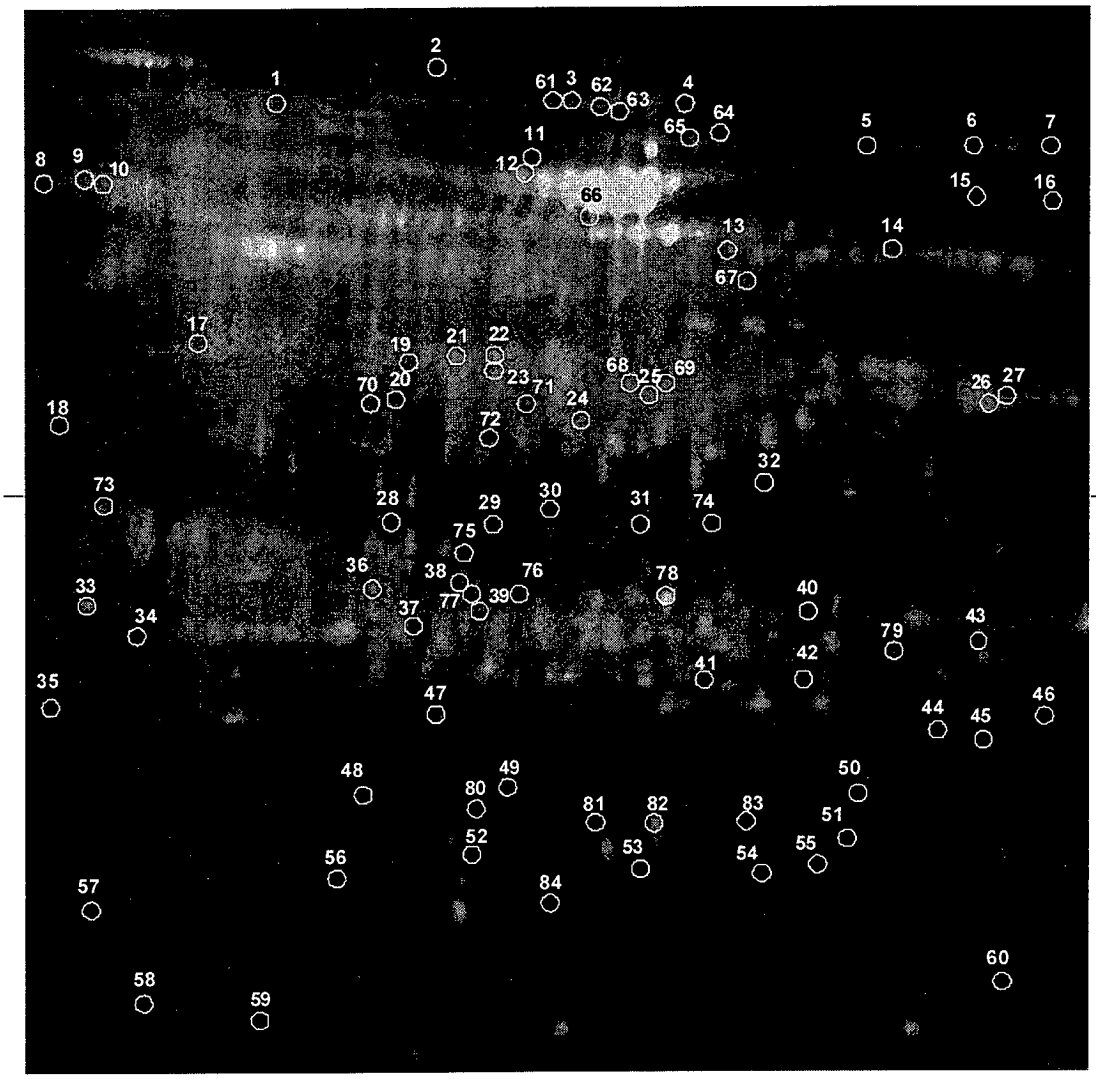

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FIG. 1: H2a / h1a.

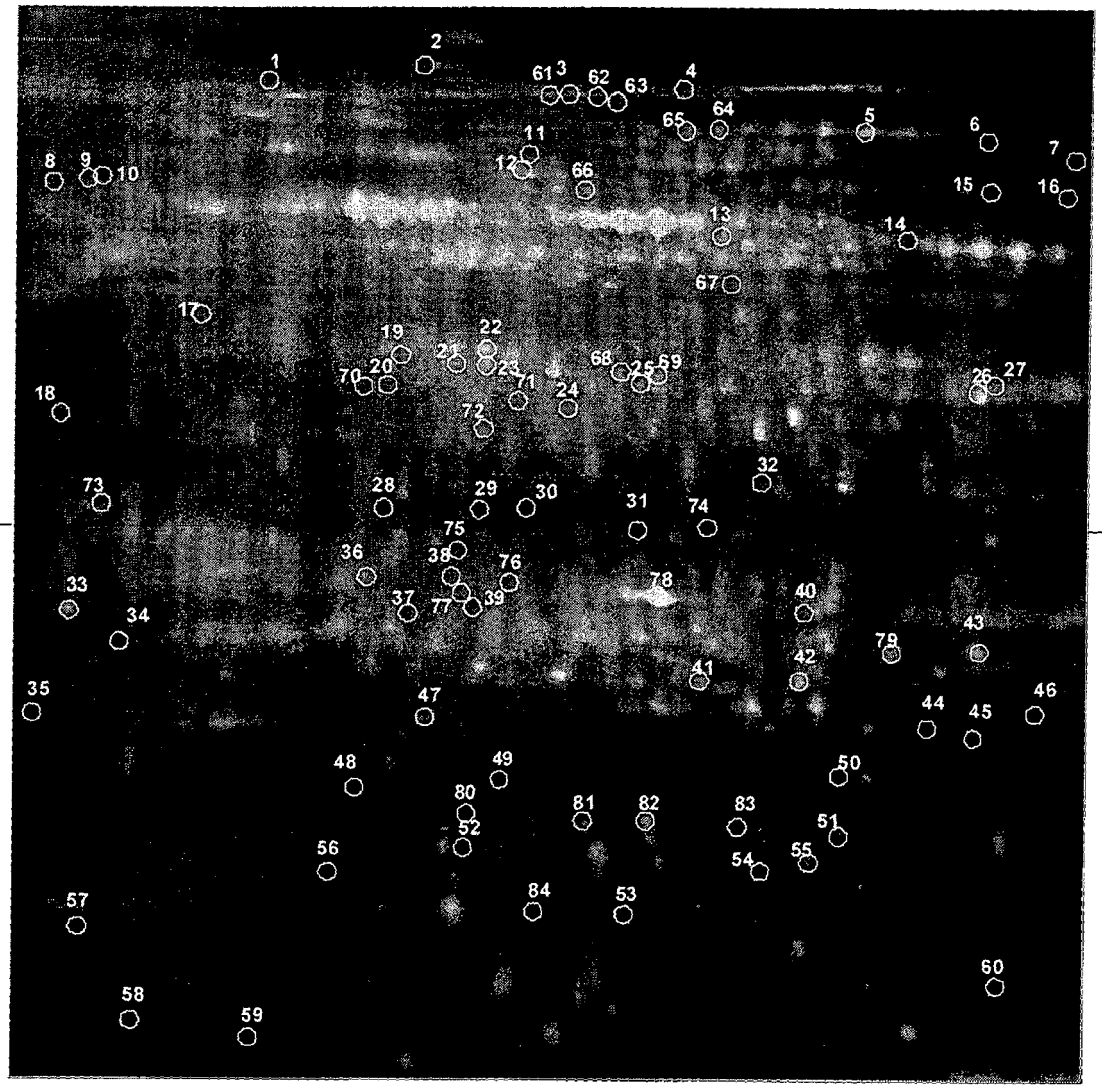

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FIG. 2: H4a / h6a.

