

## Supplementary Table 1

### A List of c-Src Kinase Substrates identified by SILAC

(Amanchy et al., Identification of c-Src Tyrosine Kinase Substrates in Platelet-Derived Growth Factor Receptor Signaling)

| Accession Number | Protein Name               | Number of Peptides | Sequence Coverage (%) | Sequence                | Charge | Score |
|------------------|----------------------------|--------------------|-----------------------|-------------------------|--------|-------|
| NP_112442.2      | heat shock protein 8       | 21                 | 37                    | ARFEELNADLFR            | 3      | 64    |
|                  |                            |                    |                       | DAGTIAGLNVLR            | 2      | 75    |
|                  |                            |                    |                       | EIAEAYLGK               | 2      | 50    |
|                  |                            |                    |                       | FDDAVVQSDMK             | 2      | 69    |
|                  |                            |                    |                       | FEELNADLFR              | 2      | 83    |
|                  |                            |                    |                       | FELTGIPPAPR             | 2      | 48    |
|                  |                            |                    |                       | IINEPTAAAIYGLDK         | 2      | 111   |
|                  |                            |                    |                       | IINEPTAAAIYGLDKK        | 3      | 88    |
|                  |                            |                    |                       | LLQDFFNGK               | 2      | 49    |
|                  |                            |                    |                       | MKEIAEAYLGK             | 2      | 58    |
|                  |                            |                    |                       | MVNHFIAEFK              | 2      | 63    |
|                  |                            |                    |                       | NQVAMNPTNTVFDK          | 2      | 115   |
|                  |                            |                    |                       | NSLESYAFNMK             | 2      | 62    |
|                  |                            |                    |                       | QTQTFTTYSQNPVLIQVYEGER  | 3      | 56    |
|                  |                            |                    |                       | RFDDAVVQSDMK            | 2      | 54    |
|                  |                            |                    |                       | SFYPEEVSSMVLTK          | 2      | 68    |
|                  |                            |                    |                       | SINPDEAVAYGAAVQAAILSGDK | 3      | 108   |
|                  |                            |                    |                       | STAGDTHLGGEDFNR         | 2      | 58    |
|                  |                            |                    |                       | TTPSYVAFTDTER           | 2      | 67    |
|                  |                            |                    |                       | TVTNAVVTVPAYFNDSQR      | 2      | 49    |
|                  |                            |                    |                       | VEIANDQGNR              | 2      | 63    |
| NP_032328.2      | heat shock protein 1, beta | 20                 | 29.4                  | ADLINNLGTIAK            | 2      | 86    |
|                  |                            |                    |                       | ALLFIPR                 | 2      | 47    |
|                  |                            |                    |                       | APFDLFENK               | 2      | 58    |
|                  |                            |                    |                       | EDQTEYLEER              | 2      | 71    |

| Accession Number    | Protein Name               | Number of Peptides | Sequence Coverage (%) | Sequence               | Charge | Score |
|---------------------|----------------------------|--------------------|-----------------------|------------------------|--------|-------|
| NP_032328.2         | heat shock protein 1, beta | 20                 | 29.4                  | EGLELPEDEEEK           | 2      | 69    |
|                     |                            |                    |                       | EKYIDQEELNK            | 2      | 57    |
|                     |                            |                    |                       | ELISNASDALDK           | 2      | 99    |
|                     |                            |                    |                       | EQVANSAFVER            | 2      | 68    |
|                     |                            |                    |                       | FYEAFSK                | 2      | 46    |
|                     |                            |                    |                       | GVVDSIDLPLNISR         | 2      | 95    |
|                     |                            |                    |                       | HFSVEGQLEFR            | 2      | 55    |
|                     |                            |                    |                       | HSQFIGYPITLYLEK        | 3      | 74    |
|                     |                            |                    |                       | IDIIPNPQER             | 2      | 58    |
|                     |                            |                    |                       | KHLEINPDHPIVETLR       | 4      | 43    |
|                     |                            |                    |                       | SIYYITGESK             | 2      | 45    |
|                     |                            |                    |                       | TLTLVDTGIGMTK          | 2      | 84    |
|                     |                            |                    |                       | YESLTDPSK              | 2      | 60    |
|                     |                            |                    |                       | YESLTDPSKLDGK          | 2      | 82    |
| YHTSQSGDEMTSLSEYVSR | 3                          | 55                 |                       |                        |        |       |
| YIDQEELNK           | 2                          | 55                 |                       |                        |        |       |
| NP_034611.1         | heat shock protein 9       | 16                 | 35.1                  | AQFEGIVTDLIK           | 2      | 73    |
|                     |                            |                    |                       | DAGQISGLNVLR           | 2      | 62    |
|                     |                            |                    |                       | EQQIVIQSSGGLSKDDIENMVK | 3      | 66    |
|                     |                            |                    |                       | LLGQFTLIGIPPAPR        | 2      | 89    |
|                     |                            |                    |                       | LYSPSQIGAFVLMK         | 2      | 68    |
|                     |                            |                    |                       | MKETAENYLGHYAK         | 3      | 53    |
|                     |                            |                    |                       | NAVITVPAYFNDSQR        | 2      | 46    |
|                     |                            |                    |                       | QAASSLQQASLK           | 2      | 71    |
|                     |                            |                    |                       | QAVTNPNTFYATK          | 2      | 94    |
|                     |                            |                    |                       | SDIGEVILVGGMTR         | 2      | 64    |
|                     |                            |                    |                       | SQVFSTAADGQTQVEIK      | 3      | 75    |
|                     |                            |                    |                       | STNGDTFLGGEDFDQALLR    | 3      | 52    |
| TTPSVVAFTADGER      | 2                          | 82                 |                       |                        |        |       |

