

Appendix III

Mascot search results

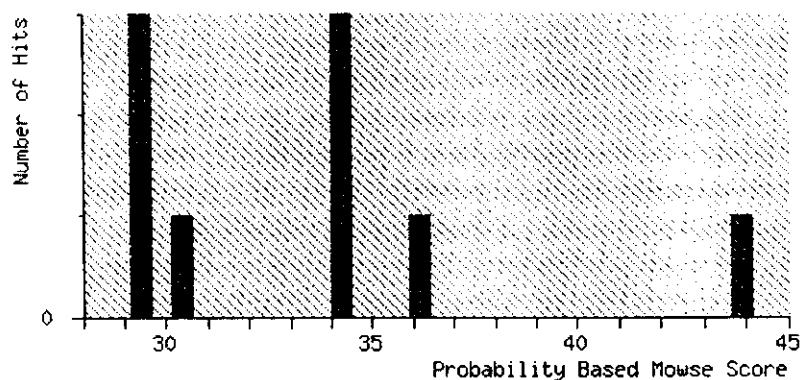
ของเมล็ดโปรตีนที่ 3

{MATRIX} *{SCIENCE}* Mascot Search Results

User : Waraporn
 Email : waraporn.p@psu.ac.th
 Search title :
 Database : SwissProt 46.6 (232847 sequences; 105413441 residues)
 Timestamp : 13 May 2005 at 11:30:03 GMT
 Top Score : 44 for Q8IZX4, (TAF1L_HUMAN) Transcription initiation factor TFIID :

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
 Protein scores greater than 66 are significant ($p < 0.05$).



Concise Protein Summary Report

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Significance threshold $p <$ Max. number of hits

[Re-Search All](#) [Search Unmatched](#)

| | | | | | |
|----|---|--------------|-----------|-------------|--------------------|
| 1. | <u>Q8IZX4</u> | Mass: 208737 | Score: 44 | Expect: 9.5 | Queries matched: 8 |
| | (TAF1L_HUMAN) Transcription initiation factor TFIID 210 kDa subunit (TBP-associ | | | | |
| | <u>P21675-01-00-00</u> | Mass: 216029 | Score: 39 | Expect: 32 | Queries matched: 8 |
| | (TAF1_HUMAN) Splice isoform 2; Variant Displayed; Conflict Displayed; from P216 | | | | |
| | <u>P21675-01-01-00</u> | Mass: 216015 | Score: 39 | Expect: 32 | Queries matched: 8 |
| | (TAF1_HUMAN) Splice isoform 2; Variant VAR_020678; Conflict Displayed; from P21 | | | | |
| | <u>P21675-00-00-00</u> | Mass: 213994 | Score: 36 | Expect: 58 | Queries matched: 8 |
| | (TAF1_HUMAN) Splice isoform 1; Variant Displayed; Conflict Displayed; from P216 | | | | |
| | <u>P21675-00-01-00</u> | Mass: 213980 | Score: 36 | Expect: 58 | Queries matched: 8 |
| | (TAF1_HUMAN) Splice isoform 1; Variant VAR_020678; Conflict Displayed; from P21 | | | | |
| | <u>Q9K998</u> | Mass: 26360 | Score: 42 | Expect: 16 | Queries matched: 6 |
| | (DCTR_BACHD) Probable C4-dicarboxylate response regulator dctR Probable C4-dica | | | | |
| | <u>P19127</u> | Mass: 16093 | Score: 39 | Expect: 27 | Queries matched: 4 |
| | (VPG_BLRV) Putative genome-linked protein precursor (VPG) (16 kDa protein) (ORF | | | | |
| | <u>Q9YCA4</u> | Mass: 16729 | Score: 36 | Expect: 52 | Queries matched: 4 |
| | (MOAC_AERPE) Probable molybdenum cofactor biosynthesis protein C Probable molyb | | | | |

| | | | | |
|------------------------|---|------------------|------------------------|---------------------------|
| <u>Q9WV85</u> | Mass: 19261 | Score: 36 | Expect: 66 | Queries matched: 3 |
| (NDK3_MOUSE) | Nucleoside diphosphate kinase 3 (EC 2.7.4.6) (NDK 3) (NDP kinase 3) | | | |
| <u>P07275</u> | Mass: 64685 | Score: 35 | Expect: 77 | Queries matched: 5 |
| (PUT2_YEAST) | Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial precu | | | |
| <u>Q81FR4</u> | Mass: 36727 | Score: 35 | Expect: 79 | Queries matched: 4 |
| (GPDA_BACCR) | Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94) (NAD(P) | | | |
| <u>Q92QI1</u> | Mass: 15114 | Score: 33 | Expect: 1.1e+02 | Queries matched |
| (RL11_RHIME) | 50S ribosomal protein L11 50S ribosomal protein L11 | | | |
| <u>O64644</u> | Mass: 17212 | Score: 33 | Expect: 1.2e+02 | Queries matched |
| (SP18_ARATH) | Probable Sin3 associated polypeptide p18 Probable Sin3 associated | | | |
| <u>P65793</u> | Mass: 39290 | Score: 33 | Expect: 1.2e+02 | Queries matched |
| (PROB_SALTI) | Glutamate 5-kinase (EC 2.7.2.11) (Gamma-glutamyl kinase) (GK) Glut | | | |
| <u>P65792</u> | Mass: 39290 | Score: 33 | Expect: 1.2e+02 | Queries matched |
| (PROB_SALTY) | Glutamate 5-kinase (EC 2.7.2.11) (Gamma-glutamyl kinase) (GK) Glut | | | |
| <u>P41457</u> | Mass: 17390 | Score: 32 | Expect: 1.4e+02 | Queries matched |
| (Y053_NPVAC) | Hypothetical 17.0 kDa protein in LEF8-FP intergenic region Hypothe | | | |
| <u>P29522</u> | Mass: 24460 | Score: 32 | Expect: 1.5e+02 | Queries matched |
| (EF1B2_BOMMO) | Elongation factor 1-beta' Elongation factor 1-beta' | | | |
| <u>O33605</u> | Mass: 16097 | Score: 32 | Expect: 1.5e+02 | Queries matched |
| (SODM_STRAY) | Superoxide dismutase [Mn/Fe] (EC 1.15.1.1) (Fragment) Superoxide d | | | |
| <u>Q84W41</u> | Mass: 101046 | Score: 32 | Expect: 1.5e+02 | Queries matched |
| (GLR36_ARATH) | Glutamate receptor 3.6 precursor (Ligand-gated ion channel 3.6) G | | | |
| <u>P20296</u> | Mass: 24797 | Score: 31 | Expect: 1.8e+02 | Queries matched |
| (YORA_PYRWO) | Hypothetical 24.7 kDa protein in GAPDH 5' region (ORF A) Hypothetic | | | |
| <u>Q87MQ1</u> | Mass: 19665 | Score: 31 | Expect: 1.9e+02 | Queries matched |
| (APT_VIBPA) | Adenine phosphoribosyltransferase (EC 2.4.2.7) (APRT) Adenine phosp | | | |
| <u>Q9XF88-01-00-00</u> | Mass: 25160 | Score: 31 | Expect: 1.9e+02 | Queries matched |
| (CB4B_ARATH) | Splice isoform 2; Variant Displayed; Conflict Displayed; from Q9XF | | | |
| <u>Q8SVF4</u> | Mass: 67658 | Score: 30 | Expect: 2.1e+02 | Queries matched |
| (Y608_ENCCU) | Hypothetical protein ECU06_0080 Hypothetical protein ECU06_0080 | | | |
| <u>Q9AI36</u> | Mass: 21003 | Score: 30 | Expect: 2.2e+02 | Queries matched |
| (GMHA_BURMA) | Phosphoheptose isomerase (EC 5.3.1.-) (Sedoheptulose 7-phosphate i | | | |
| <u>Q93UJ2</u> | Mass: 21032 | Score: 30 | Expect: 2.2e+02 | Queries matched |
| (GMHA_BURPS) | Phosphoheptose isomerase (EC 5.3.1.-) (Sedoheptulose 7-phosphate i | | | |
| <u>P66857</u> | Mass: 16639 | Score: 30 | Expect: 2.2e+02 | Queries matched |
| (SSB2_TROW8) | Single-strand binding protein 2 (SSB 2) (Helix-destabilizing prote | | | |
| <u>P66856</u> | Mass: 16639 | Score: 30 | Expect: 2.2e+02 | Queries matched |
| (SSB2_TROWT) | Single-strand binding protein 2 (SSB 2) (Helix-destabilizing prote | | | |
| <u>Q8PIF6</u> | Mass: 25119 | Score: 30 | Expect: 2.2e+02 | Queries matched |
| (Y2942_XANAC) | Hypothetical PKHD-type hydroxylase XAC2942 (EC 1.14.11.-) Hypothe | | | |
| <u>P71119</u> | Mass: 24101 | Score: 30 | Expect: 2.2e+02 | Queries matched |
| (HMUO_CORDI) | Heme oxygenase (EC 1.14.99.3) Heme oxygenase (EC 1.14.99.3) | | | |
| <u>Q58338</u> | Mass: 22101 | Score: 30 | Expect: 2.2e+02 | Queries matched |
| (Y928_METJA) | Hypothetical protein MJ0928 (M.MjaHemkP) Hypothetical protein MJ09 | | | |
| <u>Q8RH44</u> | Mass: 78810 | Score: 30 | Expect: 2.3e+02 | Queries matched |
| (SYGB_FUSNN) | Glycyl-tRNA synthetase beta chain (EC 6.1.1.14) (Glycine--tRNA lig | | | |
| <u>O49843</u> | Mass: 17887 | Score: 30 | Expect: 2.3e+02 | Queries matched |
| (PHEA_PORTE) | R-phycoerythrin alpha chain R-phycoerythrin alpha chain | | | |
| <u>O20206</u> | Mass: 17857 | Score: 30 | Expect: 2.3e+02 | Queries matched |
| (PHEA_PORYE) | R-phycoerythrin alpha chain R-phycoerythrin alpha chain | | | |
| <u>P51368</u> | Mass: 17977 | Score: 30 | Expect: 2.5e+02 | Queries matched |
| (PHEA_PORPU) | R-phycoerythrin alpha chain R-phycoerythrin alpha chain | | | |