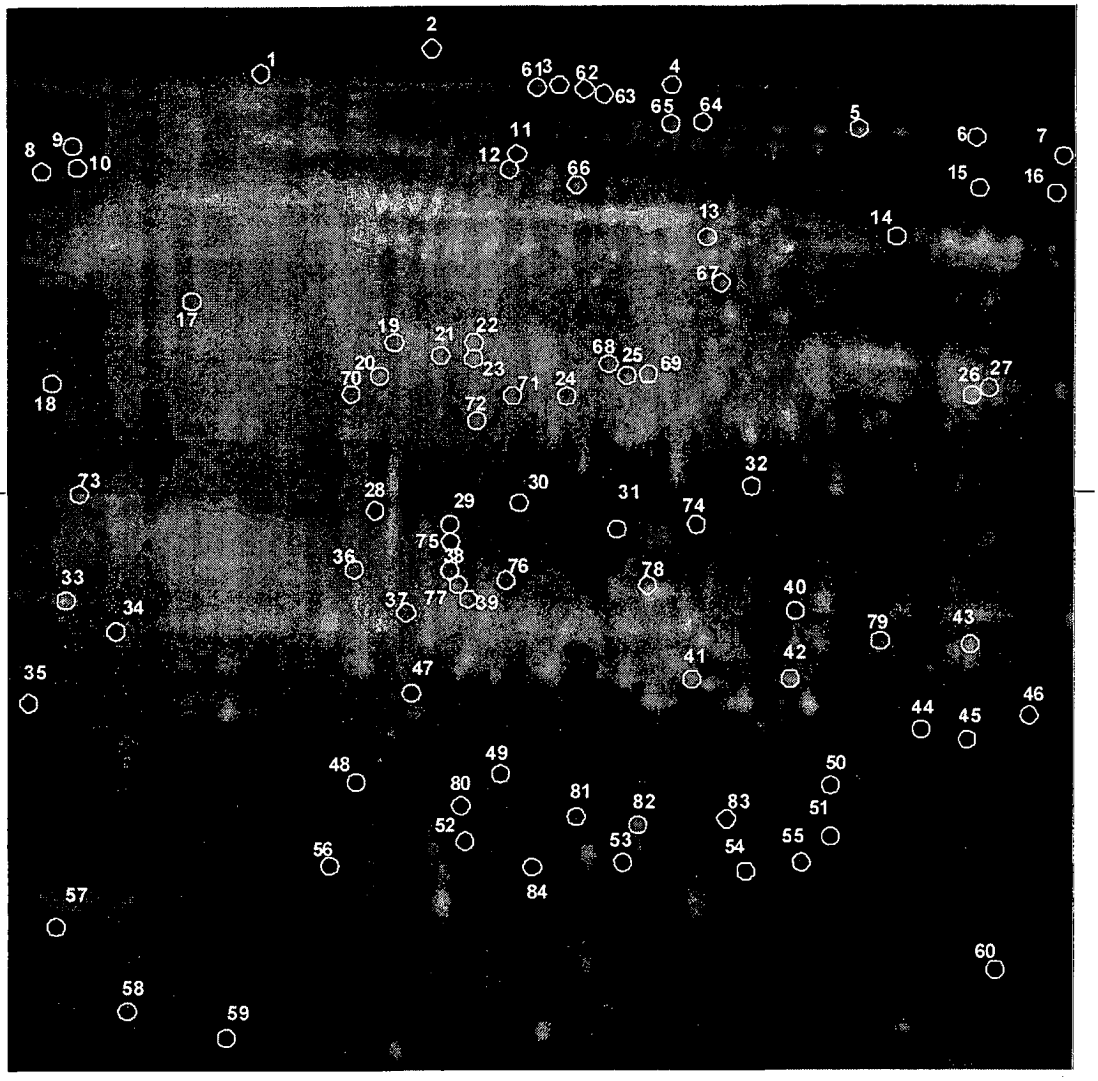

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FIG. 3: H6a / h9a.

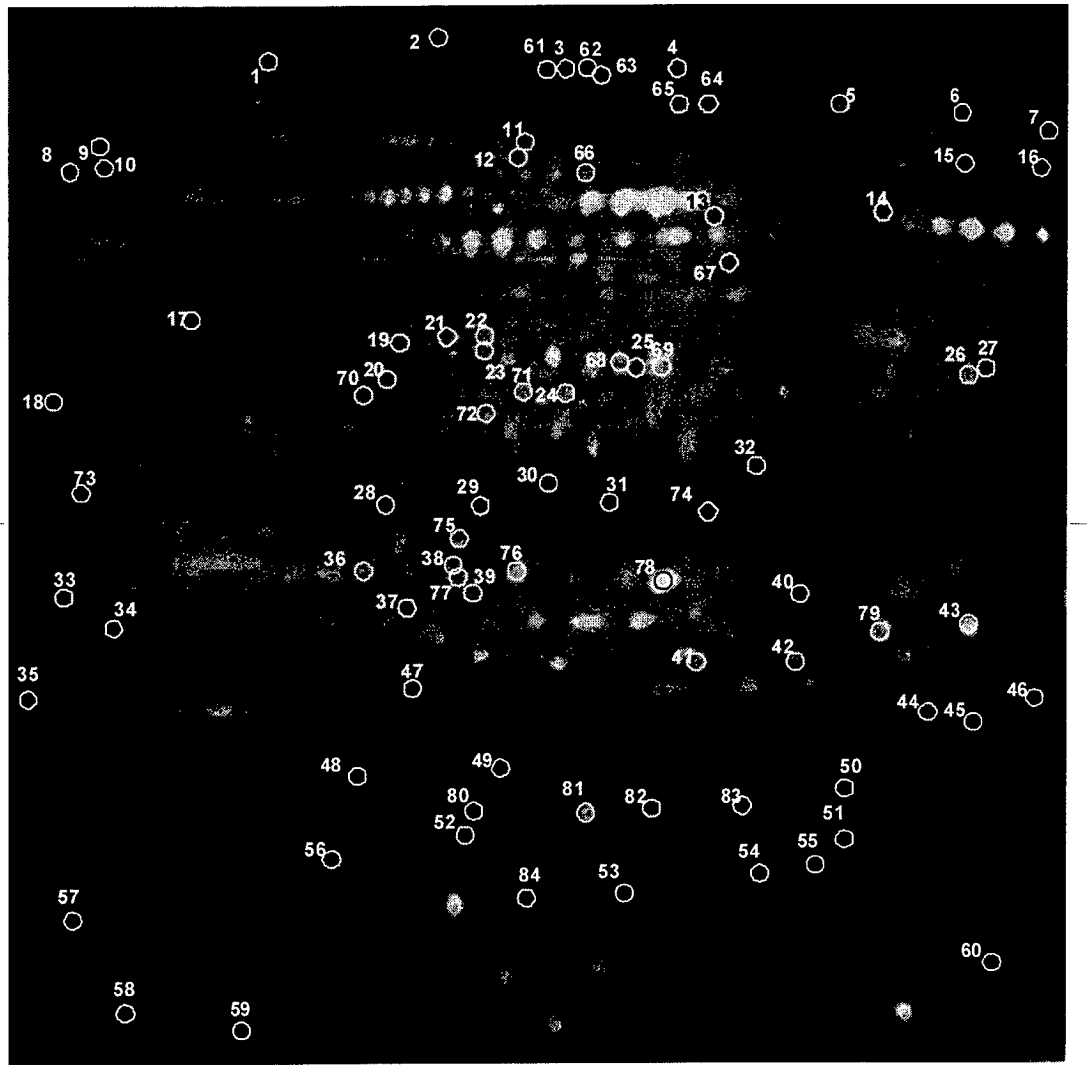

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FIG. 4: H2b / h1b.

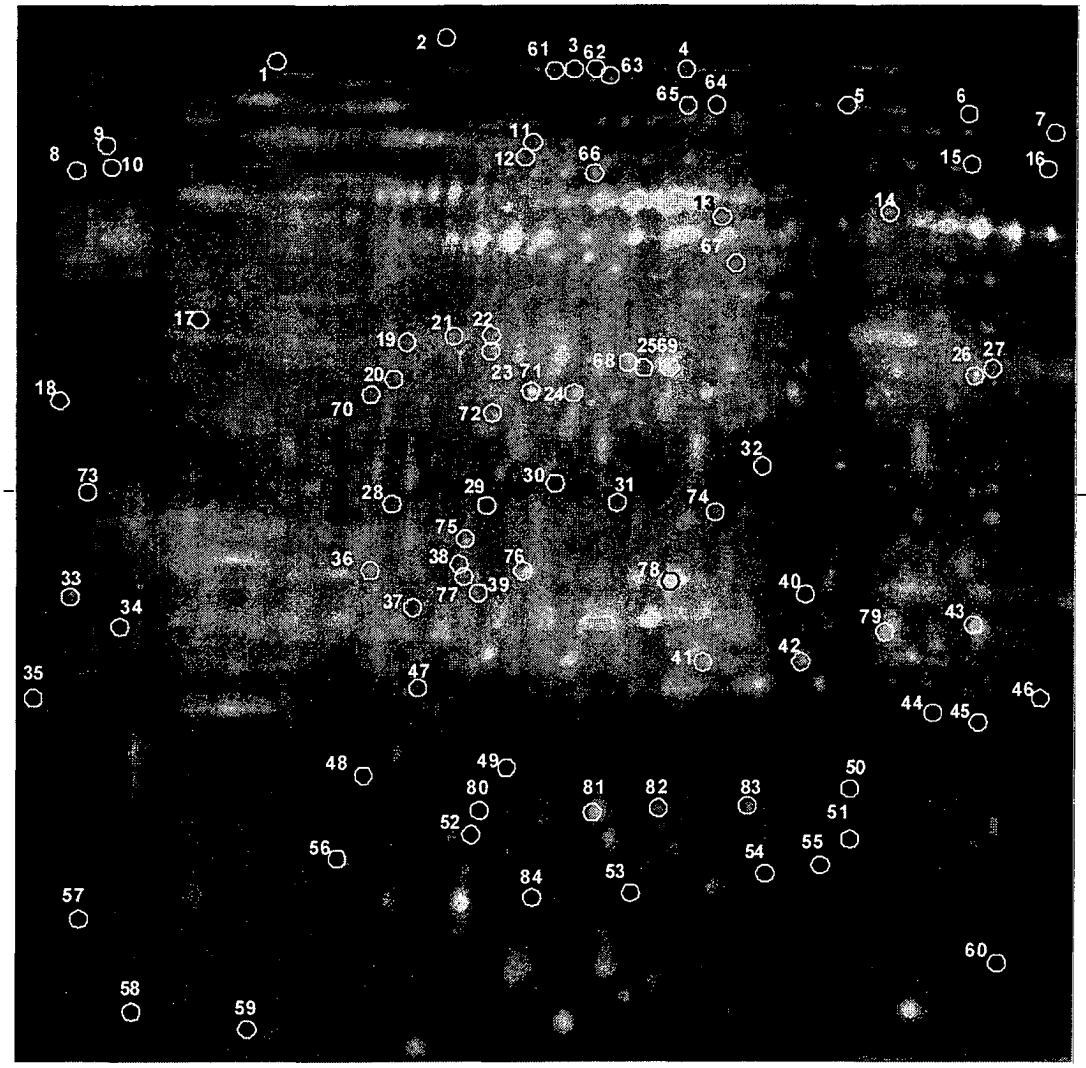

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FIG. 5: H4b / h6b.