| Accession Number | Protein Name            | Number of Peptides | Sequence Coverage (%) | Sequence                | Charge | Score |
|------------------|-------------------------|--------------------|-----------------------|-------------------------|--------|-------|
| NP_034611.1      | heat shock protein 9    | 16                 | 35.1                  | VEAVNMAEGIIHDTETK       | 3      | 74    |
|                  |                         |                    |                       | VINEPTAAALAYGLDK        | 2      | 91    |
|                  |                         |                    |                       | VQQTVQDLFGR             | 2      | 78    |
|                  |                         |                    |                       | AAYEAELGDAR             | 2      | 54    |
|                  |                         |                    |                       | DLEALLNSK               | 2      | 44    |
|                  |                         |                    |                       | EAALSTALSEK             | 2      | 69    |
|                  |                         |                    |                       | EDLQELNDR               | 2      | 60    |
|                  |                         |                    |                       | EGDLLAAQAR              | 2      | 52    |
|                  |                         |                    |                       | IDSLSAQLSQLQK           | 2      | 84    |
|                  |                         |                    |                       | ITSEEVVSR               | 2      | 91    |
| NP_001002011.1   | lamin A isoform A       | 16                 | 24.8                  | LADALQELR               | 2      | 64    |
|                  |                         |                    |                       | LKDLEALLNSK             | 2      | 49    |
|                  |                         |                    |                       | LQLELSK                 | 2      | 46    |
|                  |                         |                    |                       | LRDLEDLAR               | 3      | 45    |
|                  |                         |                    |                       | MQQQLDEYQELLDIK         | 2      | 96    |
|                  |                         |                    |                       | SGAQASSTPLSPTR          | 2      | 67    |
|                  |                         |                    |                       | SLETENAGLR              | 2      | 64    |
|                  |                         |                    |                       | TALINSTGEEVAMR          | 2      | 79    |
|                  |                         |                    |                       | VAVEEVDEEGK             | 2      | 77    |
|                  |                         |                    |                       | APIIAVTR                | 2      | 43    |
| NP_035229.2      | pyruvate kinase, muscle | 14                 | 32                    | EATESFASDPILYRPVAVALDTK | 3      | 58    |
|                  |                         |                    |                       | FGVEQDVMVFASFIR         | 2      | 74    |
|                  |                         |                    |                       | GADFLVTEVENGGSLGSK      | 2      | 72    |
|                  |                         |                    |                       | GDLGIEIPAEK             | 2      | 56    |
|                  |                         |                    |                       | GDYPLEAVR               | 2      | 46    |
|                  |                         |                    |                       | GSGTAEVELK              | 2      | 62    |
|                  |                         |                    |                       | GVNLPGAAVDLPVAVSEK      | 2      | 64    |
|                  |                         |                    |                       | ITLDNAYMEK              | 2      | 61    |
|                  |                         |                    |                       | IYVDDGLISLQVK           | 2      | 89    |
|                  |                         |                    |                       | KGVNLPGAAVDLPVAVSEK     | 3      | 57    |

