85%	8,0E-57	34,60%	492
MBN4055652.1	TolC family outer membrane protein	*Bacterium AH-315-K03*	206	206	86%	8,0E-57	31,21%	478
MBY6094322.1	Outer membrane channel protein TolC	*Priestia flexa*	205	205	85%	8,0E-57	33,73%	445
RLJ16328.1	Type I secretion protein TolC	*Bacterium endosymbiont of Escarpia laminata*	204	204	85%	1,0E-56	33,17%	422
NVN56691.1	TolC family outer membrane protein	*Bacterium Scap17*	205	205	86%	1,0E-56	31,52%	456
MBN2291186.1	TolC family outer membrane protein	*Pirellulales bacterium*	204	204	86%	3,0E-56	30,66%	468
MSM39594.1	TolC family outer membrane protein	*Geobacter sp.*	204	204	85%	4,0E-56	30,17%	453
GFD77861.1	Outer membrane channel protein TolC	*Tenacibaculum sp. KUL118*	203	203	86%	4,0E-56	31,81%	445
NWN60916.1	TolC family outer membrane protein	*Pseudomonas allii*	204	204	87%	5,0E-56	31,63%	479
KAI3491541.1	Hypothetical protein L1887_44162	*Cichorium endivia*	209	209	85%	5,0E-56	34,60%	744
VTS66135.1	Outer membrane protein tolC precursor	*Streptococcus dysgalactiae subsp. equisimilis*	203	203	86%	1,0E-55	31,93%	481
MZG80862.1	Outer membrane channel protein TolC	*PhotoBacterium lucens*	201	201	85%	2,0E-55	34,70%	432
MRR56909.1	Channel protein TolC	*Deltaproteobacteria bacterium*	201	201	85%	4,0E-55	32,94%	441
MBE8599210.1	TolC family outer membrane protein	*Pseudomonas cyclaminis*	201	201	87%	5,0E-55	31,63%	479
MAC86189.1	Transporter	*Flavobacteriales bacterium*	200	200	84%	8,0E-55	31,04%	441
ABL97260.1	Type I secretion outer membrane protein TolC	*Uncultured marine bacterium EB0_50A10*	200	200	85%	9,0E-55	31,69%	443
ABL97412.1	Putative type I secretion outer membrane protein TolC	*Uncultured marine bacterium EB80_02D08*	199	199	84%	2,0E-54	32,00%	442
MBC2380393.1	TolC family outer membrane protein	*Pseudomonas cremoris*	199	199	87%	4,0E-54	30,70%	479
MBW1860974.1	TolC family outer membrane protein	*Deltaproteobacteria bacterium*	199	199	85%	5,0E-54	30,52%	479
MBW1763624.1	TolC family outer membrane protein	*Deltaproteobacteria bacterium*	197	197	85%	8,0E-54	30,52%	450
ADI16285.1	Outer membrane protein	*Uncultured bacterium HF0010_16H03*	195	195	85%	5,0E-53	31,60%	443
GIR74193.1	Hypothetical protein CM15mP76_09200	*Prochlorococcus sp.*	195	195	85%	8,0E-53	31,69%	444
MCA9018142.1	TolC family outer membrane protein	*Planctomycetaceae bacterium*	190	190	65%	2,0E-52	32,91%	315
MBC7622923.1	TolC family outer membrane protein	*Aeromicrobium sp.*	194	194	85%	2,0E-52	33,10%	446
MCL4148690.1	Hypothetical protein	*Idotea baltica*	193	193	86%	2,0E-52	32,46%	431
PYG98110.1	Channel protein TolC	*Arthrobacter stackebrandtii*	194	194	86%	2,0E-52	33,25%	453
UTW44779.1	TolC family outer membrane protein	*Bacterium SCSIO 12696*	194	194	84%	3,0E-52	31,55%	463
MBK5304909.1	TolC family outer membrane protein	*Bacillus sp. TH86*	194	194	87%	3,0E-52	31,40%	466
