

1072/3 BLAST

Hit	Description	E-value	Score
AP009049	Clostridium kluuyveri NBRC 12016 DNA, complete genome	0.00	1,931.00
CP000673	Clostridium kluuyveri DSM 555, complete genome	0.00	1,931.00
CP000382	Clostridium novyi NT, complete genome	1.3E-108	823.00
CP000382	Clostridium novyi NT, complete genome	1.3E-108	342.00
CP000923	Thermoanaerobacter sp. X514, complete genome	1.8E-96	1,001.00
DQ831235	Heliobacillus mobilis ethanolamine utilization protein eutP (eutP), ethanolamine utilization protein eutM (eutM), and ethanolamine utilization protein eutL (eutL) genes, complete cds	1.65E-91	704.00
DQ831235	Heliobacillus mobilis ethanolamine utilization protein eutP (eutP), ethanolamine utilization protein eutM (eutM), and ethanolamine utilization protein eutL (eutL) genes, complete cds	1.65E-91	299.00
CU928162	Escherichia coli ED1a chromosome, complete genome	2.62E-85	895.00
CU928161	Escherichia coli S88 chromosome, complete genome	2.62E-85	895.00
CP000468	Escherichia coli APEC O1, complete genome	2.62E-85	895.00
CP000230	Rhodospirillum rubrum ATCC 11170, complete genome	3.02E-84	885.00
CP000301	Rhodopseudomonas palustris BisB18,	2.71E-82	867.00

Hit	Description	E-value	Score
	complete genome		
CP000416	Lactobacillus brevis ATCC 367, complete genome	9.82E-78	597.00
CP000416	Lactobacillus brevis ATCC 367, complete genome	9.82E-78	274.00
AE014075	Escherichia coli CFT073, complete genome	1.2E-75	640.00
AE014075	Escherichia coli CFT073, complete genome	1.2E-75	211.00
AY061967	Lactobacillus collinoides GldA (gldA) and GldB (gldB) genes, complete cds; and glycerol dehydratase large subunit GldC (gldC) gene, partial cds	7.96E-73	777.00
AJ297723	Lactobacillus collinoides istA, istB, pocR, pduA, pduB, pduC, pduD, pduE, pduG, pduH, pduK, pduJ, pduL, pduM, pduN, pduO, pduObis, pduP, pduQ, pduW, pduU and partial pduS genes	8.21E-73	777.00
CP000939	Clostridium botulinum B1 str. Okra, complete genome	8.66E-73	777.00
CP000728	Clostridium botulinum F str. Langeland, complete genome	1.33E-71	765.00
CP000962	Clostridium botulinum A3 str. Loch Maree, complete genome	2.87E-71	762.00
FM180568	Escherichia coli 0127: H6 E2348/69 complete genome, strain E2348/69	1.04E-62	681.00
AM236324	Escherichia coli genome fragment containing the yersiniabactin, cob and pdu gene clusters, strain A0 34/86	1.04E-62	681.00

Hit	Description	E-value	Score
CU928163	Escherichia coli UMN026 chromosome, complete genome	1.24E-62	680.00
AM498294	Citrobacter freundii cbiA gene for cobyrinic acid A,C-diamide synthase and pdu operon	2.13E-62	678.00
AL591978	Listeria monocytogenes strain EGD, complete genome, segment 6/12	2.27E-62	678.00
CP000800	Escherichia coli E24377A, complete genome	2.48E-62	677.00
CU928158	Escherichia fergusonii ATCC 35469 chromosome, complete genome	2.72E-62	677.00
CP001127	Salmonella enterica subsp. enterica serovar Schwarzengrund str. CVM19633, complete genome	6.51E-62	673.00
CP000857	Salmonella enterica subsp. enterica serovar Paratyphi C strain RKS4594, complete genome	9.67E-62	672.00
AE017220	Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67, complete genome	9.67E-62	672.00
FN424405	Salmonella enterica subsp. enterica serovar Typhimurium str. D23580 complete genome	1E-61	672.00
AE006468	Salmonella enterica subsp. enterica serovar Typhimurium str. LT2, complete genome	1E-61	672.00
AM933172	Salmonella enterica subsp. enterica serovar Enteritidis str. P125109 complete genome	1E-61	672.00
AM933173	Salmonella enterica subsp. enterica serovar Gallinarum str. 287/91	1E-61	672.00

Hit	Description	E-value	Score
	complete genome		
CP001144	Salmonella enterica subsp. enterica serovar Dublin str. CT_02021853, complete genome	1E-61	672.00
CP001113	Salmonella enterica subsp. enterica serovar Newport str. SL254, complete genome	1E-61	672.00
CP001616	Tolomonas auensis DSM 9187, complete genome	1.15E-61	671.00
CP000038	Shigella sonnei Ss046, complete genome	1.22E-61	671.00
CP001138	Salmonella enterica subsp. enterica serovar Agona str. SL483, complete genome	1.42E-61	670.00
FM200053	Salmonella enterica subsp. enterica serovar Paratyphi A str. AKU_12601 complete genome, strain AKU_12601	1.42E-61	670.00
CP000886	Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7, complete genome	1.42E-61	670.00
CP000026	Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150	1.42E-61	670.00
AE014613	Salmonella enterica subsp. enterica serovar Typhi Ty2, complete genome	1.42E-61	670.00
AL627273	Salmonella enterica serovar Typhi (Salmonella typhi) strain CT18, complete chromosome; segment 9/20	1.42E-61	670.00
AM263198	Listeria welshimeri serovar 6b str. SLCC5334 complete genome	1.47E-61	670.00
CP000822	Citrobacter koseri ATCC BAA-895,	1.77E-61	669.00

Hit	Description	E-value	Score
	complete genome		
AF026270	Salmonella enterica serovar Typhimurium PdcR (pdcR) gene, partial cds; PduF (pudF) gene, complete cds and pdu operon, complete sequence	1.8E-61	669.00
CP001120	Salmonella enterica subsp. enterica serovar Heidelberg str. SL476, complete genome	2.39E-61	668.00
CP001175	Listeria monocytogenes HCC23, complete genome	4.66E-61	665.00
FM242711	Listeria monocytogenes Clip80459 serotype 4b complete genome	4.95E-61	665.00
AE017262	Listeria monocytogenes str. 4b F2365, complete genome	4.95E-61	665.00
AL596167	Listeria innocua Clip11262 complete genome, segment 5/12	5.46E-61	665.00
AP006725	Klebsiella pneumoniae NTUH-K2044 DNA, complete genome	7.57E-61	663.00
CP000647	Klebsiella pneumoniae subsp. pneumoniae MGH 78578, complete sequence	7.57E-61	663.00
CP000721	Clostridium beijerinckii NCIMB 8052, complete genome	8.81E-61	663.00
CP000964	Klebsiella pneumoniae 342, complete genome	1.24E-60	661.00
CP000880	Salmonella enterica subsp. arizonae serovar 62:z4,z23:--, complete genome	1.8E-60	660.00
CP000387	Streptococcus sanguinis SK36, complete genome	2.51E-60	658.00
AM286415	Yersinia enterocolitica subsp. enterocolitica 8081 complete genome	6.35E-60	655.00
CP000681	Shewanella putrefaciens CN-32,	5.32E-59	646.00

Hit	Description	E-value	Score
	complete genome		
CP000503	Shewanella sp. W3-18-1, complete genome	5.32E-59	646.00
CP001322	Desulfatibacillum alkenivorans AK-01, complete genome	9.33E-59	644.00
CP001056	Clostridium botulinum B str. Eklund 17B, complete genome	1.43E-57	632.00
CP001078	Clostridium botulinum E3 str. Alaska E43, complete genome	1.75E-56	622.00
AP008232	Sodalis glossinidius str. 'morsitans' DNA, complete genome	4.92E-49	489.00
AP008232	Sodalis glossinidius str. 'morsitans' DNA, complete genome	4.92E-49	109.00
AY061969	Lactobacillus hilgardii GldA (gldA), GldB (gldB), glycerol dehydratase large subunit GldC (gldC), glycerol dehydratase medium subunit GldD (gldD), glycerol dehydratase small subunit GldE (gldE), GldG (gldG), and GldH (gldH) genes, complete cds; and GldK (gldK) gene, partial cds	6.93E-49	550.00
CP000141	Carboxydotherrmus hydrogenoformans Z-2901, complete genome	8.7E-49	549.00
AY061968	Lactobacillus diolivorans GldB (gldB), glycerol dehydratase large subunit GldC (gldC), glycerol dehydratase medium subunit GldD (gldD), and glycerol dehydratase small subunit GldE (gldE) genes, complete cds; and GldG (gldG) gene, partial cds	2.78E-48	544.00
DQ233725	Lactobacillus reuteri propanediol utilization	6.99E-45	512.00

