

BLAST result for homology analysis with *Homo sapiens* aspartate N-acetyltransferase

BLASTP 2.2.25+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference for compositional score matrix adjustment: Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schaffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

RID: TB9U2CT5014

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

13,473,798 sequences; 4,621,495,809 total letters

Query= gi|119602947|gb|EAW82541.1| hypothetical protein LOC339983 [Homo sapiens]

Length=302

Score E
Sequences producing significant alignments:
(Bits) Value

ref YP_026287.1	predicted acetyltransferase [Escherichia col...
42.0	6e-05
gb AAA97152.1	ORF_f97 [Escherichia coli str. K-12 substr. MG...
40.4	2e-04
ref NP_417898.1	predicted acetyltransferase [Escherichia col...
38.9	6e-04
ref AP_003028.1	predicted acyltransferase with acyl-CoA N-ac...
33.5	0.028
ref NP_418210.1	predicted multidrug or homocysteine efflux s...
30.4	0.23
ref NP_418790.1	ribosomal-protein-S18-alanine N-acetyltransf...
30.0	0.26
gb AAA97269.1	CG Site No. 277 [Escherichia coli str. K-12 su...
30.0	0.28

ref|NP_417296.1| exonuclease V (RecBCD complex), alpha chain ...
 30.0 0.30
 ref|NP_417625.1| predicted acyltransferase with acyl-CoA N-ac...
 28.9 0.56
 ref|NP_415597.1| flagellar protein of basal-body outer-membra...
 27.3 1.9
 ref|NP_416506.1| CP4-44 prophage; predicted DNA repair protei...
 26.2 3.7
 ref|NP_418517.1| predicted acyltransferase with acyl-CoA N-ac...
 25.4 6.3
 ref|AP_002454.1| hypothetical protein [Escherichia coli str. ...
 25.0 8.5
 ref|NP_417059.1| pyridoxine 5'-phosphate synthase [Escherichi...
 25.0 9.2

ALIGNMENTS

>ref|YP_026287.1| predicted acetyltransferase [Escherichia coli str.
 K-12 substr.
 MG1655]
 ref|AP_004752.1| predicted acetyltransferase [Escherichia coli str.
 K-12 substr.
 W3110]
 ref|YP_001733015.1| acetyltransferase [Escherichia coli str. K-12
 substr. DH10B]
 ref|YP_002929153.1| putative acetyltransferase [Escherichia coli
 BW2952]
 sp|P39337.2|YJGM_ECOLI RecName: Full=Uncharacterized N-
 acetyltransferase YjgM
 gb|AAT48245.1| predicted acetyltransferase [Escherichia coli str. K-
 12 substr.
 MG1655]
 dbj|BAE78253.1| predicted acetyltransferase [Escherichia coli str.
 K12 substr.
 W3110]
 gb|ACB05237.1| predicted acetyltransferase [Escherichia coli str. K-
 12 substr.
 DH10B]
 gb|ACR64110.1| predicted acetyltransferase [Escherichia coli BW2952]
 Length=167

Score = 42.0 bits (97), Expect = 6e-05, Method: Compositional matrix
 adjust.

Identities = 36/102 (35%), Positives = 50/102 (49%), Gaps = 3/102
 (3%)

Query 168 DMADIEQYYMKPPGSCFWVAVLDGNVVGI--
 VAARAHEEDNTVELLRMSVDSRFRGKGIA 225

++ ++ Q Y +P G +WV +G VVG +A E + EL +M

RGKG+A

Sbjct 47 NLDELYQVYSQP-

GHAYWVVEYEGEVVGGGGIAPLTGSESDICELQKMYFLPAIRGKGLA 105

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Query   226  KALGRKVLFAVVHNYSVVLTAVKVAHKLYESLGFRHM  267
          K L      +E A      +      L TTA      A  LYE LGF H+
Sbjct   106  KKLALMAMEQAREMGFKRCYLETTAFLKEAIALYEH LGFEHI  147

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>gb|AAA97152.1| ORF_f97 [Escherichia coli str. K-12 substr. MG1655]
Length=97

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Score = 40.4 bits (93), Expect = 2e-04, Method: Compositional matrix adjust.

Identities = 27/73 (37%), Positives = 34/73 (47%), Gaps = 0/73 (0%)

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Query   195
GIVAARAHEEDNTVELLRMSVDSRFRGKGIKALGRKVLFAVVHNYSVVLTAVKVA  254
          G +A      E +  EL +M      RGKG+AK L      +E A      +      L TTA
Sbjct    5
GGIAPLTGSESDICELQKMYFLPAIRGKGLAKKLALMAMEQAREMGFKRCYLETTAFLKE  64

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```

Query   255  AHKLYESLGFRHM  267
          A  LYE LGF H+
Sbjct    65  AIALYEH LGFEHI  77

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>ref|NP_417898.1| predicted acetyltransferase [Escherichia coli str.
K-12 substr.
MG1655]

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ref|AP_004351.1| predicted acetyltransferase [Escherichia coli str.
K-12 substr.
W3110]

```

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ref|YP_001732275.1| acetyltransferase [Escherichia coli str. K-12
substr. DH10B]

```

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ref|YP_002928328.1| putative acetyltransferase [Escherichia coli
BW2952]

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sp|P46854.1|YHHY_ECOLI RecName: Full=Uncharacterized N-
acetyltransferase YhhY

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gb|AAA58239.1| ORF_o162 [Escherichia coli str. K-12 substr. MG1655]

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gb|AAC76466.1| predicted acetyltransferase [Escherichia coli str. K-
12 substr.
MG1655]

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dbj|BAE77852.1| predicted acetyltransferase [Escherichia coli str.
K12 substr.
W3110]

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gb|ACB04497.1| predicted acetyltransferase [Escherichia coli str. K-
12 substr.
DH10B]

```

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gb|ACR64111.1| predicted acetyltransferase [Escherichia coli BW2952]
Length=162

```

Score = 38.9 bits (89), Expect = 6e-04, Method: Compositional matrix adjust.

Identities = 30/101 (30%), Positives = 47/101 (47%), Gaps = 7/101 (7%)

Query 180 PGSCFWVAVLDGNVVG--
 IVAARAHEEDNTVELLRMSVDSRFRGKGIKALGRKVLEFAV 237
 PG VA +DG+VVG + + + V + VDSR++ +G+A AL R+++E
 Sbjct 49
 PGIKQLVACIDGDVVGHLTIDVQQRP RRSHVADFGICVDSRWKNRGVASALMREMIEMC- 107

Query 238 VHNY---SAVVLGTTAVKVA AHKLYESLGFRHMGASDHYVL 275
 N+ + L A K+Y+ GF G Y L
 Sbjct 108 -DNWLRVDRIELTVFVDNAPAIKVYKKYGFEIEGTGKKYAL 147

>ref|AP_003028.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain
 [Escherichia coli str. K-12 substr. W3110]
 ref|NP_416929.4| predicted acyltransferase with acyl-CoA N-acyltransferase domain
 [Escherichia coli str. K-12 substr. MG1655]
 ref|YP_001731363.1| acyltransferase [Escherichia coli str. K-12 substr. DH10B]
 ref|YP_002927393.1| putative acyltransferase with acyl-CoA N-acyltransferase domain
 [Escherichia coli BW2952]
 sp|P76539.2|YPEA_ECOLI RecName: Full=Acetyltransferase YpeA
 dbj|BAE76714.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain
 [Escherichia coli str. K12 substr. W3110]
 gb|AAC75487.2| predicted acyltransferase with acyl-CoA N-acyltransferase domain
 [Escherichia coli str. K-12 substr. MG1655]
 gb|ACB03585.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain
 [Escherichia coli str. K-12 substr. DH10B]
 gb|ACR64125.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain
 [Escherichia coli BW2952]
 Length=141

Score = 33.5 bits (75), Expect = 0.028, Method: Compositional matrix adjust.