MBN2061264.1	TolC family outer membrane protein	*Deltaproteobacteria bacterium*	193	193	85%	7,0E-52	29,98%	479
GBE08362.1	Outer membrane protein TolC precursor	*Bacterium BMS3Abin11*	192	192	85%	9,0E-52	30,93%	447
NTU97568.1	TolC family outer membrane protein	*Chlorobiaceae bacterium*	191	191	85%	2,0E-51	30,50%	445
NTU57828.1	TolC family outer membrane protein	*Chlorobiaceae bacterium*	191	191	85%	2,0E-51	30,38%	444
TLU55444.1	TolC family outer membrane protein	*Chlorobium sp.*	191	191	85%	2,0E-51	30,88%	443
HAW91469.1	TPA: outer membrane channel protein TolC	*Candidatus Azambacteria bacterium*	191	191	85%	3,0E-51	32,26%	452
OHB33805.1	Type I secretion protein TolC	*Desulfuromonadaceae bacterium GWC2_58_13*	191	191	85%	3,0E-51	31,37%	449
AAY82609.1	predicted outer membrane protein TolC	*Uncultured bacterium MedeBAC35C06*	190	190	84%	4,0E-51	29,72%	445
PKN32657.1	Type I secretion protein TolC	*Deltaproteobacteria bacterium*	190	190	87%	6,0E-51	28,90%	463
NJM12632.1	TolC family outer membrane protein	*Synechococcaceae cyanoBacterium SM1_2_3*	191	191	85%	1,0E-50	32,21%	501
GFD88547.1	Outer membrane channel protein TolC	*Tenacibaculum sp. KUL152*	189	189	86%	1,0E-50	30,73%	460
NTV16040.1	TolC family outer membrane protein	*Chlorobiaceae bacterium*	188	188	85%	2,0E-50	30,64%	447
RII31317.1	Type I secretion protein TolC	*Geobacter sp.*	188	188	85%	3,0E-50	30,05%	450
TSA47941.1	Hypothetical protein D4R56_01330	*Deltaproteobacteria bacterium*	188	188	86%	3,0E-50	29,81%	459
SGD19664.1	Outer membrane protein tolC precursor	*MycoBacterium tuberculosis*	188	188	85%	3,0E-50	34,75%	452
MCP3891894.1	TolC family outer membrane protein	*Desulfobulbaceae bacterium*	189	189	85%	5,0E-50	28,84%	504
NPU83918.1	TolC family outer membrane protein	*Syntrophaceae bacterium*	187	187	85%	8,0E-50	29,34%	463
MCK4501769.1	TolC family outer membrane protein	*Desulfuromonadales bacterium*	187	187	85%	8,0E-50	29,45%	457
MPQ84623.1	TolC family outer membrane protein	*Pseudomonas kitaguniensis*	187	187	87%	1,0E-49	30,23%	479
HAY50632.1	TPA: channel protein TolC	*Acidimicrobiaceae bacterium*	188	188	85%	1,0E-49	31,15%	517
WP_275889100.1	TolC family outer membrane protein	*Desulfobulbus rhabdoformis*	186	186	85%	1,0E-49	30,95%	454
WP_083694472.1	TolC family outer membrane protein	*Chlorobium sp. KB01*	186	186	85%	2,0E-49	31,19%	456
MBM9614708.1	TolC family outer membrane protein	*Desulfobulbus rhabdoformis*	184	184	81%	3,0E-49	31,51%	412
MBT4496120.1	TolC family outer membrane protein	*Gemmatimonadota bacterium*	184	184	85%	4,0E-49	31,50%	429
WP_232209754.1	TolC family outer membrane protein	*Chlorobium ferrooxidans*	184	184	85%	5,0E-49	31,19%	447

Tabla S14. Resultados Blastp de WP_032126547.1 de *P. salmonis* contra organismos filogenéticamente cercanos a *P. salmonis*.

