

Supplementary Material

Figure S1. The sequence of the homologues of the identified barley proteins. (Matched peptides shown in Bold Red. When the protein was selected as the predicted protein, the sequence of the predicted protein was blasted using blastp algorithm. The protein with the highest score was then selected as the functional homolog of “the predicted protein” and it was also presented in Table 1).

Spot 1. Predicted protein; gi|326517328; BAK00031; Score: 3526; [Hordeum vulgare subsp. vulgare].

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1  MAPALSRTLG PSSVAALRPS PSRGLPRAAL APQGRRPAGA RGVWEAGRE
51  RLVGARCASA VAEKTAGEEE AAGEEFYQA EVSRLMDLIV HSLYSHKEVF
101 LRELVSNASD ALDKLRFLSV TDPSVLADGG DMEIRIKPDP DAGTITITDS
151 GIGMTKDELK DCLGTIAQSG TSKFLKALKE NKELGADNGL IGQFGVGFYS
201 AFLVAEKVVV STKSPKTDKQ YIWEABANSS SYVIREETDP EKMLTRGTQI
251 TLFLREDDKY EFADPTRIQG LVKNYSQFVS FIPTWQEKES RTVEVEEEES
301 KETEETAEGE KEKKKKTITE KYWDWELANE TKPIWMRNPK EVEETEYNEF
351 YKKAFNEFLD PLAHAFHTE GEVEFRSVLY IPGMAPLSNE EIMNPKTKNI
401 RLYVKRVFIS DDFDGELFPR YLSFVKGVVD SNDLPLNVSR EILQESRIVR
451 IMRKRLVRKT FDMIQDIADK DEKEDYKKFW ESFGKFMKLG CIEDSGNQKR
501 LAPLLRFYSS KNETDLISLD QYVENMPETO KAIYYIATDS LQSAKTAPFL
551 EKLLQKDIEV LYLIEPIDEV AIQNLQTYKE KKFVDISKED LELGDEDEDK
601 BESKQEYTL CDWIKQQLGD KVAKVQISKR LSSSPCVLVS GKFGWSANME
651 RLMKAQTLGD TSSLEFMRGR RIFEINPEHP IVKDLSAACK NEPESTEAKR
701 AVELLYETAL ISSGYTPESP AELGCKIYEM MTIALGGRWG RSGTBEAETN
751 VNDSSEAVVT EVVEPSEVRT ENENDPWRD
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Blast

heat-shock protein; CAA82945; [Secale cereale].

Spot 2. Predicted protein; gi|326492960; BAJ90336; Score: 2581;[Hordeum vulgare subsp. vulgare].

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1  MSIFTSQVSA MASASPSSSL FVSRRRPVAV PLQMRVARGG RPRGLTMRVT
51  CEKVVGIDLG TTNSAVAAME GGKPTVITNA EGQRTTPSVV AYTKGGERLV
101 GQIAKRQAVV NPENTFFSVK RFIGRKMAEV DDEAKQVSYN VVRDENGNVK
151 LDCPAIGKQF AABEISAQVL RKLVDASKF LNDKITKAVV TVPAYFNDSQ
201 RTATKDAGRI AGLEVLRIN BPTAASLAYC FEKKNNETIL VFDLGGGTFD
251 VSVLEVGDGV FEVLSTSGDT HLGGDDFDKK IVDWLASTFK NDEGIDLLKD
301 KQALQRLTEA AEKAKMELST LTQANISLPF ITATADGPKH IEATLSRAKF
351 BEELCSNLIDR LKTPVNNALK DAKLSISNLD EVILVGGSTR IPSVQETVRK
401 ITGKDPNVTV NPDEVVSLGA AVQGGVLAGD VKDVLVDVT PLSIGLETLG
451 GVMTKIIPRN TTLPTSKSEV FSTAADGQTS VEINVQGER EFVRDNKSLG
501 SFRLDGIPPA PRGVPQIEVK FDIDANGILS VAAVDKGTGK KQDITITGAS
551 TLPKDEVERM VEEADKFAQE DKEKRDAIDT KNQADSVVYQ TEKQLKELGD
601 KVPAPVKEKV DVKLQELKDA IAGGSTQSMK TSMEALNQEVE MQIGQAMYNQ
651 TSAGGAGSTD AEAEPSPSAG STSSGKGPND GDVIDADFTD SN
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Blast

70 kDa heat shock protein; ACT65562.1; [Triticum aestivum].