Hit	Description	E-value	Score
	protein (lr1881) gene, complete cds		
AP007281	Lactobacillus reuteri JCM 1112 DNA, complete genome	7.37E-45	512.00
CP000705	Lactobacillus reuteri DSM 20016, complete genome	7.37E-45	512.00
AP009049	Clostridium kluveri NBRC 12016 DNA, complete genome	4.27E-28	353.00
CP000673	Clostridium kluveri DSM 555, complete genome	4.27E-28	353.00
DQ831236	Heliobacillus mobilis ethanolamine utilization protein eutM (eutM), ethanolamine utilization protein pduL (pduL), ethanolamine utilization flavoprotein, ethanolamine utilization protein eutN (eutN), and ethanolamine utilization protein eutT (eutT) genes, complete cds; eutE pseudogene, complete sequence; and ethanolamine utilization Fe-S center protein eut (pduS) and ethanolamine utilization protein eutM (eutM) genes, complete cds	3.24E-22	297.00
AF026270	Salmonella enterica serovar Typhimurium PocR (pocR) gene, partial cds; PduF (pudF) gene, complete cds and pdu operon, complete sequence	7.48E-22	294.00
CP001078	Clostridium botulinum E3 str. Alaska E43, complete genome	9.04E-22	293.00
CP000885	Clostridium phytofermentans ISDg, complete genome	9.98E-22	293.00
CP001616	Tolomonas auensis DSM 9187, complete genome	1.08E-21	292.00

Hit	Description	E-value	Score
CP000681	Shewanella putrefaciens CN-32, complete genome	1.19E-21	292.00
FM180568	Escherichia coli 0127: H6 E2348/69 complete genome, strain E2348/69	1.33E-21	291.00
AM236324	Escherichia coli genome fragment containing the yersiniabactin, cob and pdu gene clusters, strain A0 34/86	1.33E-21	291.00
CU928163	Escherichia coli UMN026 chromosome, complete genome	1.33E-21	291.00
CP000800	Escherichia coli E24377A, complete genome	1.33E-21	291.00
CP001056	Clostridium botulinum B str. Eklund 17B, complete genome	1.39E-21	291.00
CP000721	Clostridium beijerinckii NCIMB 8052, complete genome	1.43E-21	291.00
CP000038	Shigella sonnei Ss046, complete genome	1.5E-21	291.00
CP000886	Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7, complete genome	1.6E-21	291.00
CP000503	Shewanella sp. W3-18-1, complete genome	1.67E-21	291.00
CP001127	Salmonella enterica subsp. enterica serovar Schwarzengrund str. CVM19633, complete genome	1.71E-21	290.00
CP000857	Salmonella enterica subsp. enterica serovar Paratyphi C strain RKS4594, complete genome	1.71E-21	290.00
AE017220	Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67, complete genome	1.71E-21	290.00

Hit	Description	E-value	Score
FN424405	Salmonella enterica subsp. enterica serovar Typhimurium str. D23580 complete genome	1.71E-21	290.00
AE006468	Salmonella enterica subsp. enterica serovar Typhimurium str. LT2, complete genome	1.71E-21	290.00
AM933172	Salmonella enterica subsp. enterica serovar Enteritidis str. P125109 complete genome	1.71E-21	290.00
CP001144	Salmonella enterica subsp. enterica serovar Dublin str. CT_02021853, complete genome	1.71E-21	290.00
CP001113	Salmonella enterica subsp. enterica serovar Newport str. SL254, complete genome	1.71E-21	290.00
CP001138	Salmonella enterica subsp. enterica serovar Agona str. SL483, complete genome	1.71E-21	290.00
AE014613	Salmonella enterica subsp. enterica serovar Typhi Ty2, complete genome	1.71E-21	290.00
AL627273	Salmonella enterica serovar Typhi (Salmonella typhi) strain CT18, complete chromosome; segment 9/20	1.71E-21	290.00
CP001120	Salmonella enterica subsp. enterica serovar Heidelberg str. SL476, complete genome	1.71E-21	290.00
AM498294	Citrobacter freundii cbiA gene for cobyrinic acid A,C-diamide synthase and pdu operon	1.74E-21	290.00
CU928158	Escherichia fergusonii ATCC 35469 chromosome, complete genome	1.9E-21	290.00

Hit	Description	E-value	Score
CP000822	Citrobacter koseri ATCC BAA-895, complete genome	2.25E-21	289.00
AL591978	Listeria monocytogenes strain EGD, complete genome, segment 6/12	2.72E-21	289.00
CP000301	Rhodopseudomonas palustris BisB18, complete genome	2.96E-21	288.00
CP001175	Listeria monocytogenes HCC23, complete genome	3.09E-21	288.00
FM242711	Listeria monocytogenes Clip80459 serotype 4b complete genome	3.09E-21	288.00
AE017262	Listeria monocytogenes str. 4b F2365, complete genome	3.09E-21	288.00
CP001056	Clostridium botulinum B str. Eklund 17B, complete genome	3.47E-21	288.00
CP001078	Clostridium botulinum E3 str. Alaska E43, complete genome	3.47E-21	288.00
AP006725	Klebsiella pneumoniae NTUH-K2044 DNA, complete genome	3.8E-21	287.00
CP000647	Klebsiella pneumoniae subsp. pneumoniae MGH 78578, complete sequence	3.8E-21	287.00
CP000964	Klebsiella pneumoniae 342, complete genome	3.8E-21	287.00
DQ299884	Roseburia inulinivorans strain A2-194 transposase gene, partial cds; and phosphohistidinol phosphatase, PduU, PduV, fucose aldolase, PduO, aldehyde dehydrogenase, alcohol dehydrogenase, PduA, PduJs, PduA, PduL, PduN, PduS, PduT, fucose operon activator, glycerol dehydratase, and glycerol dehydratase activator	3.8E-21	287.00

Hit	Description	E-value	Score
	genes, complete cds		
CP000880	Salmonella enterica subsp. arizonae serovar 62:z4,z23:--, complete genome	3.91E-21	287.00
CP000721	Clostridium beijerinckii NCIMB 8052, complete genome	4.59E-21	286.00
FM242711	Listeria monocytogenes Clip80459 serotype 4b complete genome	4.88E-21	286.00
AE017262	Listeria monocytogenes str. 4b F2365, complete genome	4.88E-21	286.00
AM263198	Listeria welshimeri serovar 6b str. SLCC5334 complete genome	4.95E-21	286.00
FM200053	Salmonella enterica subsp. enterica serovar Paratyphi A str. AKU_12601 complete genome, strain AKU_12601	5.03E-21	286.00
CP000026	Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150	5.03E-21	286.00
AL596167	Listeria innocua Clip11262 complete genome, segment 5/12	5.81E-21	285.00
CP001175	Listeria monocytogenes HCC23, complete genome	6.03E-21	285.00
CP000230	Rhodospirillum rubrum ATCC 11170, complete genome	9.52E-21	283.00
AM263198	Listeria welshimeri serovar 6b str. SLCC5334 complete genome	1.03E-20	283.00
CP000612	Desulfotomaculum reducens MI-1, complete genome	1.15E-20	283.00
AM933173	Salmonella enterica subsp. enterica serovar Gallinarum str. 287/91 complete genome	1.16E-20	283.00

Hit	Description	E-value	Score
AL596167	Listeria innocua Clip11262 complete genome, segment 5/12	1.17E-20	283.00
CP000880	Salmonella enterica subsp. arizonae serovar 62:z4,z23:--, complete genome	1.2E-20	282.00
CP000473	Solibacter usitatus Ellin6076, complete genome	1.94E-20	280.00
AL591978	Listeria monocytogenes strain EGD, complete genome, segment 6/12	2.18E-20	280.00
DQ233726	Lactobacillus reuteri propanediol utilization protein (lr1882) gene, complete cds	3.07E-20	279.00
CP000724	Alkaliphilus metalliredigens QYMF, complete genome	3.21E-20	278.00
AE015927	Clostridium tetani E88, complete genome	3.23E-20	278.00
CP001336	Desulfitobacterium hafniense DCB-2, complete genome	4.69E-20	277.00
AP008230	Desulfitobacterium hafniense Y51 DNA, complete genome	4.69E-20	277.00
CP000964	Klebsiella pneumoniae 342, complete genome	5.76E-20	276.00
CP000853	Alkaliphilus oremlandii OhILAs, complete genome	6.65E-20	275.00
CP000885	Clostridium phytofermentans ISDg, complete genome	7.28E-20	275.00
CP001100	Chloroherpeton thalassium ATCC 35110, complete genome	7.45E-20	275.00
CP001127	Salmonella enterica subsp. enterica serovar Schwarzengrund str. CVM19633, complete genome	7.92E-20	275.00
FN424405	Salmonella enterica subsp. enterica serovar	7.92E-20	275.00

