Mascot Search Results

```
User            : GM
Email           : gabriel.mazzucchelli@ulg.ac.be
Search title    : Submitted from 081205-adj-OGE34-8558-other Euc-Sprot by Mascot Daemon on MASPEC39
MS data file    : F:\DATA\Archives\ESQUIRE\2008-Esquire\Adjuvac\081205-OGE34-140min\081205-adj-OGE34_8558.mgf
Database        : Sprot 55.5 (389046 sequences; 139778124 residues)
Taxonomy        : Other Eukaryota (2925 sequences)
Timestamp       : 8 Dec 2008 at 08:25:19 GMT
Significant hits: CH60_TRYCR    Q95046|CH60_TRYCR Chaperonin HSP60, mitochondrial precursor - Trypanosoma cruzi
                  FCA1_TRYCR    P07749|FCA1_TRYCR Flagellar calcium-binding protein - Trypanosoma cruzi
                  UBIQ_TRYCR    P08565|UBIQ_TRYCR Ubiquitin - Trypanosoma cruzi
                  TBB_TRYBR     P04107|TBB_TRYBR Tubulin beta chain - Trypanosoma brucei rhodesiense
                  G3PG_TRYCR    P22513|G3PG_TRYCR Glyceraldehyde-3-phosphate dehydrogenase, glycosomal - Trypanosoma cruzi
                  RLA3_TRYCR    P26795|RLA3_TRYCR 60S acidic ribosomal protein P2-B - Trypanosoma cruzi
                  CALM_EUGGR    P11118|CALM_EUGGR Calmodulin - Euglena gracilis
                  CH60_TRYBB    Q37683|CH60_TRYBB Chaperonin HSP60, mitochondrial precursor - Trypanosoma brucei brucei
                  TBA_TRYCR     Q27352|TBA_TRYCR Tubulin alpha chain - Trypanosoma cruzi
                  EF1A_EUGGR    P14963|EF1A_EUGGR Elongation factor 1-alpha - Euglena gracilis
                  EF1AC_PORPU   P50256|EF1AC_PORPU Elongation factor 1-alpha C - Porphyra purpurea
                  HSP70_BRELC   P16394|HSP70_BRELC Heat shock 70 kDa protein - Bremia lactucae (Lettuce downy mildew)
                  RLA1_TRYCR    P26643|RLA1_TRYCR 60S acidic ribosomal protein P1 - Trypanosoma cruzi
                  H2A1_LEIIN    P27891|H2A1_LEIIN Histone H2A.1 - Leishmania infantum
                  H2A_TRYCR     P35066|H2A_TRYCR Histone H2A - Trypanosoma cruzi
                  EF1A_TRYBB    P41166|EF1A_TRYBB Elongation factor 1-alpha - Trypanosoma brucei brucei
                  HSP70_TRYCR   P05456|HSP70_TRYCR Heat shock 70 kDa protein - Trypanosoma cruzi
                  HSP70_ACHKL   P41753|HSP70_ACHKL Heat shock 70 kDa protein - Achlya klebsiana
                  HSP70_LEIMA   P14834|HSP70_LEIMA Heat shock 70 kDa protein - Leishmania major
                  EF1A_ENTHI    P31018|EF1A_ENTHI Elongation factor 1-alpha - Entamoeba histolytica
                  EF1A_GIALA    Q08046|EF1A_GIALA Elongation factor 1-alpha - Giardia lamblia (Giardia intestinalis)
                  TBAD_PHYPO    P50258|TBAD_PHYPO Tubulin alpha-1A chain - Physarum polycephalum (Slime mold)
                  RPOA_EUGGR    P48337|RPOA_EUGGR DNA-directed RNA polymerase subunit alpha - Euglena gracilis
                  KM11B_LEIIN   Q25297|KM11B_LEIIN Kinetoplastid membrane protein 11B - Leishmania infantum
                  H2B_TRYCR     P27795|H2B_TRYCR Histone H2B - Trypanosoma cruzi
                  EF1B_TRYCR    P34827|EF1B_TRYCR 25 kDa elongation factor 1-beta - Trypanosoma cruzi
                  EFTS_GALSU    P35019|EFTS_GALSU Elongation factor Ts - Galdieria sulphuraria (Red alga)
                  MYSN_ACACA    P05659|MYSN_ACACA Myosin-2 heavy chain, non muscle - Acanthamoeba castellanii (Amoeba)
                  YCF55_PORYE   Q1XDT4|YCF55_PORYE Uncharacterized protein ycf55 - Porphyra yezoensis
                  HSP71_TRYCR   P20583|HSP71_TRYCR Heat shock 70 kDa protein, mitochondrial precursor - Trypanosoma cruzi
                  CH60_GUITH    O78419|CH60_GUITH 60 kDa chaperonin - Guillardia theta (Cryptomonas phi)
                  NDUS1_DICCI   Q2LCP5|NDUS1_DICCI NADH-ubiquinone oxidoreductase 75 kDa subunit - Dictyostelium citrinum (Slime mo
```

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 23 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

Score Distribution

Peptide Summary Report

Format As | Peptide Summary ⌄ | Help

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

Standard scoring ○ | MudPIT scoring ● | Ions score cut-off 0 | Show sub-sets ☐

Show pop-ups ● | Suppress pop-ups ○ | Sort unassigned Decreasing Score ⌄ | Require bold red ☐

Select All | Select None | Search Selected | ☐ **Error tolerant** | Archive Report

1. CH60_TRYCR **Mass:** 59374 **Score:** 243 **Queries matched:** 5
Q95046|CH60_TRYCR Chaperonin HSP60, mitochondrial precursor - Trypanosoma cruzi
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☑	1503	659.93	1317.85	1317.69	0.15	0	87	1.5e-08	1	R.NVIIEQSYGAPK.I
☑	1512	670.41	1338.81	1338.61	0.20	0	75	2e-07	1	R.GLIDGETSDYNR.E

☑	380	696.47	1390.93	1390.73	0.19	0	50	0.00017	1	K.AELEDAFVLVSAK.K
☑	1667	804.02	1606.03	1605.92	0.11	0	26	0.012	1	R.AAVQEGIVPGGGVALLR.A
☑	1709	846.99	1691.97	1691.81	0.16	0	89	7e-09	1	K.VLENNDVTVGYDAQR.D

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2. FCA1_TRYCR **Mass:** 23721 **Score:** 226 **Queries matched:** 7

P07749|FCA1_TRYCR Flagellar calcium-binding protein - Trypanosoma cruzi

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☑	721	439.33	876.65	876.43	0.22	0	46	0.00019	1	K.LDEFTPR.V
☑	970	495.35	988.69	988.52	0.16	0	45	0.00021	1	K.VEDPAALFK.E
☑	1564	707.88	1413.75	1413.59	0.16	0	51	5.4e-05	1	K.LDADGDPDNVPESA.-
☑	1565	707.88	1413.75	1413.59	0.16	0	(37)	0.0015	1	K.LDADGDPDNVPESA.-
☑	1603	737.93	1473.84	1473.68	0.17	0	78	1.2e-07	1	K.GSEDFVEFLEFR.L
☑	1768	607.92	1820.74	1820.84	-0.11	0	27	0.014	1	K.LCYDEVHSGCLEVLK.L + 2 Carbamidomethyl (C)
☑	1832	979.63	1957.24	1956.92	0.32	0	62	3e-06	1	K.NGTGSVTFDEFAAWASAVK.L

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3. UBIQ_TRYCR **Mass:** 8504 **Score:** 209 **Queries matched:** 5

P08565|UBIQ_TRYCR Ubiquitin - Trypanosoma cruzi

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☑	1120	533.36	1064.70	1064.55	0.15	0	(31)	0.0041	1	R.TLADYNIQK.E
☑	138	533.40	1064.79	1064.55	0.24	0	44	0.00062	1	R.TLADYNIQK.E
☑	1126	534.41	1066.81	1066.61	0.20	0	46	0.00015	1	K.ESTLHLVLR.L
☑	1734	874.52	1747.02	1746.89	0.13	0	99	6.8e-10	1	K.TIALEVESSDTIENVK.A
☑	1735	583.36	1747.07	1746.89	0.18	0	(66)	1.6e-06	1	K.TIALEVESSDTIENVK.A

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4. TBB_TRYBR **Mass:** 49672 **Score:** 179 **Queries matched:** 4

P04107|TBB_TRYBR Tubulin beta chain - Trypanosoma brucei rhodesiense

☐ Check to include this hit in error tolerant search or archive report

```
     Query  Observed  Mr(expt)  Mr(calc)   Delta Miss Score   Expect Rank Peptide
       274    627.12   1252.24   1252.77   -0.53    1     6      4.3    2  R.KLAVNLVPFPR.L
☑     1516    671.43   1340.85   1340.64    0.21    0    87    1e-08    1  R.INVYFDEATGGR.Y
☑     1589    723.93   1445.85   1445.68    0.17    0    41   0.0004    1  K.EVDEQMLNVQNK.N
☑     1785    924.50   1846.98   1846.87    0.11    0    90  5.3e-09    1  R.EIVCVQAGQCGNQIGSK.F + 2 Carbamidomethyl (C)


      Proteins matching the same set of peptides:
      TBB_TRYCR         Mass: 49541    Score: 179    Queries matched: 4
      P08562|TBB_TRYCR Tubulin beta chain - Trypanosoma cruzi
```

```
5.    G3PG_TRYCR        Mass: 39036    Score: 149    Queries matched: 5
      P22513|G3PG_TRYCR Glyceraldehyde-3-phosphate dehydrogenase, glycosomal - Trypanosoma cruzi
    ☐ Check to include this hit in error tolerant search or archive report

     Query  Observed  Mr(expt)  Mr(calc)   Delta Miss Score   Expect Rank Peptide
☑      580    406.29    810.57    810.41    0.17    0    15     0.14    1  K.LTGMSFR.V
☑      606    412.81    823.61    823.43    0.18    0     3        2    1  K.AAAEGHLR.G
☑     1547    692.96   1383.90   1383.77    0.13    0    28    0.009    1  R.AAAVNIIPSTTGAAK.A
☑      205    596.60   1786.79   1786.95   -0.16    0   (59) 2.1e-05    1  R.VPTPDVSVVDLTFTAAR.D
☑     1751    894.56   1787.10   1786.95    0.15    0   102  3.1e-10    1  R.VPTPDVSVVDLTFTAAR.D
```

```
6.    RLA3_TRYCR        Mass: 10919    Score: 139    Queries matched: 3
      P26795|RLA3_TRYCR 60S acidic ribosomal protein P2-B - Trypanosoma cruzi
    ☐ Check to include this hit in error tolerant search or archive report

     Query  Observed  Mr(expt)  Mr(calc)   Delta Miss Score   Expect Rank Peptide
☑     1222    558.90   1115.78   1115.62    0.16    0    92  3.9e-09    1  R.SVATLVAEGAAK.M
       155    558.93   1115.84   1115.62    0.22    0   (8)        3    2  R.SVATLVAEGAAK.M
☑     1810    952.92   1903.84   1903.73    0.10    1    68  9.2e-07    1  K.KEEEEEDDDMGFGLFD.-
```

```
7.    CALM_EUGGR        Mass: 16845    Score: 139    Queries matched: 2
      P11118|CALM_EUGGR Calmodulin - Euglena gracilis
    ☐ Check to include this hit in error tolerant search or archive report
```

```
      Query  Observed  Mr(expt)  Mr(calc)   Delta Miss Score  Expect Rank Peptide
   ☑   1524    675.46   1348.90   1348.62    0.28   0     87 1.3e-08   1  K.LTDEEVDEMIR.E
   ☑   1819    964.50   1926.98   1926.85    0.13   0     73 3.3e-07   1  R.EADVDGDGQINYEEFVK.M


      Proteins matching the same set of peptides:
      CALM_TRYBB        Mass: 16828    Score: 139    Queries matched: 2
      P69097|CALM_TRYBB Calmodulin - Trypanosoma brucei brucei
      CALM_TRYBG        Mass: 16828    Score: 139    Queries matched: 2
      P69098|CALM_TRYBG Calmodulin - Trypanosoma brucei gambiense
      CALM_TRYCR        Mass: 16814    Score: 139    Queries matched: 2
      P18061|CALM_TRYCR Calmodulin - Trypanosoma cruzi
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8.    CH60_TRYBB        Mass: 59492    Score: 114    Queries matched: 3
      Q37683|CH60_TRYBB Chaperonin HSP60, mitochondrial precursor - Trypanosoma brucei brucei
   ☐  Check to include this hit in error tolerant search or archive report

      Query  Observed  Mr(expt)  Mr(calc)   Delta Miss Score  Expect Rank Peptide
       1503    659.93   1317.85   1317.69    0.15   0     87 1.5e-08   1  R.NVIIEQSYGAPK.I
        380    696.47   1390.93   1390.73    0.19   0     50 0.00017   1  K.AELEDAFVLVSAK.K
   ☑    827    925.21   1848.41   1848.89   -0.48   0      1      14   1  K.VLENTDAAVGYDAQLDR.Y

--------------------------------------------------------------------------------------------------------------
9.    TBA_TRYCR         Mass: 49696    Score: 101    Queries matched: 2
      Q27352|TBA_TRYCR Tubulin alpha chain - Trypanosoma cruzi
   ☐  Check to include this hit in error tolerant search or archive report

      Query  Observed  Mr(expt)  Mr(calc)   Delta Miss Score  Expect Rank Peptide
   ☑   1721    572.73   1715.17   1714.91    0.26   0   (45) 0.00016   1  R.AVFLDLEPTVVDEIR.T
   ☑   1722    858.61   1715.21   1714.91    0.30   0     76 1.4e-07   1  R.AVFLDLEPTVVDEIR.T

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10.   EF1A_EUGGR        Mass: 48582    Score: 100    Queries matched: 3
      P14963|EF1A_EUGGR Elongation factor 1-alpha - Euglena gracilis
   ☐  Check to include this hit in error tolerant search or archive report
```

```
     Query  Observed  Mr(expt)  Mr(calc)   Delta  Miss  Score  Expect  Rank  Peptide
☑     941    488.38    974.76    974.54    0.21    0     59   1.1e-05    1   R.LPLQDVYK.I
☑    1047    513.39   1024.76   1024.60    0.16    0     62     3e-06    1   K.IGGIGTVPVGR.V
     1368    602.39   1202.78   1202.65    0.12    1      7       1.7    2   K.ELEAEPKFIK.S
```

```
11.   EF1AC_PORPU        Mass: 49142    Score: 100    Queries matched: 3
      P50256|EF1AC_PORPU Elongation factor 1-alpha C - Porphyra purpurea
    ☐ Check to include this hit in error tolerant search or archive report

     Query  Observed  Mr(expt)  Mr(calc)   Delta  Miss  Score  Expect  Rank  Peptide
      941    488.38    974.76    974.54    0.21    0     59   1.1e-05    1   R.LPLQDVYK.I
     1047    513.39   1024.76   1024.60    0.16    0     62     3e-06    1   K.IGGIGTVPVGR.V
☑    1372    602.83   1203.64   1203.65   -0.02    2      4       2.5    1   K.KLEDSPKMIK.S + Oxidation (M)
```

```
12.   HSP70_BRELC        Mass: 74041    Score: 94     Queries matched: 2
      P16394|HSP70_BRELC Heat shock 70 kDa protein - Bremia lactucae (Lettuce downy mildew)
    ☐ Check to include this hit in error tolerant search or archive report

     Query  Observed  Mr(expt)  Mr(calc)   Delta  Miss  Score  Expect  Rank  Peptide
☑    1404    614.92   1227.83   1227.62    0.21    0     69   8.1e-07    1   R.VEIIANDQGNR.T
☑    1609    744.47   1486.92   1486.69    0.23    0     44   0.00038    1   R.TTPSYVAFTDTER.L
```

```
13.   RLA1_TRYCR         Mass: 10747    Score: 90     Queries matched: 3
      P26643|RLA1_TRYCR 60S acidic ribosomal protein P1 - Trypanosoma cruzi
    ☐ Check to include this hit in error tolerant search or archive report

     Query  Observed  Mr(expt)  Mr(calc)   Delta  Miss  Score  Expect  Rank  Peptide
☑    1220    558.86   1115.70   1115.58    0.11    0     24     0.024    1   K.NVDINDVLSK.V
     1810    952.92   1903.84   1903.73    0.10    1     68   9.2e-07    1   K.KEEEEEDDDMGFGLFD.-
☑    2072    850.54   2548.60   2548.34    0.26    0     34    0.0019    1   K.VSFGGVAPAAGGATAAPAAAAAAAAPAAAAAK.K
```