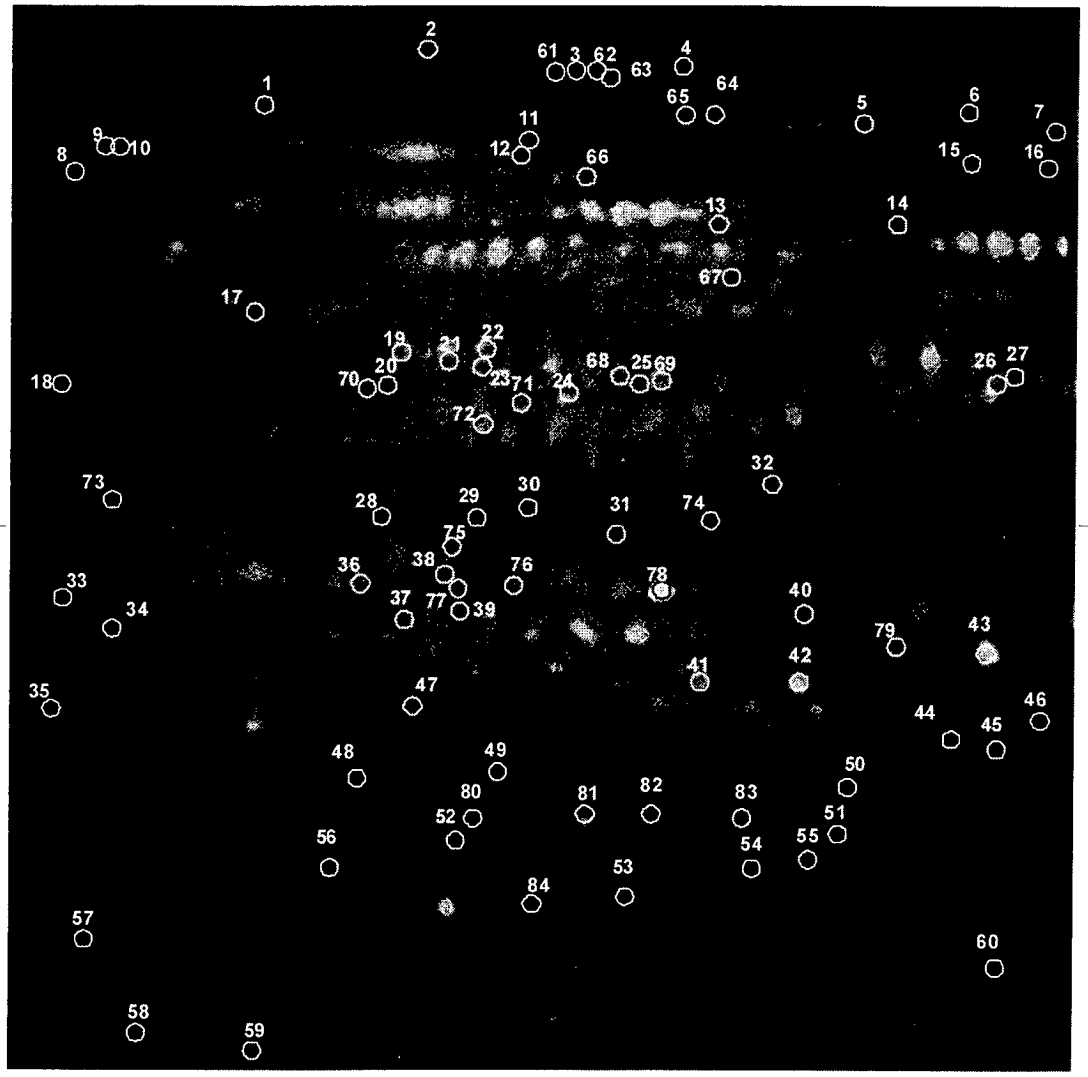

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FIG. 6: H6b / h9b.

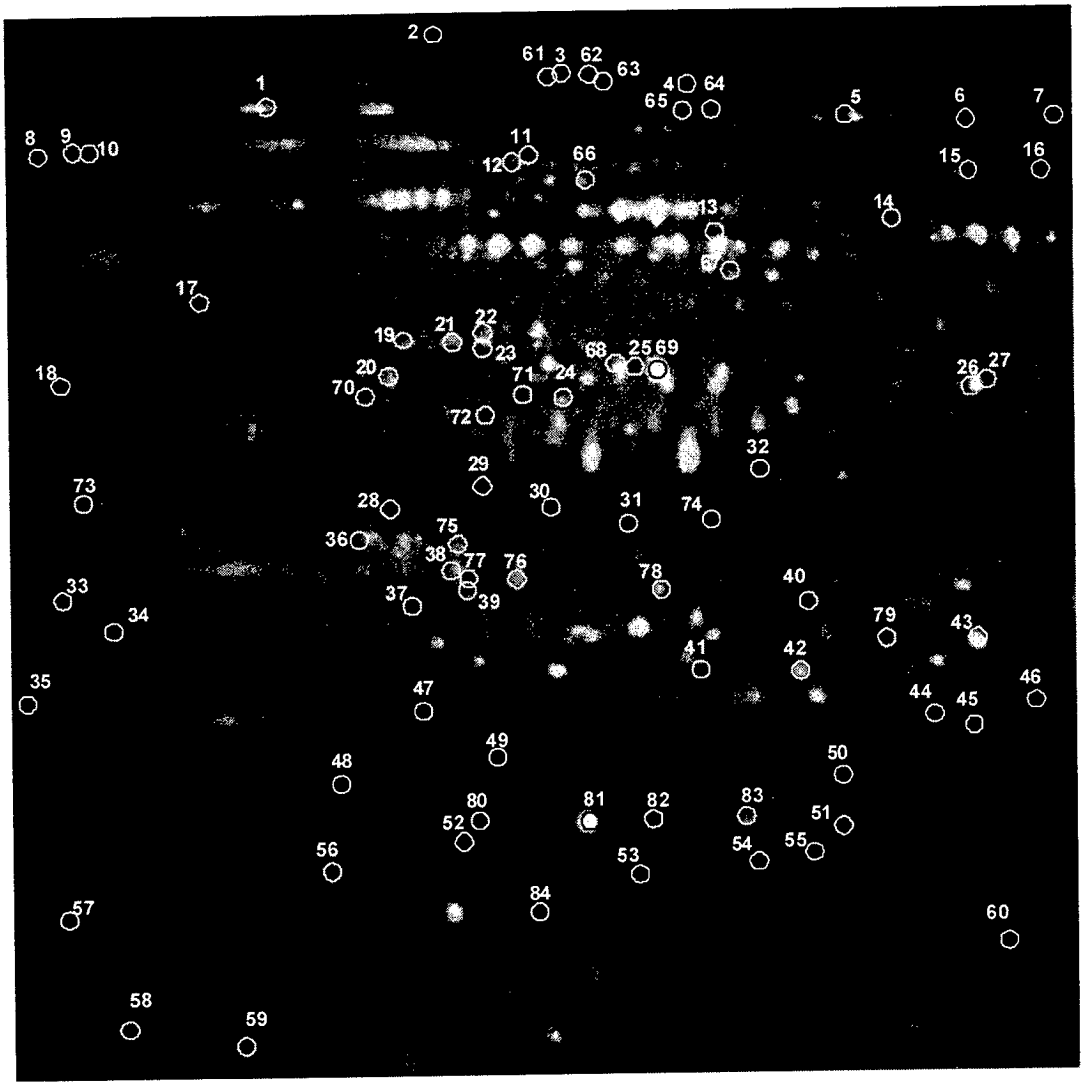

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FIG. 7: H2c / h1c.