Identities = 34/122 (28%), Positives = 49/122 (40%), Gaps = 13/122 (11%)

Query 171
 DIEQYYMKPPGSCFWVAVLDGNVVGIVAARAHEEDNTVELLRMSVDSRFRGKGIKALGR 230
 DIE+ M S F VA ++G+VVG V + L V FRG+GIA AL
 Sbjct 33 DIERK-MNHDVSLFLVAEVNGDVVGTVMGGYDGHRSAYYL--
 GVHPEFRGRGIANALLN 89

Query 231
 KVLEFAVVHNYSAVVLGTTAVKVA AHKLYESLGFRHMGASDHYVLPGMTLSLAERLFFQV 290
 ++ + + + + +YE LG+ H LSL +RL

Sbjct 90 RLEKKLIARGCPKIQINVPEDNDMVLGMYERLGYEHAD-----
VLSLGKRLIEDE 139

Query 291 RY 292
Y
Sbjct 140 EY 141

>ref|NP_418210.1| predicted multidrug or homocysteine efflux system
[Escherichia
coli str. K-12 substr. MG1655]
ref|AP_004033.1| predicted multidrug or homocysteine efflux system
[Escherichia
coli str. K-12 substr. W3110]
ref|YP_001732573.1| multidrug or homocysteine efflux system
[Escherichia coli str.
K-12 substr. DH10B]
ref|YP_002928642.1| putative multidrug or homocysteine efflux system
[Escherichia
coli BW2952]
sp|P31474.1|HSRA_ECOLI RecName: Full=Probable transport protein hsrA;
AltName: Full=High-copy
suppressor of rspA
gb|AAC76777.1| predicted multidrug or homocysteine efflux system
[Escherichia
coli str. K-12 substr. MG1655]
dbj|BAE77534.1| predicted multidrug or homocysteine efflux system
[Escherichia
coli str. K12 substr. W3110]
gb|ACB04795.1| predicted multidrug or homocysteine efflux system
[Escherichia
coli str. K-12 substr. DH10B]
gb|ACR64683.1| predicted multidrug or homocysteine efflux system
[Escherichia
coli BW2952]
Length=475

Score = 30.4 bits (67), Expect = 0.23, Method: Compositional matrix
adjust.

Identities = 23/111 (21%), Positives = 48/111 (43%), Gaps = 10/111
(9%)

Query 172
IEQYYMKPPGSCFWVAVLDGNVVGIVAARAHEEDNTVELLRMSVDSRFRGKGIKALGRK 231
I Q+ ++ P W+ +L ++G+ + NT+ L ++ D+ G +
+
Sbjct 342
IAQFSLQSPAMAIWMLILPLFILGMAMSTQFTAMNTITLADLTDDNASSGNSVLAVTQQQL 401

Query 232 VLEFAVVHNYSAVVL-----GTTAVKVAAHKLYESLGFRHMGASDHVVL 275
+ V SA VL GTT V+ H + ++G + ++ ++L
Sbjct 402 SISLGA--VSAAVLRVYEGMEGTTTVE-QFHYTFITMGIITVASAAMFML 449

```

>ref|NP_418790.1| ribosomal-protein-S18-alanine N-acetyltransferase
[Escherichia
coli str. K-12 substr. MG1655]
  ref|AP_004860.1| acetylase for 30S ribosomal subunit protein S18
[Escherichia
coli str. K-12 substr. W3110]
  ref|YP_001733078.1| acetylase for 30S ribosomal subunit protein S18
[Escherichia
coli str. K-12 substr. DH10B]
  ref|YP_002929255.1| acetylase for 30S ribosomal subunit protein S18
[Escherichia
coli BW2952]
  sp|P0A944.1|RIMI_ECOLI RecName: Full=Ribosomal-protein-alanine
acetyltransferase; AltName:
Full=Acetylating enzyme for N-terminal of ribosomal protein
S18
  gb|AAC77326.1| ribosomal-protein-S18-alanine N-acetyltransferase
[Escherichia
coli str. K-12 substr. MG1655]
  dbj|BAE78361.1| acetylase for 30S ribosomal subunit protein S18
[Escherichia
coli str. K12 substr. W3110]
  gb|ACB05300.1| acetylase for 30S ribosomal subunit protein S18
[Escherichia
coli str. K-12 substr. DH10B]
  gb|ACR61906.1| acetylase for 30S ribosomal subunit protein S18
[Escherichia
coli BW2952]
Length=148

```

Score = 30.0 bits (66), Expect = 0.26, Method: Compositional matrix adjust.

Identities = 18/64 (28%), Positives = 31/64 (48%), Gaps = 0/64 (0%)

Query 210

```

LLRMSVDSRFRGKGIAKALGRKVLFAVVHNYSVVLTAVKVAHKLYESLGFRHMGA 269
      L  ++VD  ++ +G+ +AL  +++      + + L  A  AA  LYESLGF

```

Sbjct 66

```

LFNIAVDPDYQRQGLGRALLEHLIDELEKRGVATLWLEVRASNAAAIALYESLGFNEATI 125

```

Query 270 SDHY 273

+Y

Sbjct 126 RRNY 129

```

>gb|AAA97269.1| CG Site No. 277 [Escherichia coli str. K-12 substr.
MG1655]
Length=161

```

Score = 30.0 bits (66), Expect = 0.28, Method: Compositional matrix adjust.

Identities = 18/64 (28%), Positives = 31/64 (48%), Gaps = 0/64 (0%)

Query 210

LLRMSVDSRFRGKGIKALGRKVLFAVVHNYSVVLTAVKVAAHKLYESLGFRHMGA 269
L ++VD ++ +G+ +AL +++ + + L A AA LYESLGF

Sbjct 66

LFNIAVDPDYQRQGLGRALLEHLIDELEKRGVATLWLEVRASNAAAIALYESLGFNEATI 125

Query 270 SDHY 273

+Y

Sbjct 126 RRNY 129

>ref|NP_417296.1| exonuclease V (RecBCD complex), alpha chain

[Escherichia coli

str. K-12 substr. MG1655]

ref|AP_003382.1| exonuclease V (RecBCD complex), alpha chain

[Escherichia coli

str. K-12 substr. W3110]

ref|YP_001731707.1| exonuclease V (RecBCD complex), alpha chain

[Escherichia coli

str. K-12 substr. DH10B]

ref|YP_002927750.1| exonuclease V (RecBCD complex), alpha chain

[Escherichia coli

BW2952]

sp|P04993.2|EX5A_ECOLI RecName: Full=Exodeoxyribonuclease V alpha chain; AltName: Full=Exodeoxyribonuclease V 67 kDa polypeptide

pdb|3K70|D Chain D, Crystal Structure Of The Complete Initiation Complex

Of Recbcd

pdb|3K70|G Chain G, Crystal Structure Of The Complete Initiation Complex

Of Recbcd

gb|AAB40466.1| exonuclease V alpha-subunit [Escherichia coli str. K-12 substr.

MG1655]

gb|AAC75858.1| exonuclease V (RecBCD complex), alpha chain

[Escherichia coli

str. K-12 substr. MG1655]

dbj|BAE76888.1| exonuclease V (RecBCD complex), alpha chain

[Escherichia coli

str. K12 substr. W3110]

gb|ACB03929.1| exonuclease V (RecBCD complex), alpha chain

[Escherichia coli

str. K-12 substr. DH10B]

gb|ACR63050.1| exonuclease V (RecBCD complex), alpha chain

[Escherichia coli

BW2952]

Length=608

Score = 30.0 bits (66), Expect = 0.30, Method: Compositional matrix adjust.