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14. H2A1_LEIIN **Mass:** 13884 **Score:** 81 **Queries matched:** 2
P27891|H2A1_LEIIN Histone H2A.1 - Leishmania infantum
☐ Check to include this hit in error tolerant search or archive report

	Query	**Observed**	**Mr(expt)**	**Mr(calc)**	**Delta**	**Miss**	**Score**	**Expect**	**Rank**	**Peptide**
☑	489	**759.42**	**758.41**	**758.43**	**-0.01**	**2**	**0**	**17**	**1**	**K.KGKATPSA.-**
☑	1239	**563.90**	**1125.78**	**1125.57**	**0.21**	**0**	**81**	**5e-08**	**1**	**R.HDDDIGTLLK.N**

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15. H2A_TRYCR **Mass:** 14357 **Score:** 75 **Queries matched:** 2
P35066|H2A_TRYCR Histone H2A - Trypanosoma cruzi
☐ Check to include this hit in error tolerant search or archive report

	Query	**Observed**	**Mr(expt)**	**Mr(calc)**	**Delta**	**Miss**	**Score**	**Expect**	**Rank**	**Peptide**
☑	1166	**1090.01**	**1089.00**	**1088.60**	**0.40**	**2**	**1**	**16**	**1**	**-.MATPKQAAKK.A + Oxidation (M)**
☑	1283	**578.90**	**1155.79**	**1155.56**	**0.23**	**0**	**75**	**2.3e-07**	**1**	**R.HDDDLGMLLK.D**

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16. EF1A_TRYBB **Mass:** 49003 **Score:** 72 **Queries matched:** 2
P41166|EF1A_TRYBB Elongation factor 1-alpha - Trypanosoma brucei brucei
☐ Check to include this hit in error tolerant search or archive report

	Query	**Observed**	**Mr(expt)**	**Mr(calc)**	**Delta**	**Miss**	**Score**	**Expect**	**Rank**	**Peptide**
	1047	513.39	1024.76	1024.60	0.16	0	62	3e-06	1	K.IGGIGTVPVGR.V
☑	644	**841.79**	**2522.36**	**2522.19**	**0.18**	**0**	**31**	**0.011**	**1**	**K.SIEMHHEQLAEATPGDNVGFNVK.N**

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17. HSP70_TRYCR **Mass:** 73762 **Score:** 69 **Queries matched:** 2
P05456|HSP70_TRYCR Heat shock 70 kDa protein - Trypanosoma cruzi
☐ Check to include this hit in error tolerant search or archive report

	Query	**Observed**	**Mr(expt)**	**Mr(calc)**	**Delta**	**Miss**	**Score**	**Expect**	**Rank**	**Peptide**
	1404	614.92	1227.83	1227.62	0.21	0	69	8.1e-07	1	R.VEIIANDQGNR.T
☑	1477	**650.40**	**1298.79**	**1298.60**	**0.19**	**0**	**15**	**0.19**	**1**	**R.FEELCGELFR.G + Carbamidomethyl (C)**

```
18.    HSP70_ACHKL        Mass: 71222    Score: 69     Queries matched: 2
       P41753|HSP70_ACHKL Heat shock 70 kDa protein - Achlya klebsiana
     ☐ Check to include this hit in error tolerant search or archive report

      Query  Observed  Mr(expt)  Mr(calc)    Delta Miss Score  Expect Rank Peptide
    ☑  1364    601.40   1200.78   1200.65     0.13    1     2     3.5    1  K.TMEPVEKVLR.D
       1404    614.92   1227.83   1227.62     0.21    0    69 8.1e-07    1  R.VEIIANDQGNR.T
```

```
19.    HSP70_LEIMA        Mass: 56500    Score: 69     Queries matched: 1
       P14834|HSP70_LEIMA Heat shock 70 kDa protein - Leishmania major
     ☐ Check to include this hit in error tolerant search or archive report

      Query  Observed  Mr(expt)  Mr(calc)    Delta Miss Score  Expect Rank Peptide
       1404    614.92   1227.83   1227.62     0.21    0    69 8.1e-07    1  R.LDIIANDQGNR.T
```

```
20.    EF1A_ENTHI         Mass: 47234    Score: 59     Queries matched: 4
       P31018|EF1A_ENTHI Elongation factor 1-alpha - Entamoeba histolytica
     ☐ Check to include this hit in error tolerant search or archive report

      Query  Observed  Mr(expt)  Mr(calc)    Delta Miss Score  Expect Rank Peptide
        941    488.38    974.76    974.54     0.21    0    59 1.1e-05    1  R.LPLQDVYK.I
        148    547.88   1093.76   1093.54     0.22    1     2      11    2  K.QERYEEIK.K
       1233    561.40   1120.79   1120.59     0.20    0     1     4.3    8  K.YAWVLDNLK.A
    ☑  1474    649.40   1296.78   1296.61     0.17    1     1     4.9    1  K.MDAIQYKQER.Y + Oxidation (M)
```

```
21.    EF1A_GIALA         Mass: 43922    Score: 59     Queries matched: 1
       Q08046|EF1A_GIALA Elongation factor 1-alpha - Giardia lamblia (Giardia intestinalis)
     ☐ Check to include this hit in error tolerant search or archive report

      Query  Observed  Mr(expt)  Mr(calc)    Delta Miss Score  Expect Rank Peptide
        941    488.38    974.76    974.54     0.21    0    59 1.1e-05    1  R.LPIQDVYK.I
```

```
22.    TBAD_PHYPO         Score: 53    Queries matched: 2
```

P50258|TBAD_PHYPO Tubulin alpha-1A chain - Physarum polycephalum (Slime mold)

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
	1721	572.73	1715.17	1714.91	0.26	0	(28)	0.0093	2	R.AVFLDLEPTVIDEVR.T
	1722	858.61	1715.21	1714.91	0.30	0	45	0.00019	2	R.AVFLDLEPTVIDEVR.T

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23. RPOA_EUGGR **Mass:** 25348 **Score:** 46 **Queries matched:** 2

P48337|RPOA_EUGGR DNA-directed RNA polymerase subunit alpha - Euglena gracilis

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☑	1108	**528.42**	**1054.82**	**1054.71**	**0.11**	**2**	**46**	**0.00014**	**1**	**K.ILLKIEAKK.A**
	1126	534.41	1066.81	1066.65	0.16	1	9	0.72	2	K.YLKIYVLR.S

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24. KM11B_LEIIN **Mass:** 11169 **Score:** 45 **Queries matched:** 1

Q25297|KM11B_LEIIN Kinetoplastid membrane protein 11B - Leishmania infantum

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☑	1194	**553.38**	**1104.75**	**1104.58**	**0.17**	**0**	**45**	**0.00023**	**1**	**K.FAELLEQQK.A**

Proteins matching the same set of peptides:

KM11C_LEIIN **Mass:** 11255 **Score:** 45 **Queries matched:** 1
Q25298|KM11C_LEIIN Kinetoplastid membrane protein 11C - Leishmania infantum
KM11_LEIDO **Mass:** 11254 **Score:** 45 **Queries matched:** 1
Q36736|KM11_LEIDO Kinetoplastid membrane protein 11 - Leishmania donovani
KM11_LEITR **Mass:** 11227 **Score:** 45 **Queries matched:** 1
O21436|KM11_LEITR Kinetoplastid membrane protein 11 - Leishmania tropica
KM11_TRYBB **Mass:** 11069 **Score:** 45 **Queries matched:** 1
P69300|KM11_TRYBB Kinetoplastid membrane protein 11 - Trypanosoma brucei brucei
KM11_TRYBR **Mass:** 11069 **Score:** 45 **Queries matched:** 1
P69301|KM11_TRYBR Kinetoplastid membrane protein 11 - Trypanosoma brucei rhodesiense

KM11_TRYCR **Mass:** 11004 **Score:** 45 **Queries matched:** 1
Q9U6Z1|KM11_TRYCR Kinetoplastid membrane protein 11 - Trypanosoma cruzi

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25. H2B_TRYCR **Mass:** 12368 **Score:** 36 **Queries matched:** 1
P27795|H2B_TRYCR Histone H2B - Trypanosoma cruzi
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☑	857	**470.42**	**938.83**	**938.58**	**0.25**	**0**	**36**	**0.0016**	**1**	**R.LVLPADLAK.H**

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26. EF1B_TRYCR **Mass:** 24450 **Score:** 35 **Queries matched:** 1
P34827|EF1B_TRYCR 25 kDa elongation factor 1-beta - Trypanosoma cruzi
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☑	105	**507.03**	**1518.06**	**1517.85**	**0.21**	**1**	**35**	**0.0053**	**1**	**K.LFLGGTKPSKEDVK.L**

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27. EFTS_GALSU **Score:** 31 **Queries matched:** 1
P35019|EFTS_GALSU Elongation factor Ts - Galdieria sulphuraria (Red alga)
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
	1194	553.38	1104.75	1104.58	0.16	0	31	0.005	2	-.MSEISAQLVK.E

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28. MYSN_ACACA **Mass:** 171097 **Score:** 29 **Queries matched:** 2
P05659|MYSN_ACACA Myosin-2 heavy chain, non muscle - Acanthamoeba castellanii (Amoeba)
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☑	999	**500.91**	**999.81**	**999.60**	**0.21**	**1**	**29**	**0.0083**	**1**	**K.LEKDLAALK.L**
☑	1480	**650.83**	**1299.64**	**1299.71**	**-0.07**	**1**	**12**	**0.42**	**1**	**K.CNGVLEGIRIAR.K**

29. YCF55_PORYE **Score:** 29 **Queries matched:** 1
Q1XDT4|YCF55_PORYE Uncharacterized protein ycf55 - Porphyra yezoensis
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
	1404	614.92	1227.83	1227.70	0.13	0	29	0.0087	3	K.NNLIWNTIIK.N

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30. HSP71_TRYCR **Mass:** 71102 **Score:** 28 **Queries matched:** 1
P20583|HSP71_TRYCR Heat shock 70 kDa protein, mitochondrial precursor - Trypanosoma cruzi
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☑	1551	**695.41**	**1388.81**	**1388.73**	**0.08**	**0**	**28**	**0.009**	**1**	**K.EISEVVLVGGMTR.M**

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31. CH60_GUITH **Mass:** 57367 **Score:** 27 **Queries matched:** 1
O78419|CH60_GUITH 60 kDa chaperonin - Guillardia theta (Cryptomonas phi)
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☑	1193	**1104.65**	**1103.65**	**1103.56**	**0.09**	**2**	**27**	**0.014**	**1**	**K.SRCEQIRR.Q + Carbamidomethyl (C)**

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32. NDUS1_DICCI **Mass:** 79554 **Score:** 24 **Queries matched:** 3
Q2LCP5|NDUS1_DICCI NADH-ubiquinone oxidoreductase 75 kDa subunit - Dictyostelium citrinum (Slime mo
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
	1199	554.36	1106.71	1106.65	0.06	1	4	2.1	2	K.MVFKVLLNK.K + Oxidation (M)
☑	1489	**654.42**	**1306.82**	**1306.67**	**0.15**	**2**	**24**	**0.02**	**1**	**K.KIMEAGSWKNK.T + Oxidation (M)**
☑	1490	**436.65**	**1306.92**	**1306.67**	**0.25**	**2**	**(1)**	**3.8**	**1**	**K.KIMEAGSWKNK.T + Oxidation (M)**

Peptide matches not assigned to protein hits: (no details means no match)

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide

☑	1339	593.94	1185.87	1185.62	0.25	0	22	0.039	1	EIDVIEEIAR
☑	711	437.80	873.58	873.48	0.10	0	22	0.056	1	VTVEDIAK
☑	1225	559.38	1116.74	1116.61	0.12	2	21	0.037	1	DREKEIISK
☑	1061	516.42	1030.83	1030.61	0.23	0	21	0.051	1	VIDLLAPYK
☑	1674	540.46	1618.35	1617.85	0.50	2	21	0.072	1	PIGYPLVKAMDKDR + Oxidation (M)
☑	1315	588.36	1174.70	1174.61	0.09	0	20	0.06	1	LTQESEDLLK
☑	1500	658.91	1315.81	1315.73	0.08	1	20	0.059	1	RTMFPVLDLPK
☑	1757	899.11	1796.21	1796.03	0.18	2	20	0.056	1	SRSIHKGPFIDVSLLK
☑	1478	650.41	1298.81	1298.72	0.09	1	18	0.093	1	QLEIEAKALER
☑	1259	572.40	1142.78	1142.63	0.15	2	18	0.082	1	SPEGKEKLQK
☑	20	283.12	846.34	846.39	-0.06	0	18	0.16	1	MYGYGLK + Oxidation (M)
☑	190	586.39	1170.77	1170.49	0.28	0	18	0.28	1	DFDTVCTEGK + Carbamidomethyl (C)
☑	1605	738.46	1474.90	1474.72	0.19	0	18	0.11	1	FIDCYLQFLEK + Carbamidomethyl (C)
☑	612	828.20	1654.39	1653.86	0.54	1	17	0.39	1	KLMVTGAQYMDLIR + Oxidation (M)
☑	1675	811.98	1621.95	1621.90	0.06	0	17	0.11	1	YGLPLIFEIETISK
☑	1615	751.04	1500.07	1499.85	0.22	2	16	0.18	1	ALDMKDVKQAILR
☑	147	547.83	1640.48	1640.94	-0.46	2	16	0.64	1	LARKEQCIALGAQLK
☑	1648	788.98	1575.95	1575.83	0.12	2	15	0.12	1	ASDVIGAVKKGVSDCK
☑	1601	734.95	1467.89	1467.86	0.02	2	15	0.18	1	ALSGGQKQRIAIAR
☑	902	963.48	962.47	962.49	-0.02	0	15	0.55	1	MSSNNLVAK
☑	1597	730.98	1459.95	1459.71	0.24	1	14	0.28	1	MEKEMMLYLLK + 2 Oxidation (M)
☑	1253	571.32	1140.62	1140.60	0.02	1	14	0.17	1	RSVGPGQDVAR
☑	1325	591.43	1180.85	1180.54	0.31	1	14	0.21	1	SIAPCKQCMK + Carbamidomethyl (C); Oxidation (M)
☑	611	827.51	826.50	826.39	0.11	0	14	0.23	1	SSLFMDK
☑	932	487.38	972.74	972.58	0.16	1	14	0.22	1	ELLPFAKR
☑	1542	691.42	1380.82	1380.69	0.12	1	13	0.31	1	ELESKGYEWLK
☑	1332	592.94	1183.87	1183.66	0.22	0	13	0.32	1	NVTAGANPISIK
☑	2036	814.34	2440.01	2440.20	-0.19	1	13	0.19	1	DPLNSIYMMAFSGARANISQVR
☑	1441	633.92	1265.82	1265.58	0.24	0	13	0.25	1	ICINLECIDCK
☑	1233	561.40	1120.79	1120.66	0.13	2	13	0.32	1	RNRHNIIAK
☑	155	558.93	1115.84	1115.67	0.17	1	13	1.1	1	RYVILLDPK
☑	295	642.60	1283.18	1283.69	-0.51	1	13	1.1	1	NLAREGNEIIR
☑	1171	545.86	1089.70	1089.56	0.14	1	12	0.42	1	AKVCGWIEGK
☑	1368	602.39	1202.78	1202.60	0.18	1	12	0.53	1	KINESMEPQK