| | | | | | |
|----|--|--------------|-----------|-----------------|--------------------|
| | <u>Q08704</u> | Mass: 24409 | Score: 30 | Expect: 2.6e+02 | Queries matched |
| | (CFI_MAIZE) Chalcone--flavonone isomerase (EC 5.5.1.6) (Chalcone isomerase) Cha | | | | |
| | <u>Q57773</u> | Mass: 12006 | Score: 29 | Expect: 2.7e+02 | Queries matched |
| | (Y327_METJA) Hypothetical protein MJ0327 Hypothetical protein MJ0327 | | | | |
| 2. | <u>Q8UC03</u> | Mass: 32556 | Score: 36 | Expect: 52 | Queries matched: 5 |
| | (DAPF_AGRT5) Diaminopimelate epimerase (EC 5.1.1.7) (DAP epimerase) Diaminopime | | | | |
| | <u>Q979F2</u> | Mass: 9882 | Score: 36 | Expect: 53 | Queries matched: 3 |
| | (RPOH_THEVO) DNA-directed RNA polymerase subunit H (EC 2.7.7.6) DNA-directed RN | | | | |
| 3. | <u>Q9Z7A0</u> | Mass: 72929 | Score: 35 | Expect: 79 | Queries matched: 6 |
| | (SYT_CHLPN) Threonyl-tRNA synthetase (EC 6.1.1.3) (Threonine--tRNA ligase) (Thr | | | | |
| 4. | <u>P22046</u> | Mass: 38551 | Score: 34 | Expect: 87 | Queries matched: 5 |
| | (VMAT_RINDK) Matrix protein Matrix protein | | | | |
| | <u>Q93AJ8</u> | Mass: 18516 | Score: 31 | Expect: 1.9e+02 | Queries matched |
| | (APT_STRCL) Adenine phosphoribosyltransferase (EC 2.4.2.7) (APRT) Adenine phosph | | | | |
| 5. | <u>Q47188</u> | Mass: 28670 | Score: 34 | Expect: 89 | Queries matched: 4 |
| | (EXPR_ERWCH) Transcriptional activator protein expR Transcriptional activator p | | | | |
| | <u>Q8YG94</u> | Mass: 30477 | Score: 34 | Expect: 93 | Queries matched: 4 |
| | (KSGA_BRUME) Dimethyladenosine transferase (EC 2.1.1.-) (S-adenosylmethionine-6 | | | | |
| | <u>Q8G1N0</u> | Mass: 30461 | Score: 34 | Expect: 93 | Queries matched: 4 |
| | (KSGA_BRUSU) Dimethyladenosine transferase (EC 2.1.1.-) (S-adenosylmethionine-6 | | | | |
| 6. | <u>Q931G4</u> | Mass: 39402 | Score: 31 | Expect: 2e+02 | Queries matched: |
| | (MOAA_STAAM) Molybdenum cofactor biosynthesis protein A Molybdenum cofactor bio | | | | |
| 7. | <u>Q9SP32</u> | Mass: 215469 | Score: 30 | Expect: 2.4e+02 | Queries matched |
| | (DICER_ARATH) Endoribonuclease Dicer homolog (EC 3.1.26.-) (CARPEL FACTORY prot | | | | |
| | <u>O00591-00-00-00</u> | Mass: 51014 | Score: 29 | Expect: 2.7e+02 | Queries matched |
| | (GBRP_HUMAN) Splice isoform Displayed; Variant Displayed; Conflict Displayed; f | | | | |
| | <u>O00591-00-01-00</u> | Mass: 50980 | Score: 29 | Expect: 2.7e+02 | Queries matched |
| | (GBRP_HUMAN) Splice isoform Displayed; Variant dbSNP:1063310; Conflict Displaye | | | | |
| 8. | <u>Q8TVG3</u> | Mass: 44222 | Score: 30 | Expect: 2.4e+02 | Queries matched |
| | (HIS8_METKA) Histidinol-phosphate aminotransferase (EC 2.6.1.9) (Imidazole acet | | | | |
| 9. | <u>Q8D2V8</u> | Mass: 29440 | Score: 29 | Expect: 2.7e+02 | Queries matched |
| | (LPXH_WIGBR) UDP-2,3-diacylglucosamine hydrolase (EC 3.6.1.-) UDP-2,3-diacylglu | | | | |