Hit	Description	E-value	Score
	Typhimurium str. D23580 complete genome		
AE006468	Salmonella enterica subsp. enterica serovar Typhimurium str. LT2, complete genome	7.92E-20	275.00
AM933172	Salmonella enterica subsp. enterica serovar Enteritidis str. P125109 complete genome	7.92E-20	275.00
AM933173	Salmonella enterica subsp. enterica serovar Gallinarum str. 287/91 complete genome	7.92E-20	275.00
CP001144	Salmonella enterica subsp. enterica serovar Dublin str. CT_02021853, complete genome	7.92E-20	275.00
CP001113	Salmonella enterica subsp. enterica serovar Newport str. SL254, complete genome	7.92E-20	275.00
CP001138	Salmonella enterica subsp. enterica serovar Agona str. SL483, complete genome	7.92E-20	275.00
FM200053	Salmonella enterica subsp. enterica serovar Paratyphi A str. AKU_12601 complete genome, strain AKU_12601	7.92E-20	275.00
CP000886	Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7, complete genome	7.92E-20	275.00
CP000026	Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150	7.92E-20	275.00
AE014613	Salmonella enterica subsp. enterica serovar Typhi Ty2, complete genome	7.92E-20	275.00
AL627273	Salmonella enterica serovar Typhi (Salmonella typhi) strain	7.92E-20	275.00

Hit	Description	E-value	Score
	CT18, complete chromosome; segment 9/20		
AF026270	Salmonella enterica serovar Typhimurium PocR (pocR) gene, partial cds; PduF (pudF) gene, complete cds and pdu operon, complete sequence	7.92E-20	275.00
CP001120	Salmonella enterica subsp. enterica serovar Heidelberg str. SL476, complete genome	7.92E-20	275.00
AM286415	Yersinia enterocolitica subsp. enterocolitica 8081 complete genome	1.03E-19	274.00
AP006725	Klebsiella pneumoniae NTUH-K2044 DNA, complete genome	1.4E-19	272.00
CP000647	Klebsiella pneumoniae subsp. pneumoniae MGH 78578, complete sequence	1.4E-19	272.00
CP001322	Desulfatibacillum alkenivorans AK-01, complete genome	1.42E-19	272.00
CP000724	Alkaliphilus metalliredigens QYMF, complete genome	1.63E-19	272.00
CP000939	Clostridium botulinum B1 str. Okra, complete genome	1.73E-19	271.00
CP000728	Clostridium botulinum F str. Langeland, complete genome	1.73E-19	271.00
CP000962	Clostridium botulinum A3 str. Loch Maree, complete genome	1.73E-19	271.00
AE015927	Clostridium tetani E88, complete genome	1.73E-19	271.00
CP001083	Clostridium botulinum Ba4 str. 657, complete genome	1.73E-19	271.00
CP001581	Clostridium botulinum A2 str. Kyoto, complete genome	1.73E-19	271.00
CP000727	Clostridium botulinum A	1.73E-19	271.00

Hit	Description	E-value	Score
	str. Hall, complete genome		
CP000726	Clostridium botulinum A str. ATCC 19397, complete genome	1.73E-19	271.00
AM412317	Clostridium botulinum A str. ATCC 3502 complete genome	1.73E-19	271.00
CP001616	Tolomonas auensis DSM 9187, complete genome	1.74E-19	271.00
CP001358	Desulfovibrio desulfuricans subsp. desulfuricans str. ATCC 27774, complete genome	1.88E-19	271.00
AY205335	Uncultured bacterium pdu operon, partial sequence	1.94E-19	271.00
CP000112	Desulfovibrio desulfuricans subsp. desulfuricans str. G20, complete genome	2.13E-19	271.00
AE016830	Enterococcus faecalis V583, complete genome	2.22E-19	270.00
CP001056	Clostridium botulinum B str. Eklund 17B, complete genome	2.35E-19	270.00
CP001078	Clostridium botulinum E3 str. Alaska E43, complete genome	2.35E-19	270.00
AM180355	Clostridium difficile 630 complete genome	2.47E-19	270.00
CP000885	Clostridium phytofermentans ISDg, complete genome	2.53E-19	270.00
FN545816	Clostridium difficile R20291 complete genome	2.57E-19	270.00
FN538970	Clostridium difficile CD196 complete genome, strain CD196	2.57E-19	270.00
CP001336	Desulfitobacterium hafniense DCB-2, complete genome	2.71E-19	270.00
CP000724	Alkaliphilus	2.95E-19	269.00

Hit	Description	E-value	Score
	metalliredigens QYMF, complete genome		
CP000853	Alkaliphilus oremlandii OhILAs, complete genome	3.04E-19	269.00
AP008230	Desulfitobacterium hafniense Y51 DNA, complete genome	3.46E-19	269.00
CP000857	Salmonella enterica subsp. enterica serovar Paratyphi C strain RKS4594, complete genome	4.02E-19	268.00
AE017220	Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67, complete genome	4.02E-19	268.00
AP008955	Brevibacillus brevis NBRC 100599 DNA, complete genome	4.27E-19	268.00
AP007281	Lactobacillus reuteri JCM 1112 DNA, complete genome	4.83E-19	267.00
CP000705	Lactobacillus reuteri DSM 20016, complete genome	4.83E-19	267.00
CP000556	Methylibium petroleiphilum PM1 plasmid RPME01, complete sequence	4.9E-19	267.00
CP001336	Desulfitobacterium hafniense DCB-2, complete genome	5.05E-19	267.00
AP008230	Desulfitobacterium hafniense Y51 DNA, complete genome	5.05E-19	267.00
CP001175	Listeria monocytogenes HCC23, complete genome	6.06E-19	266.00
FM242711	Listeria monocytogenes Clip80459 serotype 4b complete genome	6.06E-19	266.00
AE017262	Listeria monocytogenes str. 4b F2365, complete genome	6.06E-19	266.00
AL596167	Listeria innocua Clip11262 complete	6.11E-19	266.00

Hit	Description	E-value	Score
	genome, segment 5/12		
AL591978	Listeria monocytogenes strain EGD, complete genome, segment 6/12	6.15E-19	266.00
AM263198	Listeria welshimeri serovar 6b str. SLCC5334 complete genome	6.15E-19	266.00
CU928158	Escherichia fergusonii ATCC 35469 chromosome, complete genome	7.55E-19	265.00
CP001685	Leptotrichia buccalis DSM 1135, complete genome	8.27E-19	265.00
AM498294	Citrobacter freundii cbiA gene for cobyrinic acid A,C-diamide synthase and pdu operon	8.4E-19	265.00
CP000387	Streptococcus sanguinis SK36, complete genome	8.4E-19	265.00
CP001685	Leptotrichia buccalis DSM 1135, complete genome	8.79E-19	265.00
CP000885	Clostridium phytofermentans ISDg, complete genome	9.7E-19	264.00
CP000141	Carboxydotherrmus hydrogenoformans Z-2901, complete genome	1E-18	264.00
CP000822	Citrobacter koseri ATCC BAA-895, complete genome	1.19E-18	264.00
CP000387	Streptococcus sanguinis SK36, complete genome	1.58E-18	262.00
FM180568	Escherichia coli 0127: H6 E2348/69 complete genome, strain E2348/69	1.72E-18	262.00
AM236324	Escherichia coli genome fragment containing the yersiniabactin, cob and pdu gene clusters,	1.72E-18	262.00

Hit	Description	E-value	Score
	strain A0 34/86		
CU928163	Escherichia coli UMN026 chromosome, complete genome	1.72E-18	262.00
CP000800	Escherichia coli E24377A, complete genome	1.72E-18	262.00
CP000038	Shigella sonnei Ss046, complete genome	1.72E-18	262.00
AE009951	Fusobacterium nucleatum subsp. nucleatum ATCC 25586, complete genome	1.95E-18	261.00
CP001685	Leptotrichia buccalis DSM 1135, complete genome	2E-18	261.00
CP000612	Desulfotomaculum reducens MI-1, complete genome	2.07E-18	261.00
CP000112	Desulfovibrio desulfuricans subsp. desulfuricans str. G20, complete genome	2.34E-18	261.00
CP000509	Nocardioides sp. JS614 , complete genome	2.55E-18	260.00
CP000246	Clostridium perfringens ATCC 13124, complete genome	2.57E-18	260.00
DQ233718	Lactobacillus reuteri propanediol utilization protein (lr1874) gene, complete cds	2.57E-18	260.00
BA000016	Clostridium perfringens str. 13 DNA, complete genome	2.57E-18	260.00
AM286415	Yersinia enterocolitica subsp. enterocolitica 8081 complete genome	2.85E-18	260.00
AP007281	Lactobacillus reuteri JCM 1112 DNA, complete genome	5.44E-18	257.00
CP000705	Lactobacillus reuteri DSM 20016, complete genome	5.44E-18	257.00
CP000853	Alkaliphilus oremlandii OhILAs, complete	6.73E-18	256.00

