

Appendix II

Mascot search results

ของเมล็ดโปรตีนที่ 2

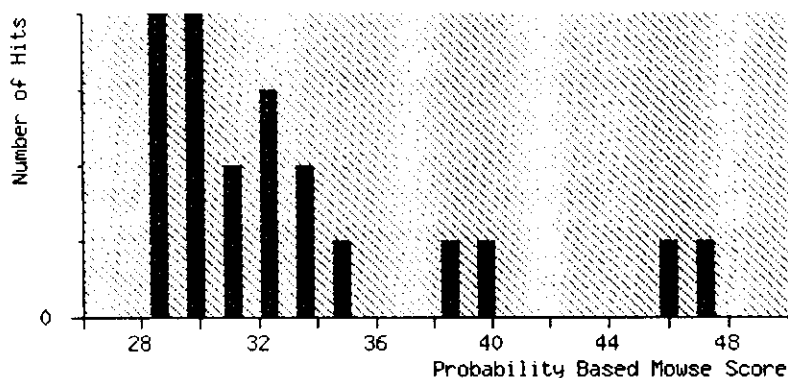
{MATRIX} Mascot Search Results

{SCIENCE}

User : Waraporn
 Email : waraporn.p@psu.ac.th
 Search title :
 Database : SwissProt 46.6 (232847 sequences; 105413441 residues)
 Timestamp : 13 May 2005 at 11:43:35 GMT
 Top Score : 47 for P14707, (YM3_STRCO) Mini-circle putative transposase for IS1:

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

 [oma AS](#)
 Concise Protein Summary

[Help](#)

 Significance threshold $p < 0.05$

 Max. number of hits 20
 [No Search All](#)
 [Search All Highlighted](#)

1.	P14707	Mass: 45868	Score: 47	Expect: 4.3	Queries matched: 7
	(YM3_STRCO) Mini-circle putative transposase for IS117 Mini-circle putative tra				
2.	P36975	Mass: 23960	Score: 46	Expect: 5.3	Queries matched: 7
	(SNP25_DROME) Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associ				
3.	P30317	Mass: 197692	Score: 40	Expect: 25	Queries matched: 12
	(DPOL_THELI) DNA polymerase (EC 2.7.7.7) (Vent DNA polymerase) [Contains: Endon				
	Q980Q9	Mass: 9664	Score: 40	Expect: 25	Queries matched: 4
	(RPOH_SULSO) DNA-directed RNA polymerase subunit H (EC 2.7.7.6) DNA-directed RN				
	Q9P429	Mass: 41445	Score: 35	Expect: 79	Queries matched: 6
	(AOX_VENIN) Alternative oxidase, mitochondrial precursor (EC 1.-.-.-) Alternati				
	O69242	Mass: 17228	Score: 34	Expect: 95	Queries matched: 4
	(HSPE_BRAJA) Small heat shock protein hspE Small heat shock protein hspE				
	P50461-00-00-00	Mass: 21883	Score: 32	Expect: 1.5e+02	Queries matched
	(CSR3_HUMAN) Splice isoform Displayed; Variant Displayed; Conflict Displayed;				
	P50462	Mass: 21809	Score: 32	Expect: 1.5e+02	Queries matched
	(CSR3_MOUSE) Cysteine and glycine-rich protein 3 (Cysteine-rich protein 3) (CR				

