Mascot Search Results

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User          : Ilya
Email         : toropygin@rambler.ru
Search title  : Submitted from Shidlovsky 080328 II by Mascot Daemon on P4P800SE
MS data file  : \\192.168.0.18\data on ultraflex-2\DATA\2008_Ilya\Shidlovsky\080328\001\0_J7\1\001__0_J7__1.dar
Database      : NCBInr 20070307 (4984280 sequences; 1723577896 residues)
Taxonomy      : Drosophila (fruit flies) (47828 sequences)
Timestamp     : 2 Apr 2008 at 19:34:01 GMT
Top Score     : 128 for gi|17137482, Origin recognition complex subunit 6 CG1584-PA [Drosophila melanogaster]
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Probability Based Mowse Score

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 59 are significant (p<0.05).

Score Distribution

Protein Summary Report

Format As	Protein Summary	Help
	Significance threshold p< 0.05	Max. number of hits 20

Overview Table

Click on column header to jump to entry in results list.
Move mouse over any indicator to highlight identical peptides.
Click on an indicator to see details of individual match.
Use check boxes to select sub-set of queries for new search.

Mouse over: -Query-

-Accession- -Sequence-

Hit:	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
☑ 1201.67 (1+)				?	?		?	?					?							
☑ 1209.61 (1+)	?	?	?			?	?	?		?	?	?		?	?		?	?	?	
☑ 1225.61 (1+)	?	?	?	?			?	?						?	?		?	?	?	
☑ 1414.71 (1+)	?	?		?	?	?		?		?	?				?					
☑ 1430.71 (1+)	?	?				?		?				?			?					
☑ 1462.72 (1+)	?	?						?	?	?	?				?	?				
☑ 1609.80 (1+)	?	?	?		?	?	?	?		?	?	?	?			?				?
☑ 1737.89 (1+)	?	?	?	?	?		?	?	?			?	?	?			?	?	?	
☑ 2045.01 (1+)	?	?	?						?	?	?					?	?	?	?	?
☑ 2663.37 (1+)	?	?															?	?	?	
☑ 2878.52 (1+)	?	?						?					?				?	?	?	

Select All   Select None   Search Selected

Index

	Accession	Mass	Score	Description
1.	gi|17137482	29220	128	Origin recognition complex subunit 6 CG1584-PA [Drosophila melanogaster]
2.	gi|5081630	29220	128	origin recognition complex subunit 6 [Drosophila melanogaster]
3.	gi|125808343	74578	47	GA11692-PA [Drosophila pseudoobscura]
4.	gi|125981065	35464	45	GA16538-PA [Drosophila pseudoobscura]
5.	gi|19920542	43668	42	Glutamate oxaloacetate transaminase 2 CG4233-PC, isoform C [Drosophila melanogaster]
6.	gi|41617892	16447	41	TPA: TPA_inf: HDC09438 [Drosophila melanogaster]
7.	gi|24580972	48142	40	Glutamate oxaloacetate transaminase 2 CG4233-PB, isoform B [Drosophila melanogaster]
8.	gi|24648595	514686	39	Dynein heavy chain at 93AB CG3723-PA [Drosophila melanogaster]
9.	gi|24652928	12308	38	CG13171-PA [Drosophila melanogaster]
10.	gi|116007482	123873	36	CG17665-PA, isoform A [Drosophila melanogaster]
11.	gi|25012218	124807	36	LD02622p [Drosophila melanogaster]
12.	gi|62862334	66917	35	CG17443-PB.3 [Drosophila melanogaster]
13.	gi|17933682	76201	35	small bristles CG1664-PA [Drosophila melanogaster]
14.	gi|37911738	27160	34	ACP29AB [Drosophila melanogaster]
15.	gi|24645951	59125	34	CG17230-PA, isoform A [Drosophila melanogaster]
16.	gi|24585597	21761	34	CG31627-PA [Drosophila melanogaster]
17.	gi|17737417	250151	33	crinkled CG7595-PB, isoform B [Drosophila melanogaster]
18.	gi|40882425	250169	33	SD18415p [Drosophila melanogaster]
19.	gi|125987181	249992	33	GA20466-PA [Drosophila pseudoobscura]
20.	gi|84912	3236	33	Cc gene smaller hypothetical protein - fruit fly (Drosophila melanogaster)

Results List

```
1.     gi|17137482     Mass: 29220     Score: 128     Expect: 7.6e-009  Queries matched: 10
       Origin recognition complex subunit 6 CG1584-PA [Drosophila melanogaster]
       Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
        1209.61   1208.60   1208.65 -36.80    113 -  122    1   R.KAEELMTLFK.G
        1225.61   1224.61   1224.64 -29.39    113 -  122    1   R.KAEELMTLFK.G + Oxidation (M)
        1414.71   1413.71   1413.73 -16.65     12 -   23    1   K.MGLREEPNVLEK.T
        1430.71   1429.70   1429.72 -17.82     12 -   23    1   K.MGLREEPNVLEK.T + Oxidation (M)
        1462.72   1461.72   1461.75 -20.52     35 -   47    0   R.STNVPLQINEYGK.I
        1609.80   1608.79   1608.79  -1.20    217 -  229    0   K.AHKPPPEDYEIWK.A
        1737.89   1736.88   1736.89  -2.97    216 -  229    1   K.KAHKPPPEDYEIWK.A
        2045.01   2044.00   2043.98   11.1    240 -  257    1   K.LKELEASQSHMDSQLLEA.- + Oxidation (M)
        2663.37   2662.37   2662.33   12.5    160 -  180    0   K.LMPFSNLRPSQFQLLEQQWER.M + Oxidation (M)
        2878.52   2877.51   2877.46   18.3    158 -  180    1   K.SKLMPFSNLRPSQFQLLEQQWER.M + Oxidation (M)
       No match to: 1201.67
```

```
2.     gi|5081630     Mass: 29220     Score: 128     Expect: 7.6e-009  Queries matched: 10
       origin recognition complex subunit 6 [Drosophila melanogaster]
       Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
        1209.61   1208.60   1208.65 -36.80    113 -  122    1   R.KAEELMTLFK.G
        1225.61   1224.61   1224.64 -29.39    113 -  122    1   R.KAEELMTLFK.G + Oxidation (M)
        1414.71   1413.71   1413.73 -16.65     12 -   23    1   K.MGLREEPNVLEK.T
        1430.71   1429.70   1429.72 -17.82     12 -   23    1   K.MGLREEPNVLEK.T + Oxidation (M)
        1462.72   1461.72   1461.75 -20.52     35 -   47    0   R.STNVPLQINEYGK.I
        1609.80   1608.79   1608.79  -1.20    217 -  229    0   K.AHKPPPEDYEIWK.A
        1737.89   1736.88   1736.89  -2.97    216 -  229    1   K.KAHKPPPEDYEIWK.A
        2045.01   2044.00   2043.98   11.1    240 -  257    1   K.LKELEASQSHMDSQLLEA.- + Oxidation (M)
        2663.37   2662.37   2662.33   12.5    160 -  180    0   K.LMPFSNLRPSQFQLLEQQWER.M + Oxidation (M)
        2878.52   2877.51   2877.46   18.3    158 -  180    1   K.SKLMPFSNLRPSQFQLLEQQWER.M + Oxidation (M)
       No match to: 1201.67
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3.     gi|125808343     Mass: 74578     Score: 47     Expect: 1.1  Queries matched: 5
       GA11692-PA [Drosophila pseudoobscura]
       Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
        1209.61   1208.60   1208.59   13.4      1 -   11    1   -.MGCMKWVGAVK.R
        1225.61   1224.61   1224.61  -6.10    287 -  297    0   R.ALTAPYPSYSR.A
        1609.80   1608.79   1608.80  -6.25     34 -   48    0   K.HGQCAFVPGICKPPR.V
        1737.89   1736.88   1736.90  -7.64     33 -   48    1   K.KHGQCAFVPGICKPPR.V
        2045.01   2044.00   2044.06 -28.79    153 -  169    1   R.NLCQFVLAIVPSPCDRK.F + 2 Propionamide (C)
       No match to: 1201.67, 1414.71, 1430.71, 1462.72, 2663.37, 2878.52
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4.     gi|125981065     Mass: 35464     Score: 45     Expect: 1.4  Queries matched: 4
       GA16538-PA [Drosophila pseudoobscura]
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        Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
         1201.67   1200.66   1200.65   9.11    291 -  301   1    K.ISAKCGDVIPK.L + Propionamide (C)
         1225.61   1224.61   1224.59   11.1    100 -  110   0    R.NFVGWPSFSGK.Q
         1414.71   1413.71   1413.76 -40.03    147 -  159   0    K.NVVELHGSGYVIK.C
         1737.89   1736.88   1736.95 -40.26    128 -  142   1    R.IQSVVTQNVDRLHTK.A
         No match to: 1209.61, 1430.71, 1462.72, 1609.80, 2045.01, 2663.37, 2878.52

   5.    gi|19920542     Mass: 43668     Score: 42     Expect: 3  Queries matched: 4
         Glutamate oxaloacetate transaminase 2 CG4233-PC, isoform C [Drosophila melanogaster]
        Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
         1201.67   1200.66   1200.66  -0.24    309 -  318   1    K.LMADRIIDVR.T
         1414.71   1413.71   1413.75 -32.09      2 -   15   0    M.GPPDAILGVTEAFK.K
         1609.80   1608.79   1608.77   13.1    148 -  162   0    K.DTCALDFGGLIEDLK.K
         1737.89   1736.88   1736.87   10.3    148 -  163   1    K.DTCALDFGGLIEDLKK.I
         No match to: 1209.61, 1225.61, 1430.71, 1462.72, 2045.01, 2663.37, 2878.52

   6.    gi|41617892     Mass: 16447     Score: 41     Expect: 4.1  Queries matched: 4
         TPA: TPA_inf: HDC09438 [Drosophila melanogaster]
        Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
         1209.61   1208.60   1208.68 -61.93     13 -   22   1    K.VHQKVVTGWR.N
         1414.71   1413.71   1413.66   33.7      1 -   12   0    -.MYFIYGPHVCGK.V
         1430.71   1429.70   1429.65   32.0      1 -   12   0    -.MYFIYGPHVCGK.V + Oxidation (M)
         1609.80   1608.79   1608.79   1.29     23 -   36   0    R.NLDAVLSTWSNYAR.N
         No match to: 1201.67, 1225.61, 1462.72, 1737.89, 2045.01, 2663.37, 2878.52

   7.    gi|24580972     Mass: 48142     Score: 40     Expect: 4.5  Queries matched: 5
         Glutamate oxaloacetate transaminase 2 CG4233-PB, isoform B [Drosophila melanogaster]
        Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
         1201.67   1200.66   1200.66  -0.24    347 -  356   1    K.LMADRIIDVR.T
         1209.61   1208.60   1208.66 -48.89      1 -   10   1    -.MSRTIIMTLK.D + Oxidation (M)
         1225.61   1224.61   1224.66 -41.33      1 -   10   1    -.MSRTIIMTLK.D + 2 Oxidation (M)
         1609.80   1608.79   1608.77   13.1    186 -  200   0    K.DTCALDFGGLIEDLK.K
         1737.89   1736.88   1736.87   10.3    186 -  201   1    K.DTCALDFGGLIEDLKK.I
         No match to: 1414.71, 1430.71, 1462.72, 2045.01, 2663.37, 2878.52

   8.    gi|24648595     Mass: 514686     Score: 39     Expect: 6.3  Queries matched: 9
         Dynein heavy chain at 93AB CG3723-PA [Drosophila melanogaster]
        Observed  Mr(expt)  Mr(calc)    ppm  Start     End Miss   Peptide
         1201.67   1200.66   1200.67  -5.68   1138 - 1148    1    R.KADEGLLQTVK.E
         1209.61   1208.60   1208.53   58.9    709 -   717    0    R.EVHYMQQMK.I + Oxidation (M)
         1225.61   1224.61   1224.53   65.1    709 -   717    0    R.EVHYMQQMK.I + 2 Oxidation (M)
         1414.71   1413.71   1413.77 -45.72   3860 - 3870    1    R.LCMIRALRPDR.M + Propionamide (C)
         1430.71   1429.70   1429.68   12.7   3871 - 3882    0    R.MTYALADFIEEK.L
         1462.72   1461.72   1461.65   46.3   3284 - 3294    0    K.FYEVYCDVEPK.R + Propionamide (C)
         1609.80   1608.79   1608.75   24.2   4241 - 4253    0    K.LPEEFNMVEIMNK.V + Oxidation (M)
         1737.89   1736.88   1736.87   9.56   4201 - 4214    1    R.AENIFRTVFEMQPR.D
         2878.52   2877.51   2877.60 -29.53   2657 - 2682    1    R.MTPNIVAATIALHNKCLQVFLPTAIK.S + Propionamide (C)
         No match to: 2045.01, 2663.37

   9.    gi|24652928     Mass: 12308     Score: 38     Expect: 7.2  Queries matched: 3
         CG13171-PA [Drosophila melanogaster]
        Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
         1462.72   1461.72   1461.73 -10.67     63 -   74   0    R.MELGLLCLQSER.N + Propionamide (C)
         1737.89   1736.88   1736.84   26.6     61 -   74   1    K.CRMELGLLCLQSER.N + Oxidation (M); Propionamide (C)
         2045.01   2044.00   2044.08 -39.11     63 -   79   1    R.MELGLLCLQSERNVQLK.G + Propionamide (C)
         No match to: 1201.67, 1209.61, 1225.61, 1414.71, 1430.71, 1609.80, 2663.37, 2878.52

   10.   gi|116007482     Mass: 123873    Score: 36     Expect: 12  Queries matched: 5
         CG17665-PA, isoform A [Drosophila melanogaster]
        Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
         1209.61   1208.60   1208.65 -40.01     85 -   94   1    K.TYRDVTLVSR.D
         1414.71   1413.71   1413.70   0.67    597 -  607   1    K.RNSYTWEAFLK.D
         1462.72   1461.72   1461.64   51.3     49 -   60   0    K.EMHDMLSQAVCK.E + Propionamide (C)
         1609.80   1608.79   1608.89 -59.58    444 -  457   0    K.QVIPNLQPLFESPK.L
         2045.01   2044.00   2044.08 -37.79    241 -  256   1    R.IPEFEQLWRDILFNPK.M
         No match to: 1201.67, 1225.61, 1430.71, 1737.89, 2663.37, 2878.52
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11.    gi|25012218     Mass: 124807    Score: 36     Expect: 13  Queries matched: 5
       LD02622p [Drosophila melanogaster]
      Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss  Peptide
       1209.61   1208.60   1208.65 -40.01    85 -   94   1   K.TYRDVTLVSR.D
       1414.71   1413.71   1413.70   0.67   597 -  607   1   K.RNSYTWEAFLK.D
       1462.72   1461.72   1461.64   51.3    49 -   60   0   K.EMHDMLSQAVCK.E + Propionamide (C)
       1609.80   1608.79   1608.89 -59.58   444 -  457   0   K.QVIPNLQPLFESPK.L
       2045.01   2044.00   2044.08 -37.79   241 -  256   1   R.IPEFEQLWRDILFNPK.M
       No match to: 1201.67, 1225.61, 1430.71, 1737.89, 2663.37, 2878.52

12.    gi|62862334     Mass: 66917     Score: 35     Expect: 14  Queries matched: 4
       CG17443-PB.3 [Drosophila melanogaster]
      Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss  Peptide
       1209.61   1208.60   1208.63 -21.37   394 -  403   1   R.IKEALEYESK.N
       1430.71   1429.70   1429.77 -48.77   351 -  362   1   R.AIDEIHHDKKPK.S
       1609.80   1608.79   1608.85 -36.95   254 -  267   0   K.LQFYINIASENIGK.M
       1737.89   1736.88   1736.95 -36.08   253 -  267   1   K.KLQFYINIASENIGK.M
       No match to: 1201.67, 1225.61, 1414.71, 1462.72, 2045.01, 2663.37, 2878.52

13.    gi|17933682     Mass: 76201     Score: 35     Expect: 17  Queries matched: 4
       small bristles CG1664-PA [Drosophila melanogaster]
      Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss  Peptide
       1201.67   1200.66   1200.62   36.2   431 -  440   1   R.LLNGEENRTR.N
       1609.80   1608.79   1608.81 -10.31   510 -  523   0   R.TYVVVPQNNGFCIR.N
       1737.89   1736.88   1736.86   16.0   444 -  458   1   K.YGRLACVSTLDEWPK.T
       2878.52   2877.51   2877.42   33.5   103 -  126   1   K.FGKLMPNSFGWYQVTLQNAQIYEK.E + Oxidation (M)
       No match to: 1209.61, 1225.61, 1414.71, 1430.71, 1462.72, 2045.01, 2663.37

14.    gi|37911738     Mass: 27160     Score: 34     Expect: 20  Queries matched: 3
       ACP29AB [Drosophila melanogaster]
      Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss  Peptide
       1209.61   1208.60   1208.64 -31.81   117 -  126   1   K.VGSRHFHIEK.N
       1225.61   1224.61   1224.52   67.8   225 -  234   0   K.SFVCQADQWA.- + Propionamide (C)
       1737.89   1736.88   1736.84   26.4    98 -  112   1   R.HHASNIEASNNIKMR.R + Oxidation (M)
       No match to: 1201.67, 1414.71, 1430.71, 1462.72, 1609.80, 2045.01, 2663.37, 2878.52

15.    gi|24645951     Mass: 59125     Score: 34     Expect: 21  Queries matched: 5
       CG17230-PA, isoform A [Drosophila melanogaster]
      Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss  Peptide
       1209.61   1208.60   1208.62 -15.98   128 -  137   1   K.LEMEAKLYGR.W
       1225.61   1224.61   1224.62  -8.85   128 -  137   1   K.LEMEAKLYGR.W + Oxidation (M)
       1414.71   1413.71   1413.72 -12.05   291 -  301   0   K.QISLCINMLHR.M + Oxidation (M); Propionamide (C)
       1430.71   1429.70   1429.68   12.8    64 -   75   1   R.DQQEKEAALNER.R
       1462.72   1461.72   1461.70   11.6   467 -  478   1   R.SEVDMQRLNQSR.S
       No match to: 1201.67, 1609.80, 1737.89, 2045.01, 2663.37, 2878.52

16.    gi|24585597     Mass: 21761     Score: 34     Expect: 21  Queries matched: 3
       CG31627-PA [Drosophila melanogaster]
      Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss  Peptide
       1462.72   1461.72   1461.69   16.5   110 -  121   1   K.DRIWDAIADEMK.A
       1609.80   1608.79   1608.82 -18.95    64 -   77   1   R.KTPITFSPSPEFMK.T
       2045.01   2044.00   2043.99   6.49   161 -  176   0   K.LFYSDNLLFLNHMFDR.E
       No match to: 1201.67, 1209.61, 1225.61, 1414.71, 1430.71, 1737.89, 2663.37, 2878.52

17.    gi|17737417     Mass: 250151    Score: 33     Expect: 22  Queries matched: 6
       crinkled CG7595-PB, isoform B [Drosophila melanogaster]
      Observed  Mr(expt)  Mr(calc)    ppm  Start     End Miss  Peptide
       1209.61   1208.60   1208.67 -55.94  1457 - 1465    1   K.YKWPLLFSR.F
       1225.61   1224.61   1224.59   14.4  1695 - 1703    1   R.SEELWRYSR.D
       1737.89   1736.88   1736.88  -0.40  1248 - 1262    0   K.KPIMLPITFMDGNTK.T + 2 Oxidation (M)
       2045.01   2044.00   2043.92   41.2  2032 - 2050    1   K.RSIVASYNQDGGMTSEDAK.V + Oxidation (M)
       2663.37   2662.37   2662.24   48.5  1584 - 1607    0   K.GDLIILEDESCGESVLNNGWCIGR.C + Propionamide (C)
       2878.52   2877.51   2877.51  -0.50   180 -  204    1   K.HSWIEQQILEANPILEAFGNAKTIR.N
       No match to: 1201.67, 1414.71, 1430.71, 1462.72, 1609.80

18.    gi|40882425     Mass: 250169    Score: 33     Expect: 23  Queries matched: 6
       SD18415p [Drosophila melanogaster]
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       Observed  Mr(expt)  Mr(calc)    ppm  Start    End  Miss   Peptide
        1209.61   1208.60   1208.67  -55.94  1457 - 1465    1    K.YKWPLLFSR.F
        1225.61   1224.61   1224.59    14.4  1695 - 1703    1    R.SEELWRYSR.D
        1737.89   1736.88   1736.88   -0.40  1248 - 1262    0    K.KPIMLPITFMDGNTK.T + 2 Oxidation (M)
        2045.01   2044.00   2043.92    41.2  2032 - 2050    1    K.RSIVASYNQDGGMTSEDAK.V + Oxidation (M)
        2663.37   2662.37   2662.24    48.5  1584 - 1607    0    K.GDLIILEDESCGESVLNNGWCIGR.C + Propionamide (C)
        2878.52   2877.51   2877.51   -0.50   180 -  204    1    K.HSWIEQQILEANPILEAFGNAKTIR.N
        No match to: 1201.67, 1414.71, 1430.71, 1462.72, 1609.80

19.     gi|125987181    Mass: 249992   Score: 33     Expect: 23  Queries matched: 6
        GA20466-PA [Drosophila pseudoobscura]
       Observed  Mr(expt)  Mr(calc)    ppm  Start    End  Miss   Peptide
        1209.61   1208.60   1208.67  -55.94  1457 - 1465    1    K.YKWPLLFSR.F
        1225.61   1224.61   1224.59    14.4  1696 - 1704    1    R.SEELWRYSR.D
        1737.89   1736.88   1736.88   -0.40  1248 - 1262    0    K.KPIMLPITFMDGNTK.T + 2 Oxidation (M)
        2045.01   2044.00   2043.92    41.2  2033 - 2051    1    K.RSIVASYNQDGGMTSEDAK.V + Oxidation (M)
        2663.37   2662.37   2662.24    48.5  1584 - 1607    0    K.GDLIILEDESCGESVLNNGWCIGR.C + Propionamide (C)
        2878.52   2877.51   2877.51   -0.50   180 -  204    1    K.HSWIEQQILEANPILEAFGNAKTIR.N
        No match to: 1201.67, 1414.71, 1430.71, 1462.72, 1609.80

20.     gi|84912    Mass: 3236     Score: 33     Expect: 25  Queries matched: 2
        Cc gene smaller hypothetical protein - fruit fly (Drosophila melanogaster)
       Observed  Mr(expt)  Mr(calc)   ppm  Start   End  Miss  Peptide
        1609.80   1608.79   1608.76   18.5     9 -   21    1   R.IGQMGSEWRFGWR.C
        2045.01   2044.00   2043.94   29.5     1 -   17    1   -.MAAQFFNRIGQMGSEWR.F + Oxidation (M)
        No match to: 1201.67, 1209.61, 1225.61, 1414.71, 1430.71, 1462.72, 1737.89, 2663.37, 2878.52
```

Search Parameters

```
Type of search          : Peptide Mass Fingerprint
Enzyme                  : Trypsin
Variable modifications : Oxidation (M),Propionamide (C)
Mass values             : Monoisotopic
Protein Mass            : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Peptide Charge State    : 1+
Max Missed Cleavages    : 1
Number of queries       : 11
```

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

Mascot Search Results

```
User            : Ilya
Email           : toropygin@rambler.ru
Search title    : Submitted from Shidlovsky 080324 II by Mascot Daemon on P4P800SE
MS data file    : \\192.168.0.18\data on ultraflex-2\DATA\2008_Ilya\Shidlovsky\080325\002\0_J12\1\002__0_J12__1.dar
Database        : NCBInr 20070307 (4984280 sequences; 1723577896 residues)
Taxonomy        : Drosophila (fruit flies) (47828 sequences)
Timestamp       : 3 Apr 2008 at 21:49:52 GMT
Top Score       : 123 for gi|21356877, CG7351-PA [Drosophila melanogaster]
```

Probability Based Mowse Score

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 59 are significant (p<0.05).

Score Distribution

Protein Summary Report

Format As	Protein Summary	Help
	Significance threshold p< 0.05	Max. number of hits 20

Overview Table

Click on column header to jump to entry in results list.
Move mouse over any indicator to highlight identical peptides.
Click on an indicator to see details of individual match.
Use check boxes to select sub-set of queries for new search.

Mouse over: -Query-

-Accession- -Sequence-

Hit:	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
☑ 807.43 (1+)									?	?	?	?	?		?		?	?		?
☑ 842.51 (1+)						?														
☑ 884.54 (1+)				?																
☑ 913.45 (1+)		?					?					?	?							
☑ 935.48 (1+)	?	?	?				?	?								?				
☑ 973.56 (1+)		?			?		?	?				?	?			?				
☑ 985.58 (1+)	?																			
☑ 988.55 (1+)	?															?				
☑ 995.53 (1+)					?						?	?	?		?					?
☑ 1009.58 (1+)																			?	
☑ 1021.61 (1+)	?		?																	
☑ 1033.51 (1+)																				
☑ 1036.56 (1+)		?			?		?	?						?		?				
☑ 1037.59 (1+)	?				?															
☑ 1098.49 (1+)																			?	

☑ 1109.54 (1+)																				
☑ 1114.49 (1+)																				
☑ 1170.86 (1+)	?																			
☑ 1174.57 (1+)		?																		
☑ 1179.58 (1+)			?			?										?			?	
☑ 1192.75 (1+)																				
☑ 1207.71 (1+)																				
☑ 1234.65 (1+)						?						?	?							
☑ 1267.67 (1+)	?										?				?		?	?		?
☑ 1277.70 (1+)				?	?															
☑ 1307.66 (1+)																				
☑ 1308.62 (1+)						?													?	
☑ 1323.66 (1+)									?	?				?						
☑ 1326.93 (1+)	?																			
☑ 1365.72 (1+)																				
☑ 1383.70 (1+)											?				?		?	?	?	?
☑ 1389.71 (1+)	?		?						?	?										
☑ 1392.71 (1+)		?			?		?	?	?	?	?			?	?	?			?	?
☑ 1407.80 (1+)	?				?							?	?							
☑ 1423.80 (1+)	?																			
☑ 1426.75 (1+)						?			?	?										
☑ 1437.74 (1+)	?	?	?		?		?	?								?				
☑ 1439.81 (1+)	?																?	?		
☑ 1441.69 (1+)																				
☑ 1461.74 (1+)		?		?			?	?											?	
☑ 1475.75 (1+)		?		?								?	?	?		?				
☑ 1493.71 (1+)				?								?	?				?	?		
☑ 1523.74 (1+)	?											?	?							
☑ 1557.70 (1+)									?	?										
☑ 1595.86 (1+)	?	?															?	?		
☑ 1638.85 (1+)						?														
☑ 1672.91 (1+)	?																		?	
☑ 1688.98 (1+)	?																			
☑ 1692.99 (1+)	?	?					?	?				?	?							
☑ 1707.77 (1+)																				
☑ 1716.83 (1+)									?	?	?				?	?				?
☑ 1744.97 (1+)	?																			
☑ 1794.84 (1+)				?															?	
☑ 1837.95 (1+)		?	?																	
☑ 1889.88 (1+)																				
☑ 1904.95 (1+)	?			?		?					?	?	?						?	
☑ 1926.89 (1+)		?					?	?				?	?				?	?	?	
☑ 1942.92 (1+)											?	?	?		?					?
☑ 1994.06 (1+)											?	?	?		?					?
☑ 2013.11 (1+)				?					?	?										
☑ 2150.16 (1+)																				
☑ 2211.10 (1+)			?						?	?	?				?					?
☑ 2225.12 (1+)			?	?							?				?		?	?		?
☑ 2284.20 (1+)	?													?						
☑ 2300.21 (1+)	?								?	?										

☑ 2357.12 (1+)		?					?	?				?	?						?	
☑ 2510.10 (1+)														?						
☑ 2705.09 (1+)																				
☑ 2788.25 (1+)					?															

Select All   Select None   Search Selected

Index

	Accession	Mass	Score	Description
1.	gi|21356877	45150	123	CG7351-PA [Drosophila melanogaster]
2.	gi|28572018	67234	60	CG31033-PC, isoform C [Drosophila melanogaster]
3.	gi|24644700	24259	48	CG31488-PA [Drosophila melanogaster]
4.	gi|24645344	49959	46	CG9356-PA, isoform A [Drosophila melanogaster]
5.	gi|46409138	41280	44	RE57519p [Drosophila melanogaster]
6.	gi|125986859	24518	43	GA21566-PA [Drosophila pseudoobscura]
7.	gi|28572022	48918	43	CG31033-PB, isoform B [Drosophila melanogaster]
8.	gi|28572020	45678	43	CG31033-PA, isoform A [Drosophila melanogaster]
9.	gi|34398667	68439	42	heat shock protein 68 [Drosophila simulans]
10.	gi|34420078	69192	42	heat shock protein 68 [Drosophila sechellia]
11.	gi|24645058	40088	42	steamer duck CG7954-PC, isoform C [Drosophila melanogaster]
12.	gi|13446608	135668	40	putative helicase Ski2 [Drosophila melanogaster]
13.	gi|17933658	135682	40	twister CG10210-PA [Drosophila melanogaster]
14.	gi|125806738	23562	40	GA17076-PA [Drosophila pseudoobscura]
15.	gi|17737847	38665	38	steamer duck CG7954-PA, isoform A [Drosophila melanogaster]
16.	gi|25012563	37492	38	RE37740p [Drosophila melanogaster]
17.	gi|2612998	44349	38	vermilion [Drosophila pallidosa]
18.	gi|2612996	44342	38	vermilion [Drosophila ananassae]
19.	gi|24640802	105649	37	CG32703-PA [Drosophila melanogaster]
20.	gi|24645056	39701	37	steamer duck CG7954-PB, isoform B [Drosophila melanogaster]