Search Parameters

Type of search : Peptide Mass Fingerprint
 Enzyme : Trypsin
 Fixed modifications : Carboxymethyl (C)
 Variable modifications : Oxidation (M)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance : ± 1 Da
 Peptide Charge State : 1+
 Max Missed Cleavages : 1
 Number of queries : 9

Mascot: <http://www.matrixscience.com/>

{MATRIX}
{SCIENCE} Mascot Search Results

Protein View

Match to: **Q8IZX4** Score: **44** Expect: **9.5**
(**TAF1L_HUMAN**) Transcription initiation factor TFIID 210 kDa subunit (TBP-associated f

Nominal mass (M_r): **208737**; Calculated pI value: **5.26**
NCBI BLAST search of **Q8IZX4** against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Homo sapiens

Fixed modifications: Carboxymethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **9**
Number of mass values matched: **8**
Sequence Coverage: **7%**

Matched peptides shown in **Bold Red**

| | | | | | |
|------|-------------------|--------------------|--------------------|--------------------|---------------------|
| 1 | MRPGCDLLLR | AAATVTAAIM | SDSDSEEDSS | GGGPFTLAGI | LFGNISGAGQ |
| 51 | LEGESVLDDE | CKKHLAAGLGA | LGLGSLITEL | TANEELTGTG | GALVNDEGWI |
| 101 | RSTEDAVDYS | DINEVAEDES | QRHQQTMGSL | QPLYHSDYDE | DDYDADCEDI |
| 151 | DKLMPPPPP | PPGPMKKDKD | QDAITCVSES | GEDIILPSII | APSFLASEKV |
| 201 | DFSSYSDES | EMGPQEATQA | ESEDGKLTLP | LAGIMQH DAT | KLLPSVTELF |
| 251 | PEFRPGKVL R | FLHLFGPGKN | VPSVWRSARR | KRKKHRELIQ | EEQIQEVECS |
| 301 | VESEVSQKSL | WNYDYAPPPP | PEQCLADDEI | TMMVPVESKF | SQSTGDVDKV |
| 351 | TDTKPRVAEW | RYGPARLWYD | MLGVSEDEGSG | FDYGFKL RKT | QHEPVIKSRM |
| 401 | MEEFRKLEES | NGTDLLADEN | FLMVTQLHWE | DSIIWDGEDI | KHKGTKPQGA |
| 451 | SLAGWLPSIK | TRNVMAYNVQ | QGFAPTLD DD | KPWYSIFPID | NEDLVYGRWE |
| 501 | DNIIWDAQAM | PRLLEPPVLA | LDPNDENLIL | EIPDEKEEAT | SNSPSKESKK |
| 551 | ESSLKKSRIL | LGKTGVIREE | PQQNMSQPEV | KDPWNLSNDE | YYFPKQOGLR |
| 601 | GTFGGNIIQH | SIPAMELWQP | FFPTHMGPIK | IRQFHRPPLK | KYSFGALSOP |
| 651 | GPHSVQPLLK | HIKKAKMRE | QERQASGGGE | LFMRT PQDL | TGKDGDLILA |
| 701 | EYSEENGPLM | MOVGMATKIK | NYKRPKPGD | PGAPDC KYGE | TVYCHTSPFL |
| 751 | GSLHPQQLLQ | ALENNLFRAP | VYLHKMPETD | FLIIRTRQGY | YIRELVDIFV |
| 801 | VGQQCPLEFV | PGPNRRANM | HIRDFLQVFI | YRLFWSKDR | PRRIRMEDIK |
| 851 | KAFPSHSESS | IRKRLKLCAD | FKRTGMDSNW | WVLKSDFRLP | TEEEIRAKVS |
| 901 | PEQCCAYYSM | IAAQRLKDA | GYGEKSFFAP | EEENEEDFOM | KIDDEVHAAP |
| 951 | WNTTRAFIAA | MKGKCLLEV T | GVADPTGCGE | GFSYVKIPNK | PTQOKDDKEP |
| 1001 | QAVKKTVTGT | DADLRRLSLK | NAQQLLRKFG | VPEEEIKKLS | RWEVIDVVRT |
| 1051 | MSTEQAHSGE | GPMSKFARG S | RFSVAEHQER | YKEECQRIFD | LQNKVLSSTE |
| 1101 | VLSTDTDSIS | AEDSDPEEMG | KNIENMLQNK | KTSSQLSREW | EEQERKELRR |
| 1151 | MLLVAGSAAS | GNNHRDDVTA | SMTSLKSSAT | GHCLKIYRTF | RDEEGKEYVR |
| 1201 | CETVRKPAVI | DAYVRIRTTK | DEKFIQKFAL | FDEKHREEMR | KERRRIQEQL |
| 1251 | RRLKRNQEKE | KLKGPPEKKP | KKMKERPDLK | LKCGACGAIG | HMRTNKF CPL |
| 1301 | YYQTNVPPSK | PVAMTEEQEE | ELEKTVIHND | NEELIKVEGT | KIVFGKQLIE |
| 1351 | NVHEVRRKSL | VLKFPEQQLP | PKKKRRVGT T | VHCDYLNIPH | KSIHRRRTDP |
| 1401 | MVTLSSILES | IINDMRDLPN | THPFHTPVNA | KVVKDYYKII | TRPMDLQTLR |
| 1451 | ENVRKCLYPS | REEFREHLEL | IVKNSATYNG | PKHSLTQISQ | SMLDLCEKLE |
| 1501 | KEKEDKLARL | EKAINPLLDD | DDQVAFS FIL | DNIVTQKMM A | VPDSWPFHHP |
| 1551 | VNKKFVPDYY | KMIVNPVDLE | TIRKNISKHK | YQSRESFLDD | VNLILANSVK |
| 1601 | YNGPESQYTK | TAQEIVNICY | QTITEYDEHL | TQLEKDICTA | KEAALEEAEL |
| 1651 | ESLDPMTPGP | YTSQPPDMYD | TNTSLSTSRD | ASVFQDES NL | SVLDISTATP |
| 1701 | EKQMCQGGQR | LGEEDSDVDV | EGYDDEEEDG | KPKPPAPEGG | DGDLADEEEE G |
| 1751 | TVQQPEASVL | YEDLLISEGE | DDEEDAGSDE | EGDNPFSAIQ | LSESGSDSDV |
| 1801 | GYGGIRPKQP | FMLQHASGEH | KDGHGK | | |