Hit	Description	E-value	Score
	genome		
CP000964	<i>Klebsiella pneumoniae</i> 342, complete genome	4.07E-17	249.00
CP000473	<i>Solibacter usitatus</i> Ellin6076, complete genome	4.13E-17	249.00
DQ299884	<i>Roseburia inulinivorans</i> strain A2-194 transposase gene, partial cds; and phosphohistidinol phosphatase, PduU, PduV, fucose aldolase, PduO, aldehyde dehydrogenase, alcohol dehydrogenase, PduA, PduJs, PduA, PduL, PduN, PduS, PduT, fucose operon activator, glycerol dehydratase, and glycerol dehydratase activator genes, complete cds	7.19E-17	247.00
AJ297723	<i>Lactobacillus collinoides</i> istA, istB, pocR, pduA, pduB, pduC, pduD, pduE, pduG, pduH, pduK, pduJ, pduL, pduM, pduN, pduO, pduObis, pduP, pduQ, pduW, pduU and partial pduS genes	7.41E-17	247.00
CP000416	<i>Lactobacillus brevis</i> ATCC 367, complete genome	9.9E-17	245.00
CU928158	<i>Escherichia fergusonii</i> ATCC 35469 chromosome, complete genome	1.04E-16	245.00
CP001358	<i>Desulfovibrio desulfuricans</i> subsp. <i>desulfuricans</i> str. ATCC 27774, complete genome	1.04E-16	245.00
AE014613	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Typhi Ty2, complete genome	1.42E-16	244.00
CP000822	<i>Citrobacter koseri</i>	1.65E-16	243.00

Hit	Description	E-value	Score
	ATCC BAA-895, complete genome		
AP006725	Klebsiella pneumoniae NTUH-K2044 DNA, complete genome	1.65E-16	243.00
CP000647	Klebsiella pneumoniae subsp. pneumoniae MGH 78578, complete sequence	1.65E-16	243.00
CP000964	Klebsiella pneumoniae 342, complete genome	1.65E-16	243.00
CP000880	Salmonella enterica subsp. arizonae serovar 62:z4,z23:--, complete genome	1.65E-16	243.00
CU928162	Escherichia coli ED1a chromosome, complete genome	1.84E-16	243.00
CP000468	Escherichia coli APEC O1, complete genome	1.84E-16	243.00
AE014075	Escherichia coli CFT073, complete genome	1.84E-16	243.00
FM180568	Escherichia coli 0127: H6 E2348/69 complete genome, strain E2348/ 69	1.84E-16	243.00
CU928163	Escherichia coli UMN026 chromosome, complete genome	1.84E-16	243.00
CP000800	Escherichia coli E24377A, complete genome	1.84E-16	243.00
CU928158	Escherichia fergusonii ATCC 35469 chromosome, complete genome	1.84E-16	243.00
CP001127	Salmonella enterica subsp. enterica serovar Schwarzengrund str. CVM19633, complete genome	3.36E-16	240.00
CP000857	Salmonella enterica subsp. enterica serovar Paratyphi C strain RKS4594, complete genome	3.36E-16	240.00
AE017220	Salmonella enterica	3.36E-16	240.00

Hit	Description	E-value	Score
	subsp. enterica serovar Choleraesuis str. SC-B67, complete genome		
FN424405	Salmonella enterica subsp. enterica serovar Typhimurium str. D23580 complete genome	3.36E-16	240.00
AE006468	Salmonella enterica subsp. enterica serovar Typhimurium str. LT2, complete genome	3.36E-16	240.00
AM933172	Salmonella enterica subsp. enterica serovar Enteritidis str. P125109 complete genome	3.36E-16	240.00
AM933173	Salmonella enterica subsp. enterica serovar Gallinarum str. 287/91 complete genome	3.36E-16	240.00
CP001144	Salmonella enterica subsp. enterica serovar Dublin str. CT_02021853, complete genome	3.36E-16	240.00
CP001113	Salmonella enterica subsp. enterica serovar Newport str. SL254, complete genome	3.36E-16	240.00
CP001138	Salmonella enterica subsp. enterica serovar Agona str. SL483, complete genome	3.36E-16	240.00
FM200053	Salmonella enterica subsp. enterica serovar Paratyphi A str. AKU_12601 complete genome, strain AKU_12601	3.36E-16	240.00
CP000886	Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7, complete genome	3.36E-16	240.00
CP000026	Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150	3.36E-16	240.00
CP001120	Salmonella enterica	3.36E-16	240.00

Hit	Description	E-value	Score
	subsp. enterica serovar Heidelberg str. SL476, complete genome		
CP000038	Shigella sonnei Ss046, complete genome	3.71E-16	240.00
CP000681	Shewanella putrefaciens CN-32, complete genome	8.55E-16	236.00
CP000503	Shewanella sp. W3-18-1, complete genome	8.55E-16	236.00
CP000964	Klebsiella pneumoniae 342, complete genome	9.66E-16	236.00
CP000964	Klebsiella pneumoniae 342, complete genome	1.12E-15	235.00
CU928158	Escherichia fergusonii ATCC 35469 chromosome, complete genome	1.26E-15	235.00
CU928158	Escherichia fergusonii ATCC 35469 chromosome, complete genome	2.01E-14	223.00
CP001336	Desulfitobacterium hafniense DCB-2, complete genome	1.53E-13	215.00
AP008230	Desulfitobacterium hafniense Y51 DNA, complete genome	1.53E-13	215.00
AP009049	Clostridium kluyveri NBRC 12016 DNA, complete genome	2.24E-13	214.00
CP000673	Clostridium kluyveri DSM 555, complete genome	2.24E-13	214.00
CU928161	Escherichia coli S88 chromosome, complete genome	2.36E-13	157.00
CU928161	Escherichia coli S88 chromosome, complete genome	2.36E-13	97.00
CP000853	Alkaliphilus oremlandii OhILAs, complete genome	3.66E-13	212.00
CP001336	Desulfitobacterium hafniense DCB-2, complete genome	8.84E-13	208.00
AP008230	Desulfitobacterium	8.84E-13	208.00

Hit	Description	E-value	Score
	hafniense Y51 DNA, complete genome		
CP000612	Desulfotomaculum reducens MI-1, complete genome	4.81E-12	201.00
CP000141	Carboxydotherrmus hydrogenoformans Z-2901, complete genome	1.03E-11	198.00
CP001083	Clostridium botulinum Ba4 str. 657, complete genome	1.62E-11	196.00
CP001581	Clostridium botulinum A2 str. Kyoto, complete genome	1.89E-11	195.00
CP000727	Clostridium botulinum A str. Hall, complete genome	1.89E-11	195.00
CP000726	Clostridium botulinum A str. ATCC 19397, complete genome	1.89E-11	195.00
AM412317	Clostridium botulinum A str. ATCC 3502 complete genome	1.89E-11	195.00
CP000939	Clostridium botulinum B1 str. Okra, complete genome	2E-11	195.00
CP000612	Desulfotomaculum reducens MI-1, complete genome	2E-11	195.00
CP000728	Clostridium botulinum F str. Langeland, complete genome	2.03E-11	195.00
CP000473	Solibacter usitatus Ellin6076, complete genome	2.61E-11	194.00
CP001078	Clostridium botulinum E3 str. Alaska E43, complete genome	3.04E-11	193.00
CP000962	Clostridium botulinum A3 str. Loch Maree, complete genome	4.95E-11	191.00
CP000939	Clostridium botulinum B1 str. Okra, complete genome	6.16E-11	190.00
CP000728	Clostridium botulinum F str. Langeland,	6.16E-11	190.00