Blastp de WP_032126547.1 de *P. salmonis* contra *L. pneumophila*, *P. aeruginosa* y *C. burnetii*								
Accesión	**Nombre descriptivo (NCBI)**	**Especie**	**Puntaje máximo**	**Puntaje total**	**Cobertura**	**E-value**	**Porcentaje identidad**	**Longitud de accesión**
WP_010957349.1	TolC family outer membrane protein	*Coxiella burnetii*	242	242	86%	4,0E-71	35,16%	616
WP_005769324.1	TolC family outer membrane protein	*Coxiella burnetii*	242	242	86%	4,0E-71	35,16%	616
WP_005772836.1	TolC family outer membrane protein	*Coxiella burnetii*	241	241	86%	6,0E-71	35,16%	616
WP_039669627.1	TolC family outer membrane protein	*Coxiella burnetii*	241	241	86%	9,0E-71	35,16%	616
WP_040953185.1	TolC family outer membrane protein	*Coxiella burnetii*	241	241	86%	1,0E-70	34,93%	616
WP_099126488.1	TolC family outer membrane protein	*Coxiella burnetii*	241	241	86%	1,0E-70	34,93%	620
WP_062727197.1	TolC family outer membrane protein	*Legionella pneumophila*	236	236	85%	1,0E-70	35,92%	455
WP_260554437.1	TolC family outer membrane protein	*Coxiella burnetii*	241	241	86%	1,0E-70	34,93%	616
WP_061513668.1	TolC family outer membrane protein	*Legionella*	236	236	85%	2,0E-70	35,92%	455
HAZ7573511.1	TPA: TolC family outer membrane protein	*Legionella pneumophila*	236	236	85%	3,0E-70	35,92%	455
WP_061640132.1	TolC family outer membrane protein	*Legionella pneumophila*	236	236	85%	3,0E-70	35,92%	455
WP_012570491.1	Unnamed protein product	*Coxiella burnetii*	239	239	86%	3,0E-70	35,16%	616
WP_061485458.1	TolC family outer membrane protein	*Legionella pneumophila*	235	235	86%	4,0E-70	35,75%	455
WP_106183394.1	TolC family outer membrane protein	*Legionella pneumophila*	235	235	85%	4,0E-70	35,92%	455
HAT2105229.1	TPA: TolC family outer membrane protein	*Legionella pneumophila*	235	235	86%	4,0E-70	35,75%	455
HAU1599702.1	TPA: TolC family outer membrane protein	*Legionella pneumophila*	235	235	86%	4,0E-70	35,75%	455
WP_042238014.1	TolC family outer membrane protein	*Legionella pneumophila*	235	235	85%	6,0E-70	35,92%	455
WP_014843521.1	TolC family outer membrane protein	*Legionella pneumophila*	234	234	85%	6,0E-70	35,92%	455
HAU1141587.1	TPA: TolC family outer membrane protein	*Legionella pneumophila*	234	234	86%	7,0E-70	35,75%	455
WP_027228387.1	TolC family outer membrane protein	*Legionella pneumophila*	234	234	85%	8,0E-70	35,68%	455
WP_027220262.1	TolC family outer membrane protein	*Legionella pneumophila*	234	234	85%	1,0E-69	35,92%	455
WP_010946436.1	TolC family outer membrane protein	*Legionella pneumophila*	234	234	85%	1,0E-69	35,92%	455
HAU3666870.1	TPA: TolC family outer membrane protein	*Legionella pneumophila*	234	234	85%	1,0E-69	35,92%	455
HAU1181436.1	TPA: TolC family outer membrane protein	*Legionella pneumophila*	234	234	85%	1,0E-69	35,68%	455
HAT1792515.1	TPA: TolC family outer membrane protein	*Legionella pneumophila*	234	234	85%	1,0E-69	35,92%	455
AEW50979.1	Outer membrane protein TolC	*Legionella pneumophila subsp. pneumophila*	234	234	86%	1,0E-69	35,51%	468
WP_011945848.1	TolC family outer membrane protein	*Legionella pneumophila*	234	234	86%	1,0E-69	35,51%	455
WP_070322120.1	TolC family outer membrane protein	*Legionella pneumophila*	234	234	85%	1,0E-69	35,45%	455
WP_110539714.1	TolC family outer membrane protein	*Legionella pneumophila*	234	234	86%	1,0E-69	35,51%	455
WP_011214910.1	TolC family outer membrane protein	*Legionella pneumophila*	233	233	85%	2,0E-69	35,45%	455
HAT8807741.1	TPA: TolC family outer membrane protein	*Legionella pneumophila*	233	233	85%	2,0E-69	35,68%	455
HAT1595445.1	TPA: TolC family outer membrane protein	*Legionella pneumophila*	233	233	85%	2,0E-69	35,68%	455
HAU1151901.1	TPA: TolC family outer membrane protein	*Legionella pneumophila*	233	233	85%	3,0E-69	35,68%	455
HAT8368461.1	TPA: TolC family outer membrane protein	*Legionella pneumophila*	233	233	86%	3,0E-69	35,28%	455
WP_027223745.1	TolC family outer membrane protein	*Legionella pneumophila*	233	233	85%	4,0E-69	35,68%	455
HAT2029575.1	TPA: TolC family outer membrane protein	*Legionella pneumophila*	232	232	86%	5,0E-69	35,28%	455
HAT1721803.1	TPA: TolC family outer membrane protein	*Legionella pneumophila*	232	232	86%	5,0E-69	35,28%	455
HAU9860334.1	TPA: TolC family outer membrane protein	*Legionella pneumophila*	232	232	86%	5,0E-69	35,51%	455
HAT8178230.1	TPA: TolC family outer membrane protein	*Legionella pneumophila*	231	231	85%	1,0E-68	35,45%	455
HAT8841709.1	TPA: TolC family outer membrane protein	*Legionella pneumophila subsp. pneumophila*	231	231	85%	1,0E-68	35,45%	455
WP_061692761.1	TolC family outer membrane protein	*Legionella pneumophila*	231	231	85%	1,0E-68	35,68%	455
HBD7396426.1	TPA: TolC family outer membrane protein	*Legionella pneumophila*	223	223	86%	1,0E-65	34,26%	457
