

Additional file 4. Raw data of sub-fraction IE3-3G1 proteomics analysis using LC-MS/MS.

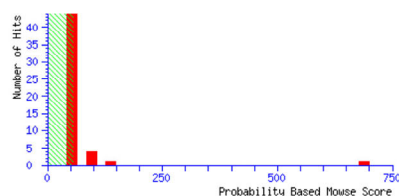
(1-1) Peptide Summary Report (protein spot 1, IE-1) Bacteria (Eubacteria)

Mascot Search Results

User : liaopc
Email :
Search title : IE-1
MS data file : merge.txt
Database : NCBI nr 090616 (9069431 sequences; 3106408609 residues)
Taxonomy : Bacteria (Eubacteria) (4853765 sequences)
Timestamp : 9 Jan 2012 at 09:15:28 CMT
Protein hits :
[gi|42518797](#) glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus johnsonii NCC 533]
[gi|227361679](#) glyceraldehyde-3-phosphate dehydrogenase [Lactobacillus sakei subsp. carnosus DSM 15831]
[gi|227525966](#) glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) [Lactobacillus jensenii JV-V16]
[gi|116492261](#) glyceraldehyde-3-phosphate dehydrogenase [Pediococcus pentosaceus ATCC 25745]
[gi|170016655](#) glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase [Leuconostoc citreum KM20]
[gi|158334876](#) hypothetical protein AM1_1713 [Acaryochloris marina MBIC11017]
[gi|148266124](#) hypothetical protein Gura_4114 [Geobacter uraniireducens Rf4]
[gi|217077222](#) chromosome segregation SMC protein, putative [Thermosiphon africanus TCF52B]
[gi|22799584](#) glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus arlettae]
[gi|182412978](#) excinuclease ABC subunit C [Opitutus terrae PB90-1]
[gi|42561108](#) holo-[acyl-carrier-protein] synthase [Mycoplasma mycoides subsp. mycoides SC str. PG1]
[gi|51244876](#) Ntr family two-component response regulator [Desulfotalea psychrophila LsV54]
[gi|172057364](#) hypothetical protein Exiq_1335 [Exiguobacterium sibiricum 255-15]
[gi|227424225](#) biopolymer transport protein [Denitrovibrio acetiphilus DSM 12809]
[gi|72382545](#) fused serine peptidase/N-terminal uncharacterized domain protein [Prochlorococcus marinus str. NATL2A]
[gi|237751407](#) glycosyl transferase [Helicobacter bilis ATCC 43879]
[gi|123965634](#) putative deoxyribodipyrimidine photolyase [Prochlorococcus marinus str. MIT 9515]
[gi|24213647](#) polynucleotide phosphorylase/polyadenylase [Leptospira interrogans serovar Lai str. 56601]
[gi|84385691](#) ISTdel, transposase [Vibrio splendidus 12B01]
[gi|88805592](#) putative two-component system sensor kinase/response regulator fusion protein [Robiginitalea bifurcata H]
[gi|15924260](#) ribosome-binding factor A [Staphylococcus aureus subsp. aureus Mu50]
[gi|1706361](#) RecName: Full=Transcriptional regulatory protein degU
[gi|223483524](#) single-strand binding protein [Brevundimonas sp. BAL3]
[gi|86131594](#) putative SpoU rRNA methylase family protein [Cellulophaga sp. MED134]
[gi|172058506](#) diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(s) [Exiguobacterium sibiricum 255-15]
[gi|110005394](#) putative atpase with chaperone activity, clp protease subunit protein [Spiriplasma citri]
[gi|150016208](#) trigger factor [Clostridium beijerinckii NCIMB 8052]
[gi|224534714](#) UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Borrelia spielmanii A14S]
[gi|153811501](#) hypothetical protein RUMOB_01893 [Ruminococcus obeum ATCC 29174]
[gi|185715004](#) aldehyde oxidase and xanthine dehydrogenase [Nitrobacter sp. Nb-311A]
[gi|84494635](#) putative glycerol phosphate dehydrogenase [Janibacter sp. HTCC2649]
[gi|160894823](#) hypothetical protein CLOL250_02373 [Clostridium sp. L2-50]
[gi|114568029](#) hypothetical protein Swol_2524 [Syntrophomonas wolfei subsp. wolfei str. Goettingen]

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
Individual ions scores > 55 indicate identity or extensive homology ($p < 0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As Peptide Summary [Help](#)

Significance threshold $p < 0.05$ Max. number of hits AUTO

Standard scoring ☒ MudPIT scoring ☐ Ions score or expect cut-off 0 Show sub-sets 0

Show pop-ups ☒ Suppress pop-ups ☐ Sort unassigned Decreasing Score Require bold red ☐

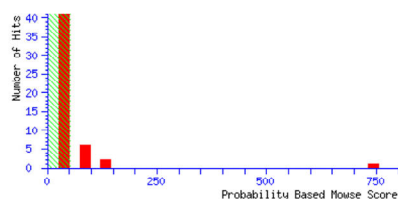
(1-2) Peptide Summary Report (protein spot 1, IE-1) Firmicutes (gram-positive bacteria)

Mascot Search Results

User : liaopc
Email :
Search title : IE-1
MS data file : merge.txt
Database : NCBIInr 090616 (9069431 sequences; 3106408609 residues)
Taxonomy : Firmicutes (gram-positive bacteria) (1006590 sequences)
Timestamp : 10 Jan 2012 at 08:20:50 GMT
Protein hits : [gi|42518797](#) glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus johnsonii NCC 533]
[gi|227361679](#) glyceraldehyde-3-phosphate dehydrogenase [Lactobacillus sakei subsp. carnosus DSM 15831]
[gi|227525966](#) glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) [Lactobacillus jensenii JV-V16]
[gi|172057364](#) hypothetical protein Exig_1335 [Exiguobacterium sibiricum 255-15]
[gi|229004124](#) hypothetical protein bmyco0002.10890 [Bacillus mycoides Rock1-4]
[gi|154502799](#) hypothetical protein RUMGNA_00613 [Ruminococcus gnavus ATCC 29149]
[gi|20799584](#) glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus arlettae]
[gi|197301564](#) hypothetical protein RUMLAC_00290 [Ruminococcus lactaris ATCC 29176]
[gi|116492261](#) glyceraldehyde-3-phosphate dehydrogenase [Pediococcus pentosaceus ATCC 25745]
[gi|149181561](#) hypothetical protein BSG1_13616 [Bacillus sp. SG-1]
[gi|150016208](#) trigger factor [Clostridium beijerinckii NCIMB 8052]
[gi|1706361](#) RecName: Full=Transcriptional regulatory protein degU
[gi|15924260](#) ribosome-binding factor A [Staphylococcus aureus subsp. aureus Mu50]
[gi|228918843](#) hypothetical protein bthur0012_59520 [Bacillus thuringiensis serovar pulsiensis BGSC 4CC1]
[gi|170016655](#) glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase [Leuconostoc citreum KM20]
[gi|228948651](#) Cell surface protein [Bacillus thuringiensis serovar monterrey BGSC 4AJ1]
[gi|172058506](#) diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(s) [Exiguobacterium sibiricum 255-15]
[gi|218273468](#) hypothetical protein ROSINTL182_01355 [Roseburia intestinalis L1-82]
[gi|150388754](#) phosphoribosylglycinamide formyltransferase [Alkaliphilus metalliredigens QYMF]
[gi|153811501](#) hypothetical protein RUMOB_01893 [Ruminococcus obeum ATCC 29174]
[gi|229229306](#) ATPase component of various ABC-type transport systems with duplicated ATPase domain [Desulfotomaculum a
conserved hypothetical protein [Selenomonas flueggei ATCC 43531]
[gi|238927776](#) hypothetical protein CLOL250_02373 [Clostridium sp. L2-50]
[gi|160894823](#) hypothetical protein BA0824 [Bacillus anthracis str. Ames]
[gi|30260965](#) terminase, small subunit, internal deletion [Enterococcus faecalis V583]
[gi|29376021](#) hypothetical protein GCWU000182_02867 [Abiotrophia defectiva ATCC 49176]
[gi|229827478](#) hypothetical protein COPCOM_01541 [Coprococcus comes ATCC 27758]
[gi|89897039](#) hypothetical protein DSY4293 [Desulfitobacterium hafniense Y51]
[gi|126700567](#) putative phage anti-repressor [Clostridium difficile 630]
[gi|116510863](#) transcriptional antiterminator [Lactococcus lactis subsp. cremoris SK11]
[gi|150391186](#) YheD [Alkaliphilus metalliredigens QYMF]
[gi|199598725](#) Chaperone ClpB [Lactobacillus rhamnosus HN001]
[gi|20808539](#) O-acetylhomoserine sulfhydrylase [Thermoanaerobacter tengcongensis MB4]
[gi|42519394](#) oligopeptide ABC transporter solute-binding component [Lactobacillus johnsonii NCC 533]
[gi|125973701](#) Alpha/beta hydrolase fold-3 [Clostridium thermocellum ATCC 27405]
[gi|167465604](#) possible phospholipase [Paenibacillus larvae subsp. larvae BRL-230010]
[gi|167750765](#) hypothetical protein EUBSIR_01743 [Eubacterium siraeum DSM 15702]
[gi|226313151](#) hypothetical protein BBR47_35640 [Brevibacillus brevis NBRC 100599]
[gi|229917100](#) nucleotide sugar dehydrogenase [Exiguobacterium sp. AT1b]
[gi|56961831](#) lysine decarboxylase [Bacillus clausii KSM-K16]
[gi|134301021](#) phenylacetate--CoA ligase [Desulfotomaculum reducens MI-1]
[gi|153953104](#) recombinase [Clostridium kluyveri DSM 555]

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Peptide Summary Report

Format As Peptide Summary [Help](#)

Significance threshold $p < 0.05$ Max. number of hits AUTO

Standard scoring ☐ MudPIT scoring ☒ Ions score or expect cut-off 0 Show sub-sets 0

Show pop-ups ☒ Suppress pop-ups ☐ Sort unassigned Decreasing Score ☒ Require bold red ☐