☑	1412	412.31	1233.92	1233.73	0.19	2	12	0.37	1	LSSAYILRRR
☑	1753	896.02	1790.02	1790.02	0.00	2	12	0.36	1	SFALTREASLRTLGLR
☑	1350	597.38	1192.75	1192.60	0.14	1	12	0.41	1	NICKISSSWR
☑	1548	462.31	1383.91	1383.72	0.19	1	12	0.4	1	HGIEKVAEQVMK + Oxidation (M)
☑	1161	544.84	1087.66	1087.63	0.03	2	11	0.41	1	LASSKRISIN
☑	416	718.83	717.82	718.39	-0.57	0	11	1.1	1	LASETAK
☑	92	483.11	964.20	964.49	-0.29	0	11	1.3	1	IADAIYDGK
☑	1496	658.43	1314.84	1314.66	0.18	1	11	0.49	1	WLRDVPSDEAK
☑	1016	1007.71	3020.10	3019.54	0.56	2	11	1.5	1	SPKPVASCAMPVMDNMKIFTNTPLVKK + Carbamidomethyl (C); Oxidation (M)
☑	1440	633.40	1264.79	1264.70	0.09	1	11	0.55	1	TNSKVLDFTIK
☑	1257	571.42	1140.83	1140.60	0.23	1	11	0.35	1	RSVGPGQDVAR
☑	1250	570.34	1138.66	1138.60	0.06	1	11	0.51	1	NTSSTNKFIK
☑	1091	523.38	1044.74	1044.63	0.11	1	11	0.69	1	SLSALAKSIR
☑	2014	793.15	2376.42	2376.15	0.27	1	10	0.46	1	IIVDTYGGWGAHGGGAFSGKDPSK
☑	1549	694.37	1386.72	1386.74	-0.02	2	10	0.61	1	RARDVEMLELR
☑	1778	613.07	1836.17	1835.97	0.20	1	10	0.6	1	SFDLDVLKDSCALILK + Carbamidomethyl (C)
☑	1664	801.57	1601.12	1600.88	0.25	1	10	0.76	1	MLQIELQKWIQR + Oxidation (M)
☑	928	972.15	971.14	970.65	0.48	2	10	1.9	1	LITGAKKIK
☑	1365	601.87	1201.73	1201.67	0.06	1	10	0.7	1	ESKINTEILR
☑	1245	567.37	1132.72	1132.61	0.11	1	10	0.65	1	KTSEVTEALR
☑	622	833.29	2496.85	2496.37	0.47	2	10	2.2	1	LVSVPTMPRVPRQELMDFLLR
☑	1431	628.99	1255.96	1255.67	0.29	1	10	0.68	1	TLPGVAVLDDKE
☑	182	580.55	1159.09	1158.65	0.45	1	9	2.1	1	IQRTLTGTNR
☑	838	465.86	929.71	929.55	0.16	1	9	0.8	1	TLIEKAQK
☑	1396	610.92	1219.82	1219.68	0.14	0	9	0.61	1	SLLSNMISIVK + Oxidation (M)
☑	1614	750.46	1498.90	1498.70	0.20	2	9	0.7	1	ECKTCSLTETKEK
☑	1046	1025.63	1024.62	1024.63	-0.01	1	9	1.7	1	KYITIFLK
☑	1199	554.36	1106.71	1106.59	0.12	1	9	0.64	1	MPLYVNSKR
☑	1072	518.42	1034.83	1034.56	0.27	0	9	0.8	1	MDLFLQIR
☑	1235	561.87	1121.72	1121.64	0.08	1	9	0.73	1	RTINQVVHR
☑	91	482.12	1443.33	1442.85	0.48	0	9	2.1	1	VLSQLGSSLVTALR
☑	784	454.40	906.79	906.53	0.26	1	9	0.79	1	KGTVSIFR
☑	367	686.84	685.83	686.43	-0.60	0	9	1.7	1	ISVLQK
☑	1758	599.75	1796.23	1796.04	0.19	1	9	0.83	1	IKIAEIINDQATNILK

☑	1241	564.39	1126.77	1126.59	0.18	0	8	0.88	1	GDLGVEIPAEK
☑	1170	545.85	1089.68	1089.62	0.05	2	8	1.1	1	MAADLLKGKK + Oxidation (M)
☑	1886	686.78	2057.33	2057.92	-0.59	1	8	0.84	1	QEANTIVKNSSTDDDFMK + Oxidation (M)
☑	1656	794.45	1586.89	1586.88	0.01	1	8	0.92	1	VQAIKGTLIVCEGTR
☑	97	491.35	980.68	980.42	0.26	0	8	2.3	1	GMLCNAGSR + Carbamidomethyl (C); Oxidation (M)
☑	764	898.24	2691.68	2692.27	-0.59	0	8	3.3	1	VPALVEAGADVLCIDSSDGFSEWQK + Carbamidomethyl (C)
☑	330	663.36	1324.71	1324.68	0.03	1	8	3.4	1	FASKIMGTTDVR
☑	124	519.25	1554.72	1554.85	-0.13	1	8	2	1	MSDILFQLGYIKK
☑	1442	634.40	1266.78	1266.71	0.07	2	8	1.1	1	MKFSQRTLLK + Oxidation (M)
☑	1486	651.98	1301.94	1301.66	0.27	0	7	1.4	1	QSVNEPMITGVK
☑	1604	738.43	1474.84	1474.72	0.12	0	7	1.2	1	FIDCYLQFLEK + Carbamidomethyl (C)
☑	1090	1045.65	1044.64	1044.63	0.01	1	7	3.4	1	SLSALAKSIR
☑	1435	631.37	1260.73	1260.66	0.07	0	7	1.5	1	QCLTAMPAGLIK + Oxidation (M)
☑	197	591.36	1180.71	1180.66	0.05	0	7	3	1	FAVFASLLASR
☑	905	482.81	963.60	963.43	0.17	0	7	1.4	1	TNFDQDPK
☑	1532	682.93	1363.85	1363.67	0.19	1	7	1.2	1	LQEQLKEMSDK + Oxidation (M)
☑	59	379.48	756.94	756.43	0.52	0	7	3.8	1	LHGVGFK
☑	101	500.44	1498.30	1498.79	-0.49	1	7	3.6	1	DNQNIKIYNHLK
☑	1484	651.42	1300.82	1300.72	0.10	1	7	1.3	1	VLVNEKLMEAR
☑	1792	931.94	1861.86	1862.00	-0.14	2	7	1.1	1	AMRLSQHVIRYMTIK + Oxidation (M)
☑	1254	571.33	1140.64	1140.56	0.08	2	7	0.94	1	YDKRTDCIK
☑	1841	656.69	1967.04	1967.12	-0.07	2	7	1.1	1	RIVENAGNNGSIIIEKIK
☑	274	627.12	1252.24	1252.54	-0.30	0	7	4.2	1	ALQECNGDFEK
☑	1855	665.77	1994.28	1994.05	0.22	2	6	1.1	1	EQYRSISSSLAQKTIQR
☑	1938	1088.80	2175.59	2175.22	0.37	2	6	1.7	1	IQTRNAKLKPYDNINLFK
☑	826	924.86	923.85	923.42	0.43	0	6	3.8	1	AFCVGGDQK
☑	451	371.14	740.27	740.53	-0.26	1	6	0.79	1	ILKVIR
☑	1392	607.88	1213.75	1213.61	0.15	0	6	1.4	1	VDIIANDQGNR
☑	948	979.46	2935.35	2935.52	-0.17	1	6	3.7	1	GEDVVCVYVAVGQKAATVASIVTTLEEK + Carbamidomethyl (C)
☑	1775	613.02	1836.04	1835.97	0.07	1	6	1.5	1	SFDLDVLKDSCALILK + Carbamidomethyl (C)
☑	1298	582.84	1163.67	1163.65	0.01	2	6	1.7	1	KEYQLVEKK
☑	1204	555.32	1108.63	1108.61	0.02	1	6	1.3	1	EGISIRHAAR
☑	1553	695.94	1389.86	1389.67	0.19	1	6	1.6	1	MQSDSEPVVSRR
☑	1521	674.97	1347.92	1347.78	0.14	1	6	1.6	1	ADLTKFIVVTNK

☑	1289	579.88	1157.75	1157.68	0.07	0	6	1.8	1	ANVPFIVAISK
☑	1344	594.90	1187.79	1187.57	0.23	1	6	1.8	1	QMVTKFGMSK + 2 Oxidation (M)
☑	799	913.26	2736.76	2736.32	0.44	2	6	5.6	1	MQHNLIDNYQLRARSFGEEPYR
☑	1269	1149.95	3446.83	3446.82	0.00	1	6	3.9	1	GPTAKHLSSIICHFQQLNTIISTAHAIYLGR + Carbamidomethyl (C)
☑	1650	792.50	1582.98	1582.81	0.17	1	6	1.6	1	FPKTNSMIEELFK
☑	364	684.44	683.43	683.33	0.10	0	6	0.85	1	GMGYLK + Oxidation (M)
☑	1763	905.63	1809.24	1808.99	0.25	2	6	1.7	1	APGSIGMGTSPGRVLPGKK
☑	332	665.11	1328.20	1328.77	-0.56	1	5	6.8	1	EILLLATGESKR
☑	1780	919.65	1837.28	1836.91	0.37	2	5	2.2	1	GHSLADPDELRSRQEK
☑	334	666.33	665.32	665.34	-0.02	0	5	1.1	1	MTISSK
☑	245	615.75	614.75	615.33	-0.59	0	5	3.6	1	LEAQR
☑	1639	778.49	1554.96	1554.87	0.09	1	5	1.5	1	EGGRTVGAGVVLSIIQ
☑	1509	665.92	1329.83	1329.73	0.10	1	5	1.8	1	IKNENPLDIFK
☑	366	686.48	1370.95	1370.80	0.15	2	5	5.8	1	NVIMLLSPKKVN + Oxidation (M)
☑	2142	991.19	2970.56	2970.56	-0.01	1	5	1.3	1	IEFEILWIGQSELFYKGIESTLIDK
☑	189	586.33	1170.65	1170.67	-0.02	2	5	5.1	1	QLQKRLEEK
☑	173	572.28	571.27	571.37	-0.10	0	5	1.5	1	LAGALK
☑	1538	687.40	1372.78	1372.81	-0.03	1	5	2.1	1	VLGGKGISLAAMIK + Oxidation (M)
☑	1508	665.49	1328.97	1328.75	0.22	2	5	1.9	1	FYKSSVRTLTK
☑	1461	643.95	1285.88	1285.66	0.22	1	5	2.4	1	MIHIGNNTKSR + Oxidation (M)
☑	1443	1270.15	3807.42	3806.99	0.43	1	5	6.1	1	IHMDPLEIDLIILATSSPNDLFGSASQVQAKIGAAR + Oxidation (M)
☑	1099	1050.86	2099.71	2099.13	0.58	2	5	5.2	1	GLINQRIHSQDIICKFSK
☑	1463	644.99	1287.97	1287.69	0.28	1	5	1.9	1	LMCIRVLGGGNR
☑	192	586.89	585.89	586.29	-0.40	0	5	3.4	1	VCHTK
☑	1369	602.42	1202.83	1202.67	0.16	0	5	2.8	1	ESTLIMQLLR
☑	650	423.27	844.52	844.47	0.06	0	5	2.7	1	IIEQASGK
☑	1499	658.88	1315.76	1315.65	0.10	1	5	2.2	1	GISAGYSKNTYR
☑	444	735.89	2204.65	2205.18	-0.53	2	5	9.9	1	SCCVRIQHVHRNVFLLPK + Carbamidomethyl (C)
☑	242	614.86	1841.56	1840.99	0.57	2	4	10	1	ARNIAALPVSMGGCGIRR
☑	266	623.27	1866.78	1866.90	-0.12	0	4	5.9	1	EMYNSLGTPISGVAEGVK + Oxidation (M)
☑	1713	850.08	1698.14	1697.97	0.17	2	4	2.1	1	MASNQQLKIRIQLR
☑	1797	626.76	1877.27	1877.01	0.26	2	4	2.5	1	KNSLTVATFMLSKFYK
☑	148	547.88	1093.76	1093.58	0.18	1	4	7	1	ELKVDFSTR
☑	160	563.04	1686.09	1685.97	0.12	1	4	6.7	1	MGMSLQLLGINLRIK

☑	277	629.36	628.35	628.40	-0.05	2	4	2.7	1	RKTPK
☑	1481	650.89	1299.76	1299.76	-0.00	0	4	2.5	1	SLTLLEAAELIK
☑	1577	714.47	1426.92	1426.73	0.19	0	4	2.4	1	LIIQIGCYSDFR
☑	523	782.88	781.88	781.32	0.55	0	4	2.2	1	EFSDER
☑	1654	793.98	1585.94	1585.89	0.06	2	4	1.9	1	IIKVSEIMHGKTSK + Oxidation (M)
☑	146	546.82	545.81	546.28	-0.47	0	4	10	1	TLGWA
☑	373	691.96	690.96	690.41	0.55	1	4	4.9	1	VYPGKK
☑	537	789.85	788.84	789.42	-0.57	0	4	9.3	1	NQLLMR + Oxidation (M)
☑	559	797.75	1593.48	1593.91	-0.43	0	4	6.5	1	LNNVDIQKPDVVIK
☑	1465	645.31	1288.61	1288.71	-0.09	0	4	2.6	1	ITSLVLDQCLK + Carbamidomethyl (C)
☑	136	531.45	530.45	530.34	0.10	0	4	1.7	1	AIVTK
☑	1482	650.94	1299.86	1299.65	0.21	2	4	2.7	1	KRDLHSNSSEK
☑	412	716.16	715.16	715.36	-0.20	0	4	3.3	1	EGGNALR
☑	1506	665.41	1328.81	1328.72	0.09	1	4	2.5	1	QVDVFVKGPGAGR
☑	1527	679.40	1356.78	1356.76	0.02	0	4	2.9	1	SAVLQNSPSTIIK
☑	328	660.89	659.89	659.39	0.50	0	4	8	1	SIDVVK
☑	1377	603.91	1205.81	1205.68	0.13	2	4	2.7	1	KTEAAGFKAGVK
☑	763	898.12	1794.23	1794.82	-0.59	1	4	7.3	1	FWSSCHAAVKAAQDMK + Oxidation (M)
☑	279	630.99	629.98	630.31	-0.33	0	4	12	1	DNNLR
☑	454	741.92	2222.74	2223.06	-0.32	1	4	9.2	1	AMIDNRMNQSILISGESGAGK + 2 Oxidation (M)
☑	1633	772.43	1542.85	1542.74	0.11	0	4	2.3	1	GYISPYFVTDPER
☑	1454	1278.52	3832.54	3832.65	-0.12	0	3	6.2	1	MSTAQSDALTFECETGNYHTFCPISCVSWLYQK + Carbamidomethyl (C); Oxidation (M
☑	1081	1040.43	2078.84	2079.08	-0.24	2	3	6	1	LDIGKLFGGLVGESESRMR + Oxidation (M)
☑	1497	658.58	1315.15	1315.56	-0.40	2	3	5.2	1	DKTGAGMMDCKK + 2 Oxidation (M)
☑	70	444.02	886.02	886.51	-0.49	2	3	9.3	1	KQATQRR
☑	456	743.48	742.47	742.48	-0.01	1	3	8.2	1	LVRTVR
☑	1191	1103.19	3306.56	3306.59	-0.03	2	3	8.3	1	MSGGDHLHSGTVVGKLEGDRAGTYGFINLMR + 2 Oxidation (M)
☑	1063	1032.56	3094.66	3094.57	0.08	0	3	7.1	1	VAVVDVQTVHGPPFFAALGGTCVNVGCVPK + 2 Carbamidomethyl (C)
☑	1265	574.01	1146.02	1145.68	0.33	2	3	5.3	1	VKDLPGVKYK
☑	1322	590.39	1178.78	1178.56	0.22	1	3	2.2	1	KNWCLIDCK + Carbamidomethyl (C)
☑	1634	773.49	1544.97	1544.78	0.19	0	3	3.2	1	HSCLIINFESNLR
☑	1196	1106.12	1105.12	1104.63	0.49	1	3	10	1	NITKIVFDR
☑	1703	843.65	1685.29	1684.87	0.42	0	3	4.2	1	ELFSLLSDFYLNPK
☑	1579	714.49	1426.96	1426.85	0.11	2	3	3.1	1	LDSIKLDVLGKAR