Spot 3. Predicted protein; gi|326506132; BAJ91305; Score: 5974; [Hordeum vulgare subsp. vulgare].

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1  MAAKGDPAP  GIDLGTTYSC  VGVWQHDRV  IANDQGNRT  TPSYVAFTDS
51  ERLIGDAAKN  QVAMNPINTV  FDAKRLIGRR  FTDSTVQSDI  KLWPFKVVAG
101 PGDKPMINVQ  YKGEEKQFAA  EBISSMVLIK  MREIABAFGL  STVKNVAVTV
151 PAYFNDSSQR  ATKDAGVIAG  INVLRIINEP  TAAAIAYGLD  KKASSVGEKN
201 VLIFDLGGGT  FDVSLLTIEE  GIFEVKATAG  DTHLGGEDFD  NRMVNHVFQE
251 PKRKNKKDIS  GNPRALRLR  TSCERAKRTL  SSTAQTITIE  DSLFEGIDFY
301 STITRARFEE  MNMDLFRKCM  EPVEKCLRDA  KMDKSTVHDV  VLVGGSTRIP
351 KVQQLQDFF  NGKELCKSIN  PDEAVAYGAA  VQAAILSGEG  NEKVQDLLLL
401 DVTPLSLGLE  TAGGVMTVLI  PRNTTIPTKK  EQVFSTYSDN  QPGVLIQVYE
451 GERTRTRDNN  LLCKFELSGI  PPAPRGVPQI  TVCFDIDANG  ILNVSAEDKT
501 TGQKNKITIT  NDKGRLSKEE  IEKMVQBAEK  YKSEDEEHKK  KVESKNALEN
551 YSYNMRNTIK  DEKIASKLPA  DDKKKIEEAI  DAAIQWLDTN  QLAEADEFED
601 KMKELEALCN  PIIAKMYQGA  GADMEGGMDD  DTPAASGGPG  PKIEEVD

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Blast

heat shock protein 70; CAA47948.2; [Oryza sativa Indica Group].

Spot 4. RuBisCO large subunit-binding protein subunit alpha, chloroplastic (60 kDa chaperonin subunit alpha); gi|134102; P08823; Score: 15416; [Triticum aestivum].

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1  GADAKEIAFD  QKSRAALQAG  VEKLANAVGV  TLGPRGRNVV  LDEYGNPKVV
51  NDGVTIARAI  ELANPMENAG  AALIREVASK  TNDSAGDGTT  TACVLAREII
101 KLGILSVTSG  ANPVSLLKGI  DKTVOGLIEE  LERKARPVKG  SGDIKAVASI
151 SAGNDELIGA  MIADAIDKVG  PDGVLSEISS  SSFETTVDVE  EGMEIDRGYI
201 SQPFVTNLEK  SIVEFENARV  LITDQKITSI  KEIIPILLEQT  TQLRCPLFIV
251 AEDITGEALA  TLVVNKLGI  INVAAIKAPS  FGERRKAVLQ  DIAIVTGABY
301 LAKDLGLLVE  NATVDQLGTA  RKITIHOTTT  TLIADAASKD  BIQARVAQLK
351 KELSETDSIY  DSEKLAERIA  KLSGGVAVIK  VGATTETELE  DRQLRIEDAK
401 NATFAAIEEG  IVPGGGAAYV  HLSTYVPAIK  ETIEDHDERL  GADIIQKALQ
451 APASLIANNA  GVEGEVVEIK  IKESWEMGY  NAMTDKYENL  IESGVIDPAK
501 VTRCALQNAA  SVSGMVLTTQ  AIVVEKPKPK  PKVAEPABEQ  LSV

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Spot 5. RuBisCO large subunit-binding protein subunit beta, chloroplastic (60 kDa chaperonin subunit beta); gi|2493650; Q43831; Score: 11239; [Secale cereale].

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1  PQIVNDGVTV  AREVELEDPV  ENIGAKLVRQ  AAKTNDLAG  DGTTSVVLV
51  QGLIAEGVKV  IAAGANPVQI  TRGIEKTAKA  LVLELKKMSK  EVEDSELADV
101 AAVSAGNNYE  IGNMIAEAMS  KVGRKGVVTL  BEGRSSENNL  YVVEGMQFER
151 GYISPYFVTD  SEKMTTEYEN  CKLLLVDKKI  TNARDLINVL  EBAIRGQYPI
201 LIIAEDIEQE  ALATLVVNKL  RGLKICAIAK  APGFGERKTQ  YLDDIAILTG
251 GTVIRDEVGL  TLDKADNTVL  GTAAKVVLTG  ESTTIVGDGS  TQREVTKRVA
301 QIKNLIEAAE  QDYEKEKLE  RIAKLAGGVA  VIQVGAQTET  ELKEKKLRVE
351 DALNATKAAV  EEGIVVGGGC  TLLRLAAKVD  AIKDTLENDE  QKVGAEIVRR
401 ALCYPLKLI  KNAGVNGSVV  TEKVLSNDNF  KFGYNAATGQ  YEDLMAAGII
451 DPTKVVRCL  EHAASVAKTF  LTSDVVVVEI  KEPEAAPLAN  PMDNSGFGY