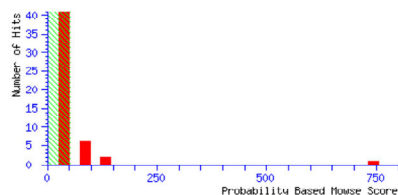
(1-3) Peptide Summary Report (protein spot 1, IE-1) Other Firmicutes

Mascot Search Results

User : liaopc
Email :
Search title : IE-1
MS data file : merge.txt
Database : NCBIInr 090616 (9069431 sequences; 3106408609 residues)
Taxonomy : Other Firmicutes (967613 sequences)
Timestamp : 10 Jan 2012 at 08:33:58 GMT
Protein hits : [gi|42518797](#) glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus johnsonii NCC 533]
[gi|1227361679](#) glyceraldehyde-3-phosphate dehydrogenase [Lactobacillus sakei subsp. carnosus DSM 15831]
[gi|1227525966](#) glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) [Lactobacillus jensenii JV-V16]
[gi|1172057364](#) hypothetical protein Exig_1335 [Exiguobacterium sibiricum 255-15]
[gi|1229004124](#) hypothetical protein bmyco0002_10890 [Bacillus mycoides Rock1-4]
[gi|154502799](#) hypothetical protein RUMGNA_00613 [Ruminococcus gnavus ATCC 29149]
[gi|120799584](#) glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus arlettae]
[gi|197301564](#) hypothetical protein RUMLAC_00290 [Ruminococcus lactaris ATCC 29176]
[gi|116492261](#) glyceraldehyde-3-phosphate dehydrogenase [Pediococcus pentosaceus ATCC 25745]
[gi|149181561](#) hypothetical protein BSG1_13616 [Bacillus sp. SG-1]
[gi|150016208](#) trigger factor [Clostridium beijerinckii NCIMB 8052]
[gi|1706361](#) RecName: Full=Transcriptional regulatory protein degU
[gi|15924260](#) ribosome-binding factor A [Staphylococcus aureus subsp. aureus Mu50]
[gi|1228918843](#) hypothetical protein bthur0012_59520 [Bacillus thuringiensis serovar pulsiensis BGSC 4CC1]
[gi|170016655](#) glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase [Leuconostoc citreum KM20]
[gi|1228948651](#) Cell surface protein [Bacillus thuringiensis serovar monterrey BGSC 4AJ1]
[gi|172058506](#) diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(s) [Exiguobacterium sibiricum 255-15]
[gi|128273468](#) hypothetical protein ROSINTL182_01355 [Roseburia intestinalis L1-82]
[gi|150388754](#) phosphoribosylglycinamide formyltransferase [Alkaliphilus metalliredigens QYMF]
[gi|153811501](#) hypothetical protein RUMOB_01893 [Ruminococcus obeum ATCC 29174]
[gi|1229229306](#) ATPase component of various ABC-type transport systems with duplicated ATPase domain [Desulfotomaculum a]
[gi|1238927776](#) conserved hypothetical protein [Selenomonas flueggei ATCC 43531]
[gi|160894823](#) hypothetical protein CLOL250_02373 [Clostridium sp. L2-50]
[gi|130260965](#) hypothetical protein BA0824 [Bacillus anthracis str. Ames]
[gi|129376021](#) terminase, small subunit, internal deletion [Enterococcus faecalis V583]
[gi|1229827478](#) hypothetical protein GCWU000182_02867 [Abiotrophia defectiva ATCC 49176]
[gi|1226323766](#) hypothetical protein COPCOM_01541 [Coprococcus comes ATCC 27758]
[gi|189897039](#) hypothetical protein DSY4293 [Desulfitobacterium hafniense Y51]
[gi|126700567](#) putative phage anti-repressor [Clostridium difficile 630]
[gi|116510863](#) transcriptional antiterminator [Lactococcus lactis subsp. cremoris SK11]
[gi|150391186](#) YheD [Alkaliphilus metalliredigens QYMF]
[gi|119598725](#) Chaperone ClpB [Lactobacillus rhamnosus HN001]
[gi|120808539](#) O-acetylhomoserine sulphydrylase [Thermoanaerobacter tengcongensis MB4]
[gi|142519394](#) oligopeptide ABC transporter solute-binding component [Lactobacillus johnsonii NCC 533]
[gi|125973701](#) Alpha/beta hydrolase fold-3 [Clostridium thermocellum ATCC 27405]
[gi|167465604](#) possible phospholipase [Paenibacillus larvae subsp. larvae BRL-230010]
[gi|167750765](#) hypothetical protein EUBSIR_01743 [Eubacterium siraeum DSM 15702]
[gi|1226313151](#) hypothetical protein BBR47_35640 [Brevibacillus brevis NBRC 100599]
[gi|1229917100](#) nucleotide sugar dehydrogenase [Exiguobacterium sp. AT1b]
[gi|156961831](#) lysine decarboxylase [Bacillus clausii KSM-K16]
[gi|134301021](#) phenylacetate--CoA ligase [Desulfotomaculum reducens MI-1]
[gi|153953104](#) recombinase [Clostridium kluyveri DSM 555]

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Peptide Summary Report

Format As [Help](#)

Significance threshold $p <$ Max. number of hits

Standard scoring ☐ MudPIT scoring ☒ Ions score or expect cut-off Show sub-sects

Show pop-ups ☒ Suppress pop-ups ☐ Sort unassigned Require bold red ☐

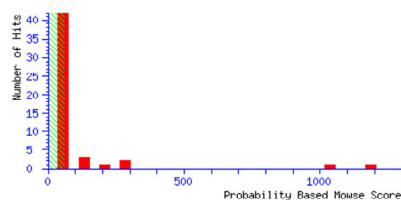
(2-1) Peptide Summary Report (protein spot 2, IE-2) Bacteria (Eubacteria)

{MATRIX} *{SCIENCE}* Mascot Search Results

User : liaopc
Email :
Search title : IE-2
MS data file : merge.txt
Database : NCBIInr 090616 (9069431 sequences; 3106408609 residues)
Taxonomy : Bacteria (Eubacteria) (4853765 sequences)
Timestamp : 10 Jan 2012 at 01:19:37 GMT
Protein hits : [gi|42518797](#) glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus johnsonii NCC 533]
[gi|227520527](#) glyceraldehyde-3-phosphate dehydrogenase, phosphorylating [Lactobacillus gasseri JV-V03]
[gi|227361679](#) glyceraldehyde-3-phosphate dehydrogenase [Lactobacillus sakei subsp. carnosus DSM 15831]
[gi|227525966](#) glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) [Lactobacillus jensenii JV-V16]
[gi|111610131](#) glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus helveticus CNR232]
[gi|90962141](#) glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus salivarius UCC118]
[gi|116492261](#) glyceraldehyde-3-phosphate dehydrogenase [Pediococcus pentosaceus ATCC 25745]
[gi|170016655](#) glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase [Leuconostoc citreum KM20]
[gi|229233449](#) dehydrogenase of unknown specificity similar to short-chain alcohol dehydrogenase [Chitinophaga pinensis]
[gi|94499337](#) hypothetical protein RED65_11124 [Oceanobacter sp. RED65]
[gi|225103805](#) glyceraldehyde-3-phosphate dehydrogenase, type I [Methylophaga sp. DMS010]
[gi|237751407](#) glycosyl transferase [Helicobacter bilis ATCC 43879]
[gi|117921863](#) prepilin-type cleavage/methylation-like protein [Shewanella sp. ANA-3]
[gi|148553294](#) beta-lactamase [Sphingomonas wittichii RW1]
[gi|111022069](#) non-ribosomal peptide synthetase [Rhodococcus jostii RHA1]
[gi|228577910](#) pilus biogenesis protein [Citrobacter sp. 30_2]
[gi|197762281](#) predicted protein [Streptomyces sp. SPB74]
[gi|167764151](#) hypothetical protein BACSTE_02535 [Bacteroides stercoris ATCC 43183]
[gi|148266124](#) hypothetical protein Gura_4114 [Geobacter uraniireducens Rf4]
[gi|1706361](#) RecName: Full=Transcriptional regulatory protein degU
[gi|118473519](#) thiocyanate hydrolase beta subunit [Mycobacterium smegmatis str. MC2 155]
[gi|20799584](#) glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus arlettae]
[gi|227424225](#) biopolymer transport protein [Denitrovibrio acetiphilus DSM 12809]
[gi|239616934](#) amidohydrolase [Kosmotoga olearia TBF 19.5.1]
[gi|224391617](#) cobalamin biosynthesis protein CobT [Candidatus Pelagibacter sp. HTCC7211]
[gi|227500542](#) DNA-binding protein [Anaerococcus tetradius ATCC 35098]
[gi|42561108](#) holo-[acyl-carrier-protein] synthase [Mycoplasma mycoides subsp. mycoides SC str. PG1]
[gi|229175622](#) Cell surface protein [Bacillus cereus MM3]
[gi|150016208](#) trigger factor [Clostridium beijerinckii NCIMB 8052]
[gi|229556841](#) glycosyltransferase [Listeria grayi DSM 20601]
[gi|196228419](#) hypothetical protein CFE428DRAFT_0450 [Chthoniobacter flavus Ellin428]
[gi|57224620](#) glyceraldehyde-3-phosphate dehydrogenase, type I [Dehalococcoides ethenogenes 195]
[gi|158337485](#) ATP-dependent metalloprotease FtsH-like protein [Acaryochloris marina MBIC11017]
[gi|150385193](#) Fibronectin, type III domain protein [Victivallis vadensis ATCC BAA-548]
[gi|146295492](#) hypothetical protein CsaC_0434 [Caldicellulosiruptor saccharolyticus DSM 8903]
[gi|197301564](#) hypothetical protein RUMILAC_00290 [Ruminococcus lactaris ATCC 29176]
[gi|227979847](#) putative proteasome component/protein of unknown function, DUF275 [Tsukamurella paurometabola DSM 20162]
[gi|20799602](#) glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus piscifermentans]
[gi|171473203](#) glyceraldehyde-3-phosphate dehydrogenase [Candidatus Phytoblasma vitis]
[gi|148380680](#) hydrolase [Clostridium botulinum A str. ATCC 3502]

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
Individual ions scores > 59 indicate identity or extensive homology ($p < 0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As [Help](#)