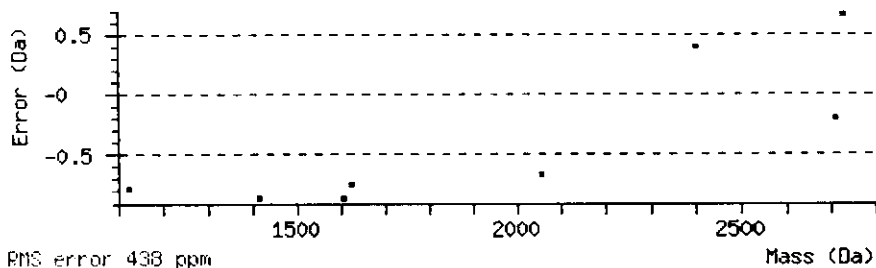
Show predicted peptides also

Sort Peptides By

Residue Number Increasing Mass Decreasing Mass

| Start - End | Observed | Mr(expt) | Mr(calc) | Delta | Miss | Sequence |
|-------------|----------|----------|----------|-------|------|------------------------------|
| 227 - 241 | 1608.02 | 1607.02 | 1607.87 | -0.85 | 0 | K.LTLPLAGIMQHDATAK.L |
| 642 - 663 | 2404.70 | 2403.69 | 2403.31 | 0.39 | 1 | K.YSFGALSQPGPHSVQPLLKHIK.K |
| 694 - 718 | 2728.91 | 2727.90 | 2727.24 | 0.66 | 0 | K.DGDLILA EYSEENGPLMMQVGMATK |
| 769 - 785 | 2058.44 | 2057.43 | 2058.10 | -0.66 | 1 | R.APVYLHKMPETDFLIIR.T Oxid: |
| 919 - 941 | 2712.92 | 2711.91 | 2712.12 | -0.21 | 1 | K.DAGYGEKSFFAPEEENEEDFQMK.I |
| 942 - 955 | 1624.03 | 1623.02 | 1623.76 | -0.74 | 0 | K.IDDEVHAAPWNTTR.A |
| 1192 - 1200 | 1123.74 | 1122.73 | 1123.51 | -0.78 | 1 | R.DEEGKEYVR.C |
| 1562 - 1573 | 1414.90 | 1413.89 | 1414.75 | -0.86 | 0 | K.MIVNPVDLETIR.K Oxidation |

No match to: 1143.77



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Full entry text for [Q8IZX4](#)

Mascot: <http://www.matrixscience.com/>

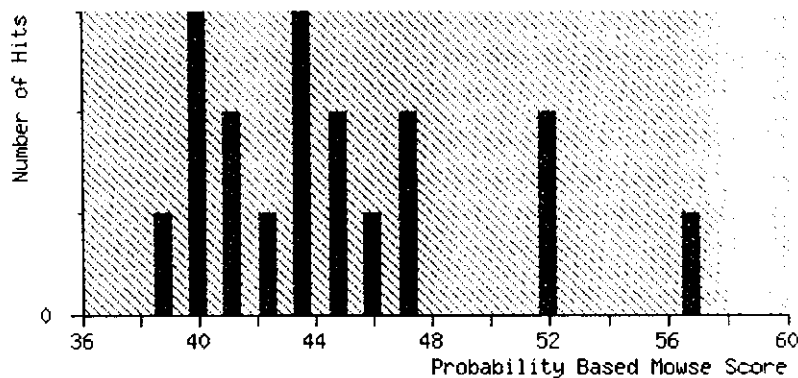
{MATRIX} Mascot Search Results

{SCIENCES}

User : Waraporn
 Email : waraporn.p@psu.ac.th
 Search title : shrimp epidermis spot3
 Database : NCBIInr 20050303 (2339066 sequences; 792779905 residues)
 Timestamp : 9 Mar 2005 at 02:27:26 GMT
 Top Score : 57 for gi|45643438, ArsR [Streptomyces ambofaciens]

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Protein scores greater than 76 are significant ($p < 0.05$).



Concise Protein Summary Report

 Format as

 Concise Protein Summary

[Help](#)

 Significance threshold $p < 0.05$

 Max. number of hits 20
 Re-Search All

 Search Unmatched

| | | | | | |
|----|-----------------------------|-------------|-----------|-----------------|---|
| 1. | gi 45643438 | Mass: 10524 | Score: 57 | Expect: 4.9 | Queries matched: ArsR [Streptomyces ambofaciens] |
| 2. | gi 48767463 | Mass: 15463 | Score: 52 | Expect: 15 | Queries matched: COG2258: Uncharacterized protein conserved in bacteria [Ralstonia metallidurans] |
| | gi 28172663 | Mass: 26147 | Score: 42 | Expect: 1.3e+02 | Queries mat p24 [Human immunodeficiency virus 1] |
| 3. | gi 15795256 | Mass: 13326 | Score: 52 | Expect: 16 | Queries matched: TRADV15D-1 [Mus musculus] |
| 4. | gi 29336555 | Mass: 18515 | Score: 47 | Expect: 43 | Queries matched: Adenine phosphoribosyltransferase (APRT) |
| | gi 46580084 | Mass: 22291 | Score: 45 | Expect: 76 | Queries matched: transcriptional regulator, putative [Desulfovibrio vulgaris subsp. vulgaris str |
| | gi 48732688 | Mass: 12584 | Score: 40 | Expect: 2.4e+02 | Queries mat hypothetical protein Pflu02000738 [Pseudomonas fluorescens Pf0-1] |
| 5. | gi 21745048 | Mass: 19762 | Score: 47 | Expect: 51 | Queries matched: putative disease resistance gene analog NBS-LRR [Malus prunifolia] |