Results List

```
1.     gi|21356877     Mass: 45150    Score: 123    Expect: 2.4e-008  Queries matched: 22
       CG7351-PA [Drosophila melanogaster]
      Observed  Mr(expt)  Mr(calc)    ppm  Start   End Miss  Peptide
        935.48    934.48    934.44   43.4    156 - 163   1   R.ASEEDTKR.L
        985.58    984.57    984.56   14.1    298 - 305   0   R.DQELVLIR.S
        988.55    987.54    987.50   39.6    387 - 395   0   K.QNPFPSVSL.-
       1021.61   1020.60   1020.59   16.7    306 - 314   0   R.SGIYLLVEK.L
       1037.59   1036.58   1036.56   15.7    258 - 266   0   K.MLLGYLPSK.S + Oxidation (M)
       1170.86   1169.86   1169.78   65.6    248 - 257   0   R.LILIYLVPVK.M
       1267.67   1266.66   1266.68 -15.07    371 - 381   1   K.IKGYISHAHNK.L
       1326.93   1325.92   1325.88   31.7    247 - 257   1   K.RLILIYLVPVK.M
       1389.71   1388.70   1388.72 -11.15    286 - 297   1   K.AGNVNRFDEIVR.D
       1407.80   1406.79   1406.74   35.0    164 - 175   0   R.LGMMNLVNQLFK.I
       1423.80   1422.80   1422.74   42.0    164 - 175   0   R.LGMMNLVNQLFK.I + Oxidation (M)
       1437.74   1436.73   1436.72   9.11    200 - 211   0   K.DSFPLPEQITYK.Y
       1439.81   1438.80   1438.73   46.9    164 - 175   0   R.LGMMNLVNQLFK.I + 2 Oxidation (M)
       1523.74   1522.73   1522.74  -2.08    126 - 138   0   K.HCQGFTPGHVLEK.A + Propionamide (C)
       1595.86   1594.85   1594.83   11.1    163 - 175   1   K.RLGMMNLVNQLFK.I + 2 Oxidation (M)
       1672.91   1671.91   1671.86   26.6    272 - 285   0   R.YDLLLFLDLAMAMK.A + Oxidation (M)
       1688.98   1687.97   1687.86   67.2    272 - 285   0   R.YDLLLFLDLAMAMK.A + 2 Oxidation (M)
       1692.99   1691.98   1691.96   10.3     52 -  66   0   R.FLKPPLDEVVSAHLK.V
       1744.97   1743.97   1743.95   7.56    292 - 305   1   R.FDEIVRDQELVLIR.S
       1904.95   1903.95   1903.95  -4.66     32 -  47   0   R.DVHVQNHNLYIAQPEK.L
       2284.20   2283.20   2283.18   9.02    272 - 291   1   R.YDLLLFLDLAMAMKAGNVNR.F + Oxidation (M)
       2300.21   2299.20   2299.17   14.5    272 - 291   1   R.YDLLLFLDLAMAMKAGNVNR.F + 2 Oxidation (M)
       No match to: 807.43, 842.51, 884.54, 913.45, 973.56, 995.53, 1009.58, 1033.51, 1036.56, 1098.49, 1109.54, 1114.49,
       1174.57, 1179.58, 1192.75, 1207.71, 1234.65, 1277.70, 1307.66, 1308.62, 1323.66, 1365.72, 1383.70, 1392.71,
       1426.75, 1441.69, 1461.74, 1475.75, 1493.71, 1557.70, 1638.85, 1707.77, 1716.83, 1794.84, 1837.95, 1889.88,
       1926.89, 1942.92, 1994.06, 2013.11, 2150.16, 2211.10, 2225.12, 2357.12, 2510.10, 2705.09, 2788.25

2.     gi|28572018     Mass: 67234    Score: 60     Expect: 0.048  Queries matched: 14
       CG31033-PC, isoform C [Drosophila melanogaster]
      Observed  Mr(expt)  Mr(calc)    ppm  Start   End Miss  Peptide
        913.45    912.45    912.47 -29.04    185 - 191   1   R.LMQYKSK.D + Oxidation (M)
        935.48    934.48    934.48  -3.49    435 - 442   0   R.SIACIETK.F + Propionamide (C)
        973.56    972.55    972.50   50.7    213 - 220   1   K.RDLEDAVR.E
       1036.56   1035.55   1035.61 -53.82     37 -  45   0   R.LIDHVAQLK.A
       1174.57   1173.56   1173.52   34.1      1 -   9   0   -.MSTEEHVWR.A
       1392.71   1391.71   1391.75 -30.41    407 - 418   1   K.VMAAKYVQEPIK.V + Oxidation (M)
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        1437.74   1436.73   1436.76  -16.70   398 - 411   1    R.HTLTGHSGKVMAAK.Y
        1461.74   1460.73   1460.72    8.09   477 - 489   1    R.TEKQADDVLMPAK.I + Oxidation (M)
        1475.75   1474.74   1474.71    20.4    95 - 107   0    K.GENSQMIVDLNQK.V
        1595.86   1594.85   1594.86   -4.12   134 - 147   0    R.AEVQLLHSSLEELK.K
        1692.99   1691.98   1691.86    68.2   518 - 531   1    R.KNQVISTFTNEHFK.I
        1837.95   1836.95   1836.92    14.4   119 - 133   1    K.EHSLVEQQTNNNRLR.A
        1926.89   1925.88   1925.94  -29.61   310 - 325   1    K.ILMKFEAHENESHAVR.W + Oxidation (M)
        2357.12   2356.11   2356.12   -3.85   572 - 594   0    K.GHSTAVNAVSWSPNNNMLASVGK.N + Oxidation (M)
       No match to: 807.43, 842.51, 884.54, 985.58, 988.55, 995.53, 1009.58, 1021.61, 1033.51, 1037.59, 1098.49, 1109.54,
       1114.49, 1170.86, 1179.58, 1192.75, 1207.71, 1234.65, 1267.67, 1277.70, 1307.66, 1308.62, 1323.66, 1326.93,
       1365.72, 1383.70, 1389.71, 1407.80, 1423.80, 1426.75, 1439.81, 1441.69, 1493.71, 1523.74, 1557.70, 1638.85,
       1672.91, 1688.98, 1707.77, 1716.83, 1744.97, 1794.84, 1889.88, 1904.95, 1942.92, 1994.06, 2013.11, 2150.16,
       2211.10, 2225.12, 2284.20, 2300.21, 2510.10, 2705.09, 2788.25

  3.   gi|24644700     Mass: 24259     Score: 48      Expect: 0.71  Queries matched: 8
       CG31488-PA [Drosophila melanogaster]
       Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
         935.48    934.48    934.46    15.5     1 -   8   0    -.MTPVICGK.T + Oxidation (M); Propionamide (C)
        1021.61   1020.60   1020.54    66.0   104 - 111   1    R.FVEDRSLR.F
        1179.58   1178.57   1178.63  -47.37    23 -  32   1    K.AFSTLVEREK.L
        1389.71   1388.70   1388.74  -31.71     2 -  14   1    M.TPVICGKTSQTVR.S
        1437.74   1436.73   1436.70    24.3    33 -  45   0    K.LSPCEAAVSELYR.T
        1837.95   1836.95   1836.87    42.0   115 - 131   0    R.IIVDSSSMGVMGHMFAR.C
        2211.10   2210.10   2210.24  -62.58   185 - 203   1    R.YFIAFLPEKIIALESLSTR.R
        2225.12   2224.11   2224.04    34.5   115 - 134   1    R.IIVDSSSMGVMGHMFARCGR.W + Propionamide (C)
       No match to: 807.43, 842.51, 884.54, 913.45, 973.56, 985.58, 988.55, 995.53, 1009.58, 1033.51, 1036.56, 1037.59,
       1098.49, 1109.54, 1114.49, 1170.86, 1174.57, 1192.75, 1207.71, 1234.65, 1267.67, 1277.70, 1307.66, 1308.62,
       1323.66, 1326.93, 1365.72, 1383.70, 1392.71, 1407.80, 1423.80, 1426.75, 1439.81, 1441.69, 1461.74, 1475.75,
       1493.71, 1523.74, 1557.70, 1595.86, 1638.85, 1672.91, 1688.98, 1692.99, 1707.77, 1716.83, 1744.97, 1794.84,
       1889.88, 1904.95, 1926.89, 1942.92, 1994.06, 2013.11, 2150.16, 2284.20, 2300.21, 2357.12, 2510.10, 2705.09, 2788.25

  4.   gi|24645344     Mass: 49959     Score: 46      Expect: 1.3  Queries matched: 9
       CG9356-PA, isoform A [Drosophila melanogaster]
       Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
         884.54    883.53    883.54   -6.18    51 -  57   1    K.RPQLSRK.D
        1277.70   1276.70   1276.61    69.2    58 -  69   0    K.DSSVVQEAVMGR.K
        1461.74   1460.73   1460.67    42.1   211 - 221   1    R.DERNYFQAQYK.F
        1475.75   1474.74   1474.68    40.7    35 -  48   0    K.TESEIPASADVDNK.V
        1493.71   1492.71   1492.71   -1.77   382 - 395   0    K.LSSASTSPLCEAEK.Y + Propionamide (C)
        1794.84   1793.84   1793.77    38.5     2 -  18   1    M.EANESAMPGTDKSQACR.T
        1904.95   1903.95   1903.97  -13.73   400 - 416   0    R.ALEFISQPLMATDEAIR.A
        2013.11   2012.10   2012.09    4.54   160 - 177   1    R.DKNNLDIAVLVDQVSTLR.T
        2225.12   2224.11   2224.12   -4.30    71 -  91   0    K.TSTSSGHSSNLPLPGLHTLYR.R
       No match to: 807.43, 842.51, 913.45, 935.48, 973.56, 985.58, 988.55, 995.53, 1009.58, 1021.61, 1033.51, 1036.56,
       1037.59, 1098.49, 1109.54, 1114.49, 1170.86, 1174.57, 1179.58, 1192.75, 1207.71, 1234.65, 1267.67, 1307.66,
       1308.62, 1323.66, 1326.93, 1365.72, 1383.70, 1389.71, 1392.71, 1407.80, 1423.80, 1426.75, 1437.74, 1439.81,
       1441.69, 1523.74, 1557.70, 1595.86, 1638.85, 1672.91, 1688.98, 1692.99, 1707.77, 1716.83, 1744.97, 1837.95,
       1889.88, 1926.89, 1942.92, 1994.06, 2150.16, 2211.10, 2284.20, 2300.21, 2357.12, 2510.10, 2705.09, 2788.25

  5.   gi|46409138     Mass: 41280     Score: 44      Expect: 2  Queries matched: 9
       RE57519p [Drosophila melanogaster]
       Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
         973.56    972.55    972.51    43.1   352 - 359   1    K.KNIPTCNI.- + Propionamide (C)
         995.53    994.52    994.53  -10.93   293 - 300   1    K.KIYEEVSK.H
        1036.56   1035.55   1035.56   -9.13     2 -  10   0    M.LAHNLGFHK.K
        1037.59   1036.58   1036.56    18.9   343 - 350   0    K.SDLIYWIK.K
        1277.70   1276.70   1276.69    2.86   220 - 230   1    K.KGGQNWFISLK.S
        1392.71   1391.71   1391.78  -54.13   340 - 350   1    K.NLKSDLIYWIK.K
        1407.80   1406.79   1406.72    50.6   294 - 304   1    K.IYEEVSKHFQK.L
        1437.74   1436.73   1436.74   -8.87    13 -  24   1    R.LFSNMKAVLQDR.G + Oxidation (M)
        2788.25   2787.24   2787.32  -27.88   251 - 274   0    K.VADCICLMSMGHLESVPVDIHIYR.I + Oxidation (M); Propionamide (C)
       No match to: 807.43, 842.51, 884.54, 913.45, 935.48, 985.58, 988.55, 1009.58, 1021.61, 1033.51, 1098.49, 1109.54,
       1114.49, 1170.86, 1174.57, 1179.58, 1192.75, 1207.71, 1234.65, 1267.67, 1307.66, 1308.62, 1323.66, 1326.93,
       1365.72, 1383.70, 1389.71, 1423.80, 1426.75, 1439.81, 1441.69, 1461.74, 1475.75, 1493.71, 1523.74, 1557.70,
       1595.86, 1638.85, 1672.91, 1688.98, 1692.99, 1707.77, 1716.83, 1744.97, 1794.84, 1837.95, 1889.88, 1904.95,
       1926.89, 1942.92, 1994.06, 2013.11, 2150.16, 2211.10, 2225.12, 2284.20, 2300.21, 2357.12, 2510.10, 2705.09

  6.   gi|125986859     Mass: 24518     Score: 43      Expect: 2.3  Queries matched: 7
       GA21566-PA [Drosophila pseudoobscura]
       Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
         842.51    841.50    841.45    64.3   212 - 219   1    K.AAKAMHIT.-
        1179.58   1178.57   1178.56    11.5   179 - 188   0    R.GTDELICTTR.R + Propionamide (C)
        1234.65   1233.64   1233.62    16.8   190 - 200   1    R.SIDEVTESARK.G
        1308.62   1307.61   1307.64  -20.38   200 - 211   1    R.KGMDEISVQASK.A + Oxidation (M)
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         1426.75   1425.75   1425.66    63.4    73 -  85   1   K.SCFASERSTVDPK.T
         1638.85   1637.84   1637.84    3.19    88 - 100   1   R.QMVLKTNNLTFCR.N + Propionamide (C)
         1904.95   1903.95   1903.93    5.36    25 -  41   0   K.YPNPMTPSIIGTDVVER.Q + Oxidation (M)
        No match to: 807.43, 884.54, 913.45, 935.48, 973.56, 985.58, 988.55, 995.53, 1009.58, 1021.61, 1033.51, 1036.56,
        1037.59, 1098.49, 1109.54, 1114.49, 1170.86, 1174.57, 1192.75, 1207.71, 1267.67, 1277.70, 1307.66, 1323.66,
        1326.93, 1365.72, 1383.70, 1389.71, 1392.71, 1407.80, 1423.80, 1437.74, 1439.81, 1441.69, 1461.74, 1475.75,
        1493.71, 1523.74, 1557.70, 1595.86, 1672.91, 1688.98, 1692.99, 1707.77, 1716.83, 1744.97, 1794.84, 1837.95,
        1889.88, 1926.89, 1942.92, 1994.06, 2013.11, 2150.16, 2211.10, 2225.12, 2284.20, 2300.21, 2357.12, 2510.10,
        2705.09, 2788.25

  7.    gi|28572022    Mass: 48918    Score: 43     Expect: 2.3  Queries matched: 10
        CG31033-PB, isoform B [Drosophila melanogaster]
        Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
          913.45    912.45    912.47  -29.04    26 -  32   1   R.LMQYKSK.D + Oxidation (M)
          935.48    934.48    934.48   -3.49   276 - 283   0   R.SIACIETK.F + Propionamide (C)
          973.56    972.55    972.50    50.7    54 -  61   1   K.RDLEDAVR.E
         1036.56   1035.55   1035.48    68.7   229 - 236   0   R.VWTVMDNR.L + Oxidation (M)
         1392.71   1391.71   1391.75  -30.41   248 - 259   1   K.VMAAKYVQEPIK.V + Oxidation (M)
         1437.74   1436.73   1436.76  -16.70   239 - 252   1   R.HTLTGHSGKVMAAK.Y
         1461.74   1460.73   1460.72    8.09   318 - 330   1   R.TEKQADDVLMPAK.I + Oxidation (M)
         1692.99   1691.98   1691.86    68.2   359 - 372   1   R.KNQVISTFTNEHFK.I
         1926.89   1925.88   1925.94  -29.61   151 - 166   1   K.ILMKFEAHENESHAVR.W + Oxidation (M)
         2357.12   2356.11   2356.12   -3.85   413 - 435   0   K.GHSTAVNAVSWSPNNNMLASVGK.N + Oxidation (M)
        No match to: 807.43, 842.51, 884.54, 985.58, 988.55, 995.53, 1009.58, 1021.61, 1033.51, 1037.59, 1098.49, 1109.54,
        1114.49, 1170.86, 1174.57, 1179.58, 1192.75, 1207.71, 1234.65, 1267.67, 1277.70, 1307.66, 1308.62, 1323.66,
        1326.93, 1365.72, 1383.70, 1389.71, 1407.80, 1423.80, 1426.75, 1439.81, 1441.69, 1475.75, 1493.71, 1523.74,
        1557.70, 1595.86, 1638.85, 1672.91, 1688.98, 1707.77, 1716.83, 1744.97, 1794.84, 1837.95, 1889.88, 1904.95,
        1942.92, 1994.06, 2013.11, 2150.16, 2211.10, 2225.12, 2284.20, 2300.21, 2510.10, 2705.09, 2788.25

  8.    gi|28572020    Mass: 45678    Score: 43     Expect: 2.5  Queries matched: 9
        CG31033-PA, isoform A [Drosophila melanogaster]
        Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
          935.48    934.48    934.48   -3.49   250 - 257   0   R.SIACIETK.F + Propionamide (C)
          973.56    972.55    972.50    50.7    28 -  35   1   K.RDLEDAVR.E
         1036.56   1035.55   1035.48    68.7   203 - 210   0   R.VWTVMDNR.L + Oxidation (M)
         1392.71   1391.71   1391.75  -30.41   222 - 233   1   K.VMAAKYVQEPIK.V + Oxidation (M)
         1437.74   1436.73   1436.76  -16.70   213 - 226   1   R.HTLTGHSGKVMAAK.Y
         1461.74   1460.73   1460.72    8.09   292 - 304   1   R.TEKQADDVLMPAK.I + Oxidation (M)
         1692.99   1691.98   1691.86    68.2   333 - 346   1   R.KNQVISTFTNEHFK.I
         1926.89   1925.88   1925.94  -29.61   125 - 140   1   K.ILMKFEAHENESHAVR.W + Oxidation (M)
         2357.12   2356.11   2356.12   -3.85   387 - 409   0   K.GHSTAVNAVSWSPNNNMLASVGK.N + Oxidation (M)
        No match to: 807.43, 842.51, 884.54, 913.45, 985.58, 988.55, 995.53, 1009.58, 1021.61, 1033.51, 1037.59, 1098.49,
        1109.54, 1114.49, 1170.86, 1174.57, 1179.58, 1192.75, 1207.71, 1234.65, 1267.67, 1277.70, 1307.66, 1308.62,
        1323.66, 1326.93, 1365.72, 1383.70, 1389.71, 1407.80, 1423.80, 1426.75, 1439.81, 1441.69, 1475.75, 1493.71,
        1523.74, 1557.70, 1595.86, 1638.85, 1672.91, 1688.98, 1707.77, 1716.83, 1744.97, 1794.84, 1837.95, 1889.88,
        1904.95, 1942.92, 1994.06, 2013.11, 2150.16, 2211.10, 2225.12, 2284.20, 2300.21, 2510.10, 2705.09, 2788.25

  9.    gi|34398667    Mass: 68439    Score: 42     Expect: 3  Queries matched: 10
        heat shock protein 68 [Drosophila simulans]
        Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
          807.43    806.42    806.38    46.8   510 - 516   0   R.MLSEAEK.Y
         1323.66   1322.65   1322.64    10.8    69 -  79   1   R.FDDSKIQDDIK.H
         1389.71   1388.70   1388.72  -14.04   229 - 239   1   R.LVNHFAEEFKR.K
         1392.71   1391.71   1391.71   -1.37   558 - 569   1   K.NSILERCSETIK.W
         1426.75   1425.75   1425.74    4.05    74 -  84   1   K.IQDDIKHWPFK.V
         1557.70   1556.69   1556.78  -55.65   118 - 131   1   K.MKETAEAYLGTTVK.D + Oxidation (M)
         1716.83   1715.82   1715.79    14.8   586 - 599   1   K.LKEMEQFCSPIMTK.M + 2 Oxidation (M)
         2013.11   2012.10   2011.96    69.5   100 - 117   1   K.GADKCFSPEEISSMVLTK.M + Propionamide (C)
         2211.10   2210.10   2210.06    16.5   532 - 551   1   R.NQLETYVFAVKEAAENGGDR.I
         2300.21   2299.20   2299.24  -16.78   462 - 483   1   R.GVPKIDVTFDLDANGILNVTAK.E
        No match to: 842.51, 884.54, 913.45, 935.48, 973.56, 985.58, 988.55, 995.53, 1009.58, 1021.61, 1033.51, 1036.56,
        1037.59, 1098.49, 1109.54, 1114.49, 1170.86, 1174.57, 1179.58, 1192.75, 1207.71, 1234.65, 1267.67, 1277.70,
        1307.66, 1308.62, 1326.93, 1365.72, 1383.70, 1407.80, 1423.80, 1437.74, 1439.81, 1441.69, 1461.74, 1475.75,
        1493.71, 1523.74, 1595.86, 1638.85, 1672.91, 1688.98, 1692.99, 1707.77, 1744.97, 1794.84, 1837.95, 1889.88,
        1904.95, 1926.89, 1942.92, 1994.06, 2150.16, 2225.12, 2284.20, 2357.12, 2510.10, 2705.09, 2788.25

 10.    gi|34420078    Mass: 69192    Score: 42     Expect: 3.2  Queries matched: 10
        heat shock protein 68 [Drosophila sechellia]
        Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
          807.43    806.42    806.38    46.8   510 - 516   0   R.MLSEAEK.Y
         1323.66   1322.65   1322.64    10.8    69 -  79   1   R.FDDSKIQDDIK.H
         1389.71   1388.70   1388.72  -14.04   229 - 239   1   R.LVNHFAEEFKR.K
         1392.71   1391.71   1391.71   -1.37   558 - 569   1   K.NSILERCSETIK.W
         1426.75   1425.75   1425.74    4.05    74 -  84   1   K.IQDDIKHWPFK.V
         1557.70   1556.69   1556.78  -55.65   118 - 131   1   K.MKETAEAYLGTTVK.D + Oxidation (M)
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          1716.83   1715.82   1715.79    14.8    586 - 599   1   K.LKEMEQFCSPIMTK.M + 2 Oxidation (M)
          2013.11   2012.10   2011.96    69.5    100 - 117   1   K.GADKCFSPEEISSMVLTK.M + Propionamide (C)
          2211.10   2210.10   2210.06    16.5    532 - 551   1   R.NQLETYVFAVKEAAENGGDR.I
          2300.21   2299.20   2299.24  -16.78    462 - 483   1   R.GVPKIDVTFDLDANGILNVTAK.E
         No match to: 842.51, 884.54, 913.45, 935.48, 973.56, 985.58, 988.55, 995.53, 1009.58, 1021.61, 1033.51, 1036.56,
         1037.59, 1098.49, 1109.54, 1114.49, 1170.86, 1174.57, 1179.58, 1192.75, 1207.71, 1234.65, 1267.67, 1277.70,
         1307.66, 1308.62, 1326.93, 1365.72, 1383.70, 1407.80, 1423.80, 1437.74, 1439.81, 1441.69, 1461.74, 1475.75,
         1493.71, 1523.74, 1595.86, 1638.85, 1672.91, 1688.98, 1692.99, 1707.77, 1744.97, 1794.84, 1837.95, 1889.88,
         1904.95, 1926.89, 1942.92, 1994.06, 2150.16, 2225.12, 2284.20, 2357.12, 2510.10, 2705.09, 2788.25

  11.    gi|24645058      Mass: 40088      Score: 42      Expect: 3.2   Queries matched: 11
         steamer duck CG7954-PC, isoform C [Drosophila melanogaster]
        Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
           807.43    806.42    806.38    54.9    108 - 113   0   R.CQLCAK.E + 2 Propionamide (C)
           995.53    994.52    994.48    43.5    114 - 122   0   K.ELADCGFIK.N
          1267.67   1266.66   1266.64    19.9    138 - 148   1   K.AEITGRYVCQK.C
          1383.70   1382.69   1382.64    37.3    324 - 333   1   K.CYDRFPNELR.R + Propionamide (C)
          1392.71   1391.71   1391.66    36.1    232 - 242   0   K.HWHVEHFVCAK.C
          1716.83   1715.82   1715.77    26.7    205 - 218   1   R.CHDKMGIPICGACR.R + 3 Propionamide (C)
          1904.95   1903.95   1903.87    39.4      6 -  23   0   K.AEVVQAANMSLGAMHCTR.C + Oxidation (M)
          1942.92   1941.91   1941.97  -29.97    209 - 224   1   K.MGIPICGACRRPIEER.V + 2 Propionamide (C)
          1994.06   1993.05   1992.95    49.3    188 - 204   0   K.SRPGLAANDMNELYCLR.C + Propionamide (C)
          2211.10   2210.10   2209.95    65.0    291 - 309   1   K.AWCVHHFACSVCDTKMTQK.S + Oxidation (M)
          2225.12   2224.11   2223.98    60.4     96 - 113   1   K.AMSASWHPQCFRCQLCAK.E + Oxidation (M); 2 Propionamide (C)
         No match to: 842.51, 884.54, 913.45, 935.48, 973.56, 985.58, 988.55, 1009.58, 1021.61, 1033.51, 1036.56, 1037.59,
         1098.49, 1109.54, 1114.49, 1170.86, 1174.57, 1179.58, 1192.75, 1207.71, 1234.65, 1277.70, 1307.66, 1308.62,
         1323.66, 1326.93, 1365.72, 1389.71, 1407.80, 1423.80, 1426.75, 1437.74, 1439.81, 1441.69, 1461.74, 1475.75,
         1493.71, 1523.74, 1557.70, 1595.86, 1638.85, 1672.91, 1688.98, 1692.99, 1707.77, 1744.97, 1794.84, 1837.95,
         1889.88, 1926.89, 2013.11, 2150.16, 2284.20, 2300.21, 2357.12, 2510.10, 2705.09, 2788.25

  12.    gi|13446608      Mass: 135668     Score: 40      Expect: 4.8   Queries matched: 15
         putative helicase Ski2 [Drosophila melanogaster]
        Observed  Mr(expt)  Mr(calc)    ppm  Start     End Miss   Peptide
           807.43    806.42    806.40    32.9    479 -  485   1   K.EMQGKAK.G + Oxidation (M)
           913.45    912.45    912.50  -60.83   1167 - 1175   0   R.IGNPGLQSK.M
           973.56    972.55    972.59  -38.41    871 -  879   0   K.AIDIISITK.S
           995.53    994.52    994.49    32.2    633 -  640   1   K.KFDGLEMR.N
          1234.65   1233.64   1233.63    6.59    486 -  498   1   K.GGGGGPRNHLNAK.Q
          1407.80   1406.79   1406.78    9.73    304 -  315   1   R.DLTRTIYTSPIK.A
          1475.75   1474.74   1474.68    37.5      1 -   12   1   -.MNEIRGEDNLER.L
          1493.71   1492.71   1492.74  -21.21    179 -  192   1   K.LTRSEETSSTGTPK.S
          1523.74   1522.73   1522.83  -66.37    548 -  560   1   K.GAVQKFFLQCLAK.L + Propionamide (C)
          1692.99   1691.98   1691.96    8.36    698 -  711   1   R.YAVILTCLRIESIK.V + Propionamide (C)
          1904.95   1903.95   1903.99  -23.77    274 -  290   1   K.LEQRQYVFVAAHTSAGK.T
          1926.89   1925.88   1926.00  -61.59    853 -  870   0   R.NMTFQPVGIGGHTVLDIK.A
          1942.92   1941.91   1942.00  -44.58    853 -  870   0   R.NMTFQPVGIGGHTVLDIK.A + Oxidation (M)
          1994.06   1993.05   1992.93    62.2    233 -  249   0   K.SDWAEMVDISQPINNFK.E
          2357.12   2356.11   2356.13   -6.98    634 -  653   1   K.FDGLEMRNLKPGEYIQMAGR.A + 2 Oxidation (M)
         No match to: 842.51, 884.54, 935.48, 985.58, 988.55, 1009.58, 1021.61, 1033.51, 1036.56, 1037.59, 1098.49, 1109.54,
         1114.49, 1170.86, 1174.57, 1179.58, 1192.75, 1207.71, 1267.67, 1277.70, 1307.66, 1308.62, 1323.66, 1326.93,
         1365.72, 1383.70, 1389.71, 1392.71, 1423.80, 1426.75, 1437.74, 1439.81, 1441.69, 1461.74, 1557.70, 1595.86,
         1638.85, 1672.91, 1688.98, 1707.77, 1716.83, 1744.97, 1794.84, 1837.95, 1889.88, 2013.11, 2150.16, 2211.10,
         2225.12, 2284.20, 2300.21, 2510.10, 2705.09, 2788.25

  13.    gi|17933658      Mass: 135682     Score: 40      Expect: 4.8   Queries matched: 15
         twister CG10210-PA [Drosophila melanogaster]
        Observed  Mr(expt)  Mr(calc)    ppm  Start     End Miss   Peptide
           807.43    806.42    806.40    32.9    479 -  485   1   K.EMQGKAK.G + Oxidation (M)
           913.45    912.45    912.50  -60.83   1167 - 1175   0   R.IGNPGLQSK.M
           973.56    972.55    972.59  -38.41    871 -  879   0   K.AIDIISITK.S
           995.53    994.52    994.49    32.2    633 -  640   1   K.KFDGLEMR.N
          1234.65   1233.64   1233.63    6.59    486 -  498   1   K.GGGGGPRNHLNAK.Q
          1407.80   1406.79   1406.78    9.73    304 -  315   1   R.DLTRTIYTSPIK.A
          1475.75   1474.74   1474.68    37.5      1 -   12   1   -.MNEIRGEDNLER.L
          1493.71   1492.71   1492.74  -21.21    179 -  192   1   K.LTRSEETSSTGTPK.S
          1523.74   1522.73   1522.83  -66.37    548 -  560   1   K.GAVQKFFLQCLAK.L + Propionamide (C)
          1692.99   1691.98   1691.96    8.36    698 -  711   1   R.YAVILTCLRIESIK.V + Propionamide (C)
          1904.95   1903.95   1903.99  -23.77    274 -  290   1   K.LEQRQYVFVAAHTSAGK.T
          1926.89   1925.88   1926.00  -61.59    853 -  870   0   R.NMTFQPVGIGGHTVLDIK.A
          1942.92   1941.91   1942.00  -44.58    853 -  870   0   R.NMTFQPVGIGGHTVLDIK.A + Oxidation (M)
          1994.06   1993.05   1992.93    62.2    233 -  249   0   K.SDWAEMVDISQPINNFK.E
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       2357.12    2356.11    2356.13    -6.98    634 -  653   1   K.FDGLEMRNLKPGEYIQMAGR.A + 2 Oxidation (M)
      No match to: 842.51, 884.54, 935.48, 985.58, 988.55, 1009.58, 1021.61, 1033.51, 1036.56, 1037.59, 1098.49, 1109.54,
      1114.49, 1170.86, 1174.57, 1179.58, 1192.75, 1207.71, 1267.67, 1277.70, 1307.66, 1308.62, 1323.66, 1326.93,
      1365.72, 1383.70, 1389.71, 1392.71, 1423.80, 1426.75, 1437.74, 1439.81, 1441.69, 1461.74, 1557.70, 1595.86,
      1638.85, 1672.91, 1688.98, 1707.77, 1716.83, 1744.97, 1794.84, 1837.95, 1889.88, 2013.11, 2150.16, 2211.10,
      2225.12, 2284.20, 2300.21, 2510.10, 2705.09, 2788.25

14.   gi|125806738     Mass: 23562     Score: 40     Expect: 4.9  Queries matched: 6
      GA17076-PA [Drosophila pseudoobscura]
      Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
       1036.56    1035.55    1035.50    51.6    131 -  139   1   K.KEEGEAFAR.E
       1323.66    1322.65    1322.70   -39.23    20 -   30   1   K.SCLLLQFTDKR.F
       1392.71    1391.71    1391.65    39.9    140 -  151   0   R.EHGLVFMETSAR.T + Oxidation (M)
       1475.75    1474.74    1474.83   -58.90    78 -   91   1   R.GAAGALLVYDITRR.E
       2284.20    2283.20    2283.22    -9.80     9 -   29   1   K.YIIIGDTGVGKSCLLLQFTDK.R
       2510.10    2509.09    2509.11    -6.61   187 -  213   0   K.IGQQHSPTNPSLPGSGGAAGAANSGCC.- + Propionamide (C)
      No match to: 807.43, 842.51, 884.54, 913.45, 935.48, 973.56, 985.58, 988.55, 995.53, 1009.58, 1021.61, 1033.51,
      1037.59, 1098.49, 1109.54, 1114.49, 1170.86, 1174.57, 1179.58, 1192.75, 1207.71, 1234.65, 1267.67, 1277.70,
      1307.66, 1308.62, 1326.93, 1365.72, 1383.70, 1389.71, 1407.80, 1423.80, 1426.75, 1437.74, 1439.81, 1441.69,
      1461.74, 1493.71, 1523.74, 1557.70, 1595.86, 1638.85, 1672.91, 1688.98, 1692.99, 1707.77, 1716.83, 1744.97,
      1794.84, 1837.95, 1889.88, 1904.95, 1926.89, 1942.92, 1994.06, 2013.11, 2150.16, 2211.10, 2225.12, 2300.21,
      2357.12, 2705.09, 2788.25

15.   gi|17737847     Mass: 38665     Score: 38     Expect: 7.1  Queries matched: 10
      steamer duck CG7954-PA, isoform A [Drosophila melanogaster]
      Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
        807.43     806.42     806.38    54.9     95 -  100   0   R.CQLCAK.E + 2 Propionamide (C)
        995.53     994.52     994.48    43.5    101 -  109   0   K.ELADCGFIK.N
       1267.67    1266.66    1266.64    19.9    125 -  135   1   K.AEITGRYVCQK.C
       1383.70    1382.69    1382.64    37.3    311 -  320   1   K.CYDRFPNELR.R + Propionamide (C)
       1392.71    1391.71    1391.66    36.1    219 -  229   0   K.HWHVEHFVCAK.C
       1716.83    1715.82    1715.77    26.7    192 -  205   1   R.CHDKMGIPICGACR.R + 3 Propionamide (C)
       1942.92    1941.91    1941.97   -29.97   196 -  211   1   K.MGIPICGACRRPIEER.V + 2 Propionamide (C)
       1994.06    1993.05    1992.95    49.3    175 -  191   0   K.SRPGLAANDMNELYCLR.C + Propionamide (C)
       2211.10    2210.10    2209.96    63.9      2 -   20   1   M.SLGAMHCTRCADGFEPTEK.I + Oxidation (M); 2 Propionamide (C)
       2225.12    2224.11    2223.98    60.4     83 -  100   1   K.AMSASWHPQCFRCQLCAK.E + Oxidation (M); 2 Propionamide (C)
      No match to: 842.51, 884.54, 913.45, 935.48, 973.56, 985.58, 988.55, 1009.58, 1021.61, 1033.51, 1036.56, 1037.59,
      1098.49, 1109.54, 1114.49, 1170.86, 1174.57, 1179.58, 1192.75, 1207.71, 1234.65, 1277.70, 1307.66, 1308.62,
      1323.66, 1326.93, 1365.72, 1389.71, 1407.80, 1423.80, 1426.75, 1437.74, 1439.81, 1441.69, 1461.74, 1475.75,
      1493.71, 1523.74, 1557.70, 1595.86, 1638.85, 1672.91, 1688.98, 1692.99, 1707.77, 1744.97, 1794.84, 1837.95,
      1889.88, 1904.95, 1926.89, 2013.11, 2150.16, 2284.20, 2300.21, 2357.12, 2510.10, 2705.09, 2788.25

16.   gi|25012563     Mass: 37492     Score: 38     Expect: 7.9  Queries matched: 9
      RE37740p [Drosophila melanogaster]
      Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
        935.48     934.48     934.44    35.5    272 -  279   0   R.ATAEECLK.S + Propionamide (C)
        973.56     972.55     972.51    43.1     37 -   45   0   K.DCLPISGLR.E
        988.55     987.54     987.58   -37.50   102 -  109   0   K.CITLQVLK.A + Propionamide (C)
       1036.56    1035.55    1035.53    24.0    126 -  134   0   K.VSNLLMTDK.G + Oxidation (M)
       1179.58    1178.57    1178.62   -41.84     1 -   10   0   -.MHLTHSVNLK.S
       1392.71    1391.71    1391.73   -19.46   123 -  134   1   R.DLKVSNLLMTDK.G + Oxidation (M)
       1437.74    1436.73    1436.74    -3.40   126 -  138   1   K.VSNLLMTDKGCIK.V + Oxidation (M)
       1475.75    1474.74    1474.76   -12.74    52 -   62   1   K.QCHHENIVRLR.E + Propionamide (C)
       1716.83    1715.82    1715.93   -65.70    37 -   51   1   K.DCLPISGLREIMILK.Q + Oxidation (M)
      No match to: 807.43, 842.51, 884.54, 913.45, 985.58, 995.53, 1009.58, 1021.61, 1033.51, 1037.59, 1098.49, 1109.54,
      1114.49, 1170.86, 1174.57, 1192.75, 1207.71, 1234.65, 1267.67, 1277.70, 1307.66, 1308.62, 1323.66, 1326.93,
      1365.72, 1383.70, 1389.71, 1407.80, 1423.80, 1426.75, 1439.81, 1441.69, 1461.74, 1493.71, 1523.74, 1557.70,
      1595.86, 1638.85, 1672.91, 1688.98, 1692.99, 1707.77, 1744.97, 1794.84, 1837.95, 1889.88, 1904.95, 1926.89,
      1942.92, 1994.06, 2013.11, 2150.16, 2211.10, 2225.12, 2284.20, 2300.21, 2357.12, 2510.10, 2705.09, 2788.25

17.   gi|2612998     Mass: 44349     Score: 38     Expect: 8.5  Queries matched: 8
      vermilion [Drosophila pallidosa]
      Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
        807.43     806.42     806.44   -21.99   157 -  162   1   R.VRYNQK.Y
       1267.67    1266.66    1266.66     2.65    70 -   79   0   K.QIIFEFDSIR.D
       1383.70    1382.69    1382.74   -33.51   273 -  284   0   R.ALQGAIMITFYR.D
       1439.81    1438.80    1438.76    29.1    251 -  263   0   R.SIFDPAVHDALVR.R
       1493.71    1492.71    1492.73   -14.25    36 -   48   1   K.LLDAQCMLSKEDK.R
       1595.86    1594.85    1594.86    -4.98   251 -  264   1   R.SIFDPAVHDALVRR.G
       1926.89    1925.88    1925.99   -56.44   269 -  284   1   R.FSHRALQGAIMITFYR.D + Oxidation (M)
       2225.12    2224.11    2224.06    24.8    193 -  210   1   R.WLERTPGLEESGFNFWEK.F
      No match to: 842.51, 884.54, 913.45, 935.48, 973.56, 985.58, 988.55, 995.53, 1009.58, 1021.61, 1033.51, 1036.56,
      1037.59, 1098.49, 1109.54, 1114.49, 1170.86, 1174.57, 1179.58, 1192.75, 1207.71, 1234.65, 1277.70, 1307.66,
      1308.62, 1323.66, 1326.93, 1365.72, 1389.71, 1392.71, 1407.80, 1423.80, 1426.75, 1437.74, 1441.69, 1461.74,
      1475.75, 1523.74, 1557.70, 1638.85, 1672.91, 1688.98, 1692.99, 1707.77, 1716.83, 1744.97, 1794.84, 1837.95,
      1889.88, 1904.95, 1942.92, 1994.06, 2013.11, 2150.16, 2211.10, 2284.20, 2300.21, 2357.12, 2510.10, 2705.09, 2788.25
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18.   gi|2612996     Mass: 44342    Score: 38     Expect: 8.5  Queries matched: 8
      vermilion [Drosophila ananassae]
     Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss    Peptide
       807.43    806.42    806.44 -21.99    157 -  162    1    R.VRYNQK.Y
      1267.67   1266.66   1266.66   2.65     70 -   79    0    K.QIIFEFDSIR.D
      1383.70   1382.69   1382.74 -33.51    273 -  284    0    R.ALQGAIMITFYR.D
      1439.81   1438.80   1438.76   29.1    251 -  263    0    R.SIFDPAVHDALVR.R
      1493.71   1492.71   1492.73 -14.25     36 -   48    1    K.LLDAQCMLSKEDK.R
      1595.86   1594.85   1594.86  -4.98    251 -  264    1    R.SIFDPAVHDALVRR.G
      1926.89   1925.88   1925.99 -56.44    269 -  284    1    R.FSHRALQGAIMITFYR.D + Oxidation (M)
      2225.12   2224.11   2224.06   24.8    193 -  210    1    R.WLERTPGLEESGFNFWEK.F
      No match to: 842.51, 884.54, 913.45, 935.48, 973.56, 985.58, 988.55, 995.53, 1009.58, 1021.61, 1033.51, 1036.56,
      1037.59, 1098.49, 1109.54, 1114.49, 1170.86, 1174.57, 1179.58, 1192.75, 1207.71, 1234.65, 1277.70, 1307.66,
      1308.62, 1323.66, 1326.93, 1365.72, 1389.71, 1392.71, 1407.80, 1423.80, 1426.75, 1437.74, 1441.69, 1461.74,
      1475.75, 1523.74, 1557.70, 1638.85, 1672.91, 1688.98, 1692.99, 1707.77, 1716.83, 1744.97, 1794.84, 1837.95,
      1889.88, 1904.95, 1942.92, 1994.06, 2013.11, 2150.16, 2211.10, 2284.20, 2300.21, 2357.12, 2510.10, 2705.09, 2788.25
```

```
19.   gi|24640802     Mass: 105649    Score: 37     Expect: 10  Queries matched: 12
      CG32703-PA [Drosophila melanogaster]
     Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss    Peptide
      1009.58   1008.57   1008.57   1.32    118 -  126    1    R.GNVLKDVHK.R
      1098.49   1097.49   1097.52 -27.66    664 -  673    0    K.DSITFGTCVR.E
      1179.58   1178.57   1178.63 -48.52    139 -  148    0    K.FIHSGNVIHR.D
      1308.62   1307.61   1307.58   21.0    287 -  297    0    K.NCCDDGISLVK.A + 2 Propionamide (C)
      1383.70   1382.69   1382.66   22.0    664 -  675    1    K.DSITFGTCVRER.I
      1392.71   1391.71   1391.75 -33.19    165 -  177    1    K.VADFGLARTLSSR.R
      1461.74   1460.73   1460.80 -47.09    200 -  212    1    R.APEILVASRNYTK.G
      1672.91   1671.91   1671.90   4.99    149 -  162    1    R.DLKPSNILIDSKCR.L + Propionamide (C)
      1794.84   1793.84   1793.88 -24.89    867 -  881    0    K.LAQNDQEELPVHHHK.A
      1904.95   1903.95   1903.94   1.24    729 -  746    0    R.ALPEGIGGPGSQNYEIFR.Q
      1926.89   1925.88   1925.85   18.2    361 -  378    1    R.ETSCSNRTVSNSTPSSNR.D
      2357.12   2356.11   2356.14 -10.12    209 -  228    1    R.NYTKGIDMWGLGCILGEMIR.Q + Oxidation (M); Propionamide (C)
      No match to: 807.43, 842.51, 884.54, 913.45, 935.48, 973.56, 985.58, 988.55, 995.53, 1021.61, 1033.51, 1036.56,
      1037.59, 1109.54, 1114.49, 1170.86, 1174.57, 1192.75, 1207.71, 1234.65, 1267.67, 1277.70, 1307.66, 1323.66,
      1326.93, 1365.72, 1389.71, 1407.80, 1423.80, 1426.75, 1437.74, 1439.81, 1441.69, 1475.75, 1493.71, 1523.74,
      1557.70, 1595.86, 1638.85, 1688.98, 1692.99, 1707.77, 1716.83, 1744.97, 1837.95, 1889.88, 1942.92, 1994.06,
      2013.11, 2150.16, 2211.10, 2225.12, 2284.20, 2300.21, 2510.10, 2705.09, 2788.25
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```
20.   gi|24645056     Mass: 39701     Score: 37     Expect: 10  Queries matched: 10
      steamer duck CG7954-PB, isoform B [Drosophila melanogaster]
     Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss    Peptide
       807.43    806.42    806.38   54.9    105 -  110    0    R.CQLCAK.E + 2 Propionamide (C)
       995.53    994.52    994.48   43.5    111 -  119    0    K.ELADCGFIK.N
      1267.67   1266.66   1266.64   19.9    135 -  145    1    K.AEITGRYVCQK.C
      1383.70   1382.69   1382.64   37.3    321 -  330    1    K.CYDRFPNELR.R + Propionamide (C)
      1392.71   1391.71   1391.66   36.1    229 -  239    0    K.HWHVEHFVCAK.C
      1716.83   1715.82   1715.77   26.7    202 -  215    1    R.CHDKMGIPICGACR.R + 3 Propionamide (C)
      1942.92   1941.91   1941.97 -29.97    206 -  221    1    K.MGIPICGACRRPIEER.V + 2 Propionamide (C)
      1994.06   1993.05   1992.95   49.3    185 -  201    0    K.SRPGLAANDMNELYCLR.C + Propionamide (C)
      2211.10   2210.10   2209.95   65.0    288 -  306    1    K.AWCVHHFACSVCDTKMTQK.S + Oxidation (M)
      2225.12   2224.11   2223.98   60.4     93 -  110    1    K.AMSASWHPQCFRCQLCAK.E + Oxidation (M); 2 Propionamide (C)
      No match to: 842.51, 884.54, 913.45, 935.48, 973.56, 985.58, 988.55, 1009.58, 1021.61, 1033.51, 1036.56, 1037.59,
      1098.49, 1109.54, 1114.49, 1170.86, 1174.57, 1179.58, 1192.75, 1207.71, 1234.65, 1277.70, 1307.66, 1308.62,
      1323.66, 1326.93, 1365.72, 1389.71, 1407.80, 1423.80, 1426.75, 1437.74, 1439.81, 1441.69, 1461.74, 1475.75,
      1493.71, 1523.74, 1557.70, 1595.86, 1638.85, 1672.91, 1688.98, 1692.99, 1707.77, 1744.97, 1794.84, 1837.95,
      1889.88, 1904.95, 1926.89, 2013.11, 2150.16, 2284.20, 2300.21, 2357.12, 2510.10, 2705.09, 2788.25
```

Search Parameters

```
Type of search          : Peptide Mass Fingerprint
Enzyme                  : Trypsin
Variable modifications : Oxidation (M),Propionamide (C)
Mass values             : Monoisotopic
Protein Mass            : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Peptide Charge State    : 1+
Max Missed Cleavages    : 1
Number of queries       : 69
```

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

Mascot Search Results

```
User          : Ilya
Email         : toropygin@rambler.ru
Search title  : Submitted from Shidlovsky 080324 II by Mascot Daemon on P4P800SE
MS data file  : \\192.168.0.18\data on ultraflex-2\DATA\2008_Ilya\Shidlovsky\080325\004\0_J14\1\004__0_J14__1.dar
Database      : NCBInr 20070307 (4984280 sequences; 1723577896 residues)
Taxonomy      : Drosophila (fruit flies) (47828 sequences)
Timestamp     : 3 Apr 2008 at 21:52:41 GMT
Top Score     : 164 for Mixture 1, gi|17137484 + gi|45549124
```

Probability Based Mowse Score

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 59 are significant (p<0.05).

Score Distribution

Protein Summary Report

Format As	Protein Summary	Help
	Significance threshold p< 0.05	Max. number of hits 20

Overview Table

Click on column header to jump to entry in results list.
Move mouse over any indicator to highlight identical peptides.
Click on an indicator to see details of individual match.
Use check boxes to select sub-set of queries for new search.

Mouse over: -Query-

-Accession- -Sequence-

Hit:	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
☑ 807.46 (1+)												?	?		?	?				?
☑ 829.41 (1+)												?	?		?	?				
☑ 842.51 (1+)								?												
☑ 913.46 (1+)												?	?		?	?				
☑ 967.49 (1+)																				
☑ 973.54 (1+)											?									
☑ 995.57 (1+)																		?	?	
☑ 1005.59 (1+)	?			?	?		?	?				?	?		?	?				
☑ 1036.57 (1+)										?										
☑ 1066.55 (1+)																				
☑ 1070.61 (1+)	?			?	?															
☑ 1089.61 (1+)																				
☑ 1106.65 (1+)	?	?	?	?	?		?	?	?	?										

☑ 1109.53 (1+)										?								?	?	
☑ 1133.68 (1+)	?			?	?															
☑ 1179.63 (1+)						?								?						
☑ 1234.67 (1+)						?								?						
☑ 1252.64 (1+)																	?			
☑ 1265.66 (1+)											?									
☑ 1267.70 (1+)	?			?							?									
☑ 1277.70 (1+)																				
☑ 1307.68 (1+)											?									
☑ 1308.67 (1+)						?						?	?		?	?				?
☑ 1319.71 (1+)	?			?	?	?					?						?			
☑ 1320.64 (1+)											?							?	?	
☑ 1323.71 (1+)									?					?				?	?	
☑ 1365.66 (1+)						?					?									
☑ 1374.64 (1+)	?	?	?				?	?	?											
☑ 1381.66 (1+)						?	?	?		?		?	?		?	?				
☑ 1383.69 (1+)						?	?											?	?	?
☑ 1397.69 (1+)							?	?		?								?	?	
☑ 1424.71 (1+)	?			?	?						?							?	?	
☑ 1434.76 (1+)																	?			
☑ 1475.76 (1+)						?				?		?	?		?	?	?			?
☑ 1493.74 (1+)						?	?	?												
☑ 1515.73 (1+)									?											
☑ 1519.70 (1+)																				?
☑ 1522.66 (1+)	?	?	?															?	?	
☑ 1536.74 (1+)	?			?	?		?				?						?	?	?	
☑ 1590.74 (1+)	?			?	?													?	?	
☑ 1604.80 (1+)	?	?	?																	
☑ 1611.89 (1+)	?	?	?							?		?	?		?	?				
☑ 1620.81 (1+)	?	?	?															?	?	
☑ 1641.83 (1+)							?	?		?		?	?		?	?				
☑ 1656.90 (1+)	?	?	?				?	?		?								?	?	?
☑ 1687.82 (1+)	?	?	?						?											?
☑ 1703.84 (1+)	?	?	?							?				?			?			
☑ 1707.74 (1+)							?	?												
☑ 1716.81 (1+)	?	?	?						?		?									
☑ 1754.92 (1+)	?	?												?						
☑ 1759.87 (1+)									?		?	?	?		?	?				?
☑ 1791.83 (1+)	?	?	?							?	?									
☑ 1796.96 (1+)	?	?	?								?							?	?	
☑ 1838.87 (1+)																		?	?	
☑ 1886.90 (1+)	?	?	?											?						?
☑ 1950.90 (1+)	?	?	?						?											?
☑ 1955.85 (1+)	?			?	?												?			
☑ 2198.89 (1+)	?			?	?															
☑ 2214.88 (1+)	?			?	?									?						
☑ 2252.97 (1+)	?	?	?														?	?	?	