Significance threshold $p <$ Max. number of hits

Standard scoring ☒ MudPIT scoring ☐ Ions score or expect cut-off Show sub-sets

Show pop-ups ☒ Suppress pop-ups ☐ Sort unassigned Require bold red ☐

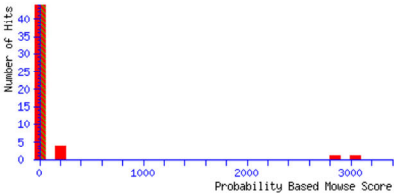
(2-2) Peptide Summary Report (protein spot 2, IE-2) Firmicutes (gram-positive bacteria)

(MATRIX)
(SCIENCE) Mascot Search Results

User	:	liaopc
Email	:	
Search title	:	IE-2
MS data file	:	merge.txt
Database	:	NCBINr 090616 (9069431 sequences; 3106408609 residues)
Taxonomy	:	Firmicutes (gram-positive bacteria) (1006590 sequences)
Timestamp	:	10 Jan 2012 at 09:18:16 GMT
Protein hits	:	gi 42518797 glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus johnsonii NCC 533] gi 227520527 glyceraldehyde-3-phosphate dehydrogenase, phosphorylating [Lactobacillus gasseri JV-V03] gi 227361679 glyceraldehyde-3-phosphate dehydrogenase [Lactobacillus sakei subsp. carnosus DSM 15831] gi 227525966 glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) [Lactobacillus jensenii JV-V16] gi 90962141 glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus salivarius UCC118] gi 20799584 glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus arlettae] gi 227500542 DNA-binding protein [Anaerococcus tetradius ATCC 35098] gi 148380680 hydrolase [Clostridium botulinum A str. ATCC 3502] gi 197301564 hypothetical protein RUMLAC_00290 [Ruminococcus lactaris ATCC 29176] gi 116492261 glyceraldehyde-3-phosphate dehydrogenase [Pediococcus pentosaceus ATCC 25745] gi 229828817 hypothetical protein GCWU000342_00900 [Shuttleworthia satelles DSM 14600] gi 146295492 hypothetical protein Csac_0434 [Caldicellulosiruptor saccharolyticus DSM 8903] gi 170016655 glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase [Leuconostoc citreum KM20] gi 229175622 Cell surface protein [Bacillus cereus MM3] gi 150016208 trigger factor [Clostridium beijerinckii NCIMB 8052] gi 20799602 glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus piscifermentans] gi 1706361 RecName: Full=Transcriptional regulatory protein degU gi 148378084 hypothetical protein CBO0076 [Clostridium botulinum A str. ATCC 3502] gi 154502799 hypothetical protein RUMGNA_00613 [Ruminococcus gnavus ATCC 29149] gi 228995199 Collagen adhesion protein [Bacillus pseudomycoides DSM 12442] gi 228583035 trigger factor protein [Clostridium sp. 7_2_43FAA] gi 149183693 hypothetical protein BSG1_13561 [Bacillus sp. SG-1] gi 150388754 phosphoribosylglycinamide formyltransferase [Alkaliphilus metalliredigens QYMF] gi 168335477 hypothetical protein Epulo_10467 [Epulopiscium sp. 'N.t. morphotype B'] gi 220930911 L-aspartate oxidase [Halothermothrix orenii H 168] gi 16079728 hypothetical protein BSU26750 [Bacillus subtilis subsp. subtilis str. 168] gi 111610131 glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus helveticus CNRZ32] gi 229229306 ATPase component of various ABC-type transport systems with duplicated ATPase domain [Desulfotomaculum a gi 150391186 YheD [Alkaliphilus metalliredigens QYMF] gi 229094029 Cell surface protein [Bacillus cereus Rock3-42] gi 229541561 two component transcriptional regulator, LuxR family [Bacillus coagulans 36D1] gi 192808885 YjgB [Geobacillus sp. Y412MC10] gi 18310785 hypothetical protein CPE1803 [Clostridium perfringens str. 13] gi 172057364 hypothetical protein Exig_1335 [Exiguobacterium sibiricum 255-15]

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Peptide Summary Report

Format As

Peptide Summary

Help

Significance threshold $p <$

0.05

Max. number of hits

AUTO

Standard scoring

☐ MudPIT scoring

☒ Ions score or expect cut-off

0

Show sub-sets

0

Show pop-ups

☒ Suppress pop-ups

☐ Sort unassigned

Decreasing Score

☒ Require bold red

☐

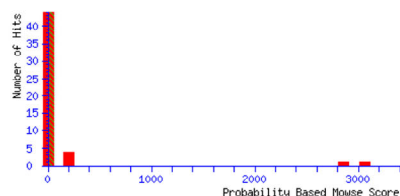
(2-3) Peptide Summary Report (protein spot 2, IE-2) Other Firmicutes

Mascot Search Results

User : liaopc
Email :
Search title : IE-2
MS data file : merge.txt
Database : NCBI nr 090616 (9069431 sequences; 3106408609 residues)
Taxonomy : Other Firmicutes (967613 sequences)
Timestamp : 10 Jan 2012 at 08:44:03 GMT
Protein hits : [gi|42518797](#) glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus johnsonii NCC 533]
[gi|227520527](#) glyceraldehyde-3-phosphate dehydrogenase, phosphorylating [Lactobacillus gasseri JV-V03]
[gi|227361679](#) glyceraldehyde-3-phosphate dehydrogenase [Lactobacillus sakei subsp. carnosus DSM 15831]
[gi|227525966](#) glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) [Lactobacillus jensenii JV-V16]
[gi|90962141](#) glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus salivarius UCC110]
[gi|20799584](#) glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus arlettae]
[gi|227500542](#) DNA-binding protein [Anaerococcus tetradus ATCC 35098]
[gi|148380680](#) hydrolase [Clostridium botulinum A str. ATCC 3502]
[gi|197301564](#) hypothetical protein RUM1AC_00290 [Ruminococcus lactaria ATCC 29176]
[gi|116492261](#) glyceraldehyde-3-phosphate dehydrogenase [Pediococcus pentosaceus ATCC 25745]
[gi|229828817](#) hypothetical protein GCWU000342_00900 [Shuttleworthia satelles DSM 14600]
[gi|146295492](#) hypothetical protein Csac_0434 [Caldicellulosiruptor saccharolyticus DSM 8903]
[gi|170016655](#) glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase [Leuconostoc citreum KM20]
[gi|229175622](#) Cell surface protein [Bacillus cereus MM3]
[gi|150016208](#) trigger factor [Clostridium beijerinckii NCIMB 8052]
[gi|20799602](#) glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus piscifermentans]
[gi|1706361](#) RecName: Full=Transcriptional regulatory protein degU
[gi|148378084](#) hypothetical protein CBO0076 [Clostridium botulinum A str. ATCC 3502]
[gi|154502799](#) hypothetical protein RUMGNA_00613 [Ruminococcus gnavus ATCC 29149]
[gi|228995199](#) Collagen adhesion protein [Bacillus pseudomycoides DSM 12442]
[gi|228583035](#) trigger factor protein [Clostridium sp. 7_2_43FAA]
[gi|149183693](#) hypothetical protein BSG1_13561 [Bacillus sp. SG-1]
[gi|150388754](#) phosphoribosylglycinamide formyltransferase [Alkaliphilus metalliredigens QYMF]
[gi|16835477](#) hypothetical protein Epulo_10467 [Epulopiscium sp. 'N.t. morphotype B']
[gi|220930911](#) L-aspartate oxidase [Halothermothrix orenii H 168]
[gi|111610131](#) glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus helveticus CNRZ32]
[gi|229229306](#) ATPase component of various ABC-type transport systems with duplicated ATPase domain [Desulfotomaculum a.
[gi|150391186](#) VheD [Alkaliphilus metalliredigens QYMF]
[gi|229094029](#) Cell surface protein [Bacillus cereus Rock3-42]
[gi|229541561](#) two component transcriptional regulator, LuxR family [Bacillus coagulans 36D1]
[gi|192808885](#) YjgB [Geobacillus sp. Y412MC10]
[gi|18310785](#) hypothetical protein CPE1803 [Clostridium perfringens str. 13]
[gi|172057364](#) hypothetical protein Exig_1335 [Exiguobacterium sibiricum 255-15]
[gi|20799590](#) glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus chromogenes]

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
Individual ions scores > 52 indicate identity or extensive homology ($p < 0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As Peptide Summary [Help](#)

Significance threshold $p < 0.05$ Max. number of hits AUTO

Standard scoring ☐ MudPIT scoring ☒ Ions score or expect cut-off 0 Show sub-sets 0

Show pop-ups ☒ Suppress pop-ups ☐ Sort unassigned Decreasing Score Require bold red ☐

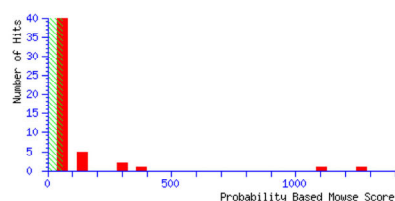
(3-1) Peptide Summary Report (protein spot 3, IE-3) Bacteria (Eubacteria)