	<u>Q9X8I6</u>	Mass: 36874	Score: 32	Expect: 1.5e+02	Queries matched
	(TILS_STRCO) tRNA(Ile)-lysidine synthase (EC 6.3.4.-) (tRNA(Ile)-lysidine synth				
	<u>O85294</u>	Mass: 17823	Score: 31	Expect: 1.7e+02	Queries matched
	(ILVH_BUCAP) Acetolactate synthase small subunit (EC 2.2.1.6) (AHAS) (Acetohydr				
	<u>P55536</u>	Mass: 4848	Score: 31	Expect: 1.8e+02	Queries matched
	(Y4KR_RHISN) Very hypothetical 4.8 kDa protein y4kR Very hypothetical 4.8 kDa p				
	<u>Q9I4U3</u>	Mass: 51509	Score: 30	Expect: 2.4e+02	Queries matched
	(RMUC_PSEAE) DNA recombination protein rmuC homolog DNA recombination protein r				
	<u>Q7NEF6</u>	Mass: 45577	Score: 30	Expect: 2.6e+02	Queries matched
	(PROA_GLOVI) Gamma-glutamyl phosphate reductase (GPR) (EC 1.2.1.41) (Glutamate-				
	<u>Q9D9W0</u>	Mass: 38604	Score: 29	Expect: 3e+02	Queries matched:
	(CU056_MOUSE) Putative protein C21orf56 homolog Putative protein C21orf56 homol				
	<u>Q60334</u>	Mass: 16458	Score: 29	Expect: 3.1e+02	Queries matched
	(Y024_METJA) Hypothetical UPF0211 protein MJ0024 Hypothetical UPF0211 protein M				
	<u>O28856</u>	Mass: 17130	Score: 28	Expect: 3.4e+02	Queries matched
	(RISC_ARCFU) Riboflavin synthase (EC 2.5.1.9) Riboflavin synthase (EC 2.5.1.9)				
	<u>P52075</u>	Mass: 54358	Score: 28	Expect: 3.5e+02	Queries matched
	(GLCD_ECOLI) Glycolate oxidase subunit glcD Glycolate oxidase subunit glcD				
4.	<u>P49340</u>	Mass: 45683	Score: 38	Expect: 35	Queries matched: 7
	(WNT1_BOMMO) Wnt-1 protein precursor Wnt-1 protein precursor				
	<u>Q8R605</u>	Mass: 17811	Score: 29	Expect: 3e+02	Queries matched:
	(Y1490_FUSNN) Hypothetical UPF0168 protein FN1490 Hypothetical UPF0168 protein				
5.	<u>Q87T10</u>	Mass: 29989	Score: 35	Expect: 81	Queries matched: 5
	(RL2_VIBPA) 50S ribosomal protein L2 50S ribosomal protein L2				
6.	<u>Q74DK5</u>	Mass: 57339	Score: 33	Expect: 1.1e+02	Queries matched
	(G6PI_GEOSL) Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose i				
7.	<u>Q03357</u>	Mass: 29331	Score: 33	Expect: 1.2e+02	Queries matched
	(MSXA_BRARE) Homeobox protein MSH-A Homeobox protein MSH-A				
8.	<u>P23069</u>	Mass: 247981	Score: 32	Expect: 1.4e+02	Queries matched
	(POLG_POL2W) Genome polyprotein [Contains: Coat protein VP4 (P1A); Coat protein				
	<u>P06210</u>	Mass: 248109	Score: 32	Expect: 1.4e+02	Queries matched
	(POLG_POL2L) Genome polyprotein [Contains: Coat protein VP4 (P1A); Coat protein				
	<u>O83644</u>	Mass: 36209	Score: 32	Expect: 1.4e+02	Queries matched
	(MIAA_TREPA) tRNA delta(2)-isopentenylpyrophosphate transferase (EC 2.5.1.8) (I				
	<u>P42035</u>	Mass: 9257	Score: 31	Expect: 2e+02	Queries matched:
	(THIO_METTM) Probable Thioredoxin (Glutaredoxin-like protein) Probable Thioredo				
	<u>O08617-01-00-00</u>	Mass: 60916	Score: 30	Expect: 2.1e+02	Queries matched
	(PTPRR_RAT) Splice isoform 1; Variant Displayed; Conflict Displayed; from O0861				
	<u>Q62GJ4</u>	Mass: 24364	Score: 30	Expect: 2.3e+02	Queries matched
	(RL1_BURMA) 50S ribosomal protein L1 50S ribosomal protein L1				
	<u>Q63Q00</u>	Mass: 24364	Score: 30	Expect: 2.3e+02	Queries matched
	(RL1_BURPS) 50S ribosomal protein L1 50S ribosomal protein L1				
	<u>Q83FB6</u>	Mass: 7682	Score: 30	Expect: 2.4e+02	Queries matched
	(CSRA1_COXBU) Carbon storage regulator homolog 1 Carbon storage regulator homol				
	<u>P46251</u>	Mass: 16390	Score: 29	Expect: 2.7e+02	Queries matched
	(ADF1_MAIZE) Actin-depolymerizing factor 1 (ADF 1) (ZmABP1) (ZmADF1) Actin-depo				
	<u>Q9JYY0</u>	Mass: 44793	Score: 29	Expect: 2.9e+02	Queries matched
	(ISCS_NEIMB) Cysteine desulfurase (EC 2.8.1.7) (NifS protein homolog) Cysteine				
	<u>Q750A9</u>	Mass: 51188	Score: 29	Expect: 3e+02	Queries matched:
	(HOG1_ASHGO) Mitogen-activated protein kinase HOG1 (EC 2.7.1.37) (MAP kinase HO				
	<u>P61465</u>	Mass: 10834	Score: 29	Expect: 3.1e+02	Queries matched
	(Y3097_CORGL) Hypothetical UPF0161 protein Cgl3097.1/cg3430 Hypothetical UPF016				