MBH4410191.1	Outer membrane channel protein TolC	*Pseudomonas aeruginosa*	216	216	85%	2,0E-62	35,31%	492
WP_009681337.1	TolC family outer membrane protein	*Pseudomonas*	210	210	87%	3,0E-60	32,48%	478
MBG7042899.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	209	209	86%	5,0E-60	31,78%	482
HCF7245706.1	TPA: efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	208	208	86%	1,0E-59	31,78%	482
VZT41389.1	Outer membrane protein TolC	*Pseudomonas aeruginosa*	207	207	85%	1,0E-59	32,86%	452
MBH9342533.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	208	208	86%	1,0E-59	31,78%	481
WP_126621707.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	207	207	86%	4,0E-59	31,54%	482
WP_126895182.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	207	207	86%	5,0E-59	31,78%	482
UTN76308.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	207	207	86%	5,0E-59	31,78%	482
WP_125032994.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	206	206	86%	6,0E-59	31,78%	482
MCO3145338.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	206	206	86%	7,0E-59	31,78%	482
WP_134278527.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	206	206	86%	9,0E-59	31,78%	482
WP_029887208.1	TolC family outer membrane protein	*Pseudomonas*	206	206	86%	9,0E-59	32,32%	478
WP_134628025.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	1,0E-58	31,54%	461
EIU4425194.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	1,0E-58	31,54%	473
HCD9087290.1	TPA: efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	206	206	86%	1,0E-58	32,17%	480
MBG5010471.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	206	206	86%	1,0E-58	31,54%	482
MBH8720123.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	474
MCO2238028.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	32,17%	482
HCD6014059.1	TPA: efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	32,17%	482
MBH8856325.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	472
MBG6761316.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	482
HBO2645427.1	TPA: efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	475
WP_244240645.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	473
MBG6951504.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	32,17%	482
WP_149809879.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	482
HCA5842261.1	TPA: efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	480
MCO3563634.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	482
WP_171958917.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	32,17%	482
WP_019726965.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas*	205	205	86%	2,0E-58	31,54%	482
MBG7570660.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	482
MBG6926369.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	482
EIU4165941.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	476
PXC01320.1	channel protein TolC	*Pseudomonas aeruginosa*	204	204	85%	2,0E-58	31,75%	452
WP_132624633.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	482
HCE7886681.1	TPA: efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	478
WP_282414043.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	482
WP_070335690.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	482
MBG5188161.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	482
WP_134329048.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	482
PBV74260.1	Channel protein TolC	*Pseudomonas aeruginosa*	204	204	85%	2,0E-58	31,75%	457
HCE6304233.1	TPA: efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	482
WP_151122752.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	482
WP_033956269.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	482
WP_070344464.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	482
MBG4390187.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	482
EIY2630997.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	480
MCO3925860.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	482
EIY2559802.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	480
EIU1646564.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	482
MCO3858357.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	482
HBN9662674.1	TPA: efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	482
HCD6622956.1	TPA: efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	480
MCO4009849.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	482
WP_003123581.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas*	205	205	86%	2,0E-58	31,54%	482
WP_017002004.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas*	205	205	86%	2,0E-58	31,54%	482
WP_048521709.1	Efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	482
HCE6866209.1	TPA: efflux transporter outer membrane subunit OpmH	*Pseudomonas aeruginosa*	205	205	86%	2,0E-58	31,54%	482