Mascot Search Results

User : liaopc
Email :
Search title : IE-3
MS data file : merge.txt
Database : NCBIInr 090616 (9069431 sequences; 3106408609 residues)
Taxonomy : Bacteria (Eubacteria) (4853765 sequences)
Timestamp : 10 Jan 2012 at 04:04:37 GMT
Protein hits : [gi|42518797](#) glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus johnsonii NCC 533]
[gi|227520527](#) glyceraldehyde-3-phosphate dehydrogenase, phosphorylating [Lactobacillus gasseri JV-V03]
[gi|227361679](#) glyceraldehyde-3-phosphate dehydrogenase [Lactobacillus sakei subsp. carnosus DSM 15831]
[gi|227525966](#) glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) [Lactobacillus jensenii JV-V16]
[gi|111610131](#) glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus helveticus GNR32]
[gi|116494473](#) glyceraldehyde-3-phosphate dehydrogenase [Lactobacillus casei ATCC 334]
[gi|90962141](#) glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus salivarius UCC118]
[gi|116492261](#) glyceraldehyde-3-phosphate dehydrogenase [Pediococcus pentosaceus ATCC 25745]
[gi|170016655](#) glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase [Leuconostoc citreum KM20]
[gi|227874212](#) zinc-exporting ATPase [Oribacterium sinus F0268]
[gi|148252055](#) glyceraldehyde-3-phosphate dehydrogenase [Bradyrhizobium sp. BTA11]
[gi|225135183](#) Helicase conserved C-terminal domain protein [Ruegeria sp. R11]
[gi|237751407](#) glycosyl transferase [Helicobacter bilis ATCC 43879]
[gi|57234620](#) glyceraldehyde-3-phosphate dehydrogenase, type I [Dehalococcoides ethenogenes 195]
[gi|20799584](#) glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus arlettae]
[gi|227979847](#) putative proteasome component/protein of unknown function, DUF275 [Tsukamurella paurometabola DSM 20162]
[gi|229880970](#) CoA-substrate-specific enzyme activase, putative [Slackia heliotrinireducens DSM 20476]
[gi|226312803](#) two-component response regulator [Brevibacillus brevis NBRC 100599]
[gi|148266124](#) hypothetical protein Gura_4114 [Geobacter uranireducens RF4]
[gi|126347884](#) putative glyceraldehyde 3-phosphate dehydrogenase [Streptomyces ambofaciens ATCC 23877]
[gi|55821675](#) penicillin binding protein 2X [Streptococcus thermophilus LMG 18311]
[gi|24213647](#) polynucleotide phosphorylase/polyadenylase [Leptospira interrogans serovar Lai str. 56601]
[gi|39996379](#) transcription elongation factor GreA [Geobacter sulfurreducens PCA]
[gi|167951074](#) hypothetical protein Epers_33717 [Endoriftia persephone 'Hot96_1+Hot96_2']
[gi|228583035](#) trigger factor protein [Clostridium sp. 7_2_43FAA]
[gi|149199701](#) hypothetical protein LNTAR_25135 [Lentisphaera araneosa HTCC2155]
[gi|154502799](#) hypothetical protein RUMGNA_00613 [Ruminococcus gnavus ATCC 29149]
[gi|227500542](#) DNA-binding protein [Anaerococcus tetradius ATCC 35098]
[gi|94972048](#) lipoprotein signal peptidase [Deinococcus geothermalis DSM 11300]
[gi|23099893](#) glyceraldehyde-3-phosphate dehydrogenase [Oceanobacillus ihayensis HTE831]
[gi|42561108](#) holo-[acyl-carrier-protein] synthase [Mycoplasmma mycoides subsp. mycoides SC str. PG1]
[gi|224476119](#) putative pyridine nucleotide-disulfide oxidoreductase [Staphylococcus carnosus subsp. carnosus TM300]
[gi|194246487](#) hypothetical protein ATP_00086 [Candidatus Phytoplasma mali]
[gi|93007110](#) ATP-dependent helicase HepA [Psychrobacter cryohalolentis K5]
[gi|226310996](#) glyceraldehyde 3-phosphate dehydrogenase [Brevibacillus brevis NBRC 100599]
[gi|197301564](#) hypothetical protein RUMMAC_00290 [Ruminococcus lactaris ATCC 29176]
[gi|91204595](#) similar to (3R)-hydroxymyristoyl acyl carrier protein dehydrase [Candidatus Kuenenia stuttgartiensis]
[gi|404160](#) outer membrane protein (40K) [Fusobacterium nucleatum]
[gi|84494635](#) putative glycerol phosphate dehydrogenase [Janibacter sp. HTCC2649]
[gi|146295492](#) hypothetical protein CsaC_0434 [Caldicellulosiruptor saccharolyticus DSM 8903]
[gi|20799590](#) glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus chromogenes]
[gi|224391617](#) cobalamin biosynthesis protein CobT [Candidatus Pelagibacter sp. HTCC7211]
[gi|172063180](#) NMT1/THI5-like domain-containing protein [Burkholderia ambifaria MC40-6]
[gi|167764151](#) hypothetical protein BACSTE_02535 [Bacteroides stercoris ATCC 43183]
[gi|162450188](#) hypothetical protein sce1916 [Sorangium cellulosum 'So ce 56']
[gi|91202749](#) strongly similar to glyceraldehyde-3-phosphate dehydrogenase [Candidatus Kuenenia stuttgartiensis]

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
Individual ions scores > 59 indicate identity or extensive homology ($p < 0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As	Peptide Summary	Help
Significance threshold p<	0.05	Max. number of hits AUTO
Standard scoring	☒ MudPIT scoring	☐ Ions score or expect cut-off 0
		Show sub-sets 0
Show pop-ups	☒ Suppress pop-ups	☐ Sort unassigned Decreasing Score
		Require bold red ☐

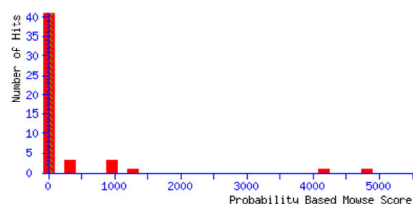
(3-2) Peptide Summary Report (protein spot 3, IE-3) Firmicutes (gram-positive bacteria)

{MATRIX} *{SCIENCE}* Mascot Search Results

User : liaopc
Email :
Search title : IE-3
MS data file : merge.txt
Database : NCBI nr 090616 (9069431 sequences; 3106408609 residues)
Taxonomy : Firmicutes (gram-positive bacteria) (1006590 sequences)
Timestamp : 10 Jan 2012 at 09:31:47 GMT
Protein hits :
[gi|142518797](#) glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus johnsonii NCC 533]
[gi|227520527](#) glyceraldehyde-3-phosphate dehydrogenase, phosphorylating [Lactobacillus gasseri JV-V03]
[gi|58337019](#) glyceraldehyde-3-p dehydrogenase [Lactobacillus acidophilus NCFM]
[gi|227361679](#) glyceraldehyde-3-phosphate dehydrogenase [Lactobacillus sakei subsp. carnosus DSM 15831]
[gi|227525966](#) glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) [Lactobacillus jensenii JV-V16]
[gi|116494473](#) glyceraldehyde-3-phosphate dehydrogenase [Lactobacillus casei ATCC 334]
[gi|20799584](#) glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus arlettae]
[gi|90962141](#) glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus salivarius UCC118]
[gi|116492261](#) glyceraldehyde-3-phosphate dehydrogenase [Pediococcus pentosaceus ATCC 25745]
[gi|111610131](#) glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus helveticus CNRZ32]
[gi|170016655](#) glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase [Leuconostoc citreum KM20]
[gi|227500542](#) DNA-binding protein [Anaerococcus tetradius ATCC 35098]
[gi|20799590](#) glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus chromogenes]
[gi|197301564](#) hypothetical protein RUM_LAC_00290 [Ruminococcus lactaris ATCC 29176]
[gi|148380680](#) hydrolase [Clostridium botulinum A str. ATCC 3502]
[gi|148378084](#) hypothetical protein CBO0076 [Clostridium botulinum A str. ATCC 3502]
[gi|228583035](#) trigger factor protein [Clostridium sp. 7.2.43FAA]
[gi|154502799](#) hypothetical protein RUM_GNA_00613 [Ruminococcus gnavus ATCC 29149]
[gi|224476119](#) putative pyridine nucleotide-disulfide oxidoreductase [Staphylococcus carnosus subsp. carnosus TM300]
[gi|146295492](#) hypothetical protein CsaC_0434 [Caldicellulosiruptor saccharolyticus DSM 8903]
[gi|150388754](#) phosphoribosylglycinamide formyltransferase [Alkaliphilus metalliredigens QYMF]
[gi|150391186](#) YheD [Alkaliphilus metalliredigens QYMF]
[gi|20799602](#) glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus piscifermentans]
[gi|1706361](#) RecName: Full=Transcriptional regulatory protein degH
[gi|229175622](#) Cell surface protein [Bacillus cereus MM3]
[gi|212640452](#) S-layer glycoprotein protein, contains three N-terminal SLH domains [Anoxybacillus flavithermus WK1]
[gi|222529355](#) von Willebrand factor type A [Anaerocellum thermophilum DSM 6725]
[gi|134298892](#) hypothetical protein Dred_1028 [Desulfotomaculum reducens MI-1]
[gi|163763733](#) tetrahydrofolate dehydrogenase/cyclohydrolase [Bacillus selenitireducens MLS10]
[gi|228982852](#) hypothetical protein bthur0002_59850 [Bacillus thuringiensis Bt407]

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
Individual ions scores > 52 indicate identity or extensive homology ($p < 0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As Peptide Summary [Help](#)

Significance threshold $p < 0.05$ Max. number of hits AUTO

Standard scoring ☐ MudPIT scoring ☒ Ions score or expect cut-off 0 Show sub-sets 0

Show pop-ups ☒ Suppress pop-ups ☐ Sort unassigned Decreasing Score ☒ Require bold red ☐

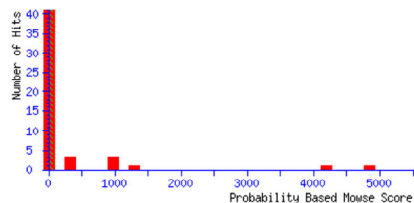
(3-3) Peptide Summary Report (protein spot 3, IE-3) Other Firmicutes