| | | | | | |
|----|---|--------------|-----------|-----------------|------------------|
| 6. | gi 18146124 | Mass: 34320 | Score: 46 | Expect: 60 | Queries matched: |
| | conserved hypothetical protein [Clostridium perfringens str. 13] | | | | |
| | gi 23003058 | Mass: 100753 | Score: 39 | Expect: 2.8e+02 | Queries mat |
| | COG0749: DNA polymerase I - 3'-5' exonuclease and polymerase domains [Lactobaci | | | | |
| | gi 28316236 | Mass: 10490 | Score: 40 | Expect: 2.4e+02 | Queries mat |
| | hypothetical protein [Escherichia coli] | | | | |
| | gi 18252405 | Mass: 16066 | Score: 39 | Expect: 2.7e+02 | Queries mat |
| | movement protein P4 [Bean leafroll virus] | | | | |
| | gi 60518 | Mass: 16093 | Score: 39 | Expect: 2.7e+02 | Queries mat |
| | unnamed protein product [Bean leafroll virus] | | | | |
| | gi 47216567 | Mass: 30570 | Score: 39 | Expect: 2.9e+02 | Queries mat |
| | unnamed protein product [Tetraodon nigroviridis] | | | | |
| 7. | gi 15222515 | Mass: 60769 | Score: 45 | Expect: 71 | Queries matched: |
| | cytochrome P450, putative [Arabidopsis thaliana] | | | | |
| | gi 17427801 | Mass: 7585 | Score: 42 | Expect: 1.6e+02 | Queries mat |
| | CONSERVED HYPOTHETICAL PROTEIN [Ralstonia solanacearum] | | | | |
| | gi 55238094 | Mass: 8125 | Score: 39 | Expect: 2.9e+02 | Queries mat |
| | ENSANGP00000027162 [Anopheles gambiae str. PEST] | | | | |
| 8. | gi 54295991 | Mass: 47847 | Score: 45 | Expect: 72 | Queries matched: |
| | hypothetical protein lpp0008 [Legionella pneumophila str. Paris] | | | | |
| | gi 631321 | Mass: 10866 | Score: 40 | Expect: 2.4e+02 | Queries mat |
| | p68 protein - human (fragments) | | | | |
| 9. | gi 24429572 | Mass: 208711 | Score: 44 | Expect: 95 | Queries matched: |
| | TBP-associated factor RNA polymerase 1-like [Homo sapiens] | | | | |
| | gi 29733 | Mass: 180089 | Score: 41 | Expect: 1.9e+02 | Queries mat |
| | CCG1 protein [Homo sapiens] | | | | |
| | gi 20357585 | Mass: 216004 | Score: 39 | Expect: 3.2e+02 | Queries mat |
| | TBP-associated factor 1 isoform 1 [Homo sapiens] | | | | |
| | gi 13605599 | Mass: 81254 | Score: 44 | Expect: 1e+02 | Queries match |
| | AT4g32910/F26P21_30 [Arabidopsis thaliana] | | | | |
| | gi 27803051 | Mass: 44119 | Score: 44 | Expect: 1e+02 | Queries match |
| | unnamed protein product [Podospira anserina] | | | | |
| | gi 19698819 | Mass: 81539 | Score: 43 | Expect: 1.1e+02 | Queries mat |
| | putative protein [Arabidopsis thaliana] | | | | |
| | gi 49653362 | Mass: 30671 | Score: 42 | Expect: 1.4e+02 | Queries mat |
| | unnamed protein product [Debaryomyces hansenii CBS767] | | | | |
| | gi 10175372 | Mass: 26360 | Score: 42 | Expect: 1.6e+02 | Queries mat |
| | two-component response regulator [Bacillus halodurans C-125] | | | | |
| | gi 15827241 | Mass: 28235 | Score: 41 | Expect: 1.7e+02 | Queries mat |
| | putative ABC transporter ATP-binding protein [Mycobacterium leprae TN] | | | | |
| | gi 24020886 | Mass: 99351 | Score: 40 | Expect: 2.1e+02 | Queries mat |
| | TBP-associated factor RNA polymerase 1-like [Pan troglodytes] | | | | |
| | gi 46156881 | Mass: 27621 | Score: 40 | Expect: 2.4e+02 | Queries mat |
| | COG1040: Predicted amidophosphoribosyltransferases [Haemophilus somnus 2336] | | | | |
| | gi 55727377 | Mass: 47923 | Score: 39 | Expect: 2.7e+02 | Queries mat |
| | hypothetical protein [Pongo pygmaeus] | | | | |
| | gi 45533192 | Mass: 26075 | Score: 39 | Expect: 2.7e+02 | Queries mat |
| | COG4221: Short-chain alcohol dehydrogenase of unknown specificity [Exiguobacter | | | | |
| | gi 16579885 | Mass: 47953 | Score: 39 | Expect: 2.7e+02 | Queries mat |
| | ribosomal protein L4 [Homo sapiens] | | | | |
| | gi 45507887 | Mass: 25265 | Score: 39 | Expect: 2.9e+02 | Queries mat |
| | COG3436: Transposase and inactivated derivatives [Anabaena variabilis ATCC 2941 | | | | |

| | | | | | |
|-----|---|--------------|-----------|-----------------|---------------|
| | gi 13160967 | Mass: 30496 | Score: 38 | Expect: 3.3e+02 | Queries mat |
| | replication initiator-like protein [Xylella fastidiosa] | | | | |
| | gi 14530637 | Mass: 28927 | Score: 38 | Expect: 3.4e+02 | Queries mat |
| | Hypothetical protein Y54E5B.3b [Caenorhabditis elegans] | | | | |
| 10. | gi 58583534 | Mass: 81226 | Score: 44 | Expect: 1e+02 | Queries match |
| | HmsH [Xanthomonas oryzae pv. oryzae KACC10331] | | | | |
| | gi 52421175 | Mass: 28419 | Score: 40 | Expect: 2.2e+02 | Queries mat |
| | crotonase [Butyrivibrio fibrisolvens] | | | | |
| 11. | gi 50305503 | Mass: 57726 | Score: 43 | Expect: 1.1e+02 | Queries mat |
| | unnamed protein product [Kluyveromyces lactis] | | | | |
| | gi 39590864 | Mass: 57946 | Score: 41 | Expect: 1.9e+02 | Queries mat |
| | Hypothetical protein CBG10121 [Caenorhabditis briggsae] | | | | |
| | gi 53714406 | Mass: 8825 | Score: 39 | Expect: 2.8e+02 | Queries mat |
| | hypothetical protein BF3119 [Bacteroides fragilis YCH46] | | | | |
| 12. | gi 37525366 | Mass: 70578 | Score: 43 | Expect: 1.3e+02 | Queries mat |
| | hypothetical protein plu1412 [Photobacterium luminescens subsp. laumondii T101] | | | | |
| 13. | gi 42524512 | Mass: 81504 | Score: 42 | Expect: 1.7e+02 | Queries mat |
| | sensor histidine kinase [Bdellovibrio bacteriovorus HD100] | | | | |
| | gi 23492093 | Mass: 45232 | Score: 40 | Expect: 2.6e+02 | Queries mat |
| | putative restriction enzyme subunit S [Corynebacterium efficiens YS-314] | | | | |
| 14. | gi 53794734 | Mass: 50118 | Score: 41 | Expect: 1.8e+02 | Queries mat |
| | COG0493: NADPH-dependent glutamate synthase beta chain and related oxidoreducta | | | | |
| 15. | gi 39936208 | Mass: 40161 | Score: 40 | Expect: 2.1e+02 | Queries mat |
| | possible transglycosylase SLT domain [Rhodopseudomonas palustris CGA009] | | | | |
| 16. | gi 23508887 | Mass: 51794 | Score: 40 | Expect: 2.1e+02 | Queries mat |
| | hypothetical protein PFL0965c [Plasmodium falciparum 3D7] | | | | |
| 17. | gi 39583256 | Mass: 42912 | Score: 40 | Expect: 2.1e+02 | Queries mat |
| | Hypothetical protein CBG03560 [Caenorhabditis briggsae] | | | | |
| 18. | gi 56474035 | Mass: 144209 | Score: 39 | Expect: 3.2e+02 | Queries mat |
| | P-glycoprotein 6 [Entamoeba histolytica HM-1:IMSS] | | | | |
| | gi 55644833 | Mass: 58881 | Score: 39 | Expect: 3.2e+02 | Queries mat |
| | PREDICTED: arrestin beta 2 [Pan troglodytes] | | | | |

Search Parameters

Type of search : Peptide Mass Fingerprint
 Enzyme : Trypsin
 Fixed modifications : Carbamidomethyl (C)
 Variable modifications : Oxidation (M)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance : ± 1 Da
 Peptide Charge State : 1+
 Max Missed Cleavages : 1
 Number of queries : 9

Mascot: <http://www.matrixscience.com/>

{MATRIX}
{SCIENCE} **Mascot Search Results**

Protein View

Match to: gi|45643438 Score: 57 Expect: 5.1
ArsR [Streptomyces ambofaciens]

Nominal mass (M_r): 10524; Calculated pI value: 6.56

NCBI BLAST search of gi|45643438 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Streptomyces ambofaciens

Fixed modifications: Carboxymethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 9
Number of mass values matched: 5
Sequence Coverage: 70%