Identities = 18/59 (31%), Positives = 28/59 (47%), Gaps = 0/59 (0%)

Query 149

RYYYSRKVIRAYLECALHTDMADIEQYYMKPPGSCFWVAVLDGNVVGIVAARAHEEDNT 207
R+Y R V+ A + AL DI + G+ W A+ DGN+ + +R E +
T

Sbjct 475

RWYEGRPVMIARNDSALGLFNGDIGIALDRGQGTRVWFAMPDGNIKSVQPSRLPEHETT 533

>ref|NP_417625.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain

[Escherichia coli str. K-12 substr. MG1655]

ref|AP_003701.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain

[Escherichia coli str. K-12 substr. W3110]

ref|YP_001732013.1| acyltransferase [Escherichia coli str. K-12 substr. DH10B]

ref|YP_002928056.1| putative acyltransferase with acyl-CoA N-acyltransferase domain

[Escherichia coli BW2952]

sp|P63417.1|YHBS_ECOLI RecName: Full=Uncharacterized N-acetyltransferase YhbS

gb|AAA57959.1| ORF_f167; end overlaps end of o100 by 14 bases; start overlaps

f174, other starts possible [Escherichia coli str. K-12 substr. MG1655]

gb|AAC76190.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain

[Escherichia coli str. K-12 substr. MG1655]

dbj|BAE77202.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain

[Escherichia coli str. K12 substr. W3110]

gb|ACB04235.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain

[Escherichia coli str. K-12 substr. DH10B]

gb|ACR64126.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain

[Escherichia coli BW2952]

Length=167

Score = 28.9 bits (63), Expect = 0.56, Method: Compositional matrix adjust.

Identities = 27/81 (33%), Positives = 40/81 (49%), Gaps = 12/81 (15%)

Query 190 DGNVVGIVA---ARAHEED-

NTVELLRMSVDSRFRGKGIKALGRKVFLEFAVVHNYSVV 245

+G V+G VA ED V + ++VD ++RG+G+A+ L + L+

Y+AVV

Sbjct 50
EGQVIGYVAFSPVDVQGEDLQWVGMAPLAVDEKYRGQGLARQLVYEGLDSLNEFGYAAVV 109

Query 246 -LGTTAVKVA AHKLYESLGFR 265
 LG A LY GF
Sbjct 110 TLGDPA-----LYSRFGFE 123

>ref|NP_415597.1| flagellar protein of basal-body outer-membrane L ring [Escherichia coli str. K-12 substr. MG1655]
 ref|AP_001705.1| flagellar protein of basal-body outer-membrane L ring [Escherichia coli str. K-12 substr. W3110]
 ref|YP_001730050.1| flagellar protein of basal-body outer-membrane L ring [Escherichia coli str. K-12 substr. DH10B]
 ref|YP_002926129.1| flagellar protein of basal-body outer-membrane L ring [Escherichia coli BW2952]
 sp|P0A6S0.1|FLGH_ECOLI RecName: Full=Flagellar L-ring protein; AltName: Full=Basal body L-ring protein; Flags: Precursor
 sp|B1X9J2.1|FLGH_ECODH RecName: Full=Flagellar L-ring protein; AltName: Full=Basal body L-ring protein; Flags: Precursor
 sp|C4ZS19.1|FLGH_ECOBW RecName: Full=Flagellar L-ring protein; AltName: Full=Basal body L-ring protein; Flags: Precursor
 gb|AAC74163.1| flagellar protein of basal-body outer-membrane L ring [Escherichia coli str. K-12 substr. MG1655]
 dbj|BAA35888.2| flagellar protein of basal-body outer-membrane L ring [Escherichia coli str. K12 substr. W3110]
 gb|ACB02272.1| flagellar protein of basal-body outer-membrane L ring [Escherichia coli str. K-12 substr. DH10B]
 gb|ACR63114.1| flagellar protein of basal-body outer-membrane L ring [Escherichia coli BW2952]
Length=232

Score = 27.3 bits (59), Expect = 1.9, Method: Compositional matrix adjust.

Identities = 13/33 (39%), Positives = 16/33 (48%), Gaps = 1/33 (3%)

Query 31 LLAAAGAMW-PPLPAAPGPAAAPPAPPPAPVAQ 62
 +L+ G W P P G +A P P P PVA
Sbjct 16 VLSLTGCAWIPSTPLVQGATSAQFVPGPTPVAN 48

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>ref|NP_416506.1| CP4-44 prophage; predicted DNA repair protein
[Escherichia coli
str. K-12 substr. MG1655]
  ref|AP_002601.1| predicted DNA repair protein [Escherichia coli str.
K-12 substr.
W3110]
  ref|YP_001730951.1| CP4-44 prophage; DNA repair protein [Escherichia
coli str. K-12
substr. DH10B]
  ref|YP_002926989.1| CP4-44 prophage; putative DNA repair protein
[Escherichia coli
BW2952]
  sp|P76362.1|YEES_ECOLI RecName: Full=UPF0758 protein yeeS
  dbj|BAA15826.1| predicted DNA repair protein [Escherichia coli str.
K12 substr.
W3110]
  gb|AAC75063.1| CP4-44 prophage; predicted DNA repair protein
[Escherichia coli
str. K-12 substr. MG1655]
  gb|ACB03173.1| CP4-44 prophage; predicted DNA repair protein
[Escherichia coli
str. K-12 substr. DH10B]
  gb|ACR62614.1| CP4-44 prophage; predicted DNA repair protein
[Escherichia coli
BW2952]
Length=148

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Score = 26.2 bits (56), Expect = 3.7, Method: Compositional matrix
adjust.
Identities = 19/66 (29%), Positives = 33/66 (50%), Gaps = 11/66 (17%)

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```

Query 230 RKVLEFAVVHNYSAVVLG-----
TTAVKVA AHKLYESLGFRHMGASDHYVLP G-M 278
          R+V++ A+ HN +AVVL          + A ++  +L ++LG  +   DH ++ G
Sbjct 79
REVIKRALYHNAAAVVLAHNHPSGEVTPSKADRLITERLVQALGLVDIRVPDHLIVGGNQ 138