Mascot Search Results

User : liaopc
Email :
Search title : IE-3
MS data file : merge.txt
Database : NCBI nr 090616 (9069431 sequences; 3106408609 residues)
Taxonomy : Other Firmicutes (967613 sequences)
Timestamp : 11 Jan 2012 at 01:21:23 GMT
Protein hits :
[gi|42518797](#) glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus johnsonii NCC 533]
[gi|227520527](#) glyceraldehyde-3-phosphate dehydrogenase, phosphorylating [Lactobacillus gasseri JV-V03]
[gi|58337019](#) glyceraldehyde-3-p dehydrogenase [Lactobacillus acidophilus NCFM]
[gi|227361679](#) glyceraldehyde-3-phosphate dehydrogenase [Lactobacillus sakei subsp. carnosus DSM 15831]
[gi|227525966](#) glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) [Lactobacillus jensenii JV-V16]
[gi|116494473](#) glyceraldehyde-3-phosphate dehydrogenase [Lactobacillus casei ATCC 334]
[gi|20799584](#) glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus arlettae]
[gi|90962141](#) glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus salivarius UCC118]
[gi|116492261](#) glyceraldehyde-3-phosphate dehydrogenase [Pediococcus pentosaceus ATCC 25745]
[gi|111610131](#) glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus helveticus CNRZ32]
[gi|170016655](#) glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase [Leuconostoc citreum KM20]
[gi|227500542](#) DNA-binding protein [Anaerococcus tetradius ATCC 35098]
[gi|20799590](#) glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus chromogenes]
[gi|197301564](#) hypothetical protein RUM1.AC_00290 [Ruminococcus lactaris ATCC 29176]
[gi|148380680](#) hydrolase [Clostridium botulinum A str. ATCC 3502]
[gi|148378084](#) hypothetical protein CB00076 [Clostridium botulinum A str. ATCC 3502]
[gi|228583035](#) trigger factor protein [Clostridium sp. 7_2_43FAA]
[gi|154502799](#) hypothetical protein RUMGNA_00613 [Ruminococcus gnavus ATCC 29149]
[gi|224476119](#) putative pyridine nucleotide-disulfide oxidoreductase [Staphylococcus carnosus subsp. carnosus TM300]
[gi|146295492](#) hypothetical protein CsaC_0434 [Caldicellulosiruptor saccharolyticus DSM 8903]
[gi|150388754](#) phosphoribosylglycinamide formyltransferase [Alkaliphilus metalliredigens QYMF]
[gi|20799602](#) glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus piscifermentans]
[gi|150391186](#) YheD [Alkaliphilus metalliredigens QYMF]
[gi|1706361](#) RecName: Full=Transcriptional regulatory protein degU
[gi|229175622](#) Cell surface protein [Bacillus cereus MM3]
[gi|212640452](#) S-layer glycoprotein protein, contains three N-terminal SLH domains [Anoxybacillus flavithermus WK1]
[gi|222529355](#) von Willebrand factor type A [Anaerocellum thermophilum DSM 6725]
[gi|134298892](#) hypothetical protein Dred_1028 [Desulfotomaculum reducens MI-1]
[gi|163763733](#) tetrahydrofolate dehydrogenase/cyclohydrolase [Bacillus selenitireducens MLS10]
[gi|228982852](#) hypothetical protein bthur0002_59850 [Bacillus thuringiensis Bt407]

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
Individual ions scores > 52 indicate identity or extensive homology ($p < 0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As Peptide Summary [Help](#)

Significance threshold $p < 0.05$ Max. number of hits AUTO

Standard scoring ☐ MudPIT scoring ☒ Ions score or expect cut-off 0 Show sub-sets 0

Show pop-ups ☒ Suppress pop-ups ☐ Sort unassigned Decreasing Score Require bold red ☐

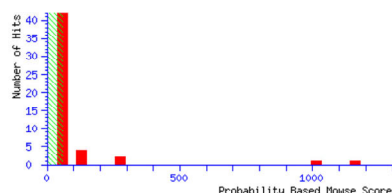
(4-1) Peptide Summary Report (protein spot 4, IE-4) Bacteria (Eubacteria)

Mascot Search Results

User : liaopc
Email :
Search title : IE-4
MS data file : merge.txt
Database : NCBIInr 090616 (9069431 sequences; 3106408609 residues)
Taxonomy : Bacteria (Eubacteria) (4853765 sequences)
Timestamp : 10 Jan 2012 at 05:46:12 GMT
Protein hits : [gi|42518797](#) glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus johnsonii NCC 533]
[gi|227520527](#) glyceraldehyde-3-phosphate dehydrogenase, phosphorylating [Lactobacillus gasseri JV-V03]
[gi|227361679](#) glyceraldehyde-3-phosphate dehydrogenase [Lactobacillus sakei subsp. carnosus DSM 15831]
[gi|227525966](#) glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) [Lactobacillus jensenii JV-V16]
[gi|116492261](#) glyceraldehyde-3-phosphate dehydrogenase [Pediococcus pentosaceus ATCC 25745]
[gi|111610131](#) glyceraldehyde 3 phosphate dehydrogenase [Lactobacillus helveticus CNR232]
[gi|90962141](#) glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus salivarius UCC118]
[gi|170016655](#) glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase [Leuconostoc citreum RM20]
[gi|225103805](#) glyceraldehyde-3-phosphate dehydrogenase, type I [Methylophaga sp. DMS010]
[gi|19499337](#) hypothetical protein RED65_11124 [Oceanobacter sp. RED65]
[gi|148252055](#) glyceraldehyde-3-phosphate dehydrogenase [Bradyrhizobium sp. BTail]
[gi|196230628](#) hypothetical protein CFE428DRAFT_2655 [Chthoniobacter flavus Ellin428]
[gi|57234620](#) glyceraldehyde-3-phosphate dehydrogenase, type I [Dehalococcoides ethenogenes 195]
[gi|87161642](#) alkyl hydroperoxide reductase subunit F [Staphylococcus aureus subsp. aureus USA300_FPR3757]
[gi|20799584](#) glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus arlettae]
[gi|126347884](#) putative glyceraldehyde 3-phosphate dehydrogenase [Streptomyces ambofaciens ATCC 23877]
[gi|84494635](#) putative glycerol phosphate dehydrogenase [Janibacter sp. HTCC2649]
[gi|218149927](#) phosphopantothencysteine decarboxylase/phosphopantothenate/cysteine ligase [Desulfovibrio salexigens]
[gi|196036424](#) phage infection protein [Bacillus cereus W]
[gi|227979847](#) putative proteasome component/protein of unknown function, DUF275 [Tsukamurella paurometabola DSM 20162]
[gi|24213647](#) polynucleotide phosphorylase/polyadenylase [Leptospira interrogans serovar Lai str. 56601]
[gi|224391617](#) cobalamin biosynthesis protein CobT [Candidatus Pelagibacter sp. HTCC7211]
[gi|23099893](#) glyceraldehyde-3-phosphate dehydrogenase [Oceanobacillus ihycynaia HTE831]
[gi|197301564](#) hypothetical protein RUMIAC_00290 [Ruminococcus lactaris ATCC 29176]
[gi|227500542](#) DNA-binding protein [Anaerococcus tetradicus ATCC 35098]
[gi|238027761](#) hypothetical protein bglu_1g21850 [Burkholderia glumae BGRI]
[gi|238927776](#) conserved hypothetical protein [Selenomonas flueggei ATCC 43531]
[gi|149199701](#) hypothetical protein LNTAR_25135 [Lentisphaera araneosa HTCC2155]
[gi|226310996](#) glyceraldehyde 3-phosphate dehydrogenase [Brevibacillus brevis NBRC 100599]
[gi|1706361](#) RecName: Full=Transcriptional regulatory protein degU
[gi|225022859](#) hypothetical protein CORMATOL_02901 [Corynebacterium matruchotii ATCC 33806]
[gi|218439438](#) DNA topoisomerase I [Cyanothera sp. PCC 7424]
[gi|20799590](#) glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus chromogenes]
[gi|114321786](#) TolC family type I secretion outer membrane protein [Alkalilimnicola ehrlichii MLHE-1]
[gi|110835656](#) aminoglycoside-3-phospho transferase [Acetobacter pasteurianus]
[gi|229175622](#) Cell surface protein [Bacillus cereus MM3]
[gi|999601](#) Chain O, The Crystal Structure Of Holo-Glyceraldehyde-3-Phosphate Dehydrogenase From The Hyperthermophil.
[gi|162450188](#) hypothetical protein sce1916 [Sorangium cellulosum 'So ce 56']
[gi|237751407](#) glycosyl transferase [Helicobacter bilis ATCC 438/19]
[gi|167764151](#) hypothetical protein BACSTE_02535 [Bacteroides stercoris ATCC 43183]

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
Individual ions scores > 59 indicate identity or extensive homology ($p < 0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As Peptide Summary [Help](#)

Significance threshold $p < 0.05$ Max. number of hits AUTO

Standard scoring ☒ MudPIT scoring ☐ Ions score or expect cut-off 0 Show sub-sets 0

Show pop-ups ☒ Suppress pop-ups ☐ Sort unassigned Decreasing Score ☒ Require bold red ☐

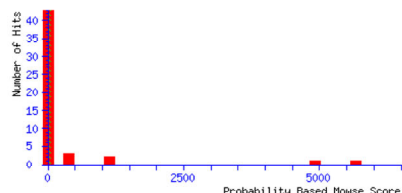
(4-2) Peptide Summary Report (protein spot 4, IE-4) Firmicutes (gram-positive bacteria)