☑	1285	578.95	1155.88	1155.68	0.20	2	3	3.3	1	CRIPVEKALK
☑	1345	594.94	1187.87	1187.57	0.30	1	3	3.4	1	QMVTKFGMSK + 2 Oxidation (M)
☑	802	457.89	913.77	913.52	0.25	0	3	3.8	1	LAQAELAAK
☑	61	423.63	1267.88	1267.71	0.17	0	3	8	1	ADPAAETLVLIR
☑	1507	665.48	1328.94	1328.79	0.15	2	3	3	1	IVSRRSNGLTVK
☑	180	579.06	1156.11	1155.62	0.49	2	3	11	1	NSAPVRSRNR
☑	1366	601.90	1201.79	1201.58	0.21	1	3	3.5	1	TNMFSKLSMK + Oxidation (M)
☑	1341	594.43	1186.84	1186.69	0.15	1	3	3.8	1	VIRVGINGFGR
☑	2093	882.16	2643.46	2643.19	0.27	1	3	2.4	1	SLIENYDCYEVKTVGDSFMIACK + Oxidation (M)
☑	301	645.87	644.87	644.39	0.48	0	3	18	1	GNTLLK
☑	314	653.18	1956.53	1956.98	-0.45	1	3	10	1	FRQYVNQGLNLYDATR
☑	1288	579.86	1157.70	1157.68	0.02	0	3	3.7	1	ANVPFIVAISK
☑	134	530.88	529.87	530.31	-0.43	0	3	4.3	1	TLLNA
☑	313	652.35	651.34	651.37	-0.03	1	3	7.9	1	YSVRK
☑	703	872.51	1743.00	1742.84	0.16	0	3	8.5	1	IVTEALNALSCMEHR + Carbamidomethyl (C)
☑	1281	578.46	1154.91	1154.74	0.17	1	3	3.6	1	IILETAKVIR
☑	1346	595.89	1189.76	1189.59	0.16	1	2	3.5	1	KVLCMGVGGGNV + Carbamidomethyl (C)
☑	81	447.67	1339.98	1339.78	0.20	1	2	6.7	1	EIVDIVLDRIR
☑	1982	762.49	2284.46	2284.18	0.28	1	2	3.2	1	YFTAASHALLMNVFASRTLR + Oxidation (M)
☑	520	780.37	2338.08	2338.24	-0.15	0	2	8.5	1	ICPIETPEGPNAGLIGSLAIFAR
☑	219	603.76	602.76	602.33	0.43	0	2	16	1	DLIDK
☑	1681	818.47	1634.93	1634.83	0.10	1	2	3	1	MVSSLANELREGTTK
☑	377	693.91	692.90	693.37	-0.47	0	2	7.6	1	FEGLTK
☑	565	802.18	2403.51	2403.21	0.31	1	2	14	1	VQSSEGTITCEVQQLLGDNKVR
☑	1074	1036.35	2070.68	2071.14	-0.47	1	2	12	1	QAVPLIRASKPYVSTGQEK
☑	1176	1092.64	1091.63	1091.59	0.04	1	2	9.7	1	NLDKTFIEL
☑	299	644.36	1286.71	1286.71	-0.00	1	2	12	1	IANQQVMKALR + Oxidation (M)
☑	755	893.89	1785.76	1785.90	-0.14	1	2	12	1	MKTPITEAIAAADNQGR
☑	806	459.33	916.65	916.57	0.08	2	2	4.6	1	VTKVTKGGK
☑	1479	650.42	1298.82	1298.62	0.20	0	2	4.1	1	MSVSQVTDASFK
☑	1203	1109.59	1108.58	1108.45	0.13	0	2	8.9	1	DVNDEQSMR + Oxidation (M)
☑	1209	1111.87	3332.58	3332.45	0.13	1	2	10	1	IYDTCIGCTQCVRACPTDVLEMVPWDGCK + 2 Carbamidomethyl (C)
☑	337	666.89	1997.65	1998.05	-0.40	1	2	12	1	MTIQKFITYTPLDLNGK + Oxidation (M)
☑	980	497.34	992.66	992.52	0.14	1	2	4.6	1	EYPELSKK

☑	1770	611.08	1830.22	1829.96	0.26	2	2	4.1	1	QGVEEELAMLKEKQAK
☑	1622	755.88	1509.75	1509.91	-0.15	1	2	4	1	VLPNKLLGVLAMAR + Oxidation (M)
☑	270	624.81	1247.61	1247.61	-0.01	0	2	15	1	LDEFQEQLAR
☑	436	731.28	2190.83	2191.09	-0.25	1	2	14	1	YDSMQASLLADELKYLGFK
☑	1449	638.43	1274.84	1274.68	0.16	1	2	3.7	1	DGLIDTAVKTSR
☑	1755	597.96	1790.86	1791.00	-0.14	1	2	3.9	1	VPVKVEVVGAPAAVDWR
☑	1844	985.52	1969.04	1968.95	0.09	0	2	3.4	1	LMSFSSLPLWTDASAEAK + Oxidation (M)
☑	1889	689.39	2065.14	2065.06	0.08	1	2	3.5	1	TDIERGMVLAQPGTISPHK + Oxidation (M)
☑	968	988.90	2963.67	2963.41	0.26	2	2	12	1	MPKSAIHPDWYPNAKVYCDGQLVMK + Carbamidomethyl (C); Oxidation (M)
☑	1267	1148.29	2294.56	2294.10	0.46	1	2	12	1	QGDIVPGNSHFDTTKGHIESR
☑	1583	718.87	1435.73	1435.74	-0.02	1	2	3.5	1	STITVELMNLMKG
☑	1545	692.42	1382.83	1382.80	0.02	2	2	3.9	1	VHDGIIFQAKKK
☑	640	840.16	839.15	839.44	-0.29	1	2	11	1	RAGFAYR
☑	1576	713.42	1424.82	1424.71	0.11	0	2	3.4	1	FSNSPIFLVCNK + Carbamidomethyl (C)
☑	1291	580.45	1158.89	1158.70	0.19	2	2	4	1	TLKLSDLKNK
☑	1205	555.35	1108.69	1108.61	0.08	1	2	3.6	1	EGISIRHAAR
☑	1069	1034.60	3100.76	3100.43	0.33	1	2	10	1	CNWGIDGTTGKLVDMEEFGVWEPFSVK + Carbamidomethyl (C)
☑	977	496.84	991.66	991.69	-0.03	2	2	5.4	1	IHKKIILK
☑	1376	603.91	1205.80	1205.63	0.16	0	2	4.5	1	QVVTLCSITDK
☑	1528	679.48	1356.94	1356.67	0.27	1	2	4.8	1	NLDFKSVDTYR
☑	1114	1060.64	1059.63	1059.57	0.07	1	2	4.1	1	SVQKLQDSR
☑	139	534.36	1066.71	1066.48	0.24	0	2	9.4	1	EMAQGPSGFK + Oxidation (M)
☑	929	486.67	971.33	971.53	-0.21	1	1	4.3	1	INTCRLPR
☑	1994	776.47	2326.38	2326.15	0.22	1	1	3.3	1	METHFHEWQKSLQLIQQK + Oxidation (M)
☑	1815	640.72	1919.14	1919.03	0.10	2	1	3.3	1	KLLNQMELLLSTCKNR + Oxidation (M)
☑	908	965.40	2893.18	2893.28	-0.10	0	1	11	1	EGIEQVECASTVCQNDNSCPIIADVEK
☑	1541	690.45	1378.88	1378.72	0.16	2	1	3.9	1	VSPGRDRHGVSGR
☑	913	484.35	966.69	966.50	0.19	1	1	3.5	1	DKLSYVDK
☑	1096	1049.17	3144.49	3144.60	-0.11	2	1	14	1	VFWRGVCEELIWFLRGETNAHVLADK + Carbamidomethyl (C)
☑	1367	602.38	1202.75	1202.63	0.12	0	1	6.2	1	MLAQLASNDIK
☑	1299	1165.07	3492.19	3492.27	-0.08	0	1	16	1	CTCPMCCENDCFYTSCDVETGSCIPWPK + 6 Carbamidomethyl (C); Oxidation (M)
☑	1668	804.98	1607.94	1607.83	0.10	1	1	4.4	1	MEIILFDNKINSR + Oxidation (M)
☑	2153	1016.96	3047.85	3047.54	0.31	1	1	3.1	1	VYYPGEIIFDNIKITQPSLCEHINNK
☑	1118	1062.48	3184.41	3184.43	-0.03	2	1	11	1	ILASFFSFNHDQKNDNSEDNRSEDDLK

☑	1303	583.40	1164.79	1164.64	0.16	1	1	3.7	1	ELRHENIVR
☑	1169	545.84	1089.67	1089.65	0.01	2	1	5.6	1	AKEIFIKNK
☑	1599	731.96	1461.91	1461.87	0.03	2	1	3.8	1	QLKQGLFMLLKK + Oxidation (M)
☑	896	961.03	1920.05	1919.91	0.13	1	1	20	1	KELDPNSESEVIEEFR
☑	1343	1188.70	1187.69	1187.63	0.06	1	1	5.2	1	KLMYTFLEK + Oxidation (M)
☑	1874	1013.60	2025.19	2025.09	0.10	1	1	3.6	1	KSHIIYDSPNIELEVLR
☑	263	621.92	620.91	620.31	0.60	0	1	15	1	TSGQTK
☑	1054	1029.63	3085.88	3085.39	0.49	0	1	12	1	NIIGSDAEDVCMCGPEGMIEYACKPALLK + Oxidation (M)
☑	1744	883.98	1765.95	1765.91	0.03	2	1	4.4	1	QQVTEFERTKLMTR
☑	787	908.70	907.70	907.40	0.30	0	1	15	1	GMLCNAGSR
☑	96	491.34	1471.00	1470.71	0.29	1	1	12	1	RFCTGGMSLGALSR + Oxidation (M)
☑	775	903.92	902.91	903.38	-0.47	0	1	8.7	1	DYFATCK + Carbamidomethyl (C)
☑	1569	710.44	1418.86	1418.74	0.12	1	1	4.5	1	VEICDTGIGISKK + Carbamidomethyl (C)
☑	1122	533.86	1065.71	1065.57	0.14	1	1	5.2	1	YLTIKADDK
☑	1790	621.15	1860.43	1859.88	0.55	2	1	7.5	1	MVQEAEKNAAQDKENR
☑	1612	747.45	1492.88	1492.79	0.09	0	1	3.8	1	VQINASNIVSFSSK
☑	1024	1013.70	3038.08	3038.52	-0.44	0	1	15	1	VAVIDVQTHHGPPHYAALGGTCVNVGCVPK
☑	246	616.56	615.56	615.32	0.24	0	1	26	1	CAIPR + Carbamidomethyl (C)
☑	878	952.13	2853.38	2853.31	0.06	1	1	15	1	YFPIFCGWMVGDEFGGVVVREDTSK + Oxidation (M)
☑	1595	726.94	1451.87	1451.90	-0.03	2	1	3.9	1	LAPLIKILWRVM
☑	336	666.82	1331.62	1331.75	-0.13	2	1	17	1	KLIVLDKTCDK + Carbamidomethyl (C)
☑	1868	1011.10	2020.18	2020.00	0.18	1	1	3.4	1	VDDGTNAPGRGAPAGGIPSSPK
☑	722	877.66	2629.96	2630.25	-0.29	2	1	18	1	DFMLNKSNIRNMCVIAHVDHGK + Carbamidomethyl (C); 2 Oxidation (M)
☑	2051	830.56	2488.65	2488.21	0.44	2	1	6.3	1	DGMSIRFDDNAAVIINKENNPR
☑	1600	734.41	1466.81	1466.91	-0.10	1	1	4.7	1	ALITRLVLQVWR
☑	1958	1126.16	2250.30	2250.09	0.21	2	0	3.1	1	AASGGFEKGLDRENEPVLSMK + Oxidation (M)
☑	1307	1167.59	3499.76	3499.76	-0.00	2	0	11	1	QSVCEPMQTGITAIDSMIPIGRGQRELIIGDR + Oxidation (M)
☑	914	967.72	966.71	966.48	0.24	0	0	4.2	1	ADISYATAR
☑	1825	648.43	1942.26	1941.89	0.37	1	0	4.6	1	MAEPFSTILGTDGSGGRCK + Oxidation (M)
☑	1689	830.93	1659.85	1659.89	-0.04	2	0	5.6	1	VNGRLFEVDKVQEK
☑	207	598.92	1195.82	1195.63	0.19	1	0	13	1	KIGMTQIFDK + Oxidation (M)
☑	1060	1031.66	1030.65	1030.61	0.05	0	0	6.1	1	VIDLLAPYK
☑	1655	529.66	1585.95	1585.89	0.06	2	0	4.5	1	IIKVSEIMHGKTSK + Oxidation (M)
☑	188	585.41	1168.81	1168.62	0.19	1	0	15	1	LYKAYTPGTR

☑	262	621.32	1860.95	1860.87	0.08	1	0	15	1	MSTKEVDEQMHAVQTK
☑	408	713.84	712.83	712.42	0.40	0	0	18	1	ISLAPGR
☑	1167	1090.29	3267.83	3267.64	0.19	1	0	19	1	SIKLHPLVCSAFNADFDGDQMGVHIPLSLK + Oxidation (M)
☑	1535	683.51	1365.01	1364.64	0.36	0	0	4.6	1	IACLECGSSQLNK
☑	1218	558.37	1114.73	1114.67	0.06	1	0	5.7	1	TIAKQINSLK
☑	626	834.43	833.42	833.46	-0.04	0	0	16	1	QVDVFVK
☑	158	561.52	1121.02	1120.59	0.43	0	0	23	1	SILQSDGVFR
☑	1076	519.34	1036.67	1036.53	0.14	1	0	4.5	1	TFISDGNKR
☑	1928	720.16	2157.47	2157.99	-0.51	1	0	5.8	1	YGLMGGEGVTMDSAKMQQQK
☑	397	705.59	1409.16	1408.70	0.46	1	0	20	1	LMRVCGLEMSVR + Oxidation (M)
☑	1354	597.85	1193.69	1193.57	0.12	1	0	3.6	1	QRCFLSNNGR
☑	2110	905.17	2712.49	2712.29	0.20	2	0	4.8	1	KRAYDCDITYITNSELGFDYLR + Carbamidomethyl (C)
☑	1638	776.96	1551.91	1551.84	0.07	0	0	5.9	1	GMVLAKPGSITPHTK + Oxidation (M)
☑	1677	542.39	1624.15	1623.87	0.28	2	0	5.8	1	MNLLKHCVVNGPRK + Oxidation (M)
☑	1505	1321.07	1320.06	1320.59	-0.53	2	0	15	1	GGGDRGGRGTGGFGGG
☑	1	*217.30*	*216.29*							
☑	2	*221.12*	*220.11*							
☑	3	*226.23*	*225.22*							
☑	4	*227.03*	*226.02*							
☑	5	*228.35*	*227.35*							
☑	6	*229.07*	*228.06*							
☑	7	*229.18*	*228.17*							
☑	8	*229.24*	*228.23*							
☑	9	*235.22*	*234.21*							
☑	10	*237.29*	*236.28*							
☑	11	*239.15*	*238.14*							
☑	12	*239.18*	*238.17*							
☑	13	*247.10*	*246.09*							
☑	14	*256.26*	*255.25*							
☑	15	*257.30*	*256.29*							
☑	16	*269.03*	*268.03*							
☑	17	*269.04*	*268.03*							
☑	18	*269.05*	*268.04*							
☑	19	*269.25*	*268.25*							

☑	21	*285.03*	*284.02*
☑	22	*285.03*	*284.02*
☑	23	*285.03*	*284.02*
☑	24	*285.06*	*284.05*
☑	25	*285.06*	*284.05*
☑	26	*285.08*	*284.07*
☑	27	*285.08*	*284.08*
☑	28	*285.13*	*284.12*
☑	29	*288.35*	*287.34*
☑	30	*296.90*	*295.90*
☑	31	*297.04*	*296.04*
☑	32	*297.10*	*296.09*
☑	33	*297.12*	*296.11*
☑	34	*297.16*	*296.16*
☑	35	*297.18*	*296.18*
☑	36	*298.27*	*297.26*
☑	37	*299.09*	*298.08*
☑	38	*299.09*	*298.09*
☑	39	*299.16*	*298.15*
☑	40	*299.20*	*298.20*
☑	41	*300.25*	*299.25*
☑	42	*300.46*	*299.46*
☑	43	*351.00*	*349.99*
☑	44	*355.14*	*354.13*
☑	45	*355.14*	*354.13*
☑	46	*355.28*	*354.28*
☑	47	*371.07*	*370.06*
☑	48	*371.08*	*370.08*
☑	49	*371.09*	*370.09*
☑	50	*371.11*	*370.10*
☑	51	*371.16*	*370.15*
☑	52	*371.16*	*370.15*
☑	53	*371.17*	*370.17*
☑	54	*371.18*	*370.17*

☑	55	371.18	370.17
☑	56	371.19	370.18
☑	57	371.19	370.18
☑	58	371.32	370.31
☑	60	388.99	387.98
☑	62	427.40	426.40
☑	63	429.03	428.02
☑	64	429.15	428.15
☑	65	429.17	428.17
☑	66	429.18	428.17
☑	67	429.21	428.20
☑	68	429.21	428.21
☑	69	429.22	428.21
☑	71	445.16	444.15
☑	72	445.17	444.16
☑	73	445.18	444.17
☑	74	445.19	444.18
☑	75	445.21	444.20
☑	76	445.25	444.24
☑	77	445.25	444.24
☑	78	445.27	444.26
☑	79	445.27	444.27
☑	80	446.11	445.10
☑	82	448.89	447.88
☑	83	449.69	448.68
☑	84	449.97	448.96
☑	85	453.91	452.91
☑	86	455.25	454.24
☑	87	460.58	459.57
☑	88	461.73	460.72
☑	89	472.04	471.03
☑	90	479.31	478.30
☑	93	486.09	485.09
☑	94	486.95	485.94