Query 279 TLSLAE 284
          S AE
Sbjct 139 VFSFAE 144

```

```

>ref|NP_418517.1| predicted acyltransferase with acyl-CoA N-
acyltransferase domain
[Escherichia coli str. K-12 substr. MG1655]
  ref|AP_004595.1| predicted acyltransferase with acyl-CoA N-
acyltransferase domain
[Escherichia coli str. K-12 substr. W3110]
  ref|YP_001732867.1| acyltransferase [Escherichia coli str. K-12
substr. DH10B]
  ref|YP_002928999.1| putative acyltransferase with acyl-CoA N-
acyltransferase domain

```

[Escherichia coli BW2952]
 sp|P16691.1|PHNO_ECOLI RecName: Full=Protein PhnO
 dbj|BAA14275.1| phnO [Escherichia coli W3110]
 gb|AAA96992.1| phnO [Escherichia coli str. K-12 substr. MG1655]
 gb|AAC77054.1| predicted acyltransferase with acyl-CoA N-
 acyltransferase domain
 [Escherichia coli str. K-12 substr. MG1655]
 dbj|BAE78096.1| predicted acyltransferase with acyl-CoA N-
 acyltransferase domain
 [Escherichia coli str. K12 substr. W3110]
 gb|ACB05089.1| predicted acyltransferase with acyl-CoA N-
 acyltransferase domain
 [Escherichia coli str. K-12 substr. DH10B]
 gb|ACR64127.1| predicted acyltransferase with acyl-CoA N-
 acyltransferase domain
 [Escherichia coli BW2952]
 Length=144

Score = 25.4 bits (54), Expect = 6.3, Method: Compositional matrix
 adjust.

Identities = 22/92 (24%), Positives = 37/92 (40%), Gaps = 4/92 (4%)

Query 177 MKPPGSCFWVAVLDGNVVGIVAA----
 RAHEEDNTVELLRMSVDSRFRGKGIKALGRKV 232
 ++ P + +A+LDG VVG++ H + E+ + V + RG + L
 Sbjct 42
 LRDPNMRHYHLALLDGEVVGMIGLHLQFHLHHVNWIGEIQELVMPQARGLNVGSKLLAWA 101

Query 233 LEFAVHNYSAAVVLGTTAVKVAAHKLYESLGF 264
 E A L T + AH+ Y G+
 Sbjct 102 EEEARQAGAEMTELSTNVKRHDAHRFYLRGY 133

>ref|AP_002454.1| hypothetical protein [Escherichia coli str. K-12
 substr. W3110]
 ref|NP_416348.2| conserved protein [Escherichia coli str. K-12
 substr. MG1655]
 ref|YP_001730810.1| hypothetical protein ECDH10B_1973 [Escherichia
 coli str. K-12
 substr. DH10B]
 ref|YP_002926845.1| hypothetical protein BWG_1648 [Escherichia coli
 BW2952]
 sp|P76272.2|YEBT_ECOLI RecName: Full=Uncharacterized protein yebT
 dbj|BAA15647.1| conserved hypothetical protein [Escherichia coli str.
 K12 substr.
 W3110]
 gb|AAC74904.2| conserved protein [Escherichia coli str. K-12 substr.
 MG1655]
 gb|ACB03032.1| conserved protein [Escherichia coli str. K-12 substr.
 DH10B]
 gb|ACR62492.1| conserved protein [Escherichia coli BW2952]
 Length=877

Score = 25.0 bits (53), Expect = 8.5, Method: Compositional matrix adjust.

Identities = 16/67 (24%), Positives = 33/67 (49%), Gaps = 9/67 (13%)

Query 153 SRKVIRAYLECALHTDMAD-----IEQYYMKPPGSCFWVAVLD----

GNVVGIVAARAHE 203

S + + ++ ++ +DM D + + + P S V+ LD GN +G++ +
E

Sbjct 82

SDDLRLKIEVKVSIKSDMKDALREETQFWLVTPKASLAGVSGLDALVGGNYIGMMPGKGKE 141

Query 204 EDNTVEL 210

+D+ V L

Sbjct 142 QDHFVAL 148

>ref|NP_417059.1| pyridoxine 5'-phosphate synthase [Escherichia coli str. K-12

substr. MG1655]

ref|AP_003150.1| pyridoxine 5'-phosphate synthase [Escherichia coli str. K-12

substr. W3110]

ref|YP_001731493.1| pyridoxine 5'-phosphate synthase [Escherichia coli str. K-12

substr. DH10B]

ref|YP_002927525.1| pyridoxine 5'-phosphate synthase [Escherichia coli BW2952]

sp|P0A794.2|PDXJ_ECOLI RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PNP synthase

gb|AAA79826.1| CG Site No. 416 [Escherichia coli str. K-12 substr. MG1655]

gb|AAC75617.1| pyridoxine 5'-phosphate synthase [Escherichia coli str. K-12

substr. MG1655]

dbj|BAE76740.1| pyridoxine 5'-phosphate synthase [Escherichia coli str. K12 substr.

W3110]

gb|ACB03715.1| pyridoxine 5'-phosphate synthase [Escherichia coli str. K-12

substr. DH10B]

gb|ACR65350.1| pyridoxine 5'-phosphate synthase [Escherichia coli BW2952]

Length=243

Score = 25.0 bits (53), Expect = 9.2, Method: Compositional matrix adjust.

Identities = 17/59 (29%), Positives = 24/59 (41%), Gaps = 12/59 (20%)

Query 190

DGNVVGIVAARAHEEDNTVELLRMSVDSRFRGKGIKALGRKVLEFAVVHNYSVVLTG 248

DG V + R H D V +LR ++D+R LE AV A+ +
T
Sbjct 40 DGITVHLREDRRHITDRDVRILRQTLDTRMN-----
LEMAVTEEMLAIAVET 86

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF
excluding environmental samples from WGS projects
Posted date: Mar 22, 2011 4:36 PM
Number of letters in database: 1,896,201
Number of sequences in database: 6,138

Lambda K H
 0.324 0.138 0.428
Gapped
Lambda K H
 0.267 0.0410 0.140
Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 6138
Number of Hits to DB: 919961
Number of extensions: 38677
Number of successful extensions: 168
Number of sequences better than 100: 73
Number of HSP's better than 100 without gapping: 0
Number of HSP's gapped: 164
Number of HSP's successfully gapped: 81
Length of query: 302
Length of database: 1896201
Length adjustment: 86
Effective length of query: 216
Effective length of database: 1368333
Effective search space: 295559928
Effective search space used: 295559928
T: 11
A: 40
X1: 15 (7.0 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 40 (20.0 bits)
S2: 44 (21.6 bits)

BLAST result for homology analysis with *Mus musculus* aspartate N-acetyltransferase

BLASTP 2.2.25+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference for compositional score matrix adjustment: Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schaffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

RID: TB9YZDB401S

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

13,473,798 sequences; 4,621,495,809 total letters

Query= gi|134288912|ref|NP_001001985.3| N-acetyltransferase 8-like protein

[Mus musculus]

Length=299

Score E

Sequences producing significant alignments:

(Bits) Value

ref|YP_026287.1| predicted acetyltransferase [Escherichia col...
42.4 6e-05

ref|NP_417898.1| predicted acetyltransferase [Escherichia col...
40.4 2e-04

gb|AAA97152.1| ORF_f97 [Escherichia coli str. K-12 substr. MG...
40.4 2e-04

ref|AP_003028.1| predicted acyltransferase with acyl-CoA N-ac...
33.9 0.020

ref|NP_417296.1| exonuclease V (RecBCD complex), alpha chain ...
32.3 0.062

gb|AAA97269.1| CG Site No. 277 [Escherichia coli str. K-12 su...
30.4 0.22

ref|NP_418790.1| ribosomal-protein-S18-alanine N-acetyltransf...
30.0 0.25

ref|NP_418210.1| predicted multidrug or homocysteine efflux s...
 29.3 0.43
 ref|NP_417625.1| predicted acyltransferase with acyl-CoA N-ac...
 28.9 0.58
 ref|NP_417454.1| DNA-binding transcriptional dual regulator, ...
 27.3 1.8
 gb|AAA69147.1| ORF_o274 [Escherichia coli str. K-12 substr. M...
 27.3 2.0
 ref|YP_001730194.1| ATP-binding subunit of oligopeptide ABC t...
 26.6 2.8
 ref|NP_415763.1| oligopeptide transporter subunit [Escherichi...
 26.6 2.8
 ref|NP_416506.1| CP4-44 prophage; predicted DNA repair protei...
 26.6 2.9
 ref|NP_418517.1| predicted acyltransferase with acyl-CoA N-ac...
 25.8 5.4
 ref|AP_004342.1| glycerol-3-phosphate transporter subunit [Es...
 25.0 7.7
 ref|AP_002454.1| hypothetical protein [Escherichia coli str. ...
 25.0 7.8
 gb|AAB18425.1| CG Site No. 17794 [Escherichia coli str. K-12 ...
 25.0 7.9
 ref|NP_417259.1| enolase [Escherichia coli str. K-12 substr. ...
 25.0 9.2
 ref|NP_418334.1| predicted peptidase [Escherichia coli str. K...
 25.0 9.4
 ref|NP_416307.1| conserved outer membrane lipoprotein [Escher...
 25.0 9.7

ALIGNMENTS

>ref|YP_026287.1| predicted acetyltransferase [Escherichia coli str.
 K-12 substr.
 MG1655]
 ref|AP_004752.1| predicted acetyltransferase [Escherichia coli str.
 K-12 substr.
 W3110]
 ref|YP_001733015.1| acetyltransferase [Escherichia coli str. K-12
 substr. DH10B]
 ref|YP_002929153.1| putative acetyltransferase [Escherichia coli
 BW2952]
 sp|P39337.2|YJGM_ECOLI RecName: Full=Uncharacterized N-
 acetyltransferase YjgM
 gb|AAT48245.1| predicted acetyltransferase [Escherichia coli str. K-
 12 substr.
 MG1655]
 dbj|BAE78253.1| predicted acetyltransferase [Escherichia coli str.
 K12 substr.
 W3110]
 gb|ACB05237.1| predicted acetyltransferase [Escherichia coli str. K-
 12 substr.
 DH10B]
 gb|ACR64110.1| predicted acetyltransferase [Escherichia coli BW2952]

Length=167

Score = 42.4 bits (98), Expect = 6e-05, Method: Compositional matrix adjust.

Identities = 36/102 (35%), Positives = 50/102 (49%), Gaps = 3/102 (3%)

```
Query 165  DMADIEQYYMKPPGSCFWVAVLDGNVVGI--
VAARAHEEDNTVELLRMSVDSRFRGKGIA 222
          ++ ++ Q Y +P G +WV +G VVG +A E + EL +M
RGKG+A
Sbjct 47  NLDELYQVYSQP-
GHAYWVVEYEGEVVGGGGIAPLTGSESDICELQKMYFLPAIRGKGLA 105
```