(MATRIX) *(SCIENCE)* Mascot Search Results

User : liaopc
Email :
Search title : IE-4
MS data file : merge.txt
Database : NCBI nr 090616 (9069431 sequences; 3106408609 residues)
Taxonomy : Firmicutes (gram-positive bacteria) (1006590 sequences)
Timestamp : 10 Jan 2012 at 09:46:08 GMT
Protein hits : [gi|42518797](#) glycerinaldehyde 3-phosphate dehydrogenase [Lactobacillus johnsonii NCC 533]
[gi|227520527](#) glycerinaldehyde-3-phosphate dehydrogenase, phosphorylating [Lactobacillus gasseri JV-V03]
[gi|227361679](#) glycerinaldehyde-3-phosphate dehydrogenase [Lactobacillus sakei subsp. carnosus DSM 15831]
[gi|227525966](#) glycerinaldehyde-3-phosphate dehydrogenase (phosphorylating) [Lactobacillus jensenii JV-V16]
[gi|20799584](#) glycerinaldehyde-3-phosphate dehydrogenase [Staphylococcus arlettae]
[gi|90962141](#) glycerinaldehyde 3-phosphate dehydrogenase [Lactobacillus salivarius UCC118]
[gi|116492261](#) glycerinaldehyde-3-phosphate dehydrogenase [Pediococcus pentosaceus ATCC 25745]
[gi|170016655](#) glycerinaldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase [Leuconostoc citreum KM20]
[gi|20799590](#) glycerinaldehyde-3-phosphate dehydrogenase [Staphylococcus chromogenes]
[gi|227500542](#) DNA-binding protein [Anaerococcus tetradius ATCC 35098]
[gi|197301564](#) hypothetical protein RUM_LAC_00290 [Ruminococcus lactaris ATCC 29176]
[gi|148380680](#) hydrolase [Clostridium botulinum A str. ATCC 3502]
[gi|148378084](#) hypothetical protein CRO0076 [Clostridium botulinum A str. ATCC 3502]
[gi|229175622](#) Cell surface protein [Bacillus cereus MM3]
[gi|49478820](#) cell surface anchor [Bacillus thuringiensis serovar konkukian str. 97-27]
[gi|228981615](#) Cell surface protein [Bacillus thuringiensis Bt407]
[gi|20799602](#) glycerinaldehyde-3-phosphate dehydrogenase [Staphylococcus piscifermentans]
[gi|238927776](#) conserved hypothetical protein [Selenomonas flueggei ATCC 43531]
[gi|1706361](#) RecName: Full=Transcriptional regulatory protein degU
[gi|111610131](#) glycerinaldehyde 3-phosphate dehydrogenase [Lactobacillus helveticus CNR232]
[gi|220931194](#) hypothetical protein Hore_03460 [Halothermothrix orenii H 168]
[gi|229229306](#) ATPase component of various ABC-type transport systems with duplicated ATPase domain [Desulfotomaculum a
[gi|169187565](#) two component transcriptional regulator, LuxR family [Paenibacillus sp. JDR-2]
[gi|146295492](#) hypothetical protein CsaC_0434 [Caldicellulosiruptor saccharolyticus DSM 8903]
[gi|229829382](#) hypothetical protein GCWU000342_01471 [Shuttleworthia satelles DSM 14600]
[gi|225027108](#) hypothetical protein EUBHAL_01364 [Eubacterium hallii DSM 3353]
[gi|154502799](#) hypothetical protein RUMGNA_00613 [Ruminococcus gnavus ATCC 29149]
[gi|212640452](#) S-layer glycoprotein protein, contains three N-terminal SLH domains [Anoxybacillus flavithermus WK1]
[gi|42519693](#) hypothetical protein LJ0632 [Lactobacillus johnsonii NCC 533]
[gi|228918843](#) hypothetical protein bthur0012_59520 [Bacillus thuringiensis serovar pulvisiensis BGSC 4CC1]
[gi|222529096](#) glycoside hydrolase family 4 [Anaerocellum thermophilum DSM 6725]
[gi|229541561](#) two component transcriptional regulator, LuxR family [Bacillus coagulans 36D1]

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
Individual ions scores > 52 indicate identity or extensive homology ($p < 0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As Peptide Summary [Help](#)

Significance threshold $p < 0.05$ Max. number of hits AUTO

Standard scoring ☐ MudPIT scoring ☒ Ions score or expect cut-off 0 Show sub-sets 0

Show pop-ups ☒ Suppress pop-ups ☐ Sort unassigned Decreasing Score Require bold red ☐

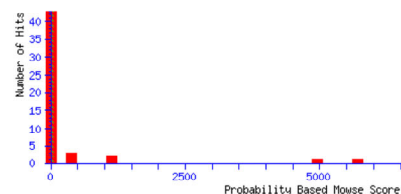
(4-3) Peptide Summary Report (protein spot 4, IE-4) Other Firmicutes

Mascot Search Results

User	:	liaopc
Email	:	
Search title	:	IE-4
MS data file	:	merge.txt
Database	:	NCBInr 090616 (9069431 sequences; 3106408609 residues)
Taxonomy	:	Other Firmicutes (967613 sequences)
Timestamp	:	11 Jan 2012 at 01:54:33 GMT
Protein hits	:	qi 42518797 glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus johnsonii NCC 533] qi 227520527 glyceraldehyde-3-phosphate dehydrogenase, phosphorylating [Lactobacillus gasseri JV-V03] qi 227361679 glyceraldehyde-3-phosphate dehydrogenase [Lactobacillus sakei subsp. carnosus DSM 15831] qi 227525966 glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) [Lactobacillus jensenii JV-V16] qi 20799584 glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus arlettae] qi 90962141 glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus salivarius UCC118] qi 116492261 glyceraldehyde-3-phosphate dehydrogenase [Pediococcus pentosaceus ATCC 25745] qi 20799590 glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus chromogenes] qi 170016655 glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase [Leuconostoc citreum KM20] qi 148300680 hydrolase [Clostridium botulinum A str. ATCC 3502] qi 227500542 DNA-binding protein [Anaerococcus tetradius ATCC 35098] qi 197301564 hypothetical protein RUM_LAC_00290 [Ruminococcus lactaris ATCC 29176] qi 148378084 hypothetical protein CBO0076 [Clostridium botulinum A str. ATCC 3502] qi 229175622 Cell surface protein [Bacillus cereus MM3] qi 49478820 cell surface anchor [Bacillus thuringiensis serovar konkukian str. 97-27] qi 228981615 Cell surface protein [Bacillus thuringiensis Bt407] qi 20799602 glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus piscifermentans] qi 238927776 conserved hypothetical protein [Selenomonas flueggei ATCC 43531] qi 1706361 RecName: Full=Transcriptional regulatory protein degU qi 111610131 glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus helveticus CNRZ32] qi 220931194 hypothetical protein Hore_03460 [Halothermothrix orenii H 168] qi 229229306 ATPase component of various ABC-type transport systems with duplicated ATPase domain [Desulfotomaculum a qi 169187565 two component transcriptional regulator, LuxR family [Paenibacillus sp. JDR-2] qi 146295492 hypothetical protein Csac 0434 [Caldicellulosiruptor saccharolyticus DSM 8903] qi 229829382 hypothetical protein GCWU000342_01471 [Shuttleworthia satelles DSM 14600] qi 225027108 hypothetical protein EUBHAL_01364 [Eubacterium hallii DSM 3353] qi 154502799 hypothetical protein RUMGNA_00613 [Ruminococcus gnavus ATCC 29149] qi 212640452 S-layer glycoprotein protein, contains three N-terminal SLH domains [Anoxybacillus flavithermus WK1] qi 42519693 hypothetical protein LJ0632 [Lactobacillus johnsonii NCC 533] qi 228918843 hypothetical protein bthur0012_59520 [Bacillus thuringiensis serovar pulsiensis BGSC 4CC1] qi 222529096 glycoside hydrolase family 4 [Anaerocellum thermophilum DSM 6725] qi 229541561 two component transcriptional regulator, LuxR family [Bacillus coagulans 36D1]

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Individual ions scores > 52 indicate identity or extensive homology ($p < 0.05$). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As	Peptide Summary	Help			
Significance threshold p<	0.05	Max. number of hits	AUTO		
Standard scoring	☒ MudPIT scoring	☒ Ions score or expect cut-off	0	Show sub-sets	0
Show pop-ups	☒ Suppress pop-ups	☐ Sort unassigned	Decreasing Score	Require bold red	☐

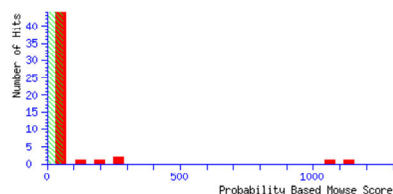
(5-1) Peptide Summary Report (protein spot 5, IE-5) Bacteria (Eubacteria)

Mascot Search Results

User : liaopc
Email :
Search title : IE-5
MS data file : merge.txt
Database : NCBI nr 090616 (9069431 sequences; 3106408609 residues)
Taxonomy : Bacteria (Eubacteria) (4853765 sequences)
Timestamp : 10 Jan 2012 at 07:20:47 GMT
Protein hits :
[gi|42518797](#) glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus johnsonii NCC 533]
[gi|227520527](#) glyceraldehyde-3-phosphate dehydrogenase, phosphorylating [Lactobacillus gasseri JV-V03]
[gi|227361679](#) glyceraldehyde-3-phosphate dehydrogenase [Lactobacillus sakei subsp. carnosus DSM 15831]
[gi|227525966](#) glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) [Lactobacillus jensenii JV-V16]
[gi|111610131](#) glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus helveticus UNK232]
[gi|90962141](#) glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus salivarius UCC118]
[gi|158334876](#) hypothetical protein AM1_1713 [Acaryochloris marina MBIC11017]
[gi|237751407](#) glycosyl transferase [Helicobacter bilis ATCC 43879]
[gi|162148108](#) putative peptidyl-prolyl cis-trans isomerase B [Gluconacetobacter diazotrophicus PAL 5]
[gi|20799584](#) glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus arlettae]
[gi|217077222](#) chromosome segregation SMC protein, putative [Thermosipho africanus TCF52B]
[gi|116492261](#) glyceraldehyde-3-phosphate dehydrogenase [Pediococcus pentosaceus ATCC 25745]
[gi|172057364](#) hypothetical protein EXig_1335 [Exiguobacterium sibiricum 255-15]
[gi|196228419](#) hypothetical protein CFE428DRAFT_0450 [Chthoniobacter flavus Ellin428]
[gi|160894823](#) hypothetical protein CLOL250_02373 [Clostridium sp. L2-50]
[gi|84494635](#) putative glycerol phosphate dehydrogenase [Janibacter sp. HTCC2649]
[gi|124024825](#) hypothetical protein NATLi_01121 [Prochlorococcus marinus str. NATLiA]
[gi|116491203](#) ABC-type metal ion transport system, periplasmic component/surface adhesin [Oenococcus oeni PSU-1]

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
Individual ions scores > 59 indicate identity or extensive homology ($p < 0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As Peptide Summary [Help](#)

Significance threshold $p <$ 0.05 Max. number of hits AUTO

Standard scoring ☒ MudPIT scoring ☐ Ions score or expect cut-off 0 Show sub-sets 0

Show pop-ups ☒ Suppress pop-ups ☐ Sort unassigned Decreasing Score ☒ Require bold red ☐

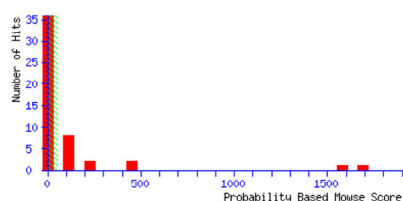
(5-2) Peptide Summary Report (protein spot 5, IE-5) Firmicutes (gram-positive bacteria)