Select All | Select None | Search Selected

Index

```
     Accession      Mass    Score  Description
 1. Mixture 1                 164  gi|17137484 + gi|45549124
 2. gi|17137484     51903     102  Origin recognition complex subunit 4 CG2917-PA [Drosophila melanogaster]
 3. gi|5081628      51733      91  origin recognition complex subunit 4 [Drosophila melanogaster]
 4. gi|45549124     51622      67  Yolk protein 2 CG2979-PA [Drosophila melanogaster]
 5. gi|14424471     49630      59  Vitellogenin-2 precursor (Vitellogenin II) (Yolk protein 2)
 6. gi|24583092     37944      45  GlcAT-S CG3881-PA, isoform A [Drosophila melanogaster]
 7. gi|24653739     57721      44  Cyp6a19 CG10243-PA [Drosophila melanogaster]
 8. gi|16768768     36749      43  LD02462p [Drosophila melanogaster]
 9. gi|24649395     43739      42  Rpn9 CG10230-PA, isoform A [Drosophila melanogaster]
10. gi|19920690     97906      41  CG17840-PA [Drosophila melanogaster]
11. gi|125977986    120600     40  GA20622-PA [Drosophila pseudoobscura]
12. gi|6649053      64394      40  dynein [Drosophila mauritiana]
13. gi|6649055      64364      40  dynein [Drosophila yakuba]
14. gi|58613897     39244      39  SR-CIV [Drosophila simulans]
15. gi|6649009      65715      39  dynein [Drosophila melanogaster]
16. gi|6649051      64846      38  dynein [Drosophila sechellia]
17. gi|24581132     42670      38  CG31948-PB, isoform B [Drosophila melanogaster]
18. gi|24641704     170230     38  strawberry notch CG1903-PB, isoform B [Drosophila melanogaster]
19. gi|2078282      170361     38  Sno [Drosophila melanogaster]
20. gi|24658169     79930      36  CG4611-PA [Drosophila melanogaster]
```

Results List

```
1.     Mixture 1     Total score: 164     Expect: 1.9e-012  Queries matched: 27
       Components: 1. gi|17137484 Origin recognition complex subunit 4 CG2917-PA [Drosophila melanogaster]
                   2. gi|45549124 Yolk protein 2 CG2979-PA [Drosophila melanogaster]
      Observed  Mr(expt)  Mr(calc)     ppm  Start   End Miss Comp  Peptide
       1005.59   1004.58   1004.54    41.1   171 -  178   0    2   K.LVQAYQQR.Y
       1070.61   1069.61   1069.57    39.1    65 -   73   0    2   R.EVEELPNLK.E
       1106.65   1105.65   1105.63    16.9   202 -  210   0    1   R.QVFLFPSLR.R
       1133.68   1132.67   1132.64    32.0   170 -  178   1    2   R.KLVQAYQQR.Y
       1267.70   1266.69   1266.66    24.9     1 -   10   1    2   -.MQYNLVRCLK.K
       1319.71   1318.71   1318.71   -5.68   128 -  138   0    2   K.IEFNLNTLVEK.V
       1374.64   1373.63   1373.66  -24.25   364 -  374   0    1   R.DSFNFEIIYAR.F
       1424.71   1423.70   1423.68    9.96   370 -  381   0    2   R.YFAESVRPGNER.N
       1522.66   1521.65   1521.66   -9.30   254 -  266   0    1   R.NHFDPGEYGFSPR.L
       1536.74   1535.73   1535.74   -3.98   437 -  448   0    2   K.QTGYHQVHQPWR.Q
       1590.74   1589.73   1589.74   -3.75   382 -  395   0    2   R.NFPSVAASSYQEYK.Q
       1604.80   1603.79   1603.79    0.14   102 -  116   0    1   K.SITVQMQLENAADGK.V
       1611.89   1610.88   1610.92  -26.09    63 -   77   0    1   K.TTLINSVLADLLPNK.S
       1620.81   1619.80   1619.78    13.0   102 -  116   0    1   K.SITVQMQLENAADGK.V + Oxidation (M)
       1656.90   1655.89   1655.89   -2.08   402 -  419   0    1   R.IAELIMPLTGGAGGGVGK.V + Oxidation (M)
       1687.82   1686.81   1686.86  -31.46    43 -   58   0    1   R.TAEMGESNSLLLLGPR.G
       1703.84   1702.83   1702.86  -12.71    43 -   58   0    1   R.TAEMGESNSLLLLGPR.G + Oxidation (M)
       1716.81   1715.80   1715.82  -14.29   429 -  442   0    1   K.LALTYSQIHHCMQR.Y + Oxidation (M)
       1754.92   1753.91   1753.98  -40.50   221 -  237   0    1   R.DLLSLPTGNSLLLAAEK.I
       1791.83   1790.83   1790.85  -12.94   254 -  268   1    1   R.NHFDPGEYGFSPRLR.D
       1796.96   1795.96   1796.01  -28.17   308 -  323   0    1   R.LVAHLRPQSPHITAEK.M
       1886.90   1885.89   1885.97  -39.31   238 -  253   0    1   K.IYNLQNIQSGALYFSR.N
       1950.90   1949.89   1949.97  -42.69   286 -  302   0    1   R.STLQALHDFDISEAYLK.N
       1955.85   1954.84   1954.91  -35.48    48 -   64   0    2   R.SNSLDNVEQPSNWVNPR.E
       2198.89   2197.88   2197.97  -39.29   319 -  339   0    2   R.GDADFVDAIHTSAYGMGTSQR.L
       2214.88   2213.87   2213.96  -41.17   319 -  339   0    2   R.GDADFVDAIHTSAYGMGTSQR.L + Oxidation (M)
       2252.97   2251.96   2252.08  -55.16    78 -   97   0    1   K.SFGENTLIVHLDGNLHTDDR.V
       No match to: 807.46, 829.41, 842.51, 913.46, 967.49, 973.54, 995.57, 1036.57, 1066.55, 1089.61, 1109.53,
       1179.63, 1234.67, 1252.64, 1265.66, 1277.70, 1307.68, 1308.67, 1320.64, 1323.71, 1365.66, 1381.66, 1383.69,
       1397.69, 1434.76, 1475.76, 1493.74, 1515.73, 1519.70, 1641.83, 1707.74, 1759.87, 1838.87

2.     gi|17137484     Mass: 51903     Score: 102     Expect: 3e-006  Queries matched: 16
       Origin recognition complex subunit 4 CG2917-PA [Drosophila melanogaster]
      Observed  Mr(expt)  Mr(calc)     ppm  Start   End Miss  Peptide
       1106.65   1105.65   1105.63    16.9   202 -  210   0    R.QVFLFPSLR.R
       1374.64   1373.63   1373.66  -24.25   364 -  374   0    R.DSFNFEIIYAR.F
       1522.66   1521.65   1521.66   -9.30   254 -  266   0    R.NHFDPGEYGFSPR.L
       1604.80   1603.79   1603.79    0.14   102 -  116   0    K.SITVQMQLENAADGK.V
       1611.89   1610.88   1610.92  -26.09    63 -   77   0    K.TTLINSVLADLLPNK.S
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      1620.81   1619.80   1619.78    13.0   102 - 116   0   K.SITVQMQLENAADGK.V + Oxidation (M)
      1656.90   1655.89   1655.89   -2.08   402 - 419   0   R.IAELIMPLTGGAGGGVGK.V + Oxidation (M)
      1687.82   1686.81   1686.86  -31.46    43 -  58   0   R.TAEMGESNSLLLLGPR.G
      1703.84   1702.83   1702.86  -12.71    43 -  58   0   R.TAEMGESNSLLLLGPR.G + Oxidation (M)
      1716.81   1715.80   1715.82  -14.29   429 - 442   0   K.LALTYSQIHHCMQR.Y + Oxidation (M)
      1754.92   1753.91   1753.98  -40.50   221 - 237   0   R.DLLSLPTGNSLLLAAEK.I
      1791.83   1790.83   1790.85  -12.94   254 - 268   1   R.NHFDPGEYGFSPRLR.D
      1796.96   1795.96   1796.01  -28.17   308 - 323   0   R.LVAHLRPQSPHITAEK.M
      1886.90   1885.89   1885.97  -39.31   238 - 253   0   K.IYNLQNIQSGALYFSR.N
      1950.90   1949.89   1949.97  -42.69   286 - 302   0   R.STLQALHDFDISEAYLK.N
      2252.97   2251.96   2252.08  -55.16    78 -  97   0   K.SFGENTLIVHLDGNLHTDDR.V
     No match to: 807.46, 829.41, 842.51, 913.46, 967.49, 973.54, 995.57, 1005.59, 1036.57, 1066.55, 1070.61,
     1089.61, 1109.53, 1133.68, 1179.63, 1234.67, 1252.64, 1265.66, 1267.70, 1277.70, 1307.68, 1308.67, 1319.71,
     1320.64, 1323.71, 1365.66, 1381.66, 1383.69, 1397.69, 1424.71, 1434.76, 1475.76, 1493.74, 1515.73, 1519.70,
     1536.74, 1590.74, 1641.83, 1707.74, 1759.87, 1838.87, 1955.85, 2198.89, 2214.88

3.   gi|5081628     Mass: 51733     Score: 91     Expect: 3.9e-005  Queries matched: 15
     origin recognition complex subunit 4 [Drosophila melanogaster]
    Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
      1106.65   1105.65   1105.63    16.9   202 - 210   0   R.QVFLFPSLR.R
      1374.64   1373.63   1373.66  -24.25   363 - 373   0   R.DSFNFEIIYAR.F
      1522.66   1521.65   1521.66   -9.30   253 - 265   0   R.NHFDPGEYGFSPR.L
      1604.80   1603.79   1603.79    0.14   102 - 116   0   K.SITVQMQLENAADGK.V
      1611.89   1610.88   1610.92  -26.09    63 -  77   0   K.TTLINSVLADLLPNK.S
      1620.81   1619.80   1619.78    13.0   102 - 116   0   K.SITVQMQLENAADGK.V + Oxidation (M)
      1656.90   1655.89   1655.89   -2.08   401 - 418   0   R.IAELIMPLTGGAGGGVGK.V + Oxidation (M)
      1687.82   1686.81   1686.86  -31.46    43 -  58   0   R.TAEMGESNSLLLLGPR.G
      1703.84   1702.83   1702.86  -12.71    43 -  58   0   R.TAEMGESNSLLLLGPR.G + Oxidation (M)
      1716.81   1715.80   1715.82  -14.29   428 - 441   0   K.LALTYSQIHHCMQR.Y + Oxidation (M)
      1791.83   1790.83   1790.85  -12.94   253 - 267   1   R.NHFDPGEYGFSPRLR.D
      1796.96   1795.96   1796.01  -28.17   307 - 322   0   R.LVAHLRPQSPHITAEK.M
      1886.90   1885.89   1885.97  -39.31   237 - 252   0   K.IYNLQNIQSGALYFSR.N
      1950.90   1949.89   1949.97  -42.69   285 - 301   0   R.STLQALHDFDISEAYLK.N
      2252.97   2251.96   2252.08  -55.16    78 -  97   0   K.SFGENTLIVHLDGNLHTDDR.V
     No match to: 807.46, 829.41, 842.51, 913.46, 967.49, 973.54, 995.57, 1005.59, 1036.57, 1066.55, 1070.61,
     1089.61, 1109.53, 1133.68, 1179.63, 1234.67, 1252.64, 1265.66, 1267.70, 1277.70, 1307.68, 1308.67, 1319.71,
     1320.64, 1323.71, 1365.66, 1381.66, 1383.69, 1397.69, 1424.71, 1434.76, 1475.76, 1493.74, 1515.73, 1519.70,
     1536.74, 1590.74, 1641.83, 1707.74, 1754.92, 1759.87, 1838.87, 1955.85, 2198.89, 2214.88

4.   gi|45549124     Mass: 51622     Score: 67     Expect: 0.011   Queries matched: 12
     Yolk protein 2 CG2979-PA [Drosophila melanogaster]
    Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
      1005.59   1004.58   1004.54    41.1   171 - 178   0   K.LVQAYQQR.Y
      1070.61   1069.61   1069.57    39.1    65 -  73   0   R.EVEELPNLK.E
      1106.65   1105.65   1105.59    53.5   118 - 127   1   R.GYIVGERGQK.I
      1133.68   1132.67   1132.64    32.0   170 - 178   1   R.KLVQAYQQR.Y
      1267.70   1266.69   1266.66    24.9     1 -  10   1   -.MQYNLVRCLK.K
      1319.71   1318.71   1318.71   -5.68   128 - 138   0   K.IEFNLNTLVEK.V
      1424.71   1423.70   1423.68    9.96   370 - 381   0   R.YFAESVRPGNER.N
      1536.74   1535.73   1535.74   -3.98   437 - 448   0   K.QTGYHQVHQPWR.Q
      1590.74   1589.73   1589.74   -3.75   382 - 395   0   R.NFPSVAASSYQEYK.Q
      1955.85   1954.84   1954.91  -35.48    48 -  64   0   R.SNSLDNVEQPSNWVNPR.E
      2198.89   2197.88   2197.97  -39.29   319 - 339   0   R.GDADFVDAIHTSAYGMGTSQR.L
      2214.88   2213.87   2213.96  -41.17   319 - 339   0   R.GDADFVDAIHTSAYGMGTSQR.L + Oxidation (M)
     No match to: 807.46, 829.41, 842.51, 913.46, 967.49, 973.54, 995.57, 1036.57, 1066.55, 1089.61, 1109.53,
     1179.63, 1234.67, 1252.64, 1265.66, 1277.70, 1307.68, 1308.67, 1320.64, 1323.71, 1365.66, 1374.64, 1381.66,
     1383.69, 1397.69, 1434.76, 1475.76, 1493.74, 1515.73, 1519.70, 1522.66, 1604.80, 1611.89, 1620.81, 1641.83,
     1656.90, 1687.82, 1703.84, 1707.74, 1716.81, 1754.92, 1759.87, 1791.83, 1796.96, 1838.87, 1886.90, 1950.90,
     2252.97

5.   gi|14424471     Mass: 49630     Score: 59     Expect: 0.065   Queries matched: 11
     Vitellogenin-2 precursor (Vitellogenin II) (Yolk protein 2)
    Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
      1005.59   1004.58   1004.54    41.1   154 - 161   0   K.LVQAYQQR.Y
      1070.61   1069.61   1069.57    39.1    48 -  56   0   R.EVEELPNLK.E
      1106.65   1105.65   1105.59    53.5   101 - 110   1   R.GYIVGERGQK.I
      1133.68   1132.67   1132.64    32.0   153 - 161   1   R.KLVQAYQQR.Y
      1319.71   1318.71   1318.71   -5.68   111 - 121   0   K.IEFNLNTLVEK.V
      1424.71   1423.70   1423.68    9.96   353 - 364   0   R.YFAESVRPGNER.N
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  1536.74   1535.73   1535.74   -3.98   420 - 431   0   K.QTGYHQVHQPWR.Q
  1590.74   1589.73   1589.74   -3.75   365 - 378   0   R.NFPSVAASSYQEYK.Q
  1955.85   1954.84   1954.91  -35.48    31 -  47   0   R.SNSLDNVEQPSNWVNPR.E
  2198.89   2197.88   2197.97  -39.29   302 - 322   0   R.GDADFVDAIHTSAYGMGTSQR.L
  2214.88   2213.87   2213.96  -41.17   302 - 322   0   R.GDADFVDAIHTSAYGMGTSQR.L + Oxidation (M)
 No match to: 807.46, 829.41, 842.51, 913.46, 967.49, 973.54, 995.57, 1036.57, 1066.55, 1089.61, 1109.53,
 1179.63, 1234.67, 1252.64, 1265.66, 1267.70, 1277.70, 1307.68, 1308.67, 1320.64, 1323.71, 1365.66, 1374.64,
 1381.66, 1383.69, 1397.69, 1434.76, 1475.76, 1493.74, 1515.73, 1519.70, 1522.66, 1604.80, 1611.89, 1620.81,
 1641.83, 1656.90, 1687.82, 1703.84, 1707.74, 1716.81, 1754.92, 1759.87, 1791.83, 1796.96, 1838.87, 1886.90,
 1950.90, 2252.97

6.      gi|24583092     Mass: 37944     Score: 45     Expect: 1.4  Queries matched: 9
 GlcAT-S CG3881-PA, isoform A [Drosophila melanogaster]
 Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
  1179.63   1178.62   1178.68  -48.78   286 - 296   0   R.SNLGALLHNLK.L
  1234.67   1233.66   1233.64    18.4     2 -  11   1   M.NLFENENKVK.D
  1308.67   1307.66   1307.71  -34.55   119 - 130   1   R.NEKPAPRGVANR.R
  1319.71   1318.71   1318.70    1.80   193 - 204   0   K.VVAFLDSWVAGR.R
  1365.66   1364.65   1364.68  -18.29     1 -  11   1   -.MNLFENENKVK.D
  1381.66   1380.66   1380.67  -10.94     1 -  11   1   -.MNLFENENKVK.D + Oxidation (M)
  1383.69   1382.68   1382.63    32.9   297 - 309   0   K.LMGVTSTTESEGR.N + Oxidation (M)
  1475.76   1474.75   1474.80  -35.83   193 - 205   1   K.VVAFLDSWVAGRR.W
  1493.74   1492.74   1492.63    68.8    91 - 101   0   K.CNDYMDTLLYR.F + Oxidation (M); Propionamide (C)
 No match to: 807.46, 829.41, 842.51, 913.46, 967.49, 973.54, 995.57, 1005.59, 1036.57, 1066.55, 1070.61,
 1089.61, 1106.65, 1109.53, 1133.68, 1252.64, 1265.66, 1267.70, 1277.70, 1307.68, 1320.64, 1323.71, 1374.64,
 1397.69, 1424.71, 1434.76, 1515.73, 1519.70, 1522.66, 1536.74, 1590.74, 1604.80, 1611.89, 1620.81, 1641.83,
 1656.90, 1687.82, 1703.84, 1707.74, 1716.81, 1754.92, 1759.87, 1791.83, 1796.96, 1838.87, 1886.90, 1950.90,
 1955.85, 2198.89, 2214.88, 2252.97

7.      gi|24653739     Mass: 57721     Score: 44     Expect: 2  Queries matched: 11
 Cyp6a19 CG10243-PA [Drosophila melanogaster]
 Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
  1005.59   1004.58   1004.53    52.2   134 - 142   0   K.LTHTFTSAK.M
  1106.65   1105.65   1105.61    30.7    92 - 100   1   K.TVLIRDFDK.F
  1374.64   1373.63   1373.58    32.0   268 - 278   0   R.NDFMDTLIDMK.Q + 2 Oxidation (M)
  1381.66   1380.66   1380.71  -37.31   252 - 262   1   K.IVQDTIDYRMK.R
  1383.69   1382.68   1382.73  -36.46   377 - 388   0   R.IATKPYQHSNPK.Y
  1397.69   1396.69   1396.70  -10.42   252 - 262   1   K.IVQDTIDYRMK.R + Oxidation (M)
  1493.74   1492.74   1492.75  -11.30   333 - 345   1   R.AEIDSVLERYNGK.L
  1536.74   1535.73   1535.76  -19.47   417 - 428   1   K.FIPERFDEEQVK.K
  1641.83   1640.82   1640.87  -31.39   218 - 231   0   R.HGWLVDLLIFGMPK.L + Oxidation (M)
  1656.90   1655.89   1655.81    47.9   203 - 216   1   K.AEFVQMGYSALRER.R
  1707.74   1706.74   1706.83  -56.69   248 - 260   1   K.FYMKIVQDTIDYR.M + Oxidation (M)
 No match to: 807.46, 829.41, 842.51, 913.46, 967.49, 973.54, 995.57, 1036.57, 1066.55, 1070.61, 1089.61,
 1109.53, 1133.68, 1179.63, 1234.67, 1252.64, 1265.66, 1267.70, 1277.70, 1307.68, 1308.67, 1319.71, 1320.64,
 1323.71, 1365.66, 1424.71, 1434.76, 1475.76, 1515.73, 1519.70, 1522.66, 1590.74, 1604.80, 1611.89, 1620.81,
 1687.82, 1703.84, 1716.81, 1754.92, 1759.87, 1791.83, 1796.96, 1838.87, 1886.90, 1950.90, 1955.85, 2198.89,
 2214.88, 2252.97

8.      gi|16768768     Mass: 36749     Score: 43     Expect: 2.3  Queries matched: 10
 LD02462p [Drosophila melanogaster]
 Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
   842.51    841.50    841.51   -8.79     1 -   8   0   -.MPLAGILK.R
  1005.59   1004.58   1004.53    52.2    85 -  93   0   K.LTHTFTSAK.M
  1106.65   1105.65   1105.61    30.7    43 -  51   1   K.TVLIRDFDK.F
  1374.64   1373.63   1373.58    32.0   219 - 229   0   R.NDFMDTLIDMK.Q + 2 Oxidation (M)
  1381.66   1380.66   1380.71  -37.31   203 - 213   1   K.IVQDTIDYRMK.R
  1397.69   1396.69   1396.70  -10.42   203 - 213   1   K.IVQDTIDYRMK.R + Oxidation (M)
  1493.74   1492.74   1492.75  -11.30   284 - 296   1   R.AEIDSVLERYNGK.L
  1641.83   1640.82   1640.87  -31.39   169 - 182   0   R.HGWLVDLLIFGMPK.L + Oxidation (M)
  1656.90   1655.89   1655.81    47.9   154 - 167   1   K.AEFVQMGYSALRER.R
  1707.74   1706.74   1706.83  -56.69   199 - 211   1   K.FYMKIVQDTIDYR.M + Oxidation (M)
 No match to: 807.46, 829.41, 913.46, 967.49, 973.54, 995.57, 1036.57, 1066.55, 1070.61, 1089.61, 1109.53,
 1133.68, 1179.63, 1234.67, 1252.64, 1265.66, 1267.70, 1277.70, 1307.68, 1308.67, 1319.71, 1320.64, 1323.71,
 1365.66, 1383.69, 1424.71, 1434.76, 1475.76, 1515.73, 1519.70, 1522.66, 1536.74, 1590.74, 1604.80, 1611.89,
 1620.81, 1687.82, 1703.84, 1716.81, 1754.92, 1759.87, 1791.83, 1796.96, 1838.87, 1886.90, 1950.90, 1955.85,
 2198.89, 2214.88, 2252.97

9.      gi|24649395     Mass: 43739     Score: 42     Expect: 2.9  Queries matched: 8
 Rpn9 CG10230-PA, isoform A [Drosophila melanogaster]
 Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
  1106.65   1105.65   1105.60    40.9    96 - 104   1   K.KEAIEFLEK.M
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     1323.71   1322.70   1322.67    20.3   295 - 306   0   R.AISFTDIAQETK.L
     1374.64   1373.63   1373.70  -50.24   371 - 382   1   K.LMENRAAEILTN.-
     1515.73   1514.72   1514.75  -23.36   277 - 288   0   K.ISLLCLMEMTFK.R + Oxidation (M); Propionamide (C)
     1687.82   1686.81   1686.85  -25.32   277 - 289   1   K.ISLLCLMEMTFKR.S + 2 Oxidation (M); Propionamide (C)
     1716.81   1715.80   1715.87  -39.02   275 - 288   1   R.QKISLLCLMEMTFK.R + 2 Oxidation (M)
     1759.87   1758.86   1758.93  -35.55     2 -  17   1   M.SNPQPNVTAYLATQKK.T
     1950.90   1949.89   1949.96  -36.90    22 -  37   0   K.ELAAEWTLIEELYNEK.L
    No match to: 807.46, 829.41, 842.51, 913.46, 967.49, 973.54, 995.57, 1005.59, 1036.57, 1066.55, 1070.61,
    1089.61, 1109.53, 1133.68, 1179.63, 1234.67, 1252.64, 1265.66, 1267.70, 1277.70, 1307.68, 1308.67, 1319.71,
    1320.64, 1365.66, 1381.66, 1383.69, 1397.69, 1424.71, 1434.76, 1475.76, 1493.74, 1519.70, 1522.66, 1536.74,
    1590.74, 1604.80, 1611.89, 1620.81, 1641.83, 1656.90, 1703.84, 1707.74, 1754.92, 1791.83, 1796.96, 1838.87,
    1886.90, 1955.85, 2198.89, 2214.88, 2252.97

10. gi|19920690      Mass: 97906     Score: 41      Expect: 4.1  Queries matched: 11
    CG17840-PA [Drosophila melanogaster]
    Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
     1036.57   1035.56   1035.53    25.0   457 - 466   0   R.TNSAQFAIGK.C
     1106.65   1105.65   1105.62    20.6    20 -  28   1   K.VVLYETRAR.L
     1109.53   1108.52   1108.46    49.1   448 - 456   0   R.TNCVDCLDR.T + Propionamide (C)
     1381.66   1380.66   1380.73  -54.05   384 - 394   0   R.YLNQFLPPPHR.M
     1397.69   1396.69   1396.68    6.63   397 - 407   1   K.HIHFDMARQSR.L
     1475.76   1474.75   1474.72    18.9   825 - 836   1   K.SLTIYAEYCRTR.S
     1611.89   1610.88   1610.78    63.7   605 - 619   1   R.ACLPYSCADSNKLVK.E
     1641.83   1640.82   1640.88  -35.77   467 - 480   1   K.CALGHQLERLGFVK.S + Propionamide (C)
     1656.90   1655.89   1655.86    16.7   384 - 396   1   R.YLNQFLPPPHRMK.H + Oxidation (M)
     1703.84   1702.83   1702.89  -32.08   370 - 383   1   K.HESIISKELEYSIR.Y
     1791.83   1790.83   1790.86  -17.07   662 - 675   1   R.YMPTFRTNFSPFQR.Q
    No match to: 807.46, 829.41, 842.51, 913.46, 967.49, 973.54, 995.57, 1005.59, 1066.55, 1070.61, 1089.61,
    1133.68, 1179.63, 1234.67, 1252.64, 1265.66, 1267.70, 1277.70, 1307.68, 1308.67, 1319.71, 1320.64, 1323.71,
    1365.66, 1374.64, 1383.69, 1424.71, 1434.76, 1493.74, 1515.73, 1519.70, 1522.66, 1536.74, 1590.74, 1604.80,
    1620.81, 1687.82, 1707.74, 1716.81, 1754.92, 1759.87, 1796.96, 1838.87, 1886.90, 1950.90, 1955.85, 2198.89,
    2214.88, 2252.97

11. gi|125977986      Mass: 120600    Score: 40      Expect: 4.7  Queries matched: 13
    GA20622-PA [Drosophila pseudoobscura]
    Observed  Mr(expt)  Mr(calc)     ppm  Start    End  Miss   Peptide
      973.54    972.53    972.52    9.59   817 -   825    0   R.QAEIVAQSK.K
     1265.66   1264.65   1264.59    45.8   128 -   139    1   K.IKFGDDGEAADK.T
     1267.70   1266.69   1266.64    42.3   739 -   748    1   K.RIDYYGDPLR.D
     1307.68   1306.67   1306.68   -5.31   782 -   793    1   R.YMAQGGRGKPVK.S + Oxidation (M)
     1319.71   1318.71   1318.70    5.24   389 -   399    0   K.EQMLLTMLVNK.L
     1320.64   1319.63   1319.71  -55.87   490 -   500    1   R.TMQAILRCLQK.A + Oxidation (M)
     1365.66   1364.65   1364.67  -12.90  1012 -  1024    1   K.GQGTSNAVFNKDK.S
     1424.71   1423.70   1423.61    62.0    60 -    71    0   R.ITFDDDGEVEER.K
     1536.74   1535.73   1535.73    2.04   212 -   223    0   K.DNEQLELFNLCK.N + Propionamide (C)
     1716.81   1715.80   1715.89  -55.42   632 -   648    0   R.QELIGGIGATDEVSSLK.T
     1759.87   1758.86   1758.92  -29.17    20 -    35    1   K.IVFDDAGEAVEKPNKK.E
     1791.83   1790.83   1790.81    8.13    97 -   111    1   K.FGDDGEVEEQQPWKK.N
     1796.96   1795.96   1795.86    54.7   337 -   349    1   R.RIYSYWYFENEVK.D
    No match to: 807.46, 829.41, 842.51, 913.46, 967.49, 995.57, 1005.59, 1036.57, 1066.55, 1070.61, 1089.61,
    1106.65, 1109.53, 1133.68, 1179.63, 1234.67, 1252.64, 1277.70, 1308.67, 1323.71, 1374.64, 1381.66, 1383.69,
    1397.69, 1434.76, 1475.76, 1493.74, 1515.73, 1519.70, 1522.66, 1590.74, 1604.80, 1611.89, 1620.81, 1641.83,
    1656.90, 1687.82, 1703.84, 1707.74, 1754.92, 1838.87, 1886.90, 1950.90, 1955.85, 2198.89, 2214.88, 2252.97

12. gi|6649053      Mass: 64394     Score: 40      Expect: 5.1  Queries matched: 10
    dynein [Drosophila mauritiana]
    Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
      807.46    806.45    806.41    55.6    57 -  62   1   K.MRDTLR.D + Oxidation (M)
      829.41    828.40    828.37    43.1     6 -  12   0   K.LYDSMGK.L + Oxidation (M)
      913.46    912.45    912.49  -46.74   350 - 357   0   R.AELPENLK.A
     1005.59   1004.58   1004.53    48.9   311 - 319   1   K.CIQDAIKSK.K
     1308.67   1307.66   1307.65    4.79     2 -  12   1   R.HLTKLYDSMGK.L + Oxidation (M)
     1381.66   1380.66   1380.73  -51.13   543 - 553   1   K.RKPHYNDLNPK.A
     1475.76   1474.75   1474.73    14.4   554 - 567   0   K.AVTNDELFGIVNPS.-
     1611.89   1610.88   1610.87    9.19   433 - 445   1   R.QRPEDQVLMRALR.D
     1641.83   1640.82   1640.84  -12.77     6 -  20   1   K.LYDSMGKLNLISGSK.N + Oxidation (M)
     1759.87   1758.86   1758.87   -2.86   402 - 415   1   K.ELLSKQDHYDWGLR.A
    No match to: 842.51, 967.49, 973.54, 995.57, 1036.57, 1066.55, 1070.61, 1089.61, 1106.65, 1109.53, 1133.68,
    1179.63, 1234.67, 1252.64, 1265.66, 1267.70, 1277.70, 1307.68, 1319.71, 1320.64, 1323.71, 1365.66, 1374.64,
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        1383.69, 1397.69, 1424.71, 1434.76, 1493.74, 1515.73, 1519.70, 1522.66, 1536.74, 1590.74, 1604.80, 1620.81,
        1656.90, 1687.82, 1703.84, 1707.74, 1716.81, 1754.92, 1791.83, 1796.96, 1838.87, 1886.90, 1950.90, 1955.85,
        2198.89, 2214.88, 2252.97

13.     gi|6649055     Mass: 64364     Score: 40     Expect: 5.1   Queries matched: 10
        dynein [Drosophila yakuba]
       Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
         807.46    806.45    806.41    55.6     57 -   62    1   K.MRDTLR.D + Oxidation (M)
         829.41    828.40    828.37    43.1      6 -   12    0   K.LYDSMGK.L + Oxidation (M)
         913.46    912.45    912.49  -46.74    350 -  357    0   R.AELPENLK.A
        1005.59   1004.58   1004.53    48.9    311 -  319    1   K.CIQDAIKSK.K
        1308.67   1307.66   1307.65    4.79      2 -   12    1   R.HLTKLYDSMGK.L + Oxidation (M)
        1381.66   1380.66   1380.73  -51.13    543 -  553    1   K.RKPHYNDLNPK.A
        1475.76   1474.75   1474.73    14.4    554 -  567    0   K.AVTNDELFGIVNPS.-
        1611.89   1610.88   1610.87    9.19    433 -  445    1   R.QRPEDQVLMRALR.D
        1641.83   1640.82   1640.84  -12.77      6 -   20    1   K.LYDSMGKLNLISGSK.N + Oxidation (M)
        1759.87   1758.86   1758.87   -2.86    402 -  415    1   K.ELLSKQDHYDWGLR.A
        No match to: 842.51, 967.49, 973.54, 995.57, 1036.57, 1066.55, 1070.61, 1089.61, 1106.65, 1109.53, 1133.68,
        1179.63, 1234.67, 1252.64, 1265.66, 1267.70, 1277.70, 1307.68, 1319.71, 1320.64, 1323.71, 1365.66, 1374.64,
        1383.69, 1397.69, 1424.71, 1434.76, 1493.74, 1515.73, 1519.70, 1522.66, 1536.74, 1590.74, 1604.80, 1620.81,
        1656.90, 1687.82, 1703.84, 1707.74, 1716.81, 1754.92, 1791.83, 1796.96, 1838.87, 1886.90, 1950.90, 1955.85,
        2198.89, 2214.88, 2252.97

14.     gi|58613897     Mass: 39244     Score: 39     Expect: 5.9   Queries matched: 7
        SR-CIV [Drosophila simulans]
       Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
        1179.63   1178.62   1178.55    56.0    243 -  252    1   K.LMTAEECARR.S
        1234.67   1233.66   1233.63    23.7     53 -   62    1   K.VFTCDRGIPR.G + Propionamide (C)
        1323.71   1322.70   1322.64    47.8    231 -  242    0   R.SQYGDIAIDDVK.L
        1703.84   1702.83   1702.74    52.6    114 -  127    0   K.DHTFQNQSDGHYVR.M
        1754.92   1753.91   1753.86    28.8     83 -   97    1   K.CGWTAELSFLGTWKR.V
        1886.90   1885.89   1885.85    22.7    215 -  230    0   K.QMDEDFQVIFTATDAR.S
        2214.88   2213.87   2214.02  -66.22    109 -  127    1   K.TGPQKDHTFQNQSDGHYVR.M
        No match to: 807.46, 829.41, 842.51, 913.46, 967.49, 973.54, 995.57, 1005.59, 1036.57, 1066.55, 1070.61,
        1089.61, 1106.65, 1109.53, 1133.68, 1252.64, 1265.66, 1267.70, 1277.70, 1307.68, 1308.67, 1319.71, 1320.64,
        1365.66, 1374.64, 1381.66, 1383.69, 1397.69, 1424.71, 1434.76, 1475.76, 1493.74, 1515.73, 1519.70, 1522.66,
        1536.74, 1590.74, 1604.80, 1611.89, 1620.81, 1641.83, 1656.90, 1687.82, 1707.74, 1716.81, 1759.87, 1791.83,
        1796.96, 1838.87, 1950.90, 1955.85, 2198.89, 2252.97

15.     gi|6649009     Mass: 65715     Score: 39     Expect: 6   Queries matched: 10
        dynein [Drosophila melanogaster]
       Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
         807.46    806.45    806.41    55.6     62 -   67    1   K.MRDTLR.D + Oxidation (M)
         829.41    828.40    828.37    43.1     11 -   17    0   K.LYDSMGK.L + Oxidation (M)
         913.46    912.45    912.49  -46.74    355 -  362    0   R.AELPENLK.A
        1005.59   1004.58   1004.53    48.9    316 -  324    1   K.CIQDAIKSK.K
        1308.67   1307.66   1307.65    4.79      7 -   17    1   R.HLTKLYDSMGK.L + Oxidation (M)
        1381.66   1380.66   1380.73  -51.13    548 -  558    1   K.RKPHYNDLNPK.A
        1475.76   1474.75   1474.73    16.6    151 -  162    0   K.IMTICTIDVHSR.D + Oxidation (M); Propionamide (C)
        1611.89   1610.88   1610.87    9.19    438 -  450    1   R.QRPEDQVLMRALR.D
        1641.83   1640.82   1640.84  -12.77     11 -   25    1   K.LYDSMGKLNLISGSK.N + Oxidation (M)
        1759.87   1758.86   1758.87   -2.86    407 -  420    1   K.ELLSKQDHYDWGLR.A
        No match to: 842.51, 967.49, 973.54, 995.57, 1036.57, 1066.55, 1070.61, 1089.61, 1106.65, 1109.53, 1133.68,
        1179.63, 1234.67, 1252.64, 1265.66, 1267.70, 1277.70, 1307.68, 1319.71, 1320.64, 1323.71, 1365.66, 1374.64,
        1383.69, 1397.69, 1424.71, 1434.76, 1493.74, 1515.73, 1519.70, 1522.66, 1536.74, 1590.74, 1604.80, 1620.81,
        1656.90, 1687.82, 1703.84, 1707.74, 1716.81, 1754.92, 1791.83, 1796.96, 1838.87, 1886.90, 1950.90, 1955.85,
        2198.89, 2214.88, 2252.97

16.     gi|6649051     Mass: 64846     Score: 38     Expect: 7.2   Queries matched: 10
        dynein [Drosophila sechellia]
       Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
         807.46    806.45    806.41    55.6     62 -   67    1   K.MRDTLR.D + Oxidation (M)
         829.41    828.40    828.37    43.1     11 -   17    0   K.LYDSMGK.L + Oxidation (M)
         913.46    912.45    912.49  -46.74    355 -  362    0   R.AELPENLK.A
        1005.59   1004.58   1004.53    48.9    316 -  324    1   K.CIQDAIKSK.K
        1308.67   1307.66   1307.65    4.79      7 -   17    1   R.HLTKLYDSMGK.L + Oxidation (M)
        1381.66   1380.66   1380.73  -51.13    548 -  558    1   K.RKPHYNDLNPK.A
        1475.76   1474.75   1474.73    14.4    559 -  572    0   K.AVTNDELFGIVNPS.-
        1611.89   1610.88   1610.87    9.19    438 -  450    1   R.QRPEDQVLMRALR.D
        1641.83   1640.82   1640.84  -12.77     11 -   25    1   K.LYDSMGKLNLISGSK.N + Oxidation (M)
        1759.87   1758.86   1758.87   -2.86    407 -  420    1   K.ELLSKQDHYDWGLR.A
```

No match to: 842.51, 967.49, 973.54, 995.57, 1036.57, 1066.55, 1070.61, 1089.61, 1106.65, 1109.53, 1133.68, 1179.63, 1234.67, 1252.64, 1265.66, 1267.70, 1277.70, 1307.68, 1319.71, 1320.64, 1323.71, 1365.66, 1374.64, 1383.69, 1397.69, 1424.71, 1434.76, 1493.74, 1515.73, 1519.70, 1522.66, 1536.74, 1590.74, 1604.80, 1620.81, 1656.90, 1687.82, 1703.84, 1707.74, 1716.81, 1754.92, 1791.83, 1796.96, 1838.87, 1886.90, 1950.90, 1955.85, 2198.89, 2214.88, 2252.97

17. gi|24581132 **Mass:** 42670 **Score:** 38 **Expect:** 7.6 **Queries matched:** 8

CG31948-PB, isoform B [Drosophila melanogaster]

Observed	Mr(expt)	Mr(calc)	ppm	Start		End	Miss	Peptide
1252.64	1251.64	1251.65	-12.66	56	-	65	1	K.DEYLLCKVAK.K + Propionamide (C)
1319.71	1318.71	1318.73	-19.82	275	-	285	0	R.SIFVIPMIVER.R + Oxidation (M)
1434.76	1433.76	1433.70	41.9	345	-	355	1	K.EYIENHCSKIK.Y + Propionamide (C)
1475.76	1474.75	1474.83	-55.16	275	-	286	1	R.SIFVIPMIVERR.L + Oxidation (M)
1536.74	1535.73	1535.79	-38.93	263	-	274	1	R.CTSFIKHFDLVR.S + Propionamide (C)
1703.84	1702.83	1702.86	-17.44	49	-	62	1	R.FFDAVLKDEYLLCK.V
1955.85	1954.84	1954.96	-58.31	253	-	268	1	R.VARPMCPPYRCTSFIK.H + Oxidation (M); Propionamide (C)
2252.97	2251.96	2251.94	7.60	167	-	185	1	K.CCDGEDNRPPYARIMPEDR.R + Oxidation (M)

No match to: 807.46, 829.41, 842.51, 913.46, 967.49, 973.54, 995.57, 1005.59, 1036.57, 1066.55, 1070.61, 1089.61, 1106.65, 1109.53, 1133.68, 1179.63, 1234.67, 1265.66, 1267.70, 1277.70, 1307.68, 1308.67, 1320.64, 1323.71, 1365.66, 1374.64, 1381.66, 1383.69, 1397.69, 1424.71, 1493.74, 1515.73, 1519.70, 1522.66, 1590.74, 1604.80, 1611.89, 1620.81, 1641.83, 1656.90, 1687.82, 1707.74, 1716.81, 1754.92, 1759.87, 1791.83, 1796.96, 1838.87, 1886.90, 1950.90, 2198.89, 2214.88

18. gi|24641704 **Mass:** 170230 **Score:** 38 **Expect:** 7.8 **Queries matched:** 15

strawberry notch CG1903-PB, isoform B [Drosophila melanogaster]

Observed	Mr(expt)	Mr(calc)	ppm	Start		End	Miss	Peptide
995.57	994.56	994.54	24.9	612	-	619	1	K.LRGMYIAR.Q + Oxidation (M)
1109.53	1108.52	1108.55	-30.72	753	-	761	1	R.HFPAPDRNR.I
1320.64	1319.63	1319.63	4.88	468	-	478	1	K.ISSDVNNNCKR.G + Propionamide (C)
1323.71	1322.70	1322.68	16.8	1191	-	1201	1	K.YGRQALETVMR.T
1383.69	1382.68	1382.69	-10.14	1250	-	1260	1	K.DYNNISKFLNR.I
1397.69	1396.69	1396.64	37.0	731	-	743	0	R.DDGELTDFVSTAK.G
1424.71	1423.70	1423.75	-38.34	1163	-	1175	1	R.LESLGALTHGDRR.A
1522.66	1521.65	1521.74	-56.70	1319	-	1332	0	K.HATGVAPTEMHTVR.V + Oxidation (M)
1536.74	1535.73	1535.81	-50.48	1111	-	1123	0	R.VHITLELPWSADR.A
1590.74	1589.73	1589.79	-35.83	1333	-	1345	1	R.VERGMIWQEAIDK.Y + Oxidation (M)
1620.81	1619.80	1619.82	-9.99	599	-	613	1	R.GVGAMEIVAMDMKLR.G
1656.90	1655.89	1655.91	-16.04	1478	-	1492	0	R.LYHVLAGSVLSVWGR.V
1796.96	1795.96	1795.89	37.0	182	-	198	0	K.LNNMVTVSYAGGASQIR.A + Oxidation (M)
1838.87	1837.86	1837.89	-18.23	642	-	656	0	K.IYDQSVELWVEAMQK.F
2252.97	2251.96	2252.08	-54.56	724	-	743	1	R.TLDQLERDDGELTDFVSTAK.G

No match to: 807.46, 829.41, 842.51, 913.46, 967.49, 973.54, 1005.59, 1036.57, 1066.55, 1070.61, 1089.61, 1106.65, 1133.68, 1179.63, 1234.67, 1252.64, 1265.66, 1267.70, 1277.70, 1307.68, 1308.67, 1319.71, 1365.66, 1374.64, 1381.66, 1434.76, 1475.76, 1493.74, 1515.73, 1519.70, 1604.80, 1611.89, 1641.83, 1687.82, 1703.84, 1707.74, 1716.81, 1754.92, 1759.87, 1791.83, 1886.90, 1950.90, 1955.85, 2198.89, 2214.88

19. gi|2078282 **Mass:** 170361 **Score:** 38 **Expect:** 8.3 **Queries matched:** 15

Sno [Drosophila melanogaster]

Observed	Mr(expt)	Mr(calc)	ppm	Start		End	Miss	Peptide
995.57	994.56	994.54	24.9	612	-	619	1	K.LRGMYIAR.Q + Oxidation (M)
1109.53	1108.52	1108.55	-30.72	753	-	761	1	R.HFPAPDRNR.I
1320.64	1319.63	1319.63	4.88	468	-	478	1	K.ISSDVNNNCKR.G + Propionamide (C)
1323.71	1322.70	1322.68	16.8	1191	-	1201	1	K.YGRQALETVMR.T
1383.69	1382.68	1382.69	-10.14	1250	-	1260	1	K.DYNNISKFLNR.I
1397.69	1396.69	1396.64	37.0	731	-	743	0	R.DDGELTDFVSTAK.G
1424.71	1423.70	1423.75	-38.34	1163	-	1175	1	R.LESLGALTHGDRR.A
1522.66	1521.65	1521.74	-56.70	1319	-	1332	0	K.HATGVAPTEMHTVR.V + Oxidation (M)
1536.74	1535.73	1535.81	-50.48	1111	-	1123	0	R.VHITLELPWSADR.A
1590.74	1589.73	1589.79	-35.83	1333	-	1345	1	R.VERGMIWQEAIDK.Y + Oxidation (M)
1620.81	1619.80	1619.82	-9.99	599	-	613	1	R.GVGAMEIVAMDMKLR.G
1656.90	1655.89	1655.91	-16.04	1478	-	1492	0	R.LYHVLAGSVLSVWGR.V
1796.96	1795.96	1795.89	37.0	182	-	198	0	K.LNNMVTVSYAGGASQIR.A + Oxidation (M)
1838.87	1837.86	1837.89	-18.23	642	-	656	0	K.IYDQSVELWVEAMQK.F
2252.97	2251.96	2252.08	-54.56	724	-	743	1	R.TLDQLERDDGELTDFVSTAK.G

No match to: 807.46, 829.41, 842.51, 913.46, 967.49, 973.54, 1005.59, 1036.57, 1066.55, 1070.61, 1089.61, 1106.65, 1133.68, 1179.63, 1234.67, 1252.64, 1265.66, 1267.70, 1277.70, 1307.68, 1308.67, 1319.71, 1365.66, 1374.64, 1381.66, 1434.76, 1475.76, 1493.74, 1515.73, 1519.70, 1604.80, 1611.89, 1641.83, 1687.82, 1703.84, 1707.74, 1716.81, 1754.92, 1759.87, 1791.83, 1886.90, 1950.90, 1955.85, 2198.89, 2214.88

20. gi|24658169 **Mass:** 79930 **Score:** 36 **Expect:** 12 **Queries matched:** 10

CG4611-PA [Drosophila melanogaster]

```
Observed   Mr(expt)   Mr(calc)     ppm   Start    End  Miss   Peptide
  807.46     806.45     806.40    69.5    174 -  179    1    R.MLKEDR.A + Oxidation (M)
 1308.67    1307.66    1307.71  -39.69    483 -  493    0    K.ADIDFFNILIK.K
 1383.69    1382.68    1382.72  -30.77    538 -  549    0    R.ELLEQMHVAGIK.M + Oxidation (M)
 1475.76    1474.75    1474.76   -2.61     75 -   87    0    R.EEVFEELITAAPK.E
 1519.70    1518.70    1518.79  -59.95    313 -  324    0    R.HALLTWHNMLQR.G
 1656.90    1655.89    1655.80    54.7    253 -  266    1    K.GYEPNVKNYNAMIK.A + Oxidation (M)
 1687.82    1686.81    1686.69    69.2    339 -  352    1    R.CARDCGFGDLDSMR.E + 2 Propionamide (C)
 1759.87    1758.86    1758.86    1.22      9 -   24    1    R.SMSCHIRGLQLNATGR.R + Oxidation (M)
 1886.90    1885.89    1885.82    40.2    342 -  357    1    R.DCGFGDLDSMREVIDK.I + Oxidation (M); Propionamide (C)
 1950.90    1949.89    1949.93  -20.78    550 -  566    1    K.MNMPILGAMLRQGCANK.S + 2 Oxidation (M); Propionamide (C)
 No match to: 829.41, 842.51, 913.46, 967.49, 973.54, 995.57, 1005.59, 1036.57, 1066.55, 1070.61, 1089.61,
 1106.65, 1109.53, 1133.68, 1179.63, 1234.67, 1252.64, 1265.66, 1267.70, 1277.70, 1307.68, 1319.71, 1320.64,
 1323.71, 1365.66, 1374.64, 1381.66, 1397.69, 1424.71, 1434.76, 1493.74, 1515.73, 1522.66, 1536.74, 1590.74,
 1604.80, 1611.89, 1620.81, 1641.83, 1703.84, 1707.74, 1716.81, 1754.92, 1791.83, 1796.96, 1838.87, 1955.85,
 2198.89, 2214.88, 2252.97
```

Search Parameters

```
Type of search         : Peptide Mass Fingerprint
Enzyme                 : Trypsin
Variable modifications : Oxidation (M),Propionamide (C)
Mass values            : Monoisotopic
Protein Mass           : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Peptide Charge State   : 1+
Max Missed Cleavages   : 1
Number of queries      : 60
```

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

Mascot Search Results

```
User          : Ilya
Email         : toropygin@rambler.ru
Search title  : Submitted from Shidlovsky 080324 II by Mascot Daemon on P4P800SE
MS data file  : \\192.168.0.18\data on ultraflex-2\DATA\2008_Ilya\Shidlovsky\080325\005\0_J15\1\005__0_J15__1.dar
Database      : NCBInr 20070307 (4984280 sequences; 1723577896 residues)
Taxonomy      : Drosophila (fruit flies) (47828 sequences)
Timestamp     : 3 Apr 2008 at 21:53:38 GMT
Top Score     : 140 for gi|17137148, Origin recognition complex subunit 5 CG7833-PA [Drosophila melanogaster]
```

Probability Based Mowse Score

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 59 are significant (p<0.05).