☑	95	488.07	487.06
☑	98	492.45	491.44
☑	99	494.36	493.35
☑	100	496.42	495.41
☑	102	503.09	502.08
☑	103	503.17	502.16
☑	104	505.30	504.29
☑	106	507.11	506.10
☑	107	507.67	506.67
☑	108	508.39	507.38
☑	109	509.85	508.84
☑	110	510.67	509.66
☑	111	512.09	511.08
☑	112	512.26	511.25
☑	113	257.24	512.46
☑	114	513.71	512.71
☑	115	514.43	513.43
☑	116	515.40	514.39
☑	117	515.43	514.42
☑	118	517.00	515.99
☑	119	518.93	517.92
☑	120	519.15	518.15
☑	121	519.16	518.16
☑	122	519.17	518.16
☑	123	519.20	518.19
☑	125	519.25	518.24
☑	126	519.35	518.34
☑	127	523.39	522.38
☑	128	523.83	522.82
☑	129	524.34	523.33
☑	130	524.81	523.80
☑	131	525.08	524.07
☑	132	528.38	527.38
☑	133	528.99	527.99

☑	135	531.33	530.32
☑	137	533.33	532.32
☑	140	536.58	535.57
☑	141	538.19	537.18
☑	142	538.28	537.27
☑	143	542.61	541.60
☑	144	543.96	542.95
☑	145	544.02	543.01
☑	149	548.55	547.54
☑	150	550.06	549.06
☑	151	552.39	551.38
☑	152	552.64	551.64
☑	153	554.04	553.03
☑	154	554.11	553.10
☑	156	559.66	558.66
☑	157	560.64	559.63
☑	159	562.97	561.96
☑	161	563.35	562.34
☑	162	563.58	562.57
☑	163	565.23	564.23
☑	164	567.17	566.16
☑	165	567.30	566.30
☑	166	567.41	566.40
☑	167	568.70	567.69
☑	168	569.00	567.99
☑	169	569.84	568.83
☑	170	571.03	570.02
☑	171	571.61	570.61
☑	172	571.70	570.69
☑	174	572.91	571.90
☑	175	573.09	572.08
☑	176	576.38	575.37
☑	177	576.90	575.89
☑	178	578.40	577.39

☑	179	578.98	577.97
☑	181	579.87	578.86
☑	183	582.09	581.08
☑	184	582.10	581.09
☑	185	582.95	581.94
☑	186	584.38	583.37
☑	187	584.42	583.41
☑	191	586.84	585.83
☑	193	587.39	586.38
☑	194	587.67	586.67
☑	195	589.31	588.30
☑	196	590.36	589.35
☑	198	591.90	590.89
☑	199	592.60	591.59
☑	200	593.14	592.13
☑	201	594.31	593.30
☑	202	594.45	593.45
☑	203	595.03	594.03
☑	204	596.56	595.55
☑	206	597.98	596.97
☑	208	599.13	598.13
☑	209	599.44	598.44
☑	210	599.75	598.74
☑	211	599.80	598.79
☑	212	599.89	598.89
☑	213	600.15	599.14
☑	214	601.92	600.91
☑	215	602.84	601.83
☑	216	603.38	602.37
☑	217	603.61	602.60
☑	218	603.66	602.65
☑	220	603.95	602.95
☑	221	604.05	603.05
☑	222	604.07	603.06

☑	223	604.10	603.10
☑	224	604.72	603.71
☑	225	606.98	605.97
☑	226	606.98	605.97
☑	227	607.39	606.38
☑	228	608.02	607.01
☑	229	608.07	607.06
☑	230	608.31	607.31
☑	231	608.36	607.35
☑	232	609.38	608.38
☑	233	609.64	608.63
☑	234	609.79	608.79
☑	235	611.09	610.08
☑	236	611.93	610.92
☑	237	611.94	610.93
☑	238	612.02	611.02
☑	239	612.80	611.80
☑	240	613.79	612.79
☑	241	613.87	612.86
☑	243	615.02	614.02
☑	244	615.37	614.36
☑	247	617.29	616.29
☑	248	617.62	616.61
☑	249	618.54	617.54
☑	250	618.72	617.71
☑	251	618.82	617.81
☑	252	618.86	617.85
☑	253	619.01	618.00
☑	254	619.02	618.01
☑	255	619.09	618.09
☑	256	619.65	618.65
☑	257	619.89	618.89
☑	258	620.26	619.26
☑	259	620.39	619.38

☑	260	620.48	619.48
☑	261	620.74	619.74
☑	264	622.11	621.10
☑	265	622.80	621.80
☑	267	623.47	622.46
☑	268	623.54	622.53
☑	269	624.79	623.79
☑	271	625.33	624.33
☑	272	626.46	625.45
☑	273	627.08	626.07
☑	275	628.01	627.00
☑	276	628.65	627.64
☑	278	630.64	629.64
☑	280	632.08	631.07
☑	281	633.20	632.19
☑	282	633.95	632.94
☑	283	635.01	634.01
☑	284	637.34	636.33
☑	285	637.37	636.36
☑	286	637.46	636.45
☑	287	637.73	636.73
☑	288	639.09	638.08
☑	289	639.55	638.55
☑	290	640.96	639.96
☑	291	641.16	640.16
☑	292	641.92	640.91
☑	293	641.95	640.94
☑	294	642.38	641.37
☑	296	643.04	642.03
☑	297	643.54	642.54
☑	298	644.21	643.20
☑	300	645.03	644.02
☑	302	646.35	645.34
☑	303	646.60	645.60

☑	304	647.47	646.47
☑	305	647.66	646.65
☑	306	649.74	648.73
☑	307	649.91	648.91
☑	308	650.46	649.45
☑	309	650.50	649.49
☑	310	650.82	649.82
☑	311	651.16	650.15
☑	312	651.33	650.32
☑	315	653.95	652.94
☑	316	654.00	652.99
☑	317	654.09	653.08
☑	318	654.29	653.29
☑	319	327.77	653.52
☑	320	327.81	653.61
☑	321	654.70	653.69
☑	322	656.08	655.07
☑	323	657.11	656.10
☑	324	657.27	656.26
☑	325	657.32	656.31
☑	326	657.43	656.42
☑	327	658.06	657.06
☑	329	661.97	660.96
☑	331	664.47	663.46
☑	333	665.38	664.37
☑	335	666.65	665.64
☑	338	666.95	665.94
☑	339	667.13	666.12
☑	340	667.27	666.27
☑	341	669.45	668.45
☑	342	672.18	671.18
☑	343	672.31	671.31
☑	344	672.66	671.65
☑	345	673.44	672.44

☑	346	673.84	672.84
☑	347	675.33	674.32
☑	348	675.62	674.61
☑	349	675.77	674.77
☑	350	676.74	675.73
☑	351	677.42	676.42
☑	352	678.38	677.37
☑	353	678.54	677.54
☑	354	679.07	678.06
☑	355	681.52	680.52
☑	356	682.11	681.10
☑	357	682.16	681.15
☑	358	682.41	681.40
☑	359	682.55	681.55
☑	360	683.34	682.33
☑	361	683.35	682.34
☑	362	683.40	682.40
☑	363	683.64	682.63
☑	365	685.73	684.72
☑	368	687.62	686.61
☑	369	345.03	688.05
☑	370	689.95	688.95
☑	371	690.02	689.01
☑	372	690.90	689.89
☑	374	692.53	691.53
☑	375	693.12	692.11
☑	376	693.79	692.78
☑	378	694.79	693.78
☑	379	694.84	693.83
☑	381	697.46	696.45
☑	382	698.03	697.02
☑	383	698.42	697.41
☑	384	698.79	697.78
☑	385	699.87	698.86

☑	386	700.49	699.48
☑	387	701.02	700.02
☑	388	702.55	701.54
☑	389	702.84	701.83
☑	390	703.18	702.18
☑	391	703.57	702.56
☑	392	235.24	702.70
☑	393	703.96	702.95
☑	394	704.55	703.54
☑	395	704.71	703.70
☑	396	705.30	704.29
☑	398	706.69	705.68
☑	399	709.52	708.52
☑	400	710.08	709.08
☑	401	710.70	709.69
☑	402	711.10	710.09
☑	403	711.28	710.27
☑	404	712.57	711.56
☑	405	713.23	712.23
☑	406	713.71	712.70
☑	407	713.78	712.77
☑	409	714.77	713.76
☑	410	715.14	714.13
☑	411	239.08	714.23
☑	413	717.60	716.59
☑	414	717.89	716.88
☑	415	718.47	717.46
☑	417	718.96	717.95
☑	418	720.05	719.04
☑	419	720.24	719.24
☑	420	720.29	719.29
☑	421	720.40	719.40
☑	422	722.16	721.15
☑	423	722.42	721.41

☑	424	723.33	722.33
☑	425	723.36	722.35
☑	426	723.52	722.51
☑	427	723.62	722.62
☑	428	724.31	723.30
☑	429	724.38	723.37
☑	430	724.96	723.95
☑	431	728.32	727.31
☑	432	728.85	727.84
☑	433	729.26	728.26
☑	434	729.54	728.53
☑	435	730.05	729.04
☑	437	732.23	731.22
☑	438	732.57	731.56
☑	439	733.20	732.20
☑	440	733.40	732.39
☑	441	734.32	733.31
☑	442	735.01	734.00
☑	443	735.18	734.17
☑	445	737.47	736.46
☑	446	737.69	736.68
☑	447	738.28	737.27
☑	448	739.63	738.62
☑	449	740.06	739.05
☑	450	371.14	740.26
☑	452	741.45	740.44
☑	453	741.58	740.57
☑	455	742.47	741.46
☑	457	743.89	742.88
☑	458	744.04	743.03
☑	459	744.08	743.07
☑	460	745.90	744.89
☑	461	746.03	745.02
☑	462	746.20	745.19

☑	463	746.31	745.30
☑	464	746.72	745.72
☑	465	747.12	746.11
☑	466	747.51	746.50
☑	467	747.70	746.69
☑	468	749.56	748.55
☑	469	751.58	750.57
☑	470	751.89	750.88
☑	471	752.50	751.49
☑	472	752.74	751.73
☑	473	753.00	751.99
☑	474	753.18	752.17
☑	475	754.10	753.09
☑	476	755.39	754.39
☑	477	755.68	754.68
☑	478	755.77	754.76
☑	479	755.80	754.79
☑	480	756.39	755.38
☑	481	756.67	755.67
☑	482	757.15	756.15
☑	483	757.43	756.43
☑	484	757.71	756.70
☑	485	758.45	757.44
☑	486	758.84	757.84
☑	487	759.06	758.05
☑	488	759.33	758.32
☑	490	759.52	758.52
☑	491	760.22	759.21
☑	492	760.32	759.31
☑	493	760.86	759.85
☑	494	761.10	760.10
☑	495	761.52	760.51
☑	496	762.27	761.26
☑	497	762.52	761.51

☑	498	762.96	761.95
☑	499	763.48	762.47
☑	500	764.03	763.02
☑	501	765.02	764.01
☑	502	765.79	764.79
☑	503	766.01	765.00
☑	504	766.28	765.27
☑	505	766.53	765.52
☑	506	766.90	765.89
☑	507	767.46	766.45
☑	508	768.96	767.95
☑	509	769.55	768.55
☑	510	769.89	768.89
☑	511	770.47	769.47
☑	512	771.98	770.97
☑	513	773.46	772.45
☑	514	773.70	772.69
☑	515	774.30	773.30
☑	516	774.55	773.55
☑	517	776.54	775.54
☑	518	777.42	776.41
☑	519	780.13	779.12
☑	521	780.59	779.58
☑	522	782.74	781.73
☑	524	784.55	783.55
☑	525	784.99	783.98
☑	526	785.11	784.10
☑	527	785.53	784.53
☑	528	785.59	784.58
☑	529	785.74	784.73
☑	530	786.99	785.98
☑	531	787.01	786.00
☑	532	787.53	786.53
☑	533	788.04	787.03

☑	534	*788.92*	*787.91*
☑	535	*788.95*	*787.94*
☑	536	*789.78*	*788.78*
☑	538	*790.38*	*789.37*
☑	539	*791.63*	*790.62*
☑	540	*791.98*	*790.97*
☑	541	*791.98*	*790.97*
☑	542	*792.27*	*791.26*
☑	543	*792.52*	*791.52*
☑	544	*792.57*	*791.56*
☑	545	*793.47*	*792.46*
☑	546	*793.55*	*792.54*
☑	547	*793.60*	*792.59*
☑	548	*793.96*	*792.95*
☑	549	*793.97*	*792.96*
☑	550	*794.39*	*793.38*
☑	551	*795.05*	*794.04*
☑	552	*795.23*	*794.22*
☑	553	*796.37*	*795.36*
☑	554	*796.64*	*795.63*
☑	555	*796.69*	*795.68*
☑	556	*797.23*	*796.22*
☑	557	*797.31*	*796.30*
☑	558	*797.49*	*796.49*
☑	560	*798.54*	*797.53*
☑	561	*799.37*	*798.36*
☑	562	*799.43*	*798.42*
☑	563	*799.47*	*798.46*
☑	564	*799.88*	*798.87*
☑	566	*802.48*	*801.47*
☑	567	*803.90*	*802.89*
☑	568	*804.06*	*803.05*
☑	569	*804.14*	*803.13*
☑	570	*804.53*	*803.53*

☑	571	804.59	803.58
☑	572	269.00	803.97
☑	573	805.23	804.22
☑	574	806.12	805.11
☑	575	807.18	806.17
☑	576	807.27	806.26
☑	577	810.28	809.28
☑	578	810.51	809.50
☑	579	811.55	810.54
☑	581	811.76	810.75
☑	582	812.41	811.40
☑	583	812.89	811.88
☑	584	813.05	812.05
☑	585	813.34	812.33
☑	586	814.05	813.04
☑	587	814.84	813.84
☑	588	814.98	813.98
☑	589	815.00	813.99
☑	590	815.38	814.37
☑	591	816.09	815.08
☑	592	816.50	815.49
☑	593	816.51	815.50
☑	594	816.56	815.55
☑	595	817.24	816.23
☑	596	817.30	816.29
☑	597	819.27	818.26
☑	598	819.60	818.60
☑	599	819.89	818.89
☑	600	820.03	819.03
☑	601	820.48	819.47
☑	602	821.27	820.26
☑	603	821.84	820.83
☑	604	822.90	821.89
☑	605	824.57	823.57

☑	607	413.34	824.67
☑	608	826.15	825.14
☑	609	826.41	825.40
☑	610	827.32	826.32
☑	613	414.79	827.56
☑	614	828.84	827.83
☑	615	828.89	827.88
☑	616	829.33	828.32
☑	617	829.82	828.81
☑	618	831.67	830.66
☑	619	831.84	830.83
☑	620	833.15	832.14
☑	621	833.20	832.19
☑	623	833.41	832.41
☑	624	833.44	832.43
☑	625	833.61	832.60
☑	627	835.00	834.00
☑	628	835.44	834.44
☑	629	836.61	835.60
☑	630	836.68	835.68
☑	631	836.77	835.76
☑	632	837.56	836.56
☑	633	837.81	836.80
☑	634	838.15	837.14
☑	635	839.47	838.46
☑	636	420.32	838.63
☑	637	839.66	838.65
☑	638	839.67	838.67
☑	639	840.02	839.01
☑	641	840.47	839.46
☑	642	840.48	839.47
☑	643	840.52	839.51
☑	645	842.49	841.49
☑	646	842.57	841.56

☑	647	421.85	841.68
☑	648	843.82	842.81
☑	649	844.41	843.40
☑	651	845.95	844.94
☑	652	847.46	846.45
☑	653	848.48	847.47
☑	654	848.97	847.96
☑	655	849.61	848.60
☑	656	850.21	849.20
☑	657	850.65	849.64
☑	658	851.20	850.19
☑	659	852.06	851.06
☑	660	285.02	852.04
☑	661	285.06	852.16
☑	662	285.13	852.37
☑	663	853.77	852.76
☑	664	854.28	853.27
☑	665	855.47	854.46
☑	666	855.73	854.72
☑	667	856.73	855.72
☑	668	857.18	856.17
☑	669	429.19	856.37
☑	670	857.87	856.86
☑	671	858.63	857.63
☑	672	860.01	859.00
☑	673	860.68	859.68
☑	674	860.90	859.90
☑	675	861.04	860.03
☑	676	861.45	860.44
☑	677	861.72	860.71
☑	678	862.54	861.53
☑	679	862.76	861.75
☑	680	863.38	862.37
☑	681	863.43	862.42