```
Query 223  KALGRRVLEFAMLHNYSAVVLGTTAVKVAAHKLYESLGFRHM 264
          K L +E A + L TTA A LYE LGF H+
Sbjct 106  KKLALMAMEQAREMGFKRCYLETTAFLKEAIALYEH LGFEHI 147
```

>ref|NP_417898.1| predicted acetyltransferase [Escherichia coli str. K-12 substr.

MG1655]

ref|AP_004351.1| predicted acetyltransferase [Escherichia coli str. K-12 substr.

W3110]

ref|YP_001732275.1| acetyltransferase [Escherichia coli str. K-12 substr. DH10B]

ref|YP_002928328.1| putative acetyltransferase [Escherichia coli BW2952]

sp|P46854.1|YHHY_ECOLI RecName: Full=Uncharacterized N-acetyltransferase YhhY

gb|AAA58239.1| ORF_o162 [Escherichia coli str. K-12 substr. MG1655]

gb|AAC76466.1| predicted acetyltransferase [Escherichia coli str. K-12 substr.

MG1655]

dbj|BAE77852.1| predicted acetyltransferase [Escherichia coli str. K12 substr.

W3110]

gb|ACB04497.1| predicted acetyltransferase [Escherichia coli str. K-12 substr.

DH10B]

gb|ACR64111.1| predicted acetyltransferase [Escherichia coli BW2952]

Length=162

Score = 40.4 bits (93), Expect = 2e-04, Method: Compositional matrix adjust.

Identities = 31/101 (31%), Positives = 47/101 (47%), Gaps = 7/101 (7%)

```
Query 177  PGSCFWVAVLDGNVVG--
IVAARAHEEDNTVELLRMSVDSRFRGKGIAKALGRRVLEFAM 234
```

PG VA +DG+VVG + + + V + VDSR++ +G+A AL R ++E
M
Sbjct 49 PGIKQLVACIDGDVVGHLTIDVQQRPRRSHVADFGICVDSRWKNRGVASALMREMIE-
-M 106

Query 235 LHNY---SAVVLGTTAVKVA AHKLYESLGFRHMGASDHYVL 272
N+ + L A K+Y+ GF G Y L
Sbjct 107 CDNWL RVDRIELTVFVDNAPA IKVYKKYGFEIEGTGKKYAL 147

>gb|AAA97152.1| ORF_f97 [Escherichia coli str. K-12 substr. MG1655]
Length=97

Score = 40.4 bits (93), Expect = 2e-04, Method: Compositional matrix
adjust.
Identities = 27/73 (37%), Positives = 34/73 (47%), Gaps = 0/73 (0%)

Query 192
GIVAARAHEEDNTVELLRMSVDSRFRGKGI AKALGRRVLEFAMLHNYSAVVLGTTAVKVA 251
G +A E + EL +M RGKG+AK L +E A + L TTA
Sbjct 5
GGIAPLTGSESDICELQKMYFLPAIRGKGLAKKLALMAMEQAREMGFKRCYLETTAFLKE 64

Query 252 AHKLYESLGFRHM 264
A LYE LGF H+
Sbjct 65 AIALYEH LGFEHI 77

>ref|AP_003028.1| predicted acyltransferase with acyl-CoA N-
acyltransferase domain
[Escherichia coli str. K-12 substr. W3110]
ref|NP_416929.4| predicted acyltransferase with acyl-CoA N-
acyltransferase domain
[Escherichia coli str. K-12 substr. MG1655]
ref|YP_001731363.1| acyltransferase [Escherichia coli str. K-12
substr. DH10B]
ref|YP_002927393.1| putative acyltransferase with acyl-CoA N-
acyltransferase domain
[Escherichia coli BW2952]
sp|P76539.2|YPEA_ECOLI RecName: Full=Acetyltransferase YpeA
dbj|BAE76714.1| predicted acyltransferase with acyl-CoA N-
acyltransferase domain
[Escherichia coli str. K12 substr. W3110]
gb|AAC75487.2| predicted acyltransferase with acyl-CoA N-
acyltransferase domain
[Escherichia coli str. K-12 substr. MG1655]
gb|ACB03585.1| predicted acyltransferase with acyl-CoA N-
acyltransferase domain
[Escherichia coli str. K-12 substr. DH10B]
gb|ACR64125.1| predicted acyltransferase with acyl-CoA N-
acyltransferase domain
[Escherichia coli BW2952]

Length=141

Score = 33.9 bits (76), Expect = 0.020, Method: Compositional matrix adjust.

Identities = 35/122 (29%), Positives = 49/122 (40%), Gaps = 13/122 (11%)

Query 168

```
DIEQYMKPPGSCFWVAVLDGNVVGIVAARAHEEDNTVELLRMSVDSRFRGKGIKALGR 227
          DIE+  M      S F VA ++G+VVG V          +  L  V  FRG+GIA AL
Sbjct 33  DIERK-MNHDVSLFLVAEVNGDVVGTVMGGYDGHGRGSAYYL--
GVHPEFRGRGIANALLN 89
```

Query 228

```
RVLEFAMLHNYSAVVLGTTAVKVAAHKLYESLGFRHMGASDHVYVLPGMTLSLAERLFFQV 287
          R+ + +      + +      +YE LG+ H          LSL +RL
Sbjct 90  RLEKKLIARGCPKIQINVPEDNDMVLGMYERLGYEHAD-----
VLSLGKRLIEDE 139
```

Query 288 RY 289