Score Distribution

Protein Summary Report

Format As	Protein Summary	Help
	Significance threshold p< 0.05	Max. number of hits 20

Overview Table

Click on column header to jump to entry in results list.
Move mouse over any indicator to highlight identical peptides.
Click on an indicator to see details of individual match.
Use check boxes to select sub-set of queries for new search.

Mouse over: -Query-

-Accession- -Sequence-

Hit:	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
☑ 842.51 (1+)				?	?							?								
☑ 913.43 (1+)																?				
☑ 973.52 (1+)						?	?	?	?				?			?	?			
☑ 1082.55 (1+)	?	?	?	?					?	?	?						?			
☑ 1098.56 (1+)	?	?	?		?					?	?					?				
☑ 1141.61 (1+)	?									?	?	?					?			
☑ 1162.61 (1+)	?											?	?							
☑ 1173.58 (1+)				?	?										?				?	?
☑ 1179.59 (1+)		?	?			?		?								?				
☑ 1333.67 (1+)	?			?	?				?					?			?	?		
☑ 1395.75 (1+)	?			?			?									?			?	
☑ 1461.77 (1+)	?					?		?						?				?	?	

☑ 1475.75 (1+)							?							?		?		?		
☑ 1494.71 (1+)	?									?	?					?				
☑ 1567.74 (1+)					?					?	?		?		?	?				?
☑ 1586.90 (1+)	?				?															
☑ 1634.86 (1+)	?	?	?				?		?	?	?									
☑ 1640.91 (1+)	?	?	?			?		?					?			?				
☑ 1650.82 (1+)	?			?	?	?		?	?						?		?			?
☑ 1675.82 (1+)	?	?	?																	
☑ 1795.79 (1+)		?	?							?	?		?		?		?			?
☑ 2211.10 (1+)										?	?									
☑ 2225.11 (1+)		?	?				?													
☑ 2305.12 (1+)	?						?										?			
☑ 2433.21 (1+)	?	?	?						?								?	?	?	

Select All   Select None   Search Selected

Index

	Accession	Mass	Score	Description
1.	gi|17137148	52082	140	Origin recognition complex subunit 5 CG7833-PA [Drosophila melanogaster]
2.	gi|24650048	108801	44	CG10669-PA [Drosophila melanogaster]
3.	gi|19528115	108736	44	AT25429p [Drosophila melanogaster]
4.	gi|125776637	45640	42	GA18345-PA [Drosophila pseudoobscura]
5.	gi|24642019	93877	40	CG14411-PA, isoform A [Drosophila melanogaster]
6.	gi|20128991	30427	40	CG17764-PA [Drosophila melanogaster]
7.	gi|125982920	59375	40	GA17465-PA [Drosophila pseudoobscura]
8.	gi|18447016	30557	40	AT19038p [Drosophila melanogaster]
9.	gi|125986756	46335	39	GA12523-PA [Drosophila pseudoobscura]
10.	gi|24646878	92725	38	CG7886-PA [Drosophila melanogaster]
11.	gi|21064159	92755	38	AT27185p [Drosophila melanogaster]
12.	gi|20151513	3968	38	GM09207p [Drosophila melanogaster]
13.	gi|125986509	39107	37	GA18584-PA [Drosophila pseudoobscura]
14.	gi|224804	8951	37	caudal 38E gene
15.	gi|6531636	19387	37	TC21 ras-related [Drosophila melanogaster]
16.	gi|6665667	198883	36	UNC-13 [Drosophila melanogaster]
17.	gi|24653385	149429	36	centrosomin CG4832-PC, isoform C [Drosophila melanogaster]
18.	gi|578301	22233	35	put. cad fragment [Drosophila melanogaster]
19.	gi|17016304	27877	35	dacapo [Drosophila virilis]
20.	gi|24657269	22221	35	Ras oncogene at 64B CG1167-PA [Drosophila melanogaster]

Results List

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1.     gi|17137148     Mass: 52082    Score: 140    Expect: 4.8e-010  Queries matched: 15
       Origin recognition complex subunit 5 CG7833-PA [Drosophila melanogaster]
      Observed  Mr(expt)  Mr(calc)   ppm  Start   End Miss   Peptide
       1082.55   1081.55   1081.56 -10.62   285 - 293   0    R.SALTQIYMR.I
       1098.56   1097.55   1097.55  -5.32   285 - 293   0    R.SALTQIYMR.I + Oxidation (M)
       1141.61   1140.60   1140.61  -9.96   243 - 252   0    R.DVPELQLTAR.K
       1162.61   1161.61   1161.61  -7.87   191 - 200   0    R.ILGSDFQQVR.N
       1333.67   1332.66   1332.67  -4.48   201 - 211   0    R.NQLLEQFAQDK.K
       1395.75   1394.74   1394.74  -2.80   315 - 326   0    K.LAQSLELPYYAK.F
       1461.77   1460.76   1460.76  -1.43   201 - 212   1    R.NQLLEQFAQDKK.R
       1494.71   1493.70   1493.72 -10.14    98 - 109   0    K.VDNMLDFVEQLR.R + Oxidation (M)
       1586.90   1585.89   1585.90  -4.39   327 - 341   0    K.FLLIAAFLASHNAAK.Q
       1634.86   1633.85   1633.82   16.4    98 - 110   1    K.VDNMLDFVEQLRR.Q
       1640.91   1639.90   1639.91  -5.19   131 - 144   1    R.LRDMDANVLPVLLR.L + Oxidation (M)
       1650.82   1649.81   1649.82  -3.78    98 - 110   1    K.VDNMLDFVEQLRR.Q + Oxidation (M)
       1675.82   1674.81   1674.82  -4.09   116 - 130   0    R.VEDQGFLIAVDNAER.L
       2305.12   2304.12   2304.11   2.35   294 - 313   0    R.IEKPAEEVEDFTAIEDQSVR.K
       2433.21   2432.20   2432.21  -1.17   294 - 314   1    R.IEKPAEEVEDFTAIEDQSVRK.L
      No match to: 842.51, 913.43, 973.52, 1173.58, 1179.59, 1475.75, 1567.74, 1795.79, 2211.10, 2225.11

2.     gi|24650048     Mass: 108801    Score: 44     Expect: 2  Queries matched: 9
       CG10669-PA [Drosophila melanogaster]
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       Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss  Peptide
        1082.55   1081.55   1081.53   12.6    442 -  450   1   R.DLRMGVYGR.Y + Oxidation (M)
        1098.56   1097.55   1097.48   57.9    765 -  773   1   R.TQCMNTEKK.F + Oxidation (M)
        1179.59   1178.58   1178.60 -13.62    380 -  388   1   K.EIKCMICLR.R + Propionamide (C)
        1634.86   1633.85   1633.86  -5.88    660 -  673   1   K.ICDIQFVSVADLRR.H
        1640.91   1639.90   1639.79   63.7    851 -  865   0   K.YLCSLCGLESLTPNK.L
        1675.82   1674.81   1674.78   23.5    365 -  379   1   R.VDGFDFHRSEPNGAK.E
        1795.79   1794.78   1794.79  -3.01    873 -  887   1   R.HTGEKPFKCDLCDMR.F + Oxidation (M)
        2225.11   2224.10   2223.96   62.5     82 -  102   0   K.IGDSLNGDDEMEGTAALECLR.E + Oxidation (M)
        2433.21   2432.20   2432.33 -53.71     28 -   48   1   K.TFVQLLVELTRIEVVMAQAEK.F + Oxidation (M)
        No match to: 842.51, 913.43, 973.52, 1141.61, 1162.61, 1173.58, 1333.67, 1395.75, 1461.77, 1475.75, 1494.71,
        1567.74, 1586.90, 1650.82, 2211.10, 2305.12

  3.    gi|19528115     Mass: 108736    Score: 44     Expect: 2  Queries matched: 9
        AT25429p [Drosophila melanogaster]
       Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss  Peptide
        1082.55   1081.55   1081.53   12.6    442 -  450   1   R.DLRMGVYGR.Y + Oxidation (M)
        1098.56   1097.55   1097.48   57.9    765 -  773   1   R.TQCMNTEKK.F + Oxidation (M)
        1179.59   1178.58   1178.60 -13.62    380 -  388   1   K.EIKCMICLR.R + Propionamide (C)
        1634.86   1633.85   1633.86  -5.88    660 -  673   1   K.ICDIQFVSVADLRR.H
        1640.91   1639.90   1639.79   63.7    851 -  865   0   K.YLCSLCGLESLTPNK.L
        1675.82   1674.81   1674.78   23.5    365 -  379   1   R.VDGFDFHRSEPNGAK.E
        1795.79   1794.78   1794.79  -3.01    873 -  887   1   R.HTGEKPFKCDLCDMR.F + Oxidation (M)
        2225.11   2224.10   2223.96   62.5     82 -  102   0   K.IGDSLNGDDEMEGTAALECLR.E + Oxidation (M)
        2433.21   2432.20   2432.33 -53.71     28 -   48   1   K.TFVQLLVELTRIEVVMAQAEK.F + Oxidation (M)
        No match to: 842.51, 913.43, 973.52, 1141.61, 1162.61, 1173.58, 1333.67, 1395.75, 1461.77, 1475.75, 1494.71,
        1567.74, 1586.90, 1650.82, 2211.10, 2305.12

  4.    gi|125776637     Mass: 45640     Score: 42     Expect: 2.8  Queries matched: 6
        GA18345-PA [Drosophila pseudoobscura]
       Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss  Peptide
         842.51    841.50    841.50   0.00     17 -   23   1   K.RIEISPK.S
        1082.55   1081.55   1081.55  -0.28    334 -  343   0   K.FVTICVTGDK.T
        1173.58   1172.57   1172.60 -21.82    175 -  184   0   K.CQPSAITLNR.Q + Propionamide (C)
        1333.67   1332.66   1332.61   36.1    189 -  199   0   R.HVDNVMFENTK.I
        1395.75   1394.74   1394.75  -3.77    200 -  209   1   K.IVERFLNYWR.T
        1650.82   1649.81   1649.83 -10.58    175 -  188   1   K.CQPSAITLNRQTYR.H
        No match to: 913.43, 973.52, 1098.56, 1141.61, 1162.61, 1179.59, 1461.77, 1475.75, 1494.71, 1567.74,
        1586.90, 1634.86, 1640.91, 1675.82, 1795.79, 2211.10, 2225.11, 2305.12, 2433.21

  5.    gi|24642019     Mass: 93877     Score: 40     Expect: 5.1  Queries matched: 7
        CG14411-PA, isoform A [Drosophila melanogaster]
       Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss  Peptide
         842.51    841.50    841.54 -43.24    240 -  247   0   K.LIASALVR.F
        1098.56   1097.55   1097.51   30.9    222 -  230   0   K.FAFQQQDSK.M
        1173.58   1172.57   1172.59 -12.24    415 -  424   1   R.RLCTPETPEK.F
        1333.67   1332.66   1332.71 -34.31    374 -  384   1   K.SENVMLELVRK.C + Oxidation (M)
        1567.74   1566.73   1566.81 -48.81    504 -  515   1   K.EWVALEHPFQRR.L
        1586.90   1585.89   1585.78   68.5    615 -  626   1   K.MFFSNPLYQRQR.G
        1650.82   1649.81   1649.84 -16.99     25 -   39   0   R.NTFTSYVAPLPGDLR.A
        No match to: 913.43, 973.52, 1082.55, 1141.61, 1162.61, 1179.59, 1395.75, 1461.77, 1475.75, 1494.71,
        1634.86, 1640.91, 1675.82, 1795.79, 2211.10, 2225.11, 2305.12, 2433.21

  6.    gi|20128991     Mass: 30427     Score: 40     Expect: 5.1  Queries matched: 5
        CG17764-PA [Drosophila melanogaster]
       Observed  Mr(expt)  Mr(calc)   ppm  Start    End Miss  Peptide
         973.52    972.51    972.51 -0.58     36 -   43   0   K.FSSINLHR.M
        1179.59   1178.58   1178.59 -7.36      1 -   10   1   -.MSKAQQLMAR.D + Oxidation (M)
        1461.77   1460.76   1460.69  46.1    236 -  248   0   R.NIDIAESPMAQTR.R + Oxidation (M)
        1640.91   1639.90   1639.82  46.0     71 -   86   1   K.APVETNADAPAMPTKK.E
        1650.82   1649.81   1649.83 -8.53     30 -   43   1   R.QSYGNKFSSINLHR.M
        No match to: 842.51, 913.43, 1082.55, 1098.56, 1141.61, 1162.61, 1173.58, 1333.67, 1395.75, 1475.75,
        1494.71, 1567.74, 1586.90, 1634.86, 1675.82, 1795.79, 2211.10, 2225.11, 2305.12, 2433.21

  7.    gi|125982920     Mass: 59375     Score: 40     Expect: 5.2  Queries matched: 6
        GA17465-PA [Drosophila pseudoobscura]
       Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss  Peptide
         973.52    972.51    972.50   17.7     61 -   68   0   K.QAVLHFCR.N
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        1395.75   1394.74   1394.81  -52.12    407 - 419    0    K.LASDLVPDVVLVR.K
        1475.75   1474.75   1474.69    36.4     61 -  72    1    K.QAVLHFCRNCER.Y
        1634.86   1633.85   1633.87  -12.74    274 - 287    0    R.HQLGNLSPICLVNR.V + Propionamide (C)
        2225.11   2224.10   2224.11   -4.78    323 - 340    1    K.QLVEYVVMDIEVIMEKDR.K + Oxidation (M)
        2305.12   2304.12   2304.18  -26.99     50 -  68    1    R.NHVDITENIPKQAVLHFCR.N + Propionamide (C)
       No match to: 842.51, 913.43, 1082.55, 1098.56, 1141.61, 1162.61, 1173.58, 1179.59, 1333.67, 1461.77,
       1494.71, 1567.74, 1586.90, 1640.91, 1650.82, 1675.82, 1795.79, 2211.10, 2433.21

  8.   gi|18447016     Mass: 30557     Score: 40     Expect: 5.4  Queries matched: 5
       AT19038p [Drosophila melanogaster]
       Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
         973.52    972.51    972.51  -0.58    36 -  43    0    K.FSSINLHR.M
        1179.59   1178.58   1178.59  -7.36     1 -  10    1    -.MSKAQQLMAR.D + Oxidation (M)
        1461.77   1460.76   1460.69   46.1   238 - 250    0    R.NIDIAESPMAQTR.R + Oxidation (M)
        1640.91   1639.90   1639.82   46.0    71 -  86    1    K.APVETNADAPAMPTKK.E
        1650.82   1649.81   1649.83  -8.53    30 -  43    1    R.QSYGNKFSSINLHR.M
       No match to: 842.51, 913.43, 1082.55, 1098.56, 1141.61, 1162.61, 1173.58, 1333.67, 1395.75, 1475.75,
       1494.71, 1567.74, 1586.90, 1634.86, 1675.82, 1795.79, 2211.10, 2225.11, 2305.12, 2433.21

  9.   gi|125986756     Mass: 46335     Score: 39     Expect: 6.3  Queries matched: 6
       GA12523-PA [Drosophila pseudoobscura]
       Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
         973.52    972.51    972.49    25.3    175 - 182    1    R.STRGPNWR.Q
        1082.55   1081.55   1081.56  -11.24    255 - 262    0    R.NIFDWLFK.R
        1333.67   1332.66   1332.65    5.96    238 - 249    1    R.NKHPSVGNSHEK.A
        1634.86   1633.85   1633.81    25.7     17 -  32    0    K.GTSTVITTTAPQMGNR.S
        1650.82   1649.81   1649.80    5.45     17 -  32    0    K.GTSTVITTTAPQMGNR.S + Oxidation (M)
        2433.21   2432.20   2432.34  -55.29    289 - 309    1    R.KPHTTERPTEKTTEKPTVKPK.L
       No match to: 842.51, 913.43, 1098.56, 1141.61, 1162.61, 1173.58, 1179.59, 1395.75, 1461.77, 1475.75,
       1494.71, 1567.74, 1586.90, 1640.91, 1675.82, 1795.79, 2211.10, 2225.11, 2305.12

 10.   gi|24646878     Mass: 92725     Score: 38     Expect: 7.4  Queries matched: 8
       CG7886-PA [Drosophila melanogaster]
       Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
        1082.55   1081.55   1081.54    9.50      2 -  10    1    M.SVSRVTMMR.K + Oxidation (M)
        1098.56   1097.55   1097.53    14.5      2 -  10    1    M.SVSRVTMMR.K + 2 Oxidation (M)
        1141.61   1140.60   1140.54    56.0    758 - 766    0    K.YSSMHVFVR.R + Oxidation (M)
        1494.71   1493.70   1493.65    33.3    584 - 595    1    K.SDHEFANERDFK.L
        1567.74   1566.73   1566.78  -34.05    335 - 347    1    R.SIHDRLGCLPEEK.Q + Propionamide (C)
        1634.86   1633.85   1633.78    41.5    106 - 119    0    R.TYPQTNIDPIDTEK.R
        1795.79   1794.78   1794.86  -43.06    436 - 450    1    R.NDVMPEVIKNSQSYR.Q + Oxidation (M)
        2211.10   2210.10   2210.12  -10.18    451 - 470    1    R.QSHFNRLVNSAATSPEVTPR.S
       No match to: 842.51, 913.43, 973.52, 1162.61, 1173.58, 1179.59, 1333.67, 1395.75, 1461.77, 1475.75, 1586.90,
       1640.91, 1650.82, 1675.82, 2225.11, 2305.12, 2433.21

 11.   gi|21064159     Mass: 92755     Score: 38     Expect: 8.1  Queries matched: 8
       AT27185p [Drosophila melanogaster]
       Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
        1082.55   1081.55   1081.54    9.50      2 -  10    1    M.SVSRVTMMR.K + Oxidation (M)
        1098.56   1097.55   1097.53    14.5      2 -  10    1    M.SVSRVTMMR.K + 2 Oxidation (M)
        1141.61   1140.60   1140.54    56.0    758 - 766    0    K.YSSMHVFVR.R + Oxidation (M)
        1494.71   1493.70   1493.65    33.3    584 - 595    1    K.SDHEFANERDFK.L
        1567.74   1566.73   1566.73   -3.66    174 - 187    0    K.ALADNECLETVSFR.K
        1634.86   1633.85   1633.78    41.5    106 - 119    0    R.TYPQTNIDPIDTEK.R
        1795.79   1794.78   1794.86  -43.06    436 - 450    1    R.NDVMPEVIKNSQSYR.Q + Oxidation (M)
        2211.10   2210.10   2210.12  -10.18    451 - 470    1    R.QSHFNRLVNSAATSPEVTPR.S
       No match to: 842.51, 913.43, 973.52, 1162.61, 1173.58, 1179.59, 1333.67, 1395.75, 1461.77, 1475.75, 1586.90,
       1640.91, 1650.82, 1675.82, 2225.11, 2305.12, 2433.21

 12.   gi|20151513     Mass: 3968     Score: 38     Expect: 8.3  Queries matched: 3
       GM09207p [Drosophila melanogaster]
       Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
         842.51    841.50    841.55  -56.59     11 -  17    1    K.AIRILTR.D
        1141.61   1140.60   1140.68  -65.08     22 -  31    0    R.IPHHTALKPK.S
        1162.61   1161.61   1161.62  -10.75      1 -  10    1    -.MVLDAIRSNK.A + Oxidation (M)
       No match to: 913.43, 973.52, 1082.55, 1098.56, 1173.58, 1179.59, 1333.67, 1395.75, 1461.77, 1475.75,
       1494.71, 1567.74, 1586.90, 1634.86, 1640.91, 1650.82, 1675.82, 1795.79, 2211.10, 2225.11, 2305.12, 2433.21
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13.   gi|125986509    Mass: 39107    Score: 37     Expect: 10  Queries matched: 5
      GA18584-PA [Drosophila pseudoobscura]
     Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss  Peptide
       973.52    972.51    972.49   29.2   248 -  255   0    R.DKPHAMFK.R
      1162.61   1161.61   1161.55   48.6    74 -   85   1    K.SGGTRNGGNTNK.T
      1567.74   1566.73   1566.78 -31.04    47 -   60   1    K.EVAEAYEVLSDKSK.R
      1640.91   1639.90   1639.93 -18.47   207 -  220   1    K.EDKVLQISIKPGWK.S
      1795.79   1794.78   1794.86 -47.21   271 -  287   0    K.QALCGVVFQVPTMSGDK.L + Oxidation (M)
      No match to: 842.51, 913.43, 1082.55, 1098.56, 1141.61, 1173.58, 1179.59, 1333.67, 1395.75, 1461.77,
      1475.75, 1494.71, 1586.90, 1634.86, 1650.82, 1675.82, 2211.10, 2225.11, 2305.12, 2433.21

14.   gi|224804     Mass: 8951     Score: 37     Expect: 10  Queries matched: 3
      caudal 38E gene
     Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss  Peptide
      1333.67   1332.66   1332.69 -20.33    39 -   50   0    K.SELAQTLSLSER.Q
      1461.77   1460.76   1460.78 -15.88    38 -   50   1    R.KSELAQTLSLSER.Q
      1475.75   1474.75   1474.72   14.9    26 -   36   1    K.EYCTSRYITIR.R + Propionamide (C)
      No match to: 842.51, 913.43, 973.52, 1082.55, 1098.56, 1141.61, 1162.61, 1173.58, 1179.59, 1395.75, 1494.71,
      1567.74, 1586.90, 1634.86, 1640.91, 1650.82, 1675.82, 1795.79, 2211.10, 2225.11, 2305.12, 2433.21

15.   gi|6531636     Mass: 19387    Score: 37     Expect: 10  Queries matched: 4
      TC21 ras-related [Drosophila melanogaster]
     Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss  Peptide
      1173.58   1172.57   1172.55   18.8    18 -   27   0    K.QCNIDDVPAK.L + Propionamide (C)
      1567.74   1566.73   1566.72   7.67    80 -   92   1    K.DRDEFPMLMVGNK.C + Oxidation (M)
      1650.82   1649.81   1649.86 -30.29   112 -  125   1    R.NLMIPYIECSAKLR.V
      1795.79   1794.78   1794.85 -36.80    28 -   43   0    K.LDILDTAGQEEFSAMR.E
      No match to: 842.51, 913.43, 973.52, 1082.55, 1098.56, 1141.61, 1162.61, 1179.59, 1333.67, 1395.75, 1461.77,
      1475.75, 1494.71, 1586.90, 1634.86, 1640.91, 1675.82, 2211.10, 2225.11, 2305.12, 2433.21

16.   gi|6665667     Mass: 198883   Score: 36     Expect: 12  Queries matched: 9
      UNC-13 [Drosophila melanogaster]
     Observed  Mr(expt)  Mr(calc)    ppm  Start     End Miss  Peptide
       913.43    912.42    912.44 -18.07   993 -   999   0    R.IDLSMYR.N + Oxidation (M)
       973.52    972.51    972.51   7.51  1538 -  1545   0    K.SPELQMLR.Y
      1098.56   1097.55   1097.55  -2.25   970 -   979   1    R.FAASNFGKEK.F
      1179.59   1178.58   1178.55   23.5   628 -   638   1    R.QGVRCTECGVK.C
      1395.75   1394.74   1394.76 -13.30    73 -    86   1    K.KASTVGMFGSILGK.A
      1475.75   1474.75   1474.75  -5.35  1700 -  1711   1    K.GSVACWLPLMRR.I + Oxidation (M); Propionamide (C)
      1494.71   1493.70   1493.74 -22.01   392 -   405   0    K.VDSNIEASFASLNK.K
      1567.74   1566.73   1566.75 -15.01   406 -   419   1    K.KSDSFTPTNDSLQK.H
      1640.91   1639.90   1639.80   61.4   474 -   488   0    R.GETEEVVGGHMQVLR.Q
      No match to: 842.51, 1082.55, 1141.61, 1162.61, 1173.58, 1333.67, 1461.77, 1586.90, 1634.86, 1650.82,
      1675.82, 1795.79, 2211.10, 2225.11, 2305.12, 2433.21

17.   gi|24653385     Mass: 149429   Score: 36     Expect: 12  Queries matched: 8
      centrosomin CG4832-PC, isoform C [Drosophila melanogaster]
     Observed  Mr(expt)  Mr(calc)    ppm  Start     End Miss  Peptide
       973.52    972.51    972.56 -48.17   575 -   582   1    K.QLQTEVKK.K
      1082.55   1081.55   1081.55  -3.35  1215 -  1223   1    R.AMLKTVEMK.T + 2 Oxidation (M)
      1141.61   1140.60   1140.55   49.7   489 -   497   1    R.ERIHEQACR.T
      1333.67   1332.66   1332.67  -6.99    44 -    54   1    R.ELEEQMSALRK.E
      1650.82   1649.81   1649.77   27.5   527 -   542   1    K.ENDCAKTVISPSSSGR.S
      1795.79   1794.78   1794.81 -14.77   910 -   923   0    R.MLNVQCQMVELDNR.Y + 2 Oxidation (M); Propionamide (C)
      2305.12   2304.12   2304.21 -42.17   304 -   323   1    K.NVLNYEALIAKLNAELETMR.Q
      2433.21   2432.20   2432.23 -12.06  1048 -  1067   0    R.DWVALTTYQEQAQQLLELQR.S
      No match to: 842.51, 913.43, 1098.56, 1162.61, 1173.58, 1179.59, 1395.75, 1461.77, 1475.75, 1494.71,
      1567.74, 1586.90, 1634.86, 1640.91, 1675.82, 2211.10, 2225.11

18.   gi|578301     Mass: 22233    Score: 35     Expect: 14  Queries matched: 4
      put. cad fragment [Drosophila melanogaster]
     Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss  Peptide
      1333.67   1332.66   1332.69 -20.33    92 -  103   0    K.SELAQTLSLSER.Q
      1461.77   1460.76   1460.78 -15.88    91 -  103   1    R.KSELAQTLSLSER.Q
      1475.75   1474.75   1474.72   14.9    79 -   89   1    K.EYCTSRYITIR.R + Propionamide (C)
      2433.21   2432.20   2432.26 -21.85   175 -  197   0    R.LHPHLAAHSHSLAAVAAHSHQLQ.-
      No match to: 842.51, 913.43, 973.52, 1082.55, 1098.56, 1141.61, 1162.61, 1173.58, 1179.59, 1395.75, 1494.71,
```

```
       1567.74, 1586.90, 1634.86, 1640.91, 1650.82, 1675.82, 1795.79, 2211.10, 2225.11, 2305.12

19.    gi|17016304    Mass: 27877    Score: 35     Expect: 15  Queries matched: 4
       dacapo [Drosophila virilis]
      Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
       1173.58   1172.57   1172.53    33.9    13 -   22    1    R.SEFCKMSVSR.N
       1395.75   1394.74   1394.76  -16.67     1 -   12    1    -.MVSARMLHPVVR.S
       1461.77   1460.76   1460.73    22.9     6 -   17    1    R.MLHPVVRSEFCK.M + Oxidation (M)
       2433.21   2432.20   2432.10    41.8   105 - 126    0    R.AAHVRPDAYDSASDMDALLNER.A + Oxidation (M)
       No match to: 842.51, 913.43, 973.52, 1082.55, 1098.56, 1141.61, 1162.61, 1179.59, 1333.67, 1475.75, 1494.71,
       1567.74, 1586.90, 1634.86, 1640.91, 1650.82, 1675.82, 1795.79, 2211.10, 2225.11, 2305.12

20.    gi|24657269    Mass: 22221    Score: 35     Expect: 17  Queries matched: 4
       Ras oncogene at 64B CG1167-PA [Drosophila melanogaster]
      Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
       1173.58   1172.57   1172.55    18.8    45 -   54    0    K.QCNIDDVPAK.L + Propionamide (C)
       1567.74   1566.73   1566.72    7.67   107 - 119    1    K.DRDEFPMLMVGNK.C + Oxidation (M)
       1650.82   1649.81   1649.86  -30.29   139 - 152    1    R.NLMIPYIECSAKLR.V
       1795.79   1794.78   1794.85  -36.80    55 -   70    0    K.LDILDTAGQEEFSAMR.E
       No match to: 842.51, 913.43, 973.52, 1082.55, 1098.56, 1141.61, 1162.61, 1179.59, 1333.67, 1395.75, 1461.77,
       1475.75, 1494.71, 1586.90, 1634.86, 1640.91, 1675.82, 2211.10, 2225.11, 2305.12, 2433.21
```

Search Parameters

```
Type of search         : Peptide Mass Fingerprint
Enzyme                 : Trypsin
Variable modifications : Oxidation (M),Propionamide (C)
Mass values            : Monoisotopic
Protein Mass           : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Peptide Charge State   : 1+
Max Missed Cleavages   : 1
Number of queries      : 25
```

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

Mascot Search Results

```
User            : Ilya
Email           : toropygin@rambler.ru
Search title    : Submitted from Shidlovsky 080328 II by Mascot Daemon on P4P800SE
MS data file    : \\192.168.0.18\data on ultraflex-2\DATA\2008_Ilya\Shidlovsky\080328\010\0_J24\1\010__0_J24__1.dar
Database        : NCBInr 20070307 (4984280 sequences; 1723577896 residues)
Taxonomy        : Drosophila (fruit flies) (47828 sequences)
Timestamp       : 2 Apr 2008 at 19:56:31 GMT
Top Score       : 100 for gi|5081626, origin recognition complex subunit 3 [Drosophila melanogaster]
```

Probability Based Mowse Score

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 59 are significant (p<0.05).

Score Distribution

Protein Summary Report

Format As	Protein Summary	Help
	Significance threshold p< 0.05	Max. number of hits 20

Overview Table

Click on column header to jump to entry in results list.
Move mouse over any indicator to highlight identical peptides.
Click on an indicator to see details of individual match.
Use check boxes to select sub-set of queries for new search.

Mouse over: -Query-

-Accession- -Sequence-

Hit:	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
☑ 1015.53 (1+)					?				?		?	?	?			?	?		?	?
☑ 1171.55 (1+)																		?		
☑ 1201.58 (1+)						?		?										?		
☑ 1320.71 (1+)								?	?	?										
☑ 1351.75 (1+)	?	?	?						?			?	?					?		
☑ 1399.73 (1+)	?	?	?	?	?		?		?		?					?	?		?	?
☑ 1518.72 (1+)	?	?	?									?		?						
☑ 1553.85 (1+)	?	?	?	?									?							
☑ 1569.85 (1+)	?	?	?		?					?										
☑ 1586.79 (1+)	?	?	?		?		?				?					?	?	?	?	?
☑ 1703.94 (1+)	?	?	?	?		?				?					?					
☑ 1714.89 (1+)	?	?	?		?		?				?					?	?	?	?	?
☑ 1807.04 (1+)	?	?	?																	
☑ 1830.96 (1+)	?	?	?					?	?			?	?							
☑ 1936.91 (1+)								?	?	?				?	?					

☑ **1952.91 (1+)**				?		?		?		?					?					
☑ **2023.07 (1+)**									?											
☑ **2102.12 (1+)**									?					?				?		
☑ **2124.98 (1+)**				?			?	?	?							?	?		?	?
☑ **2137.17 (1+)**						?					?									
☑ **2284.23 (1+)**							?							?						
☑ **2339.29 (1+)**	?	?	?							?										
☑ **2499.24 (1+)**	?	?			?													?		
☑ **2585.28 (1+)**								?			?					?	?		?	?
☑ **2722.45 (1+)**									?					?	?					
☑ **2808.38 (1+)**					?		?					?	?		?					
☑ **3362.75 (1+)**	?	?	?												?					
☑ **3570.52 (1+)**						?												?		

Select All   Select None   Search Selected

Index

	Accession	Mass	Score	Description
1.	gi|5081626	82120	100	origin recognition complex subunit 3 [Drosophila melanogaster]
2.	gi|5391451	82151	100	LATHEO [Drosophila melanogaster]
3.	gi|17136788	82201	86	latheo CG4088-PA, isoform A [Drosophila melanogaster]
4.	gi|125976956	23171	43	GA20782-PA [Drosophila pseudoobscura]
5.	gi|24648911	82796	41	CG31423-PA [Drosophila melanogaster]
6.	gi|24644214	29890	40	CG14667-PA, isoform A [Drosophila melanogaster]
7.	gi|28137740	69054	39	xanthine dehydrogenase [Drosophila koepferae]
8.	gi|24646727	68953	39	Origin recognition complex subunit 2 CG3041-PA [Drosophila melanogaster]
9.	gi|125777612	219672	38	GA19970-PA [Drosophila pseudoobscura]
10.	gi|3342458	36651	37	thymidylate synthase [Drosophila melanogaster]
11.	gi|37788606	68676	37	xanthine dehydrogenase [Drosophila buzzatii]
12.	gi|3915203	42995	37	Uroporphyrinogen decarboxylase (URO-D) (UPD)
13.	gi|125810666	39351	36	GA14829-PA [Drosophila pseudoobscura]
14.	gi|125986649	51171	36	GA11518-PA [Drosophila pseudoobscura]
15.	gi|21711659	61204	36	GH23001p [Drosophila melanogaster]
16.	gi|37788628	69063	36	xanthine dehydrogenase [Drosophila buzzatii]
17.	gi|37788634	69032	36	xanthine dehydrogenase [Drosophila buzzatii]
18.	gi|125808420	153274	36	GA10856-PA [Drosophila pseudoobscura]
19.	gi|37788610	69055	36	xanthine dehydrogenase [Drosophila buzzatii]
20.	gi|37788616	69055	36	xanthine dehydrogenase [Drosophila buzzatii]

Results List

1. gi|5081626 **Mass:** 82120 **Score:** 100 **Expect:** 4.9e-006 **Queries matched:** 13

origin recognition complex subunit 3 [Drosophila melanogaster]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1351.75	1350.74	1350.75	-9.81	696 -	707	0	R.AVAELQFLGYIK.M
1399.73	1398.73	1398.70	19.2	552 -	563	0	R.HQLNTPTTQFGR.A
1518.72	1517.71	1517.64	43.5	190 -	201	0	K.SWYTNNFDSEQK.R
1553.85	1552.84	1552.79	34.4	658 -	669	0	R.MINLFDWLQAFR.S
1569.85	1568.84	1568.78	38.6	658 -	669	0	R.MINLFDWLQAFR.S + Oxidation (M)
1586.79	1585.79	1585.74	28.4	43 -	54	0	K.EVVQQPFYEEYR.K
1703.94	1702.94	1702.89	27.0	75 -	89	0	R.TLEQLVDFVVGQAER.D
1714.89	1713.88	1713.84	26.4	43 -	55	1	K.EVVQQPFYEEYRK.A
1807.04	1806.04	1806.00	20.6	568 -	582	0	K.TLQLIETQIVQDHLR.A
1830.96	1829.96	1829.95	2.31	265 -	281	0	R.VFQTQAAPTGLNEVLDK.V
2339.29	2338.29	2338.23	23.6	583 -	603	0	R.ALQDAPPIHELFVFSDIATVR.R
2499.24	2498.23	2498.19	18.4	670 -	692	0	R.SVVSGSDNEEVAQEQIDPQIQAR.F
3362.75	3361.74	3361.72	6.81	90 -	120	0	R.DTPDEVLPTAALLTGINQPDHLSQFTALTQR.L

No match to: 1015.53, 1171.55, 1201.58, 1320.71, 1936.91, 1952.91, 2023.07, 2102.12, 2124.98, 2137.17, 2284.23, 2585.28, 2722.45, 2808.38, 3570.52

2. gi|5391451 **Mass:** 82151 **Score:** 100 **Expect:** 4.9e-006 **Queries matched:** 13

LATHEO [Drosophila melanogaster]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1351.75	1350.74	1350.75	-9.81	696 -	707	0	R.AVAELQFLGYIK.M
1399.73	1398.73	1398.70	19.2	552 -	563	0	R.HQLNTPTTQFGR.A
1518.72	1517.71	1517.64	43.5	190 -	201	0	K.SWYTNNFDSEQK.R
1553.85	1552.84	1552.79	34.4	658 -	669	0	R.MINLFDWLQAFR.S
1569.85	1568.84	1568.78	38.6	658 -	669	0	R.MINLFDWLQAFR.S + Oxidation (M)

```
          1586.79    1585.79    1585.74    28.4     43 -   54    0    K.EVVQQPFYEEYR.K
          1703.94    1702.94    1702.89    27.0     75 -   89    0    R.TLEQLVDFVVGQAER.D
          1714.89    1713.88    1713.84    26.4     43 -   55    1    K.EVVQQPFYEEYRK.A
          1807.04    1806.04    1806.00    20.6    568 -  582    0    K.TLQLIETQIVQDHLR.A
          1830.96    1829.96    1829.95    2.31    265 -  281    0    R.VFQTQAAPTGLNEVLDK.V
          2339.29    2338.29    2338.23    23.6    583 -  603    0    R.ALQDAPPIHELFVFSDIATVR.R
          2499.24    2498.23    2498.19    18.4    670 -  692    0    R.SVVSGSDNEEVAQEQIDPQIQAR.F
          3362.75    3361.74    3361.72    6.81     90 -  120    0    R.DTPDEVLPTAALLTGINQPDHLSQFTALTQR.L
         No match to: 1015.53, 1171.55, 1201.58, 1320.71, 1936.91, 1952.91, 2023.07, 2102.12, 2124.98, 2137.17, 2284.23,
         2585.28, 2722.45, 2808.38, 3570.52

   3.    gi|17136788      Mass: 82201      Score: 86      Expect: 0.00012  Queries matched: 12
         latheo CG4088-PA, isoform A [Drosophila melanogaster]
         Observed   Mr(expt)   Mr(calc)    ppm  Start    End Miss   Peptide
          1351.75    1350.74    1350.75   -9.81    696 -  707    0    R.AVAELQFLGYIK.M
          1399.73    1398.73    1398.70    19.2    552 -  563    0    R.HQLNTPTTQFGR.A
          1518.72    1517.71    1517.64    43.5    190 -  201    0    K.SWYTNNFDSEQK.R
          1553.85    1552.84    1552.79    34.4    658 -  669    0    R.MINLFDWLQAFR.S
          1569.85    1568.84    1568.78    38.6    658 -  669    0    R.MINLFDWLQAFR.S + Oxidation (M)
          1586.79    1585.79    1585.74    28.4     43 -   54    0    K.EVVQQPFYEEYR.K
          1703.94    1702.94    1702.89    27.0     75 -   89    0    R.TLEQLVDFVVGQAER.D
          1714.89    1713.88    1713.84    26.4     43 -   55    1    K.EVVQQPFYEEYRK.A
          1807.04    1806.04    1806.00    20.6    568 -  582    0    K.TLQLIETQIVQDHLR.A
          1830.96    1829.96    1829.95    2.31    265 -  281    0    R.VFQTQAAPTGLNEVLDK.V
          2339.29    2338.29    2338.23    23.6    583 -  603    0    R.ALQDAPPIHELFVFSDIATVR.R
          3362.75    3361.74    3361.72    6.81     90 -  120    0    R.DTPDEVLPTAALLTGINQPDHLSQFTALTQR.L
         No match to: 1015.53, 1171.55, 1201.58, 1320.71, 1936.91, 1952.91, 2023.07, 2102.12, 2124.98, 2137.17, 2284.23,
         2499.24, 2585.28, 2722.45, 2808.38, 3570.52