9.	<u>Q9CB26</u> (CLPB_MYCLE) Chaperone clpB Chaperone clpB	Mass: 93208	Score: 32	Expect: 1.4e+02	Queries matched
10.	<u>P25558</u> (BUD3_YEAST) Bud site selection protein BUD3 Bud site selection protein BUD3	Mass: 185591	Score: 32	Expect: 1.4e+02	Queries matched
	<u>Q88R97</u> (SSUE_PSEPK) FMN reductase (EC 1.5.1.29) FMN reductase (EC 1.5.1.29)	Mass: 21558	Score: 31	Expect: 1.9e+02	Queries matched
11.	<u>P55691</u> (Y4WM_RHISN) Hypothetical protein y4wM precursor Hypothetical protein y4wM prec	Mass: 75052	Score: 31	Expect: 1.8e+02	Queries matched
12.	<u>Q82SV5</u> (Y2194_NITEU) Hypothetical UPF0307 protein NE2194 Hypothetical UPF0307 protein	Mass: 20657	Score: 31	Expect: 2e+02	Queries matched:
13.	<u>O72896</u> (V091_FOWPV) Protein FPV091 Protein FPV091	Mass: 77767	Score: 30	Expect: 2.4e+02	Queries matched
14.	<u>Q9P2N4-01-00-00</u> (ATS9_HUMAN) Splice isoform 2; Variant Displayed; Conflict Displayed; from Q9P2	Mass: 188820	Score: 30	Expect: 2.6e+02	Queries matched
	<u>Q7VB62</u> (DXR_PROMA) 1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267) (DXP	Mass: 45493	Score: 28	Expect: 3.4e+02	Queries matched
15.	<u>P11511-00-05-00</u> (CP19A_HUMAN) Splice isoform Displayed; Variant dbSNP:700519; Conflict Displaye	Mass: 58241	Score: 29	Expect: 2.7e+02	Queries matched
	<u>P11511-00-00-00</u> (CP19A_HUMAN) Splice isoform Displayed; Variant Displayed; Conflict Displayed;	Mass: 58236	Score: 29	Expect: 3e+02	Queries matched:
16.	<u>P05679</u> (YI32_AGRT7) Insertion element IS136 hypothetical 21.2 kDa protein Insertion el	Mass: 21631	Score: 29	Expect: 2.7e+02	Queries matched
17.	<u>P58694</u> (SYN_ECO57) Asparaginyl-tRNA synthetase (EC 6.1.1.22) (Asparagine--tRNA ligase)	Mass: 52682	Score: 29	Expect: 2.8e+02	Queries matched
	<u>P17242-00-00-00</u> (SYN_ECOLI) Splice isoform Displayed; Variant Displayed; Conflict Displayed; fr	Mass: 52638	Score: 29	Expect: 2.8e+02	Queries matched
18.	<u>P00813-00-28-00</u> (ADA_HUMAN) Splice isoform Displayed; Variant SCID-VAR_002237; Conflict Display	Mass: 40924	Score: 29	Expect: 2.9e+02	Queries matched
19.	<u>P38345</u> (YB9N_YEAST) Hypothetical 14.6 kDa protein in MRPL37-RIF1 intergenic region Hyp	Mass: 14665	Score: 29	Expect: 3.1e+02	Queries matched
20.	<u>P81831</u> (CAPP1_CHLRE) Phosphoenolpyruvate carboxylase 1 (EC 4.1.1.31) (PEP carboxylase	Mass: 109418	Score: 29	Expect: 3.2e+02	Queries matched

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 : 14

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

{MATRIX} {SCIENCE} Mascot Search Results

Protein View

Match to: P14707 Score: 47 Expect: 4.3

(YM3_STRCO) Mini-circle putative transposase for IS117 Mini-circle putative transposase

Nominal mass (M_r): 45868; Calculated pI value: 9.83

NCBI BLAST search of P14707 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Streptomyces coelicolor

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: 14
Number of mass values matched: 7
Sequence Coverage: 21%

Matched peptides shown in **Bold Red**

```

1 MWEDSLTVFC GIDWAERHHD VAIVDDTGTL LAKARITDDV AGYNKLLDLL
51 AEHGDSATP IPVAIETSHG LLVAALRTGS RKVFAINPLA AARYRDRHGV
101 SRKKSDFGDA LVLANILRTD MHAHRPLPAD SELAQAITVL ARAQQDAVWN
151 RQQVANQVRS LLREYPAAL HAFQSKDGGL TRPDARVILT MAPTPAKAAK
201 LTLAQLRAGL KRSGRTRAFN TEIERLRGIF RSEYARQLPA VEDAFGHQLL
251 ALLRQLDATC LAADDLAKAV EDAFREHADS EILLSPGLG PLLGARVLAE
301 IGDDRSRFTD ARALKSYAGS APITRASGRK HFVGRRFVKN NRLMNAGFLW
351 AFAALQASPG ANAHYRRRRE HGDWHAAAQR HLLNRFLGQL HHCLQTRQHF
401 DEQRAFAPLL QAAA
    
```

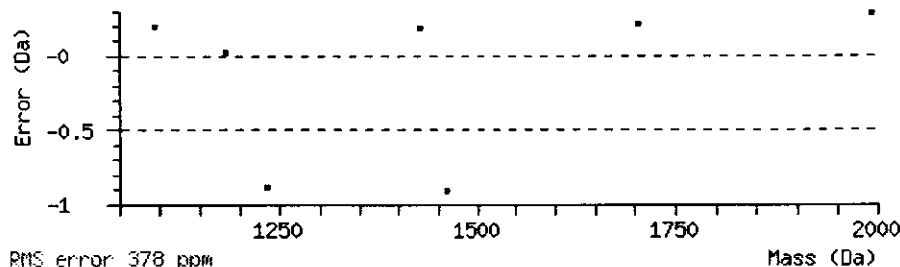
Show predicted peptides also

Sort Peptides By

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
18 - 33	1705.10	1704.09	1703.88	0.21	0	R.HHDVAIVDDTGTLLAK.A
36 - 45	1095.73	1094.72	1094.52	0.20	0	R.ITDDVAGYNK.L
83 - 95	1460.91	1459.91	1460.83	-0.92	1	K.VFAINPLAAARYR.D
160 - 176	1994.32	1993.32	1993.04	0.27	1	R.SLLREYYPALHAFQSK.D
187 - 200	1428.01	1427.00	1426.82	0.18	1	R.VILTMAPTPAKAAK.L Oxidation
201 - 211	1183.77	1182.77	1182.74	0.02	1	K.LTLAQLRAGLK.R
216 - 225	1235.74	1234.73	1235.63	-0.89	1	R.TRAFNTEIER.L

