

Supplemental File 4. Sequences of the predominant proteins in 2-DE spots identified by MS/MS. For spots 2c and 2d, sequences of both the predominant protein and the purinin are provided.

gi|224589270 (spots 1a,1c)

MATTLATDVRLSIAHQTRFALRLASTISSNPKSAASNAAFSPVSLHSALSLAAGAGSATRDQLVATLGTGE
VEGLHALAEQVVQFVLADASSAGGPRVAFANGVFVDASLLLKPSFQELAVCKYKAETQSVDFQTKAAEVTTQ
VNSWVEKVTSGRIKNILPSGSVDNNTTKLVLANALYFKGAWTDQFDSYGTKNDFYLLDGSSVQTPFMSSMDD
DQYISSSDGLKVLKLPYKQGGDNRFQSMYILLPEAPGGLSLLAEKLSAEPDFLERHIPRQRVAIRQFKLPKF
KISFGIEASDLLKCLGLQLPFSDEADFSEMVDSPMPQGLRVSSVFHQAFVEVNEQGTEAAASTAIKMVPQQA
RPPSVMDFIADHPFLFLLREDISGVVLFMGHVVNPLRSL

BU_serpin#2 (spots 1b,1d)

MATTLATDVRLSIAHQTRFALRLASTISSNPKSAASNAVFSPVSLHVALSLAAGAGSATRDQLVTTLGTGE
VEGLHALAEQVVQFVLADASSAGGPHVAFANGVFVDASLLLKPSFQELAVCKYKAETQSVDFQTKAAEVTAQ
VNSWVEKVTSGRIKDILPSGSVDNNTTKLVLANALYFKGAWTDQFDSYGTKNDFYLLPDGSSVQTPFMSSMDD
QYLSDDGLKVLKLPYKQGGDKRQFSMYILLPEAPGGLSNLAEKLSAEPDFLERHIPRQRVALRQFKLPKFK
ISFETEASDLLKCLGLQLPFSNEADFSEMVDSPMAHGLRVSSVFHQAFVEVNEQGTEAAASTAIKMALLQAR
PPSVMDFIADHPFLFLLREDISGVVLFMGHVVNPLSS

gi|475621781 (spots 1e,1g)

MATTLATDVRLSIAHQTRFAFRLASAISSNPSTVNNAAFSPVSLHVALSLITAGAGGATRNLAAATLGE
VEGLHALAEQVVQFVLADASNIGGPRVAFANGVFVDASLQLKPSFQELAVCKYKAEAQSVDFQTKAAEVTAQ
VNSWVEKVTGLIKDILPAGSIDNNTTLVLGNALYFKGAWTDQFDPRAQSDDFYLLDGSSIQTPFMYSSEE
QYISSSDGLKVLKLPYKQGGDKRQFSMYILLPEALSGLWSLAEKLSAEPDFLEQHIPRQKVALRQFKLPKFK
ISLGIASDLLKCLGLQLPFGAEADLSEMVDSPMAQNLIISSIFHKAFVEVNETGTEAAATTIAKVVLRQAP
PPSVLDFIVDHPFLFLIREDTSGVVLFIGHVVNPLSS

gi|871551 (spot 1f)

MATTLATDVRLSIAHQTRFALRLASTISSNPKSAASNAAFSPVSLYSALSLAAGAGSATRDQLVATLGT
GKVEGLHALAEQVVQFVLADASSSTGGSACRFANGVFVDASLLLKPSFQEIIVCKYKAETQSVDFQTKAAE
VTTQVNSWVEKVTSGRIKDILPPGSIDNNTTKLVLANALYFKGAWTEQFDSYGTKNDFYLLDGSSVQTPF
MSSMDDQYLLSSDGLKVLKLPYKQGGDNRFQFMYILLPEAPGGLSLLAEKLSAEPDFLERHIPRQRVALR
QFKLPKFKISFGIEASDLLKCLGLQLPFGDEADFSEMVDSPMAQNLIISSIFHKAFVEVNETGTEAAAST
AIKMVLQQAARPPSVMDFIADHPFLFLVREDISGVVLFMGHVVNPLSS

BU_purin#3 (spots 2a,2e)

MKKFLVLAALIVVAATTTAAEPFTAFRSAWEPQHPSPEHQPTPQPQEHVPVHQKLNPCRDALLQCCSPVADM
SFLRSQVVQHSSCLVMWEQCCQQLKAIPKQSRCEAIHNVVHAIILQQQQQLVQATSTQPQQQQQQGQQQQGQ
LGSSQPQQQTQLDQGWIAVIGTWVIQTIPAMCDVHVPPYCYTTIISPSDVTTDMGGY