{MATRIX} *{SCIENCE}* Mascot Search Results

User : liaopc
Email :
Search title : IE-5
MS data file : merge.txt
Database : NCBIInr 090616 (9069431 sequences; 3106408609 residues)
Taxonomy : Firmicutes (gram-positive bacteria) (1006590 sequences)
Timestamp : 11 Jan 2012 at 02:17:38 GMT
Protein hits : [gi|42518797](#) glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus johnsonii NCC 533]
[gi|227520527](#) glyceraldehyde-3-phosphate dehydrogenase, phosphorylating [Lactobacillus gasseri JV-V03]
[gi|227361679](#) glyceraldehyde-3-phosphate dehydrogenase [Lactobacillus sakei subsp. carnosus DSM 15831]
[gi|227525966](#) glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) [Lactobacillus jensenii JV-V16]
[gi|116494473](#) glyceraldehyde-3-phosphate dehydrogenase [Lactobacillus casei ATCC 334]
[gi|111610131](#) glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus helveticus CNR232]
[gi|20799584](#) glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus arlettae]
[gi|116492261](#) glyceraldehyde-3-phosphate dehydrogenase [Pediococcus pentosaceus ATCC 25745]
[gi|172057364](#) hypothetical protein Exig_1335 [Exiguobacterium sibiricum 255-15]
[gi|160894823](#) hypothetical protein CLOL250_02373 [Clostridium sp. L2-50]
[gi|90962141](#) glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus salivarius UCC118]
[gi|150016208](#) trigger factor [Clostridium beijerinckii NCIMB 8052]
[gi|150391186](#) YheD [Alkaliphilus metalliredigens QYMF]
[gi|154502799](#) hypothetical protein RUMGNA_00613 [Ruminococcus gnavus ATCC 29149]
[gi|148380680](#) hydrolase [Clostridium botulinum A str. ATCC 3502]
[gi|20799590](#) glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus chromogenes]
[gi|170016659](#) glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase [Leuconostoc citreum KM20]
[gi|227500542](#) DNA-binding protein [Anaerococcus tetradius ATCC 35098]
[gi|192808885](#) YjgB [Geobacillus sp. Y412MC10]
[gi|225390610](#) hypothetical protein CLOSTASPAR_04365 [Clostridium asparagiforme DSM 15981]
[gi|150388754](#) phosphoribosylglycinamide formyltransferase [Alkaliphilus metalliredigens QYMF]

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
Individual ions scores > 52 indicate identity or extensive homology ($p < 0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As [Help](#)

Significance threshold $p <$ Max. number of hits

Standard scoring ☐ MudPIT scoring ☒ Ions score or expect cut-off Show sub-sets

Show pop-ups ☒ Suppress pop-ups ☐ Sort unassigned ☒ Require bold red ☐

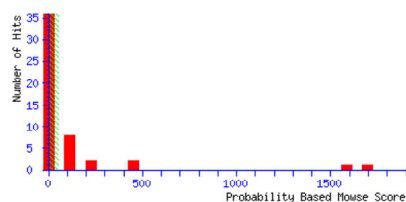
(5-3) Peptide Summary Report (protein spot 5, IE-5) Other Firmicutes

Mascot Search Results

User : liaopc
Email :
Search title : IE-5
MS data file : merge.txt
Database : NCBI nr 090616 (9069431 sequences; 3106408609 residues)
Taxonomy : Other Firmicutes (967613 sequences)
Timestamp : 11 Jan 2012 at 02:05:35 GMT
Protein hits :
[gi|142518797](#) glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus johnsonii NCC 533]
[gi|227520527](#) glyceraldehyde-3-phosphate dehydrogenase, phosphorylating [Lactobacillus gasseri JV-V03]
[gi|227361679](#) glyceraldehyde-3-phosphate dehydrogenase [Lactobacillus sakei subsp. carnosus DSM 15831]
[gi|227525966](#) glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) [Lactobacillus jensenii JV-V16]
[gi|116494473](#) glyceraldehyde-3-phosphate dehydrogenase [Lactobacillus casei ATCC 334]
[gi|111610131](#) glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus helveticus CNRZ32]
[gi|20799584](#) glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus arlettae]
[gi|116492261](#) glyceraldehyde-3-phosphate dehydrogenase [Pediococcus pentosaceus ATCC 25745]
[gi|172057364](#) hypothetical protein Exig_1335 [Exiguobacterium sibiricum 255-15]
[gi|160894823](#) hypothetical protein CLOL250_02373 [Clostridium sp. L2-50]
[gi|90962141](#) glyceraldehyde 3-phosphate dehydrogenase [Lactobacillus salivarius UCC118]
[gi|150016208](#) trigger factor [Clostridium beijerinckii NCIMB 8052]
[gi|150391186](#) YheD [Alkaliphilus metalliredigens QYMF]
[gi|154502799](#) hypothetical protein RUMGNA_00613 [Ruminococcus gnavus ATCC 29149]
[gi|148380680](#) hydrolase [Clostridium botulinum A str. ATCC 3502]
[gi|20799590](#) glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus chromogenes]
[gi|170016655](#) glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase [Leuconostoc citreum KM20]
[gi|227500542](#) DNA-binding protein [Anaerococcus tetradius ATCC 35098]
[gi|192808885](#) YjgB [Geobacillus sp. Y412MC10]
[gi|225390610](#) hypothetical protein CLOSTASPAR_04365 [Clostridium asparagiforme DSM 15981]
[gi|150388754](#) phosphoribosylglycinamide formyltransferase [Alkaliphilus metalliredigens QYMF]
[gi|220932533](#) DegT/DnrJ/EryC1/StrS aminotransferase [Halothermothrix orenii H 168]

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
Individual ions scores > 52 indicate identity or extensive homology ($p < 0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As [Help](#)

Significance threshold $p <$ Max. number of hits

Standard scoring ☐ MudPIT scoring ☒ Ions score or expect cut-off Show sub-sets

Show pop-ups ☒ Suppress pop-ups ☐ Sort unassigned Require bold red ☐

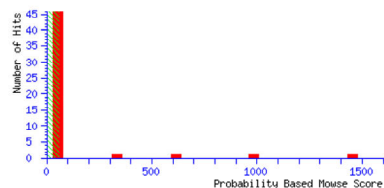
(6-1) Peptide Summary Report (protein spot 6, IE-6) Bacteria (Eubacteria)

MASCOT **SCIENCE** Mascot Search Results

User : liaopc
Email :
Search title : IE-6
MS data file : mesre.txt
Database : NCBI nr 090616 (9069431 sequences; 3106408609 residues)
Taxonomy : Bacteria (Eubacteria) (4853765 sequences)
Timestamp : 10 Jan 2012 at 02:16:55 GMT
Protein hits : [gi|116629131](#) fructose/tagatose bisphosphate aldolase [Lactobacillus gasseri ATCC 33323]
[gi|42518609](#) fructose-bisphosphate aldolase [Lactobacillus johnsonii NCC 533]
[gi|227360402](#) fructose-bisphosphate aldolase [Lactobacillus sakei subsp. carnosus DSM 15831]
[gi|227876934](#) fructose-bisphosphate aldolase [Lactobacillus crispatus JV-V01]
[gi|164687868](#) hypothetical protein CLOBAR_01512 [Clostridium bartlettii DSM 16795]
[gi|119961101](#) hypothetical protein AAur_3947 [Arthrobacter aureescens TC1]
[gi|228948651](#) Cell surface protein [Bacillus thuringiensis serovar monterrey BGSC 4AJ1]
[gi|229541583](#) galactokinase [Bacillus coagulans 36D1]
[gi|114561971](#) UspA domain-containing protein [Shewanella frigidimarina NCIMB 400]
[gi|229135967](#) transposase, IS605 [Bacillus cereus BDRD-ST196]
[gi|196157130](#) DNA polymerase III subunit delta [Alteromonas macleodii 'Deep ecotype']
[gi|237712148](#) alpha-1,2-fucosyltransferase [Bacteroides sp. 9_1_42FAA]
[gi|224437247](#) lipid A biosynthesis lauroyl acyltransferase [Helicobacter cinaedi CCUG 18818]
[gi|19704335](#) biotin synthase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]
[gi|67922674](#) hypothetical protein CwatDRAFT_3622 [Crocospaera watsonii WH 8501]
[gi|1706361](#) RecName: Full-Transcriptional regulatory protein degU
[gi|158321234](#) adenosylcobinamide-phosphate guanylyltransferase [Alkaliphilus oremlandii OhILAs]
[gi|90407501](#) stringent starvation protein A [Psychromonas sp. CNPT3]
[gi|73667069](#) hypothetical protein Ecaj_0447 [Ehrlichia canis str. Jake]
[gi|237751407](#) glycosyl transferase [Helicobacter bilis ATCC 43879]
[gi|197301564](#) hypothetical protein RUMLAC_00290 [Ruminococcus lactaris ATCC 29176]
[gi|110638554](#) Zn-binding alcohol dehydrogenase [Cytophaga hutchinsonii ATCC 33406]
[gi|123442441](#) hemin storage receptor protein [Yersinia enterocolitica subsp. enterocolitica 8081]
[gi|149199701](#) hypothetical protein LNTAR_25135 [Lentisphaera araneosa HTCC2155]
[gi|224391617](#) cobalamin biosynthesis protein CobT [Candidatus Pelagibacter sp. HTCC7211]
[gi|163786638](#) hypothetical protein FBALC1_15672 [Flavobacteriales bacterium ALC-1]
[gi|29840049](#) polymorphic outer membrane protein G family protein/autotransporter, putative [Chlamydomonas caviae GPIC]
[gi|30262473](#) hypothetical protein BA2474 [Bacillus anthracis str. Ames]
[gi|167764151](#) hypothetical protein BACSTE_02535 [Bacteroides stercoris ATCC 43183]
[gi|42561108](#) holo-[acyl-carrier-protein] synthase [Mycoplasma mycoides subsp. mycoides SC str. PG1]
[gi|15594477](#) fused transcript cleavage factor/uncharacterized domain-containing protein [Borrelia burgdorferi B31]
[gi|153813549](#) hypothetical protein RUMOB_03971 [Ruminococcus obeum ATCC 29174]

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
Individual ions scores > 59 indicate identity or extensive homology ($p < 0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As Peptide Summary [Help](#)