```
          Y
Sbjct 140 EY 141
```

```
>ref|NP_417296.1| exonuclease V (RecBCD complex), alpha chain
[Escherichia coli
str. K-12 substr. MG1655]
  ref|AP_003382.1| exonuclease V (RecBCD complex), alpha chain
[Escherichia coli
str. K-12 substr. W3110]
  ref|YP_001731707.1| exonuclease V (RecBCD complex), alpha chain
[Escherichia coli
str. K-12 substr. DH10B]
  ref|YP_002927750.1| exonuclease V (RecBCD complex), alpha chain
[Escherichia coli
BW2952]
  sp|P04993.2|EX5A_ECOLI RecName: Full=Exodeoxyribonuclease V alpha
chain; AltName: Full=Exodeoxyribonuclease
V 67 kDa polypeptide
  pdb|3K70|D Chain D, Crystal Structure Of The Complete Initiation
Complex
Of Recbcd
  pdb|3K70|G Chain G, Crystal Structure Of The Complete Initiation
Complex
Of Recbcd
  gb|AAB40466.1| exonuclease V alpha-subunit [Escherichia coli str. K-
12 substr.
MG1655]
  gb|AAC75858.1| exonuclease V (RecBCD complex), alpha chain
[Escherichia coli
str. K-12 substr. MG1655]
```

dbj|BAE76888.1| exonuclease V (RecBCD complex), alpha chain
[Escherichia coli
str. K12 substr. W3110]
gb|ACB03929.1| exonuclease V (RecBCD complex), alpha chain
[Escherichia coli
str. K-12 substr. DH10B]
gb|ACR63050.1| exonuclease V (RecBCD complex), alpha chain
[Escherichia coli
BW2952]
Length=608

Score = 32.3 bits (72), Expect = 0.062, Method: Compositional matrix
adjust.

Identities = 18/59 (31%), Positives = 29/59 (49%), Gaps = 0/59 (0%)

Query 146
RYYYSRKVILAYLECALHTDMADIEQYYMKPPGSCFWVAVLDGNVVGIVAARAHEEDNT 204
R+Y R V++A + AL DI + G+ W A+ DGN+ + +R E +
T
Sbjct 475
RWYEGRPVMIARNDSALGLFNGDIGIALDRGQGTRVWFAMPDGNIKSVQPSRLPEHETT 533

>gb|AAA97269.1| CG Site No. 277 [Escherichia coli str. K-12 substr.
MG1655]
Length=161

Score = 30.4 bits (67), Expect = 0.22, Method: Compositional matrix
adjust.

Identities = 18/64 (28%), Positives = 31/64 (48%), Gaps = 0/64 (0%)

Query 207
LLRMSVDSRFRGKGIKALGRRVLEFAMLNYSVVGLTTAVKVAAHKLYESLGFHRMGA 266
L ++VD ++ +G+ +AL +++ + + L A AA LYESLGF
Sbjct 66
LFNIAVDPDYQRQGLGRALLEHLIDELEKRGVATLWLEVRASNAAAIALYESLGFNEATI 125

Query 267 SDHY 270
+Y
Sbjct 126 RRNY 129

>ref|NP_418790.1| ribosomal-protein-S18-alanine N-acetyltransferase
[Escherichia
coli str. K-12 substr. MG1655]
ref|AP_004860.1| acetylase for 30S ribosomal subunit protein S18
[Escherichia
coli str. K-12 substr. W3110]
ref|YP_001733078.1| acetylase for 30S ribosomal subunit protein S18
[Escherichia
coli str. K-12 substr. DH10B]

ref|YP_002929255.1| acetylase for 30S ribosomal subunit protein S18
[Escherichia coli BW2952]
sp|P0A944.1|RIMI_ECOLI RecName: Full=Ribosomal-protein-alanine acetyltransferase; AltName: Full=Acetylating enzyme for N-terminal of ribosomal protein S18
gb|AAC77326.1| ribosomal-protein-S18-alanine N-acetyltransferase [Escherichia coli str. K-12 substr. MG1655]
dbj|BAE78361.1| acetylase for 30S ribosomal subunit protein S18 [Escherichia coli str. K12 substr. W3110]
gb|ACB05300.1| acetylase for 30S ribosomal subunit protein S18 [Escherichia coli str. K-12 substr. DH10B]
gb|ACR61906.1| acetylase for 30S ribosomal subunit protein S18 [Escherichia coli BW2952]
Length=148

Score = 30.0 bits (66), Expect = 0.25, Method: Compositional matrix adjust.

Identities = 18/64 (28%), Positives = 31/64 (48%), Gaps = 0/64 (0%)

Query 207

LLRMSVDSRFRGKGIKALGRRVLEFAMLNYSVVLTAVKVAHKLYESLGFRHMGA 266
L ++VD ++ +G+ +AL +++ + + L A AA LYESLGF

Sbjct 66

LFNIAVDPDYQRQGLGRALLEHLIDELEKRGVATLWLEVRASNAAAIALYESLGFNEATI 125

Query 267 SDHY 270

+Y

Sbjct 126 RRYN 129

>ref|NP_418210.1| predicted multidrug or homocysteine efflux system

[Escherichia

coli str. K-12 substr. MG1655]

ref|AP_004033.1| predicted multidrug or homocysteine efflux system

[Escherichia

coli str. K-12 substr. W3110]

ref|YP_001732573.1| multidrug or homocysteine efflux system

[Escherichia coli str.

K-12 substr. DH10B]

ref|YP_002928642.1| putative multidrug or homocysteine efflux system

[Escherichia

coli BW2952]

sp|P31474.1|HSRA_ECOLI RecName: Full=Probable transport protein hsrA; AltName: Full=High-copy

suppressor of rspA

gb|AAC76777.1| predicted multidrug or homocysteine efflux system
 [Escherichia coli str. K-12 substr. MG1655]
 dbj|BAE77534.1| predicted multidrug or homocysteine efflux system
 [Escherichia coli str. K12 substr. W3110]
 gb|ACB04795.1| predicted multidrug or homocysteine efflux system
 [Escherichia coli str. K-12 substr. DH10B]
 gb|ACR64683.1| predicted multidrug or homocysteine efflux system
 [Escherichia coli BW2952]
 Length=475

Score = 29.3 bits (64), Expect = 0.43, Method: Compositional matrix
 adjust.
 Identities = 23/111 (21%), Positives = 49/111 (44%), Gaps = 10/111
 (9%)

Query 169
 IEQYMKPPGSCFWVAVLDGNVVGIVAARAHEEDNTVELLRMSVDSRFRGKGIKALGRR 228
 I Q+ ++ P W+ +L ++G+ + NT+ L ++ D+ G +
 +
 Sbjct 342 IAQFSLQSPAMAIWMLILPLFILGMAMSTQFTAMNTITLADLTDDNASSGNSVLAV--
 TQ 399

Query 229 VLEFAMLNYSYAVVL-----GTTAVKVAHKLYESLGFRHMGASDHVYL 272
 L ++ SA VL GTT V+ H + ++G + ++ ++L
 Sbjct 400 QLSISLGVAVSAAVLRVYEGMEGTTTVE-QFHYTFITMGIITVASAAMFML 449

>ref|NP_417625.1| predicted acyltransferase with acyl-CoA N-
 acyltransferase domain
 [Escherichia coli str. K-12 substr. MG1655]
 ref|AP_003701.1| predicted acyltransferase with acyl-CoA N-
 acyltransferase domain
 [Escherichia coli str. K-12 substr. W3110]
 ref|YP_001732013.1| acyltransferase [Escherichia coli str. K-12
 substr. DH10B]
 ref|YP_002928056.1| putative acyltransferase with acyl-CoA N-
 acyltransferase domain
 [Escherichia coli BW2952]
 sp|P63417.1|YHBS_ECOLI RecName: Full=Uncharacterized N-
 acetyltransferase YhbS
 gb|AAA57959.1| ORF_f167; end overlaps end of o100 by 14 bases; start
 overlaps
 f174, other starts possible [Escherichia coli str. K-12 substr.
 MG1655]
 gb|AAC76190.1| predicted acyltransferase with acyl-CoA N-
 acyltransferase domain
 [Escherichia coli str. K-12 substr. MG1655]

dbj|BAE77202.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain

[Escherichia coli str. K12 substr. W3110]

gb|ACB04235.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain

[Escherichia coli str. K-12 substr. DH10B]

gb|ACR64126.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain

[Escherichia coli BW2952]

Length=167

Score = 28.9 bits (63), Expect = 0.58, Method: Compositional matrix adjust.

Identities = 27/81 (33%), Positives = 39/81 (48%), Gaps = 12/81 (15%)

Query 187 DGNVVGIVA---ARAHEED-

NTVELLRMSVDSRFRGKGIKALGRRVLEFAMLHNYSVV 242

+G V+G VA ED V + ++VD ++RG+G+A+ L L+

Y+AVV

Sbjct 50

EGQVIGYVAFSPVDVQGEDLQWVGMAPLAVDEKYRGQGLARQLVYEGLDSLNEFGYAAVV 109

Query 243 -LGTTAVKVAAHKLYESLGFR 262

LG A LY GF

Sbjct 110 TLGDPA-----LYSRFGFE 123

>ref|NP_417454.1| DNA-binding transcriptional dual regulator, glycolate-binding

[Escherichia coli str. K-12 substr. MG1655]

ref|AP_003535.1| DNA-binding transcriptional dual regulator, glycolate-binding

[Escherichia coli str. K-12 substr. W3110]

ref|YP_001731848.1| DNA-binding transcriptional dual regulator, glycolate-binding

[Escherichia coli str. K-12 substr. DH10B]

ref|YP_002927895.1| DNA-binding transcriptional dual regulator, glycolate-binding

[Escherichia coli BW2952]

sp|P0ACL5.1|GLCC_ECOLI RecName: Full=Glc operon transcriptional activator

gb|AAB02529.1| regulatory protein [Escherichia coli str. K-12 substr. W3110]

gb|AAC76016.1| DNA-binding transcriptional dual regulator, glycolate-binding

[Escherichia coli str. K-12 substr. MG1655]

dbj|BAE77041.1| DNA-binding transcriptional dual regulator, glycolate-binding

[Escherichia coli str. K12 substr. W3110]

gb|ACB04070.1| DNA-binding transcriptional dual regulator, glycolate-binding

[Escherichia coli str. K-12 substr. DH10B]

gb|ACR62941.1| DNA-binding transcriptional dual regulator, glycolate-binding
[Escherichia coli BW2952]
Length=254

Score = 27.3 bits (59), Expect = 1.8, Method: Compositional matrix adjust.

Identities = 10/23 (43%), Positives = 15/23 (65%), Gaps = 0/23 (0%)