Hit	Description	E-value	Score
	complete genome		
CP001083	Clostridium botulinum Ba4 str. 657, complete genome	6.16E-11	190.00
CP001581	Clostridium botulinum A2 str. Kyoto, complete genome	6.16E-11	190.00
CP000727	Clostridium botulinum A str. Hall, complete genome	7.68E-11	190.00
CP000726	Clostridium botulinum A str. ATCC 19397, complete genome	7.68E-11	190.00
AM412317	Clostridium botulinum A str. ATCC 3502 complete genome	7.68E-11	190.00
CP000473	Solibacter usitatus Ellin6076, complete genome	8.1E-11	189.00
CP000382	Clostridium novyi NT, complete genome	8.74E-11	189.00
CP000962	Clostridium botulinum A3 str. Loch Maree, complete genome	9.22E-11	189.00
CP000724	Alkaliphilus metalliredigens QYMF, complete genome	1.78E-10	186.00
CP000724	Alkaliphilus metalliredigens QYMF, complete genome	1.93E-10	186.00
CP001078	Clostridium botulinum E3 str. Alaska E43, complete genome	2.84E-10	184.00
CP000885	Clostridium phytofermentans ISDg, complete genome	3.3E-10	184.00
CP001056	Clostridium botulinum B str. Eklund 17B, complete genome	3.33E-10	183.00
CP000473	Solibacter usitatus Ellin6076, complete genome	3.33E-10	183.00
CP000939	Clostridium botulinum B1 str. Okra, complete genome	3.9E-10	183.00
CP000728	Clostridium botulinum F str. Langeland,	3.9E-10	183.00

Hit	Description	E-value	Score
	complete genome		
CP000962	Clostridium botulinum A3 str. Loch Maree, complete genome	3.9E-10	183.00
CP001083	Clostridium botulinum Ba4 str. 657, complete genome	3.9E-10	183.00
CP000724	Alkaliphilus metalliredigens QYMF, complete genome	3.99E-10	183.00
CP000724	Alkaliphilus metalliredigens QYMF, complete genome	4.24E-10	182.00
CP001581	Clostridium botulinum A2 str. Kyoto, complete genome	4.72E-10	182.00
CP000727	Clostridium botulinum A str. Hall, complete genome	4.72E-10	182.00
CP000726	Clostridium botulinum A str. ATCC 19397, complete genome	4.72E-10	182.00
AM412317	Clostridium botulinum A str. ATCC 3502 complete genome	4.72E-10	182.00
AP009049	Clostridium kluyveri NBRC 12016 DNA, complete genome	5.05E-10	182.00
CP000673	Clostridium kluyveri DSM 555, complete genome	5.05E-10	182.00
AE015927	Clostridium tetani E88, complete genome	5.79E-10	181.00
CP000853	Alkaliphilus oremlandii OhILAs, complete genome	6.44E-10	181.00
CP000556	Methylibium petroleiphilum PM1 plasmid RPME01, complete sequence	1.02E-9	179.00
CP000112	Desulfovibrio desulfuricans subsp. desulfuricans str. G20, complete genome	1.06E-9	179.00
CP001056	Clostridium botulinum B str. Eklund 17B, complete genome	2.43E-9	175.00

Hit	Description	E-value	Score
CP001078	<i>Clostridium botulinum</i> E3 str. Alaska E43, complete genome	2.62E-9	175.00
CP000853	<i>Alkaliphilus oremlandii</i> OhILAs, complete genome	2.9E-9	175.00
CP001056	<i>Clostridium botulinum</i> B str. Eklund 17B, complete genome	3.53E-9	174.00
CP000885	<i>Clostridium phytofermentans</i> ISDg, complete genome	4.27E-9	173.00
AE015927	<i>Clostridium tetani</i> E88, complete genome	4.82E-9	172.00
CP001358	<i>Desulfovibrio desulfuricans</i> subsp. <i>desulfuricans</i> str. ATCC 27774, complete genome	5.16E-9	172.00
AE015927	<i>Clostridium tetani</i> E88, complete genome	6.78E-9	171.00
AP008232	<i>Sodalis glossinidius</i> str. 'morsitans' DNA, complete genome	1.09E-8	169.00
CP001358	<i>Desulfovibrio desulfuricans</i> subsp. <i>desulfuricans</i> str. ATCC 27774, complete genome	1.62E-8	167.00
CP000112	<i>Desulfovibrio desulfuricans</i> subsp. <i>desulfuricans</i> str. G20, complete genome	1.83E-8	167.00
AP008230	<i>Desulfitobacterium hafniense</i> Y51 DNA, complete genome	1.88E-8	167.00
CP001336	<i>Desulfitobacterium hafniense</i> DCB-2, complete genome	4.53E-8	163.00
CP000885	<i>Clostridium phytofermentans</i> ISDg, complete genome	6.62E-8	162.00
CP000612	<i>Desulfotomaculum reducens</i> MI-1, complete genome	7.59E-8	161.00
CP000246	<i>Clostridium perfringens</i> ATCC 13124, complete	8.37E-8	161.00

Hit	Description	E-value	Score
	genome		
BA000016	<i>Clostridium perfringens</i> str. 13 DNA, complete genome	9.17E-8	160.00
CP000141	<i>Carboxydotherrmus hydrogenoformans</i> Z-2901, complete genome	1.41E-7	159.00
CP000853	<i>Alkaliphilus oremlandii</i> OhILAs, complete genome	3.31E-7	155.00
CP001056	<i>Clostridium botulinum</i> B str. Eklund 17B, complete genome	5.18E-7	153.00
AE009951	<i>Fusobacterium nucleatum</i> subsp. <i>nucleatum</i> ATCC 25586, complete genome	6.03E-7	153.00
CP000724	<i>Alkaliphilus metalliredigens</i> QYMF, complete genome	6.26E-7	152.00
CP001078	<i>Clostridium botulinum</i> E3 str. Alaska E43, complete genome	6.36E-7	152.00
FN545816	<i>Clostridium difficile</i> R20291 complete genome	7.93E-7	151.00
FN538970	<i>Clostridium difficile</i> CD196 complete genome, strain CD196	7.93E-7	151.00
CP000612	<i>Desulfotomaculum reducens</i> MI-1, complete genome	1.03E-6	110.00
CP000612	<i>Desulfotomaculum reducens</i> MI-1, complete genome	1.03E-6	80.00
CP001358	<i>Desulfovibrio desulfuricans</i> subsp. <i>desulfuricans</i> str. ATCC 27774, complete genome	1.35E-6	149.00
AM180355	<i>Clostridium difficile</i> 630 complete genome	1.41E-6	149.00
AE014075	<i>Escherichia coli</i> CFT073, complete genome	2.4E-6	147.00

Hit	Description	E-value	Score
AE015927	Clostridium tetani E88, complete genome	3.21E-6	146.00
AP006725	Klebsiella pneumoniae NTUH-K2044 DNA, complete genome	4.15E-6	145.00
CU928162	Escherichia coli ED1a chromosome, complete genome	6.65E-6	143.00
CU928161	Escherichia coli S88 chromosome, complete genome	6.65E-6	143.00
CP000468	Escherichia coli APEC O1, complete genome	6.65E-6	143.00
FM180568	Escherichia coli 0127: H6 E2348/69 complete genome, strain E2348/69	6.65E-6	143.00
CU928163	Escherichia coli UMN026 chromosome, complete genome	6.65E-6	143.00
CP000038	Shigella sonnei Ss046, complete genome	6.65E-6	143.00
CP000800	Escherichia coli E24377A, complete genome	7.01E-6	143.00
CP000112	Desulfovibrio desulfuricans subsp. desulfuricans str. G20, complete genome	9.28E-6	141.00
CP001175	Listeria monocytogenes HCC23, complete genome	1.2E-5	140.00
CU928158	Escherichia fergusonii ATCC 35469 chromosome, complete genome	1.24E-5	140.00
AM263198	Listeria welshimeri serovar 6b str. SLCC5334 complete genome	1.4E-5	140.00
AL591978	Listeria monocytogenes strain EGD, complete genome, segment 6/12	1.73E-5	139.00
AL596167	Listeria innocua Clip11262 complete genome, segment 5/12	2.03E-5	138.00
CP000923	Thermoanaerobacter	3.56E-5	136.00