BU_purin#2 (spots 2b,2d)

MKKFLVLAALIVIAATTTAAEPFTAFRIASEPQHPSPEQQPTLQPQEHVPVHQKLNPCRDALLHQCS
SFLRSQVVQHSSCLVMWEQCCQQLKAIPKQSRCEAIHNVVHAIILQQQQLVQGTSTQPQQQQQQGQQEHGQ
GSSQPQHQQQQQLDQGWIAVIGTWVIQTVAMPVHVPPYCYTTIISPSDVTTDMGGY

RS_UWI_15510 (spot 2c)

gsqqqrarsslvsimpGLTIGDTPVNLLELDSTHGKIWIHDYVGNVYVILFVSHPGDFTPVCTTELAAMANY
AKEFEKRGVKLLGISCDVQSHKEWTKDIEAYKAGSKVTYPIMADPDRSAIKQLNMVDPDEKDAEQLP
LHIVGPDKKVLSFLYPSCTGRNMDEVVRAVDSLLTAAKHKVPANWKPGEVVIAPGVSDDAEAKMFPQG
FETADLPSSKGYLRFTKVacvrassaparlllavcvvvvrayfcggtcrffckstsvselcmctvtlslsc
vfffagvscvrspvypcvgrllkkkkk

BU_purin#1 (spot 2c)

MKKFLVLAALIVVAATTTAAEPFTAFRTAWEPHPHPSPEQQPTPQPQEQPVVHQKLNPCRDALLQCCSPVADM
SFLRSQVVQHSSCLVMWEQCCQQLKAIPKQSRCEAIHNVVHAIIVLQQQQQLVQGI STQPQQQQQQGQQQQGQ
GSSQPQQQTQLDQGWIAVIGTWVIQTIPAMCDVHVPPYCYTTIISPSIDVTTDMGGY

gi|475538570 (spot 2d)

MSRGSAGYDRHITIFSPEGRLYQVEYAFKAVKSAGVTSIGVRGKDSVCVVTQKKVPDKLLDDTSITHLF
SITKYTGLLATGLTADARSLVSQARNEAAEFKRWGYEMPVDVLAKWIADKAQIYTTQHAYMRPLGVVAMV
LGYDEEKNAQLFKCDPAGHFFGHKATSAGLKEQEAINFLEKKMKDSPQFTYDETVOIAIASALQSVLQEDF
KATEIEVGVVRKEDRVFRSLTTEEIDQHLTAISERD

gi|56480630 (spot 3a)
SGPWWCYPGQAFQVPALPGCRPLLKLCNQSQVPEAVLRDCCQQLADI SEWCRCGALYSMLDSMYKEHGVSE
GQAGTGAFPSRREVVKLTAA SITAVCRLPIVVDASGDGAYVCKDVAAYPDA

gi|253783731 (spot 3b)
TGPYCYAGMGLPINPLEGCREYVAQQTGCGISISGSAVSTEPGNTPRDRCCCKELYDASQHCRCCEAVRYFIGRR
SDPNSSVLKDLPGCPREPQRDFAKVLVTPGHCVNMTVHNAPYCLGLDI

gi|134034637 (spots 3c, 3d)
SGPWSWCDPATGYKVSALTGCRAMVKLQCVGSQVPEAVLRDCCQQLADINNEWCRCDLSSMLRSVYQELGV
REGKEVLPGCRKEVMKLTAA SVPEVCKVPIPNPSGDRAGVCYWAAYPDA

gi|123956 (spot 3e)
MASKSSITHLLLA AVLVS VFAAAAATGPYCYPGMGLPSNPLEGCREYVAQQTGCGVIGVSPVSTEPGNTF
RDRCCCKELYDASQHCRCCEAVRYFIGRTSDPNSGVLKDLPGCPREPQRDFAKVLVTPGHCVNMTVHNTPYC
LGLDI

gi|54778511 (spot 3f)
SGPWWCYPGYAFKVPALPGCRPVLLKLCNQSQVPEAVLRECCQQLADI SEWCRCGALYSMLDSMYKEHGVQE
GQAGTGAFPSRREVVKLTAA SITAVCKLPIVIDASGDGAYVCKGVAAYPDA

gi|123958 (spot 3g)
MASKSNCVLLLLAAVLVS IFAAVAAIGNEDCTPWWSTLITPLPSCRDYVEQQACRIETPGSPYLAKQQCCGEL
ANIPQQCRCQALRYFMGPKSRPDQSGLMELPGCPREVQMDVFRILVTPGYCNLTTVHNTPYCLAMEESQWS