☑	682	863.52	862.51
☑	683	863.54	862.54
☑	684	432.33	862.64
☑	685	864.12	863.11
☑	686	864.15	863.14
☑	687	865.10	864.09
☑	688	865.83	864.82
☑	689	865.96	864.95
☑	690	866.44	865.44
☑	691	866.80	865.79
☑	692	868.14	867.14
☑	693	869.30	868.30
☑	694	435.27	868.53
☑	695	869.61	868.60
☑	696	869.94	868.93
☑	697	870.79	869.79
☑	698	870.80	869.79
☑	699	871.04	870.03
☑	700	871.40	870.39
☑	701	871.54	870.53
☑	702	872.05	871.04
☑	704	872.59	871.58
☑	705	873.04	872.03
☑	706	873.16	872.16
☑	707	874.06	873.06
☑	708	874.08	873.07
☑	709	874.31	873.31
☑	710	874.47	873.46
☑	712	874.71	873.70
☑	713	875.33	874.32
☑	714	876.38	875.38
☑	715	876.60	875.59
☑	716	876.87	875.86
☑	717	876.91	875.90

☑	718	877.24	876.24
☑	719	877.59	876.58
☑	720	877.66	876.65
☑	723	878.26	877.25
☑	724	878.27	877.26
☑	725	879.05	878.05
☑	726	879.75	878.74
☑	727	880.38	879.38
☑	728	880.71	879.70
☑	729	881.13	880.12
☑	730	881.29	880.28
☑	731	881.46	880.45
☑	732	882.63	881.63
☑	733	882.65	881.64
☑	734	883.34	882.33
☑	735	883.48	882.47
☑	736	883.55	882.55
☑	737	885.21	884.20
☑	738	885.30	884.29
☑	739	885.55	884.54
☑	740	886.48	885.47
☑	741	444.23	886.44
☑	742	888.13	887.12
☑	743	888.39	887.38
☑	744	888.92	887.92
☑	745	889.03	888.02
☑	746	889.25	888.24
☑	747	889.33	888.32
☑	748	890.34	889.33
☑	749	890.48	889.47
☑	750	890.57	889.57
☑	751	892.39	891.39
☑	752	892.96	891.95
☑	753	893.37	892.37

☑	754	893.53	892.52
☑	756	893.94	892.93
☑	757	894.84	893.84
☑	758	895.56	894.55
☑	759	896.10	895.09
☑	760	896.58	895.57
☑	761	449.28	896.54
☑	762	897.63	896.62
☑	765	898.44	897.43
☑	766	898.70	897.69
☑	767	899.21	898.20
☑	768	899.38	898.37
☑	769	899.48	898.47
☑	770	902.67	901.66
☑	771	902.89	901.89
☑	772	903.23	902.22
☑	773	903.37	902.37
☑	774	903.86	902.85
☑	776	904.54	903.53
☑	777	904.71	903.70
☑	778	904.81	903.80
☑	779	905.10	904.09
☑	780	905.58	904.57
☑	781	905.77	904.76
☑	782	906.13	905.13
☑	783	907.43	906.43
☑	785	907.85	906.84
☑	786	908.39	907.38
☑	788	908.96	907.95
☑	789	909.17	908.16
☑	790	909.57	908.57
☑	791	909.77	908.76
☑	792	910.23	909.22
☑	793	910.57	909.56

☑	794	*910.86*	*909.85*
☑	795	*911.92*	*910.92*
☑	796	*912.08*	*911.07*
☑	797	*912.68*	*911.67*
☑	798	*912.73*	*911.72*
☑	800	*914.02*	*913.01*
☑	801	*914.22*	*913.21*
☑	803	*915.05*	*914.05*
☑	804	*915.22*	*914.21*
☑	805	*915.76*	*914.76*
☑	807	*459.61*	*917.21*
☑	808	*918.39*	*917.39*
☑	809	*919.57*	*918.56*
☑	810	*919.81*	*918.81*
☑	811	*920.17*	*919.17*
☑	812	*920.33*	*919.32*
☑	813	*921.72*	*920.71*
☑	814	*922.07*	*921.07*
☑	815	*922.10*	*921.09*
☑	816	*922.12*	*921.11*
☑	817	*922.12*	*921.12*
☑	818	*922.14*	*921.13*
☑	819	*922.20*	*921.19*
☑	820	*922.53*	*921.53*
☑	821	*922.79*	*921.78*
☑	822	*923.05*	*922.04*
☑	823	*924.00*	*923.00*
☑	824	*924.21*	*923.20*
☑	825	*924.30*	*923.30*
☑	828	*925.52*	*924.51*
☑	829	*925.67*	*924.67*
☑	830	*926.26*	*925.26*
☑	831	*464.38*	*926.75*
☑	832	*928.11*	*927.10*

☑	833	928.41	927.40
☑	834	928.99	927.98
☑	835	929.22	928.21
☑	836	929.90	928.89
☑	837	930.35	929.34
☑	839	931.00	929.99
☑	840	931.46	930.45
☑	841	931.64	930.64
☑	842	931.87	930.86
☑	843	931.93	930.93
☑	844	932.73	931.72
☑	845	933.36	932.36
☑	846	935.11	934.10
☑	847	935.13	934.13
☑	848	936.56	935.55
☑	849	936.95	935.94
☑	850	937.23	936.23
☑	851	937.32	936.31
☑	852	937.63	936.62
☑	853	938.45	937.44
☑	854	939.22	938.22
☑	855	939.53	938.52
☑	856	939.53	938.53
☑	858	939.90	938.89
☑	859	940.44	939.44
☑	860	941.51	940.51
☑	861	941.61	940.60
☑	862	941.66	940.65
☑	863	942.93	941.93
☑	864	943.13	942.13
☑	865	943.56	942.55
☑	866	945.48	944.48
☑	867	945.61	944.60
☑	868	945.81	944.80

☑	869	946.23	945.22
☑	870	946.34	945.33
☑	871	473.87	945.72
☑	872	947.28	946.28
☑	873	948.03	947.03
☑	874	949.31	948.30
☑	875	949.40	948.39
☑	876	949.53	948.53
☑	877	950.12	949.11
☑	879	952.22	951.21
☑	880	954.21	953.20
☑	881	954.71	953.70
☑	882	955.21	954.20
☑	883	955.54	954.54
☑	884	956.56	955.55
☑	885	956.71	955.70
☑	886	957.28	956.27
☑	887	958.10	957.09
☑	888	958.35	957.34
☑	889	958.89	957.88
☑	890	959.10	958.09
☑	891	959.70	958.70
☑	892	480.49	958.96
☑	893	960.08	959.07
☑	894	960.26	959.25
☑	895	960.45	959.45
☑	897	961.11	960.10
☑	898	961.26	960.26
☑	899	962.73	961.72
☑	900	962.76	961.76
☑	901	962.78	961.77
☑	903	964.06	963.05
☑	904	482.60	963.18
☑	906	964.63	963.62

☑	907	964.73	963.72
☑	909	965.65	964.64
☑	910	966.26	965.25
☑	911	966.91	965.90
☑	912	484.30	966.58
☑	915	967.84	966.83
☑	916	968.09	967.08
☑	917	968.81	967.80
☑	918	968.86	967.85
☑	919	969.46	968.45
☑	920	970.37	969.36
☑	921	970.76	969.75
☑	922	970.80	969.79
☑	923	971.04	970.03
☑	924	971.41	970.41
☑	925	971.42	970.42
☑	926	971.87	970.86
☑	927	972.10	971.09
☑	930	973.17	972.17
☑	931	973.28	972.28
☑	933	973.77	972.77
☑	934	974.75	973.74
☑	935	974.81	973.80
☑	936	975.11	974.10
☑	937	975.17	974.17
☑	938	975.52	974.51
☑	939	975.57	974.56
☑	940	975.73	974.72
☑	942	976.08	975.07
☑	943	976.75	975.74
☑	944	977.49	976.48
☑	945	489.67	977.33
☑	946	978.71	977.70
☑	947	978.98	977.97

☑	949	979.46	978.46
☑	950	979.49	978.48
☑	951	980.07	979.06
☑	952	981.05	980.05
☑	953	491.11	980.21
☑	954	982.13	981.12
☑	955	982.23	981.22
☑	956	982.49	981.48
☑	957	982.70	981.69
☑	958	983.36	982.36
☑	959	983.55	982.54
☑	960	492.70	983.38
☑	961	984.42	983.42
☑	962	984.92	983.92
☑	963	985.06	984.06
☑	964	985.82	984.81
☑	965	986.70	985.69
☑	966	987.83	986.83
☑	967	988.65	987.64
☑	969	494.99	987.97
☑	971	990.19	989.18
☑	972	990.99	989.98
☑	973	991.54	990.53
☑	974	496.34	990.66
☑	975	991.91	990.90
☑	976	992.61	991.60
☑	978	993.45	992.44
☑	979	993.66	992.66
☑	981	993.77	992.76
☑	982	993.85	992.84
☑	983	993.99	992.98
☑	984	994.42	993.41
☑	985	995.16	994.16
☑	986	498.29	994.56

☑	987	*997.34*	*996.34*
☑	988	*997.42*	*996.41*
☑	989	*499.42*	*996.82*
☑	990	*998.26*	*997.26*
☑	991	*998.45*	*997.45*
☑	992	*998.46*	*997.45*
☑	993	*999.06*	*998.05*
☑	994	*999.15*	*998.15*
☑	995	*999.52*	*998.51*
☑	996	*999.67*	*998.67*
☑	997	*999.91*	*998.90*
☑	998	*1000.21*	*999.20*
☑	1000	*1001.65*	*1000.65*
☑	1001	*1002.07*	*1001.06*
☑	1002	*1002.76*	*1001.75*
☑	1003	*502.27*	*1002.52*
☑	1004	*1003.72*	*1002.72*
☑	1005	*1004.43*	*1003.43*
☑	1006	*1004.58*	*1003.57*
☑	1007	*1004.64*	*1003.63*
☑	1008	*502.91*	*1003.81*
☑	1009	*1005.09*	*1004.08*
☑	1010	*1005.51*	*1004.50*
☑	1011	*1005.91*	*1004.90*
☑	1012	*1006.05*	*1005.04*
☑	1013	*1006.09*	*1005.08*
☑	1014	*1006.39*	*1005.39*
☑	1015	*1006.98*	*1005.97*
☑	1017	*1008.33*	*1007.32*
☑	1018	*1008.34*	*1007.33*
☑	1019	*1010.40*	*1009.40*
☑	1020	*1011.03*	*1010.02*
☑	1021	*1011.34*	*1010.33*
☑	1022	*1011.48*	*1010.48*

☑	1023	*1011.54*	*1010.53*
☑	1025	*1014.03*	*1013.02*
☑	1026	*1014.14*	*1013.13*
☑	1027	*1014.33*	*1013.32*
☑	1028	*1015.39*	*1014.38*
☑	1029	*1015.96*	*1014.95*
☑	1030	*1016.53*	*1015.53*
☑	1031	*1016.99*	*1015.98*
☑	1032	*1017.24*	*1016.23*
☑	1033	*1017.48*	*1016.48*
☑	1034	*1017.85*	*1016.85*
☑	1035	*1018.49*	*1017.48*
☑	1036	*1019.61*	*1018.60*
☑	1037	*1020.21*	*1019.20*
☑	1038	*1022.15*	*1021.14*
☑	1039	*1022.55*	*1021.54*
☑	1040	*1023.16*	*1022.16*
☑	1041	*1023.20*	*1022.19*
☑	1042	*1023.53*	*1022.52*
☑	1043	*1023.72*	*1022.71*
☑	1044	*1024.15*	*1023.14*
☑	1045	*1025.08*	*1024.07*
☑	1048	*1026.64*	*1025.64*
☑	1049	*1026.70*	*1025.70*
☑	1050	*1028.37*	*1027.36*
☑	1051	*1028.77*	*1027.77*
☑	1052	*1029.20*	*1028.19*
☑	1053	*1029.36*	*1028.36*
☑	1055	*1030.18*	*1029.17*
☑	1056	*1030.53*	*1029.53*
☑	1057	*1030.96*	*1029.95*
☑	1058	*1031.32*	*1030.31*
☑	1059	*1031.64*	*1030.63*
☑	1062	*1031.95*	*1030.94*

☑	1064	517.35	1032.69
☑	1065	1033.82	1032.82
☑	1066	1033.85	1032.84
☑	1067	1033.91	1032.90
☑	1068	1034.25	1033.24
☑	1070	1034.62	1033.62
☑	1071	1035.66	1034.66
☑	1073	1035.92	1034.91
☑	1075	1036.80	1035.79
☑	1077	1038.51	1037.50
☑	1078	1038.73	1037.72
☑	1079	1039.28	1038.27
☑	1080	1040.02	1039.01
☑	1082	1041.08	1040.08
☑	1083	1041.10	1040.09
☑	1084	521.39	1040.76
☑	1085	1041.83	1040.82
☑	1086	1042.03	1041.02
☑	1087	1043.01	1042.00
☑	1088	1043.77	1042.76
☑	1089	1044.05	1043.04
☑	1092	1046.59	1045.59
☑	1093	1048.15	1047.15
☑	1094	1048.37	1047.36
☑	1095	1048.71	1047.71
☑	1097	1049.27	1048.26
☑	1098	1050.07	1049.06
☑	1100	1051.44	1050.43
☑	1101	1051.73	1050.72
☑	1102	526.38	1050.76
☑	1103	1052.32	1051.31
☑	1104	527.39	1052.77
☑	1105	1054.02	1053.01
☑	1106	1054.08	1053.07

☑	1107	1054.27	1053.26
☑	1109	1056.36	1055.35
☑	1110	1056.46	1055.46
☑	1111	1058.39	1057.38
☑	1112	1058.62	1057.62
☑	1113	1060.04	1059.03
☑	1115	1061.13	1060.13
☑	1116	1061.31	1060.30
☑	1117	1061.90	1060.89
☑	1119	1064.65	1063.64
☑	1121	533.43	1064.86
☑	1123	1066.96	1065.95
☑	1124	1067.19	1066.19
☑	1125	1067.20	1066.19
☑	1127	1068.06	1067.05
☑	1128	1068.43	1067.42
☑	1129	1068.68	1067.67
☑	1130	1069.60	1068.59
☑	1131	1070.09	1069.09
☑	1132	1071.36	1070.35
☑	1133	1071.72	1070.72
☑	1134	1072.13	1071.12
☑	1135	1072.21	1071.20
☑	1136	1072.40	1071.39
☑	1137	1072.91	1071.90
☑	1138	1073.09	1072.09
☑	1139	1074.57	1073.56
☑	1140	1074.65	1073.64
☑	1141	1075.72	1074.71
☑	1142	1076.12	1075.11
☑	1143	1078.00	1077.00
☑	1144	1079.05	1078.04
☑	1145	540.06	1078.10
☑	1146	1079.82	1078.81

☑	1147	1079.87	1078.86
☑	1148	1080.15	1079.15
☑	1149	1081.89	1080.89
☑	1150	1082.13	1081.12
☑	1151	1083.55	1082.55
☑	1152	1084.22	1083.21
☑	1153	1084.74	1083.73
☑	1154	1084.99	1083.98
☑	1155	1085.18	1084.17
☑	1156	1085.54	1084.53
☑	1157	1086.17	1085.17
☑	1158	1087.72	1086.72
☑	1159	1087.99	1086.98
☑	1160	1088.34	1087.34
☑	1162	1089.14	1088.14
☑	1163	1089.19	1088.19
☑	1164	1089.73	1088.72
☑	1165	1089.83	1088.82
☑	1168	545.78	1089.55
☑	1172	1090.87	1089.86
☑	1173	1091.12	1090.11
☑	1174	1091.17	1090.16
☑	1175	1092.38	1091.37
☑	1177	1093.54	1092.53
☑	1178	1097.08	1096.08
☑	1179	1097.20	1096.19
☑	1180	1097.33	1096.32
☑	1181	1098.24	1097.24
☑	1182	549.90	1097.79
☑	1183	1099.24	1098.23
☑	1184	1099.89	1098.89
☑	1185	550.53	1099.04
☑	1186	1100.61	1099.60
☑	1187	550.87	1099.72

☑	1188	1101.27	1100.26
☑	1189	1101.83	1100.82
☑	1190	1102.24	1101.23
☑	1192	1103.59	1102.59
☑	1195	1106.06	1105.05
☑	1197	1106.65	1105.64
☑	1198	1106.97	1105.96
☑	1200	1108.42	1107.42
☑	1201	1108.63	1107.62
☑	1202	555.26	1108.51
☑	1206	1109.70	1108.69
☑	1207	1109.86	1108.85
☑	1208	556.40	1110.80
☑	1210	1111.90	1110.90
☑	1211	1112.05	1111.04
☑	1212	1113.42	1112.41
☑	1213	1113.50	1112.49
☑	1214	1113.64	1112.64
☑	1215	557.42	1112.83
☑	1216	1114.67	1113.67
☑	1217	1115.45	1114.45
☑	1219	1116.25	1115.24
☑	1221	1116.72	1115.71
☑	1223	1116.84	1115.83
☑	1224	1117.02	1116.02
☑	1226	1118.06	1117.05
☑	1227	1118.76	1117.75
☑	1228	1119.09	1118.08
☑	1229	1119.40	1118.39
☑	1230	1120.16	1119.15
☑	1231	1121.04	1120.03
☑	1232	1121.67	1120.66
☑	1234	1122.40	1121.40
☑	1236	1123.67	1122.66