Matched peptides shown in **Bold Red**

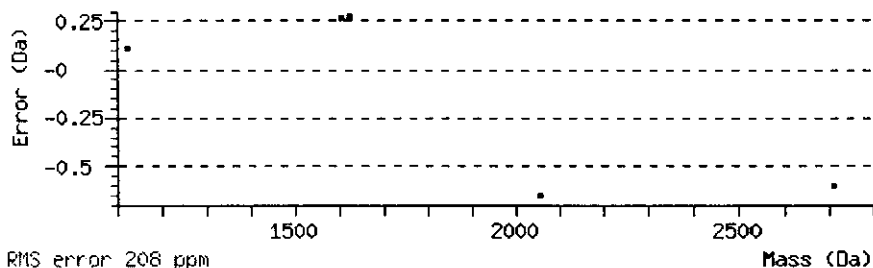
1 MGPLPGLPGI RASGEISVTT RQSWENALTE MSRRHAEVSY VELSGVRFVD
51 VAGVTALAVT AMNLPGGRV VEQPPPQLPR VLELFWPSLN RIEVAPR

Show predicted peptides also

Sort Peptides By Residue Number Increasing Mass Decreasing Mass

| Start - End | Observed | Mr(expt) | Mr(calc) | Delta | Miss | Sequence |
|-------------|----------|----------|----------|-------|------|-----------------------------|
| 1 - 11 | 1123.74 | 1122.73 | 1122.62 | 0.11 | 0 | -.MGPLPGLPGIR.A Oxidation |
| 22 - 34 | 1608.02 | 1607.02 | 1606.75 | 0.26 | 1 | R.QSWENALTEMSRR.H |
| 22 - 34 | 1624.03 | 1623.02 | 1622.75 | 0.28 | 1 | R.QSWENALTEMSRR.H Oxidation |
| 48 - 68 | 2058.44 | 2057.43 | 2058.09 | -0.66 | 0 | R.FVDVAGVTALAVTAMNLPGGR.V |
| 69 - 91 | 2712.92 | 2711.91 | 2712.51 | -0.60 | 1 | R.VVVEQPPPQLPRVLELFWPSLNR.I |

No match to: 1143.77, 1414.90, 2404.70, 2728.91



LOCUS AAS72557 97 aa linear BCT 04-AUG-2004
 DEFINITION ArsR [Streptomyces ambofaciens].
 ACCESSION AAS72557
 VERSION AAS72557.1 GI:45643438
 DBSOURCE accession AF050150.2
 KEYWORDS
 SOURCE Streptomyces ambofaciens
 ORGANISM Streptomyces ambofaciens
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Streptomycineae; Streptomycetaceae; Streptomyces.
 REFERENCE 1 (residues 1 to 97)
 AUTHORS Fischer,G., Wenner,T., Decaris,B. and Leblond,P.

TITLE Chromosomal arm replacement generates a high level of intraspecific polymorphism in the terminal inverted repeats of the linear chromosomal DNA of *Streptomyces ambofaciens*
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (24), 14296-14301 (1998)
PUBMED [9826694](#)
REFERENCE 2 (residues 1 to 97)
AUTHORS Roth,V., Aigle,B., Bunet,R., Wenner,T., Fourrier,C., Decaris,B. and Leblond,P.
TITLE Differential and Cross-Transcriptional Control of Duplicated Genes Encoding Alternative Sigma Factors in *Streptomyces ambofaciens*
JOURNAL J. Bacteriol. 186 (16), 5355-5365 (2004)
PUBMED [15292136](#)
REFERENCE 3 (residues 1 to 97)
AUTHORS Fischer,G., Wenner,T., Decaris,B. and Leblond,P.
TITLE Direct Submission
JOURNAL Submitted (23-FEB-1998) Genetique et Microbiologie, Universite Henri Poincare Nancy1, Boulevard des Aiguillettes, Vandoeuvre les Nancy 54506, France
REFERENCE 4 (residues 1 to 97)
AUTHORS Virginie,R., Bertrand,A., Bunet,R., Wenner,T., Fourrier,C., Decaris,B. and Leblond,P.
TITLE Direct Submission
JOURNAL Submitted (23-MAR-2004) UMR UHP-INRA 1128, IFR110, Faculte des Sciences et Techniques, Universite Henri Poincare, Nancy 1, Laboratoire de Genetique et Microbiologie, Boulevard des Aiguillettes, BP 239, Vandoeuvre-les-Nancy 54506, France
REMARK Sequence update by submitter
COMMENT Method: conceptual translation.
FEATURES Location/Qualifiers
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 /db_xref="taxon:1889"
 Protein 1..97
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 CDS 1..97
 /gene="arsR"
 /coded_by="AF050150.2:758..1051"
 /note="putative anti-anti-sigma factor; similar to Streptomyces coelicolor putative anti-anti-sigma factor SCF55.22"
 /transl_table=11

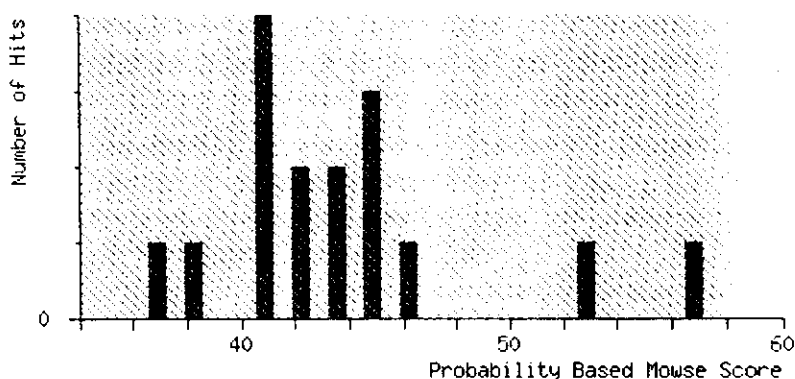
Mascot: <http://www.matrixscience.com/>

{MATRIX}
{SCIENCE} Mascot Search Results

User : Waraporn
 Email : waraporn.p@psu.ac.th
 Search title :
 Database : MSDB 20050227 (1942918 sequences; 629040812 residues)
 Timestamp : 13 May 2005 at 11:29:09 GMT
 Top Score : 57 for Q7BU49_STRAM, ArsR.- Streptomyces ambofaciens.

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
 Protein scores greater than 75 are significant ($p < 0.05$).

**Concise Protein Summary Report**

Format As Concise Protein Summary

[Help](#)

Significance threshold $p <$

Max. number of hits

Re-Search All Search Unmatched

| | | | | | |
|----|--|-------------|-----------|-----------------|--------------------|
| 1. | <u>Q7BU49_STRAM</u> ArsR.- Streptomyces ambofaciens. | Mass: 10524 | Score: 57 | Expect: 4.1 | Queries matched: 5 |
| | <u>T17987</u> hypothetical protein A485R - Chlorella virus PBCV-1 | Mass: 17223 | Score: 37 | Expect: 3.9e+02 | Queries matched: 3 |
| 2. | <u>Q8N2W5_HUMAN</u> Hypothetical protein (Fragment).- Homo sapiens (Human). | Mass: 3095 | Score: 53 | Expect: 10 | Queries matched: 3 |
| 3. | <u>Q7NVM4_CHRVO</u> Hypothetical protein.- Chromobacterium violaceum. | Mass: 19928 | Score: 47 | Expect: 43 | Queries matched: 4 |
| 4. | <u>Q5X983_LEGPA</u> Hypothetical protein.- Legionella pneumophila (strain Paris). | Mass: 47855 | Score: 45 | Expect: 56 | Queries matched: 5 |
| | <u>S43974</u> p68 protein - human (fragments) | Mass: 10866 | Score: 40 | Expect: 2e+02 | Queries matched: 3 |
| | <u>O90984_9HIV1</u> Gp120 (Fragment).- Human immunodeficiency virus 1. | Mass: 9721 | Score: 38 | Expect: 3.2e+02 | Queries matched: 3 |
| | <u>Q9CWA5_MOUSE</u> Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone: | Mass: 18943 | Score: 37 | Expect: 4.3e+02 | Queries matched: 3 |