| Accession Number | Protein Name                      | Number of Peptides | Sequence Coverage (%) | Sequence                  | Charge | Score |
|------------------|-----------------------------------|--------------------|-----------------------|---------------------------|--------|-------|
| NP_035229.2      | pyruvate kinase, muscle           | 14                 | 32                    | LAPITSDPTEAAAVGAVEASFK    | 2      | 82    |
|                  |                                   |                    |                       | LDIDSAPITAR               | 2      | 57    |
|                  |                                   |                    |                       | VNLAMDVGK                 | 2      | 58    |
| NP_034607.3      | heat shock protein 1 (chaperonin) | 14                 | 19.5                  | ALMLQGVDLLADAVAVTMGPK     | 3      | 78    |
|                  |                                   |                    |                       | GVMLAVDAVIAELKK           | 3      | 59    |
|                  |                                   |                    |                       | GYISPYFINTSK              | 2      | 45    |
|                  |                                   |                    |                       | ILQSSSEVGYDAMLGDFVNMVEK   | 3      | 82    |
|                  |                                   |                    |                       | ISSVQSIVPALEIANAHR        | 3      | 48    |
|                  |                                   |                    |                       | KISSVQSIVPALEIANAHR       | 4      | 45    |
|                  |                                   |                    |                       | LSDGVAVLK                 | 2      | 75    |
|                  |                                   |                    |                       | LVQDVANNTNEEAGDGTATVLR    | 3      | 84    |
|                  |                                   |                    |                       | NAGVEGSLIVEK              | 2      | 49    |
|                  |                                   |                    |                       | TALLDAAGVASLLTTAEAVVTEIPK | 3      | 107   |
|                  |                                   |                    |                       | TLNDELEIIIEGMK            | 2      | 78    |
|                  |                                   |                    |                       | VGEVIVTKDDAMLLK           | 3      | 43    |
|                  |                                   |                    |                       | VGGTSDVEVNEK              | 2      | 91    |
|                  |                                   |                    |                       | VGLQVVAVK                 | 2      | 78    |
| NP_033529.3      | Valosin containing protein        | 14                 | 22.7                  | ELQELVQYPVEHPDK           | 2      | 81    |
|                  |                                   |                    |                       | ESIESEIR                  | 2      | 74    |
|                  |                                   |                    |                       | EVDIGIPDATGR              | 2      | 47    |
|                  |                                   |                    |                       | GDDLSTAILK                | 2      | 88    |
|                  |                                   |                    |                       | GDIFLVR                   | 2      | 44    |
|                  |                                   |                    |                       | IVSQLLTMDGLK              | 2      | 87    |
|                  |                                   |                    |                       | KYEMFAQTLQQSR             | 3      | 60    |
|                  |                                   |                    |                       | LDQLIYIPLPDEK             | 2      | 71    |
|                  |                                   |                    |                       | LIVDEAINEDNSVVSLSQPK      | 2      | 84    |
|                  |                                   |                    |                       | MDELQLFR                  | 2      | 66    |
|                  |                                   |                    |                       | NAPAIIFIDELDAIAPK         | 3      | 99    |
|                  |                                   |                    |                       | QTNPSAMEVEEDDPVPEIR       | 3      | 50    |
|                  |                                   |                    |                       | VINQILTEMDGMSTK           | 2      | 75    |
|                  |                                   |                    |                       | VLFFDELDSIAK              | 2      | 65    |