```
Query   92   FYDGILERIPNTAFRGLRQHPRT   114
          Y+ +L+R+P+ A R   R H RT
Sbjct   205  IYNAVLQRLPHVAQRAARDHVRT   227
```

>gb|AAA69147.1| ORF_o274 [Escherichia coli str. K-12 substr. MG1655]
Length=274

Score = 27.3 bits (59), Expect = 2.0, Method: Compositional matrix adjust.

Identities = 10/23 (43%), Positives = 15/23 (65%), Gaps = 0/23 (0%)

```
Query   92   FYDGILERIPNTAFRGLRQHPRT   114
          Y+ +L+R+P+ A R   R H RT
Sbjct   225  IYNAVLQRLPHVAQRAARDHVRT   247
```

>ref|YP_001730194.1| ATP-binding subunit of oligopeptide ABC transporter [Escherichia coli str. K-12 substr. DH10B]
ref|YP_002926275.1| oligopeptide transporter subunit [Escherichia coli BW2952]
gb|ACB02416.1| ATP-binding subunit of oligopeptide ABC transporter [Escherichia coli str. K-12 substr. DH10B]
gb|ACR63934.1| oligopeptide transporter subunit [Escherichia coli BW2952]
Length=334

Score = 26.6 bits (57), Expect = 2.8, Method: Compositional matrix adjust.

Identities = 13/50 (26%), Positives = 27/50 (54%), Gaps = 5/50 (10%)

```
Query   151  RKVILAYLECALHTDMADIEQYYMKPPGSCFWVA-----VLDGNVVGIVA   195
          RKV+L   +   +H ++ D +Q++ +PP +   V           + +G +G+V
Sbjct    8   RKVLEIADLKVHFEIKDGKQWFWQPPKTLKAVDGVTLRRLYEGETLGVVG   57
```

>ref|NP_415763.1| oligopeptide transporter subunit [Escherichia coli str. K-12 substr. MG1655]
ref|AP_001873.1| oligopeptide transporter subunit [Escherichia coli str. K-12]

substr. W3110]
 sp|P77737.1|OPPF_ECOLI RecName: Full=Oligopeptide transport ATP-binding protein OppF
 dbj|BAA14779.1| oligopeptide transporter subunit [Escherichia coli str. K12 substr.
 W3110]
 gb|AAC74329.1| oligopeptide transporter subunit [Escherichia coli str. K-12
 substr. MG1655]
 Length=334

Score = 26.6 bits (57), Expect = 2.8, Method: Compositional matrix adjust.
 Identities = 13/50 (26%), Positives = 27/50 (54%), Gaps = 5/50 (10%)

Query	151	RKVILAYLECALHTDMADIEQYYMKPPGSCFWVA-----VLDGNVVGIVA	195
		RKV+L + +H ++ D +Q++ +PP + V + +G +G+V	
Sbjct	8	RKVLEIADLKVHFEIKDGKQWFWQPPKTLKAVDGVTLRLYEGETLGVVG	57

>ref|NP_416506.1| CP4-44 prophage; predicted DNA repair protein [Escherichia coli str. K-12 substr. MG1655]
 ref|AP_002601.1| predicted DNA repair protein [Escherichia coli str. K-12 substr. W3110]
 ref|YP_001730951.1| CP4-44 prophage; DNA repair protein [Escherichia coli str. K-12 substr. DH10B]
 ref|YP_002926989.1| CP4-44 prophage; putative DNA repair protein [Escherichia coli BW2952]
 sp|P76362.1|YEES_ECOLI RecName: Full=UPF0758 protein yeeS
 dbj|BAA15826.1| predicted DNA repair protein [Escherichia coli str. K12 substr. W3110]
 gb|AAC75063.1| CP4-44 prophage; predicted DNA repair protein [Escherichia coli str. K-12 substr. MG1655]
 gb|ACB03173.1| CP4-44 prophage; predicted DNA repair protein [Escherichia coli str. K-12 substr. DH10B]
 gb|ACR62614.1| CP4-44 prophage; predicted DNA repair protein [Escherichia coli BW2952]
 Length=148

Score = 26.6 bits (57), Expect = 2.9, Method: Compositional matrix adjust.
 Identities = 19/66 (29%), Positives = 32/66 (48%), Gaps = 11/66 (17%)

Query 227 RRVLEFAMLHNYSAVVLG-----
 TTAVKVAAHKLYESLGFRHMGASDHYVLP-G-M 275
 R V++ A+ HN +AVVL + A ++ +L ++LG + DH ++ G
 Sbjct 79
 REVIKRALYHNAAAVVLAHNHPSGEVTPSKADRLITERLVQALGLVDIRVPDHLIVGGNQ 138

Query 276 TLSLAE 281
 S AE
 Sbjct 139 VFSFAE 144

>ref|NP_418517.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain
 [Escherichia coli str. K-12 substr. MG1655]
 ref|AP_004595.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain
 [Escherichia coli str. K-12 substr. W3110]
 ref|YP_001732867.1| acyltransferase [Escherichia coli str. K-12 substr. DH10B]
 ref|YP_002928999.1| putative acyltransferase with acyl-CoA N-acyltransferase domain
 [Escherichia coli BW2952]
 sp|P16691.1|PHNO_ECOLI RecName: Full=Protein PhnO
 dbj|BAA14275.1| phnO [Escherichia coli W3110]
 gb|AAA96992.1| phnO [Escherichia coli str. K-12 substr. MG1655]
 gb|AAC77054.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain
 [Escherichia coli str. K-12 substr. MG1655]
 dbj|BAE78096.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain
 [Escherichia coli str. K12 substr. W3110]
 gb|ACB05089.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain
 [Escherichia coli str. K-12 substr. DH10B]
 gb|ACR64127.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain
 [Escherichia coli BW2952]
 Length=144

Score = 25.8 bits (55), Expect = 5.4, Method: Compositional matrix adjust.

Identities = 22/92 (24%), Positives = 37/92 (40%), Gaps = 4/92 (4%)

Query 174 MKPPGSCFWVAVLDGNVVGIVAA----
 RAHEEDNTVELLRMSVDSRFRGKGIKALGRRV 229
 ++ P + +A+LDG VVG++ H + E+ + V + RG + L
 Sbjct 42
 LRDPNMRYHLALLDGEVVGMIGLHLQFHLHHVNWIGEIQELVVMPPQARGLNVGSKLLAWA 101

Query 230 LEFAMLHNYSAVVLGTTAVKVAAHKLYESLGF 261
 E A L T + AH+ Y G+
 Sbjct 102 EEEARQAGAEMTELSTNVKRHDAHRFYLRGY 133

```

>ref|AP_004342.1| glycerol-3-phosphate transporter subunit
[Escherichia coli str.
K-12 substr. W3110]
  ref|NP_417907.2| glycerol-3-phosphate transporter subunit
[Escherichia coli str.
K-12 substr. MG1655]
  ref|YP_001732284.1| glycerol-3-phosphate ABC transporter ATP-binding
protein [Escherichia
coli str. K-12 substr. DH10B]
  ref|YP_002928337.1| glycerol-3-phosphate transporter subunit
[Escherichia coli BW2952]
  sp|P10907.3|UGPC_ECOLI RecName: Full=sn-glycerol-3-phosphate import
ATP-binding protein
UgpC
  dbj|BAE77843.1| glycerol-3-phosphate transporter subunit [Escherichia
coli str.
K12 substr. W3110]
  gb|AAC76475.2| glycerol-3-phosphate transporter subunit [Escherichia
coli str.
K-12 substr. MG1655]
  gb|ACB04506.1| glycerol-3-phosphate transporter subunit; ATP-binding
component
of ABC superfamily [Escherichia coli str. K-12 substr. DH10B]
  gb|ACR63359.1| glycerol-3-phosphate transporter subunit [Escherichia
coli BW2952]
Length=356

```

Score = 25.0 bits (53), Expect = 7.7, Method: Compositional matrix adjust.

Identities = 14/38 (37%), Positives = 21/38 (55%), Gaps = 0/38 (0%)