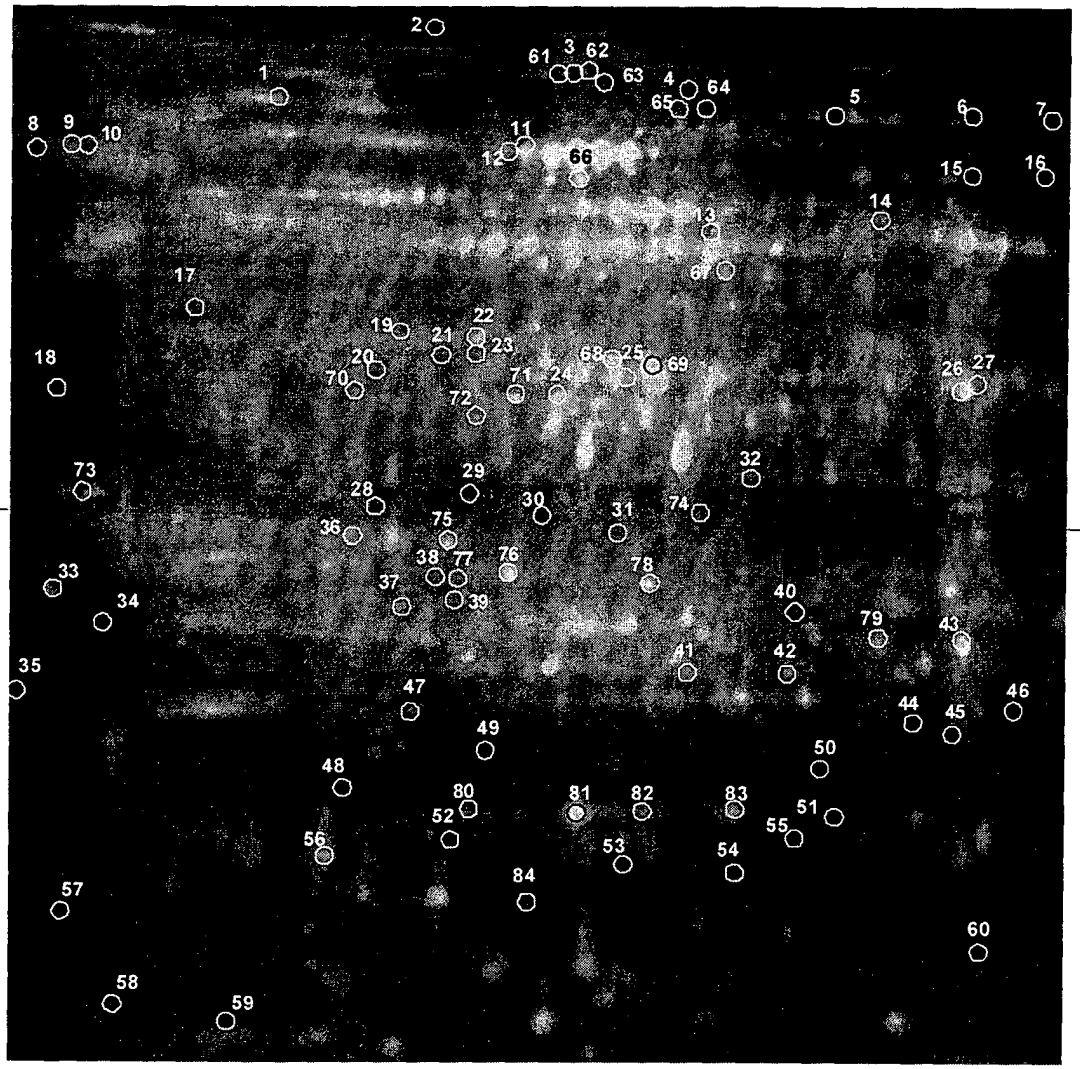

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FIG. 8: H4c / h6c.

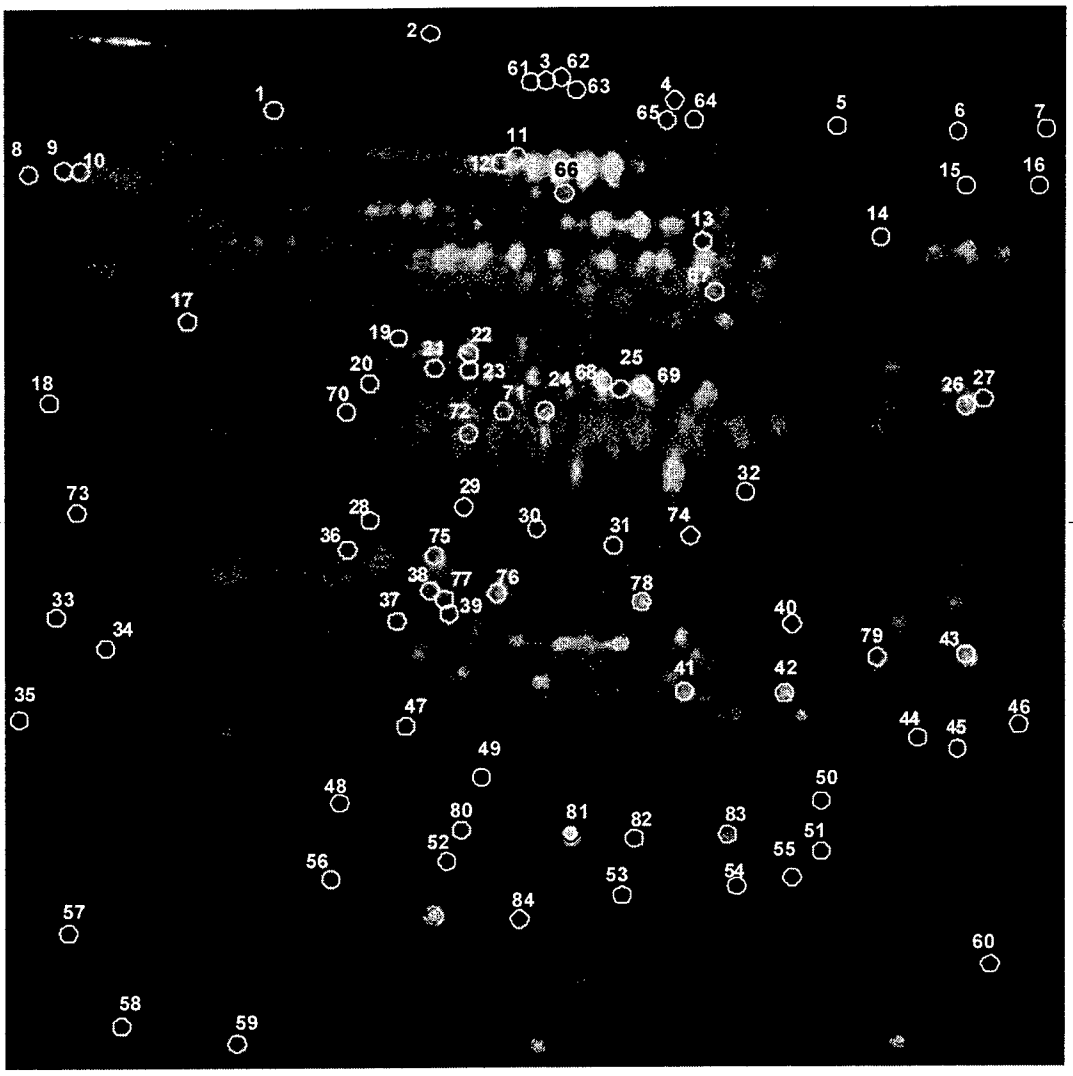

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FIG. 9: H6c / h9c.

SEQ ID NO: 1
>Top Ranked Protein Name [Species]: 5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase [Oryza sativa] (Spot 65)
MASHVVGYPRMGPKRELKFALESFWDGKSSAADLQKVSQDLRCSIWKQMSDAGVKYIPSN
TFSYYDQVLDATAMLGAVPQRYGWSGGEIGFDTYFSMARGNASVPAMEMTKWFDTNYHYI
VPELAPDTKFTYASHKAVSEYKEAKALGIDTVPVLIGPVTYLLLSKPAKGVEKAFPLLSL
LGNVLPVYKEVIAELKAAGASWVQFDEPHL*

Predicted MW= 23.25kDa; Predicted pI= 6.96

SEQ ID NO: 2
>Top Ranked Protein Name [Species]: abscisic stress ripening protein [Musa acuminata subsp. burmannicoides] (spot 78)
MEHLGEMGAVAAGAFALYEKHEAKKHPEHAHRHKIEEEIAAAVAVGSGGYAFHEHHEKKA
AKKEAEES

This is not a full-length protein sequence.

SEQ ID NO: 3
>Top Ranked Protein Name [Species]: actin 6 [Populus trichocarpa] (Spot 22)
MADAEDIQPLVCDNGTGMVKAGFAGDDAPRAVFPSIVGRPRHTGVMVGMGQKDAYVGDEA
QSKRGILTLKYPIEHGIVSNWDDMEKIWHHTFYNELRVAPEEHPVLLTEAPLNPKANREK
MTQIMFETFNVPAMYVAIQAVLSLYASGRTTGIVLDSGDGVSHTVPIYEGYALPHAILRL
DLAGRDLTDALMKILTERGYSFTTTAEREIVRDMKEKLAYVALDYEQELETAKSSSSVEK
SYELPDGQVITIGAERFRCPEVLFQPSLIGMEAAGIHETTYNSIMKCDVDIRKDLYGNIV
LSGGSTMFPGIADRMSKEITALAPSSMKIKVVAPPERKYSVWIGGSILASLSTFQQMWIS
KGEYDESGPSIVHRKCF*

Predicted MW= 41.63kDa; Predicted pI= 5.16

SEQ ID NO: 4
>Top Ranked Protein Name [Species]: actin E [Elaeis guineensis] (spot 76)
MAEAEDIQPLVCDNGTGMVKAGFAGDDAPRAVFPSIVGRPRHTGVMVGMGQKDAYVGDEA
QSKRGILTLKYPIEHGIVTNWDDMEKIWHHTFYNELRVAPEEHPVLLTEAPLNPKANREK
MTQIMFETFNVPAMYVAIQAVLSLYASGRTTGIVLDSGDGVTHTVPIYEGFALPHAILRL
DLAGRDLTDALMKILTERGYSFTTTAEREIVRDIKEKLGYVALDYEQELETAKSSSSVEK
SYELPDGQVITIGAERFRCPEVLFQPSLIGMEAAGIHETTYNSIMKCDVDIRKDLYGNIV
LSGGSTMFPGIADRMSKEISALAPSSMKIKVVAPPERKYSVWIGGSILASLSTFQQMWIS
KEEYDECGPAIVHRKCF*

Predicted MW= 41.68kDa; Predicted pI= 5.06

FIG. 10A: Sequences of the forty-five proteins.