Hit	Description	E-value	Score
	sp. X514, complete genome		
AE017262	Listeria monocytogenes str. 4b F2365, complete genome	4.61E-5	135.00
FM242711	Listeria monocytogenes Clip80459 serotype 4b complete genome	6.15E-5	134.00
CP000885	Clostridium phytofermentans ISDg, complete genome	8.72E-5	132.00
CP000473	Solibacter usitatus Ellin6076, complete genome	9.06E-5	132.00
CP000721	Clostridium beijerinckii NCIMB 8052, complete genome	1.71E-4	129.00
CP000964	Klebsiella pneumoniae 342, complete genome	1.79E-4	129.00
CP001322	Desulfatibacillum alkenivorans AK-01, complete genome	2.56E-4	128.00
CP000724	Alkaliphilus metalliredigens QYMF, complete genome	4.6E-4	125.00
CP001175	Listeria monocytogenes HCC23, complete genome	6.23E-4	124.00
FM242711	Listeria monocytogenes Clip80459 serotype 4b complete genome	1.02E-3	122.00
AE017262	Listeria monocytogenes str. 4b F2365, complete genome	1.02E-3	122.00
AP008955	Brevibacillus brevis NBRC 100599 DNA, complete genome	1.04E-3	122.00
AE016830	Enterococcus faecalis V583, complete genome	3.19E-3	117.00
DQ299884	Roseburia inulinivorans strain A2-194 transposase gene, partial cds; and phosphohistidinol phosphatase, PduU, PduV, fucose aldolase, PduO, aldehyde	6.82E-3	114.00

Hit	Description	E-value	Score
	dehydrogenase, alcohol dehydrogenase, PduA, PduJs, PduA, PduL, PduN, PduS, PduT, fucose operon activator, glycerol dehydratase, and glycerol dehydratase activator genes, complete cds		
AL591978	Listeria monocytogenes strain EGD, complete genome, segment 6/12	7.03E-3	114.00
AL596167	Listeria innocua Clip11262 complete genome, segment 5/12	9.03E-3	113.00
CU928162	Escherichia coli ED1a chromosome, complete genome	9.45E-3	113.00
CU928161	Escherichia coli S88 chromosome, complete genome	9.45E-3	113.00
CP000468	Escherichia coli APEC O1, complete genome	9.45E-3	113.00
AE014075	Escherichia coli CFT073, complete genome	9.45E-3	113.00
CU928158	Escherichia fergusonii ATCC 35469 chromosome, complete genome	0.02	110.00
CU928161	Escherichia coli S88 chromosome, complete genome	0.02	110.00
CP000468	Escherichia coli APEC O1, complete genome	0.02	110.00
AE014075	Escherichia coli CFT073, complete genome	0.02	110.00
CP000800	Escherichia coli E24377A, complete genome	0.02	110.00
CP000038	Shigella sonnei Ss046, complete genome	0.02	110.00
CP001685	Leptotrichia buccalis DSM 1135, complete genome	0.02	109.00
FM180568	Escherichia coli 0127: H6 E2348/69 complete	0.03	108.00

Hit	Description	E-value	Score
	genome, strain E2348/69		
CU928163	Escherichia coli UMN026 chromosome, complete genome	0.03	108.00
AM263198	Listeria welshimeri serovar 6b str. SLCC5334 complete genome	0.04	106.00
CP000038	Shigella sonnei Ss046, complete genome	0.05	106.00
CP000416	Lactobacillus brevis ATCC 367, complete genome	0.05	106.00
AP006725	Klebsiella pneumoniae NTUH-K2044 DNA, complete genome	0.06	105.00
CP000647	Klebsiella pneumoniae subsp. pneumoniae MGH 78578, complete sequence	0.06	105.00
CP000800	Escherichia coli E24377A, complete genome	0.06	105.00
CU928163	Escherichia coli UMN026 chromosome, complete genome	0.06	105.00
AM236324	Escherichia coli genome fragment containing the yersiniabactin, cob and pdu gene clusters, strain A0 34/86	0.07	105.00
FM180568	Escherichia coli 0127: H6 E2348/69 complete genome, strain E2348/69	0.07	105.00
CP000301	Rhodopseudomonas palustris BisB18, complete genome	0.08	104.00
CP001127	Salmonella enterica subsp. enterica serovar Schwarzengrund str. CVM19633, complete genome	0.11	103.00
AY205335	Uncultured bacterium pdu operon, partial sequence	0.11	103.00

Hit	Description	E-value	Score
CP000230	Rhodospirillum rubrum ATCC 11170, complete genome	0.11	103.00
CP000880	Salmonella enterica subsp. arizonae serovar 62:z4,z23:--, complete genome	0.11	103.00
CU928162	Escherichia coli ED1a chromosome, complete genome	0.12	102.00
CP000822	Citrobacter koseri ATCC BAA-895, complete genome	0.12	102.00
CP000857	Salmonella enterica subsp. enterica serovar Paratyphi C strain RKS4594, complete genome	0.14	102.00
AE017220	Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67, complete genome	0.14	102.00
FN424405	Salmonella enterica subsp. enterica serovar Typhimurium str. D23580 complete genome	0.14	102.00
AE006468	Salmonella enterica subsp. enterica serovar Typhimurium str. LT2, complete genome	0.14	102.00
AM933172	Salmonella enterica subsp. enterica serovar Enteritidis str. P125109 complete genome	0.14	102.00
AM933173	Salmonella enterica subsp. enterica serovar Gallinarum str. 287/91 complete genome	0.14	102.00
CP001144	Salmonella enterica subsp. enterica serovar Dublin str. CT_ 02021853, complete genome	0.14	102.00
CP001113	Salmonella enterica subsp. enterica serovar Newport str. SL254, complete genome	0.14	102.00

Hit	Description	E-value	Score
CP001138	Salmonella enterica subsp. enterica serovar Agona str. SL483, complete genome	0.14	102.00
CP000886	Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7, complete genome	0.14	102.00
AE014613	Salmonella enterica subsp. enterica serovar Typhi Ty2, complete genome	0.14	102.00
CP001120	Salmonella enterica subsp. enterica serovar Heidelberg str. SL476, complete genome	0.14	102.00
FM200053	Salmonella enterica subsp. enterica serovar Paratyphi A str. AKU_12601 complete genome, strain AKU_12601	0.15	101.00
CP000026	Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150	0.15	101.00
CP000880	Salmonella enterica subsp. arizonae serovar 62:z4,z23:--, complete genome	0.16	101.00
CU928158	Escherichia fergusonii ATCC 35469 chromosome, complete genome	0.17	101.00
CP000885	Clostridium phytofermentans ISDg, complete genome	0.21	100.00
CP000964	Klebsiella pneumoniae 342, complete genome	0.22	100.00
AM286415	Yersinia enterocolitica subsp. enterocolitica 8081 complete genome	0.30	99.00
CP001336	Desulfitobacterium hafniense DCB-2, complete genome	0.30	99.00
AP008230	Desulfitobacterium hafniense Y51 DNA, complete genome	0.30	99.00

Hit	Description	E-value	Score
AM498294	<i>Citrobacter freundii</i> cbiA gene for cobyrinic acid A,C-diamide synthase and pdu operon	0.33	98.00
CP001685	<i>Leptotrichia buccalis</i> DSM 1135, complete genome	0.45	97.00
AE016830	<i>Enterococcus faecalis</i> V583, complete genome	0.46	97.00
CP000964	<i>Klebsiella pneumoniae</i> 342, complete genome	0.55	96.00
CP000853	<i>Alkaliphilus oremlandii</i> OhILAs, complete genome	0.60	96.00
CP000822	<i>Citrobacter koseri</i> ATCC BAA-895, complete genome	0.61	96.00
CU928158	<i>Escherichia fergusonii</i> ATCC 35469 chromosome, complete genome	0.63	96.00
CP000822	<i>Citrobacter koseri</i> ATCC BAA-895, complete genome	0.65	95.00
AP007281	<i>Lactobacillus reuteri</i> JCM 1112 DNA, complete genome	0.80	95.00
CP000705	<i>Lactobacillus reuteri</i> DSM 20016, complete genome	0.80	95.00
CP001113	<i>Salmonella enterica</i> subsp. enterica serovar Newport str. SL254, complete genome	1.30	93.00
CP000886	<i>Salmonella enterica</i> subsp. enterica serovar Paratyphi B str. SPB7, complete genome	1.30	93.00
AM933172	<i>Salmonella enterica</i> subsp. enterica serovar Enteritidis str. P125109 complete genome	1.44	92.00
AM933173	<i>Salmonella enterica</i> subsp. enterica serovar Gallinarum str. 287/91 complete genome	1.44	92.00

Hit	Description	E-value	Score
CP000880	Salmonella enterica subsp. arizonae serovar 62:z4,z23:--, complete genome	1.57	92.00
AE017220	Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67, complete genome	1.58	92.00
CP000853	Alkaliphilus oremlandii OhILAs, complete genome	1.68	92.00
CP001127	Salmonella enterica subsp. enterica serovar Schwarzengrund str. CVM19633, complete genome	1.69	92.00
CP000857	Salmonella enterica subsp. enterica serovar Paratyphi C strain RKS4594, complete genome	1.69	92.00
FN424405	Salmonella enterica subsp. enterica serovar Typhimurium str. D23580 complete genome	1.69	92.00
AE006468	Salmonella enterica subsp. enterica serovar Typhimurium str. LT2, complete genome	1.69	92.00
CP001144	Salmonella enterica subsp. enterica serovar Dublin str. CT_02021853, complete genome	1.69	92.00
CP001138	Salmonella enterica subsp. enterica serovar Agona str. SL483, complete genome	1.69	92.00
FM200053	Salmonella enterica subsp. enterica serovar Paratyphi A str. AKU_12601 complete genome, strain AKU_12601	1.69	92.00
CP000026	Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC	1.69	92.00