| | | | | | |
|----|--|--------------|-----------|-----------------|--------------------|
| 5. | <u>B96662</u> | Mass: 60777 | Score: 45 | Expect: 59 | Queries matched: 6 |
| | probable cytochrome P450 F24D7.10 [imported] - Arabidopsis thaliana | | | | |
| | <u>AAF09150</u> | Mass: 61009 | Score: 45 | Expect: 60 | Queries matched: 6 |
| | AE005173 NID: - Arabidopsis thaliana | | | | |
| | <u>Q8Y1A1_RALSO</u> | Mass: 7585 | Score: 42 | Expect: 1.3e+02 | Queries matched |
| | Hypothetical protein RSc0789.- Ralstonia solanacearum (Pseudomonas solanacearum) | | | | |
| | <u>Q95M43_BOVIN</u> | Mass: 6029 | Score: 38 | Expect: 2.9e+02 | Queries matched |
| | Insulin receptor (Fragment).- Bos taurus (Bovine). | | | | |
| | <u>Q9VR25_DROME</u> | Mass: 51086 | Score: 37 | Expect: 3.7e+02 | Queries matched |
| | CG15630-PA.- Drosophila melanogaster (Fruit fly). | | | | |
| | <u>AAP24796</u> | Mass: 11956 | Score: 37 | Expect: 4.2e+02 | Queries matched |
| | AE016879 NID: - Bacillus anthracis str. Ames | | | | |
| 6. | <u>Q9XZ87_PLAFA</u> | Mass: 17004 | Score: 45 | Expect: 60 | Queries matched: 4 |
| | DBL alpha protein (Fragment).- Plasmodium falciparum. | | | | |
| | <u>S11438</u> | Mass: 16093 | Score: 39 | Expect: 2.2e+02 | Queries matched |
| | coat protein 2 - bean leaf roll virus | | | | |
| | <u>Q8V2F4_BLRV</u> | Mass: 16066 | Score: 39 | Expect: 2.2e+02 | Queries matched |
| | Movement protein P4.- Bean leafroll virus (BLRV). | | | | |
| 7. | <u>AAN40840</u> | Mass: 208737 | Score: 44 | Expect: 79 | Queries matched: 8 |
| | AF390562 NID: - Homo sapiens | | | | |
| | <u>CAA30073</u> | Mass: 180114 | Score: 41 | Expect: 1.6e+02 | Queries matched |
| | HSCCG1 NID: - Homo sapiens | | | | |
| | <u>A40262</u> | Mass: 216029 | Score: 39 | Expect: 2.7e+02 | Queries matched |
| | transcription initiation factor IID 250K chain splice form 1 - human | | | | |
| | <u>Q86ZJ9_PODAN</u> | Mass: 44121 | Score: 44 | Expect: 87 | Queries matched: 5 |
| | Similar to Regulatory Particle Non-ATPase Rpn9p of Saccharomyces cerevisiae.- P | | | | |
| | <u>Q7ZNT7_9HIV1</u> | Mass: 26149 | Score: 42 | Expect: 1.1e+02 | Queries matched |
| | P24 (Fragment).- Human immunodeficiency virus 1. | | | | |
| | <u>G83993</u> | Mass: 26360 | Score: 42 | Expect: 1.3e+02 | Queries matched |
| | two-component response regulator BH2751 [imported] - Bacillus halodurans (strai | | | | |
| | <u>S72767</u> | Mass: 28236 | Score: 41 | Expect: 1.4e+02 | Queries matched |
| | probable ABC-type transport protein B1496_C3_228 - Mycobacterium leprae | | | | |
| | <u>T34386</u> | Mass: 55782 | Score: 40 | Expect: 1.7e+02 | Queries matched |
| | hypothetical protein T26A5.4 - Caenorhabditis elegans | | | | |
| | <u>Q8HZW0_PANTR</u> | Mass: 99366 | Score: 40 | Expect: 1.7e+02 | Queries matched |
| | TBP-associated factor RNA polymerase 1-like (Fragment).- Pan troglodytes (Chimp | | | | |
| | <u>Q6YSX4_ORYSA</u> | Mass: 11086 | Score: 40 | Expect: 1.9e+02 | Queries matched |
| | Hypothetical protein OSJNBa0004F07.30 (Hypothetical protein B1100H02.7).- Oryza | | | | |
| | <u>B56679</u> | Mass: 102912 | Score: 40 | Expect: 2.1e+02 | Queries matched |
| | probable reverse transcriptase - house mosquito | | | | |
| | <u>Q6PJN8_MOUSE</u> | Mass: 59566 | Score: 39 | Expect: 2.6e+02 | Queries matched |
| | 6330580J24Rik protein.- Mus musculus (Mouse). | | | | |
| | <u>Q9AMP2_XYLFA</u> | Mass: 30497 | Score: 38 | Expect: 2.7e+02 | Queries matched |
| | Replication initiator-like protein.- Xylella fastidiosa. | | | | |
| | <u>CAC08865</u> | Mass: 144723 | Score: 38 | Expect: 2.9e+02 | Queries matched |
| | Sequence 20 from Patent EP0999284 (Fragment).- Candida albicans (Yeast). | | | | |
| | <u>Q7VWT3_BORPE</u> | Mass: 29674 | Score: 38 | Expect: 3.3e+02 | Queries matched |
| | Putative exodeoxyribonuclease III (EC 3.1.11.2).- Bordetella pertussis. | | | | |
| | <u>Q7WAF5_BORPA</u> | Mass: 29616 | Score: 38 | Expect: 3.3e+02 | Queries matched |
| | Putative exodeoxyribonuclease III (EC 3.1.11.2).- Bordetella parapertussis. | | | | |
| | <u>Q6CQK3_KLUJLA</u> | Mass: 96847 | Score: 38 | Expect: 3.5e+02 | Queries matched |
| | Kluyveromyces lactis strain NRRL Y-1140 chromosome D of strain NRRL Y- 1140 of | | | | |