SEQ ID NO: 5
>Top Ranked Protein Name [Species]: biotin carboxylase precursor [Glycine max] (Spot 67)
MDSMIACKSGCLPPGLFIRPTRGIRSSQCSFMVGNDPKFCKISFPRKRTACAIRKSKKNG
GALNATCYDEKILVANRGEIAVRVIRTAHEMGIPCVAVHSTIDQDALHVRLADEAVCIGE
APSSQSYLFIPNVLSAAVSRGCTMLHPGYGFLAENAGFVDICKEHGINFIGPNPDSIRVM
GDKSTARETMKKAGVPTVPGSDGLLQSTEEAVKLAHEIGFPVMIKATAGGGGRGMRLAYE
PEQFVKLLQQAKSEAAAAFGNDGVYLEKYIQNPRHIEFQVLADKYGNVVHFGERDCSIQR
RNQKLLEEAPSPALTPELRKAMGDAAVAAAASIGYIGVGTVEFLLDERGSFYFMEMNTRI
QVEHPVTEMISSTDLIEEQIRVALGERLTYKQEDIVLRGHSIECRINAEDAFKGFRPGPG
KITSYLPSGGPFVRMDSHVYPGYVVPPSYDSLLGKLIVWAPTREKAIERMKRALDDTIIT
GIPTTIEYHKLILDIEDFRNGKVDTAFIPKHEKDLTAPHKLVLSTSEKELAGVGA*

Predicted MW= 58.48kDa; Predicted pI= 7.51

SEQ ID NO: 6
>Top Ranked Protein Name [Species]: caffeic acid O-methyltransferase [Vanilla planifolia](Spot 23)
MGSIEKQGMPAPSVENQAGDEASCMYALQLASSSILPMTLKAAIELGVLEIIAKAGSVGK
LSPAQVAAQLPTENPMAATMLDRMLRLLASYNILTCSVEVDADGKPLRRYGPAPVCKWLT
KNEDGVSMAALTLMNQDKVLMESWYYLKDAVLDGGIPFNKAYGMTAFEYHGTDPRFNKVF
NEGMKNHSIIITKKLLEFYKGFEDVNVLVDVGGGIGATLHMITSKYPHIKGINFDLPHVI
SEAPPFPGVEHIGGDMFASVPSGDAILMKWIMHDWSDEHCAKILENCYKALPNNGKVILC
ECILPVAPEPVPSAQGVFHVDMIMLAHNPGGKERTEKEYQDLAKGAGFTGFKAQYCFSTA
WVLEFTK*

Predicted MW= 40.06kDa; Predicted pI= 5.80

SEQ ID NO: 7
>Top Ranked Protein Name [Species]: catalase 2 [Elaeis guineensis] (Spot 9)
MDPYKFRPSSANNSPFWTTNSGAPVWNNNSSLTVGNRGPILLEDYHVIEKLAQFDRERIP
ERVVHARGASAKGFFEVTHDVSHLTCADFLHAPGVQTPVIVRFSTVIHERGSPETLRDPR
GFAVKFYTREGNFDLVGNNFPVFFVRDGIKFPDMVHALKPNPKSHIQENWRIVDFFSHHP
ESLHMFTFLFDDVGVPADYRHMDGSGVNTYTLINKEGKARYVKFHWRPTCGVKCLLEDEA
VIVGGNNHSHATKDLYDSIAAGNYPEWKLFIQTIDPDHEDRFDFDPLDVTKTWPEDILPL
QPVGRMVLNKNIDNFFAENEQLAFCP

This is not a full-length protein sequence.

SEQ ID NO: 8
>Top Ranked Protein Name [Species]: conserved hypothetical protein [Ricinus communis] (Spot 59)
MAAIANSFVSIRDLRPPALSGCPLKPSPQSLVSCSPMNLSLSTIRWRRAKIATYKSRITV
QAAYSDGGRPNSASIFIGGFVLGGIIVGTLGCVYAPQISKILAGADRKDLMRKLPKFIYD
EEKALERTRKILADKIEQLNSAIDDVSSQLRADDGPNGVAVASDEVEAAI*

Predicted MW= 18.21kDa; Predicted pI= 9.53

FIG. 10B: Sequences of the forty-five proteins.

SEQ ID NO: 9
>Top Ranked Protein Name [Species]: fibrillin-like protein [Elaeis guineensis] (Spot 73)
MAGVASWKPMALKAPPAAPPLRYHSSIHPIPIGAPASVFQKAPILRSAMGLPLAAAPIRP
RAIADDEEWGGELGEEEGAAAGGLAVAEQEEEEVKVEPIEVGELKRKLMDLLYGTDRGLQ
ASSETRAEIVEVINQLEVRNPTPAPTEALTLLNGKWILAYTSFSPLFPLLGSARLPELVK
VEEISQTIDSENFTVQNSVQFAVPLATTSVTTNAKFEVRSPKRVQIKFEEGIIGTPQLTD
SIVLPEKVEFLGQNIDLSPFKSVITSVQNAASSVARTISERPPWKISINNDNAQSWLLTT
YLDEELKISRADGGGIFLLIKEGSSLLN*

Predicted MW= 35.47kDa; Predicted pI= 4.57

SEQ ID NO: 10
>Top Ranked Protein Name [Species]: FQR1 (FLAVODOXIN-LIKE QUINONE REDUCTASE 1) [Arabidopsis thaliana] (Spot46)
MATKVYIVYYSMYGHVEKLAEEIKRGASTVGGVEAKMWQVPETLPEEVLGKMGAPPKSDV
PIITPNELAEADGIIFGFPTRFGMMAAQFKAFLDATGGLWRAQQLAGKPAGIFYSTGSQG
GGQETTPLTAITQLVHHGMIFVPIGYTFGAGMFEMEKVKGGSPYGAGTYAGDGSRFPSEL
ELEQAFHQGKYFAGIAKKFKSSS*

Predicted MW= 21.75kDa; Predicted pI= 6.97

SEQ ID NO: 11
>Top Ranked Protein Name [Species]: fructose-bisphosphate aldolase [Elaeis guineensis] (spot 74)
MSAYCGKYHDELIKNAAYIGTPGKGILAADESTGTIGKRLASINVENVEENRRALRELLF
CTPGALQYLSGVILFEETLYQKTKDGKPFVEVLKEGGVLPGIKVDKGTIELAGTNGETTT
QGHDDLAKRCQKYYEAGARFAKWRAVLKIGPTEPSQLAIDLNAHGLARYAIICQENGLVP
IVEPEILVDGPHDIKRCADVTERVLAACYKALNDHHVLLEGTLLKPNMVTPGSESAKVAP
EVVAEYAVRALQRTVPAAVPAIVFLSGGQSEEEATLNLNAMNKLGGKKPWSLSFSFGRAL
QQSTLKAWAGKVENVEKARAAFLARCKANSEATLGKYEGDAAGGEGVSESLHVKDYKY*

Predicted MW= 38.61kDa; predicted pI= 7.14

SEQ ID NO: 12
>Top Ranked Protein Name [Species]: glyceraldehyde 3-phosphate dehydrogenase [Elaeis guineensis] (Spot 26)
MFVVGVNEKEYKSDINVVSNASCTTNCLAPLAKVIHDKFGIVEGLMTTVHSITATQKTVD
GPSSKDWRGGRAASFNIIPSSTGAAKAVGKVLPALNGKLTGMAFRVPTVDVSVVDLTVRL
EKSATYDQIKDAIKEESEGKMKGILGYVDEDLVSTDFLGDSRSSIFDAKAGIALNGNFVK
LVSWYDNEWGYSSRVVDLIRHIHGTQ*

Predicted MW= 22.20kDa; Predicted pI= 6.95

FIG. 10C: Sequences of the forty-five proteins.

SEQ ID NO: 13
>Top Ranked Protein Name [Species]: H0825G02.11 [Oryza sativa (indica cultivar-group)] (Spot 19)
MDLGKSASTSATLK----------
----------FYYELR----------YVPFQCPSSR----------
----------RIQPLQAR----------

----------ELAEAHEDLTK------

----------LSCPELDLREILDQGAASDVR----------
----------FEVAELER-------EKAVETLRGREVWFSSYL
QSCCTSMARVCR----------
----------SMSPLAEK

This is not a full-length protein sequence.

SEQ ID NO: 14
>Top Ranked Protein Name [Species]: Large subunit of ribulose-1, 5-bisphosphate carboxylase/oxygenase [Chlorogonium elongatum] (Spot 56)
--------DYRLTYYTPDYVVRDTDVLAAFR----------
----------ALRLEDLR----------

SQAETGEVKGHYLNVTAGTAEEMLK

This is not a full-length protein sequence.

SEQ ID NO: 15
>Top Ranked Protein Name [Species]: Lea1P [Daucus carota] (Spot 48)
MASHQDTSYK----------DQTGSYVSDKASAAR--
SCETGQAAK----------EKASQMGESAK---------TGGVISSAAEQVKGMAQGATEAVKNTFGMGGGNEEK

This is not a full-length protein sequence.