No match to: 1207.83, 1300.79, 1474.01, 1624.14, 1689.13, 1960.29, 1978.34



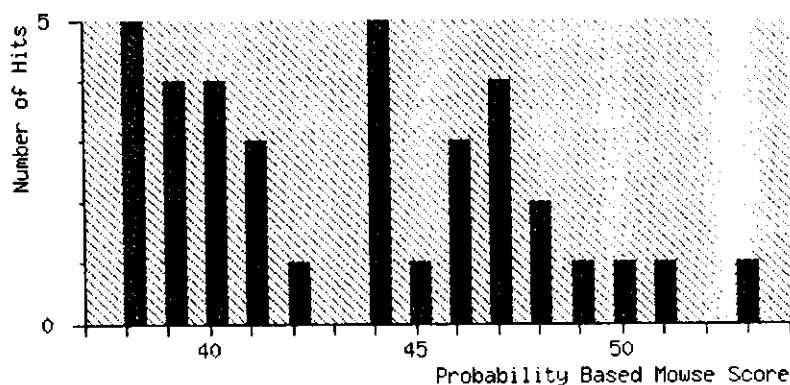
SWISS-PROT is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European

{MATRIX}
{SCIENCE} Mascot Search Results

User : Waraporn
 Email : waraporn.p@psu.ac.th
 Search title :
 Database : NCBI nr 20050501 (2452561 sequences; 830617002 residues)
 Timestamp : 13 May 2005 at 11:41:22 GMT
 Top Score : 53 for gi|722334, RNA6 [Grapevine leafroll virus-associated RNA6]

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

Concise Protein Summary

[Help](#)Significance threshold $p < 0.05$

Max. number of hits 20

No Search Hit

Search Unmatched

1.	gi 722334	Mass: 34467	Score: 53	Expect: 12	Queries matched: 8
	RNA6 [Grapevine leafroll virus-associated RNA6]				
	gi 39583033	Mass: 10211	Score: 45	Expect: 83	Queries matched: 4
	Hypothetical protein CBG18827 [Caenorhabditis briggsae]				
	gi 27377602	Mass: 25457	Score: 39	Expect: 3e+02	Queries matched:
	hypothetical protein bll2491 [Bradyrhizobium japonicum USDA 110]				
2.	gi 24461597	Mass: 41316	Score: 51	Expect: 18	Queries matched: 7
	conserved hypothetical plasmid protein [Pseudomonas aeruginosa]				
3.	gi 3881234	Mass: 13083	Score: 50	Expect: 26	Queries matched: 5
	Hypothetical protein Y63D3A.7 [Caenorhabditis elegans]				
4.	gi 20808796	Mass: 6306	Score: 49	Expect: 32	Queries matched: 5
	hypothetical protein TTE2436 [Thermoanaerobacter tengcongensis MB4]				
5.	gi 46133065	Mass: 15878	Score: 48	Expect: 40	Queries matched: 5
	COG3499: Phage protein U [Haemophilus influenzae R2866]				