| Accession Number | Protein Name                               | Number of Peptides | Sequence Coverage (%) | Sequence                | Charge | Score |
|------------------|--|--------------------|-----------------------|-------------------------|--------|-------|
| NP_598862.1      | proteasome 26S non-ATPase subunit 2        | 11                 | 16                    | AVPLALALISVSNPR         | 2      | 110   |
|                  |  |                    |                       | DKEQELSEEDKQLQDELEMLVER | 4      | 56    |
|                  |  |                    |                       | DKTPVQSQQPSATTPSGADEK   | 3      | 47    |
|                  |  |                    |                       | EDVLTLLLPMGDSK          | 2      | 57    |
|                  |  |                    |                       | EPLTLVK                 | 2      | 47    |
|                  |  |                    |                       | LAQGLTHLGK              | 2      | 57    |
|                  |  |                    |                       | LKEIYENMAPGENK          | 3      | 46    |
|                  |  |                    |                       | SSTTSMTSVPKPLK          | 2      | 73    |
|                  |  |                    |                       | TPVQSQQPSATTPSGADEK     | 2      | 91    |
|                  |  |                    |                       | VGQAVDVVGQAGKPK         | 3      | 61    |
|                  |  |                    |                       | YLYSSEDYIK              | 2      | 47    |
| NP_031933.1      | eukaryotic translation elongation factor 2 | 10                 | 15.9                  | ALLELQLEPEELYQTFQR      | 3      | 60    |
|                  |  |                    |                       | ARPPDGLAEDIDKGEVSAR     | 3      | 66    |
|                  |  |                    |                       | EGIPALDNFLDKL           | 2      | 66    |
|                  |  |                    |                       | GHVFEESQVAGTPMFVVK      | 3      | 80    |
|                  |  |                    |                       | GPLMMYISK               | 2      | 46    |
|                  |  |                    |                       | IMGPNYTPGK              | 2      | 45    |
|                  |  |                    |                       | QFAEMYVAK               | 2      | 61    |
|                  |  |                    |                       | STAISLFYELSENDLNFIK     | 3      | 90    |
|                  |  |                    |                       | VFSGVVSTGLK             | 2      | 49    |
| VNFTVDQIR        | 2  | 71                 |                       |                         |        |       |
| NP_001003908.1   | clathrin, heavy polypeptide (Hc)           | 10                 | 7.3                   | AFMTADLPNELIELLEK       | 3      | 63    |
|                  |  |                    |                       | ALEHFTDLYDIK            | 3      | 47    |
|                  |  |                    |                       | GQFSTDELVAEVEK          | 2      | 104   |
|                  |  |                    |                       | IYIDSNNNPER             | 2      | 82    |
|                  |  |                    |                       | LLYNNVSNFGR             | 2      | 74    |
|                  |  |                    |                       | NLQNLLILTAIK            | 2      | 61    |
|                  |  |                    |                       | NNLAGAEELFAR            | 2      | 68    |
| RPISADSAIMNPASK  | 3  | 56                 |                       |                         |        |       |

| Accession Number    | Protein Name                     | Number of Peptides | Sequence Coverage (%) | Sequence             | Charge  | Score |
|---------------------|----------------------------------|--------------------|-----------------------|----------------------|---|-------|
| NP_001003908.1      | clathrin, heavy polypeptide (Hc) | 10                 | 7.3                   | TLQIFNIEMK           | 2   | 60    |
|                     |                                  |                    |                       | VANVELYYK            | 2   | 48    |
| NP_031623.1         | calnexin                         | 9                  | 19.1                  | AEDEILNR             | 2   | 58    |
|                     |                                  |                    |                       | APVPTGEVYFADSFDR     | 2   | 77    |
|                     |                                  |                    |                       | DEEEEEKLEEK          | 2   | 97    |
|                     |                                  |                    |                       | IPNPdffedLEPFK       | 2   | 65    |
|                     |                                  |                    |                       | KIPNPdffedLEPFK      | 3   | 62    |
|                     |                                  |                    |                       | SDAEEDGVTGSQDEEDSKPK | 3   | 59    |
|                     |                                  |                    |                       | TAELSLDQFHDK         | 2   | 72    |
|                     |                                  |                    |                       | TDAPQPDVKDEEGKEEEK   | 3   | 58    |
|                     |                                  |                    |                       | TPYTIMFGPDK          | 2   | 54    |
|                     |                                  |                    |                       | NP_031969.1          | epidermal growth factor receptor pathway substrate 15 | 9     |
| DQFALAFHLINQK       | 3                                | 48                 |                       |                      |   |       |
| IDPFGGDPFK          | 2                                | 47                 |                       |                      |   |       |
| LNQQEQEDLELAIALSK   | 3                                | 48                 |                       |                      |   |       |
| NITGSSPVADFSAIK     | 2                                | 64                 |                       |                      |   |       |
| QQVQELLGELDEQK      | 2                                | 59                 |                       |                      |   |       |
| SGLPDLILGK          | 2                                | 52                 |                       |                      |   |       |
| VLALDAAFLK          | 2                                | 60                 |                       |                      |   |       |
| YDAIFDSLSPVDGFLSGDK | 2                                | 61                 |                       |                      |   |       |
| NP_598798.1         | ATP citrate lyase                | 9                  | 12.7                  |                      |   |       |
|                     |                                  |                    |                       | DEPSVAAMVYPFTGDHK    | 3   | 48    |
|                     |                                  |                    |                       | DLVSSLTSGLLTIGDR     | 2   | 95    |
|                     |                                  |                    |                       | EAYPEEAYIADLDAK      | 2   | 70    |
|                     |                                  |                    |                       | GQELIYAGMPITEVFK     | 2   | 64    |
|                     |                                  |                    |                       | IGNTGGMLDNILASK      | 2   | 97    |
|                     |                                  |                    |                       | LGLVGVNLSLDGVK       | 2   | 66    |
|                     |                                  |                    |                       | QHFPATPLLDYALEVEK    | 3   | 47    |
| TIAIAEGIPEALTR      | 2                                | 103                |                       |                      |   |       |