   4.    gi|125976956      Mass: 23171      Score: 43      Expect: 2.3  Queries matched: 5
         GA20782-PA [Drosophila pseudoobscura]
         Observed   Mr(expt)   Mr(calc)     ppm  Start    End Miss   Peptide
          1399.73    1398.73    1398.78  -35.23     56 -   67    1    R.LGLNTLPTRQMR.Y
          1553.85    1552.84    1552.82     15.8     68 -   79    0    R.YEQALPLHQLWR.G
          1703.94    1702.94    1702.92     11.5      1 -   14    0    -.LQEFITDLVVPHHR.C
          1952.91    1951.90    1951.99  -42.02     15 -   31    0    R.CNVNIIPEHITMLEGAK.S + Propionamide (C)
          2124.98    2123.97    2124.08  -52.51     15 -   33    1    R.CNVNIIPEHITMLEGAKSR.K
         No match to: 1015.53, 1171.55, 1201.58, 1320.71, 1351.75, 1518.72, 1569.85, 1586.79, 1714.89, 1807.04, 1830.96,
         1936.91, 2023.07, 2102.12, 2137.17, 2284.23, 2339.29, 2499.24, 2585.28, 2722.45, 2808.38, 3362.75, 3570.52

   5.    gi|24648911      Mass: 82796      Score: 41      Expect: 3.7  Queries matched: 7
         CG31423-PA [Drosophila melanogaster]
         Observed   Mr(expt)   Mr(calc)     ppm  Start    End Miss   Peptide
          1015.53    1014.53    1014.60  -68.93    132 -  139    1    K.NPQLKFLR.E
          1399.73    1398.73    1398.81  -56.09    401 -  412    1    R.FMDVLHKLGVLK.L
          1569.85    1568.84    1568.85   -6.79    140 -  152    1    R.ELINVIEEGREIR.T
          1586.79    1585.79    1585.87  -54.18     60 -   73    1    K.IVARPTLSIDSRCR.S
          1714.89    1713.88    1713.86     14.1    344 -  357    1    K.YNLSLKLYDQNESK.S
          2499.24    2498.23    2498.19     17.8    586 -  606    1    K.SFDERVFCESESLTIAWNLPR.M
          2808.38    2807.37    2807.31     19.6    188 -  212    0    R.ISGYFNDQAVILACMGENSDYGLLK.S + Oxidation (M); Propionamide (C)
         No match to: 1171.55, 1201.58, 1320.71, 1351.75, 1518.72, 1553.85, 1703.94, 1807.04, 1830.96, 1936.91, 1952.91,
         2023.07, 2102.12, 2124.98, 2137.17, 2284.23, 2339.29, 2585.28, 2722.45, 3362.75, 3570.52

   6.    gi|24644214      Mass: 29890      Score: 40      Expect: 5.4  Queries matched: 5
         CG14667-PA, isoform A [Drosophila melanogaster]
         Observed   Mr(expt)   Mr(calc)     ppm  Start    End Miss   Peptide
          1201.58    1200.57    1200.62  -36.97     20 -   28    1    R.DRNIFIHMR.G
          1703.94    1702.94    1703.00  -37.06     31 -   45    1    K.YLGQLKLITGVELTR.N
          1952.91    1951.90    1951.94  -18.32    237 -  253    1    R.RFQCTICHEAFASLGAK.L + Propionamide (C)
          2137.17    2136.16    2136.06     47.2    238 -  255    1    R.FQCTICHEAFASLGAKLR.H + 2 Propionamide (C)
          3570.52    3569.51    3569.59  -21.78    174 -  202    0    R.SNFFICDECGTLFHDAFLYTEHLNGHQNR.R + 2 Propionamide (C)
         No match to: 1015.53, 1171.55, 1320.71, 1351.75, 1399.73, 1518.72, 1553.85, 1569.85, 1586.79, 1714.89, 1807.04,
         1830.96, 1936.91, 2023.07, 2102.12, 2124.98, 2284.23, 2339.29, 2499.24, 2585.28, 2722.45, 2808.38, 3362.75

   7.    gi|28137740      Mass: 69054      Score: 39      Expect: 5.9  Queries matched: 6
         xanthine dehydrogenase [Drosophila koepferae]
         Observed   Mr(expt)   Mr(calc)     ppm  Start    End Miss   Peptide
          1399.73    1398.73    1398.70     22.0     32 -   43    0    R.CTGYRPILEGYK.T
          1586.79    1585.79    1585.81  -12.53    481 -  494    0    R.MDGELYLAFVLSTK.A
          1714.89    1713.88    1714.00  -67.43    151 -  164    1    K.FKHFLYPVLINPVK.V
          2124.98    2123.97    2124.10  -61.27      1 -   19    1    -.GIVMSMYALLRNAAKPSMR.D + Oxidation (M)
          2284.23    2283.22    2283.19     15.0    460 -  480    1    K.VHVSALKQATGEAIYTDDIPR.M
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          2808.38   2807.37   2807.36    2.88    225 - 252   0   R.NVACLGGNIMTASPISDMNTVLTAAGVR.L + 2 Oxidation (M)
         No match to: 1015.53, 1171.55, 1201.58, 1320.71, 1351.75, 1518.72, 1553.85, 1569.85, 1703.94, 1807.04, 1830.96,
         1936.91, 1952.91, 2023.07, 2102.12, 2137.17, 2339.29, 2499.24, 2585.28, 2722.45, 3362.75, 3570.52

   8.    gi|24646727     Mass: 68953    Score: 39     Expect: 6.3  Queries matched: 7
         Origin recognition complex subunit 2 CG3041-PA [Drosophila melanogaster]
         Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
          1201.58   1200.57   1200.61  -33.05   576 - 585   0   R.AQLTEFLDHK.L
          1320.71   1319.71   1319.71   -0.79   564 - 575   0   R.EAFLVSSDLALR.A
          1830.96   1829.96   1829.91    23.9   140 - 156   1   K.RDAMALAALNATPCTPK.T + Oxidation (M); Propionamide (C)
          1936.91   1935.90   1935.86    20.3   321 - 337   0   K.TSAEHEGSINAIMEEYR.S
          1952.91   1951.90   1951.86    23.4   321 - 337   0   K.TSAEHEGSINAIMEEYR.S + Oxidation (M)
          2124.98   2123.97   2123.92    24.5   273 - 291   0   K.SNEFVPESDGYFHSHASSK.I
          2585.28   2584.27   2584.23    16.2   116 - 138   0   K.DLHLIQSEYNVAGTSMFGFNTPK.K + Oxidation (M)
         No match to: 1015.53, 1171.55, 1351.75, 1399.73, 1518.72, 1553.85, 1569.85, 1586.79, 1703.94, 1714.89, 1807.04,
         2023.07, 2102.12, 2137.17, 2284.23, 2339.29, 2499.24, 2722.45, 2808.38, 3362.75, 3570.52

   9.    gi|125777612     Mass: 219672    Score: 38     Expect: 7.4  Queries matched: 10
         GA19970-PA [Drosophila pseudoobscura]
         Observed  Mr(expt)  Mr(calc)    ppm  Start     End Miss   Peptide
          1015.53   1014.53   1014.50    23.6  1474 - 1481   0   K.EWLAFGHR.F
          1320.71   1319.71   1319.77  -48.45   413 -  423   1   R.IHPKTVITFHK.A
          1351.75   1350.74   1350.78  -28.94   406 -  416   1   R.SCLTIIRIHPK.T + Propionamide (C)
          1399.73   1398.73   1398.63    69.2  1815 - 1825   1   K.CTELSMKNCTK.Y + 2 Propionamide (C)
          1830.96   1829.96   1829.87    46.8  1763 - 1777   1   K.GRLAGYQDNYFHPHR.F
          1936.91   1935.90   1935.88    10.6   855 -  871   0   R.FIDCVCTEGGVTSEHIR.N + Propionamide (C)
          2023.07   2022.07   2022.01    30.2  1011 - 1027   1   K.VAFDTEVTPEQIENFRK.I
          2102.12   2101.11   2101.11   -0.74   637 -  653   1   K.AILDHQQFELVLRFMNK.A
          2124.98   2123.97   2123.94    13.9  1858 - 1875   0   R.TSSHHFYNQFSSNVAENR.T
          2722.45   2721.44   2721.45   -5.71  1918 - 1944   1   K.GIIELAEVQSVTAAQPAQIGAKGVDEK.G
         No match to: 1171.55, 1201.58, 1518.72, 1553.85, 1569.85, 1586.79, 1703.94, 1714.89, 1807.04, 1952.91, 2137.17,
         2284.23, 2339.29, 2499.24, 2585.28, 2808.38, 3362.75, 3570.52

  10.    gi|3342458     Mass: 36651     Score: 37     Expect: 9.1  Queries matched: 6
         thymidylate synthase [Drosophila melanogaster]
         Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
          1320.71   1319.71   1319.62    67.8     35 -  44   0   R.DEMHYLDLLR.H + Oxidation (M)
          1569.85   1568.84   1568.80    25.1     71 -  83   1   R.FDMRNSFPLLTTK.R
          1703.94   1702.94   1702.85    47.9    182 - 195   1   R.RIIMSAWNPLDMPK.M + 2 Oxidation (M)
          1936.91   1935.90   1935.90   -1.04    196 - 212   0   K.MALPPCHCLAQFYVSEK.R
          1952.91   1951.90   1951.90    2.28    196 - 212   0   K.MALPPCHCLAQFYVSEK.R + Oxidation (M)
          2339.29   2338.29   2338.15    59.2     35 -  53   1   R.DEMHYLDLLRHIIANGEQR.M + Oxidation (M)
         No match to: 1015.53, 1171.55, 1201.58, 1351.75, 1399.73, 1518.72, 1553.85, 1586.79, 1714.89, 1807.04, 1830.96,
         2023.07, 2102.12, 2124.98, 2137.17, 2284.23, 2499.24, 2585.28, 2722.45, 2808.38, 3362.75, 3570.52

  11.    gi|37788606     Mass: 68676    Score: 37     Expect: 10  Queries matched: 6
         xanthine dehydrogenase [Drosophila buzzatii]
         Observed  Mr(expt)  Mr(calc)    ppm  Start    End  Miss   Peptide
          1015.53   1014.53   1014.56  -29.11   253 - 262    1   R.LEVASRAGGR.R
          1399.73   1398.73   1398.70    22.0    32 -  43    0   R.CTGYRPILEGYK.T
          1586.79   1585.79   1585.81  -12.53   481 - 494    0   R.MDGELYLAFVLSTK.A
          1714.89   1713.88   1714.00  -67.43   151 - 164    1   K.FKHFLYPVLINPVK.V
          2137.17   2136.16   2136.10    28.6     1 -  19    1   -.GIVMPMYALVRNAAKPSMR.D + 2 Oxidation (M)
          2585.28   2584.27   2584.36  -35.70   309 - 332    1   R.RDDDIAIVNSAVNVNFKPGTNVVK.S
         No match to: 1171.55, 1201.58, 1320.71, 1351.75, 1518.72, 1553.85, 1569.85, 1703.94, 1807.04, 1830.96, 1936.91,
         1952.91, 2023.07, 2102.12, 2124.98, 2284.23, 2339.29, 2499.24, 2722.45, 2808.38, 3362.75, 3570.52

  12.    gi|3915203     Mass: 42995     Score: 37     Expect: 11  Queries matched: 5
         Uroporphyrinogen decarboxylase (URO-D) (UPD)
         Observed  Mr(expt)  Mr(calc)    ppm  Start    End  Miss   Peptide
          1015.53   1014.53   1014.52    10.5   344 - 352    0   R.SLATEMVHK.C
          1351.75   1350.74   1350.65    67.5    58 -  67    1   R.KQHDFFTVCR.T + Propionamide (C)
          1518.72   1517.71   1517.76  -35.34     1 -  13    1   -.MTIKNNNNNNTLK.H
          1830.96   1829.96   1829.91    23.9    68 -  82    1   R.TPELACEVTMQPLRR.F + Oxidation (M); Propionamide (C)
          2808.38   2807.37   2807.32    17.9    59 -  81    1   K.QHDFFTVCRTPELACEVTMQPLR.R + Oxidation (M); Propionamide (C)
         No match to: 1171.55, 1201.58, 1320.71, 1399.73, 1553.85, 1569.85, 1586.79, 1703.94, 1714.89, 1807.04, 1936.91,
         1952.91, 2023.07, 2102.12, 2124.98, 2137.17, 2284.23, 2339.29, 2499.24, 2585.28, 2722.45, 3362.75, 3570.52

  13.    gi|125810666     Mass: 39351     Score: 36     Expect: 11  Queries matched: 5
         GA14829-PA [Drosophila pseudoobscura]
         Observed  Mr(expt)  Mr(calc)    ppm  Start    End  Miss   Peptide
          1015.53   1014.53   1014.55  -18.04   231 - 238    1   R.IRDELVDR.L
```

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        1351.75    1350.74    1350.65     67.5     43 -   52   1   R.KQHDFFTVCR.T + Propionamide (C)
        1553.85    1552.84    1552.87   -21.28      1 -   13   1   -.QPFPVLKNDNLLR.A
        1830.96    1829.96    1829.91     23.9     53 -   67   1   R.TPELACEVTMQPLRR.F + Oxidation (M); Propionamide (C)
        2808.38    2807.37    2807.32     17.9     44 -   66   1   K.QHDFFTVCRTPELACEVTMQPLR.R + Oxidation (M); Propionamide (C)
       No match to: 1171.55, 1201.58, 1320.71, 1399.73, 1518.72, 1569.85, 1586.79, 1703.94, 1714.89, 1807.04, 1936.91,
       1952.91, 2023.07, 2102.12, 2124.98, 2137.17, 2284.23, 2339.29, 2499.24, 2585.28, 2722.45, 3362.75, 3570.52

  14.   gi|125986649     Mass: 51171     Score: 36     Expect: 12  Queries matched: 5
       GA11518-PA [Drosophila pseudoobscura]
       Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
        1518.72    1517.71    1517.80   -59.77    234 - 247   1   R.KVFFHTDAAQAVGK.I
        1936.91    1935.90    1935.90     3.47    443 - 458   0   R.EMSPLWEMVQEGIDLK.S + 2 Oxidation (M)
        2102.12    2101.11    2101.00     53.3    248 - 266   0   K.IPMDVNAMNIDLMSISGHK.I + Oxidation (M)
        2284.23    2283.22    2283.11     50.3    380 - 401   0   K.DVALSSGSACTSASLEPSYVLR.A + Propionamide (C)
        2722.45    2721.44    2721.32     45.1    301 - 327   0   R.SGTVPASLAVGLGAAAELSQQEMEYDK.K
       No match to: 1015.53, 1171.55, 1201.58, 1320.71, 1351.75, 1399.73, 1553.85, 1569.85, 1586.79, 1703.94, 1714.89,
       1807.04, 1830.96, 1952.91, 2023.07, 2124.98, 2137.17, 2339.29, 2499.24, 2585.28, 2808.38, 3362.75, 3570.52

  15.   gi|21711659     Mass: 61204     Score: 36     Expect: 12  Queries matched: 6
       GH23001p [Drosophila melanogaster]
       Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
        1703.94    1702.94    1702.82     67.4      7 -   21   0   K.TNASTDVIFSPFNYK.M
        1936.91    1935.90    1935.98   -39.92    382 - 397   1   R.LQIQWELMSKDSSMLK.E
        1952.91    1951.90    1951.97   -36.27    382 - 397   1   R.LQIQWELMSKDSSMLK.E + Oxidation (M)
        2722.45    2721.44    2721.42     6.85     87 - 109   1   K.HLVRQLDAELSQRPLFCMSPPLR.R + Oxidation (M)
        2808.38    2807.37    2807.44   -25.99    468 - 494   1   K.SHNKPGLFTSPRPSRLTSAQEAAGGNK.V
        3362.75    3361.74    3361.51     68.5      7 -   38   1   K.TNASTDVIFSPFNYKMTMDGATGSTSSSGSLR.K + 2 Oxidation (M)
       No match to: 1015.53, 1171.55, 1201.58, 1320.71, 1351.75, 1399.73, 1518.72, 1553.85, 1569.85, 1586.79, 1714.89,
       1807.04, 1830.96, 2023.07, 2102.12, 2124.98, 2137.17, 2284.23, 2339.29, 2499.24, 2585.28, 3570.52

  16.   gi|37788628     Mass: 69063     Score: 36     Expect: 12  Queries matched: 6
       xanthine dehydrogenase [Drosophila buzzatii]
       Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
        1015.53    1014.53    1014.56   -29.11    253 - 262   1   R.LEVASRAGGR.R
        1399.73    1398.73    1398.70     22.0     32 -   43   0   R.CTGYRPILEGYK.T
        1586.79    1585.79    1585.81   -12.53    481 - 494   0   R.MDGELYLAFVLSTK.A
        1714.89    1713.88    1714.00   -67.43    151 - 164   1   K.FKHFLYPVLINPVK.V
        2124.98    2123.97    2124.10   -61.27      1 -   19   1   -.GIVMSMYALLRNAAKPSMR.D + Oxidation (M)
        2585.28    2584.27    2584.36   -35.70    309 - 332   1   R.RDDDIAIVNSAVNVNFKPGTNVVK.S
       No match to: 1171.55, 1201.58, 1320.71, 1351.75, 1518.72, 1553.85, 1569.85, 1703.94, 1807.04, 1830.96, 1936.91,
       1952.91, 2023.07, 2102.12, 2137.17, 2284.23, 2339.29, 2499.24, 2722.45, 2808.38, 3362.75, 3570.52

  17.   gi|37788634     Mass: 69032     Score: 36     Expect: 12  Queries matched: 6
       xanthine dehydrogenase [Drosophila buzzatii]
       Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
        1015.53    1014.53    1014.56   -29.11    253 - 262   1   R.LEVASRAGGR.R
        1399.73    1398.73    1398.70     22.0     32 -   43   0   R.CTGYRPILEGYK.T
        1586.79    1585.79    1585.81   -12.53    481 - 494   0   R.MDGELYLAFVLSTK.A
        1714.89    1713.88    1714.00   -67.43    151 - 164   1   K.FKHFLYPVLINPVK.V
        2124.98    2123.97    2124.10   -61.27      1 -   19   1   -.GIVMSMYALLRNAAKPSMR.D + Oxidation (M)
        2585.28    2584.27    2584.36   -35.70    309 - 332   1   R.RDDDIAIVNSAVNVNFKPGTNVVK.S
       No match to: 1171.55, 1201.58, 1320.71, 1351.75, 1518.72, 1553.85, 1569.85, 1703.94, 1807.04, 1830.96, 1936.91,
       1952.91, 2023.07, 2102.12, 2137.17, 2284.23, 2339.29, 2499.24, 2722.45, 2808.38, 3362.75, 3570.52

  18.   gi|125808420     Mass: 153274    Score: 36     Expect: 12  Queries matched: 8
       GA10856-PA [Drosophila pseudoobscura]
       Observed  Mr(expt)  Mr(calc)     ppm  Start     End Miss   Peptide
        1171.55    1170.54    1170.57   -24.32    658 -    666   1   R.LRNYDEAYK.L
        1201.58    1200.57    1200.61   -33.07    262 -    271   0   K.DVGQELWQVK.N
        1351.75    1350.74    1350.71     24.9    742 -    753   1   K.GVYTRAALELCR.D
        1586.79    1585.79    1585.79    -3.74   1147 -   1158   1   R.DLLYSMYQELRR.N
        1714.89    1713.88    1713.78     58.0    883 -    897   0   R.GGFYDEACGHYIALK.M + Propionamide (C)
        2102.12    2101.11    2101.12    -5.46     89 -    106   1   K.ISVETGLRDPLTCILWSK.Q + Propionamide (C)
        2499.24    2498.23    2498.20     14.9    564 -    584   0   K.QCLGCLWDLTQPNIFISYDAK.I + Propionamide (C)
        3570.52    3569.51    3569.62   -29.44    433 -    465   0   R.NVSSMMMNAEYCAALCPPQLILQAITADNPNCK.D + Oxidation (M)
       No match to: 1015.53, 1320.71, 1399.73, 1518.72, 1553.85, 1569.85, 1703.94, 1807.04, 1830.96, 1936.91, 1952.91,
       2023.07, 2124.98, 2137.17, 2284.23, 2339.29, 2585.28, 2722.45, 2808.38, 3362.75

  19.   gi|37788610     Mass: 69055     Score: 36     Expect: 13  Queries matched: 6
       xanthine dehydrogenase [Drosophila buzzatii]
       Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
        1015.53    1014.53    1014.56   -29.11    253 - 262   1   R.LEVASRAGGR.R
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         1399.73   1398.73   1398.70    22.0    32 -  43   0   R.CTGYRPILEGYK.T
         1586.79   1585.79   1585.81  -12.53   481 - 494   0   R.MDGELYLAFVLSTK.A
         1714.89   1713.88   1714.00  -67.43   151 - 164   1   K.FKHFLYPVLINPVK.V
         2124.98   2123.97   2124.10  -61.27     1 -  19   1   -.GIVMSMYALLRNAAKPSMR.D + Oxidation (M)
         2585.28   2584.27   2584.36  -35.70   309 - 332   1   R.RDDDIAIVNSAVNVNFKPGTNVVK.S
        No match to: 1171.55, 1201.58, 1320.71, 1351.75, 1518.72, 1553.85, 1569.85, 1703.94, 1807.04, 1830.96, 1936.91,
        1952.91, 2023.07, 2102.12, 2137.17, 2284.23, 2339.29, 2499.24, 2722.45, 2808.38, 3362.75, 3570.52

 20.    gi|37788616     Mass: 69055    Score: 36     Expect: 13  Queries matched: 6
        xanthine dehydrogenase [Drosophila buzzatii]
        Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
         1015.53   1014.53   1014.56  -29.11   253 - 262   1   R.LEVASRAGGR.R
         1399.73   1398.73   1398.70    22.0    32 -  43   0   R.CTGYRPILEGYK.T
         1586.79   1585.79   1585.81  -12.53   481 - 494   0   R.MDGELYLAFVLSTK.A
         1714.89   1713.88   1714.00  -67.43   151 - 164   1   K.FKHFLYPVLINPVK.V
         2124.98   2123.97   2124.10  -61.27     1 -  19   1   -.GIVMSMYALLRNAAKPSMR.D + Oxidation (M)
         2585.28   2584.27   2584.36  -35.70   309 - 332   1   R.RDDDIAIVNSAVNVNFKPGTNVVK.S
        No match to: 1171.55, 1201.58, 1320.71, 1351.75, 1518.72, 1553.85, 1569.85, 1703.94, 1807.04, 1830.96, 1936.91,
        1952.91, 2023.07, 2102.12, 2137.17, 2284.23, 2339.29, 2499.24, 2722.45, 2808.38, 3362.75, 3570.52
```

Search Parameters

```
Type of search         : Peptide Mass Fingerprint
Enzyme                 : Trypsin
Variable modifications : Oxidation (M),Propionamide (C)
Mass values            : Monoisotopic
Protein Mass           : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Peptide Charge State   : 1+
Max Missed Cleavages   : 1
Number of queries      : 28
```

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

Mascot Search Results

```
User          : Ilya
Email         : toropygin@rambler.ru
Search title  : Submitted from Shidlovsky 080324 II by Mascot Daemon on P4P800SE
MS data file  : \\192.168.0.18\data on ultraflex-2\DATA\2008_Ilya\Shidlovsky\080325\013\0_K13\3\013__0_K13__3.dar
Database      : NCBInr 20070307 (4984280 sequences; 1723577896 residues)
Taxonomy      : Drosophila (fruit flies) (47828 sequences)
Timestamp     : 3 Apr 2008 at 22:05:12 GMT
Top Score     : 158 for gi|17137456, Origin recognition complex subunit 1 CG10667-PA [Drosophila melanogaster]
```

Probability Based Mowse Score

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 59 are significant (p<0.05).

Score Distribution

Protein Summary Report

Format As | Protein Summary | Help

Significance threshold p< 0.05 | Max. number of hits 20

Overview Table

Click on column header to jump to entry in results list.
Move mouse over any indicator to highlight identical peptides.
Click on an indicator to see details of individual match.
Use check boxes to select sub-set of queries for new search.

Mouse over: -Query-

-Accession- -Sequence-

Hit:	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
☑ 829.46 (1+)																			?	
☑ 835.46 (1+)						?		?	?				?							
☑ 847.46 (1+)	?	?																		?
☑ 901.50 (1+)									?						?					
☑ 936.51 (1+)			?	?					?	?	?		?							
☑ 942.56 (1+)	?	?			?			?					?					?		?
☑ 944.55 (1+)	?	?			?								?	?	?					
☑ 954.56 (1+)	?	?			?															
☑ 961.51 (1+)	?	?	?			?	?					?					?			
☑ 1020.53 (1+)	?	?			?		?		?				?			?	?			
☑ 1057.62 (1+)	?	?			?				?				?	?	?					
☑ 1058.58 (1+)													?		?					
☑ 1074.62 (1+)	?	?	?	?							?						?			

☑ 1090.60 (1+)	?	?	?	?				?					?		?	?				
☑ 1111.60 (1+)													?							
☑ 1120.64 (1+)	?	?						?	?						?					
☑ 1137.62 (1+)							?									?			?	
☑ 1143.60 (1+)							?			?			?					?		?
☑ 1202.64 (1+)														?	?				?	?
☑ 1295.76 (1+)	?	?													?					
☑ 1318.81 (1+)															?					
☑ 1329.66 (1+)									?											
☑ 1368.76 (1+)	?	?						?												
☑ 1392.74 (1+)	?	?	?	?	?	?	?				?		?							
☑ 1399.77 (1+)								?												?
☑ 1410.81 (1+)	?	?										?								
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☑ 1433.78 (1+)								?								?				
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☑ 1511.85 (1+)	?	?	?	?							?			?						
☑ 1590.91 (1+)	?	?			?															
☑ 1671.01 (1+)	?	?			?										?					
☑ 1687.00 (1+)	?	?			?										?					
☑ 1713.04 (1+)	?	?			?							?	?							
☑ 1719.99 (1+)	?	?				?								?	?					
☑ 1736.00 (1+)	?	?				?														
☑ 1744.95 (1+)	?	?	?	?								?	?					?		
☑ 1747.00 (1+)	?	?			?															
☑ 1762.03 (1+)	?	?																		
☑ 1840.01 (1+)						?							?			?	?	?		
☑ 1887.10 (1+)	?	?			?						?									
☑ 1903.08 (1+)			?	?				?			?	?					?			
☑ 1925.01 (1+)			?	?									?							
☑ 2163.18 (1+)											?	?								
☑ 2193.13 (1+)						?														
☑ 2230.32 (1+)																				
☑ 2241.33 (1+)	?	?													?	?				
☑ 2273.29 (1+)					?					?										
☑ 2284.30 (1+)														?	?					?
☑ 2298.31 (1+)														?						
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☑ 2485.33 (1+)	?	?											?		?					
☑ 2550.37 (1+)										?										
☑ 2780.09 (1+)																				
☑ 2780.57 (1+)																				?
☑ 2809.47 (1+)			?	?			?		?		?		?		?					?
☑ 3211.66 (1+)									?										?	
☑ 3338.94 (1+)																				

Select All

Select None

Search Selected

Index

	Accession	Mass	Score	Description
1.	gi|17137456	103217	158	Origin recognition complex subunit 1 CG10667-PA [Drosophila melanogaster]
2.	gi|2576416	103233	158	origin recognition complex subunit 1 [Drosophila melanogaster]
3.	gi|18858175	58027	51	CG7033-PA, isoform A [Drosophila melanogaster]
4.	gi|24640724	57767	45	CG7033-PB, isoform B [Drosophila melanogaster]
5.	gi|125810214	103475	40	GA10479-PA [Drosophila pseudoobscura]
6.	gi|17136328	44374	38	meiotic from via Salaria 332 CG5303-PA [Drosophila melanogaster]
7.	gi|125775894	38343	38	GA11231-PA [Drosophila pseudoobscura]
8.	gi|28572961	56392	37	CG7718-PA [Drosophila melanogaster]
9.	gi|125778456	75568	37	GA19806-PA [Drosophila pseudoobscura]
10.	gi|125986487	20539	37	GA18414-PA [Drosophila pseudoobscura]
11.	gi|125981859	57604	36	GA20046-PA [Drosophila pseudoobscura]
12.	gi|85725184	41233	36	CG4174-PB, isoform B [Drosophila melanogaster]
13.	gi|125776677	320654	35	GA10452-PA [Drosophila pseudoobscura]
14.	gi|125773325	43719	34	GA18617-PA [Drosophila pseudoobscura]
15.	gi|125773639	263763	33	GA18916-PA [Drosophila pseudoobscura]
16.	gi|21358017	35026	32	CG11837-PA [Drosophila melanogaster]
17.	gi|24581278	24830	31	Peroxiredoxin 6005 CG3083-PA [Drosophila melanogaster]
18.	gi|24658952	26800	31	CG9897-PA [Drosophila melanogaster]
19.	gi|49066183	13716	30	ACP53C14C [Drosophila simulans]
20.	gi|125979875	59422	30	GA18684-PA [Drosophila pseudoobscura]

Results List

1. gi|17137456 **Mass:** 103217 **Score:** 158 **Expect:** 7.6e-012 **Queries matched:** 29

Origin recognition complex subunit 1 CG10667-PA [Drosophila melanogaster]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
847.46	846.45	846.47	-27.88	614	620	1	R.TLQRMAK.Q
942.56	941.55	941.58	-24.64	267	275	1	K.IVGGRSVVR.L
944.55	943.54	943.51	30.9	315	322	0	R.NLNLSLDR.G
954.56	953.55	953.53	22.2	890	897	0	R.LIISEHSR.N
961.51	960.50	960.48	24.3	1	8	1	-.MVNKENAR.S
1020.53	1019.52	1019.53	-11.16	140	148	0	K.CIVLEGTSK.T + Propionamide (C)
1057.62	1056.61	1056.59	20.4	749	757	0	K.QLQEIVTAR.L
1074.62	1073.61	1073.57	36.2	74	81	0	R.ILHMYELR.E
1090.60	1089.59	1089.56	24.7	74	81	0	R.ILHMYELR.E + Oxidation (M)
1120.64	1119.63	1119.57	52.5	740	748	0	R.LTFQPYSHK.Q
1295.76	1294.75	1294.70	40.6	443	453	0	R.SIHLSNIVEQR.V
1368.76	1367.75	1367.71	31.7	16	27	0	K.WIGSQDELPPVK.N
1392.74	1391.73	1391.68	35.2	454	465	0	R.VFEDDEIISTPK.R
1410.81	1409.80	1409.72	58.2	162	173	1	K.LKSTACPMFVSR.Y + Propionamide (C)
1459.77	1458.77	1458.70	44.0	574	585	0	R.EFENIYAFLEGK.I
1511.85	1510.84	1510.78	42.8	655	667	0	K.TVSWEQAHALLEK.R
1590.91	1589.90	1589.81	56.6	694	706	0	R.QDVVYNLLDWPTK.S
1671.01	1670.00	1669.91	55.3	711	725	0	K.LVVVTIANTMDLPER.L
1687.00	1686.00	1685.90	55.9	711	725	0	K.LVVVTIANTMDLPER.L + Oxidation (M)
1713.04	1712.03	1711.93	61.9	904	918	0	K.ILLNVSADDIHYALR.V
1719.99	1718.99	1718.90	48.9	832	846	0	R.MEQIFLQAIAAEVTR.T
1736.00	1734.99	1734.90	53.4	832	846	0	R.MEQIFLQAIAAEVTR.T + Oxidation (M)
1744.95	1743.94	1743.85	54.0	572	585	1	R.EREFENIYAFLEGK.I
1747.00	1745.99	1745.91	46.8	693	706	1	R.RQDVVYNLLDWPTK.S
1762.03	1761.03	1760.94	48.5	758	774	1	R.LGGSETFKGEAVQLVAR.K
1887.10	1886.09	1886.02	37.2	677	692	0	R.VTTVLLVDELDILCNR.R + Propionamide (C)
2241.33	2240.32	2240.19	58.4	185	203	0	R.LIPLEIHLEQPEDNARPTR.S
2469.34	2468.33	2468.19	58.7	366	388	0	R.LASMDVDPLSLEEAVQEPNAQGR.K
2485.33	2484.33	2484.18	59.4	366	388	0	R.LASMDVDPLSLEEAVQEPNAQGR.K + Oxidation (M)

No match to: 829.46, 835.46, 901.50, 936.51, 1058.58, 1111.60, 1137.62, 1143.60, 1202.64, 1318.81, 1329.66, 1399.77, 1420.83, 1433.78, 1840.01, 1903.08, 1925.01, 2163.18, 2193.13, 2230.32, 2273.29, 2284.30, 2298.31, 2550.37, 2780.09, 2780.57, 2809.47, 3211.66, 3338.94

2. gi|2576416 **Mass:** 103233 **Score:** 158 **Expect:** 7.6e-012 **Queries matched:** 29

origin recognition complex subunit 1 [Drosophila melanogaster]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
847.46	846.45	846.47	-27.88	614	620	1	R.TLQRMAK.Q
942.56	941.55	941.58	-24.64	267	275	1	K.IVGGRSVVR.L
944.55	943.54	943.51	30.9	315	322	0	R.NLNLSLDR.G
954.56	953.55	953.53	22.2	890	897	0	R.LIISEHSR.N
961.51	960.50	960.48	24.3	1	8	1	-.MVNKENAR.S
1020.53	1019.52	1019.53	-11.16	140	148	0	K.CIVLEGTSK.T + Propionamide (C)
1057.62	1056.61	1056.59	20.4	749	757	0	K.QLQEIVTAR.L
1074.62	1073.61	1073.57	36.2	74	81	0	R.ILHMYELR.E
1090.60	1089.59	1089.56	24.7	74	81	0	R.ILHMYELR.E + Oxidation (M)

1120.64	1119.63	1119.57	52.5	740	748	0	R.LTFQPYSHK.Q
1295.76	1294.75	1294.70	40.6	443	453	0	R.SIHLSNIVEQR.V
1368.76	1367.75	1367.71	31.7	16	27	0	K.WIGSQDELPPVK.N
1392.74	1391.73	1391.68	35.2	454	465	0	R.VFEDDEIISTPK.R
1410.81	1409.80	1409.72	58.2	162	173	1	K.LKSTACPMFVSR.Y + Propionamide (C)
1459.77	1458.77	1458.70	44.0	574	585	0	R.EFENIYAFLEGK.I
1511.85	1510.84	1510.78	42.8	655	667	0	K.TVSWEQAHALLEK.R
1590.91	1589.90	1589.81	56.6	694	706	0	R.QDVVYNLLDWPTK.S
1671.01	1670.00	1669.91	55.3	711	725	0	K.LVVVTIANTMDLPER.L
1687.00	1686.00	1685.90	55.9	711	725	0	K.LVVVTIANTMDLPER.L + Oxidation (M)
1713.04	1712.03	1711.93	61.9	904	918	0	K.ILLNVSADDIHYALR.V
1719.99	1718.99	1718.90	48.9	832	846	0	R.MEQIFLQAIAAEVTR.T
1736.00	1734.99	1734.90	53.4	832	846	0	R.MEQIFLQAIAAEVTR.T + Oxidation (M)
1744.95	1743.94	1743.85	54.0	572	585	1	R.EREFENIYAFLEGK.I
1747.00	1745.99	1745.91	46.8	693	706	1	R.RQDVVYNLLDWPTK.S
1762.03	1761.03	1760.94	48.5	758	774	1	R.LGGSETFKGEAVQLVAR.K
1887.10	1886.09	1886.02	37.2	677	692	0	R.VTTVLLVDELDILCNR.R + Propionamide (C)
2241.33	2240.32	2240.19	58.4	185	203	0	R.LIPLEIHLEQPEDNARPTR.S
2469.34	2468.33	2468.19	58.7	366	388	0	R.LASMDVDPLSLEEAVQEPNAQGR.K
2485.33	2484.33	2484.18	59.4	366	388	0	R.LASMDVDPLSLEEAVQEPNAQGR.K + Oxidation (M)

No match to: 829.46, 835.46, 901.50, 936.51, 1058.58, 1111.60, 1137.62, 1143.60, 1202.64, 1318.81, 1329.66, 1399.77, 1420.83, 1433.78, 1840.01, 1903.08, 1925.01, 2163.18, 2193.13, 2230.32, 2273.29, 2284.30, 2298.31, 2550.37, 2780.09, 2780.57, 2809.47, 3211.66, 3338.94

3. gi|18858175 **Mass:** 58027 **Score:** 51 **Expect:** 0.35 **Queries matched:** 10

CG7033-PA, isoform A [Drosophila melanogaster]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
936.51	935.51	935.46	45.1	287	293	0	K.CNVFINR.Q + Propionamide (C)
961.51	960.50	960.47	36.0	2	9	0	M.EMSLNPVR.V + Oxidation (M)
1074.62	1073.61	1073.59	16.5	367	376	0	K.LGEACTIVIR.G
1090.60	1089.59	1089.58	8.38	432	441	0	K.EAIAIEAFAR.A
1392.74	1391.73	1391.79	-41.26	165	176	1	R.TTLSSKILHQHK.D
1511.85	1510.84	1510.82	16.4	389	402	0	R.SLHDALCVLAATVK.E + Propionamide (C)
1744.95	1743.94	1743.92	12.7	474	489	1	K.QTLGLDMELGKVADVR.E
1903.08	1902.07	1902.08	-7.05	116	131	1	K.LVEQKLHPQIIVSGWR.Q
1925.01	1924.01	1924.02	-4.94	406	424	1	R.IIFGGGCSEALMATAVLKK.A + Oxidation (M)
2809.47	2808.46	2808.44	5.62	377	402	1	R.GATQQILDEADRSLHDALCVLAATVK.E + Propionamide (C)

No match to: 829.46, 835.46, 847.46, 901.50, 942.56, 944.55, 954.56, 1020.53, 1057.62, 1058.58, 1111.60, 1120.64, 1137.62, 1143.60, 1202.64, 1295.76, 1318.81, 1329.66, 1368.76, 1399.77, 1410.81, 1420.83, 1433.78, 1459.77, 1590.91, 1671.01, 1687.00, 1713.04, 1719.99, 1736.00, 1747.00, 1762.03, 1840.01, 1887.10, 2163.18, 2193.13, 2230.32, 2241.33, 2273.29, 2284.30, 2298.31, 2469.34, 2485.33, 2550.37, 2780.09, 2780.57, 3211.66, 3338.94

4. gi|24640724 **Mass:** 57767 **Score:** 45 **Expect:** 1.5 **Queries matched:** 9

CG7033-PB, isoform B [Drosophila melanogaster]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
936.51	935.51	935.46	45.1	285	291	0	K.CNVFINR.Q + Propionamide (C)
1074.62	1073.61	1073.59	16.5	365	374	0	K.LGEACTIVIR.G
1090.60	1089.59	1089.58	8.38	430	439	0	K.EAIAIEAFAR.A
1392.74	1391.73	1391.79	-41.26	163	174	1	R.TTLSSKILHQHK.D
1511.85	1510.84	1510.82	16.4	387	400	0	R.SLHDALCVLAATVK.E + Propionamide (C)
1744.95	1743.94	1743.92	12.7	472	487	1	K.QTLGLDMELGKVADVR.E
1903.08	1902.07	1902.08	-7.05	114	129	1	K.LVEQKLHPQIIVSGWR.Q
1925.01	1924.01	1924.02	-4.94	404	422	1	R.IIFGGGCSEALMATAVLKK.A + Oxidation (M)
2809.47	2808.46	2808.44	5.62	375	400	1	R.GATQQILDEADRSLHDALCVLAATVK.E + Propionamide (C)

No match to: 829.46, 835.46, 847.46, 901.50, 942.56, 944.55, 954.56, 961.51, 1020.53, 1057.62, 1058.58, 1111.60, 1120.64, 1137.62, 1143.60, 1202.64, 1295.76, 1318.81, 1329.66, 1368.76, 1399.77, 1410.81, 1420.83, 1433.78, 1459.77, 1590.91, 1671.01, 1687.00, 1713.04, 1719.99, 1736.00, 1747.00, 1762.03, 1840.01, 1887.10, 2163.18, 2193.13, 2230.32, 2241.33, 2273.29, 2284.30, 2298.31, 2469.34, 2485.33, 2550.37, 2780.09, 2780.57, 3211.66, 3338.94

5. gi|125810214 **Mass:** 103475 **Score:** 40 **Expect:** 4.6 **Queries matched:** 13

GA10479-PA [Drosophila pseudoobscura]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
942.56	941.55	941.53	26.0	775	783	0	K.GEAVQLVAR.K
944.55	943.54	943.51	30.9	323	330	0	R.NLNLSLDR.G
954.56	953.55	953.53	22.2	899	906	0	R.LIISEHSR.N
1020.53	1019.52	1019.58	-57.86	735	743	1	R.LLMGKVTSR.L + Oxidation (M)
1057.62	1056.61	1056.59	20.4	758	766	0	K.QLQEIVTAR.L
1392.74	1391.73	1391.65	55.6	5	15	0	K.ENVISCCQQVK.W + 2 Propionamide (C)

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      1590.91    1589.90    1589.81     56.6    703 - 715    0    R.QDVVYNLLDWPTK.S
      1671.01    1670.00    1669.91     55.3    720 - 734    0    R.LVVVTIANTMDLPER.L
      1687.00    1686.00    1685.90     55.9    720 - 734    0    R.LVVVTIANTMDLPER.L + Oxidation (M)
      1713.04    1712.03    1711.93     61.9    913 - 927    0    K.ILLNVSADDIHYALR.V
      1747.00    1745.99    1745.91     46.8    702 - 715    1    R.RQDVVYNLLDWPTK.S
      1887.10    1886.09    1886.02     37.2    686 - 701    0    R.VTTVLLVDELDILCNR.R + Propionamide (C)
      2273.29    2272.28    2272.14     63.4    811 - 831    1    R.DKCVTMLHVQQALGEMIASAK.V
     No match to: 829.46, 835.46, 847.46, 901.50, 936.51, 961.51, 1058.58, 1074.62, 1090.60, 1111.60, 1120.64,
     1137.62, 1143.60, 1202.64, 1295.76, 1318.81, 1329.66, 1368.76, 1399.77, 1410.81, 1420.83, 1433.78, 1459.77,
     1511.85, 1719.99, 1736.00, 1744.95, 1762.03, 1840.01, 1903.08, 1925.01, 2163.18, 2193.13, 2230.32, 2241.33,
     2284.30, 2298.31, 2469.34, 2485.33, 2550.37, 2780.09, 2780.57, 2809.47, 3211.66, 3338.94