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Spot 6. RuBisCO large subunit-binding protein subunit beta, chloroplastic (60 kDa chaperonin subunit beta); gi|2493650; Q43831; Score: 4325; [Secale cereale].

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1  PQIVNDGVTV  AREVELEDPV  ENIGAKLVRQ  AAKTNDLAG  DGTTSVVLV
51  QGLIAEGVKV  IAAGANPVQI  TRGIEKTAKA  LVLELKKMSK  EVEDSELADV
101 AAVSAGNNYE  IGNMIAEAMS  KVGRKGVVTL  BEGRSSENNL  YVVEGMQFER
151 GYISPYFVTD  SEKMTTEYEN  CKLLLVDKKI  TNARDLINVL  EBAIRGQYPI
201 LIIAEDIEQE  ALATLVVNKL  RGLKICAIAK  APGFGERKTQ  YLDDIAILTG
251 GTVIRDEVGL  TLDKADNTVL  GTAAKVVLTG  ESTTIVGDGS  TQREVTKRVA
301 QIKNLIEAAE  QDYEKEKLE  RIAKLAGGVA  VIQVGAQTET  ELKEKKLRVE
351 DALNATKAAV  EEGIVVGGGC  TLLRLAAKVD  AIKDTLENDE  QKVGAEIVRR
401 ALCYPLKLI  KNAGVNGSVV  TEKVLSNDNF  KFGYNAATGQ  YEDLMAAGII
451 DPTKVVRCL  EHAASVAKTF  LTSDVVVVEI  KEPEAAPLAN  PMDNSGFGY

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Spot 7. RuBisCO large subunit-binding protein subunit beta, chloroplastic (60 kDa chaperonin subunit beta); gi|2493650; Q43831; Score: 2326; [Secale cereale].

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1 PQIVNDGVTV AREVELEDPV ENIGAKLVRQ AAKTNDLAG DGTTSVVL
51 QGLIABGVKV IAAGANPVQI TRGIEKTAKA LVLELKKMSK EVEDSELADV
101 AAVSAGNNYE IGNMIAEAMS KVGGRGVVTL EEGRSSENNL YVVEGMQFER
151 GYISPYFVTD SEKMTTEYEN CKLLLVDDKI TNARDLINVL EEAIRGQYPI
201 LIIAEDIEQE ALATLVVNKL RGSLLKICAIK APGFGERKTQ YLDDIAILTG
251 GTVIRDEVGL TLDKADNTVL GTAAKVVLTK ESTTIVGDGS TQEEVTKRVA
301 QIKNLIEAAE QDYEEKLNE RIAKLAGGVA VIQVGAQTET ELKEKKLRVE
351 DALNATKAAV EEGIVVGGGC TLLRLAAKVD AIKDTLENDE QKVGAEIVRR
401 ALCYPLKLIK KNAGVNGSVV TEKVLSNDNF KPGYNAATGQ YEDLMAAGII
451 DPTKVVRCCLEHAASVAKTF LTSDVVVVEI KEPEAAPLAN PMDNSGFGY

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Spot 8. Predicted protein; gi|326490439; BAJ84883; Score: 2492; [Hordeum vulgare subsp. vulgare].

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1 MLSVSHPHPA ASTGPRHRKP LSTAHRRRRR CTYTIAALIL PGGGGPRGSP
51 PNGGKLILPG SGGGGGRGGG VGGGMLPRT PPTAPPQQLY QPFHPPSPSL
101 PENYRNLDLT ERLAVLRDRM GRWYEPAPLI SLSRSGFTT ASIEEATGMS
151 GVEQNRLVVA SQVRDSLSD DFPDDLHYF DSYGGPDLLY ELRFLNARQR
201 IVATKHTIER RLESGVREL ARSMKDFPQR RGDEGWDAFD RASAGDCRAY
251 ARFRLSREAI ANEDRIPELE RSLDVVETES ARARVELEVE RAIKKAAGEE
301 VEELEAKVDA RPAVPVVRML YGEISEASIV LLLPVVKETD GVQAVDLAPR
351 RSQTDADLGI VEVDKGWARW AVLPGWAPVM AVADEAVVIE LADGRVLPWR
401 SAENERVLVV ADRKRKEVVD EGIYVLEKGG KLVVERGNKL LEEGISQAAA
451 EVVTVVRPPK DEEDIIVGDE WD

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Blast

Any recognized protein with high homology.