6.	gi 50875611	Mass: 25768	Score: 48	Expect: 43	Queries matched: 7
	probable orotidine 5'-phosphate decarboxylase [Desulfotalea psychrophila LSV54]				
	gi 50911497	Mass: 20877	Score: 38	Expect: 3.7e+02	Queries matched
	hypothetical protein [Oryza sativa (japonica cultivar-group)]				
7.	gi 46444236	Mass: 34386	Score: 47	Expect: 45	Queries matched: 7
	hypothetical protein Ca019.12418 [Candida albicans SC5314]				
	gi 38106784	Mass: 11352	Score: 42	Expect: 1.5e+02	Queries matched
	hypothetical protein MG06177.4 [Magnaporthe grisea 70-15]				
8.	gi 3218352	Mass: 45868	Score: 47	Expect: 46	Queries matched: 7
	putative IS117 transposase [Streptomyces coelicolor A3(2)]				
9.	gi 45644671	Mass: 50683	Score: 47	Expect: 49	Queries matched: 7
	predicted acetyl-CoA carboxylase, biotin carboxylase [uncultured marine gamma p				
10.	gi 57086505	Mass: 54022	Score: 47	Expect: 51	Queries matched: 7
	PREDICTED: similar to Angiopoietin-related protein 3 precursor (Angiopoietin-li				
11.	gi 51951046	Mass: 23960	Score: 46	Expect: 56	Queries matched: 7
	CG40452-PA.3 [Drosophila melanogaster]				
12.	gi 58532667	Mass: 35119	Score: 46	Expect: 60	Queries matched: 7
	sphingosine kinase [Sphingomonas chungbukensis]				
13.	gi 27383374	Mass: 8477	Score: 46	Expect: 66	Queries matched: 4
	hypothetical protein bsr8263 [Bradyrhizobium japonicum USDA 110]				
14.	gi 42524362	Mass: 19200	Score: 45	Expect: 83	Queries matched: 6
	50S ribosomal protein L6 [Bdellovibrio bacteriovorus HD100]				
15.	gi 34452201	Mass: 162182	Score: 44	Expect: 89	Queries matched: 10
	three rows [Drosophila virilis]				
	gi 55823563	Mass: 9991	Score: 44	Expect: 1.1e+02	Queries matched
	hypothetical protein str1659 [Streptococcus thermophilus CNRZ1066]				
	gi 51893858	Mass: 54233	Score: 42	Expect: 1.6e+02	Queries matched
	transposase [Symbiobacterium thermophilum IAM 14863]				
	gi 48890477	Mass: 22634	Score: 40	Expect: 2.2e+02	Queries matched
	COG5635: Predicted NTPase (NACHT family) [Trichodesmium erythraeum IMS101]				
	gi 31747688	Mass: 10790	Score: 40	Expect: 2.5e+02	Queries matched
	Lfe142p1 [Leptospirillum ferrooxidans]				
16.	gi 55240814	Mass: 23925	Score: 44	Expect: 95	Queries matched: 6
	ENSANGP00000016957 [Anopheles gambiae str. PEST]				
17.	gi 20177105	Mass: 141702	Score: 44	Expect: 95	Queries matched: 10
	LD41783p [Drosophila melanogaster]				
18.	gi 14669786	Mass: 59997	Score: 44	Expect: 1e+02	Queries matched:
	marginal coil Xmc [Xenopus laevis]				
	gi 15897174	Mass: 9664	Score: 40	Expect: 2.6e+02	Queries matched
	DNA-directed RNA polymerase, subunit H (rpoH) [Sulfolobus solfataricus P2]				
19.	gi 28900178	Mass: 17822	Score: 44	Expect: 1e+02	Queries matched:
	hypothetical protein VPA0323 [Vibrio parahaemolyticus RIMD 2210633]				
20.	gi 53797873	Mass: 23628	Score: 42	Expect: 1.5e+02	Queries matched
	COG0237: Dephospho-CoA kinase [Chloroflexus aurantiacus]				

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 : 14

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

{MATRIX} Mascot Search Results
{SCIENCE}

Protein View

Match to: gi|722334 Score: 53 Expect: 12
 RNA6 [Grapevine leafroll virus-associated RNA6]

Nominal mass (M_r): 34467; Calculated pI value: 9.49
 NCBI BLAST search of gi|722334 against nr
 Unformatted sequence string for pasting into other applications

Taxonomy: Grapevine leafroll virus-associated RNA6

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: 14
 Number of mass values matched: 8
 Sequence Coverage: 27%