SEQ ID NO: 16
>Top Ranked Protein Name [Species]: methionine synthase protein [Sorghum bicolor] (Spot 5)
MGPKRELKFALESFWDGKSSADDLQKVAADLRCSIWKQMADAGIKYIPSNTFSYYDQVLD
TTAMLGAVPQRYGWSGAEIGFDTYFSMARGNALVPAMEMTKWFDTNYHYIVPELAPDTKF
TYASHKAVSEYKEAKALGIDTVPVLIGPVTYLLLSKPAKGVEKSFATLSLLGNVLPIYQE
VIMELKAAGASWIQFDEPTLVMDLDAHQLEAFTKAYSELESSFSGLNVLVETYFADVPAE
AYKTITTLNGVSGFGFDLVRGTNTLDLIKSAGFPSGKYLFAGVVDGRNIWANDLASSLSS
LGVLEAIVGKDNLVVSTSCSLMHTAVDLVNETKLDGEIKSWLAFAAQKVVEVNALAKALA
GHKDEAFFSANAAAQASRKSSPRVTNEEVQTAAAALKGSDHCRATNVSARLDA

This is not a full-length protein sequence.

FIG. 10D: Sequences of the forty-five proteins.

SEQ ID NO: 17
>Top Ranked Protein Name [Species]: Mitochondrial peroxiredoxin [Pisum sativum] (Spot 51)
MASALMRARRSAALPSAAVMALRRAFAAASVGCDIVSAAPGVALQKARSWDEGVSSKFST
TPLKDIFLGKQVVVFGLPGAFTGVCSAQHVPSYKNNIDKFKAKGIDSVICVAVNDPYVLN
GWAENLQAKEAIDFYGDFDGSFHKSLELDLDLSAALLGHRSQRWSAYVVDGKIKVLNVEK
VPSEFKVSGGEVILGQF*

Predicted MW= 21.06kDa; Predicted pI= 8.83

SEQ ID NO: 18
>Top Ranked Protein Name [Species]: Os02g0753300 [Oryza sativa (japonica cultivar-group)] (Spot 58)
MMKGTKKAIFLFLLLSSLVIISHCVTPLTIKPVNRDDDEYQCVYTVYIRTGSIWKGGTDS
VISLVLAGSDGWGVAITDIESWGGIMEAGHNYFERGNLDIFSGRGPCLSTPPCWMNLTSD
GSGSHHGWYCNYVEVTTTGPHMGCAQQLFTVEQWLATDAAPYQLYATRDSCTGRGNAEEE
PKIGDRIGRHVTHVA*

Predicted MW= 21.38kDa; Predicted pI= 5.85

SEQ ID NO: 19
>Top Ranked Protein Name [Species]: unknown protein Os05g0482700 [Oryza sativa (japonica cultivar-group)] (Spot 66)
MGSSEFSWKLADHPKLPKGKTVAVVVLDGWGEANPDKYNCIHVAETPAMDSLKKGAPDRW
RLVRAHGTAVGLPTEDDMGNSEVGHNALGAGRIYAQGAKLVDLALASGKIYEGEGFKYIK
ECFDQGTLHLIGLLSDGGVHSRLDQLQLLLKGASENGAKRIRVHVLTDGRDVLDGSSVGF
VETLENDLLKLREKGVDAQIASGGGRMYVTMDRYENDWGVVKRGWDAQVLGEAPHKFQSA
VEAVKKLREVPKANDQYLAPFVIVDESGKAVGPIVDGDAVVTFNFRADRMVMLAKALEYE
DFDKFDRVRFPKIQYAGMLQYDGELKLPSHYLVSPPEIERTSGEYLVHNGIRTFACSETV
KFGHVTFFWNGNRSGYFDPSMEEYVEIPSDAGITFNVKPKMKAVEIAEKARDAILSRKFD
QVRVNLPNGDMVGHTGDIEATVVACKAADDAVKMILDAIEQVGGIYVVTADHGNAEDMVK
RNKSGQPQLDKNGDIQILTSHTLQPVPVAIGGPGLAPGVGFRKDVPNGGLANIAATVMNL
HGFEAPSDYEPTLIEVVDN*

Predicted MW= 60.86kDa; Predicted pI= 5.39

SEQ ID NO: 20
>Top Ranked Protein Name [Species]: unknown protein Os12g0163700 [Oryza sativa (japonica cultivar-group)] (Spot 68)
MADAEDIQPLVCDNGTGMVKAGFAGDDAPRAVFPSIVGRPRHTGVMVGMGQKDAYVGDEA
QSKRGILTLKYPIEHGIVSNWDDMEKIWHHTFYNELRVAPEEHPILLTEAPLNPKANREK
MTQIMFETFDVPAMYVAIQAVLSLYASGRTTGIVLDSGDGVSHTVPIYEGYALPHAILRL
DLAGRDLTDALMKILTERGYSFTTTAEREIVRDIKEKLAYVALDYEQELETAKSSSAVEK
SYELPDGQVITIGAERFRCPEVLFQPSLIGMESPGIHETTYNSIMKCDVDIRKDLYGNIV
LSGGSTMFPGIGDRMSKEITALAPSSMKIKVVAPPERKYSVWIGGSILASLSTFQQMWIT
KAEYDESGPAIVHRKCF*

Predicted MW= 41.65kDa; Predicted pI= 5.06

FIG. 10E: Sequences of the forty-five proteins.

SEQ ID NO: 21
>Top Ranked Protein Name [Species]: OSJNBb0085F13.17 [Oryza sativa (japonica cultivar- group)] (Spot 7)
MADIQMGEAETFAFQAEINQLLSLIINTFYSNKEIFLRELISNSSDALDKIRYEGLTDKS
KLDAQPELFIRLVPDKANKTLSIIDSGIGMTKADLVNNLGTIARSGTKEFMEALQAGADV
SMIGQFGVGFYSAYLVAEKVVVTTKHNDDEQYIWESQAGGSFTVTRDVSGEQLGRGTKIT
LYLKEDQLDYLEERRLKDLVKKHSEFISYPIYLWTEKTTEKEISDDEDEETKKEEEGDVE
NIDEEKETKSKKKKVKEVLHEWSLVNKQKPIWLRKPEEITKEEYASFYKSLTNDWEDHLA
VKHFSVEGQLEFKAILFVPKRAPFDLFDTRKKMNNIKLYVRRVFIMDNCEELIPEYLGFV
KGVVDSDDLPLNISREMLQQNKILKVIRKNLVKKCIELFSEIAENKEDYNKFYEAFSKNL
KLGIHEDSQNRAKLADLLRYHSTKSGDEMTSLKDYVTRMKEDQKDIYYITGESKKAVENS
PFLEKLKKKGYEVLFMVDAIDEYAVGQLKEYDGKKLVSATKEGLKIDESEDEKKRKEEKK
AAFESLCKVMKDILGDKVEKVVVSDRIVDSPCCLVTGEYGWTANMERIMKAQALKDNSMG
SYMSSKKTMEINPENGIMEEMRKRAEADKNDKSVKDLVLLLFETAILTSGFSLDDPNTFA
GRIHRMLKLGLSIDEDEAAGDDTDMPALEEDGNEESKMEEVD*

Predicted MW= 80.51kDa; Predicted pI= 4.72

SEQ ID NO: 22
>Top Ranked Protein Name [Species]: predicted protein [Ostreococcus lucimarinus CCE9901] (Spot 34)
---MKWCER---VYLTIELPDAKDAEVTIEAR

This is not a full-length protein sequence.

SEQ ID NO: 23
>Top Ranked Protein Name [Species]: predicted protein [Physcomitrella patens subsp. patens] (spot 79)

YIANKFEGQGTPIYGSTPVEK----------VLDIYEAR----

This is not a full-length protein sequence.

FIG. 10F: Sequences of the forty-five proteins.

SEQ ID NO: 24
>Top Ranked Protein Name [Species]: Predicted protein [Populus trichocarpa] (Spot 20)
MASSSAQIHVLGSAAAFPSSRKPSARISSSKSLFFGNRHSNGINGAFLSIRRGAGRGNRG
YGGPLRVVSEKVVGIDLGTTNSAVAAMEGGKPTIVTNAEGQRTTPSVVAYTKNGDRLVGQ
IAKRQAVVNPENTFFSVKRFIGRKMSEVDEESKQVSYRVVKDENGNVKLECPAIGKQFAA
EEISAQVLRKLVDDASKFLNDKVTKAVVTVPAYFNDSQRTATKDAGRIAGLDVLRIINEP
TAASLAYGFEKKNNETILVFDLGGGTFDVSVLEVGDGVFEVLSTSGDTHLGGDDFDKRVV
DWLAGNFKRDEGIDLLKDKQALQRLTETAEKAKMELSSLTQTNISLPFITATADGPKHIE
TTITRAKFEELCSDLLDRLRTPVDNALKDAKLSFKDIDEVILVGGSTRIPAVQELVKKMT
GKEPNVTVNPDEVVALGAAVQAGVLAGDVSDIVLLDVTPLSLGLETLGGVMTKIIPRNTT
LPTSKSEVFSTAADGQTSVEINVLQGEREFVRDNKSLGSFRLDGIPPAPRGVPQIEVKFD
IDANGILSVTAVDKGTGKKQDITITGASTLPGDEVDRMVKEAERYAKEDKEKRDAIDTKN
QSESVVYQTEKQLKELGDKVPAAVKEKVEAKLKELKDAIAGGSTQSMKDAMAALNQEVMQ
LGQSLYNQPGAAGAGPAPGADAGSAGSTGKGPDDGGDVIDADFTDSK*

Predicted MW= 75.17kDa; Predicted pI= 5.18

SEQ ID NO: 25
>Top Ranked Protein Name [Species]: PREDICTED: hypothetical protein isoform 1 [Vitis vinifera] (Spot 55)
MQGALQAIRAQGNVLKCAVLRHVRIMNPAMLPTAISRFESTSPAQLEEHGFESTTISDVL
KAKGKGADGSWLWCTTDDTVYDAVKSMTQHNVGALVVVKPGADKAIAGIITERDYLRKII
VQGRSSKSTKVGDIMTEENKLITVTPDTKVLQAMQLMTDNRIRHIPVIDAKGMMGMVSIG
DVVRAVVTEHREELDRLNAYIQGGY*

Predicted MW= 22.44kDa; Predicted pI= 8.70

SEQ ID NO: 26
>Top Ranked Protein Name [Species]: PREDICTED: similar to nascent polypeptide associated (Spot 33)
MTAQTQEELLAAHLEQQKIDYDEPVVEDEDDDEDDEDDDDKDEDDAEGQAGDASGRSKQS
RSEKKSRKAMLKLGMKPIPGVSRVTVKKSKNILFVISKPDVFKSPTSDTYVIFGEAKIED
LSSQLQTQAAEQFKAPDLSHVISKPETSAMAQDDEEVDETGVEPKDIELVMTQAGVSRSK
AVKALKAADGDIVTAIMELTN*

Predicted MW= 22.02kDa; Predicted pI= 4.13

FIG. 10G: Sequences of the forty-five proteins.