| | | | | | |
|-----|---|-------------|-----------|-----------------|--------------------|
| | <u>Q8EMA4_OCEIH</u> | Mass: 67061 | Score: 37 | Expect: 4.1e+02 | Queries matched |
| | Hypothetical conserved protein.- Oceanobacillus iheyensis. | | | | |
| 8. | <u>Q6CTM8_KLULA</u> | Mass: 57731 | Score: 43 | Expect: 93 | Queries matched: 6 |
| | Kluyveromyces lactis strain NRRL Y-1140 chromosome C of strain NRRL Y- 1140 of | | | | |
| | <u>Q64RL7_BACFR</u> | Mass: 8826 | Score: 39 | Expect: 2.3e+02 | Queries matched |
| | Hypothetical protein.- Bacteroides fragilis. | | | | |
| | <u>Q6AVK1_ORYSA</u> | Mass: 9632 | Score: 39 | Expect: 2.4e+02 | Queries matched |
| | Striated muscle activator-like protein.- Oryza sativa (japonica cultivar-group) | | | | |
| 9. | <u>Q7N6X3_PHOLL</u> | Mass: 70589 | Score: 43 | Expect: 1e+02 | Queries matched: |
| | Similar to hemolysin erythrocyte lysis protein 2.- Photorhabdus luminescens (su | | | | |
| 10. | <u>Q8AD09_9HIV1</u> | Mass: 21253 | Score: 42 | Expect: 1.2e+02 | Queries matched |
| | Envelope glycoprotein (Fragment).- Human immunodeficiency virus 1. | | | | |
| | <u>Q96L06_HUMAN</u> | Mass: 26971 | Score: 38 | Expect: 2.7e+02 | Queries matched |
| | Hypothetical protein MGC26856.- Homo sapiens (Human). | | | | |
| | <u>Q6UWM5_HUMAN</u> | Mass: 27975 | Score: 38 | Expect: 3.2e+02 | Queries matched |
| | ALKN2972.- Homo sapiens (Human). | | | | |
| 11. | <u>Q6MIM8_BDEBA</u> | Mass: 81505 | Score: 42 | Expect: 1.4e+02 | Queries matched |
| | Sensor histidine kinase precursor.- Bdellovibrio bacteriovorus. | | | | |
| | <u>Q8FTX0_COREF</u> | Mass: 45235 | Score: 40 | Expect: 2.2e+02 | Queries matched |
| | Putative restriction enzyme subunit S.- Corynebacterium efficiens. | | | | |
| 12. | <u>Q7Q030_ANOGA</u> | Mass: 47743 | Score: 41 | Expect: 1.6e+02 | Queries matched |
| | ENSANGP00000016550 (Fragment).- Anopheles gambiae str. PEST. | | | | |
| | <u>Q7XLP6_ORYSA</u> | Mass: 29661 | Score: 38 | Expect: 3.2e+02 | Queries matched |
| | OSJNBa0044M19.10 protein.- Oryza sativa (japonica cultivar-group). | | | | |
| 13. | <u>Q61YF8_CAEBR</u> | Mass: 42917 | Score: 40 | Expect: 1.8e+02 | Queries matched |
| | Hypothetical protein CBG03560 (Fragment).- Caenorhabditis briggsae. | | | | |
| 14. | <u>Q65Y12_BUTFI</u> | Mass: 28424 | Score: 40 | Expect: 1.8e+02 | Queries matched |
| | Crotonase.- Butyrivibrio fibrisolvens. | | | | |
| 15. | <u>Q9DKH3_9HIV1</u> | Mass: 56188 | Score: 38 | Expect: 3.3e+02 | Queries matched |
| | Gag protein.- Human immunodeficiency virus 1. | | | | |
| 16. | <u>Q8T5H4_ANOGA</u> | Mass: 65837 | Score: 37 | Expect: 4e+02 | Queries matched: |
| | Putative sodium channel.- Anopheles gambiae (African malaria mosquito). | | | | |

Search Parameters

Type of search : Peptide Mass Fingerprint
 Enzyme : Trypsin
 Fixed modifications : Carboxymethyl (C)
 Variable modifications : Oxidation (M)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance : ± 1 Da
 Peptide Charge State : 1+
 Max Missed Cleavages : 1
 Number of queries : 9

Mascot: <http://www.matrixscience.com/>

{MATRIX} {SCIENCE} Mascot Search Results

Protein View

Match to: **Q7BU49_STRAM** Score: 57 Expect: 4.1
ArsR.- Streptomyces ambofaciens.

Nominal mass (M_r): 10524; Calculated pI value: 6.56

NCBI BLAST search of **Q7BU49_STRAM** against nr
 Unformatted sequence string for pasting into other applications

Taxonomy: Streptomyces ambofaciens
 Links to retrieve other entries containing this sequence from NCBI Entrez:
AAS72557 from Streptomyces ambofaciens

Fixed modifications: Carboxymethyl (C)
 Variable modifications: Oxidation (M)
 Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
 Number of mass values searched: 9
 Number of mass values matched: 5
 Sequence Coverage: 70%

Matched peptides shown in **Bold Red**

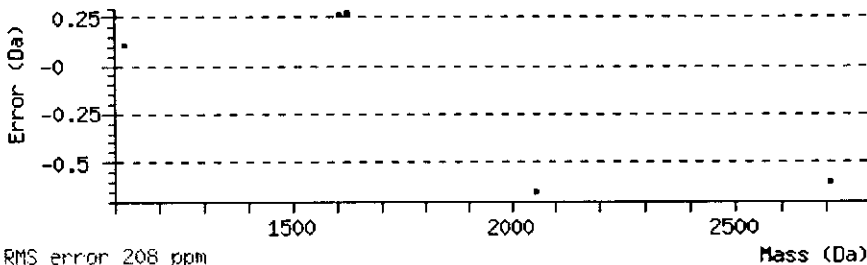
1 MGPLPGLPGI RASGEISVTT QSWENALTE MSRRHAEVSY VELSGVRFVD
51 VAGVTALAVT AMNLPGGRV VEQPPPQLPR VLELFWPSLN RIEVAPR

Show predicted peptides also

Sort Peptides By Residue Number Increasing Mass Decreasing Mass

| Start - End | Observed | Mr(expt) | Mr(calc) | Delta | Miss | Sequence |
|-------------|----------|----------|----------|-------|------|-----------------------------|
| 1 - 11 | 1123.74 | 1122.73 | 1122.62 | 0.11 | 0 | -.MGPLPGLPGIR.A Oxidation |
| 22 - 34 | 1608.02 | 1607.02 | 1606.75 | 0.26 | 1 | R.QSWENALTEMSRR.H |
| 22 - 34 | 1624.03 | 1623.02 | 1622.75 | 0.28 | 1 | R.QSWENALTEMSRR.H Oxidation |
| 48 - 68 | 2058.44 | 2057.43 | 2058.09 | -0.66 | 0 | R.FVDVAGVTALAVTAMNLPGGR.V |
| 69 - 91 | 2712.92 | 2711.91 | 2712.51 | -0.60 | 1 | R.VVVEQPPPQLPRVLELFWPSLNR.I |

No match to: 1143.77, 1414.90, 2404.70, 2728.91



>P1;Q7BU49_STRAM
 ArsR.- Streptomyces ambofaciens.
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 C;Species AAS72557: Streptomyces ambofaciens
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 C;NUCLEOTIDE SEQUENCE.

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R;Fischer G., Wenner T., Decaris B., Leblond P.;
Proc. Natl. Acad. Sci. U.S.A. 95:14296-14301(1998).
C;Reference [2]
C;NUCLEOTIDE SEQUENCE.
C;STRAIN=DSM40697;
C;PubMed=15292136; DOI=10.1128/JB.186.16.5355-5365.2004;
R;Roth V., Aigle B., Bunet R., Wenner T., Fourrier C., Decaris B., Leblond P.;
J. Bacteriol. 186:5355-5365(2004).
C;Reference [3]
C;NUCLEOTIDE SEQUENCE.
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R;Virginie R., Bertrand A., Bunet R., Wenner T., Fourrier C., Decaris B., Leblond P.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
C;05-JUL-2004 (TrEMBLrel. 27, Created)
C;05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
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C;Keywords:
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C;IDN_GENBANK AAS72557;

Mascot: <http://www.matrixscience.com/>