6.   gi|17136328     Mass: 44374     Score: 38     Expect: 7.2  Queries matched: 8
     meiotic from via Salaria 332 CG5303-PA [Drosophila melanogaster]
    Observed  Mr(expt)  Mr(calc)    ppm  Start   End Miss   Peptide
       835.46     834.45     834.46   -12.81    317 - 324    0    R.SLFNGIGK.M
       961.51     960.50     960.51    -1.89     57 -  64    0    R.MENISIVR.S
      1392.74    1391.73    1391.69     30.1    138 - 150    0    R.SSAEVQSEVVTTR.I
      1719.99    1718.99    1718.89     57.8     65 -  80    0    R.SLMLSLNVDSDSLAVR.Q
      1736.00    1734.99    1734.88     62.1     65 -  80    0    R.SLMLSLNVDSDSLAVR.Q + Oxidation (M)
      1840.01    1839.00    1839.02    -8.99    248 - 264    1    R.ALREVDTNIPVAVSLSR.G
      2193.13    2192.13    2192.11     5.84      5 -  22    1    K.VEQQYKLLNAELMDQVQK.Q + Oxidation (M)
      2469.34    2468.33    2468.20     52.5    271 - 293    0    K.GSWLAISVAVEDSPQEPSIQCPR.L
     No match to: 829.46, 847.46, 901.50, 936.51, 942.56, 944.55, 954.56, 1020.53, 1057.62, 1058.58, 1074.62,
     1090.60, 1111.60, 1120.64, 1137.62, 1143.60, 1202.64, 1295.76, 1318.81, 1329.66, 1368.76, 1399.77, 1410.81,
     1420.83, 1433.78, 1459.77, 1511.85, 1590.91, 1671.01, 1687.00, 1713.04, 1744.95, 1747.00, 1762.03, 1887.10,
     1903.08, 1925.01, 2163.18, 2230.32, 2241.33, 2273.29, 2284.30, 2298.31, 2485.33, 2550.37, 2780.09, 2780.57,
     2809.47, 3211.66, 3338.94

7.   gi|125775894     Mass: 38343     Score: 38     Expect: 7.8  Queries matched: 7
     GA11231-PA [Drosophila pseudoobscura]
    Observed  Mr(expt)  Mr(calc)    ppm  Start   End Miss   Peptide
       961.51     960.50     960.49     17.5     77 -  85    1    K.ENKGLSDAK.N
      1020.53    1019.52    1019.54   -22.16     27 -  35    1    K.MNIGLSNKK.Q + Oxidation (M)
      1137.62    1136.61    1136.68   -59.92    318 - 326    1    K.RRPDQKPLK.V
      1143.60    1142.59    1142.67   -68.15    219 - 227    1    K.RVKPNFNLR.K
      1392.74    1391.73    1391.74    -9.45     22 -  34    1    K.AISTKMNIGLSNK.K + Oxidation (M)
      1459.77    1458.77    1458.73     23.6    294 - 308    0    R.GASRPVAAAGNGFER.V
      2809.47    2808.46    2808.37     32.2     86 - 110    1    K.NIVHIPSNENNRFGGVDFGNDIPQR.Q
     No match to: 829.46, 835.46, 847.46, 901.50, 936.51, 942.56, 944.55, 954.56, 1057.62, 1058.58, 1074.62, 1090.60,
     1111.60, 1120.64, 1202.64, 1295.76, 1318.81, 1329.66, 1368.76, 1399.77, 1410.81, 1420.83, 1433.78, 1511.85,
     1590.91, 1671.01, 1687.00, 1713.04, 1719.99, 1736.00, 1744.95, 1747.00, 1762.03, 1840.01, 1887.10, 1903.08,
     1925.01, 2163.18, 2193.13, 2230.32, 2241.33, 2273.29, 2284.30, 2298.31, 2469.34, 2485.33, 2550.37, 2780.09,
     2780.57, 3211.66, 3338.94

8.   gi|28572961     Mass: 56392     Score: 37     Expect: 8.9  Queries matched: 8
     CG7718-PA [Drosophila melanogaster]
    Observed  Mr(expt)  Mr(calc)    ppm  Start   End Miss   Peptide
       835.46     834.45     834.45    -4.97      2 -   7    1    M.MPYLRR.L
       942.56     941.55     941.57   -20.54    136 - 143    0    K.TMLLPLVR.D
      1090.60    1089.59    1089.62   -25.05    118 - 126    0    R.LNVLLDFTR.G
      1120.64    1119.63    1119.57     53.1    312 - 321    0    R.LLSNCLSGSR.L + Propionamide (C)
      1368.76    1367.75    1367.70     36.5    171 - 181    0    R.WNELLGLQHMK.V
      1399.77    1398.76    1398.79   -18.06    364 - 378    0    K.GPAGGIPAAYTLIAK.S
      1433.78    1432.77    1432.72     31.4    438 - 450    0    R.DLETQVCLVTANK.D
      1903.08    1902.07    1902.03     21.4    166 - 181    1    R.LAPPRWNELLGLQHMK.V
     No match to: 829.46, 847.46, 901.50, 936.51, 944.55, 954.56, 961.51, 1020.53, 1057.62, 1058.58, 1074.62,
     1111.60, 1137.62, 1143.60, 1202.64, 1295.76, 1318.81, 1329.66, 1392.74, 1410.81, 1420.83, 1459.77, 1511.85,
     1590.91, 1671.01, 1687.00, 1713.04, 1719.99, 1736.00, 1744.95, 1747.00, 1762.03, 1840.01, 1887.10, 1925.01,
     2163.18, 2193.13, 2230.32, 2241.33, 2273.29, 2284.30, 2298.31, 2469.34, 2485.33, 2550.37, 2780.09, 2780.57,
     2809.47, 3211.66, 3338.94

9.   gi|125778456     Mass: 75568     Score: 37     Expect: 10  Queries matched: 9
     GA19806-PA [Drosophila pseudoobscura]
    Observed  Mr(expt)  Mr(calc)    ppm  Start   End Miss   Peptide
       835.46     834.45     834.47   -26.25    131 - 136    1    K.LYREVR.I
       901.50     900.50     900.54   -50.71    318 - 325    0    K.FLVLNPAK.R
       936.51     935.51     935.44     69.3    503 - 510    1    R.SENSSRTR.S
      1020.53    1019.52    1019.49     26.5    627 - 635    0    R.ATFHFGQGR.S
      1057.62    1056.61    1056.64   -28.50    318 - 326    1    K.FLVLNPAKR.T
      1120.64    1119.63    1119.59     33.7    149 - 157    0    R.LFQVIESER.S
      1329.66    1328.65    1328.64     7.74    353 - 363    0    R.EKPMELQDPAR.V + Oxidation (M)
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        2809.47   2808.46   2808.27    69.0     62 -  88   1   K.DVGDGMTSGSDLKFQSYVNGNGNGVYK.I
        3211.66   3210.65   3210.65    1.49    260 - 290   0   K.YAGPEVDAWSLGVVLYTLVSGSLPFDGGTLK.E
       No match to: 829.46, 847.46, 942.56, 944.55, 954.56, 961.51, 1058.58, 1074.62, 1090.60, 1111.60, 1137.62,
       1143.60, 1202.64, 1295.76, 1318.81, 1368.76, 1392.74, 1399.77, 1410.81, 1420.83, 1433.78, 1459.77, 1511.85,
       1590.91, 1671.01, 1687.00, 1713.04, 1719.99, 1736.00, 1744.95, 1747.00, 1762.03, 1840.01, 1887.10, 1903.08,
       1925.01, 2163.18, 2193.13, 2230.32, 2241.33, 2273.29, 2284.30, 2298.31, 2469.34, 2485.33, 2550.37, 2780.09,
       2780.57, 3338.94

 10.   gi|125986487     Mass: 20539     Score: 37     Expect: 10  Queries matched: 5
       GA18414-PA [Drosophila pseudoobscura]
      Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss  Peptide
        936.51    935.51    935.51  -0.77    174 - 180   1   K.VERIEYK.K
       1143.60   1142.59   1142.58   8.73     15 -  23   1   R.CSSLPYKFK.K + Propionamide (C)
       1420.83   1419.82   1419.77   38.5     31 -  43   0   R.IHHILATGNICTK.E
       2273.29   2272.28   2272.24   19.5     74 -  93   1   K.VVTVGQFRIGLCHGHQVVPR.G + Propionamide (C)
       2550.37   2549.36   2549.36  -1.43     82 - 104   1   R.IGLCHGHQVVPRGDPEALALIQR.Q + Propionamide (C)
       No match to: 829.46, 835.46, 847.46, 901.50, 942.56, 944.55, 954.56, 961.51, 1020.53, 1057.62, 1058.58, 1074.62,
       1090.60, 1111.60, 1120.64, 1137.62, 1202.64, 1295.76, 1318.81, 1329.66, 1368.76, 1392.74, 1399.77, 1410.81,
       1433.78, 1459.77, 1511.85, 1590.91, 1671.01, 1687.00, 1713.04, 1719.99, 1736.00, 1744.95, 1747.00, 1762.03,
       1840.01, 1887.10, 1903.08, 1925.01, 2163.18, 2193.13, 2230.32, 2241.33, 2284.30, 2298.31, 2469.34, 2485.33,
       2780.09, 2780.57, 2809.47, 3211.66, 3338.94

 11.   gi|125981859     Mass: 57604     Score: 36     Expect: 11  Queries matched: 8
       GA20046-PA [Drosophila pseudoobscura]
      Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss  Peptide
        936.51    935.51    935.46     45.1    285 - 291   0   K.CNVFINR.Q + Propionamide (C)
       1074.62   1073.61   1073.59     16.5    365 - 374   0   K.LGEACTIVIR.G
       1392.74   1391.73   1391.79   -41.26    163 - 174   1   R.TTLSSKILHQHK.E
       1511.85   1510.84   1510.82     16.4    387 - 400   0   R.SLHDALCVLAATVK.E + Propionamide (C)
       1887.10   1886.09   1885.98     56.5    230 - 246   1   R.IENAKILIANTPMDTDK.I
       1903.08   1902.07   1902.08    -7.05    114 - 129   1   K.LVEQKLHPQIIVSGWR.M
       2163.18   2162.17   2162.06     50.9    341 - 359   0   K.LGECDVIEQIMIGEDTLLR.F + Oxidation (M)
       2809.47   2808.46   2808.44     5.62    375 - 400   1   R.GATQQILDEADRSLHDALCVLAATVK.E + Propionamide (C)
       No match to: 829.46, 835.46, 847.46, 901.50, 942.56, 944.55, 954.56, 961.51, 1020.53, 1057.62, 1058.58, 1090.60,
       1111.60, 1120.64, 1137.62, 1143.60, 1202.64, 1295.76, 1318.81, 1329.66, 1368.76, 1399.77, 1410.81, 1420.83,
       1433.78, 1459.77, 1590.91, 1671.01, 1687.00, 1713.04, 1719.99, 1736.00, 1744.95, 1747.00, 1762.03, 1840.01,
       1925.01, 2193.13, 2230.32, 2241.33, 2273.29, 2284.30, 2298.31, 2469.34, 2485.33, 2550.37, 2780.09, 2780.57,
       3211.66, 3338.94

 12.   gi|85725184     Mass: 41233     Score: 36     Expect: 13  Queries matched: 7
       CG4174-PB, isoform B [Drosophila melanogaster]
      Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss  Peptide
        961.51    960.50    960.50     1.59    308 - 316   0   K.GGEIVFPSR.H
       1410.81   1409.80   1409.76     25.1    242 - 254   0   K.IGNLSTSLHDVVR.K
       1459.77   1458.77   1458.80   -23.60     38 -  49   0   R.FSLNMLIHISIR.N + Oxidation (M)
       1713.04   1712.03   1711.99     23.2     36 -  49   1   R.LRFSLNMLIHISIR.N
       1744.95   1743.94   1743.94    -0.58    292 - 307   1   K.IHNKANAFIFLSNAGK.G
       1903.08   1902.07   1901.99     43.0     96 - 111   0   K.LWNYPNLLESLVEANK.G
       2163.18   2162.17   2162.03     67.0     50 -  67   0   R.NWSADECLMLGLMYLFLK.D + Oxidation (M)
       No match to: 829.46, 835.46, 847.46, 901.50, 936.51, 942.56, 944.55, 954.56, 1020.53, 1057.62, 1058.58, 1074.62,
       1090.60, 1111.60, 1120.64, 1137.62, 1143.60, 1202.64, 1295.76, 1318.81, 1329.66, 1368.76, 1392.74, 1399.77,
       1420.83, 1433.78, 1511.85, 1590.91, 1671.01, 1687.00, 1719.99, 1736.00, 1747.00, 1762.03, 1840.01, 1887.10,
       1925.01, 2193.13, 2230.32, 2241.33, 2273.29, 2284.30, 2298.31, 2469.34, 2485.33, 2550.37, 2780.09, 2780.57,
       2809.47, 3211.66, 3338.94

 13.   gi|125776677     Mass: 320654     Score: 35     Expect: 15  Queries matched: 20
       GA10452-PA [Drosophila pseudoobscura]
      Observed  Mr(expt)  Mr(calc)     ppm  Start     End Miss  Peptide
        835.46    834.45    834.49   -42.97    928 -  934   0   K.LTFEVVK.L
        936.51    935.51    935.51    -4.39   1018 - 1025   1   R.KSVSQLMK.E + Oxidation (M)
        942.56    941.55    941.58   -27.46    821 -  828   0   R.LDIDLILK.C
        944.55    943.54    943.48     57.4   1925 - 1931   1   K.VFFEKMK.D + Oxidation (M)
       1020.53   1019.52   1019.51     9.57    226 -  233   0   K.ISLFMEHK.E + Oxidation (M)
       1057.62   1056.61   1056.63   -14.05   2321 - 2329   1   K.IKILNTAER.D
       1058.58   1057.57   1057.60   -25.88    687 -  695   0   K.DILIETQVK.A
       1090.60   1089.59   1089.61   -15.96    264 -  271   1   K.KQYHVFLR.T
       1111.60   1110.59   1110.53     55.3   1026 - 1034   0   K.EYPLVMDTK.L + Oxidation (M)
       1143.60   1142.59   1142.52     59.6   2717 - 2726   0   K.TTCFVCSLNR.S
       1392.74   1391.73   1391.67     42.2     58 -   68   1   R.DCLIKICPMNR.Y + Oxidation (M); Propionamide (C)
       1420.83   1419.82   1419.77     33.9    173 -  185   1   K.LRSIGDYVVVGDK.V
       1459.77   1458.77   1458.74     21.8    559 -  571   1   R.LDELGDPKNAPYK.N
       1713.04   1712.03   1712.06   -16.56   1035 - 1048   1   K.LKIIEILQFILDVR.L
       1744.95   1743.94   1743.90     24.0   1392 - 1405   0   K.VVQHFVHCIEIHGR.H + Propionamide (C)
```

1840.01	1839.00	1838.94	36.2	2712	2726	1	K.EAILKTTCFVCSLNR.S + 2 Propionamide (C)
1925.01	1924.01	1923.91	51.1	1627	1641	1	K.WMSLADRFNVENCIR.T + Propionamide (C)
2469.34	2468.33	2468.20	52.7	821	840	1	R.LDIDLILKCMSDETMPYELR.A + Propionamide (C)
2485.33	2484.33	2484.19	53.4	821	840	1	R.LDIDLILKCMSDETMPYELR.A + Oxidation (M); Propionamide (C)
2809.47	2808.46	2808.54	-29.24	2805	2828	1	R.SMQTQLLETQLLIKNLSTQLHELK.D

No match to: 829.46, 847.46, 901.50, 954.56, 961.51, 1074.62, 1120.64, 1137.62, 1202.64, 1295.76, 1318.81, 1329.66, 1368.76, 1399.77, 1410.81, 1433.78, 1511.85, 1590.91, 1671.01, 1687.00, 1719.99, 1736.00, 1747.00, 1762.03, 1887.10, 1903.08, 2163.18, 2193.13, 2230.32, 2241.33, 2273.29, 2284.30, 2298.31, 2550.37, 2780.09, 2780.57, 3211.66, 3338.94

14. gi|125773325 **Mass:** 43719 **Score:** 34 **Expect:** 18 **Queries matched:** 7

GA18617-PA [Drosophila pseudoobscura]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
944.55	943.54	943.49	54.7	386	393	0	K.LPDTEELK.L
1057.62	1056.61	1056.61	2.75	63	71	0	K.GMIILNRPK.A + Oxidation (M)
1202.64	1201.63	1201.58	42.2	116	127	0	R.ALVDAGPTDESK.S
1511.85	1510.84	1510.76	57.5	301	314	1	K.TLATLCKMSPTSMK.V
1719.99	1718.99	1718.92	37.8	2	15	1	M.QNPIQRLVYTFGQR.T
2284.30	2283.29	2283.23	26.9	145	167	0	K.IPYIAIIDGITMGGGVGLSVHGK.Y + Oxidation (M)
2298.31	2297.30	2297.27	11.9	63	82	1	K.GMIILNRPKALNAINLEMVR.K + 2 Oxidation (M)

No match to: 829.46, 835.46, 847.46, 901.50, 936.51, 942.56, 954.56, 961.51, 1020.53, 1058.58, 1074.62, 1090.60, 1111.60, 1120.64, 1137.62, 1143.60, 1295.76, 1318.81, 1329.66, 1368.76, 1392.74, 1399.77, 1410.81, 1420.83, 1433.78, 1459.77, 1590.91, 1671.01, 1687.00, 1713.04, 1736.00, 1744.95, 1747.00, 1762.03, 1840.01, 1887.10, 1903.08, 1925.01, 2163.18, 2193.13, 2230.32, 2241.33, 2273.29, 2469.34, 2485.33, 2550.37, 2780.09, 2780.57, 2809.47, 3211.66, 3338.94

15. gi|125773639 **Mass:** 263763 **Score:** 33 **Expect:** 23 **Queries matched:** 17

GA18916-PA [Drosophila pseudoobscura]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
901.50	900.50	900.50	-5.82	38	44	1	R.EEVRQIK.H
944.55	943.54	943.52	14.7	1736	1743	1	K.VALGKWDR.D
1057.62	1056.61	1056.58	29.8	1823	1830	1	R.AIEYLHRR.R
1058.58	1057.57	1057.61	-36.50	62	71	0	R.VLLSALGTER.Q
1090.60	1089.59	1089.56	27.5	1533	1541	1	R.MVLCPRCLR.K
1120.64	1119.63	1119.56	63.2	2234	2242	1	R.IENKLDCSK.L + Propionamide (C)
1202.64	1201.63	1201.58	44.5	2037	2047	1	K.TPENGAQSRSR.S
1295.76	1294.75	1294.69	48.2	1013	1024	1	K.RSPGSHGPVVFR.T
1318.81	1317.80	1317.75	38.6	929	941	1	R.MKLMVVGVAGIGK.S + Oxidation (M)
1671.01	1670.00	1669.92	48.6	1119	1133	1	K.IGLPRVIDSIEISCR.T
1687.00	1686.00	1685.93	42.2	1046	1059	1	R.SLYLVLWRISDGHK.G
1719.99	1718.99	1718.87	68.1	891	905	1	R.GCLLQEPLRSMIESK.K + Oxidation (M)
2241.33	2240.32	2240.18	61.6	1295	1313	1	R.SYIVSLLNKFEVALTWDSR.T
2284.30	2283.29	2283.19	42.3	2357	2375	1	K.SLPPVDVDNHIHCLLWRAK.H + Propionamide (C)
2469.34	2468.33	2468.33	-0.83	2098	2120	1	K.SAVISLVYMENIARVAVGLHNGR.V
2485.33	2484.33	2484.33	0.24	2098	2120	1	K.SAVISLVYMENIARVAVGLHNGR.V + Oxidation (M)
2809.47	2808.46	2808.33	44.5	2329	2356	1	R.SLISRYVDSAESSNACSAVSTPTHGAAK.S

No match to: 829.46, 835.46, 847.46, 936.51, 942.56, 954.56, 961.51, 1020.53, 1074.62, 1111.60, 1137.62, 1143.60, 1329.66, 1368.76, 1392.74, 1399.77, 1410.81, 1420.83, 1433.78, 1459.77, 1511.85, 1590.91, 1713.04, 1736.00, 1744.95, 1747.00, 1762.03, 1840.01, 1887.10, 1903.08, 1925.01, 2163.18, 2193.13, 2230.32, 2273.29, 2298.31, 2550.37, 2780.09, 2780.57, 3211.66, 3338.94

16. gi|21358017 **Mass:** 35026 **Score:** 32 **Expect:** 33 **Queries matched:** 7

CG11837-PA [Drosophila melanogaster]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1020.53	1019.52	1019.55	-29.43	178	186	1	R.VDMLMKVGK.N
1090.60	1089.59	1089.55	38.7	74	82	0	K.VIACEIDTR.L + Propionamide (C)
1137.62	1136.61	1136.67	-50.05	90	99	1	K.RVQATPLQPK.L
1433.78	1432.77	1432.79	-12.51	156	167	1	R.LVAKPGDKLYCR.L + Propionamide (C)
1459.77	1458.77	1458.78	-10.83	151	163	1	R.EFAERLVAKPGDK.L
1840.01	1839.00	1838.90	59.7	206	221	0	K.NPPPPVNFTEWDGLTR.I
2241.33	2240.32	2240.19	56.9	45	66	1	K.AALRATDVVLEIGPGTGNMTVR.M

No match to: 829.46, 835.46, 847.46, 901.50, 936.51, 942.56, 944.55, 954.56, 961.51, 1057.62, 1058.58, 1074.62, 1111.60, 1120.64, 1143.60, 1202.64, 1295.76, 1318.81, 1329.66, 1368.76, 1392.74, 1399.77, 1410.81, 1420.83, 1511.85, 1590.91, 1671.01, 1687.00, 1713.04, 1719.99, 1736.00, 1744.95, 1747.00, 1762.03, 1887.10, 1903.08, 1925.01, 2163.18, 2193.13, 2230.32, 2273.29, 2284.30, 2298.31, 2469.34, 2485.33, 2550.37, 2780.09, 2780.57, 2809.47, 3211.66, 3338.94

17. gi|24581278 **Mass:** 24830 **Score:** 31 **Expect:** 36 **Queries matched:** 5

Peroxiredoxin 6005 CG3083-PA [Drosophila melanogaster]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
961.51	960.50	960.51	-9.61	185	192	0	K.CMVLPTVK.A + Propionamide (C)
1020.53	1019.52	1019.57	-43.56	131	139	1	R.AVFVVDDKK.K

```
         1074.62    1073.61    1073.59    19.6   214 - 222   1   K.SYLRITPQP.-
         1840.01    1839.00    1838.97    20.5    65 -  81   1   K.RGVKPIALSCDTVESHK.G
         1903.08    1902.07    1901.94    68.1    89 - 105   1   K.SFGKLSSFDYPIIADDK.R
        No match to: 829.46, 835.46, 847.46, 901.50, 936.51, 942.56, 944.55, 954.56, 1057.62, 1058.58, 1090.60, 1111.60,
        1120.64, 1137.62, 1143.60, 1202.64, 1295.76, 1318.81, 1329.66, 1368.76, 1392.74, 1399.77, 1410.81, 1420.83,
        1433.78, 1459.77, 1511.85, 1590.91, 1671.01, 1687.00, 1713.04, 1719.99, 1736.00, 1744.95, 1747.00, 1762.03,
        1887.10, 1925.01, 2163.18, 2193.13, 2230.32, 2241.33, 2273.29, 2284.30, 2298.31, 2469.34, 2485.33, 2550.37,
        2780.09, 2780.57, 2809.47, 3211.66, 3338.94

18.     gi|24658952     Mass: 26800     Score: 31     Expect: 38  Queries matched: 5
        CG9897-PA [Drosophila melanogaster]
       Observed   Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
          942.56     941.55     941.52   37.9   206 - 214   0   R.GSPLVIDNK.L
         1143.60    1142.59    1142.54   40.7   133 - 142   1   K.VPDDNSRANR.I
         1744.95    1743.94    1743.86   45.7    56 -  71   1   K.NYILTAAKCVDGYSAR.S
         1840.01    1839.00    1838.92   44.5    77 -  95   1   R.LGTSSCGTSGSIAGICKVK.V + Propionamide (C)
         2469.34    2468.33    2468.28   18.5   143 - 164   1   R.ISSGIEEKCFQLPVQLHGTQVR.I
        No match to: 829.46, 835.46, 847.46, 901.50, 936.51, 944.55, 954.56, 961.51, 1020.53, 1057.62, 1058.58, 1074.62,
        1090.60, 1111.60, 1120.64, 1137.62, 1202.64, 1295.76, 1318.81, 1329.66, 1368.76, 1392.74, 1399.77, 1410.81,
        1420.83, 1433.78, 1459.77, 1511.85, 1590.91, 1671.01, 1687.00, 1713.04, 1719.99, 1736.00, 1747.00, 1762.03,
        1887.10, 1903.08, 1925.01, 2163.18, 2193.13, 2230.32, 2241.33, 2273.29, 2284.30, 2298.31, 2485.33, 2550.37,
        2780.09, 2780.57, 2809.47, 3211.66, 3338.94

19.     gi|49066183     Mass: 13716     Score: 30     Expect: 45  Queries matched: 4
        ACP53C14C [Drosophila simulans]
       Observed   Mr(expt)  Mr(calc)     ppm   Start    End Miss   Peptide
          829.46     828.45     828.49  -46.99     52 -  58   1   R.AIPCVKK.L + Propionamide (C)
         1137.62    1136.61    1136.54    62.8     34 -  43   0   R.LSECTESGLK.V + Propionamide (C)
         1202.64    1201.63    1201.60    26.7    114 - 124   0   K.LISENCVPGLS.- + Propionamide (C)
         3211.66    3210.65    3210.76  -33.53      1 -  28   1   -.MKSNQVYYIALSLILLGFLLPNEVESLK.V + Oxidation (M)
        No match to: 835.46, 847.46, 901.50, 936.51, 942.56, 944.55, 954.56, 961.51, 1020.53, 1057.62, 1058.58, 1074.62,
        1090.60, 1111.60, 1120.64, 1143.60, 1295.76, 1318.81, 1329.66, 1368.76, 1392.74, 1399.77, 1410.81, 1420.83,
        1433.78, 1459.77, 1511.85, 1590.91, 1671.01, 1687.00, 1713.04, 1719.99, 1736.00, 1744.95, 1747.00, 1762.03,
        1840.01, 1887.10, 1903.08, 1925.01, 2163.18, 2193.13, 2230.32, 2241.33, 2273.29, 2284.30, 2298.31, 2469.34,
        2485.33, 2550.37, 2780.09, 2780.57, 2809.47, 3338.94

20.     gi|125979875     Mass: 59422     Score: 30     Expect: 47  Queries matched: 8
        GA18684-PA [Drosophila pseudoobscura]
       Observed   Mr(expt)  Mr(calc)     ppm   Start    End Miss   Peptide
          847.46     846.45     846.42    32.3    478 - 484   0   R.FEPIGER.Q
          942.56     941.55     941.51    44.8    467 - 474   0   K.SVMAHLLR.S + Oxidation (M)
         1143.60    1142.59    1142.61  -16.66    210 - 218   0   R.EVLHVIDYR.L
         1202.64    1201.63    1201.65  -10.11    478 - 487   1   R.FEPIGERQVK.M
         1399.77    1398.76    1398.72    28.7    133 - 144   0   K.TLTPAFNYTMIK.Q
         2284.30    2283.29    2283.15    59.9    488 - 505   1   K.MKLNFVVTLHTVEPYYCR.V + Propionamide (C)
         2780.57    2779.56    2779.61  -19.03      1 -  23   0   -.VVWLGLCLLLIVLSLYLLYAFER.Q + Propionamide (C)
         2809.47    2808.46    2808.59  -46.91     27 -  51   1   R.IDRLTHNWPAPPSLPILGHLHILAK.L
        No match to: 829.46, 835.46, 901.50, 936.51, 944.55, 954.56, 961.51, 1020.53, 1057.62, 1058.58, 1074.62,
        1090.60, 1111.60, 1120.64, 1137.62, 1295.76, 1318.81, 1329.66, 1368.76, 1392.74, 1410.81, 1420.83, 1433.78,
        1459.77, 1511.85, 1590.91, 1671.01, 1687.00, 1713.04, 1719.99, 1736.00, 1744.95, 1747.00, 1762.03, 1840.01,
        1887.10, 1903.08, 1925.01, 2163.18, 2193.13, 2230.32, 2241.33, 2273.29, 2298.31, 2469.34, 2485.33, 2550.37,
        2780.09, 3211.66, 3338.94
```

Search Parameters

```
Type of search         : Peptide Mass Fingerprint
Enzyme                 : Trypsin
Variable modifications : Oxidation (M),Propionamide (C)
Mass values            : Monoisotopic
Protein Mass           : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Peptide Charge State   : 1+
Max Missed Cleavages   : 1
Number of queries      : 58
```

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

Mascot Search Results