SEQ ID NO: 27
>Top Ranked Protein Name [Species]: proline iminopeptidase, putative [Ricinus communis] (Spot 24)
METSKESQELNRSLYPHIEPYSSGFLKVSDIHTLYWEQSGNPNGHPVVFLHGGPGAGTSA
SNRRFFDPEFYRIILFDQRGSGKSTPHACLEDNTTWDLVNDIEKLREHLEIPEWQVTGII
LRGIFLLRKKELDWFYEGGAAAIFPDAWEPFRDFIPENERNNFIVAYHKRLNSDDNHIQV
TAAKIWTTWELMTAHLIQNEENIKRGEDDDFSLAFARIENHYFVNKGFFPSDSYLLDNVD
KIRHISTVIVQGRYDVCCPMMSAWDLHKAWPEAELKVVPDAGHSANEIGIAAELVAANEK
FKNILKSGGFKM*

Predicted MW= 35.79kDa; Predicted pI= 5.39

SEQ ID NO: 28
>Top Ranked Protein Name [Species]: protein transporter [Elaeis guineensis] (Spot39)
MASSGPDHLFNLRNSFYLGAYQDAINKSDIPNLSGDDAVERDSIVYRSYIALGSYQLVIN
EIDSSAPTALQAVKLLALYLAGDKESAIASLQEWLNDAAIGNNHVLRLIAGIIYMHEQNY
VEALKHTNSGGTMELHALNVQIYLKMHRSDYAEKQLKIMLQIDEDHTLTQLANAWVNLAV
GGSKIQEAYLIYQDFSEKNQMTPLILNGKAVCCLHMGRFDEAESLLLDALNKDAKDAETL
ANLVVCSLHLGKSAARYLNQLKLSHPDHMLVQRASSAEDSFERAVQSIA*

Predicted MW= 32.00kDa; Predicted pI= 5.31

SEQ ID NO: 29
>Top Ranked Protein Name [Species]: putative NBS-LRR disease resistance protein homologue [Oryza sativa Japonica Group] (Spot 12)
-------ERQEIDRSAMVGALASASTGVMNSVIAKLSKLLEDEYAK----------
----------AHVVEESKR--

----------LRDTLQDK-
YLVVIDDVWATEAWETIKLALLSNNCDSR----------CSYHGGYVYHMEPLSFVDSKR----------
----------VLAAIGSALAKDPNAGNMRR----------
----------SLIQPVDVQYGKPVACR----------
----------ENVIMATNLSLK----------

-MQSLEELQTFDIFTYSSR----------
----------WMNMLACLTELDLTLCSTK----------
----------LQHLMIK-------CLNGASDLGIR----------
----------SVNYEIEVNLGEVR

This is not a full-length protein sequence.

FIG. 10H: Sequences of the forty-five proteins.

SEQ ID NO: 30
>Top Ranked Protein Name [Species]: Ran GTPase binding protein, putative [Ricinus communis] (Spot 32)

----------FQKDMSFRFVTPAYGCTQIGKNDSLKDVLMWGEGVEGGNIGGMVQR----------
----------VNMDVGMPKVVESLDDVHIK----------

----------FNAVGGKLFTWGDGDK----------

----------SISVTDQSSCSGCRMPFGLTR--HNCYNCGLLFCHSCS
SK----------MSKPGTHGSK----------
----------DQGEHQHHVETVSSLSAGLPR----------
----------AMSEKISAGR---
GGVELSVSQNTPAYK

This is not a full-length protein sequence.

SEQ ID NO: 31
>Top Ranked Protein Name [Species]: RecName: Full=Triosephosphate isomerase, chloroplastic; Short=TIM; Short=Triose-phosphate (Spot37)
MAAASSLVPQFSGLAVARERAPSLSSILFFHDASSQRRPFSTRRAPRGVVAMAGTGKFFV
GGNWKCNGMKDSISKLVADLNDAKMENDVDVAVAPPFIYIDQVNNSLTDRIDISAQNCWV
GKGGAFTGEISAEQLIDMGCKWVILGHSERRHIIGEDDQFIGKKAAYALSQNLKVIACIG
EKLEEREAGKTFEVCFQQMQAFADSITSWENVVIAYEPVWAIGTGKVATPEQAQEVHVAV
RDWLKKNISAEVASSTRIIYGGSVNGSNCSELAKQEDIDGFLVGGASLKGPEFATIVNSV
TSKKVAV*

Predicted MW= 33.10kDa; Predicted pI= 6.15

SEQ ID NO: 32
>Top Ranked Protein Name [Species]: RecName: Full=V-type proton ATPase catalytic subunit A; Short=V-ATPase subunit A; AltName: Full=Vac (Spot 13)
MAYGDRLTTFEDSEKESEYGYVRKVSGPVVVADGMGGAAMYELVRVGHDNLIGEIIRLEG
DSATIQVYEETAGLMVNDPVLRTHKPLSVELGPGILGNIFDGIQRPLKTIALKSGDVYIP
RGVSVPALDKDTLWEFEPKKLAAGDLLTGGDLYATVFENTLMQHHVALPPGSMGKITYIA
PAGQYSLKDTVLELEFQGVKKQFTMLQTWPVRTPRPVAAKLAADTPLLTGQRVLDALFPS
VLGGTCAIPGAFGCGKTVISQALSKYSNSDTVVYVGCGERGNEMAEVLMDFPQLTMTLPD
GREESVMKRTTLVANTSNMPVAAREASIYTGITIAEYFRDMGYNVSMMADSTSRWAEALR
EISGRLAEMPADSGYPAYLAARLASFYERAGKVKCLGGPDRTGSVTIVGAVSPPGGDFSD
PVTSATLGIVQVFWGLDKKLAQRKHFPSVNWLISYSKYSKALESFYEKFDPDFIDIRTKA
REVLQREDDLNEIVQLVGKDALAESDKITLETAKLLREDYLAQNAFTPYDKFCPFYKSVW
MMRNIIHFNALANQAVERGAGSDGQKITYSVIKHRLGDLFYRLVSQKFEDPAEGEEVLVA
KFKKLYDDLSAGFRNLEDETR*

Predicted MW= 68.36kDa; Predicted pI= 5.09

FIG. 10I: Sequences of the forty-five proteins.

SEQ ID NO: 33
>Top Ranked Protein Name [Species]: regulator of ribonuclease activity A [Zea mays] (spot 84)
MAALPLATAEVCDANAHLIQNGELRALQPIFQIYGRRQVFAGPIVTLKVFEDNVLVREFL
EEKGNGRVLVVDGGGSMRCAILGGNPVQQAQNNGWAGIVVNGCIRDVDEINGCDIGVRAL
ASHPMKANKKGFGEKHVPVNIAGTRICDGEWLYADSDGILVSRMELTV*

Predicted MW= 18.06kDa; Predicted pI= 5.68

SEQ ID NO: 34
>Top Ranked Protein Name [Species]: retroelement pol polyprotein-like [Arabidopsis thaliana] (Spot36)

----------MTIDSELLTNISHRDVAR----------MKADLATCKQEGMTMEGYYGK---
----------ICASHHMTGNLELLSDMR----------

----------TPSYSGARYFLTIVDDYS--------
----------SDNGTEFLCMR----------
--FQSYLPIQFWGECILSAAYLINRTPSMLLQGKSPYEMLYK----------
----------LFDLEEQK----------
--------VNQTFSIVNLPPGK----------
----------EEVYMKLPQGFQCDDPSK----------

AMAFLTQELMWLK----------
QLADILTKALGEK

This is not a full-length protein sequence.

SEQ ID NO: 35
>Top Ranked Protein Name [Species]: ribosomal protein L10 [Elaeis guineensis] (Spot 72)
MTVKLSKSEKKIEYDKKLCRLLDEYSQVLIAAADNVGSNQLQNIRKGLRGDSVVLMGKNT
LIRRCIKIHAEKTGNKDYLNLLPLLVGNVGLIFTKGDLKEVREEVAKYKVGAPARVGLVA
PIDVVVPPGNTGLDPSQTSFFQVLNIPTKINKGTVEIITPVELIRKGDKVGSSEAALLAK
LGIRPFSYGLVIQAVYDNGSVFSPEVLDLTEDDLVEKFAAGVSMVTSLSLALSYPTLVAA
PHMFINAYKNVLAVAIATEYTFEQAEKVKEYLKDPSKFAVAVPVEAAAAAAAAPAAAAKE
EEKKEEPAEESDEDMGFSLFD*

Predicted MW= 34.66kDa; Predicted pI= 5.15

FIG. 10J: Sequences of the forty-five proteins.