Significance threshold $p < 0.05$ Max. number of hits AUTO

Standard scoring ☒ MudPIT scoring ☐ Ions score or expect cut-off 0 Show sub-sets 0

Show pop-ups ☒ Suppress pop-ups ☐ Sort unassigned Decreasing Score ☒ Require bold red ☐

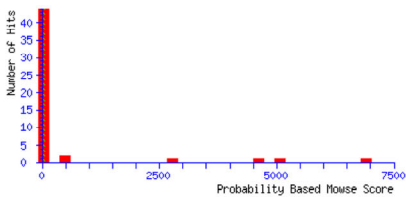
(6-2) Peptide Summary Report (protein spot 6, IE-6) Firmicutes (gram-positive bacteria)

(MATRIX) *(SCIENCE)* Mascot Search Results

User	: liaopc
Email	:
Search title	: IE-6
MS data file	: merge.txt
Database	: NCBI nr 090616 (9069431 sequences; 3106408609 residues)
Taxonomy	: Firmicutes (gram-positive bacteria) (1006590 sequences)
Timestamp	: 11 Jan 2012 at 02:57:03 GMT
Protein hits	: qi 116629131 fructose/tagatose bisphosphate aldolase [Lactobacillus gasserii ATCC 33323] qi 42518609 fructose-bisphosphate aldolase [Lactobacillus johnsonii NCC 533] qi 227360402 fructose-bisphosphate aldolase [Lactobacillus sakei subsp. carnosus DSM 15831] qi 227876934 fructose-bisphosphate aldolase [Lactobacillus crispatus JV-V01] qi 164687868 hypothetical protein CLOBAR_01512 [Clostridium bartlettii DSM 16795] qi 229135967 transposase, IS605 [Bacillus cereus BDRD-ST196] qi 197301564 hypothetical protein RUMLAC_00290 [Ruminococcus lactaris ATCC 29176] qi 30262473 hypothetical protein BA2474 [Bacillus anthracis str. Ames] qi 158321234 adenosylcobinamide-phosphate guanylyltransferase [Alkaliphilus oremlandii OhILAs] qi 169191287 UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Paenibacillus sp. JDR-2] qi 47567502 ABC transporter, ATP-binding protein [Bacillus cereus G9241] qi 153813549 hypothetical protein RUMOB_03971 [Ruminococcus obeum ATCC 29174] qi 81429140 fructose-bisphosphate aldolase [Lactobacillus sakei subsp. sakei 23K] qi 1706361 RecName: Full=Transcriptional regulatory protein degU qi 168333288 hypothetical protein Epulo_00390 [Epulopiscium sp. 'N.t. morphotype B'] qi 228948651 Cell surface protein [Bacillus thuringiensis serovar monterrey BGSC 4AJ1] qi 172058143 glutamate-1-semialdehyde-2,1-aminomutase [Exiguobacterium sibiricum 255-15] qi 145952657 hypothetical protein CdifQ_04004036 [Clostridium difficile QCD-32q58] qi 229229306 ATPase component of various ABC-type transport systems with duplicated ATPase domain [Desulfotomaculum a qi 229092047 beta-lactamase class C [Bacillus cereus Rock3-42] qi 228583035 trigger factor protein [Clostridium sp. 7_2_43FAA] qi 229106627 hypothetical protein boere0019_54130 [Bacillus cereus Rock3-28] qi 187935417 serine protein kinase [Clostridium botulinum B str. Eklund 17B] qi 229172724 Fis-type helix-turn-helix domain protein [Bacillus cereus MM3] qi 152974405 sortase family protein [Bacillus cereus subsp. cytotoxica NVH 391-98] qi 194398220 ABC transporter, ATP-binding protein [Streptococcus pneumoniae G54] qi 238916527 basic amino acid/polyamine antiporter, APA family [Eubacterium eligens ATCC 27750] qi 167766734 hypothetical protein CLOSS21_01240 [Clostridium sp. SS2/1] qi 150391186 YheD [Alkaliphilus metalliredigens QYMF] qi 222529355 von Willebrand factor type A [Anaerocellum thermophilum DSM 6725] qi 192808568 hypothetical protein GYMC10DRAFT_1077 [Geobacillus sp. Y412MC10] qi 212640452 S-layer glycoprotein protein, contains three N-terminal SLH domains [Anoxybacillus flavithermus WK1] qi 52078774 putative lipoprotein [Bacillus licheniformis ATCC 14580] qi 229541561 two component transcriptional regulator, LuxR family [Bacillus coagulans 36D1] qi 194016979 YpiF [Bacillus pumilus ATCC 7061] qi 160939974 hypothetical protein CLOBOL_04864 [Clostridium bolteae ATCC BAA-613] qi 229051384 hypothetical protein boere0027_53120 [Bacillus cereus AH676] qi 218284163 hypothetical protein EUBIFOR_02562 [Eubacterium bifforme DSM 3989] qi 15614407 3-oxoacyl-[acyl-carrier-protein] synthase III [Bacillus halodurans C-125] qi 16799344 2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase [Listeria innocua Clip11262]

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
Individual ions scores > 52 indicate identity or extensive homology ($p < 0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As	Peptide Summary	Help
Significance threshold p<	0.05	Max. number of hits AUTO
Standard scoring	☐ MudPIT scoring ☒ Ions score or expect cut-off	0 Show sub-sets 0
Show pop-ups	☒ Suppress pop-ups ☐ Sort unassigned	Decreasing Score Require bold red ☐

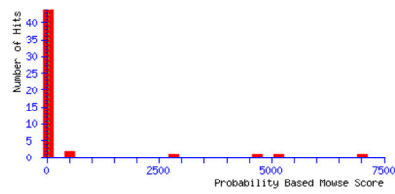
(6-3) Peptide Summary Report (protein spot 6, IE-6) Other Firmicutes

Mascot Search Results

User	: liaopc
Email	:
Search title	: IE-6
MS data file	: merge.txt
Database	: NCBI nr 090616 (9069431 sequences; 3106408609 residues)
Taxonomy	: Other Firmicutes (967613 sequences)
Timestamp	: 11 Jan 2012 at 03:19:47 GMT
Protein hits	: gi 116629131 fructose/tagatose biphosphate aldolase [Lactobacillus gasseri ATCC 33323] gi 42518609 fructose-bisphosphate aldolase [Lactobacillus johnsonii NCC 533] gi 227360402 fructose-bisphosphate aldolase [Lactobacillus sakei subsp. carnosus DSM 15831] gi 227876934 fructose-bisphosphate aldolase [Lactobacillus crispatus JV-V01] gi 164687868 hypothetical protein CLOBAR_01512 [Clostridium bartlettii DSM 16795] gi 229135967 transposase, IS605 [Bacillus cereus BDRD-ST196] gi 197301564 hypothetical protein RUMIAC_00290 [Ruminococcus lactaria ATCC 29176] gi 30262473 hypothetical protein BA2474 [Bacillus anthracis str. Ames] gi 158321234 adenosylcobinamide-phosphate guanylyltransferase [Alkaliphilus oremlandii OhILAs] gi 181429140 fructose-bisphosphate aldolase [Lactobacillus sakei subsp. sakei 23K] gi 169191287 UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Paenibacillus sp. JDR-2] gi 47567502 ABC transporter, ATP-binding protein [Bacillus cereus G9241] gi 153813549 hypothetical protein RUMOB_03971 [Ruminococcus obeum ATCC 29174] gi 1706361 RecName: Full=Transcriptional regulatory protein degU gi 168333288 hypothetical protein Epulo_00390 [Epulopiscium sp. 'N.t. morphotype B'] gi 228948651 Cell surface protein [Bacillus thuringiensis serovar monterrey BGSC 4AJ1] gi 172058143 glutamate-1-semialdehyde-2,1-aminomutase [Exiguobacterium sibiricum 255-15] gi 145952657 hypothetical protein CdifQ_04004036 [Clostridium difficile QCD-32g58] gi 229229306 ATPase component of various ABC-type transport systems with duplicated ATPase domain [Desulfotomaculum a gi 229092047 beta-lactamase class C [Bacillus cereus Rock3-42] gi 228583035 trigger factor protein [Clostridium sp. 7_2_43FAA] gi 229106627 hypothetical protein bcere0019_54130 [Bacillus cereus Rock3-28] gi 187935417 serine protein kinase [Clostridium botulinum B str. Eklund 17B] gi 229172724 Fis-type helix-turn-helix domain protein [Bacillus cereus MM3] gi 152974405 sortase family protein [Bacillus cereus subsp. cytotoxis NVH 391-98] gi 238916527 basic amino acid/polyamine antiporter, APA family [Eubacterium eligens ATCC 27750] gi 167766734 hypothetical protein CLOSS21_01240 [Clostridium sp. SS2/1] gi 150391186 YheD [Alkaliphilus metalliredigens QYMF] gi 222529355 von Willebrand factor type A [Anaerocellum thermophilum DSM 6725] gi 192808568 hypothetical protein GYMC10DRAFT_1077 [Geobacillus sp. Y412MC10] gi 212640452 S-layer glycoprotein protein, contains three N-terminal SLH domains [Anoxybacillus flavithermus WK1] gi 52078774 putative lipoprotein [Bacillus licheniformis ATCC 14580] gi 229541561 two component transcriptional regulator, LuxR family [Bacillus coagulans 36D1] gi 194016979 YpiF [Bacillus pumilus ATCC 7061] gi 160939974 hypothetical protein CLOBOL_04864 [Clostridium bolteae ATCC BAA-613] gi 229051384 hypothetical protein bcere0027_53120 [Bacillus cereus AH676] gi 218284163 hypothetical protein EUBIFOR_02562 [Eubacterium biforme DSM 3989] gi 15614407 3-oxoacyl-[acyl-carrier-protein] synthase III [Bacillus halodurans C-125] gi 16799344 2-C-methyl-D-erythritol 4-phosphate cytidyltransferase [Listeria innocua Clip11262]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 52 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As

Peptide Summary

Help

Significance threshold p<

0.05

Max. number of hits

AUTO

Standard scoring

☐ MudPIT scoring

☒ Ions score or expect cut-off

0

Show sub-sets

0

Show pop-ups

☒ Suppress pop-ups

☐ Sort unassigned

Decreasing Score

Require bold red

☐

If readers are interested in further analysis of this proteomic data, we can make it available upon reasonable request.