☑	1237	1124.18	1123.17
☑	1238	563.16	1124.32
☑	1240	1127.30	1126.29
☑	1242	564.90	1127.79
☑	1243	1132.85	1131.84
☑	1244	1133.10	1132.10
☑	1246	1133.82	1132.82
☑	1247	1134.38	1133.37
☑	1248	1135.68	1134.67
☑	1249	1138.65	1137.64
☑	1251	1140.66	1139.65
☑	1252	1140.79	1139.78
☑	1255	1141.70	1140.69
☑	1256	571.40	1140.80
☑	1258	1142.65	1141.65
☑	1260	572.61	1143.20
☑	1261	1144.86	1143.85
☑	1262	1145.61	1144.60
☑	1263	1146.70	1145.69
☑	1264	1146.73	1145.73
☑	1266	1147.06	1146.05
☑	1268	1148.83	1147.82
☑	1270	1150.19	1149.18
☑	1271	1150.32	1149.31
☑	1272	1150.74	1149.73
☑	1273	1151.00	1149.99
☑	1274	1151.65	1150.65
☑	1275	1151.86	1150.85
☑	1276	576.46	1150.91
☑	1277	576.75	1151.48
☑	1278	1152.52	1151.51
☑	1279	576.77	1151.52
☑	1280	577.38	1152.75
☑	1282	578.89	1155.76

☑	1284	1156.83	1155.83
☑	1286	1157.54	1156.53
☑	1287	1158.42	1157.42
☑	1290	1159.70	1158.69
☑	1292	1161.08	1160.08
☑	1293	1161.74	1160.74
☑	1294	1161.83	1160.82
☑	1295	581.96	1161.91
☑	1296	1164.43	1163.42
☑	1297	1164.59	1163.58
☑	1300	1165.37	1164.36
☑	1301	1165.47	1164.46
☑	1302	1165.75	1164.75
☑	1304	583.90	1165.78
☑	1305	1166.89	1165.88
☑	1306	1167.36	1166.36
☑	1308	1168.70	1167.69
☑	1309	1169.04	1168.03
☑	1310	585.90	1169.79
☑	1311	1171.90	1170.89
☑	1312	1173.56	1172.56
☑	1313	1173.58	1172.57
☑	1314	1174.73	1173.73
☑	1316	1177.72	1176.71
☑	1317	1177.85	1176.85
☑	1318	1178.00	1176.99
☑	1319	1178.09	1177.08
☑	1320	1178.24	1177.23
☑	1321	1178.84	1177.83
☑	1323	1179.87	1178.86
☑	1324	1181.20	1180.20
☑	1326	1182.52	1181.51
☑	1327	591.90	1181.78
☑	1328	1182.80	1181.79

☑	1329	1183.05	1182.05
☑	1330	1183.84	1182.83
☑	1331	592.56	1183.10
☑	1333	593.08	1184.14
☑	1334	1185.34	1184.33
☑	1335	1185.71	1184.71
☑	1336	1186.36	1185.35
☑	1337	1186.50	1185.49
☑	1338	593.94	1185.86
☑	1340	594.40	1186.79
☑	1342	1188.01	1187.00
☑	1347	1192.17	1191.16
☑	1348	1192.27	1191.26
☑	1349	1193.69	1192.68
☑	1351	1193.88	1192.87
☑	1352	1194.14	1193.14
☑	1353	1194.55	1193.54
☑	1355	1196.07	1195.06
☑	1356	1196.82	1195.82
☑	1357	599.43	1196.84
☑	1358	1198.31	1197.30
☑	1359	599.90	1197.78
☑	1360	1199.39	1198.39
☑	1361	600.20	1198.39
☑	1362	1200.78	1199.77
☑	1363	1201.63	1200.62
☑	1370	1204.00	1203.00
☑	1371	1204.38	1203.38
☑	1373	1205.30	1204.29
☑	1374	1205.79	1204.78
☑	1375	1205.95	1204.95
☑	1378	1207.39	1206.38
☑	1379	1207.60	1206.59
☑	1380	1208.51	1207.50

☑	1381	*604.91*	*1207.80*
☑	1382	*604.96*	*1207.91*
☑	1383	*1209.77*	*1208.76*
☑	1384	*1210.52*	*1209.52*
☑	1385	*1211.02*	*1210.01*
☑	1386	*606.39*	*1210.77*
☑	1387	*1212.47*	*1211.47*
☑	1388	*1213.51*	*1212.50*
☑	1389	*1214.17*	*1213.16*
☑	1390	*1214.32*	*1213.31*
☑	1391	*1214.72*	*1213.71*
☑	1393	*1215.85*	*1214.84*
☑	1394	*1217.35*	*1216.34*
☑	1395	*1219.90*	*1218.89*
☑	1397	*611.44*	*1220.87*
☑	1398	*1221.96*	*1220.96*
☑	1399	*611.67*	*1221.33*
☑	1400	*1222.61*	*1221.61*
☑	1401	*1225.89*	*1224.89*
☑	1402	*1226.83*	*1225.82*
☑	1403	*1227.31*	*1226.30*
☑	1405	*1231.35*	*1230.34*
☑	1406	*1231.47*	*1230.46*
☑	1407	*617.00*	*1231.99*
☑	1408	*1234.04*	*1233.03*
☑	1409	*1234.27*	*1233.26*
☑	1410	*1234.48*	*1233.47*
☑	1411	*1234.54*	*1233.53*
☑	1413	*1236.05*	*1235.04*
☑	1414	*1236.46*	*1235.45*
☑	1415	*1240.17*	*1239.16*
☑	1416	*1243.24*	*1242.23*
☑	1417	*622.39*	*1242.76*
☑	1418	*1244.53*	*1243.52*

☑	1419	1245.27	1244.26
☑	1420	1247.69	1246.68
☑	1421	1249.64	1248.64
☑	1422	1250.12	1249.11
☑	1423	1251.41	1250.41
☑	1424	1252.21	1251.21
☑	1425	1252.51	1251.50
☑	1426	626.96	1251.91
☑	1427	1254.61	1253.60
☑	1428	627.89	1253.77
☑	1429	1255.05	1254.04
☑	1430	1255.57	1254.56
☑	1432	629.38	1256.74
☑	1433	1258.87	1257.86
☑	1434	1260.85	1259.84
☑	1436	1262.26	1261.26
☑	1437	632.43	1262.85
☑	1438	1265.09	1264.08
☑	1439	633.38	1264.74
☑	1444	1270.52	1269.51
☑	1445	1271.61	1270.60
☑	1446	1272.71	1271.70
☑	1447	636.91	1271.81
☑	1448	638.25	1274.49
☑	1450	1276.15	1275.14
☑	1451	638.78	1275.54
☑	1452	1277.77	1276.76
☑	1453	639.42	1276.83
☑	1455	640.42	1278.82
☑	1456	641.04	1280.07
☑	1457	1281.58	1280.57
☑	1458	1281.89	1280.88
☑	1459	1282.77	1281.76
☑	1460	642.49	1282.96

☑	1462	1287.25	1286.24
☑	1464	1289.57	1288.56
☑	1466	645.34	1288.66
☑	1467	645.56	1289.11
☑	1468	1290.37	1289.36
☑	1469	1291.27	1290.26
☑	1470	1291.72	1290.71
☑	1471	1293.94	1292.93
☑	1472	1295.67	1294.66
☑	1473	1296.12	1295.11
☑	1475	1297.83	1296.82
☑	1476	650.40	1298.78
☑	1483	1301.23	1300.22
☑	1485	1302.33	1301.33
☑	1487	1304.33	1303.32
☑	1488	653.01	1304.01
☑	1491	1308.67	1307.66
☑	1492	654.95	1307.89
☑	1493	655.47	1308.92
☑	1494	656.47	1310.92
☑	1495	1315.70	1314.69
☑	1498	658.86	1315.70
☑	1501	1317.48	1316.47
☑	1502	1317.49	1316.48
☑	1504	660.45	1318.88
☑	1510	666.32	1330.62
☑	1511	667.86	1333.71
☑	1513	1340.27	1339.26
☑	1514	670.87	1339.72
☑	1515	1340.99	1339.98
☑	1517	671.99	1341.97
☑	1518	672.94	1343.87
☑	1519	673.10	1344.19
☑	1520	1347.63	1346.62

☑	1522	675.39	1348.76
☑	1523	1349.77	1348.76
☑	1525	676.02	1350.03
☑	1526	676.95	1351.89
☑	1529	680.34	1358.67
☑	1530	681.43	1360.84
☑	1531	1363.67	1362.66
☑	1533	1365.61	1364.60
☑	1534	683.41	1364.81
☑	1536	1366.22	1365.21
☑	1537	684.44	1366.86
☑	1539	689.44	1376.87
☑	1540	1379.77	1378.76
☑	1543	691.99	1381.96
☑	1544	692.41	1382.80
☑	1546	692.72	1383.43
☑	1550	1388.71	1387.70
☑	1552	1390.44	1389.43
☑	1554	697.47	1392.92
☑	1555	697.51	1393.01
☑	1556	698.01	1394.00
☑	1557	698.49	1394.96
☑	1558	1399.55	1398.54
☑	1559	1401.68	1400.67
☑	1560	702.46	1402.90
☑	1561	703.37	1404.73
☑	1562	703.88	1405.75
☑	1563	703.96	1405.90
☑	1566	708.42	1414.82
☑	1567	709.96	1417.91
☑	1568	710.37	1418.73
☑	1570	710.47	1418.92
☑	1571	710.84	1419.67
☑	1572	710.99	1419.96

☑	1573	711.34	1420.67
☑	1574	711.45	1420.88
☑	1575	712.42	1422.83
☑	1578	476.65	1426.93
☑	1580	714.93	1427.84
☑	1581	717.54	1433.06
☑	1582	717.95	1433.89
☑	1584	719.42	1436.83
☑	1585	719.52	1437.03
☑	1586	720.97	1439.93
☑	1587	722.44	1442.86
☑	1588	1446.15	1445.15
☑	1590	724.56	1447.11
☑	1591	724.93	1447.84
☑	1592	725.45	1448.88
☑	1593	725.82	1449.62
☑	1594	725.91	1449.81
☑	1596	727.46	1452.90
☑	1598	488.30	1461.89
☑	1602	736.48	1470.95
☑	1606	738.47	1474.93
☑	1607	1478.64	1477.63
☑	1608	740.71	1479.40
☑	1610	744.91	1487.81
☑	1611	747.20	1492.39
☑	1613	748.97	1495.93
☑	1616	751.31	1500.60
☑	1617	751.55	1501.09
☑	1618	752.46	1502.91
☑	1619	753.08	1504.14
☑	1620	753.48	1504.94
☑	1621	755.45	1508.88
☑	1623	755.90	1509.78
☑	1624	755.92	1509.82

☑	1625	756.11	1510.21
☑	1626	760.49	1518.96
☑	1627	764.93	1527.85
☑	1628	765.01	1528.00
☑	1629	765.80	1529.59
☑	1630	770.00	1537.98
☑	1631	514.64	1540.91
☑	1632	771.84	1541.67
☑	1635	774.25	1546.49
☑	1636	775.33	1548.65
☑	1637	775.47	1548.93
☑	1640	522.09	1563.25
☑	1641	782.75	1563.50
☑	1642	784.28	1566.55
☑	1643	785.92	1569.83
☑	1644	786.06	1570.10
☑	1645	786.30	1570.59
☑	1646	787.03	1572.04
☑	1647	788.55	1575.08
☑	1649	789.79	1577.56
☑	1651	793.04	1584.07
☑	1652	793.15	1584.29
☑	1653	793.89	1585.76
☑	1657	794.48	1586.95
☑	1658	794.64	1587.26
☑	1659	794.86	1587.71
☑	1660	795.13	1588.24
☑	1661	795.36	1588.70
☑	1662	800.05	1598.08
☑	1663	800.83	1599.65
☑	1665	803.43	1604.85
☑	1666	803.45	1604.89
☑	1669	537.01	1608.01
☑	1670	538.63	1612.86

☑	1671	807.92	1613.84
☑	1672	540.23	1617.67
☑	1673	809.91	1617.80
☑	1676	812.81	1623.60
☑	1678	813.63	1625.25
☑	1679	814.53	1627.04
☑	1680	815.05	1628.09
☑	1682	547.42	1639.23
☑	1683	820.84	1639.67
☑	1684	820.96	1639.91
☑	1685	821.17	1640.32
☑	1686	821.44	1640.87
☑	1687	829.46	1656.91
☑	1688	829.93	1657.86
☑	1690	832.02	1662.02
☑	1691	556.50	1666.48
☑	1692	834.95	1667.89
☑	1693	835.56	1669.10
☑	1694	836.10	1670.18
☑	1695	836.37	1670.73
☑	1696	836.54	1671.07
☑	1697	836.60	1671.18
☑	1698	837.56	1673.10
☑	1699	838.00	1673.98
☑	1700	838.46	1674.90
☑	1701	841.91	1681.80
☑	1702	842.30	1682.60
☑	1704	844.48	1686.94
☑	1705	563.59	1687.74
☑	1706	845.28	1688.55
☑	1707	846.50	1690.99
☑	1708	846.96	1691.91
☑	1710	847.89	1693.77
☑	1711	849.06	1696.10

☑	1712	*850.06*	*1698.10*
☑	1714	*850.19*	*1698.37*
☑	1715	*850.74*	*1699.46*
☑	1716	*851.43*	*1700.84*
☑	1717	*851.59*	*1701.16*
☑	1718	*568.61*	*1702.81*
☑	1719	*854.47*	*1706.93*
☑	1720	*857.83*	*1713.64*
☑	1723	*859.03*	*1716.05*
☑	1724	*859.51*	*1717.00*
☑	1725	*860.53*	*1719.04*
☑	1726	*864.03*	*1726.05*
☑	1727	*870.08*	*1738.15*
☑	1728	*870.41*	*1738.81*
☑	1729	*580.78*	*1739.32*
☑	1730	*581.79*	*1742.34*
☑	1731	*872.53*	*1743.05*
☑	1732	*872.54*	*1743.06*
☑	1733	*873.09*	*1744.17*
☑	1736	*875.23*	*1748.44*
☑	1737	*876.44*	*1750.86*
☑	1738	*584.83*	*1751.46*
☑	1739	*877.09*	*1752.16*
☑	1740	*879.80*	*1757.58*
☑	1741	*881.51*	*1761.01*
☑	1742	*881.53*	*1761.05*
☑	1743	*883.45*	*1764.88*
☑	1745	*592.01*	*1773.01*
☑	1746	*592.03*	*1773.08*
☑	1747	*888.05*	*1774.09*
☑	1748	*892.88*	*1783.74*
☑	1749	*596.02*	*1785.05*
☑	1750	*894.06*	*1786.10*
☑	1752	*896.00*	*1789.98*

☑	1754	*896.42*	*1790.82*
☑	1756	*898.44*	*1794.87*
☑	1759	*899.34*	*1796.67*
☑	1760	*899.87*	*1797.72*
☑	1761	*900.05*	*1798.09*
☑	1762	*600.38*	*1798.13*
☑	1764	*604.12*	*1809.34*
☑	1765	*909.04*	*1816.06*
☑	1766	*909.33*	*1816.65*
☑	1767	*607.43*	*1819.26*
☑	1769	*915.35*	*1828.68*
☑	1771	*916.32*	*1830.62*
☑	1772	*916.60*	*1831.18*
☑	1773	*611.79*	*1832.34*
☑	1774	*612.35*	*1834.01*
☑	1776	*919.03*	*1836.05*
☑	1777	*919.04*	*1836.06*
☑	1779	*613.08*	*1836.23*
☑	1781	*613.61*	*1837.81*
☑	1782	*920.06*	*1838.11*
☑	1783	*923.13*	*1844.26*
☑	1784	*615.93*	*1844.77*
☑	1786	*926.24*	*1850.46*
☑	1787	*926.59*	*1851.17*
☑	1788	*619.09*	*1854.24*
☑	1789	*929.09*	*1856.17*
☑	1791	*621.32*	*1860.93*
☑	1793	*932.30*	*1862.60*
☑	1794	*933.86*	*1865.70*
☑	1795	*937.40*	*1872.79*
☑	1796	*938.83*	*1875.64*
☑	1798	*939.65*	*1877.28*
☑	1799	*942.23*	*1882.45*
☑	1800	*942.69*	*1883.37*