SEQ ID NO: 36
>Top Ranked Protein Name [Species]: short chain type dehydrogenase, putative [Ricinus communis] (spot 75)
MIKTAVDAWGTVDILVNNAGITRDTLLMRMKKPQWQEVIDLNLTGVFLCTQAAAKLMMKK
KKGKIINMTSVIGLTGNIGQANYSAAKAGVIGFTKTVAREYASRNINVNAVAPGFIASDM
TAKLGADIETKFLQTIPLGRFGQPEEVAGLVEFLALNPAANYITGQVFTIDGGLVM*

predicted MW=18.84kDa; predicted pI=9.99

SEQ ID NO: 37
>Top Ranked Protein Name [Species]: Temperature-induced lipocalin [Elaeis guineensis] (Spot 53 & 82)
MATTSTKEMTVVKGLDVERYMGRWYEIASFPSFFQPKNGENTRATYTLNSDGTVHVLNET
WSDGKRDAIEGTAYKANPNSDEAKLKVKFYVPPFFPIIPVTGDYWVLYIDDDYQYALIGQ
PSRKYLWILCRQTHMDDEVYNLLLEKAKEEGYDVKKLHKTPQADPPPEAEAGPKDTKGIW
WIKSLEGK*

Predicted MW= 21.63kDa; Predicted pI= 5.77

SEQ ID NO: 38
>Top Ranked Protein Name [Species]: unknown [Picea sitchensis] (Spot38)
MAASIAFNPHVIPARSAAPRRVAPLQTLSAAPRLAARSLCFKSSLRSDGTAAFSGVRTQA
AVVEQASIEQAQNVEAPVAIVTGGSRGIGKAIALALGKAGCKVLINYATSTEEAEEVSKE
IEASGGQAIIFFGDISKEDDVESMIKIAADAWGTVDILVNNAGITRDTLLMRMKKSQWQE
VIDVNLTGVFLCTQAAAKLMMKKKKGKIINIASVVGLTGNAGQANYSASKAGVIGFTKTV
AREYASRNINVNAVAPGFIASPMTAQLGEDVEKKILQTIPLGRYGQPEEVAGLVEFLALN
PAADYITGQVFTIDGGMVM*

Predicted MW= 33.44kDa; Predicted pI= 8.79

SEQ ID NO: 39
>Top Ranked Protein Name [Species]: 17.6 kDa class I small heat shock protein (HSP17.6C-CI) (AA 1-156) [Arabidopsis thaliana](spot 81)
MSLIPRGWGFGSSIFDPWDSFEGFPFNSSLSSFPRPSFPSESSAFANARIDWKETPEAHV
FKADLPGLKKEEVKVEVEEGNVLQISGERSREQEEKTDTWHRVERSSGKFLRRFRLPENA
KMDRVKAAMENGVLTVTVPKEEVKKLEVRSIEISG*

Predicted MW= 17.63kDa; Predicted pI= 5.88

FIG. 10K: Sequences of the forty-five proteins.

SEQ ID NO: 40
>Top Ranked Protein Name [Species]: ABC1 family protein [Arabidopsis thaliana] (Spot 49)
MEFYTTCLPRSSMSYCAHPRLSPPVPRSKQFLSFRIKNAASTSSVPAPPATTPSSSRNGN
ITTKSLTEKLSSAMDQLDIERGVCIPFRKYTPETVRNKVLESRGAILSLIGRGVEIVWNL
GLYWSALTYDCLVGRDEEVVPYRARQLRNLLCNLGPSFIKAGQVLANRPDIIREDYMNEL
CILQDDVPPFPNQEAFSIIEEELGQPLEKVFSRISSETIAAASLGQVYRATLRETREDVA
IKVQRPGIEPIIYRDLFLFRTLASFLNGISLQKLGCNAELIVDEFGEKLLEELDYTLEAR
NIEDFLENFKNDPTVKIPRVYKQLSGRRVLVMEWIDGIRCTDPEAVKEAGIDVNGFLTVG
VSAALRQLLEFGLFHGDPHPGNIFAMRDGRIAYVDFGNVAVLSQQNKQILIDAVVHAVNE
DYAEMANDFTRLGFLASGTDVSPIIPALEAIWQNSAGKGLADFNFRSVTGKFNQLVYNYP
IRIPERFSLVIRSLLTQEGICFTLKPDFKFLEVAYPYIAKRLLTDPNPALRERLIQVLFK
DGLFQWKRLENLIVLAKENVAKMNQNPALQVTNTQNSRNWQVEKKLDLTETIKDGARMFL
IDAGIRRQLIMALTEDSKLHIQELVDVYRLVEDDVDIPAVAFEVLQDLPSVTRDLMLSWS
EAVLSDR*

Predicted MW= 75.32kDa; Predicted pI= 5.21

SEQ ID NO: 41
>Top Ranked Protein Name [Species]: Glutathione peroxidase [Triticum monococcum subsp. aegilopoides] (Spot 54)
MAGNSSQATQTVHDFTVKDARGNDVNLGTYKGKVLLIVNVASQCGLTNSNYTELTALYEK
YKDKGLEILAFPCNQFGAQEPGSNEQILEFACTRFKAEYPIFDKVDVNGDNAAPIYKFLK
SSKGGLFGESIKWNFSKFLVDKEGHVVDRYAPTTSPLSIEKDVKKLLGLN*

Predicted MW= 18.76kDa; Predicted pI= 7.34

SEQ ID NO: 42
>Top Ranked Protein Name [Species]: glutathione S-transferase [Matricaria chamomilla] (Spot41)
----------GIEYEYK-------SSLLLEMNPVHK----------
----------FWADFVDKK-----------GEEQETAKK

This is not a full-length protein sequence.

SEQ ID NO: 43
>Top Ranked Protein Name [Species]: glutathione-s-transferase theta, gst, putative [Ricinus communis] (spot43)
MGVKVYGPTMSTCTARVLLCLEEVGAEYELVPINLSTGEHKQPAHLARNPFGQVPAFEDG
ALMLHESRAIARYVSRKYKSSGADLLKEGGLEESAMVDVWLEVESHQFDPAIGPIFFQSF
IVPMIGGVPDQTVINTNLEKLCKVLDIYEARLSKTKYLAGDFFSLADLSHVPLLYYFMGS
PHASVVNSRPHVKAWWEAVSSRPACKKVTSAMPGSA*

Predicted MW= 23.72kDa; Predicted pI= 6.62

FIG. 10L: Sequences of the forty-five proteins.

SEQ ID NO: 44
>Top Ranked Protein Name [Species]: phospholipase D [Oryza sativa Japonica Group] (Spot 63)
MAQILLHGTLHVTIFEANSLSNPNRASGGAPKFIRQLVEGIEDTIGLGKGSSKLYATIDL
EKARVGRTRLITKEPVNPRWYESFHIYCAHMSANVIFTVKFDNPIGASLIGRAYLPVTEI
LNGEEVDRWIEICDEDRNPLDGGARIHVKVQYFDISKDRNWARGIRSAKYPGVPYTFFSQ
RQGCKVTLYQDAHVPDNFIPKIPLADGKYYEPHRCWEDIFDAISNAQHLIYITGWSVYTE
ITLVRDAKRQKPGGDVTLGELLKRKASEGVRVLMLVWDDRTSVGLLKKDGLMATHDEETA
NYFQDTDVHCVLCPRNPDDGGSFVQDLQISTMFTHHQKIVVVDHEMPNKSSQQRRIVSFV
GGIDLCDGRYDTQFHSLFRTLDTAHHDDFHQPNFADASIKKGGPREPWHDIHSRLEGPIA
WDVLYNFEQRWRKQGGKDLLVQLRDLADIVIPPSPVMFPEDRETWNVQLFRSIDGGAAFG
FPETPEDAARAGLVSGKDNIIDRSIQDAYINAIRRAKNFIYIENQYFLGSSFGWRADDIK
PEEVGALHLIPKELSLKIVSKIEAGERFTVYVVVPMWPEGVPESGSVQAILDWQRRTMEM
MYTDIILALQAKGIEANPKDYLTFFCLGNREVKKGGEYEPEEQPEADTDYSRAQQARRFM
IYVHTKMMIVDDEYIIIGSANINQRSMDGARDSEIAMGAYQPFYLSTRGLARGRIHGFRM
ALWYEHLGMLDDAFLHPESVECVQKVNRIADKYWDLYSSDNLDRDLPGHLLSYPIGVSSD
GVITELPGMEFFPDTRARVLGTKADYLPPILTT*

Predicted MW= 92.37kDa; Predicted pI= 5.85

SEQ ID NO: 45
>Top Ranked Protein Name [Species]: VFB2 (VIER F-BOX PROTEINE 2); ubiquitin-protein ligase [Arabidopsis thaliana](Spot 30)

----LSLDAKSEILPFLPCIFNRFDSVTK----------EITDLGMESFAR-
------LSCGSCTFGAKGINAMLEHCK----------
----------LQVTDIGLFGISK----------
----------RIGDQGLMSVAK----------

----------NLVACTLRR

This is not a full-length protein sequence.

FIG. 10M: Sequences of the forty-five proteins.