Matched peptides shown in Bold Red

```

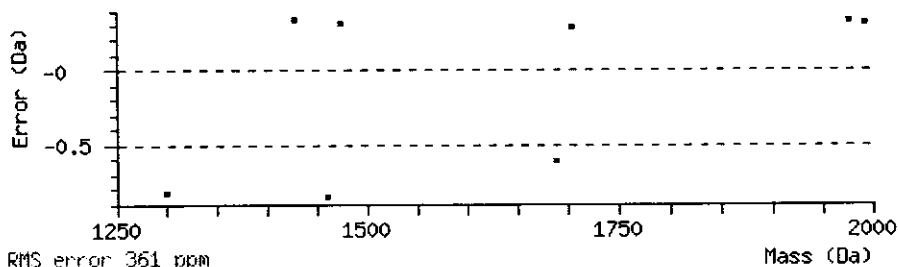
1  VILKYTGITM SQSALADLIL RSSLALQOGI FVKKEYGGYH AYQCANKKNI
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101 KLRKKQKSSV AASSVAKVSA WQREAEYRG AMSNKLEILE EKLSTSQRSS
151 ESESVMKSLQ RSIDSSASEL NEKLQVVMKR LNSITAE LRA LQASVETV GK
201 PNSVGDNGEG EARDMLESQT FVAMRTMIDA AYHSHRRQHE MYVSLEHLYR
251 IFGNPKITSK SPLILHTVEE LARASLKHRE LORKYTS LLE EYRHLTSVDY
301 GG
    
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Show predicted peptides also

Sort Peptides By Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
35 - 48	1689.13	1688.12	1688.73	-0.61	1	K.EYGGYHAYQCANKK.N
130 - 142	1460.91	1459.91	1460.75	-0.85	1	R.GAMSNKLEILEEK.L
162 - 179	1978.34	1977.33	1977.01	0.32	1	R.SIDSSASELNEKLQVVMK.R
162 - 179	1994.32	1993.32	1993.00	0.31	1	R.SIDSSASELNEKLQVVMK.R Oxidation
214 - 225	1428.01	1427.00	1426.66	0.34	0	R.DMLESQTFVAMR.T
226 - 236	1300.79	1299.78	1300.60	-0.82	0	R.TMIDAAYHSHR.R
226 - 237	1474.01	1473.00	1472.69	0.31	1	R.TMIDAAYHSHRR.Q Oxidation
238 - 250	1705.10	1704.09	1703.81	0.28	0	R.QHEMYVSLEHLYR.I

No match to: 1095.73, 1183.77, 1207.83, 1235.74, 1624.14, 1960.29



LOCUS AAB52903 302 aa linear VRL 07-JAN-2003
 DEFINITION RNA6 [Grapevine leafroll virus-associated RNA6].
 ACCESSION AAB52903
 VERSION AAB52903.1 GI:722334

DBSOURCE locus GLU22170 accession [U22170.1](#)
 KEYWORDS .
 SOURCE Grapevine leafroll virus-associated RNA6
 ORGANISM [Grapevine leafroll virus-associated RNA6](#)
 Viruses; Satellites; Satellite Nucleic Acids; unclassified
 Satellite Nucleic Acids.
 REFERENCE 1 (residues 1 to 302)
 AUTHORS Habili,N. and Rezaian,M.A.
 TITLE Cloning and molecular analysis of double-stranded RNA associated
 with grapevine leafroll disease
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 302)
 AUTHORS Habili,N.
 TITLE Direct Submission
 JOURNAL Submitted (05-MAR-1995) Div. of Horticulture, CSIRO, GPO Box 350,
 Adelaide, SA 5001, Australia
 COMMENT Method: conceptual translation.
 FEATURES Location/Qualifiers
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 /isolation_source="phloem tissue"
 /specific_host="grape, cv. Sultana"
 /db_xref="taxon:217616"
 /note="subgenomic RNA"
 Protein <1..302
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 CDS 1..302
 /coded_by="U22170.1:<1..909"

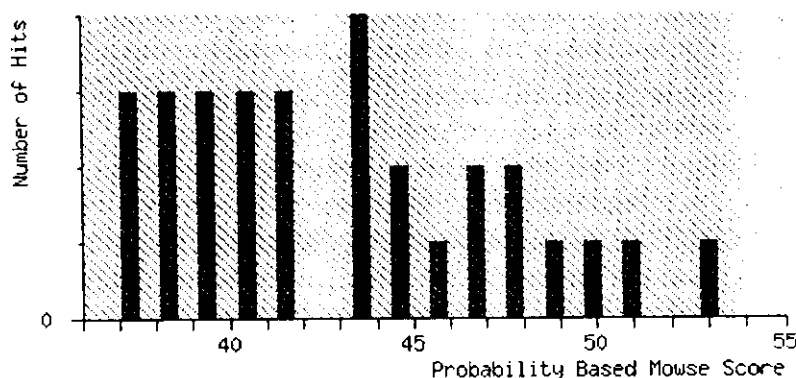
Mascot: <http://www.matrixscience.com/>

{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 11:27:53 GMT
 Top Score : 53 for Q67651_9VIRU, RNA6 (Fragment).- Grapevine leafroll virus-assoc

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 $p < 0.05$

Max. number of hits 20

Re-Search All**Search Unmatched**

- | | | | | | |
|----|---|-------------|-----------|-----------------|--------------------|
| 1. | <u>Q67651_9VIRU</u>
RNA6 (Fragment).- Grapevine leafroll virus-associated RNA6. | Mass: 34467 | Score: 53 | Expect: 9.7 | Queries matched: 8 |
| | <u>Q60X53_CAEBR</u>
Hypothetical protein CBG18827.- Caenorhabditis briggsae. | Mass: 10211 | Score: 45 | Expect: 66 | Queries matched: 4 |
| | <u>Q89SB4_BRAJA</u>
Bll12491 protein.- Bradyrhizobium japonicum. | Mass: 25457 | Score: 39 | Expect: 2.4e+02 | Queries matched: 1 |
| 2. | <u>Q8GQ36_PSEAE</u>
Conserved hypothetical plasmid protein.- Pseudomonas aeruginosa. | Mass: 41316 | Score: 51 | Expect: 14 | Queries matched: 7 |
| 3. | <u>T27273</u>
hypothetical protein Y63D3A.7 - Caenorhabditis elegans | Mass: 13083 | Score: 50 | Expect: 20 | Queries matched: 5 |
| 4. | <u>Q8R7H3_THETN</u>
Hypothetical protein.- Thermoanaerobacter tengcongensis. | Mass: 6306 | Score: 49 | Expect: 25 | Queries matched: 5 |
| | <u>AAM25571</u>
AE008691 NID: - Thermoanaerobacter tengcongensis MB4 | Mass: 6506 | Score: 48 | Expect: 30 | Queries matched: 5 |
| 5. | <u>Q6AQC2_DESPS</u>
Probable orotidine 5'-phosphate decarboxylase.- Desulfotalea psychrophila. | Mass: 25768 | Score: 48 | Expect: 34 | Queries matched: 7 |

	<u>Q6H6A2_ORYSA</u>	Mass: 20877	Score: 38	Expect: 2.9e+02	Queries matched
	Hypothetical protein P0708H12.27 (Hypothetical protein P0516F12.1).- <i>Oryza sativa</i>				
6.	<u>S06729</u>	Mass: 45868	Score: 47	Expect: 36	Queries matched: 7
	probable IS117 transposase - <i>Streptomyces coelicolor</i>				