gi|123957 (spots 3h, 3i)
MACKSSCSLLLLAAVLLSVLAAASASGSCVPGVAFRTNLLPHCRDYVLQQTGTFTPGSKLPEWMTSASIYS
PGPKYLAKLYCCQELAEISQQCRCEALRYFIALPVPSPQVDPDRSGNVGESGLIDLPGCPREMOWDFVRLLLVA
PGQCNLATIHNVRYCPAVEQPLWI

gi|390979705 (spots 4a, 4b, 4c)
MATRGRATIPLLFLLGTSLLFAAAVSASHDEEEDRRGGRS LQRCVQRCQQDRPRYSHARCVQECRDDQQQH
RHEQEEQGRGHGRHGEGEREEEEQGRGRGRRGQGEREEEEQGRGRGRRGEGEGERDEEHGDGRRPYVFGPRSFRI
IRSDHGFVKALRPFDEVSRLLRGIRNYRVAIMEVNPRAFVVPGLTDADGVGYVAQGEGLTVIENGEKRSYT
VRQGDVIVAPAGS IMHLANTDGRKLVIAKILHTISVPGKFQYFSAKPLLASLSKRVLTAALKTSDERLGS
LGSRQGEKEEKSISIVRASEEQRLRELRRQASEGDQGHWWPLPPFRGDSRDTFNLLEQRPKIANRHGRLYEA
DARSFHALAQH DVRVAVANITPGSMTAPYLNTQSFKLAVVLEGEGEVEIVCPHLGRD SERREQE H GKGRWRS
EEEEDDRRQRRRGSGSESEEEQDQORYETVRARVSRGSAFVVPVPPGHPVVEIASRGS SNLQVVCFEINAER
NERVWLAGRNNVIAKLDDPAQELAFGRPAREVQEVFRAKDQQDEG FVAGPEQQQEHEHGRDRRRGDRGRGDEA
VEAFLRMATAAL

RS_UWI_15518 (spot 4d)
ELASSTMATRARVTIPLLLGTSLLFAAAVSASHDEEEDRRGGHSLQQCVQRCQQDRPRYSHARCVQECRG
DQQQHGRHEQEEQGRGRGRHGEGEREEEEQGGGRGRHGEGEREEEEEGRGRGRHGEGEREEHGRHEQGRGRGE
GERDEEQGSRRPYVFGPRNFRSIIIRSDHGFVKALRPFDEVSRLLRGIRNYRVAIMEVNPRAFVVPGLTDAD
GVGYVAQGEGLTVIENGEKRSYTVRQGDVIVAPAGS IMHLANTDGRKLVIAKILHTISVPGRFQYFSAKPL
LLASLSKRVLRAALKTSDEQLGRLLGRRQGEKEESRSISIIIRASEEQRLREL SRQASEGGQGHWWPLPPFRGD
SRDTFNLLEQRPKIANRHGRLYQADARSFHALAQH DVRVAVANITPGSMTAPYLNTQSFKLAVVLEGEGEVE
IVCPHLGRD SERREH GKGRWSEEEEEDDRRQRRRGSGSESESEEEQDQORYETVRARVSRGSAFVVPVPPGHPV
VEISSSQGSSNLQVVCFEINAERNERVWLAGRNNVIAKLDSPAQELTFGRPAREVQEVFRAKDQQDEG FVAG
PEQQSHEQE QERGD RRRGDRGRGDDAVGAF LRMATGAFGCMATVEVWVGAGARAVELDLYGVCYCVVVRTY
AGVEMRVARARYDDASYQPTYQQGMSMSIHKIQWALRSSSKKKKX

gi|475609166 (spots 5a, 5b, 5c)
MKTMFILALLALAASTAI AQLETIC SQFGQCQHHQQLGQQQLLDQMPCVAFVQHQCSPVRTPFQTRGEO
HSSCQTVQHCCRQLVQIPEQARCKAIQSVEEAI IQQQPQQQWNEPQQEAHLKSMRMSLQTLPSMCNIYVPV
QCQQQQQLGRQQQQQLQEQLKPCATFLQHQC RPMTVPFPHTPVQKPTSCQNVQSQCCRQLAQIPEQFRCQAI
HNVVESIRQQQHHQPQQEVQLEGLRMSLHTLPSMCKIYIPVQCPATTTTPYSITMTASYTDGTC