```
User            : Ilya
Email           : toropygin@rambler.ru
Search title    : Submitted from Shidlovsky 080328 II by Mascot Daemon on P4P800SE
MS data file    : \\192.168.0.18\data on ultraflex-2\DATA\2008_Ilya\Shidlovsky\080328\015\0_K21\1\015__0_K21__1.dar
Database        : NCBInr 20070307 (4984280 sequences; 1723577896 residues)
Taxonomy        : Drosophila (fruit flies) (47828 sequences)
Timestamp       : 2 Apr 2008 at 20:06:24 GMT
Top Score       : 61 for gi|24642732, xmas-2 CG32562-PA [Drosophila melanogaster]
```

Probability Based Mowse Score

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 59 are significant (p<0.05).

Score Distribution

Protein Summary Report

Format As	Protein Summary	Help
	Significance threshold p< 0.05	Max. number of hits 20

Overview Table

Click on column header to jump to entry in results list.
Move mouse over any indicator to highlight identical peptides.
Click on an indicator to see details of individual match.
Use check boxes to select sub-set of queries for new search.

Mouse over: -Query-

-Accession- -Sequence-

Hit:	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
☑ 1038.69 (1+)																				?
☑ 1062.66 (1+)		?																		
☑ 1090.65 (1+)	?					?									?					
☑ 1163.69 (1+)	?					?									?					
☑ 1191.69 (1+)																			?	
☑ 1196.65 (1+)																			?	
☑ 1202.66 (1+)			?			?				?	?							?		
☑ 1235.74 (1+)			?			?	?	?												
☑ 1273.73 (1+)				?														?	?	
☑ 1292.79 (1+)				?																
☑ 1302.72 (1+)				?					?			?								
☑ 1306.80 (1+)																				
☑ 1309.74 (1+)	?		?		?								?		?					

☑ **1363.71 (1+)**				?		?	?			?	?								?	?
☑ **1370.77 (1+)**				?		?								?		?				
☑ **1372.80 (1+)**		?	?														?			
☑ **1392.82 (1+)**						?														
☑ **1416.78 (1+)**						?						?							?	
☑ **1422.79 (1+)**	?	?													?					
☑ **1424.74 (1+)**				?																
☑ **1434.80 (1+)**						?	?										?			
☑ **1436.75 (1+)**						?	?			?	?									
☑ **1439.78 (1+)**										?	?									
☑ **1466.82 (1+)**				?								?								
☑ **1482.82 (1+)**						?						?								
☑ **1493.79 (1+)**		?				?							?					?		
☑ **1520.84 (1+)**		?			?		?									?				?
☑ **1530.85 (1+)**		?																		
☑ **1532.86 (1+)**					?	?		?									?			
☑ **1552.85 (1+)**	?					?							?		?		?			?
☑ **1564.83 (1+)**	?	?				?						?	?		?			?		
☑ **1572.97 (1+)**	?			?														?	?	
☑ **1577.85 (1+)**	?		?												?				?	
☑ **1579.81 (1+)**	?					?										?				
☑ **1590.85 (1+)**	?					?														
☑ **1600.90 (1+)**				?		?														
☑ **1611.83 (1+)**				?				?												
☑ **1631.83 (1+)**	?	?											?	?	?					
☑ **1635.87 (1+)**			?									?						?		
☑ **1649.85 (1+)**	?			?		?			?						?				?	?
☑ **1655.89 (1+)**						?						?		?						
☑ **1658.86 (1+)**		?								?	?			?		?			?	
☑ **1687.91 (1+)**				?	?								?				?			
☑ **1706.83 (1+)**				?	?	?	?					?								
☑ **1739.89 (1+)**						?														
☑ **1750.91 (1+)**						?						?								
☑ **1770.90 (1+)**	?					?		?							?					
☑ **1775.89 (1+)**			?			?			?								?			
☑ **1782.90 (1+)**			?			?								?		?			?	
☑ **1814.00 (1+)**	?	?				?									?					
☑ **1842.98 (1+)**	?	?						?												
☑ **1878.94 (1+)**				?		?														
☑ **1948.97 (1+)**	?					?		?					?							
☑ **1978.97 (1+)**				?		?							?				?			
☑ **1988.05 (1+)**		?				?			?											
☑ **2070.01 (1+)**						?														
☑ **2075.06 (1+)**									?	?	?			?		?		?		
☑ **2084.09 (1+)**		?	?			?														
☑ **2086.05 (1+)**	?											?			?					
☑ **2090.04 (1+)**									?								?			
☑ **2101.09 (1+)**						?			?			?							?	
☑ **2251.10 (1+)**					?			?	?											

☑ 2298.15 (1+)				?		?			?									?	?	
☑ 2351.11 (1+)	?					?									?					?
☑ 2724.38 (1+)					?															
☑ 2780.43 (1+)					?	?								?		?				
☑ 2780.92 (1+)																				

Select All Select None Search Selected

Index

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    Accession     Mass    Score  Description
 1. gi|24642732   158081     61  xmas-2 CG32562-PA [Drosophila melanogaster]
 2. gi|125807138  76227      56  GA11026-PA [Drosophila pseudoobscura]
 3. gi|21428826   52159      40  GH06222p [Drosophila melanogaster]
 4. gi|125985555  153282     39  GA10974-PA [Drosophila pseudoobscura]
 5. gi|17136796   54515      39  Vacuolar H[+]-ATPase 55kD B subunit CG17369-PB, isoform B [Drosophila melanogaster]
 6. gi|78706842   888438     39  Muscle-specific protein 300 CG33715-PB, isoform B [Drosophila melanogaster]
 7. gi|41615732   15450      38  TPA: TPA_inf: HDC02496 [Drosophila melanogaster]
 8. gi|24642691   35887      38  CG13001-PA [Drosophila melanogaster]
 9. gi|28573188   64835      37  alpha-Esterase-1 CG1031-PA [Drosophila melanogaster]
10. gi|24644665   19860      37  CG1307-PB [Drosophila melanogaster]
11. gi|4389444    18795      37  hypothetical 23.1kd-like protein [Drosophila melanogaster]
12. gi|19528039   62994      36  AT22192p [Drosophila melanogaster]
13. gi|24639878   20523      36  CG4151-PA [Drosophila melanogaster]
14. gi|7572       42939      36  aldolase-related protein [Drosophila melanogaster]
15. gi|6685149    137181     35  xmas-2 [Drosophila melanogaster]
16. gi|45551983   43217      35  Aldolase CG6058-PA, isoform A [Drosophila melanogaster]
17. gi|21430850   43587      35  SD20045p [Drosophila melanogaster]
18. gi|125978701  30284      35  GA16922-PA [Drosophila pseudoobscura]
19. gi|27544248   118888     35  supressor of Ty element 16 [Drosophila melanogaster]
20. gi|21356157   27835      35  Aly CG1101-PA [Drosophila melanogaster]
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Results List

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1.     gi|24642732     Mass: 158081    Score: 61     Expect: 0.035  Queries matched: 18
       xmas-2 CG32562-PA [Drosophila melanogaster]
      Observed  Mr(expt)  Mr(calc)    ppm  Start     End Miss   Peptide
       1090.65   1089.64   1089.61   30.3   1048 - 1057    0    R.LMIALESAVK.F + Oxidation (M)
       1163.69   1162.68   1162.63   37.4    524 -  532    1    R.QYELVEVKR.V
       1309.74   1308.73   1308.68   38.8    928 -  939    0    R.GLLQQPQSPDAR.F
       1422.79   1421.78   1421.75   20.4    535 -  548    0    K.SVGEVVSGEPLPPR.D
       1552.85   1551.84   1551.83   9.44   1078 - 1090    0    R.EYLLVNLGSELFR.R
       1564.83   1563.82   1563.80   13.1    735 -  746    0    K.LEQLFFVQQQER.E
       1572.97   1571.96   1571.87   58.5   1257 - 1270    1    R.NPPQGIVYNTKTLK.R
       1577.85   1576.85   1576.86  -9.99     18 -   30    1    R.NIPELFLDKYVAR.S
       1579.81   1578.81   1578.76   27.5    245 -  258    0    R.SSADQETPLPHELR.N
       1590.85   1589.84   1589.77   49.9    153 -  165    1    R.TPAQLRDLENMMR.R + Oxidation (M)
       1631.83   1630.82   1630.77   30.1    643 -  656    0    R.AQEFQEQAPATQQR.R
       1649.85   1648.84   1648.91  -43.69   533 -  548    1    R.VKSVGEVVSGEPLPPR.D
       1770.90   1769.89   1769.86   18.2    353 -  365    1    K.CLQTLKYMYHDLR.I + Oxidation (M); Propionamide (C)
       1814.00   1813.00   1812.97   12.0   1144 - 1159    0    R.VFVQPLPIESSLNTNR.L
       1842.98   1841.98   1841.94   21.1    166 -  181    1    R.RPAHTSEEKFSVLDAR.D
       1948.97   1947.96   1947.82   69.8    194 -  211    1    K.LSGATQGHCADMCPEKER.V + Oxidation (M)
       2086.05   2085.04   2085.08  -18.25   969 -  988    0    K.ATDLAEANGIICLIGLDDIR.L
       2351.11   2350.10   2350.08   9.47    549 -  567    0    R.DLYLNHRPHNSFDDYGMLK.S + Oxidation (M)
       No match to: 1038.69, 1062.66, 1191.69, 1196.65, 1202.66, 1235.74, 1273.73, 1292.79, 1302.72, 1306.80, 1363.71,
       1370.77, 1372.80, 1392.82, 1416.78, 1424.74, 1434.80, 1436.75, 1439.78, 1466.82, 1482.82, 1493.79, 1520.84,
       1530.85, 1532.86, 1600.90, 1611.83, 1635.87, 1655.89, 1658.86, 1687.91, 1706.83, 1739.89, 1750.91, 1775.89,
       1782.90, 1878.94, 1978.97, 1988.05, 2070.01, 2075.06, 2084.09, 2090.04, 2101.09, 2251.10, 2298.15, 2724.38,
       2780.43, 2780.92

2.     gi|125807138     Mass: 76227     Score: 56     Expect: 0.13  Queries matched: 13
       GA11026-PA [Drosophila pseudoobscura]
      Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
       1062.66   1061.65   1061.59   53.6    380 - 388    1    K.MDKFLAPIK.K
       1372.80   1371.79   1371.77   18.6    447 - 457    1    R.QCNVQLRSILK.N + Propionamide (C)
       1422.79   1421.78   1421.71   50.6    458 - 469    1    K.NLVYVGCVDERR.A
       1493.79   1492.78   1492.75   24.7    458 - 469    1    K.NLVYVGCVDERR.A + Propionamide (C)
       1520.84   1519.83   1519.84  -4.58    211 - 224    1    R.SENIRIIYGAGISK.E
       1530.85   1529.84   1529.77   44.1    442 - 453    1    R.QSVERQCNVQLR.S + Propionamide (C)
       1564.83   1563.82   1563.91  -54.14    17 -  31    0    R.IAAGEIIQRPANALK.E
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         1631.83   1630.82   1630.93  -68.53   577 - 590   0   R.HKPSATHLPVYLLR.L
         1658.86   1657.86   1657.85    2.25   561 - 576   0   R.ISEEGSVESLPSLVGR.H
         1814.00   1813.00   1812.88    63.8   310 - 323   0   K.HEVHFLYQDEIVER.L
         1842.98   1841.98   1841.97    5.24    83 -  98   1   K.LAKFEDLSQIATFGFR.G
         1988.05   1987.04   1986.96    41.6   344 - 361   1   K.QLKLPGASDMDETQPVDK.S + Oxidation (M)
         2084.09   2083.08   2083.17  -42.16   536 - 554   1   K.TELVASAVQILQQKAPIMK.E + Oxidation (M)
        No match to: 1038.69, 1090.65, 1163.69, 1191.69, 1196.65, 1202.66, 1235.74, 1273.73, 1292.79, 1302.72, 1306.80,
        1309.74, 1363.71, 1370.77, 1392.82, 1416.78, 1424.74, 1434.80, 1436.75, 1439.78, 1466.82, 1482.82, 1532.86,
        1552.85, 1572.97, 1577.85, 1579.81, 1590.85, 1600.90, 1611.83, 1635.87, 1649.85, 1655.89, 1687.91, 1706.83,
        1739.89, 1750.91, 1770.90, 1775.89, 1782.90, 1878.94, 1948.97, 1978.97, 2070.01, 2075.06, 2086.05, 2090.04,
        2101.09, 2251.10, 2298.15, 2351.11, 2724.38, 2780.43, 2780.92

   3.   gi|21428826    Mass: 52159    Score: 40     Expect: 4.6  Queries matched: 9
        GH06222p [Drosophila melanogaster]
        Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
         1202.66   1201.66   1201.62    32.9    43 -  52   1   R.TSNQQNINKR.R
         1235.74   1234.73   1234.65    66.1   217 - 228   1   R.SKSLSSADALTR.G
         1309.74   1308.73   1308.66    52.4   119 - 131   0   R.QAGHSLGNMPGLK.A
         1372.80   1371.79   1371.73    42.2    69 -  80   0   R.GKPAMDIYRPPK.L
         1577.85   1576.85   1576.80    31.6   427 - 441   1   R.DAFLNAGESAASIRR.T
         1635.87   1634.86   1634.78    49.3    54 -  68   0   R.SLAFNVPGNQTGQMR.G + Oxidation (M)
         1775.89   1774.89   1774.89   -1.14    53 -  68   1   R.RSLAFNVPGNQTGQMR.G
         1782.90   1781.89   1781.92  -16.07   265 - 279   1   K.LNSRCLMELTSQFIK.R
         2084.09   2083.08   2083.01    35.5   340 - 356   1   R.FTAFMAFLTEMFCQLKR.R
        No match to: 1038.69, 1062.66, 1090.65, 1163.69, 1191.69, 1196.65, 1273.73, 1292.79, 1302.72, 1306.80, 1363.71,
        1370.77, 1392.82, 1416.78, 1422.79, 1424.74, 1434.80, 1436.75, 1439.78, 1466.82, 1482.82, 1493.79, 1520.84,
        1530.85, 1532.86, 1552.85, 1564.83, 1572.97, 1579.81, 1590.85, 1600.90, 1611.83, 1631.83, 1649.85, 1655.89,
        1658.86, 1687.91, 1706.83, 1739.89, 1750.91, 1770.90, 1814.00, 1842.98, 1878.94, 1948.97, 1978.97, 1988.05,
        2070.01, 2075.06, 2086.05, 2090.04, 2101.09, 2251.10, 2298.15, 2351.11, 2724.38, 2780.43, 2780.92

   4.   gi|125985555    Mass: 153282    Score: 39     Expect: 5.5  Queries matched: 16
        GA10974-PA [Drosophila pseudoobscura]
        Observed  Mr(expt)  Mr(calc)    ppm  Start     End Miss   Peptide
         1273.73   1272.72   1272.66    48.5    11 -   21    0   R.LAQMTGQQQLR.A
         1292.79   1291.78   1291.70    61.8   361 -  371    1   R.KEIEAFESLVK.Q
         1302.72   1301.71   1301.63    65.2   965 -  974    1   R.FQEHKEDLEK.A
         1363.71   1362.70   1362.66    34.2   558 -  568    1   K.EERNLSVQCSK.L + Propionamide (C)
         1370.77   1369.77   1369.72    33.3   414 -  424    1   K.ELEDLRTLPER.N
         1424.74   1423.73   1423.68    36.1  1103 - 1114    0   K.EFMDGFAIITHK.L + Oxidation (M)
         1466.82   1465.81   1465.88  -43.99    72 -   83    1   R.LIIKQIVNHNFK.S
         1572.97   1571.96   1571.90    35.4   999 - 1012    0   K.VEIPAHQAELKPLK.L
         1600.90   1599.89   1599.85    23.3    11 -   24    1   R.LAQMTGQQQLRAQK.E
         1611.83   1610.83   1610.86  -23.00   202 -  214    1   K.LLKTHHVDLEHNR.F
         1649.85   1648.84   1648.86  -13.29  1103 - 1116    1   K.EFMDGFAIITHKLK.E
         1687.91   1686.90   1686.80    59.6   670 -  684    1   R.REACSTIDTPENVPR.L
         1706.83   1705.82   1705.74    48.3   178 -  192    0   R.TAMSDNSSYYQINGR.R
         1878.94   1877.93   1877.83    51.1   178 -  193    1   R.TAMSDNSSYYQINGRR.A + Oxidation (M)
         1978.97   1977.96   1977.89    38.1   110 -  126    1   K.SNVIDSMMFVFGCRANR.I + 2 Oxidation (M)
         2298.15   2297.15   2297.06    36.5   380 -  399    1   K.LVSAERACTEVQSTMENTNK.Q + Oxidation (M); Propionamide (C)
        No match to: 1038.69, 1062.66, 1090.65, 1163.69, 1191.69, 1196.65, 1202.66, 1235.74, 1306.80, 1309.74, 1372.80,
        1392.82, 1416.78, 1422.79, 1434.80, 1436.75, 1439.78, 1482.82, 1493.79, 1520.84, 1530.85, 1532.86, 1552.85,
        1564.83, 1577.85, 1579.81, 1590.85, 1631.83, 1635.87, 1655.89, 1658.86, 1739.89, 1750.91, 1770.90, 1775.89,
        1782.90, 1814.00, 1842.98, 1948.97, 1988.05, 2070.01, 2075.06, 2084.09, 2086.05, 2090.04, 2101.09, 2251.10,
        2351.11, 2724.38, 2780.43, 2780.92

   5.   gi|17136796    Mass: 54515    Score: 39     Expect: 6.5  Queries matched: 8
        Vacuolar H[+]-ATPase 55kD B subunit CG17369-PB, isoform B [Drosophila melanogaster]
        Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
         1309.74   1308.73   1308.65    58.4   381 - 392   1   R.LMKSAIGEGMTR.K + Oxidation (M)
         1520.84   1519.83   1519.79    26.7    73 -  87   0   K.AVVQVFEGTSGIDAK.N
         1532.86   1531.85   1531.85   -2.06   474 - 486   1   K.RIPASILAEFYPR.D
         1687.91   1686.90   1686.94  -24.71    47 -  61   1   K.FAEIVQLRLADGTVR.S
         1706.83   1705.82   1705.90  -45.89     2 -  16   1   M.NAQQAQREHVLAVSR.D
         2251.10   2250.09   2250.21  -51.98   252 - 271   1   R.IITPRLALTAAEFLAYQCEK.H
         2724.38   2723.37   2723.27    36.5   198 - 222   0   K.SVLDDHTDNFAIVFAAMGVNMETAR.F
         2780.43   2779.43   2779.39    13.6   143 - 167   1   R.IYPEEMIQTGISAIDVMNSIARGQK.I + Oxidation (M)
        No match to: 1038.69, 1062.66, 1090.65, 1163.69, 1191.69, 1196.65, 1202.66, 1235.74, 1273.73, 1292.79, 1302.72,
        1306.80, 1363.71, 1370.77, 1372.80, 1392.82, 1416.78, 1422.79, 1424.74, 1434.80, 1436.75, 1439.78, 1466.82,
        1482.82, 1493.79, 1530.85, 1552.85, 1564.83, 1572.97, 1577.85, 1579.81, 1590.85, 1600.90, 1611.83, 1631.83,
        1635.87, 1649.85, 1655.89, 1658.86, 1739.89, 1750.91, 1770.90, 1775.89, 1782.90, 1814.00, 1842.98, 1878.94,
        1948.97, 1978.97, 1988.05, 2070.01, 2075.06, 2084.09, 2086.05, 2090.04, 2101.09, 2298.15, 2351.11, 2780.92
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6.   gi|78706842     Mass: 888438    Score: 39     Expect: 6.8  Queries matched: 37
     Muscle-specific protein 300 CG33715-PB, isoform B [Drosophila melanogaster]
     Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
      1090.65   1089.64   1089.62    23.1  3196 - 3204   0    K.QLFQSIVQK.S
      1163.69   1162.68   1162.61    55.6  6962 - 6971   0    K.IFFGNEAPIR.N
      1202.66   1201.66   1201.63    21.4  6384 - 6394   1    K.AELDRALEASK.A
      1235.74   1234.73   1234.66    60.1  5122 - 5132   0    R.ISNAIMQLTTK.Y + Oxidation (M)
      1363.71   1362.70   1362.71   -2.72  6161 - 6172   1    K.LESELMDAIAKK.Q + Oxidation (M)
      1370.77   1369.77   1369.77   -4.45  7615 - 7625   1    R.LSIEKLEVHFR.N
      1392.82   1391.81   1391.77    33.3  5992 - 6003   0    K.LEDLLDQKPPPK.T
      1416.78   1415.77   1415.74    22.6  4802 - 4812   1    K.ELQTEWDRLVK.K
      1434.80   1433.79   1433.71    60.3  5707 - 5719   1    K.VAPETKGELSEMK.T + Oxidation (M)
      1436.75   1435.75   1435.66    60.1  2752 - 2763   1    K.AVTLCDDESERK.T + Propionamide (C)
      1482.82   1481.81   1481.80    5.82  1187 - 1198   1    R.REVHEVVCLLSK.V + Propionamide (C)
      1493.79   1492.78   1492.80  -11.53  6972 - 6984   1    R.NLVHKQIQEAADK.I
      1532.86   1531.85   1531.77    53.2  5217 - 5230   1    K.EKVIMNTEQNGAAK.I
      1552.85   1551.84   1551.75    60.5  1727 - 1738   0    K.LVNFSNWMEQLR.N + Oxidation (M)
      1564.83   1563.82   1563.74    52.4  3656 - 3667   1    K.AQQDYQKNLWDR.L
      1579.81   1578.81   1578.80    4.49  3738 - 3752   1    K.FGASLSDVKSGLENR.L
      1590.85   1589.84   1589.83    6.25  4635 - 4647   1    K.NHKLNLCPNLPEK.E + Propionamide (C)
      1600.90   1599.89   1599.81    48.9  4902 - 4917   0    K.ASVLQQGAPGTEISDK.Y
      1649.85   1648.84   1648.82    11.2  6622 - 6635   0    R.LAECSQFLGNIQQK.L + Propionamide (C)
      1655.89   1654.89   1654.88    2.30     9 -   21   1    K.TFTNWINSYLLKR.V
      1706.83   1705.82   1705.81    7.58  3753 - 3765   0    R.LQQWNDYEINLDR.L
      1739.89   1738.89   1738.88    1.45  1199 - 1214   1    K.VKDQTANIPAPDSLDR.V
      1750.91   1749.90   1749.84    37.6  3813 - 3828   1    K.VKDDTSELVQSSGETR.I
      1770.90   1769.89   1769.89   -1.83  2031 - 2045   1    K.YNLISQALREYADSK.D
      1775.89   1774.89   1774.94  -26.82  6647 - 6662   0    R.IEDVQDLLGAYEGILK.E
      1782.90   1781.89   1781.90   -6.10   451 -  465   1    K.CCLIAFLNLVENKMR.G + Oxidation (M)
      1814.00   1813.00   1812.97    16.3  1448 - 1464   1    R.MKQLDLLAADASELAPK.E
      1878.94   1877.93   1877.87    31.6  7459 - 7473   0    R.FMNLYQIVMSWASEK.R + 2 Oxidation (M)
      1948.97   1947.96   1947.83    68.4  4307 - 4323   1    K.LDYCSDMSSMSPKELDK.K
      1978.97   1977.96   1977.91    25.8  4794 - 4809   1    R.DAINTEMKELQTEWDR.L
      1988.05   1987.04   1987.10  -28.60  1330 - 1346   1    K.RDLNVQLQQASHQLLPK.L
      2070.01   2069.00   2069.06  -30.11  1419 - 1436   1    K.NIEALQSEDLTPEERVVK.V
      2084.09   2083.08   2083.13  -23.08   156 -  174   1    K.TLLNWVTNALPKDSGVEVK.D
      2101.09   2100.08   2100.06    8.82  3344 - 3361   1    R.SAEAVFREQQLQSTLHEK.V
      2298.15   2297.15   2297.22  -30.61  7046 - 7065   1    R.TKFVDEPVQNLAGLHFNIQK.L
      2351.11   2350.10   2350.19  -36.40  4617 - 4634   1    K.EEYERLMEWLQQIDILVK.N + Oxidation (M)
      2780.43   2779.43   2779.38    16.2  2598 - 2623   1    K.IEFQELARMGSPGSSSATAQQLQTVK.N + Oxidation (M)
     No match to: 1038.69, 1062.66, 1191.69, 1196.65, 1273.73, 1292.79, 1302.72, 1306.80, 1309.74, 1372.80, 1422.79,
     1424.74, 1439.78, 1466.82, 1520.84, 1530.85, 1572.97, 1577.85, 1611.83, 1631.83, 1635.87, 1658.86, 1687.91,
     1842.98, 2075.06, 2086.05, 2090.04, 2251.10, 2724.38, 2780.92

7.   gi|41615732     Mass: 15450     Score: 38     Expect: 7.4  Queries matched: 6
     TPA: TPA_inf: HDC02496 [Drosophila melanogaster]
     Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss  Peptide
      1235.74   1234.73   1234.65    68.1    28 -   38   0   R.MGRPSAVFINK.K + Oxidation (M)
      1363.71   1362.70   1362.74  -30.42    28 -   39   1   R.MGRPSAVFINKK.K + Oxidation (M)
      1434.80   1433.79   1433.77    18.8    41 -   53   1   K.KESPVFFGTLGPR.Q
      1436.75   1435.75   1435.71    24.1    98 -  110   0   R.ENICISLGDFGLR.A
      1520.84   1519.83   1519.78    35.0    14 -   26   1   R.HSSHGGNIITRWR.R
      1706.83   1705.82   1705.88  -37.05    98 -  113   1   R.ENICISLGDFGLRAAK.S
     No match to: 1038.69, 1062.66, 1090.65, 1163.69, 1191.69, 1196.65, 1202.66, 1273.73, 1292.79, 1302.72, 1306.80,
     1309.74, 1370.77, 1372.80, 1392.82, 1416.78, 1422.79, 1424.74, 1439.78, 1466.82, 1482.82, 1493.79, 1530.85,
     1532.86, 1552.85, 1564.83, 1572.97, 1577.85, 1579.81, 1590.85, 1600.90, 1611.83, 1631.83, 1635.87, 1649.85,
     1655.89, 1658.86, 1687.91, 1739.89, 1750.91, 1770.90, 1775.89, 1782.90, 1814.00, 1842.98, 1878.94, 1948.97,
     1978.97, 1988.05, 2070.01, 2075.06, 2084.09, 2086.05, 2090.04, 2101.09, 2251.10, 2298.15, 2351.11, 2724.38,
     2780.43, 2780.92

8.   gi|24642691     Mass: 35887     Score: 38     Expect: 7.6  Queries matched: 7
     CG13001-PA [Drosophila melanogaster]
     Observed  Mr(expt)  Mr(calc)   ppm  Start   End Miss  Peptide
      1235.74   1234.73   1234.67   50.5    13 -  22   1   R.HYYAKLEAIK.D
      1532.86   1531.85   1531.74   69.2   254 - 268   0   K.GDFSAPPPPPPPSNR.L
      1611.83   1610.83   1610.75   45.6   130 - 143   1   R.DLHEEEGSPISKDR.F
      1770.90   1769.89   1769.89   1.83   285 - 299   1   R.SDFNVNLRQQPPPMK.S
      1842.98   1841.98   1841.85   66.7     2 -  17   1   M.ATSEISSSNERHYYAK.L
      1948.97   1947.96   1947.94   10.1    97 - 112   1   R.SFDMANRVYEEYLALK.Y
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       2251.10   2250.09   2250.06    12.0    300 - 319    1   K.SCLSCHQQIHRNAPICPLCK.A
      No match to: 1038.69, 1062.66, 1090.65, 1163.69, 1191.69, 1196.65, 1202.66, 1273.73, 1292.79, 1302.72, 1306.80,
      1309.74, 1363.71, 1370.77, 1372.80, 1392.82, 1416.78, 1422.79, 1424.74, 1434.80, 1436.75, 1439.78, 1466.82,
      1482.82, 1493.79, 1520.84, 1530.85, 1552.85, 1564.83, 1572.97, 1577.85, 1579.81, 1590.85, 1600.90, 1631.83,
      1635.87, 1649.85, 1655.89, 1658.86, 1687.91, 1706.83, 1739.89, 1750.91, 1775.89, 1782.90, 1814.00, 1878.94,
      1978.97, 1988.05, 2070.01, 2075.06, 2084.09, 2086.05, 2090.04, 2101.09, 2298.15, 2351.11, 2724.38, 2780.43,
      2780.92

  9.  gi|28573188     Mass: 64835     Score: 37     Expect: 8.7  Queries matched: 9
      alpha-Esterase-1 CG1031-PA [Drosophila melanogaster]
     Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
       1302.72   1301.71   1301.72  -10.05    540 - 550    0   K.QLEFIVLPESK.Q
       1649.85   1648.84   1648.80    28.8    408 - 420    0   R.MEFNECLHILSVK.H + Oxidation (M); Propionamide (C)
       1775.89   1774.89   1774.89    1.03    406 - 420    1   R.GRMEFNECLHILSVK.H
       1988.05   1987.04   1986.97    35.9    286 - 304    0   K.APASEMAAQGITLVSQEER.R
       2075.06   2074.05   2073.96    45.1    260 - 277    1   R.WAYRLACQLGYSGSENEK.E
       2090.04   2089.04   2089.03    2.92     76 -  93    1   R.APQPPHPWLGVRDCTYPR.A
       2101.09   2100.08   2099.99    40.0    264 - 281    1   R.LACQLGYSGSENEKEVFR.Y + Propionamide (C)
       2251.10   2250.09   2250.01    36.1    447 - 464    1   R.FDVDSPHFNHFRQVMCGK.H + Oxidation (M); Propionamide (C)
       2298.15   2297.15   2297.24  -39.81    168 - 190    1   R.VGALGFLSLADRDLDVPGNAGLK.D
      No match to: 1038.69, 1062.66, 1090.65, 1163.69, 1191.69, 1196.65, 1202.66, 1235.74, 1273.73, 1292.79, 1306.80,
      1309.74, 1363.71, 1370.77, 1372.80, 1392.82, 1416.78, 1422.79, 1424.74, 1434.80, 1436.75, 1439.78, 1466.82,
      1482.82, 1493.79, 1520.84, 1530.85, 1532.86, 1552.85, 1564.83, 1572.97, 1577.85, 1579.81, 1590.85, 1600.90,
      1611.83, 1631.83, 1635.87, 1655.89, 1658.86, 1687.91, 1706.83, 1739.89, 1750.91, 1770.90, 1782.90, 1814.00,
      1842.98, 1878.94, 1948.97, 1978.97, 2070.01, 2084.09, 2086.05, 2351.11, 2724.38, 2780.43, 2780.92

 10.  gi|24644665     Mass: 19860     Score: 37     Expect: 11  Queries matched: 6
      CG1307-PB [Drosophila melanogaster]
     Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
       1202.66   1201.66   1201.69  -24.45     74 -  83    1   K.MVLVVRNDLK.M + Oxidation (M)
       1363.71   1362.70   1362.71   -2.72    127 - 138    1   R.VESEAELMAIKK.E + Oxidation (M)
       1436.75   1435.75   1435.67    54.0    114 - 126    1   R.SWENCGCAKIAVR.V
       1439.78   1438.77   1438.78   -2.27    164 - 178    0   K.TVLAVGPAAAADIDR.V
       1658.86   1657.86   1657.91  -30.91    123 - 137    1   K.IAVRVESEAELMAIK.K
       2075.06   2074.05   2074.15  -49.28    164 - 184    1   K.TVLAVGPAAAADIDRVTGHLK.L
      No match to: 1038.69, 1062.66, 1090.65, 1163.69, 1191.69, 1196.65, 1235.74, 1273.73, 1292.79, 1302.72, 1306.80,
      1309.74, 1370.77, 1372.80, 1392.82, 1416.78, 1422.79, 1424.74, 1434.80, 1466.82, 1482.82, 1493.79, 1520.84,
      1530.85, 1532.86, 1552.85, 1564.83, 1572.97, 1577.85, 1579.81, 1590.85, 1600.90, 1611.83, 1631.83, 1635.87,
      1649.85, 1655.89, 1687.91, 1706.83, 1739.89, 1750.91, 1770.90, 1775.89, 1782.90, 1814.00, 1842.98, 1878.94,
      1948.97, 1978.97, 1988.05, 2070.01, 2084.09, 2086.05, 2090.04, 2101.09, 2251.10, 2298.15, 2351.11, 2724.38,
      2780.43, 2780.92

 11.  gi|4389444     Mass: 18795     Score: 37     Expect: 11  Queries matched: 6
      hypothetical 23.1kd-like protein [Drosophila melanogaster]
     Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
       1202.66   1201.66   1201.69  -24.45     64 -  73    1   K.MVLVVRNDLK.M + Oxidation (M)
       1363.71   1362.70   1362.71   -2.72    117 - 128    1   R.VESEAELMAIKK.E + Oxidation (M)
       1436.75   1435.75   1435.67    54.0    104 - 116    1   R.SWENCGCAKIAVR.V
       1439.78   1438.77   1438.78   -2.27    154 - 168    0   K.TVLAVGPAAAADIDR.V
       1658.86   1657.86   1657.91  -30.91    113 - 127    1   K.IAVRVESEAELMAIK.K
       2075.06   2074.05   2074.15  -49.28    154 - 174    1   K.TVLAVGPAAAADIDRVTGHLK.L
      No match to: 1038.69, 1062.66, 1090.65, 1163.69, 1191.69, 1196.65, 1235.74, 1273.73, 1292.79, 1302.72, 1306.80,
      1309.74, 1370.77, 1372.80, 1392.82, 1416.78, 1422.79, 1424.74, 1434.80, 1466.82, 1482.82, 1493.79, 1520.84,
      1530.85, 1532.86, 1552.85, 1564.83, 1572.97, 1577.85, 1579.81, 1590.85, 1600.90, 1611.83, 1631.83, 1635.87,
      1649.85, 1655.89, 1687.91, 1706.83, 1739.89, 1750.91, 1770.90, 1775.89, 1782.90, 1814.00, 1842.98, 1878.94,
      1948.97, 1978.97, 1988.05, 2070.01, 2084.09, 2086.05, 2090.04, 2101.09, 2251.10, 2298.15, 2351.11, 2724.38,
      2780.43, 2780.92

 12.  gi|19528039     Mass: 62994     Score: 36     Expect: 11  Queries matched: 11
      AT22192p [Drosophila melanogaster]
     Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
       1302.72   1301.71   1301.66    34.6    413 - 423    0   R.CLIVAEDELAR.C + Propionamide (C)
       1416.78   1415.77   1415.74    21.6     61 -  72    1   K.YNHIPGSFRIGR.K
       1466.82   1465.81   1465.88  -43.99    119 - 131    1   K.LTKWIVKPPASAR.G
       1482.82   1481.81   1481.75    42.4    465 - 476    1   R.EMGIALLSRYCR.D + Propionamide (C)
       1564.83   1563.82   1563.75    45.2    384 - 395    1   K.HNQYTNRSIEFR.E
       1635.87   1634.86   1634.79    46.8    238 - 250    0   K.WTLQSLWSCLENR.G
       1655.89   1654.89   1654.94  -30.02    263 - 278    1   R.NLVIKGIVSGESGLNR.M
       1706.83   1705.82   1705.82   -3.34    238 - 250    0   K.WTLQSLWSCLENR.G + Propionamide (C)
       1750.91   1749.90   1749.88    15.9     32 -  45    1   R.IIKNTTDWMAVWEK.H + Oxidation (M)
       2086.05   2085.04   2085.17  -62.39    171 - 187    1   R.LYVVLTSINPLRIYMYK.D
       2101.09   2100.08   2100.09   -7.33    424 - 441    1   R.CQPLERIFPTAGTHVYLR.Y
      No match to: 1038.69, 1062.66, 1090.65, 1163.69, 1191.69, 1196.65, 1202.66, 1235.74, 1273.73, 1292.79, 1306.80,
      1309.74, 1363.71, 1370.77, 1372.80, 1392.82, 1422.79, 1424.74, 1434.80, 1436.75, 1439.78, 1493.79, 1520.84,
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        1530.85, 1532.86, 1552.85, 1572.97, 1577.85, 1579.81, 1590.85, 1600.90, 1611.83, 1631.83, 1649.85, 1658.86,
        1687.91, 1739.89, 1770.90, 1775.89, 1782.90, 1814.00, 1842.98, 1878.94, 1948.97, 1978.97, 1988.05, 2070.01,
        2075.06, 2084.09, 2090.04, 2251.10, 2298.15, 2351.11, 2724.38, 2780.43, 2780.92

13.     gi|24639878     Mass: 20523     Score: 36     Expect: 11  Queries matched: 8
        CG4151-PA [Drosophila melanogaster]
       Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
        1309.74   1308.73   1308.74  -6.17    97 - 107    1   R.LRPRPQSDGKR.I
        1493.79   1492.78   1492.72   44.2   115 - 126    1   R.ICLDDKLASCWR.D + Propionamide (C)
        1552.85   1551.84   1551.75   60.9    31 -  45    1   R.CTGLSSGQSVCIRNK.V
        1564.83   1563.82   1563.75   45.5   115 - 126    1   R.ICLDDKLASCWR.D + 2 Propionamide (C)
        1631.83   1630.82   1630.80   9.67    81 -  96    1   R.CRNIPGTSGVGQCAIR.L
        1687.91   1686.90   1686.84   38.0    67 -  80    1   R.DNGLEPIRETCITR.C + Propionamide (C)
        1948.97   1947.96   1947.94   9.73   121 - 137    1   K.LASCWRDQQGACILQTR.C
        1978.97   1977.96   1977.97  -2.39    25 -  43    1   R.RPCVGRCTGLSSGQSVCIR.N
        No match to: 1038.69, 1062.66, 1090.65, 1163.69, 1191.69, 1196.65, 1202.66, 1235.74, 1273.73, 1292.79, 1302.72,
        1306.80, 1363.71, 1370.77, 1372.80, 1392.82, 1416.78, 1422.79, 1424.74, 1434.80, 1436.75, 1439.78, 1466.82,
        1482.82, 1520.84, 1530.85, 1532.86, 1572.97, 1577.85, 1579.81, 1590.85, 1600.90, 1611.83, 1635.87, 1649.85,
        1655.89, 1658.86, 1706.83, 1739.89, 1750.91, 1770.90, 1775.89, 1782.90, 1814.00, 1842.98, 1878.94, 1988.05,
        2070.01, 2075.06, 2084.09, 2086.05, 2090.04, 2101.09, 2251.10, 2298.15, 2351.11, 2724.38, 2780.43, 2780.92

14.     gi|7572     Mass: 42939     Score: 36     Expect: 12  Queries matched: 7
        aldolase-related protein [Drosophila melanogaster]
       Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
        1370.77   1369.77   1369.78  -12.65   304 - 316    1   R.ALQASVLRAWAGK.K
        1631.83   1630.82   1630.82   -2.85   380 - 395    1   R.LPAMPTSLSPSTNTKS.-
        1655.89   1654.89   1654.89   -1.25   243 - 257    0   K.NTPEEIALTTVQALR.R
        1658.86   1657.86   1657.80    32.6    44 -  57    1   R.LQDIGVENTEDNRR.A
        1782.90   1781.89   1781.84    28.9   331 - 348    1   R.AKANGEAACGNYTAGSVK.G + Propionamide (C)
        2075.06   2074.05   2074.11  -28.25    70 -  87    0   K.LAENISGVILFHETLYQK.A
        2780.43   2779.43   2779.43   -2.35   216 - 241    0   K.ALSDHHVYLEGTLLKPNMVTAGQSAK.K
        No match to: 1038.69, 1062.66, 1090.65, 1163.69, 1191.69, 1196.65, 1202.66, 1235.74, 1273.73, 1292.79, 1302.72,
        1306.80, 1309.74, 1363.71, 1372.80, 1392.82, 1416.78, 1422.79, 1424.74, 1434.80, 1436.75, 1439.78, 1466.82,
        1482.82, 1493.79, 1520.84, 1530.85, 1532.86, 1552.85, 1564.83, 1572.97, 1577.85, 1579.81, 1590.85, 1600.90,
        1611.83, 1635.87, 1649.85, 1687.91, 1706.83, 1739.89, 1750.91, 1770.90, 1775.89, 1814.00, 1842.98, 1878.94,
        1948.97, 1978.97, 1988.05, 2070.01, 2084.09, 2086.05, 2090.04, 2101.09, 2251.10, 2298.15, 2351.11, 2724.38,
        2780.92

15.     gi|6685149     Mass: 137181     Score: 35     Expect: 14  Queries matched: 13
        xmas-2 [Drosophila melanogaster]
       Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
        1090.65   1089.64   1089.61    30.3   862 - 871    0   R.LMIALESAVK.F + Oxidation (M)
        1163.69   1162.68   1162.63    37.4   338 - 346    1   R.QYELVEVKR.V
        1309.74   1308.73   1308.68    38.8   742 - 753    0   R.GLLQQPQSPDAR.F
        1422.79   1421.78   1421.75    20.4   349 - 362    0   K.SVGEVVSGEPLPPR.D
        1552.85   1551.84   1551.83    9.44   892 - 904    0   R.EYLLVNLGSELFR.R
        1564.83   1563.82   1563.80    13.1   549 - 560    0   K.LEQLFFVQQQER.E
        1577.85   1576.85   1576.86   -9.99    18 -  30    1   R.NIPELFLDKYVAR.S
        1631.83   1630.82   1630.77    30.1   457 - 470    0   R.AQEFQEQAPATQQR.R
        1649.85   1648.84   1648.91  -43.69   347 - 362    1   R.VKSVGEVVSGEPLPPR.D
        1770.90   1769.89   1769.86    18.2   167 - 179    1   K.CLQTLKYMYHDLR.I + Oxidation (M); Propionamide (C)
        1814.00   1813.00   1812.97    12.0   958 - 973    0   R.VFVQPLPIESSLNTNR.L
        2086.05   2085.04   2085.08  -18.25   783 - 802    0   K.ATDLAEANGIICLIGLDDIR.L
        2351.11   2350.10   2350.08    9.47   363 - 381    0   R.DLYLNHRPHNSFDDYGMLK.S + Oxidation (M)
        No match to: 1038.69, 1062.66, 1191.69, 1196.65, 1202.66, 1235.74, 1273.73, 1292.79, 1302.72, 1306.80, 1363.71,
        1370.77, 1372.80, 1392.82, 1416.78, 1424.74, 1434.80, 1436.75, 1439.78, 1466.82, 1482.82, 1493.79, 1520.84,
        1530.85, 1532.86, 1572.97, 1579.81, 1590.85, 1600.90, 1611.83, 1635.87, 1655.89, 1658.86, 1687.91, 1706.83,
        1739.89, 1750.91, 1775.89, 1782.90, 1842.98, 1878.94, 1948.97, 1978.97, 1988.05, 2070.01, 2075.06, 2084.09,
        2090.04, 2101.09, 2251.10, 2298.15, 2724.38, 2780.43, 2780.92

16.     gi|45551983     Mass: 43217     Score: 35     Expect: 14  Queries matched: 7
        Aldolase CG6058-PA, isoform A [Drosophila melanogaster]
       Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
        1370.77   1369.77   1369.78  -12.65   337 - 349    1   R.ALQASVLRAWAGK.K
        1520.84   1519.83   1519.86  -21.15   235 - 248    1   R.AQKVTETVLAAVYK.A
        1579.81   1578.81   1578.78    20.3    31 -  43    1   R.ISKMTTYFNYPSK.E
        1658.86   1657.86   1657.80    32.6    77 -  90    1   R.LQDIGVENTEDNRR.A
        1782.90   1781.89   1781.84    28.9   364 - 381    1   R.AKANGEAACGNYTAGSVK.G + Propionamide (C)
        2075.06   2074.05   2074.11  -28.25   103 - 120    0   K.LAENISGVILFHETLYQK.A
        2780.43   2779.43   2779.43   -2.35   249 - 274    0   K.ALSDHHVYLEGTLLKPNMVTAGQSAK.K
        No match to: 1038.69, 1062.66, 1090.65, 1163.69, 1191.69, 1196.65, 1202.66, 1235.74, 1273.73, 1292.79, 1302.72,
        1306.80, 1309.74, 1363.71, 1372.80, 1392.82, 1416.78, 1422.79, 1424.74, 1434.80, 1436.75, 1439.78, 1466.82,
        1482.82, 1493.79, 1530.85, 1532.86, 1552.85, 1564.83, 1572.97, 1577.85, 1590.85, 1600.90, 1611.83, 1631.83,
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        1635.87, 1649.85, 1655.89, 1687.91, 1706.83, 1739.89, 1750.91, 1770.90, 1775.89, 1814.00, 1842.98, 1878.94,
        1948.97, 1978.97, 1988.05, 2070.01, 2084.09, 2086.05, 2090.04, 2101.09, 2251.10, 2298.15, 2351.11, 2724.38,
        2780.92

17.     gi|21430850     Mass: 43587     Score: 35     Expect: 15  Queries matched: 8
        SD20045p [Drosophila melanogaster]
       Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
        1372.80   1371.79   1371.75    29.3   331 - 342    1    K.LGKIQLYEGHSK.E
        1434.80   1433.79   1433.74    37.3   285 - 298    0    K.TLDAAFEAAIEVGK.W
        1532.86   1531.85   1531.75    64.8   201 - 213    1    K.ESKEMLAALCPNR.N + Propionamide (C)
        1552.85   1551.84   1551.78    39.7   237 - 249    1    K.LRNAFNEAMTLTR.H + Oxidation (M)
        1687.91   1686.90   1686.89    6.99   271 - 284    0    K.QTGVFHPLNVWYVK.T
        1775.89   1774.89   1774.93  -26.17   316 - 330    0    K.YHGPWNPLLGLLHMK.L
        1978.97   1977.96   1977.93    16.4   250 - 265    1    R.HNLENMKDVAYLDVCK.V + Oxidation (M); Propionamide (C)
        2090.04   2089.04   2088.99    24.4   204 - 223    1    K.EMLAALCPNRNCGAGISVDR.N
        No match to: 1038.69, 1062.66, 1090.65, 1163.69, 1191.69, 1196.65, 1202.66, 1235.74, 1273.73, 1292.79, 1302.72,
        1306.80, 1309.74, 1363.71, 1370.77, 1392.82, 1416.78, 1422.79, 1424.74, 1436.75, 1439.78, 1466.82, 1482.82,
        1493.79, 1520.84, 1530.85, 1564.83, 1572.97, 1577.85, 1579.81, 1590.85, 1600.90, 1611.83, 1631.83, 1635.87,
        1649.85, 1655.89, 1658.86, 1706.83, 1739.89, 1750.91, 1770.90, 1782.90, 1814.00, 1842.98, 1878.94, 1948.97,
        1988.05, 2070.01, 2075.06, 2084.09, 2086.05, 2101.09, 2251.10, 2298.15, 2351.11, 2724.38, 2780.43, 2780.92

18.     gi|125978701     Mass: 30284     Score: 35     Expect: 15  Queries matched: 8
        GA16922-PA [Drosophila pseudoobscura]
       Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
        1202.66   1201.66   1201.60    45.5     1 -  12    0    -.SEDPAAIAGLMK.L
        1273.73   1272.72   1272.71    13.8    43 -  52    1    R.LRYNLEGRPR.H
        1493.79   1492.78   1492.69    58.9    59 -  69    1    R.WREFDVEIEDR.L
        1564.83   1563.82   1563.76    40.5   179 - 190    1    R.FQWGILECQERR.L
        1572.97   1571.96   1571.86    63.5     1 -  15    1    -.SEDPAAIAGLMKLLK.Q + Oxidation (M)
        1635.87   1634.86   1634.80    40.0   179 - 190    1    R.FQWGILECQERR.L + Propionamide (C)
        2075.06   2074.05   2073.99    29.0    90 - 108    1    R.GRQSLGCYVVACCAASIFR.R + Propionamide (C)
        2298.15   2297.15   2297.21  -29.02   230 - 247    1    R.QLMVLLYCMVVTLNLRCK.K + Oxidation (M); 2 Propionamide (C)
        No match to: 1038.69, 1062.66, 1090.65, 1163.69, 1191.69, 1196.65, 1235.74, 1292.79, 1302.72, 1306.80, 1309.74,
        1363.71, 1370.77, 1372.80, 1392.82, 1416.78, 1422.79, 1424.74, 1434.80, 1436.75, 1439.78, 1466.82, 1482.82,
        1520.84, 1530.85, 1532.86, 1552.85, 1577.85, 1579.81, 1590.85, 1600.90, 1611.83, 1631.83, 1649.85, 1655.89,
        1658.86, 1687.91, 1706.83, 1739.89, 1750.91, 1770.90, 1775.89, 1782.90, 1814.00, 1842.98, 1878.94, 1948.97,
        1978.97, 1988.05, 2070.01, 2084.09, 2086.05, 2090.04, 2101.09, 2251.10, 2351.11, 2724.38, 2780.43, 2780.92

19.     gi|27544248     Mass: 118888    Score: 35     Expect: 17  Queries matched: 12
        supressor of Ty element 16 [Drosophila melanogaster]
       Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss  Peptide
        1191.69   1190.68   1190.63    46.2    76 -  85    1   K.DQGNFEKLIK.A
        1196.65   1195.64   1195.59    46.1   760 - 769    0   K.SVVEFDTPFR.E
        1273.73   1272.72   1272.64    66.2   298 - 308    0   K.EKPSMVDNLPK.S + Oxidation (M)
        1363.71   1362.70   1362.65    38.5   537 - 548    0   R.INFFHPGATMGR.N + Oxidation (M)
        1416.78   1415.77   1415.71    45.9   481 - 492    1   K.SISQMPREPEVK.E + Oxidation (M)
        1572.97   1571.96   1571.94    12.2   629 - 641    1   K.LKDLYIRPNIVTK.R
        1577.85   1576.85   1576.85   -5.02   277 - 290    1   K.LLVPGTKLCDVYEK.T
        1649.85   1648.84   1648.81    20.1   549 - 563    0   R.NEGGLYPQPEATFVK.E
        1658.86   1657.86   1657.79    37.0   523 - 536    0   K.NISQSVEGEYTYLR.I
        1782.90   1781.89   1781.90   -6.11   835 - 850    0   K.VAMVNAIPMNMLDHVK.E
        2101.09   2100.08   2100.09   -3.16    53 -  70    0   K.QTQNITEEGFPEINLLVR.D
        2298.15   2297.15   2297.13    5.96   549 - 568    1   R.NEGGLYPQPEATFVKEVTYR.S
        No match to: 1038.69, 1062.66, 1090.65, 1163.69, 1202.66, 1235.74, 1292.79, 1302.72, 1306.80, 1309.74, 1370.77,
        1372.80, 1392.82, 1422.79, 1424.74, 1434.80, 1436.75, 1439.78, 1466.82, 1482.82, 1493.79, 1520.84, 1530.85,
        1532.86, 1552.85, 1564.83, 1579.81, 1590.85, 1600.90, 1611.83, 1631.83, 1635.87, 1655.89, 1687.91, 1706.83,
        1739.89, 1750.91, 1770.90, 1775.89, 1814.00, 1842.98, 1878.94, 1948.97, 1978.97, 1988.05, 2070.01, 2075.06,
        2084.09, 2086.05, 2090.04, 2251.10, 2351.11, 2724.38, 2780.43, 2780.92

20.     gi|21356157     Mass: 27835     Score: 35     Expect: 17  Queries matched: 6
        Aly CG1101-PA [Drosophila melanogaster]
       Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
        1038.69   1037.68   1037.63    47.8    58 -  67    1    R.KPGSVLKGPR.G
        1363.71   1362.70   1362.73  -16.76   148 - 159    1    R.SLGTADVIFERR.A
        1520.84   1519.83   1519.79    24.5     5 -  17    1    K.IEMSLDDIIKSTR.S
        1552.85   1551.84   1551.85   -2.46    48 -  64    1    R.GGANAGGSPRKPGSVLK.G
        1649.85   1648.84   1648.84    0.74     1 -  14    1    -.MVDKIEMSLDDIIK.S
        2351.11   2350.10   2350.09    5.84   246 - 266    1    K.APPTAEELDAELDSYINDMKI.- + Oxidation (M)
        No match to: 1062.66, 1090.65, 1163.69, 1191.69, 1196.65, 1202.66, 1235.74, 1273.73, 1292.79, 1302.72, 1306.80,
        1309.74, 1370.77, 1372.80, 1392.82, 1416.78, 1422.79, 1424.74, 1434.80, 1436.75, 1439.78, 1466.82, 1482.82,
        1493.79, 1530.85, 1532.86, 1564.83, 1572.97, 1577.85, 1579.81, 1590.85, 1600.90, 1611.83, 1631.83, 1635.87,
        1655.89, 1658.86, 1687.91, 1706.83, 1739.89, 1750.91, 1770.90, 1775.89, 1782.90, 1814.00, 1842.98, 1878.94,
        1948.97, 1978.97, 1988.05, 2070.01, 2075.06, 2084.09, 2086.05, 2090.04, 2101.09, 2251.10, 2298.15, 2724.38,
        2780.43, 2780.92
```

Search Parameters

```
Type of search         : Peptide Mass Fingerprint
Enzyme                 : Trypsin
Variable modifications : Oxidation (M),Propionamide (C)
Mass values            : Monoisotopic
Protein Mass           : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Peptide Charge State   : 1+
Max Missed Cleavages   : 1
Number of queries      : 67
```

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

Mascot Search Results

```
User             : Ilya
Email            : toropygin@rambler.ru
Search title     : Submitted from Shidlovsky 080328 II by Mascot Daemon on P4P800SE
MS data file     : \\192.168.0.18\data on ultraflex-2\DATA\2008_Ilya\Shidlovsky\080328\016\0_K22\1\016__0_K22__1.dar
Database         : NCBInr 20070307 (4984280 sequences; 1723577896 residues)
Taxonomy         : Drosophila (fruit flies) (47828 sequences)
Timestamp        : 2 Apr 2008 at 20:07:31 GMT
Top Score        : 147 for gi|24642732, xmas-2 CG32562-PA [Drosophila melanogaster]
```

Probability Based Mowse Score

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 59 are significant (p<0.05).

Score Distribution

Protein Summary Report

Format As	Protein Summary	Help
	Significance threshold p< 0.05	Max. number of hits 20

Overview Table

Click on column header to jump to entry in results list.
Move mouse over any indicator to highlight identical peptides.
Click on an indicator to see details of individual match.
Use check boxes to select sub-set of queries for new search.

Mouse over: -Query-

-Accession- -Sequence-

Hit:	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
☑ 865.45 (1+)	?					?			?	?	?					?				
☑ 947.51 (1+)	?						?	?										?	?	
☑ 1034.56 (1+)				?	?								?	?				?	?	?
☑ 1079.53 (1+)						?		?						?	?		?	?		
☑ 1163.59 (1+)	?	?						?	?	?	?		?			?				
☑ 1228.65 (1+)								?												
☑ 1293.60 (1+)												?								
☑ 1309.64 (1+)	?	?				?						?								
☑ 1341.67 (1+)			?						?	?	?	?	?	?					?	?
☑ 1418.78 (1+)	?	?						?	?	?	?									
☑ 1422.71 (1+)	?	?		?																
☑ 1503.73 (1+)	?	?						?							?			?		
☑ 1519.75 (1+)	?	?		?				?							?			?		
☑ 1530.77 (1+)				?	?	?	?						?	?	?	?	?			
☑ 1577.84 (1+)	?	?					?		?	?	?									
☑ 1631.77 (1+)	?	?						?												?
☑ 1649.88 (1+)	?	?				?			?	?	?				?					