```

Query   73   RGVCIREFRAAEQEAARRIFYDGILERIPNTAFRGLRQ   110
          RG+  ++      +EAAR +  DG+L+R P      G RQ
Sbjct   104  RGMGKQQIAERVKEAARILELDGLLKRRPRELSGGQRQ   141

```

```

>ref|AP_002454.1| hypothetical protein [Escherichia coli str. K-12
substr. W3110]
  ref|NP_416348.2| conserved protein [Escherichia coli str. K-12
substr. MG1655]
  ref|YP_001730810.1| hypothetical protein ECDH10B_1973 [Escherichia
coli str. K-12
substr. DH10B]
  ref|YP_002926845.1| hypothetical protein BWG_1648 [Escherichia coli
BW2952]
  sp|P76272.2|YEBT_ECOLI RecName: Full=Uncharacterized protein yebT
  dbj|BAA15647.1| conserved hypothetical protein [Escherichia coli str.
K12 substr.
W3110]

```

gb|AAC74904.2| conserved protein [Escherichia coli str. K-12 substr. MG1655]
gb|ACB03032.1| conserved protein [Escherichia coli str. K-12 substr. DH10B]
gb|ACR62492.1| conserved protein [Escherichia coli BW2952]
Length=877

Score = 25.0 bits (53), Expect = 7.8, Method: Compositional matrix adjust.

Identities = 15/59 (25%), Positives = 30/59 (51%), Gaps = 9/59 (15%)

Query 158 LECALHTDMAD-----IEQYYMKPPGSCFWVAVLD----
GNVVGIVAARAHEEDNTVEL 207

++ ++ +DM D + + + P S V+ LD GN +G++ + E+D+ V
L

Sbjct 90

VKVSISKMDKDALREETQFWLVTPKASLAGVSGLDALVGGNYIGMMPGKGKEQDHFVAL 148

>gb|AAB18425.1| CG Site No. 17794 [Escherichia coli str. K-12 substr. MG1655]
Length=369

Score = 25.0 bits (53), Expect = 7.9, Method: Compositional matrix adjust.

Identities = 14/38 (37%), Positives = 21/38 (55%), Gaps = 0/38 (0%)

Query 73 RGVCIREFRAAEQEAARRIFYDGILERIPNTAFRGLRQ 110
RG+ ++ +EAAR + DG+L+R P G RQ

Sbjct 117 RGMGKQQIAERVKEAARILELDGLLKRRPRELSGGQRQ 154

>ref|NP_417259.1| enolase [Escherichia coli str. K-12 substr. MG1655]
ref|AP_003345.1| enolase [Escherichia coli str. K-12 substr. W3110]
ref|YP_001731671.1| enolase [Escherichia coli str. K-12 substr. DH10B]
ref|YP_002927711.1| enolase [Escherichia coli BW2952]
sp|P0A6P9.2|ENO_ECOLI RecName: Full=Enolase; AltName: Full=2-phospho-D-glycerate hydro-lyase;
AltName: Full=2-phosphoglycerate dehydratase
sp|B1XDI9.1|ENO_ECODH RecName: Full=Enolase; AltName: Full=2-phospho-D-glycerate hydro-lyase;
AltName: Full=2-phosphoglycerate dehydratase
sp|C4ZZT2.1|ENO_ECOBW RecName: Full=Enolase; AltName: Full=2-phospho-D-glycerate hydro-lyase;
AltName: Full=2-phosphoglycerate dehydratase
gb|AAA69289.1| enolase [Escherichia coli str. K-12 substr. MG1655]
gb|AAC75821.1| enolase [Escherichia coli str. K-12 substr. MG1655]
dbj|BAE76853.1| enolase [Escherichia coli str. K12 substr. W3110]
gb|ACB03893.1| enolase [Escherichia coli str. K-12 substr. DH10B]
gb|ACR63031.1| enolase [Escherichia coli BW2952]
Length=432

Score = 25.0 bits (53), Expect = 9.2, Method: Compositional matrix adjust.

Identities = 17/42 (40%), Positives = 23/42 (55%), Gaps = 2/42 (5%)

```
Query   186  LDGNVVGIVAARAHEEDNTVELL--RMSVDSRFRGKGIKAL   225
          L+G  VG+ AA +      + E L R      SRF GK+ KA+
Sbjct   27   LEGGFVGMAAAPSGASTGSREALELRDGDKSRLGKGVTKAV   68
```

```
>ref|NP_418334.1| predicted peptidase [Escherichia coli str. K-12
substr. MG1655]
  ref|AP_003910.1| predicted endo-1,4-beta-glucanase [Escherichia coli
str. K-12
substr. W3110]
  ref|YP_001732690.1| endo-1,4-beta-glucanase [Escherichia coli str. K-
12 substr. DH10B]
  ref|YP_002928761.1| putative endo-1,4-beta-glucanase [Escherichia
coli BW2952]
  sp|P32153.1|FRVX_ECOLI RecName: Full=Putative aminopeptidase frvX
  gb|AAB03031.1| ORF_f356 [Escherichia coli str. K-12 substr. MG1655]
  gb|AAC76880.1| predicted peptidase [Escherichia coli str. K-12
substr. MG1655]
  dbj|BAE77411.1| predicted endo-1,4-beta-glucanase [Escherichia coli
str. K12
substr. W3110]
  gb|ACB04912.1| predicted endo-1,4-beta-glucanase [Escherichia coli
str. K-12
substr. DH10B]
  gb|ACR64341.1| predicted endo-1,4-beta-glucanase [Escherichia coli
BW2952]
Length=356
```

Score = 25.0 bits (53), Expect = 9.4, Method: Compositional matrix adjust.

Identities = 9/25 (36%), Positives = 15/25 (60%), Gaps = 0/25 (0%)

```
Query   142  LLALRYYYSRKVILAYLECALHTDM   166
          L   RY+ ++K++ A   CA H D+
Sbjct   255  LFDKRYFPNQKLVAALKSCAAHNDL   279
```

```
>ref|NP_416307.1| conserved outer membrane lipoprotein [Escherichia
coli str. K-12
substr. MG1655]
  ref|AP_002412.1| conserved outer membrane protein [Escherichia coli
str. K-12
substr. W3110]
  ref|YP_001730769.1| outer membrane protein [Escherichia coli str. K-
12 substr. DH10B]
  ref|YP_002926803.1| conserved outer membrane protein [Escherichia
coli BW2952]
```

sp|P64493.1|YOAF_ECOLI RecName: Full=Uncharacterized protein yoaF
gb|AAC74863.1| conserved outer membrane lipoprotein [Escherichia coli
str. K-12
substr. MG1655]
dbj|BAE76530.1| conserved outer membrane protein [Escherichia coli
str. K12 substr.
W3110]
gb|ACB02991.1| conserved outer membrane protein [Escherichia coli
str. K-12
substr. DH10B]
gb|ACR62258.1| conserved outer membrane protein [Escherichia coli
BW2952]
Length=84

Score = 25.0 bits (53), Expect = 9.7, Method: Composition-based
stats.

Identities = 16/37 (43%), Positives = 17/37 (46%), Gaps = 3/37 (8%)

```
Query   31  LLVAAGAMWPPLPAAPGP---AAAPPPAAGPQPHGGT   64
          LLV AG  P  P AP P      A P +   Q  GGT
Sbjct   11  LLVLAGCSTPSQPEAPKPPQIGMANPASVYCQQKGGT  47
```

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF
excluding environmental samples from WGS projects
Posted date: Mar 22, 2011 4:36 PM
Number of letters in database: 1,896,392
Number of sequences in database: 6,139

Lambda	K	H
0.324	0.139	0.429

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 6139

Number of Hits to DB: 14580

Number of extensions: 649

Number of successful extensions: 0

Number of sequences better than 100: 0

Number of HSP's better than 100 without gapping: 0

Number of HSP's gapped: 0

Number of HSP's successfully gapped: 0

Length of query: 299

Length of database: 1896392

Length adjustment: 85

Effective length of query: 214

Effective length of database: 1374577

Effective search space: 294159478

Effective search space used: 294159478

T: 11
A: 40
X1: 15 (7.0 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 40 (20.0 bits)
S2: 44 (21.6 bits)