Hit	Description	E-value	Score
	9150		
CP001120	Salmonella enterica subsp. enterica serovar Heidelberg str. SL476, complete genome	1.69	92.00
CP001100	Chloroherpeton thalassium ATCC 35110, complete genome	1.94	91.00
AJ297723	Lactobacillus collinoides istA, istB, pocR, pduA, pduB, pduC, pduD, pduE, pduG, pduH, pduK, pduJ, pduL, pduM, pduN, pduO, pduObis, pduP, pduQ, pduW, pduU and partial pduS genes	2.57	90.00
CP000647	Klebsiella pneumoniae subsp. pneumoniae MGH 78578, complete sequence	2.92	89.00
AM286415	Yersinia enterocolitica subsp. enterocolitica 8081 complete genome	4.75	87.00
AM498294	Citrobacter freundii cbiA gene for cobyrinic acid A,C-diamide synthase and pdu operon	5.40	87.00
AE014613	Salmonella enterica subsp. enterica serovar Typhi Ty2, complete genome	8.71	85.00
AM286415	Yersinia enterocolitica subsp. enterocolitica 8081 complete genome	8.91	85.00
AP008955	Brevibacillus brevis NBRC 100599 DNA, complete genome	9.84	84.00

%Identity	%Positive	%Gaps
98.00	98.00	2.00
98.00	98.00	2.00
56.00	73.00	6.00
95.00	98.00	0.00
57.00	71.00	8.00
53.00	69.00	7.00
83.00	96.00	0.00
51.00	67.00	14.00
51.00	67.00	14.00
51.00	67.00	14.00
52.00	65.00	11.00
54.00	66.00	14.00
45.00	67.00	2.00
79.00	87.00	0.00
44.00	61.00	17.00
86.00	94.00	0.00
46.00	62.00	14.00
46.00	62.00	14.00
63.00	82.00	0.00
63.00	81.00	0.00
62.00	81.00	0.00
58.00	77.00	1.00
58.00	77.00	1.00
58.00	77.00	1.00
54.00	73.00	3.00
57.00	77.00	1.00
54.00	72.00	2.00
58.00	77.00	1.00
53.00	74.00	3.00
54.00	74.00	3.00
54.00	74.00	3.00
54.00	74.00	3.00
54.00	74.00	3.00
54.00	74.00	3.00
54.00	74.00	3.00
54.00	74.00	3.00
54.00	74.00	3.00

%Identity	%Positive	%Gaps
54.00	74.00	3.00
56.00	78.00	1.00
58.00	76.00	1.00
53.00	74.00	3.00
53.00	74.00	3.00
53.00	74.00	3.00
53.00	74.00	3.00
53.00	74.00	3.00
53.00	74.00	3.00
53.00	74.00	3.00
57.00	76.00	1.00
53.00	73.00	3.00
53.00	73.00	3.00
53.00	74.00	3.00
56.00	76.00	1.00
56.00	76.00	1.00
56.00	76.00	1.00
56.00	76.00	1.00
56.00	76.00	1.00
53.00	74.00	3.00
53.00	74.00	3.00
52.00	70.00	1.00
53.00	73.00	3.00
58.00	77.00	0.00
52.00	71.00	4.00
55.00	76.00	1.00
51.00	71.00	1.00
51.00	71.00	1.00
56.00	72.00	1.00
48.00	65.00	1.00
51.00	69.00	0.00
41.00	56.00	22.00
42.00	64.00	4.00
41.00	56.00	13.00
42.00	62.00	5.00
49.00	69.00	1.00
44.00	65.00	2.00
45.00	66.00	1.00

%Identity	%Positive	%Gaps
45.00	66.00	1.00
77.00	84.00	11.00
77.00	84.00	11.00
84.00	93.00	0.00
84.00	93.00	0.00
82.00	95.00	0.00
78.00	91.00	0.00
80.00	91.00	0.00
80.00	93.00	0.00
82.00	91.00	1.00
82.00	91.00	1.00
82.00	91.00	1.00
81.00	90.00	1.00
82.00	95.00	0.00
85.00	92.00	0.00
82.00	90.00	1.00
83.00	92.00	0.00
79.00	93.00	0.00
84.00	93.00	0.00
84.00	93.00	0.00
84.00	93.00	0.00
84.00	93.00	0.00
84.00	93.00	0.00
84.00	93.00	0.00
84.00	93.00	0.00
84.00	93.00	0.00
84.00	93.00	0.00
84.00	93.00	0.00
84.00	93.00	0.00
84.00	93.00	0.00
84.00	93.00	0.00
84.00	93.00	0.00
84.00	93.00	0.00
84.00	93.00	0.00
80.00	91.00	1.00
84.00	93.00	0.00
85.00	94.00	0.00
77.00	90.00	0.00
84.00	94.00	0.00

%Identity	%Positive	%Gaps
84.00	94.00	0.00
84.00	94.00	0.00
79.00	94.00	0.00
79.00	94.00	0.00
82.00	92.00	0.00
82.00	92.00	0.00
82.00	92.00	0.00
74.00	87.00	0.00
81.00	91.00	1.00
82.00	88.00	0.00
87.00	95.00	0.00
87.00	95.00	0.00
87.00	95.00	0.00
83.00	92.00	0.00
83.00	92.00	0.00
85.00	93.00	0.00
85.00	93.00	0.00
74.00	91.00	0.00
83.00	94.00	0.00
85.00	95.00	0.00
83.00	92.00	0.00
83.00	92.00	0.00
79.00	89.00	0.00
61.00	75.00	10.00
85.00	93.00	0.00
76.00	89.00	0.00
82.00	94.00	0.00
86.00	95.00	0.00
86.00	94.00	0.00
86.00	94.00	0.00
82.00	92.00	0.00
82.00	92.00	0.00
84.00	97.00	0.00
81.00	90.00	0.00
81.00	91.00	0.00
81.00	91.00	0.00

%Identity	%Positive	%Gaps
81.00	91.00	0.00
81.00	91.00	0.00
81.00	91.00	0.00
81.00	91.00	0.00
81.00	91.00	0.00
81.00	91.00	0.00
81.00	91.00	0.00
81.00	91.00	0.00
81.00	91.00	0.00
81.00	91.00	0.00
81.00	91.00	0.00
81.00	91.00	0.00
81.00	91.00	0.00
81.00	91.00	0.00
81.00	91.00	0.00
80.00	88.00	0.00
81.00	91.00	0.00
81.00	91.00	0.00
81.00	91.00	0.00
78.00	91.00	0.00
80.00	92.00	0.00
80.00	92.00	0.00
80.00	92.00	0.00
80.00	92.00	0.00
80.00	92.00	0.00
80.00	92.00	0.00
80.00	92.00	0.00
80.00	92.00	0.00
80.00	92.00	0.00
80.00	92.00	0.00
80.00	92.00	0.00
78.00	90.00	0.00
80.00	93.00	0.00
80.00	90.00	0.00
83.00	93.00	0.00
81.00	95.00	0.00
81.00	92.00	0.00
81.00	92.00	0.00
67.00	76.00	12.00
81.00	92.00	0.00

%Identity	%Positive	%Gaps
67.00	76.00	12.00
67.00	76.00	12.00
81.00	91.00	0.00
83.00	92.00	0.00
80.00	94.00	0.00
81.00	91.00	0.00
80.00	90.00	0.00
80.00	90.00	0.00
51.00	65.00	8.00
72.00	88.00	0.00
72.00	88.00	0.00
82.00	93.00	0.00
82.00	90.00	0.00
82.00	90.00	0.00
81.00	95.00	0.00
81.00	95.00	0.00
81.00	95.00	0.00
66.00	80.00	5.00
81.00	95.00	0.00
81.00	95.00	0.00
79.00	90.00	0.00
81.00	92.00	0.00
79.00	90.00	0.00
81.00	94.00	0.00
81.00	92.00	0.00
80.00	89.00	0.00
78.00	92.00	2.00
81.00	91.00	0.00
82.00	94.00	0.00
80.00	91.00	0.00
80.00	91.00	0.00
80.00	91.00	0.00
80.00	91.00	0.00
80.00	91.00	0.00
81.00	91.00	0.00
80.00	92.00	0.00