☑	1801	943.04	1884.06
☑	1802	630.03	1887.06
☑	1803	944.60	1887.19
☑	1804	631.85	1892.52
☑	1805	949.54	1897.07
☑	1806	949.92	1897.82
☑	1807	951.01	1900.01
☑	1808	635.02	1902.04
☑	1809	952.40	1902.78
☑	1811	955.47	1908.92
☑	1812	955.64	1909.26
☑	1813	960.25	1918.48
☑	1814	960.26	1918.51
☑	1816	641.09	1920.26
☑	1817	641.45	1921.32
☑	1818	963.07	1924.12
☑	1820	966.72	1931.43
☑	1821	967.47	1932.93
☑	1822	969.77	1937.52
☑	1823	970.48	1938.94
☑	1824	971.93	1941.85
☑	1826	972.60	1943.19
☑	1827	973.64	1945.28
☑	1828	974.07	1946.12
☑	1829	975.42	1948.82
☑	1830	975.71	1949.41
☑	1831	979.42	1956.82
☑	1833	979.93	1957.86
☑	1834	980.03	1958.04
☑	1835	980.56	1959.11
☑	1836	982.58	1963.14
☑	1837	982.61	1963.21
☑	1838	655.82	1964.45
☑	1839	983.69	1965.37

☑	1840	656.41	1966.20
☑	1842	984.55	1967.09
☑	1843	984.78	1967.56
☑	1845	987.74	1973.46
☑	1846	991.45	1980.89
☑	1847	992.26	1982.50
☑	1848	993.61	1985.21
☑	1849	994.08	1986.15
☑	1850	994.26	1986.51
☑	1851	994.54	1987.06
☑	1852	997.56	1993.10
☑	1853	997.59	1993.17
☑	1854	665.41	1993.22
☑	1856	665.85	1994.53
☑	1857	999.06	1996.10
☑	1858	999.54	1997.07
☑	1859	999.58	1997.14
☑	1860	1003.51	2005.01
☑	1861	1003.71	2005.40
☑	1862	1004.06	2006.11
☑	1863	1006.47	2010.92
☑	1864	1008.83	2015.64
☑	1865	672.95	2015.83
☑	1866	673.22	2016.63
☑	1867	1011.06	2020.10
☑	1869	674.64	2020.90
☑	1870	1011.56	2021.10
☑	1871	674.81	2021.40
☑	1872	1011.99	2021.97
☑	1873	1013.00	2023.99
☑	1875	676.77	2027.29
☑	1876	677.53	2029.58
☑	1877	1015.89	2029.76
☑	1878	1016.09	2030.16

☑	1879	678.14	2031.40
☑	1880	678.15	2031.44
☑	1881	678.38	2032.13
☑	1882	679.22	2034.63
☑	1883	679.96	2036.85
☑	1884	682.25	2043.74
☑	1885	1027.52	2053.03
☑	1887	687.40	2059.19
☑	1888	688.20	2061.57
☑	1890	689.92	2066.73
☑	1891	1036.75	2071.49
☑	1892	1040.09	2078.16
☑	1893	1041.03	2080.05
☑	1894	1042.44	2082.86
☑	1895	1046.25	2090.49
☑	1896	699.41	2095.21
☑	1897	1048.64	2095.27
☑	1898	699.45	2095.32
☑	1899	1048.91	2095.81
☑	1900	700.41	2098.21
☑	1901	1050.18	2098.34
☑	1902	1050.71	2099.41
☑	1903	1051.44	2100.88
☑	1904	1051.61	2101.20
☑	1905	1053.04	2104.07
☑	1906	703.05	2106.12
☑	1907	1057.17	2112.33
☑	1908	706.03	2115.08
☑	1909	707.26	2118.76
☑	1910	708.89	2123.65
☑	1911	1064.13	2126.25
☑	1912	1067.10	2132.19
☑	1913	714.07	2139.20
☑	1914	1070.64	2139.26

☑	1915	714.48	2140.41
☑	1916	1071.72	2141.43
☑	1917	1073.41	2144.81
☑	1918	1075.28	2148.54
☑	1919	1075.71	2149.40
☑	1920	718.00	2150.98
☑	1921	718.13	2151.38
☑	1922	719.02	2154.04
☑	1923	1078.81	2155.61
☑	1924	1079.02	2156.02
☑	1925	720.10	2157.28
☑	1926	1079.67	2157.33
☑	1927	720.13	2157.36
☑	1929	1081.47	2160.93
☑	1930	722.13	2163.36
☑	1931	1082.90	2163.78
☑	1932	1083.12	2164.24
☑	1933	1084.79	2167.57
☑	1934	1086.11	2170.20
☑	1935	724.41	2170.22
☑	1936	724.44	2170.30
☑	1937	725.56	2173.66
☑	1939	726.41	2176.21
☑	1940	728.11	2181.31
☑	1941	1094.09	2186.16
☑	1942	729.74	2186.19
☑	1943	732.67	2194.99
☑	1944	1100.90	2199.78
☑	1945	1101.45	2200.89
☑	1946	1103.51	2205.00
☑	1947	737.81	2210.40
☑	1948	1109.32	2216.62
☑	1949	740.74	2219.19
☑	1950	741.98	2222.92

☑	1951	*1114.91*	*2227.82*
☑	1952	*744.15*	*2229.42*
☑	1953	*1117.09*	*2232.16*
☑	1954	*746.80*	*2237.39*
☑	1955	*1119.90*	*2237.78*
☑	1956	*747.51*	*2239.50*
☑	1957	*750.19*	*2247.55*
☑	1959	*751.14*	*2250.40*
☑	1960	*751.43*	*2251.27*
☑	1961	*751.48*	*2251.41*
☑	1962	*1126.99*	*2251.96*
☑	1963	*1127.34*	*2252.66*
☑	1964	*753.03*	*2256.07*
☑	1965	*1129.63*	*2257.24*
☑	1966	*1132.72*	*2263.43*
☑	1967	*1135.43*	*2268.85*
☑	1968	*1136.32*	*2270.62*
☑	1969	*1138.10*	*2274.19*
☑	1970	*1140.53*	*2279.05*
☑	1971	*1140.88*	*2279.74*
☑	1972	*1141.25*	*2280.49*
☑	1973	*761.54*	*2281.61*
☑	1974	*761.59*	*2281.76*
☑	1975	*761.61*	*2281.82*
☑	1976	*761.75*	*2282.24*
☑	1977	*761.82*	*2282.43*
☑	1978	*1142.34*	*2282.66*
☑	1979	*762.12*	*2283.33*
☑	1980	*762.15*	*2283.44*
☑	1981	*762.36*	*2284.06*
☑	1983	*1144.06*	*2286.10*
☑	1984	*763.08*	*2286.22*
☑	1985	*766.07*	*2295.20*
☑	1986	*1148.69*	*2295.37*

☑	1987	766.15	2295.43
☑	1988	767.23	2298.67
☑	1989	767.47	2299.39
☑	1990	767.54	2299.61
☑	1991	770.42	2308.25
☑	1992	1162.04	2322.07
☑	1993	1162.64	2323.27
☑	1995	1166.66	2331.31
☑	1996	1167.62	2333.22
☑	1997	1168.64	2335.27
☑	1998	1170.72	2339.43
☑	1999	783.87	2348.60
☑	2000	1175.80	2349.59
☑	2001	1177.02	2352.02
☑	2002	1177.64	2353.26
☑	2003	785.75	2354.24
☑	2004	1181.56	2361.11
☑	2005	788.77	2363.29
☑	2006	789.23	2364.68
☑	2007	1183.69	2365.37
☑	2008	789.54	2365.60
☑	2009	1184.27	2366.53
☑	2010	1184.30	2366.58
☑	2011	1188.18	2374.34
☑	2012	792.48	2374.43
☑	2013	1188.49	2374.97
☑	2015	1192.06	2382.11
☑	2016	795.42	2383.24
☑	2017	1192.63	2383.25
☑	2018	1195.72	2389.42
☑	2019	1195.95	2389.90
☑	2020	798.33	2391.98
☑	2021	1197.08	2392.15
☑	2022	799.14	2394.39

☑	2023	802.15	2403.43
☑	2024	1202.83	2403.64
☑	2025	802.72	2405.14
☑	2026	1203.60	2405.18
☑	2027	1209.86	2417.70
☑	2028	807.85	2420.53
☑	2029	808.41	2422.22
☑	2030	808.54	2422.60
☑	2031	1215.93	2429.86
☑	2032	812.03	2433.07
☑	2033	812.47	2434.39
☑	2034	1219.94	2437.87
☑	2035	1220.06	2438.11
☑	2037	814.85	2441.53
☑	2038	1227.28	2452.55
☑	2039	1227.73	2453.44
☑	2040	818.86	2453.56
☑	2041	820.89	2459.65
☑	2042	823.38	2467.12
☑	2043	824.74	2471.20
☑	2044	1237.19	2472.37
☑	2045	825.51	2473.51
☑	2046	826.14	2475.40
☑	2047	826.29	2475.86
☑	2048	828.46	2482.37
☑	2049	1243.39	2484.78
☑	2050	1243.75	2485.48
☑	2052	1245.41	2488.81
☑	2053	831.17	2490.49
☑	2054	1249.53	2497.05
☑	2055	835.60	2503.77
☑	2056	836.50	2506.46
☑	2057	836.60	2506.77
☑	2058	1255.67	2509.32

☑	2059	837.47	2509.40
☑	2060	839.42	2515.25
☑	2061	839.49	2515.43
☑	2062	1258.75	2515.49
☑	2063	840.87	2519.59
☑	2064	842.39	2524.16
☑	2065	842.51	2524.52
☑	2066	1263.54	2525.06
☑	2067	843.16	2526.45
☑	2068	845.12	2532.34
☑	2069	846.16	2535.47
☑	2070	849.20	2544.57
☑	2071	1274.09	2546.16
☑	2073	850.85	2549.52
☑	2074	852.73	2555.16
☑	2075	1280.13	2558.24
☑	2076	854.59	2560.76
☑	2077	855.80	2564.38
☑	2078	855.84	2564.50
☑	2079	1283.60	2565.19
☑	2080	856.19	2565.55
☑	2081	857.13	2568.37
☑	2082	858.55	2572.63
☑	2083	1287.67	2573.33
☑	2084	1290.81	2579.60
☑	2085	863.71	2588.12
☑	2086	866.88	2597.62
☑	2087	867.17	2598.49
☑	2088	868.52	2602.53
☑	2089	875.78	2624.32
☑	2090	876.22	2625.63
☑	2091	876.84	2627.50
☑	2092	877.60	2629.79
☑	2094	882.85	2645.51

☑	2095	889.37	2665.08
☑	2096	890.64	2668.90
☑	2097	1345.27	2688.53
☑	2098	899.44	2695.29
☑	2099	900.66	2698.96
☑	2100	901.58	2701.71
☑	2101	901.73	2702.16
☑	2102	902.36	2704.05
☑	2103	902.46	2704.37
☑	2104	902.56	2704.66
☑	2105	903.77	2708.28
☑	2106	904.67	2711.00
☑	2107	904.73	2711.18
☑	2108	904.99	2711.93
☑	2109	905.09	2712.25
☑	2111	905.76	2714.27
☑	2112	905.78	2714.31
☑	2113	906.47	2716.39
☑	2114	906.48	2716.41
☑	2115	906.94	2717.79
☑	2116	907.41	2719.21
☑	2117	910.45	2728.32
☑	2118	911.04	2730.10
☑	2119	913.75	2738.24
☑	2120	914.87	2741.60
☑	2121	918.85	2753.53
☑	2122	924.49	2770.43
☑	2123	926.97	2777.87
☑	2124	929.51	2785.50
☑	2125	931.65	2791.93
☑	2126	936.83	2807.47
☑	2127	937.37	2809.09
☑	2128	943.04	2826.10
☑	2129	947.10	2838.28

☑	2130	*954.79*	*2861.36*
☑	2131	*958.23*	*2871.67*
☑	2132	*964.35*	*2890.04*
☑	2133	*968.20*	*2901.58*
☑	2134	*968.63*	*2902.87*
☑	2135	*969.26*	*2904.75*
☑	2136	*977.13*	*2928.38*
☑	2137	*984.33*	*2949.98*
☑	2138	*985.44*	*2953.31*
☑	2139	*988.17*	*2961.49*
☑	2140	*988.46*	*2962.34*
☑	2141	*990.77*	*2969.29*
☑	2143	*992.73*	*2975.16*
☑	2144	*995.45*	*2983.33*
☑	2145	*995.46*	*2983.36*
☑	2146	*996.91*	*2987.71*
☑	2147	*999.61*	*2995.81*
☑	2148	*1001.63*	*3001.86*
☑	2149	*1002.72*	*3005.13*
☑	2150	*1007.27*	*3018.78*
☑	2151	*1007.89*	*3020.64*
☑	2152	*1009.43*	*3025.27*
☑	2154	*1017.51*	*3049.50*
☑	2155	*1018.26*	*3051.75*
☑	2156	*1020.47*	*3058.39*
☑	2157	*1021.02*	*3060.03*
☑	2158	*1021.05*	*3060.13*
☑	2159	*1021.79*	*3062.35*
☑	2160	*1026.11*	*3075.29*
☑	2161	*1027.09*	*3078.24*
☑	2162	*1030.23*	*3087.68*
☑	2163	*1031.68*	*3092.02*
☑	2164	*1032.25*	*3093.72*
☑	2165	*1034.91*	*3101.70*

☑	2166	*1038.30*	*3111.86*
☑	2167	*1038.89*	*3113.66*
☑	2168	*1040.68*	*3119.02*
☑	2169	*1043.54*	*3127.60*
☑	2170	*1045.45*	*3133.33*
☑	2171	*1046.70*	*3137.07*
☑	2172	*1047.83*	*3140.47*
☑	2173	*1054.56*	*3160.66*
☑	2174	*1057.24*	*3168.69*
☑	2175	*1057.98*	*3170.92*
☑	2176	*1066.97*	*3197.89*
☑	2177	*1074.53*	*3220.56*
☑	2178	*1075.17*	*3222.50*
☑	2179	*1075.45*	*3223.33*
☑	2180	*1079.50*	*3235.48*
☑	2181	*1082.46*	*3244.37*
☑	2182	*1084.11*	*3249.31*
☑	2183	*1088.92*	*3263.73*
☑	2184	*1088.94*	*3263.79*
☑	2185	*1095.52*	*3283.53*
☑	2186	*1095.77*	*3284.30*
☑	2187	*1095.87*	*3284.59*
☑	2188	*1100.42*	*3298.25*
☑	2189	*1102.84*	*3305.49*
☑	2190	*1104.87*	*3311.60*
☑	2191	*1117.47*	*3349.39*
☑	2192	*1117.67*	*3350.00*
☑	2193	*1117.72*	*3350.13*
☑	2194	*1121.69*	*3362.05*
☑	2195	*1121.73*	*3362.18*
☑	2196	*1130.15*	*3387.44*
☑	2197	*1131.55*	*3391.63*
☑	2198	*1141.06*	*3420.16*
☑	2199	*1142.61*	*3424.81*

☑	2200	*1146.78*	*3437.31*
☑	2201	*1151.24*	*3450.69*
☑	2202	*1155.62*	*3463.83*
☑	2203	*1158.78*	*3473.30*
☑	2204	*1180.13*	*3537.38*
☑	2205	*1180.22*	*3537.65*
☑	2206	*1183.24*	*3546.70*
☑	2207	*1187.16*	*3558.47*
☑	2208	*1188.93*	*3563.76*
☑	2209	*1190.06*	*3567.15*
☑	2210	*1210.71*	*3629.12*
☑	2211	*1231.51*	*3691.50*
☑	2212	*1240.37*	*3718.09*
☑	2213	*1246.90*	*3737.68*

Search Parameters

```
Type of search         : MS/MS Ion Search
Enzyme                 : Trypsin
Variable modifications : Carbamidomethyl (C),Oxidation (M)
Mass values            : Monoisotopic
Protein Mass           : Unrestricted
Peptide Mass Tolerance : ± 0.6 Da
Fragment Mass Tolerance: ± 0.3 Da
Max Missed Cleavages   : 2
Instrument type        : ESI-TRAP
Number of queries      : 2213
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Mascot: http://www.matrixscience.com/