Spot 9. Os06g0114000—hypothetical protein similar to 60 kDa chaperonin (Protein Cpn60); gi|115466004; NP_001056601; Score: 2136; [Oryza sativa Japonica Group].

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1 MASTFGATST VGLMAAPTGI VSDKKPSSL SSVSSVSVASR PRNARLQKRC
51 NFRVKAARKEL YFNKDGSAIK KLQTVGNKLA DLVGVTLGPK GRNVVLESKY
101 GSPRIVNDGV TVAREVELED PVENIGAKLV RQAAAKTNDL AGDGTTSVSV
151 LAQGLIABGV KVVAAGANPV QITRGIEKTA KALVEELKKL SKEVEDSELA
201 DVAASAGNN YEIGNMIAEA MSKVGGRGVV TLEGRSSEN NLYVVEGMQF
251 ERGYISPYFV TDSEKMSAEY ENCKLLLVDK KITNARDLIN VLEEIRGAY
301 PILIIAEDIE QEALATLVVN KLRGSLKIAA IKAPGFGERK TQYLLDIAIL
351 TGATVIRDEV GLSLDKADKS VLGTAAKVVL NKESTTIVGD GSTQEEVTKR
401 VAQIKNLIEA AEQEYEKEKL NERIAKLAGG VAVIQVGAQT ETELKEKKLR
451 VEDALNATKA AVEEGIVVGG GCTLLRLAAR VDAIKDNLEN DEQKVGAEIV
501 RRALSYPKLK IAKNAGVNGS VVTEKVLSND NFKPGYNAAT GQYEDLMAAG
551 IIDPTKVVRRC CLEHAASVAK TFLTSDVVVV EIKEPEPAPV TNPMDNSGYG
601 Y

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Spot 10. Ribulose biphosphate carboxylase/oxygenase activase A, chloroplastic; (RuBisCO activase A); gi|12643756; Q40073; Score: 4802; [Hordeum vulgare subsp. vulgare].

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1 MAAAFSSTVG APASTPTNFL GKLLKKQVTS AVNYHGKSSK ANRFTVMAAE
51 NIDEKRNTDK WKGLAYDISD DQQDITRGKG IVDLSLQAPT GHGTHEAVLS
101 SYEYVSQGLR KYDFDNTMGG FYIAPAFMDK LVVHLSKNFM TLPNIKIPLI
151 LGIWGGKGGG KSFQCELVFA KMGINPIMMS AGELESGNAG EPAKLIRQRY
201 REAADMIKKG KMCCFLINDL DAGAGRMGGT TQYTVNNQMV NATLMNIADA
251 PTVVQLPGMY NKRENPRVPI VVTGNDFTSL YAPLIRDRM EKFYWAPTRD
301 DRIGVCKGIF QTDNVSDSV VKIVDTFPGQ SIDFFGALRA RYVDDEVKRW
351 VGSTGIENIG KRLVNSRDGP VTFEQPKMTV EKLLEYGHML VQEQDNVKKV
401 QLADTYMSQA ALGDANQDAM KTGsfYgKGA QQGTLPVPEG CTDQNAKNYD
451 PTARSDDGSC LYTF

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Spot 11. RuBisCO large subunit-binding protein subunit beta, chloroplastic; (60 kDa chaperonin subunit beta); gi|2493650; Q43831; Score: 1048; [Secale cereale].