%Identity	%Positive	%Gaps
79.00	88.00	3.00
78.00	91.00	0.00
81.00	92.00	0.00
80.00	93.00	0.00
79.00	87.00	0.00
80.00	93.00	0.00
80.00	88.00	0.00
77.00	86.00	0.00
77.00	86.00	0.00
77.00	87.00	0.00
72.00	84.00	0.00
75.00	88.00	1.00
71.00	83.00	1.00
72.00	85.00	0.00
78.00	87.00	0.00
69.00	84.00	0.00
79.00	92.00	0.00
70.00	86.00	0.00
71.00	87.00	0.00
71.00	87.00	0.00
71.00	87.00	0.00
71.00	87.00	0.00
71.00	87.00	0.00
67.00	84.00	1.00
67.00	84.00	1.00
67.00	84.00	1.00
67.00	84.00	1.00
67.00	84.00	1.00
67.00	84.00	1.00
67.00	84.00	1.00
67.00	84.00	1.00
67.00	84.00	1.00
70.00	86.00	0.00
70.00	86.00	0.00
70.00	86.00	0.00
70.00	86.00	0.00
70.00	86.00	0.00
70.00	86.00	0.00

%Identity	%Positive	%Gaps
70.00	86.00	0.00
70.00	86.00	0.00
70.00	86.00	0.00
70.00	86.00	0.00
70.00	86.00	0.00
70.00	86.00	0.00
70.00	86.00	0.00
70.00	86.00	0.00
70.00	86.00	0.00
66.00	84.00	1.00
72.00	85.00	0.00
72.00	85.00	0.00
68.00	82.00	1.00
70.00	84.00	1.00
68.00	82.00	1.00
67.00	82.00	1.00
41.00	58.00	18.00
41.00	58.00	18.00
64.00	84.00	1.00
64.00	84.00	1.00
70.00	83.00	0.00
57.00	83.00	3.00
42.00	64.00	8.00
60.00	80.00	0.00
60.00	80.00	0.00
57.00	74.00	0.00
60.00	80.00	1.00
37.00	55.00	13.00
38.00	55.00	13.00
38.00	55.00	13.00
38.00	55.00	13.00
38.00	55.00	13.00
36.00	53.00	19.00
58.00	78.00	0.00
36.00	53.00	19.00
67.00	79.00	4.00
40.00	61.00	8.00

%Identity	%Positive	%Gaps
54.00	71.00	2.00
54.00	71.00	2.00
54.00	71.00	2.00
54.00	71.00	2.00
54.00	71.00	2.00
54.00	71.00	2.00
54.00	71.00	2.00
54.00	71.00	2.00
54.00	71.00	2.00
61.00	81.00	0.00
45.00	63.00	10.00
38.00	53.00	16.00
53.00	77.00	0.00
47.00	73.00	5.00
55.00	78.00	0.00
56.00	78.00	0.00
55.00	78.00	0.00
60.00	78.00	0.00
60.00	80.00	0.00
60.00	80.00	0.00
60.00	80.00	0.00
60.00	80.00	0.00
60.00	80.00	0.00
59.00	79.00	2.00
50.00	70.00	6.00
60.00	80.00	0.00
60.00	80.00	0.00
60.00	80.00	0.00
60.00	80.00	0.00
54.00	70.00	3.00
54.00	70.00	3.00
56.00	75.00	5.00
66.00	86.00	0.00
63.00	79.00	0.00
61.00	81.00	0.00
52.00	70.00	2.00
52.00	70.00	2.00
52.00	72.00	1.00

%Identity	%Positive	%Gaps
40.00	61.00	8.00
57.00	74.00	2.00
57.00	74.00	2.00
58.00	74.00	2.00
59.00	78.00	0.00
79.00	88.00	0.00
58.00	81.00	0.00
35.00	50.00	28.00
40.00	61.00	4.00
54.00	77.00	2.00
55.00	72.00	1.00
51.00	72.00	2.00
52.00	69.00	1.00
52.00	69.00	1.00
54.00	75.00	4.00
54.00	76.00	2.00
40.00	59.00	16.00
51.00	67.00	0.00
46.00	63.00	4.00
55.00	75.00	0.00
35.00	56.00	17.00
35.00	56.00	17.00
58.00	78.00	0.00
57.00	80.00	0.00
49.00	69.00	1.00
51.00	77.00	0.00
48.00	67.00	2.00
34.00	61.00	2.00
49.00	75.00	0.00
47.00	67.00	2.00
47.00	67.00	2.00
47.00	67.00	2.00
47.00	67.00	2.00
47.00	67.00	2.00
47.00	67.00	2.00
47.00	67.00	2.00
47.00	67.00	2.00

%Identity	%Positive	%Gaps
50.00	71.00	2.00
41.00	57.00	6.00
60.00	78.00	0.00
41.00	61.00	2.00
41.00	56.00	6.00
45.00	62.00	4.00
68.00	80.00	1.00
41.00	56.00	6.00
40.00	56.00	6.00
56.00	72.00	6.00
43.00	64.00	0.00
51.00	63.00	1.00
57.00	72.00	0.00
33.00	53.00	18.00
51.00	68.00	4.00
49.00	61.00	1.00
48.00	61.00	1.00
48.00	61.00	1.00
43.00	61.00	6.00
47.00	63.00	0.00
40.00	55.00	9.00
45.00	60.00	1.00
42.00	58.00	8.00
48.00	71.00	1.00
48.00	71.00	1.00
48.00	71.00	1.00
48.00	71.00	1.00
28.00	41.00	10.00
28.00	41.00	10.00
28.00	41.00	10.00
28.00	41.00	10.00
28.00	41.00	10.00
28.00	41.00	10.00
28.00	41.00	10.00
28.00	42.00	9.00
28.00	40.00	10.00
28.00	40.00	10.00

%Identity	%Positive	%Gaps
45.00	59.00	1.00
40.00	62.00	4.00
51.00	66.00	2.00
27.00	41.00	11.00
27.00	41.00	11.00
40.00	62.00	4.00
40.00	62.00	4.00
40.00	62.00	4.00
40.00	62.00	4.00
48.00	65.00	1.00
27.00	40.00	10.00
32.00	49.00	18.00
60.00	74.00	2.00
38.00	61.00	1.00
28.00	42.00	11.00
27.00	41.00	10.00
27.00	40.00	10.00
27.00	40.00	10.00
27.00	40.00	10.00
27.00	40.00	10.00
27.00	40.00	10.00
27.00	40.00	10.00
27.00	40.00	10.00
27.00	40.00	10.00
27.00	40.00	10.00
27.00	40.00	10.00
27.00	40.00	10.00
27.00	40.00	10.00
27.00	40.00	10.00
27.00	40.00	10.00
27.00	40.00	10.00
27.00	40.00	10.00
27.00	40.00	10.00
27.00	40.00	10.00
27.00	40.00	10.00
27.00	40.00	10.00
27.00	40.00	10.00
27.00	40.00	10.00
27.00	40.00	10.00
27.00	40.00	10.00
27.00	40.00	10.00
27.00	40.00	10.00
27.00	40.00	10.00
27.00	40.00	10.00
44.00	67.00	2.00
39.00	55.00	10.00
27.00	40.00	11.00
52.00	67.00	2.00
30.00	45.00	15.00

%Identity	%Positive	%Gaps
30.00	45.00	15.00
44.00	67.00	2.00
51.00	68.00	0.00
27.00	43.00	22.00
46.00	73.00	0.00
42.00	55.00	20.00
41.00	63.00	1.00
46.00	67.00	2.00
48.00	73.00	0.00
48.00	63.00	2.00
48.00	63.00	2.00
46.00	73.00	0.00
46.00	73.00	0.00
46.00	73.00	0.00
46.00	73.00	0.00
46.00	73.00	0.00
46.00	73.00	0.00
27.00	40.00	18.00
46.00	73.00	0.00
46.00	73.00	0.00
46.00	73.00	0.00
46.00	73.00	0.00
46.00	73.00	0.00
46.00	73.00	0.00
46.00	73.00	0.00
46.00	73.00	0.00
46.00	73.00	0.00
46.00	73.00	0.00
46.00	73.00	0.00
46.00	73.00	0.00
46.00	73.00	0.00
46.00	73.00	0.00
46.00	73.00	0.00
46.00	73.00	0.00
48.00	73.00	0.00
47.00	64.00	2.00
49.00	75.00	0.00
35.00	52.00	15.00
27.00	49.00	14.00
45.00	71.00	0.00
36.00	52.00	4.00
26.00	43.00	9.00