7.	<u>Q6Q934_9GAMM</u>	Mass: 50683	Score: 47	Expect: 39	Queries matched: 7
	Predicted acetyl-CoA carboxylase, biotin carboxylase.- uncultured marine gamma				
	<u>Q8WNG9_PANTR</u>	Mass: 5141	Score: 38	Expect: 3.2e+02	Queries matched
	NPIP-like protein (Fragment).- Pan troglodytes (Chimpanzee).				
8.	<u>Q7PLV2_DROME</u>	Mass: 23960	Score: 46	Expect: 45	Queries matched: 7
	CG40452-PA.3.- <i>Drosophila melanogaster</i> (Fruit fly).				
	<u>Q5LJU6_DROME</u>	Mass: 17601	Score: 37	Expect: 3.5e+02	Queries matched
	CG40452-PB.3.- <i>Drosophila melanogaster</i> (Fruit fly).				
9.	<u>Q89BA1_BRAJA</u>	Mass: 8477	Score: 46	Expect: 52	Queries matched: 4
	Bsr8263 protein.- <i>Bradyrhizobium japonicum</i> .				
10.	<u>Q6MJ27_BDEBA</u>	Mass: 19200	Score: 45	Expect: 66	Queries matched: 6
	50S ribosomal protein L6.- <i>Bdellovibrio bacteriovorus</i> .				
11.	<u>Q6V3V8_DROVI</u>	Mass: 162182	Score: 44	Expect: 71	Queries matched: 10
	Three rows.- <i>Drosophila virilis</i> (Fruit fly).				
	<u>Q5LYB9_STRTR</u>	Mass: 9991	Score: 44	Expect: 85	Queries matched: 4
	Hypothetical protein.- <i>Streptococcus thermophilus</i> CNRZ1066.				
	<u>Q67KU1_SYMTH</u>	Mass: 54233	Score: 42	Expect: 1.3e+02	Queries matched
	Transposase.- <i>Symbiobacterium thermophilum</i> .				
	<u>Q7X1H3_9BACT</u>	Mass: 10790	Score: 40	Expect: 2e+02	Queries matched:
	Lfe142p1.- <i>Leptospirillum ferrooxidans</i> .				
12.	<u>Q7QA47_ANOGA</u>	Mass: 23925	Score: 44	Expect: 76	Queries matched: 6
	ENSANGP00000016957 (Fragment).- <i>Anopheles gambiae</i> str. PEST.				
13.	<u>Q8SWR4_DROME</u>	Mass: 141702	Score: 44	Expect: 76	Queries matched: 10
	LD41783p (Fragment).- <i>Drosophila melanogaster</i> (Fruit fly).				
	<u>Q7QXH2_GIALA</u>	Mass: 10740	Score: 38	Expect: 3.2e+02	Queries matched
	GLP_14_13300_13022.- <i>Giardia lamblia</i> ATCC 50803.				
	<u>Q6NIQ6_CORDI</u>	Mass: 13039	Score: 38	Expect: 3.5e+02	Queries matched
	Hypothetical protein.- <i>Corynebacterium diphtheriae</i> .				
14.	<u>Q90YY8_XENLA</u>	Mass: 59997	Score: 44	Expect: 79	Queries matched: 8
	Marginal coil Xmc.- <i>Xenopus laevis</i> (African clawed frog).				
	<u>B90164</u>	Mass: 9664	Score: 40	Expect: 2.1e+02	Queries matched
	DNA-directed RNA polymerase, subunit H (rpoH) [imported] - <i>Sulfolobus solfataricus</i>				
	<u>AAK40569</u>	Mass: 9864	Score: 40	Expect: 2.1e+02	Queries matched
	AE006641 NID: - <i>Sulfolobus solfataricus</i> P2				
15.	<u>Q87JD0_VIBPA</u>	Mass: 17822	Score: 44	Expect: 83	Queries matched: 5
	Hypothetical protein VPA0323.- <i>Vibrio parahaemolyticus</i> .				
	<u>Q6D1U3_ERWCT</u>	Mass: 13992	Score: 37	Expect: 3.7e+02	Queries matched
	Hypothetical protein.- <i>Erwinia carotovora</i> (subsp. atroseptica) (<i>Pectobacterium</i>				
16.	<u>Q5Z2W2_NOCHA</u>	Mass: 39486	Score: 41	Expect: 1.4e+02	Queries matched
	Hypothetical protein.- <i>Nocardia farcinica</i> .				
17.	<u>Q76Z18_9CAUD</u>	Mass: 35359	Score: 41	Expect: 1.5e+02	Queries matched
	Hypothetical protein.- Bacteriophage Aeh1.				
18.	<u>Q88QG0_PSEPK</u>	Mass: 25666	Score: 41	Expect: 1.5e+02	Queries matched
	Transcriptional regulator PfeR, putative.- <i>Pseudomonas putida</i> (strain KT2440).				
	<u>AAN66161</u>	Mass: 25866	Score: 41	Expect: 1.6e+02	Queries matched
	AE015451 NID: - <i>Pseudomonas putida</i> KT2440				

19.	<u>CAF01840</u>	Mass: 11017	Score: 41	Expect: 1.7e+02	Queries matched
	AX887702 NID: - Homo sapiens				
20.	<u>Q6PTE3_9BILA</u>	Mass: 22878	Score: 40	Expect: 1.8e+02	Queries matched
	Triosephosphate isomerase (Fragment).- Priapulus caudatus.				

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 : 14

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

{MATRIX} {SCIENCE} Mascot Search Results

Protein View

Match to: Q67651_9VIRU Score: 53 Expect: 9.7
 RNA6 (Fragment).- Grapevine leafroll virus-associated RNA6.

Nominal mass (M_r): 34467; Calculated pI value: 9.49

NCBI BLAST search of Q67651_9VIRU against nr
 Unformatted sequence string for pasting into other applications

Taxonomy: Grapevine leafroll virus-associated RNA6
 Links to retrieve other entries containing this sequence from NCBI Entrez:
AAB52903 from Grapevine leafroll virus-associated RNA6

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: 14
 Number of mass values matched: 8
 Sequence Coverage: 27%

Matched peptides shown in **Bold Red**