| Accession Number | Protein Name                    | Number of Peptides | Sequence Coverage (%) | Sequence          | Charge | Score |
|------------------|---------------------------------|--------------------|-----------------------|-------------------|--------|-------|
| NP_034610.1      | heat shock protein 1, alpha     | 8                  | 25.9                  | ALLFVPR           | 2      | 48    |
|                  |                                 |                    |                       | APFDLFENR         | 2      | 52    |
|                  |                                 |                    |                       | DQVANSAFVER       | 2      | 74    |
|                  |                                 |                    |                       | ELISNSSDALDK      | 2      | 87    |
|                  |                                 |                    |                       | HIYFITGETK        | 2      | 56    |
|                  |                                 |                    |                       | HSQFIGYPITLFVEK   | 3      | 68    |
|                  |                                 |                    |                       | NPDDITNEEYGEFYK   | 2      | 62    |
|                  |                                 |                    |                       | YYTSASGDEMVSLLK   | 2      | 43    |
| NP_075373.1      | vacuolar protein sorting 35     | 7                  | 10.8                  | ESPESEGPIYEGLLI   | 2      | 49    |
|                  |                                 |                    |                       | ILVGTNLVR         | 2      | 58    |
|                  |                                 |                    |                       | IPVDTYNNILTVLK    | 2      | 81    |
|                  |                                 |                    |                       | LFDIFSQQVATVIQSR  | 3      | 51    |
|                  |                                 |                    |                       | LLDEAIQAVK        | 2      | 76    |
|                  |                                 |                    |                       | LSQLEGVNVER       | 2      | 75    |
|                  |                                 |                    |                       | VLETTVEIFNK       | 2      | 61    |
| NP_031829.2      | cortactin                       | 6                  | 11.4                  | ANFENLAK          | 2      | 44    |
|                  |                                 |                    |                       | NASTFEEVVQVPSAYQK | 2      | 78    |
|                  |                                 |                    |                       | QDSSAVGFDYK       | 2      | 66    |
|                  |                                 |                    |                       | VDKSAVGFEYQGK     | 2      | 104   |
|                  |                                 |                    |                       | YGLFPANYVELR      | 2      | 60    |
|                  |                                 |                    |                       | YGLFPANYVELRQ     | 2      | 44    |
| NP_034963.2      | moesin                          | 6                  | 12.3                  | ALTSELANAR        | 2      | 64    |
|                  |                                 |                    |                       | APDFVIFYAPR       | 2      | 51    |
|                  |                                 |                    |                       | EDAVLEYLK         | 2      | 71    |
|                  |                                 |                    |                       | FYPEDVSEELIQDITQR | 2      | 71    |
|                  |                                 |                    |                       | IAQDLEMYGVNYFSIK  | 2      | 78    |
|                  |                                 |                    |                       | QRIDEFESM         | 2      | 46    |
| NP_058017.1      | stress-induced phosphoprotein 1 | 6                  | 10.3                  | AAALEFLNR         | 2      | 70    |
|                  |                                 |                    |                       | DPQALSEHLK        | 2      | 45    |