☑ **1686.85** (1+)				?	?			?								?	?	?		
☑ **1706.82** (1+)												?								
☑ **1745.91** (1+)	?	?										?		?	?			?		
☑ **1753.87** (1+)	?	?					?					?				?			?	
☑ **1787.89** (1+)	?	?		?		?	?	?	?	?	?			?	?	?				
☑ **1842.94** (1+)	?							?						?						
☑ **1874.91** (1+)	?	?					?	?												
☑ **1877.95** (1+)				?	?											?			?	
☑ **1925.00** (1+)			?										?							?
☑ **1934.02** (1+)	?	?		?	?				?	?	?	?								
☑ **2031.01** (1+)				?				?	?	?	?									
☑ **2033.10** (1+)																	?			
☑ **2086.04** (1+)	?	?	?					?										?		
☑ **2321.11** (1+)	?		?													?				
☑ **2342.18** (1+)	?	?	?				?	?					?		?	?				
☑ **2351.11** (1+)	?	?				?		?							?			?		?
☑ **2430.17** (1+)	?																			
☑ **2437.17** (1+)	?	?	?			?											?	?	?	
☑ **2468.35** (1+)						?		?					?							
☑ **2617.36** (1+)							?	?					?	?	?		?			
☑ **2724.38** (1+)			?									?				?				
☑ **2865.52** (1+)					?															
☑ **2918.50** (1+)			?					?												
☑ **3159.59** (1+)								?						?						
☑ **3338.75** (1+)			?					?					?							

Select All Select None Search Selected

Index

```
    Accession      Mass     Score   Description
 1. gi|24642732    158081     147   xmas-2 CG32562-PA [Drosophila melanogaster]
 2. gi|6685149     137181     102   xmas-2 [Drosophila melanogaster]
 3. gi|125978973   59427       57   GA10863-PA [Drosophila pseudoobscura]
 4. gi|62472746    56049       54   munin CG33518-PA [Drosophila melanogaster]
 5. gi|125986167   26383       46   GA12955-PA [Drosophila pseudoobscura]
 6. gi|125776225   88474       45   GA20047-PA [Drosophila pseudoobscura]
 7. gi|21357939    34785       45   CG16984-PA [Drosophila melanogaster]
 8. gi|45552865    455345      45   Dynein heavy chain at 62B CG15804-PB, isoform B [Drosophila melanogaster]
 9. gi|6118254     68888       45   DEAD-box protein abstrakt [Drosophila melanogaster]
10. gi|17977678    69444       45   abstrakt CG14637-PA [Drosophila melanogaster]
11. gi|125777504   69135       44   GA13135-PA [Drosophila pseudoobscura]
12. gi|17136796    54515       42   Vacuolar H[+]-ATPase 55kD B subunit CG17369-PB, isoform B [Drosophila melanogaster]
13. gi|45550626    95197       41   CG6114-PA [Drosophila melanogaster]
14. gi|125807930   89695       41   GA19661-PA [Drosophila pseudoobscura]
15. gi|24585660    100234      40   CG8665-PA [Drosophila melanogaster]
16. gi|125987453   136258      39   GA12952-PA [Drosophila pseudoobscura]
17. gi|66773024    42756       39   IP10422p [Drosophila melanogaster]
18. gi|24639719    93167       39   cap binding protein 80 CG7035-PA, isoform A [Drosophila melanogaster]
19. gi|19920610    39966       39   CG3165-PA [Drosophila melanogaster]
20. gi|19921938    23839       39   CG1648-PA, isoform A [Drosophila melanogaster]
```

Results List

```
1.    gi|24642732     Mass: 158081    Score: 147     Expect: 9.5e-011  Queries matched: 23
      xmas-2 CG32562-PA [Drosophila melanogaster]
     Observed  Mr(expt)  Mr(calc)    ppm  Start    End  Miss   Peptide
       865.45    864.44    864.48 -49.29    238 -  244     1   R.ALKQYSR.S
       947.51    946.50    946.53 -36.70    212 -  218     1   R.VLREFQR.Q
      1163.59   1162.58   1162.63 -44.41    524 -  532     1   R.QYELVEVKR.V
      1309.64   1308.63   1308.68 -35.04    928 -  939     0   R.GLLQQPQSPDAR.F
      1418.78   1417.77   1417.82 -35.67     36 -   47     0   R.FGTLVNFVLRPR.R
      1422.71   1421.70   1421.75 -35.46    535 -  548     0   K.SVGEVVSGEPLPPR.D
      1503.73   1502.73   1502.76 -20.04    512 -  523     1   R.MHTVETEYKLPR.Q
      1519.75   1518.74   1518.75  -7.45    512 -  523     1   R.MHTVETEYKLPR.Q + Oxidation (M)
      1577.84   1576.83   1576.86 -21.13     18 -   30     1   R.NIPELFLDKYVAR.S
      1631.77   1630.76   1630.77  -7.02    643 -  656     0   R.AQEFQEQAPATQQR.R
```

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        1649.88   1648.87   1648.91  -28.01   533 -  548   1   R.VKSVGEVVSGEPLPPR.D
        1745.91   1744.90   1744.95  -31.97    13 -   26   1   K.TLLCRNIPELFLDK.Y + Propionamide (C)
        1753.87   1752.87   1752.87   -0.01   318 -  332   1   K.LVEQCARFHIHCAAR.L
        1787.89   1786.88   1786.87    5.71   643 -  657   1   R.AQEFQEQAPATQQRR.A
        1842.94   1841.93   1841.94   -5.22   166 -  181   1   R.RPAHTSEEKFSVLDAR.D
        1874.91   1873.91   1873.90    2.25   641 -  656   1   K.SRAQEFQEQAPATQQR.R
        1934.02   1933.02   1933.04  -13.66   732 -  746   1   R.QLKLEQLFFVQQQER.E
        2086.04   2085.03   2085.08  -23.66   969 -  988   0   K.ATDLAEANGIICLIGLDDIR.L
        2321.11   2320.11   2320.08    11.5   219 -  237   0   R.QVAYYELQPGSDELICHER.A + Propionamide (C)
        2342.18   2341.18   2341.16    7.03  1124 - 1143   0   R.LQLVAGEDLSDWPQFPEELR.V
        2351.11   2350.11   2350.08    10.7   549 -  567   0   R.DLYLNHRPHNSFDDYGMLK.S + Oxidation (M)
        2430.17   2429.16   2429.15    3.46    91 -  111   0   K.TEEWVDPDIQAELSALQSGWR.N
        2437.17   2436.16   2436.15    6.59  1228 - 1247   0   K.ILQYDTDDYLNFVEYLAGER.M
       No match to: 1034.56, 1079.53, 1228.65, 1293.60, 1341.67, 1530.77, 1686.85, 1706.82, 1877.95, 1925.00, 2031.01, 2033.10,
       2468.35, 2617.36, 2724.38, 2865.52, 2918.50, 3159.59, 3338.75

  2.   gi|6685149     Mass: 137181   Score: 102     Expect: 3e-006  Queries matched: 18
       xmas-2 [Drosophila melanogaster]
       Observed  Mr(expt)  Mr(calc)     ppm  Start     End  Miss   Peptide
        1163.59   1162.58   1162.63  -44.41   338 -  346   1   R.QYELVEVKR.V
        1309.64   1308.63   1308.68  -35.04   742 -  753   0   R.GLLQQPQSPDAR.F
        1418.78   1417.77   1417.82  -35.67    36 -   47   0   R.FGTLVNFVLRPR.R
        1422.71   1421.70   1421.75  -35.46   349 -  362   0   K.SVGEVVSGEPLPPR.D
        1503.73   1502.73   1502.76  -20.04   326 -  337   1   R.MHTVETEYKLPR.Q
        1519.75   1518.74   1518.75   -7.45   326 -  337   1   R.MHTVETEYKLPR.Q + Oxidation (M)
        1577.84   1576.83   1576.86  -21.13    18 -   30   1   R.NIPELFLDKYVAR.S
        1631.77   1630.76   1630.77   -7.02   457 -  470   0   R.AQEFQEQAPATQQR.R
        1649.88   1648.87   1648.91  -28.01   347 -  362   1   R.VKSVGEVVSGEPLPPR.D
        1745.91   1744.90   1744.95  -31.97    13 -   26   1   K.TLLCRNIPELFLDK.Y + Propionamide (C)
        1753.87   1752.87   1752.87   -0.01   132 -  146   1   K.LVEQCARFHIHCAAR.L
        1787.89   1786.88   1786.87    5.71   457 -  471   1   R.AQEFQEQAPATQQRR.A
        1874.91   1873.91   1873.90    2.25   455 -  470   1   K.SRAQEFQEQAPATQQR.R
        1934.02   1933.02   1933.04  -13.66   546 -  560   1   R.QLKLEQLFFVQQQER.E
        2086.04   2085.03   2085.08  -23.66   783 -  802   0   K.ATDLAEANGIICLIGLDDIR.L
        2342.18   2341.18   2341.16    7.03   938 -  957   0   R.LQLVAGEDLSDWPQFPEELR.V
        2351.11   2350.11   2350.08    10.7   363 -  381   0   R.DLYLNHRPHNSFDDYGMLK.S + Oxidation (M)
        2437.17   2436.16   2436.15    6.59  1042 - 1061   0   K.ILQYDTDDYLNFVEYLAGER.M
       No match to: 865.45, 947.51, 1034.56, 1079.53, 1228.65, 1293.60, 1341.67, 1530.77, 1686.85, 1706.82, 1842.94, 1877.95,
       1925.00, 2031.01, 2033.10, 2321.11, 2430.17, 2468.35, 2617.36, 2724.38, 2865.52, 2918.50, 3159.59, 3338.75

  3.   gi|125978973     Mass: 59427     Score: 57     Expect: 0.098  Queries matched: 9
       GA10863-PA [Drosophila pseudoobscura]
       Observed  Mr(expt)  Mr(calc)     ppm  Start    End  Miss   Peptide
        1341.67   1340.66   1340.61    33.1   210 - 221    0   K.CSASFSTNANLR.V + Propionamide (C)
        1925.00   1923.99   1923.89    55.3   210 - 226    1   K.CSASFSTNANLRVHMMR.H
        2086.04   2085.03   2085.06  -14.73    11 -  31    0   K.EDAVSLLTDSGISLSSPPAAR.G
        2321.11   2320.11   2320.11   -1.42   284 - 302    1   K.HAAIKTHVCEVCNSYFTQK.S + 2 Propionamide (C)
        2342.18   2341.18   2341.11    26.7   164 - 182    1   R.LHMRLHSGEKPYQCPICDK.R + Oxidation (M); Propionamide (C)
        2437.17   2436.16   2436.10    27.2   200 - 221    1   K.TCIQQFNCTKCSASFSTNANLR.V
        2724.38   2723.38   2723.28    34.0   187 - 209    1   R.GGQLQQHMVSHHKTCIQQFNCTK.C + Propionamide (C)
        2918.50   2917.50   2917.45    15.3    11 -  40    1   K.EDAVSLLTDSGISLSSPPAARGSSPTSSTK.L
        3338.75   3337.74   3337.62    37.0   402 - 432    1   K.CPAVEGDNTDSQSDDALVLSTIRFNMAVILK.K + Oxidation (M)
       No match to: 865.45, 947.51, 1034.56, 1079.53, 1163.59, 1228.65, 1293.60, 1309.64, 1418.78, 1422.71, 1503.73, 1519.75,
       1530.77, 1577.84, 1631.77, 1649.88, 1686.85, 1706.82, 1745.91, 1753.87, 1787.89, 1842.94, 1874.91, 1877.95, 1934.02,
       2031.01, 2033.10, 2351.11, 2430.17, 2468.35, 2617.36, 2865.52, 3159.59

  4.   gi|62472746     Mass: 56049     Score: 54     Expect: 0.17  Queries matched: 9
       munin CG33518-PA [Drosophila melanogaster]
       Observed  Mr(expt)  Mr(calc)     ppm  Start    End  Miss   Peptide
        1034.56   1033.56   1033.49    62.1   301 - 310    1   K.KCAGRPSGCR.T
        1422.71   1421.70   1421.67    20.3   477 - 489    0   K.ADNMPHNIPGQTK.V
        1519.75   1518.74   1518.75  -10.53     1 -  12    1   -.MLRICNYSHNIR.I
        1530.77   1529.76   1529.77   -6.98   344 - 356    0   R.LLWMNPCVVEAQK.D
        1686.85   1685.85   1685.87  -17.47   343 - 356    1   R.RLLWMNPCVVEAQK.D
        1787.89   1786.88   1786.84    24.1   203 - 218    0   K.GPHEDLNLDIAFCLCK.K
        1877.95   1876.95   1876.84    57.6   188 - 202    1   R.CNRNACMSSLQAFYK.G + 2 Propionamide (C)
        1934.02   1933.02   1932.92    48.2   451 - 467    0   R.FVFCFPISTQSVAQMGR.R + Oxidation (M)
        2031.01   2030.00   2030.00    0.03   284 - 300    1   R.LKLEYYEQACAVDSVTK.K + Propionamide (C)
       No match to: 865.45, 947.51, 1079.53, 1163.59, 1228.65, 1293.60, 1309.64, 1341.67, 1418.78, 1503.73, 1577.84, 1631.77,
       1649.88, 1706.82, 1745.91, 1753.87, 1842.94, 1874.91, 1925.00, 2033.10, 2086.04, 2321.11, 2342.18, 2351.11, 2430.17,
       2437.17, 2468.35, 2617.36, 2724.38, 2865.52, 2918.50, 3159.59, 3338.75

  5.   gi|125986167     Mass: 26383     Score: 46     Expect: 1.1  Queries matched: 6
       GA12955-PA [Drosophila pseudoobscura]
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```
       Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
        1034.56   1033.56   1033.52   34.8    40 -   48   1    R.ADYPRDVAK.I
        1530.77   1529.76   1529.82 -35.90   120 -  131   0    R.FHCLFKPAQLQK.I + Propionamide (C)
        1686.85   1685.85   1685.92 -43.72   119 -  131   1    R.RFHCLFKPAQLQK.I + Propionamide (C)
        1877.95   1876.95   1876.92   13.2   146 -  162   0    K.ASAMAAFLYQLYMVGNK.D
        1934.02   1933.02   1932.92   52.0   179 -  195   1    R.YKSGGQQRPEFGSYMAK.M
        2865.52   2864.51   2864.47   13.2    12 -   37   1    K.RMLSLIEGLNGTVDEQLSLAAFTWGK.L + Oxidation (M)
        No match to: 865.45, 947.51, 1079.53, 1163.59, 1228.65, 1293.60, 1309.64, 1341.67, 1418.78, 1422.71, 1503.73, 1519.75,
        1577.84, 1631.77, 1649.88, 1706.82, 1745.91, 1753.87, 1787.89, 1842.94, 1874.91, 1925.00, 2031.01, 2033.10, 2086.04,
        2321.11, 2342.18, 2351.11, 2430.17, 2437.17, 2468.35, 2617.36, 2724.38, 2918.50, 3159.59, 3338.75

  6.    gi|125776225     Mass: 88474     Score: 45     Expect: 1.4  Queries matched: 9
        GA20047-PA [Drosophila pseudoobscura]
       Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
         865.45    864.44    864.42   21.9   274 -  279   1    K.DYRQQR.R
        1079.53   1078.52   1078.57 -43.38   616 -  625   0    K.LPHIAQAACR.R
        1309.64   1308.63   1308.71 -59.90   363 -  373   0    K.NLIMLSINTFK.C + Oxidation (M)
        1530.77   1529.76   1529.86 -66.15   164 -  176   0    R.FATQMQIQIPIIK.E
        1649.88   1648.87   1648.82   31.4    74 -   87   0    K.QLHDEVHSLDTSLR.Q
        1787.89   1786.88   1786.87   7.49   432 -  446   0    R.FPFHSEQLENAPFPK.K
        2351.11   2350.11   2350.19 -36.85   138 -  156   1    K.QYYQALRTLETLETEHLSR.L
        2437.17   2436.16   2436.21 -18.94   281 -  301   1    R.DQAKLVLQPPPNMHDNLEAYK.T + Oxidation (M)
        2468.35   2467.34   2467.19   60.1   412 -  431   0    K.EQFLPMVVQNVEEYESIIER.F + Oxidation (M)
        No match to: 947.51, 1034.56, 1163.59, 1228.65, 1293.60, 1341.67, 1418.78, 1422.71, 1503.73, 1519.75, 1577.84, 1631.77,
        1686.85, 1706.82, 1745.91, 1753.87, 1842.94, 1874.91, 1877.95, 1925.00, 1934.02, 2031.01, 2033.10, 2086.04, 2321.11,
        2342.18, 2430.17, 2617.36, 2724.38, 2865.52, 2918.50, 3159.59, 3338.75

  7.    gi|21357939     Mass: 34785     Score: 45     Expect: 1.5  Queries matched: 8
        CG16984-PA [Drosophila melanogaster]
       Observed  Mr(expt)  Mr(calc)    ppm  Start   End Miss   Peptide
         947.51    946.50    946.51  -8.70   280 - 287   1   K.SKLESDLR.Q
        1530.77   1529.76   1529.70   43.2   224 - 238   0   R.ASVQSSGPPPMPGMR.V + 2 Oxidation (M)
        1577.84   1576.83   1576.79   27.0   143 - 156   0   K.ICAGQTVPCPPPPR.Y + 2 Propionamide (C)
        1753.87   1752.87   1752.80   40.4   196 - 210   1   R.MLADMNAVCAKEQAR.L + 2 Oxidation (M); Propionamide (C)
        1787.89   1786.88   1786.89  -6.71   112 - 129   1   K.CPKMPPMPPLPPPGSGGK.K
        1874.91   1873.91   1873.93  -9.59   112 - 129   1   K.CPKMPPMPPLPPPGSGGK.K + Oxidation (M); Propionamide (C)
        2342.18   2341.18   2341.10   33.2   224 - 245   1   R.ASVQSSGPPPMPGMRVMEQAER.N
        2617.36   2616.35   2616.36  -4.71   115 - 139   1   K.MPPMPPLPPPGSGGKKPAMVPNFIK.R + 2 Oxidation (M)
        No match to: 865.45, 1034.56, 1079.53, 1163.59, 1228.65, 1293.60, 1309.64, 1341.67, 1418.78, 1422.71, 1503.73, 1519.75,
        1631.77, 1649.88, 1686.85, 1706.82, 1745.91, 1842.94, 1877.95, 1925.00, 1934.02, 2031.01, 2033.10, 2086.04, 2321.11,
        2351.11, 2430.17, 2437.17, 2468.35, 2724.38, 2865.52, 2918.50, 3159.59, 3338.75

  8.    gi|45552865     Mass: 455345    Score: 45     Expect: 1.6  Queries matched: 21
        Dynein heavy chain at 62B CG15804-PB, isoform B [Drosophila melanogaster]
       Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
         947.51    946.50    946.53 -28.43  2122 - 2130   0    R.VVTGCTLVR.K
        1079.53   1078.52   1078.47   51.0   691 -  697   0    K.CCIEWQR.Y + 2 Propionamide (C)
        1163.59   1162.58   1162.63 -44.41  3128 - 3137   1    K.ETVAKIEAFR.L
        1228.65   1227.64   1227.68 -33.54  1883 - 1894   0    K.TGVIVPTVDTAR.Y
        1418.78   1417.77   1417.77  -1.63  2118 - 2130   1    R.DISRVVTGCTLVR.K
        1503.73   1502.73   1502.83 -68.46  2679 - 2691   1    K.RLLGEMNFLPGLK.E + Oxidation (M)
        1519.75   1518.74   1518.77 -21.79   598 -  609   0    K.FTFEEHLQEVIK.K
        1631.77   1630.76   1630.80 -24.92   402 -  414   0    R.TYQEVIQYVEGFR.D
        1686.85   1685.85   1685.85  -1.25  2586 - 2601   0    R.DEEVASVQAEAAQVLK.Q
        1787.89   1786.88   1786.82   31.5  2143 - 2155   1    R.VWYHEAMRVFYDR.L + Oxidation (M)
        1842.94   1841.93   1841.95 -10.59  2585 - 2601   1    K.RDEEVASVQAEAAQVLK.Q
        1874.91   1873.91   1873.92  -7.33   402 -  416   1    R.TYQEVIQYVEGFRDK.Y
        2031.01   2030.00   2029.97   18.0  2755 - 2772   1    K.LAGAEKEYADTMEFLAQK.R + Oxidation (M)
        2086.04   2085.03   2085.00   12.4   777 -  794   0    K.DFTTGVFIVNTMCNPALR.K + Oxidation (M); Propionamide (C)
        2342.18   2341.18   2341.07   47.1   427 -  445   0    R.DALNQFLSEPHEFEEYFAR.I
        2351.11   2350.11   2350.09   4.36   680 -  697   1    K.TFVYPFAELMKCCIEWQR.Y + Oxidation (M); Propionamide (C)
        2468.35   2467.34   2467.32   8.08   395 -  414   1    K.VQNIILRTYQEVIQYVEGFR.D
        2617.36   2616.35   2616.46 -40.26  3036 - 3059   0    K.VTVINFALTQNALMDQLLSIVVAK.E + Oxidation (M)
        2918.50   2917.50   2917.43   22.0  1640 - 1664   1    K.WVIFDGPVDAVWIENMNTVLDDNKK.L
        3159.59   3158.58   3158.60  -6.94  3084 - 3113   1    R.DAENMILKTLSAGGDILENEAAIQILADSK.G + Oxidation (M)
        3338.75   3337.74   3337.61   39.5  1726 - 1752   1    R.WADEEGVPYVMALMQWLLPPCQTFVRR.F + 2 Oxidation (M); Propionamide (C)
        No match to: 865.45, 1034.56, 1293.60, 1309.64, 1341.67, 1422.71, 1530.77, 1577.84, 1649.88, 1706.82, 1745.91, 1753.87,
        1877.95, 1925.00, 1934.02, 2033.10, 2321.11, 2430.17, 2437.17, 2724.38, 2865.52

  9.    gi|6118254     Mass: 68888     Score: 45     Expect: 1.6  Queries matched: 9
        DEAD-box protein abstrakt [Drosophila melanogaster]
       Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
         865.45    864.44    864.41   35.4   315 -  321   0    R.LMDMLDK.K
        1163.59   1162.58   1162.62 -32.04   322 -  330   1    K.KILTLDMCR.Y + Propionamide (C)
        1341.67   1340.66   1340.63   19.3   274 -  284   0    K.HLQACGMPEIR.S + Oxidation (M); Propionamide (C)
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        1418.78   1417.77   1417.70    46.9   246 - 258   0   R.NEGPYGLIICPSR.E
        1577.84   1576.83   1576.84   -7.33   358 - 371   1   K.GQRQTLLFSATMPK.K
        1649.88   1648.87   1648.89  -10.41   408 - 421   1   K.QEAKVVYLLDCLQK.T
        1787.89   1786.88   1786.93  -26.57   433 - 446   1   K.KQDVDCIHEYLLLK.G + Propionamide (C)
        1934.02   1933.02   1932.96    26.3   285 - 303   0   R.SCLAMGGLPVSEALDVISR.G + Oxidation (M)
        2031.01   2030.00   2030.09  -43.00   107 - 125   1   K.IMESIAQQKALMGVAELAK.G
       No match to: 947.51, 1034.56, 1079.53, 1228.65, 1293.60, 1309.64, 1422.71, 1503.73, 1519.75, 1530.77, 1631.77, 1686.85,
       1706.82, 1745.91, 1753.87, 1842.94, 1874.91, 1877.95, 1925.00, 2033.10, 2086.04, 2321.11, 2342.18, 2351.11, 2430.17,
       2437.17, 2468.35, 2617.36, 2724.38, 2865.52, 2918.50, 3159.59, 3338.75

  10.  gi|17977678     Mass: 69444     Score: 45     Expect: 1.6  Queries matched: 9
       abstrakt CG14637-PA [Drosophila melanogaster]
       Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss  Peptide
         865.45    864.44    864.41    35.4   320 - 326   0   R.LMDMLDK.K
        1163.59   1162.58   1162.62  -32.04   327 - 335   1   K.KILTLDMCR.Y + Propionamide (C)
        1341.67   1340.66   1340.63    19.3   279 - 289   0   K.HLQACGMPEIR.S + Oxidation (M); Propionamide (C)
        1418.78   1417.77   1417.70    46.9   251 - 263   0   R.NEGPYGLIICPSR.E
        1577.84   1576.83   1576.84   -7.33   363 - 376   1   K.GQRQTLLFSATMPK.K
        1649.88   1648.87   1648.89  -10.41   413 - 426   1   K.QEAKVVYLLDCLQK.T
        1787.89   1786.88   1786.93  -26.57   438 - 451   1   K.KQDVDCIHEYLLLK.G + Propionamide (C)
        1934.02   1933.02   1932.96    26.3   290 - 308   0   R.SCLAMGGLPVSEALDVISR.G + Oxidation (M)
        2031.01   2030.00   2030.09  -43.00   112 - 130   1   K.IMESIAQQKALMGVAELAK.G
       No match to: 947.51, 1034.56, 1079.53, 1228.65, 1293.60, 1309.64, 1422.71, 1503.73, 1519.75, 1530.77, 1631.77, 1686.85,
       1706.82, 1745.91, 1753.87, 1842.94, 1874.91, 1877.95, 1925.00, 2033.10, 2086.04, 2321.11, 2342.18, 2351.11, 2430.17,
       2437.17, 2468.35, 2617.36, 2724.38, 2865.52, 2918.50, 3159.59, 3338.75

  11.  gi|125777504     Mass: 69135     Score: 44     Expect: 1.8  Queries matched: 9
       GA13135-PA [Drosophila pseudoobscura]
       Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss  Peptide
         865.45    864.44    864.41    35.4   320 - 326   0   R.LMDMLDK.K
        1163.59   1162.58   1162.62  -32.04   327 - 335   1   K.KILTLDMCR.Y + Propionamide (C)
        1341.67   1340.66   1340.57    63.1   345 - 355   0   R.MIDMGFEEDVR.T
        1418.78   1417.77   1417.70    46.9   251 - 263   0   R.NEGPYGLIICPSR.E
        1577.84   1576.83   1576.84   -7.33   363 - 376   1   K.GQRQTLLFSATMPK.K
        1649.88   1648.87   1648.89  -10.41   413 - 426   1   K.QEAKVVYLLDCLQK.T
        1787.89   1786.88   1786.93  -26.57   438 - 451   1   K.KQDVDCIHEYLLLK.G + Propionamide (C)
        1934.02   1933.02   1932.96    26.3   290 - 308   0   R.SCLAMGGLPVSEALDVISR.G + Oxidation (M)
        2031.01   2030.00   2030.09  -43.00   112 - 130   1   K.IMESIAQQKALMGVAELAK.G
       No match to: 947.51, 1034.56, 1079.53, 1228.65, 1293.60, 1309.64, 1422.71, 1503.73, 1519.75, 1530.77, 1631.77, 1686.85,
       1706.82, 1745.91, 1753.87, 1842.94, 1874.91, 1877.95, 1925.00, 2033.10, 2086.04, 2321.11, 2342.18, 2351.11, 2430.17,
       2437.17, 2468.35, 2617.36, 2724.38, 2865.52, 2918.50, 3159.59, 3338.75

  12.  gi|17136796     Mass: 54515     Score: 42     Expect: 2.9  Queries matched: 8
       Vacuolar H[+]-ATPase 55kD B subunit CG17369-PB, isoform B [Drosophila melanogaster]
       Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss  Peptide
        1293.60   1292.60   1292.66  -48.76   381 - 392   1   R.LMKSAIGEGMTR.K
        1309.64   1308.63   1308.65  -15.45   381 - 392   1   R.LMKSAIGEGMTR.K + Oxidation (M)
        1341.67   1340.66   1340.61    35.7   441 - 451   0   K.NFISQGNYENR.T
        1706.82   1705.81   1705.90  -50.61     2 -  16   1   M.NAQQAQREHVLAVSR.D
        1745.91   1744.90   1744.82    46.9   438 - 451   1   K.FEKNFISQGNYENR.T
        1753.87   1752.87   1752.93  -34.63     9 -  23   1   R.EHVLAVSRDFISQPR.L
        1934.02   1933.02   1933.00    9.24   272 - 288   0   K.HVLVILTDMSSYAEALR.E + Oxidation (M)
        2724.38   2723.38   2723.27    39.9   198 - 222   0   K.SVLDDHTDNFAIVFAAMGVNMETAR.F
       No match to: 865.45, 947.51, 1034.56, 1079.53, 1163.59, 1228.65, 1418.78, 1422.71, 1503.73, 1519.75, 1530.77, 1577.84,
       1631.77, 1649.88, 1686.85, 1787.89, 1842.94, 1874.91, 1877.95, 1925.00, 2031.01, 2033.10, 2086.04, 2321.11, 2342.18,
       2351.11, 2430.17, 2437.17, 2468.35, 2617.36, 2865.52, 2918.50, 3159.59, 3338.75

  13.  gi|45550626     Mass: 95197     Score: 41     Expect: 3.5  Queries matched: 9
       CG6114-PA [Drosophila melanogaster]
       Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss  Peptide
        1034.56   1033.56   1033.54    14.3   415 - 424   0   R.SPTTVTSSVR.S
        1163.59   1162.58   1162.63  -37.64    52 -  61   1   R.EKLSESVLMK.V
        1341.67   1340.66   1340.67   -7.24   357 - 368   1   K.SRSELDAVDPPR.K
        1530.77   1529.76   1529.74    12.1   741 - 753   1   R.ICEHIQSQVCSKR.F
        1925.00   1923.99   1924.00   -4.38   478 - 495   1   R.TPSHSSQKSIEGDVVVVR.E
        2342.18   2341.18   2341.15    12.1   614 - 634   1   R.KMQVSADEVHLTPESSPELTK.R + Oxidation (M)
        2468.35   2467.34   2467.29    21.5   716 - 737   1   K.QGDIADMLFALTFTLLSGNIRR.F + Oxidation (M)
        2617.36   2616.35   2616.21    52.5   434 - 459   0   R.CNSPMSSAQQQANAISRPSSPAAGTR.H
        3338.75   3337.74   3337.52    64.8   156 - 187   0   K.IADFGMASLQPAGSMLETSCGSPHYACPEVIR.G
       No match to: 865.45, 947.51, 1079.53, 1228.65, 1293.60, 1309.64, 1418.78, 1422.71, 1503.73, 1519.75, 1577.84, 1631.77,
       1649.88, 1686.85, 1706.82, 1745.91, 1753.87, 1787.89, 1842.94, 1874.91, 1877.95, 1934.02, 2031.01, 2033.10, 2086.04,
       2321.11, 2351.11, 2430.17, 2437.17, 2724.38, 2865.52, 2918.50, 3159.59

  14.  gi|125807930     Mass: 89695     Score: 41     Expect: 4.1  Queries matched: 9
       GA19661-PA [Drosophila pseudoobscura]
       Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss  Peptide
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         1034.56   1033.56   1033.56   -0.46   172 - 179   0   R.QLQQYVQK.L
         1079.53   1078.52   1078.60  -66.72   788 - 797   1   K.SLIGGRFCVK.Q
         1341.67   1340.66   1340.65    8.87   690 - 700   1   R.CKACDELIFTK.E + Propionamide (C)
         1530.77   1529.76   1529.66    67.0    32 -  46   0   K.LGHESGAGAPCTECK.D + Propionamide (C)
         1745.91   1744.90   1744.79    63.9    30 -  46   1   R.SKLGHESGAGAPCTECK.D + Propionamide (C)
         1787.89   1786.88   1786.79    53.6   646 - 660   1   K.EIAWHPGCFKCHTCR.E
         1842.94   1841.93   1841.86    35.9   794 - 809   1   R.FCVKQDLPFCSPTCVR.S
         2617.36   2616.35   2616.34    3.77   193 - 216   1   R.VGNRLTHGYVEHVTPPIQSEAANK.T
         3159.59   3158.58   3158.43    46.3   581 - 607   0   K.FTTIPGIEDMNMYPNCVGMPEQFQQLR.L
        No match to: 865.45, 947.51, 1163.59, 1228.65, 1293.60, 1309.64, 1418.78, 1422.71, 1503.73, 1519.75, 1577.84, 1631.77,
        1649.88, 1686.85, 1706.82, 1753.87, 1874.91, 1877.95, 1925.00, 1934.02, 2031.01, 2033.10, 2086.04, 2321.11, 2342.18,
        2351.11, 2430.17, 2437.17, 2468.35, 2724.38, 2865.52, 2918.50, 3338.75

  15.   gi|24585660     Mass: 100234   Score: 40     Expect: 4.8  Queries matched: 10
        CG8665-PA [Drosophila melanogaster]
        Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
         1079.53   1078.52   1078.50    25.3   464 - 474   0   K.VACASATDVDK.A
         1503.73   1502.73   1502.76  -22.28   496 - 508   0   R.GQLMLNLADLMER.N
         1519.75   1518.74   1518.75   -9.66   496 - 508   0   R.GQLMLNLADLMER.N + Oxidation (M)
         1530.77   1529.76   1529.85  -54.00    27 -  40   0   R.SNIQIVGVFTIPDK.G
         1649.88   1648.87   1648.80    42.2   714 - 728   1   K.GENCIAAGRLFVEDR.I
         1745.91   1744.90   1744.90    1.37   496 - 510   1   R.GQLMLNLADLMERNK.E
         1787.89   1786.88   1786.92  -20.66   494 - 508   1   R.QRGQLMLNLADLMER.N
         2342.18   2341.18   2341.10    32.1   680 - 700   1   K.CSLELGGKSPLIIFADCDMDK.A + Oxidation (M); Propionamide (C)
         2351.11   2350.11   2350.23  -51.76   509 - 530   1   R.NKEELATIESVDSGAVYTLALK.T
         2617.36   2616.35   2616.35   -0.59    44 -  65   1   R.EDILATTATIHNIPVFKFACWR.R + Propionamide (C)
        No match to: 865.45, 947.51, 1034.56, 1163.59, 1228.65, 1293.60, 1309.64, 1341.67, 1418.78, 1422.71, 1577.84, 1631.77,
        1686.85, 1706.82, 1753.87, 1842.94, 1874.91, 1877.95, 1925.00, 1934.02, 2031.01, 2033.10, 2086.04, 2321.11, 2430.17,
        2437.17, 2468.35, 2724.38, 2865.52, 2918.50, 3159.59, 3338.75

  16.   gi|125987453     Mass: 136258   Score: 39     Expect: 5.5  Queries matched: 10
        GA12952-PA [Drosophila pseudoobscura]
        Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
          865.45    864.44    864.40    44.0   710 - 717   0   K.QSMTPSSK.Q
         1163.59   1162.58   1162.60  -16.02   707 - 717   1   R.LGKQSMTPSSK.Q
         1530.77   1529.76   1529.84  -49.71   881 - 893   1   K.GMAYLTELKLVHR.D
         1686.85   1685.85   1685.95  -60.12   141 - 156   1   R.TFEPVLIGALNSRAAK.Y
         1753.87   1752.87   1752.86    5.37    13 -  27   0   K.FNLPINEESESIFSK.I
         1787.89   1786.88   1786.83    26.3   512 - 526   1   R.SQTCAQIKYQSQCTK.F + Propionamide (C)
         1877.95   1876.95   1876.89    31.2   852 - 869   0   K.IECAGVDFSDGVEPVNVK.M
         2321.11   2320.11   2320.02    37.6   520 - 540   1   K.YQSQCTKFCGLATNGGPCTWR.G
         2342.18   2341.18   2341.17    1.95   186 - 206   1   R.HPLDHDELNGLMARAGQLQAR.I
         2724.38   2723.38   2723.43  -20.06   819 - 843   1   K.LLGACTQSSEAPLLIIEYARYGSLR.S
        No match to: 947.51, 1034.56, 1079.53, 1228.65, 1293.60, 1309.64, 1341.67, 1418.78, 1422.71, 1503.73, 1519.75, 1577.84,
        1631.77, 1649.88, 1706.82, 1745.91, 1842.94, 1874.91, 1925.00, 1934.02, 2031.01, 2033.10, 2086.04, 2351.11, 2430.17,
        2437.17, 2468.35, 2617.36, 2865.52, 2918.50, 3159.59, 3338.75

  17.   gi|66773024     Mass: 42756    Score: 39     Expect: 5.5  Queries matched: 6
        IP10422p [Drosophila melanogaster]
        Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
         1079.53   1078.52   1078.55  -26.12    86 -  94   0   R.ISISHTEHR.I
         1530.77   1529.76   1529.72    27.3   171 - 184   0   R.EEATPILISDDGDR.E
         1686.85   1685.85   1685.82    13.7   170 - 184   1   R.REEATPILISDDGDR.E
         2033.10   2032.09   2032.04    26.9   185 - 201   0   R.EVFSVEGQNLTLWQVQR.S
         2437.17   2436.16   2436.18   -5.42   147 - 169   0   R.STGQNVTLTCSATGVPMPTITWR.R + Oxidation (M)
         2617.36   2616.35   2616.33    7.66   356 - 376   1   K.SCSFQPLWIMFLCFVNKVSLL.- + 2 Propionamide (C)
        No match to: 865.45, 947.51, 1034.56, 1163.59, 1228.65, 1293.60, 1309.64, 1341.67, 1418.78, 1422.71, 1503.73, 1519.75,
        1577.84, 1631.77, 1649.88, 1706.82, 1745.91, 1753.87, 1787.89, 1842.94, 1874.91, 1877.95, 1925.00, 1934.02, 2031.01,
        2086.04, 2321.11, 2342.18, 2351.11, 2430.17, 2468.35, 2724.38, 2865.52, 2918.50, 3159.59, 3338.75

  18.   gi|24639719     Mass: 93167    Score: 39     Expect: 5.9  Queries matched: 10
        cap binding protein 80 CG7035-PA, isoform A [Drosophila melanogaster]
        Observed  Mr(expt)  Mr(calc)     ppm  Start    End Miss   Peptide
          947.51    946.50    946.49    10.0    74 -  81   0   R.ILSDCAVR.M + Propionamide (C)
         1034.56   1033.56   1033.59  -35.64   202 - 209   1   R.IEVYLNKR.S
         1079.53   1078.52   1078.48    40.6   121 - 128   1   K.MCRWDAAR.Y + Propionamide (C)
         1503.73   1502.73   1502.74   -9.87   705 - 717   1   R.MEEKLEAANVNQK.R
         1519.75   1518.74   1518.73    2.62   705 - 717   1   R.MEEKLEAANVNQK.R + Oxidation (M)
         1686.85   1685.85   1685.79    34.3   100 - 113   1   K.NYKFGGEFVDHMVK.T + Oxidation (M)
         1745.91   1744.90   1744.88    11.9   370 - 384   0   R.YLDICYGSILIELCK.L
         2086.04   2085.03   2085.00    12.4   462 - 478   1   R.LSYHQRITEMMPTTYAK.L + Oxidation (M)
         2351.11   2350.11   2350.00    45.0   294 - 314   0   R.MFDYTDCPDGPNLPGAHSIER.F + Oxidation (M)
         2437.17   2436.16   2436.28  -45.78   490 - 512   0   K.YANEEAANLPGTTVAHQLVVAIR.Q
        No match to: 865.45, 1163.59, 1228.65, 1293.60, 1309.64, 1341.67, 1418.78, 1422.71, 1530.77, 1577.84, 1631.77, 1649.88,
        1706.82, 1753.87, 1787.89, 1842.94, 1874.91, 1877.95, 1925.00, 1934.02, 2031.01, 2033.10, 2321.11, 2342.18, 2430.17,
        2468.35, 2617.36, 2724.38, 2865.52, 2918.50, 3159.59, 3338.75
```

```
19.    gi|19920610    Mass: 39966    Score: 39     Expect: 6.5  Queries matched: 6
       CG3165-PA [Drosophila melanogaster]
      Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
        947.51    946.50    946.50   1.75    256 - 262    1    K.RKPDEFR.S
       1034.56   1033.56   1033.53   23.9    257 - 264    1    R.KPDEFRSR.R
       1341.67   1340.66   1340.59   49.9    166 - 176    0    R.AFMEIDDTQQK.E + Oxidation (M)
       1753.87   1752.87   1752.79   42.8     59 -  73    0    K.EQDQDEQQELPAAPR.V
       1877.95   1876.95   1876.98 -17.01    106 - 122    0    R.ESQLDTDAAQLIVSFLK.H
       2437.17   2436.16   2436.28 -48.82     74 -  94    1    R.VLHKLNVLFQPSMVVDPEAER.I + Oxidation (M)
       No match to: 865.45, 1079.53, 1163.59, 1228.65, 1293.60, 1309.64, 1418.78, 1422.71, 1503.73, 1519.75, 1530.77, 1577.84,
       1631.77, 1649.88, 1686.85, 1706.82, 1745.91, 1787.89, 1842.94, 1874.91, 1925.00, 1934.02, 2031.01, 2033.10, 2086.04,
       2321.11, 2342.18, 2351.11, 2430.17, 2468.35, 2617.36, 2724.38, 2865.52, 2918.50, 3159.59, 3338.75

20.    gi|19921938    Mass: 23839    Score: 39     Expect: 6.6  Queries matched: 5
       CG1648-PA, isoform A [Drosophila melanogaster]
      Observed  Mr(expt)  Mr(calc)    ppm  Start    End Miss   Peptide
       1034.56   1033.56   1033.50   49.5    176 - 184    0    K.QTSQTVDQK.L
       1341.67   1340.66   1340.67 -10.25     11 -  22    1    K.NFGDKTANLFSK.K
       1631.77   1630.76   1630.80 -26.98      1 -  15    1    -.MFSSISASLKNFGDK.T
       1925.00   1923.99   1923.99   2.86     82 - 101    1    K.AGQAIDQGVNRAAGAVNQGK.Q
       2351.11   2350.11   2350.14 -14.89    176 - 195    1    K.QTSQTVDQKLQEANQYVDQK.R
       No match to: 865.45, 947.51, 1079.53, 1163.59, 1228.65, 1293.60, 1309.64, 1418.78, 1422.71, 1503.73, 1519.75, 1530.77,
       1577.84, 1649.88, 1686.85, 1706.82, 1745.91, 1753.87, 1787.89, 1842.94, 1874.91, 1877.95, 1934.02, 2031.01, 2033.10,
       2086.04, 2321.11, 2342.18, 2430.17, 2437.17, 2468.35, 2617.36, 2724.38, 2865.52, 2918.50, 3159.59, 3338.75
```

Search Parameters

```
Type of search         : Peptide Mass Fingerprint
Enzyme                 : Trypsin
Variable modifications : Oxidation (M),Propionamide (C)
Mass values            : Monoisotopic
Protein Mass           : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Peptide Charge State   : 1+
Max Missed Cleavages   : 1
Number of queries      : 42
```

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