```

1 VILKYTGITM SQSALADLIL RSSLALQOGI FVKKEYGGYH AYQCANKKNI
51 FLYHNTGTGR VMIPIWDYDE SPGYKSLTQG AQYRFRVLRV SVIEEIFKEK
101 KLRKKQKSSV AASSVAKVSA WQREAETYRG AMSNKLEILE EKLSTSQRSS
151 ESESYMKSLQ RSIDSSASEL NEKLQVVMKR LNSITAE LRA LQASVETVGK
201 PNSVGDNGEG EARDMLESQT FVAMRTMIDA AYHSHRRQHE MYVSLEHLYR
251 IFGNPKITSK SPLILHTVEE LARASLKHRE LQRKYTSLE EYRHLTSVDY
301 GG
    
```

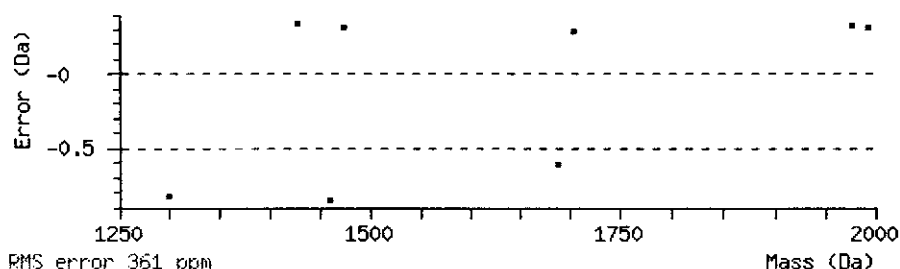
Show predicted peptides also

Sort Peptides By

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
35 - 48	1689.13	1688.12	1688.73	-0.61	1	K.EYGGYHAYQCANKK.N
130 - 142	1460.91	1459.91	1460.75	-0.85	1	R.GAMSNKLEILEEK.L
162 - 179	1978.34	1977.33	1977.01	0.32	1	R.SIDSSASELNEKLQVVMK.R
162 - 179	1994.32	1993.32	1993.00	0.31	1	R.SIDSSASELNEKLQVVMK.R Oxid
214 - 225	1428.01	1427.00	1426.66	0.34	0	R.DMLESQTFVAMR.T
226 - 236	1300.79	1299.78	1300.60	-0.82	0	R.TMIDAAYHSHR.R
226 - 237	1474.01	1473.00	1472.69	0.31	1	R.TMIDAAYHSHRR.Q Oxidation
238 - 250	1705.10	1704.09	1703.81	0.28	0	R.QHEMYVSLEHLYR.I

No match to: 1095.73, 1183.77, 1207.83, 1235.74, 1624.14, 1960.29



>P1;Q67651_9VIRU
 RNA6 (Fragment).- Grapevine leafroll virus-associated RNA6.

C;Species Q67651_9VIRU: Grapevine leafroll virus-associated RNA6.
C;Species AAB52903: Grapevine leafroll virus-associated RNA6
C;Family: Viruses; Satellites; Satellite Nucleic Acids; unclassified Satellite Nucleic Acids
C;Accession: Q67651;

C;Reference [1]
C;NUCLEOTIDE SEQUENCE.
R;Habibi N., Rezaian M.A.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
C;01-NOV-1996 (TrEMBLrel. 01, Created)
C;01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
C;01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
C;EMBL; U22170; AAB52903.1; -.
C;NON_TER 1 1
C;Keywords:
C;SRCDB TREMBL
C;IDN_GENBANK AAB52903;

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