| Accession Number | Protein Name  | Number of Peptides | Sequence Coverage (%) | Sequence                | Charge | Score |
|------------------|---|--------------------|-----------------------|-------------------------|--------|-------|
| NP_058017.1      | stress-induced phosphoprotein 1   | 6                  | 10.3                  | FMNPFNLPNLYQK           | 2      | 54    |
|                  |   |                    |                       | KFMNPFNLPNLYQK          | 3      | 46    |
|                  |   |                    |                       | LAYINPDLALEEK           | 2      | 71    |
|                  |   |                    |                       | LMDVGLIAIR              | 2      | 75    |
| NP_032867.1      | phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2 (p85 beta) | 6                  | 15.1                  | APSPDTAVHALASAFGPLLLR   | 3      | 51    |
|                  |   |                    |                       | GFLALPAAVVTPEAAAEAYR    | 3      | 45    |
|                  |   |                    |                       | IPPSGGEGDGESEVPDFPVLLER | 3      | 56    |
|                  |   |                    |                       | TAIEAFNETIK             | 2      | 75    |
|                  |   |                    |                       | TATGFGFAEPYNLYGSLK      | 2      | 61    |
| VALQALGVADGGER   | 2   | 47                 |                       |                         |        |       |
| NP_035853.2      | xanthine dehydrogenase  | 5                  | 5.2                   | DPPANVQLFQEVPK          | 2      | 74    |
|                  |   |                    |                       | IPAFGSIPIEFR            | 2      | 56    |
|                  |   |                    |                       | ITYEDLPAIITIQDAIK       | 3      | 53    |
|                  |   |                    |                       | LDPTFASATLLFQK          | 2      | 51    |
|                  |   |                    |                       | QLFQLDSPATPEK           | 2      | 66    |
| NP_035500.1      | cytoplasmic FMR1 interacting protein 1                                      | 5                  | 4.5                   | LADQIFAYYK              | 2      | 62    |
|                  |   |                    |                       | NVIQSVLQAIR             | 2      | 50    |
|                  |   |                    |                       | SLLQGTILQYVK            | 2      | 75    |
|                  |   |                    |                       | SSLEGPTILDIEK           | 2      | 49    |
|                  |   |                    |                       | TMLESLIADK              | 2      | 44    |
| NP_035945.1      | FYN binding protein   | 4                  | 6.1                   | DLQIKPGESLEVIQSTDDTK    | 3      | 60    |
|                  |   |                    |                       | FMPAAQDTDSKPR           | 3      | 49    |
|                  |   |                    |                       | NSLNAVPPR               | 2      | 43    |
|                  |   |                    |                       | VSESDNNEGSSLPSQHK       | 3      | 72    |
| NP_079555.1      | heterogeneous nuclear ribonucleoprotein K                                   | 4                  | 14                    | GSYGDLDGGPIITTQVTIPK    | 2      | 76    |
|                  |   |                    |                       | IDEPLEGSEDR             | 2      | 54    |
|                  |   |                    |                       | IILDLISESPIK            | 2      | 97    |
|                  |   |                    |                       | IITITGTQDQIQNAQYLLQNSVK | 3      | 67    |
| NP_149065.2      | threonyl-tRNA synthetase  | 4                  | 6.4                   | IYGISFPDPK              | 2      | 57    |
|                  |   |                    |                       | MIAILTENYGGK            | 2      | 72    |

| Accession Number | Protein Name   | Number of Peptides | Sequence Coverage (%) | Sequence             | Charge | Score |
|------------------|--|--------------------|-----------------------|----------------------|--------|-------|
| NP_149065.2      | threonyl-tRNA synthetase   | 4                  | 6.4                   | NELSGALTGLTR         | 2      | 74    |
|                  |  |                    |                       | QLENSLNEFGEK         | 2      | 71    |
| NP_038744.1      | ras-GTPase-activating protein SH3-domain binding protein                   | 3                  | 9.9                   | DFFQNFQNVVELR        | 2      | 61    |
|                  |  |                    |                       | FMQTFVLAPEGSVANK     | 2      | 82    |
|                  |  |                    |                       | LPNFGFVVFDDSEPVQK    | 2      | 73    |
| NP_035332.1      | protein tyrosine phosphatase, non-receptor type 11 isoform                 | 3                  | 6.2                   | FDSLTDLVEHYK         | 3      | 56    |
|                  |  |                    |                       | NPMVETLGTVLQLK       | 3      | 48    |
|                  |  |                    |                       | SNPGDFTLSVR          | 2      | 45    |
| NP_001020126.1   | phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1 isoform 1 | 3                  | 12.3                  | DTADGTFLVR           | 2      | 45    |
|                  |  |                    |                       | TATGYGFAEPYNLYSSLK   | 3      | 48    |
|                  |  |                    |                       | YQQDQVVKEDNIEAVGK    | 3      | 58    |
| NP_058028.1      | cytidine 5'-triphosphate synthase  | 3                  | 6.4                   | FSDSYASVIK           | 2      | 62    |
|                  |  |                    |                       | GVIASSVGTILK         | 2      | 68    |
|                  |  |                    |                       | VPLLLLEEQQVVDYFLR    | 3      | 48    |
| NP_032835.1      | platelet derived growth factor receptor, beta polypeptide                  | 3                  | 3.6                   | LLETLGDEVEIAELHR     | 3      | 44    |
|                  |  |                    |                       | LVEPVTDYLFVPSR       | 2      | 78    |
|                  |  |                    |                       | YVSELILVR            | 2      | 55    |
| NP_067255.2      | phospholipase C, gamma 1   | 3                  | 2.6                   | NMLSQVNYR            | 2      | 51    |
|                  |  |                    |                       | NNYSEDLELASLLIK      | 2      | 82    |
|                  |  |                    |                       | YPINEEALEK           | 2      | 53    |
| NP_001028472.2   | guanine monphosphate synthetase  | 3                  | 7.4                   | EPPTDVTPTFLTGTGLSTLR | 3      | 44    |
|                  |  |                    |                       | LMQITSLHSLNAFLPIK    | 3      | 44    |
|                  |  |                    |                       | SGNIVAGIANESK        | 2      | 59    |
| NP_033536.2      | villin 2   | 3                  | 11.6                  | DSAMLEYLK            | 2      | 52    |
|                  |  |                    |                       | IALLEEAR             | 2      | 43    |
|                  |  |                    |                       | SQEQLAAELAEYTK       | 3      | 57    |
| NP_034743.2      | KH-type splicing regulatory protein  | 3                  | 5.4                   | IGQQPQQPGAPPQQDYTK   | 3      | 51    |
|                  |  |                    |                       | IINDLLQSLR           | 2      | 43    |
|                  |  |                    |                       | VGGGIDVPVPR          | 2      | 60    |

| Accession Number | Protein Name                                       | Number of Peptides | Sequence Coverage (%) | Sequence           | Charge | Score |
|------------------|--|--------------------|-----------------------|--------------------|--------|-------|
| NP_742012.1      | isoleucyl-tRNA synthetase                          | 3                  | 2.1                   | FFIQNVFR           | 2      | 51    |
|                  |  |                    |                       | LFILTEAR           | 2      | 44    |
|                  |  |                    |                       | TVVTSVFGVK         | 2      | 51    |
| NP_032895.1      | cytosolic phospholipase A2, group IVA              | 3                  | 6.1                   | LHDLMYFNTLNNIDVIK  | 3      | 50    |
|                  |  |                    |                       | DVPVVAILGSGGGFR    | 2      | 61    |
|                  |  |                    |                       | NVSHNPLLLLTPOK     | 3      | 44    |
| NP_034200.4      | docking protein 1                                  | 2                  | 3.9                   | GLYDLPQEPR         | 2      | 43    |
|                  |  |                    |                       | VGQAQDILR          | 2      | 68    |
| NP_035718.1      | tripartite motif protein 28                        | 2                  | 1.8                   | LDLDTSDSQPPVFK     | 2      | 91    |
|                  |  |                    |                       | ADVQSIIGLQR        | 2      | 45    |
| NP_035449.1      | seryl-aminoacyl-tRNA synthetase                    | 2                  | 4.9                   | EVMQEVAQLSQFDEELYK | 3      | 46    |
|                  |  |                    |                       | VLDLDFR            | 2      | 54    |
| NP_919323.1      | unc-84 homolog B                                   | 2                  | 3                     | EAAASLGQILQK       | 2      | 63    |
|                  |  |                    |                       | LEAQLASLR          | 2      | 51    |
| NP_001028465.1   | UDP-N-acetylglucosamine pyrophosphorylase 1-like 1 | 2                  | 5.1                   | AALLAELASLEADALR   | 3      | 57    |
|                  |  |                    |                       | FVFDVFQFAK         | 2      | 46    |
| NP_032080.2      | protein-tyrosine kinase fyn                        | 2                  | 3                     | GSLLDFLK           | 2      | 47    |
|                  |  |                    |                       | IADFGLAR           | 2      | 47    |
| NP_476513.2      | far upstream element (FUSE) binding protein 1      | 2                  | 2.5                   | EMVLEIIR           | 2      | 45    |
|                  |  |                    |                       | LLDQIVEK           | 2      | 45    |
| NP_033924.2      | calpain 2  | 2                  | 3                     | IMVDMLDEDGSGK      | 2      | 46    |
|                  |  |                    |                       | SDTFINLR           | 2      | 51    |