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1 PQIVNDGVTV AREVELEDPV ENIGAKLVRQ AAKTNDLAG DGTTSVVL
51 QGLIAEGVKV IAAGANPVQI TRGIEKTAKA LVLELKKMSK EVEDSELADV
101 AAVSAGNNYE IGMNIAEAMS KVGRRKGVVTL EGRSSNNL YVVEGMQFER
151 GYISPYFVTD SEKMTTEYEN CKLLLVDDKI TNARDLINVL EEAIRGQYPI
201 LIIAEDIEQE ALATLVVNKL RGSLLKCAIK APGFGERKTQ YLDDIAILTG
251 GTVIRDEVGL TLDKADNTVL GTAAKVVLTK ESTTIVGDGS TQEEVTKRVA
301 QIKNLIEAAE QDYEKEKLE RIAKLAGGVA VIQVGAQTET ELKEKKLRVE
351 DALNATKAAV EGGIVVGGGC TLLRLAAKVD AIKDTLENDE QKVGAEIVRR
401 ALCYPLKLI KAGVNGSVV TEKVLSNDF KPGYNAATGQ YEDLMAAGII
451 DPTKVVRCCLEHAASVAKTF LTSDVVVEI KEPEAAPLAN PMDNSGFGY

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Spot 12. Chloroplast translational elongation factor Tu; gi|6525065; AAF15312; Score: 1269; [Oryza sativa Japonica Group].

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1 MASLASASAS TSLVFSTSSS KPRLGSSVGF SSPARFRRTA AAAASKGTGR
51 RAGLLVMRAA RGKFERTKPH VNIGTIGHVD HGKTTILTAAL TMVLASVGS
101 APKHYDEIDA APEERARGIT INTATVEYET ETRHYAHVDC PGHADYVKNM
151 ITGAAQMDGA ILVVSADGP MPQTKHILL AKQGVGPKIV VFLNKKDQVD
201 DEELLQLVEL EVRELLSSYE YDGDEVPIVA GSALKALENL MANPAIKRGD
251 DEWVDGIFSL IDSVNYIPV PQRQTDLPFL LAVEDVFSIT GRGTVATGRI
301 ERGTVKVGDI VDIVGIRETR NCTVTGVEMF QKTMDAMAG DNVGLLLRCM
351 QKDDIERGMV LAKPASITPH TKFDVVVVL KKDEGGRHSP FPGYRPFY
401 MRTTDTGNV PKIMNDKDEE AKMCMGDRV KVVVELIQPV ACEQGMFAI
451 PEGGKTVGAG VINTILK

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Spot 13. Ribulose biphosphate carboxylase activase B; gi|7960277; AAF71272; Score: 1735; [Triticum aestivum].

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1 MASAFSSTVG APASTPTTFL GKKVKKQAGA LNYHGGNKI NNRVVRMAA
51 KKELDEGKQT DADRWKGLAY DISDDQDIT RGKGIVDSL FQAPMGDGTHE
101 AILSSYEYIS QGLRKYDFDN TMDGLYIAPA FMDKLIVHLA KNFMTLPNIK
151 VPLILGIWGG KGQKSFQCE LVFAKMGINP IMMSAGELES GNAGEPAKLI
201 RQRYREAAI IKKGKMCCLF INDLADAGAR MGGTTQYTVN NQMVNATLMN
251 IADAPTNVQF PGMYNKEENP RVPIIVTGND FSTLYAPLIR DGRMEKFYWA
301 PTREDRIGVC KGIFRTDNVP DEAVVRLVDT FPGQSIDFFG ALRARVYDDE
351 VRKWVGEIGV ENISKRLVNS REGPPTFDQP KMTIEKLMEY GHMLVQEQEN
401 VKRVQLADKY LSEALGQAN DDAMATGAFY GK

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Spot 14. RuBisCO large subunit-binding protein subunit beta, chloroplastic (60 kDa chaperonin subunit beta); gi|2493650; Q43831; Score: 1075; [Secale cereale].

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1 PQIVNDGVTV AREVELEDPV ENIGAKLVRQ AAKTNDLAG DGTTSVVL
51 QGLIAEGVKV IAAGANPVQI TRGIEKTAKA LVLELKKMSK EVEDSELADV
101 AAVSAGNNYE IGMNIAEAMS KVGRRKGVVTL EGRSSNNL YVVEGMQFER
151 GYISPYFVTD SEKMTTEYEN CKLLLVDDKI TNARDLINVL EEAIRGQYPI
201 LIIAEDIEQE ALATLVVNKL RGSLLKCAIK APGFGERKTQ YLDDIAILTG
251 GTVIRDEVGL TLDKADNTVL GTAAKVVLTK ESTTIVGDGS TQEEVTKRVA
301 QIKNLIEAAE QDYEKEKLE RIAKLAGGVA VIQVGAQTET ELKEKKLRVE
351 DALNATKAAV EGGIVVGGGC TLLRLAAKVD AIKDTLENDE QKVGAEIVRR
401 ALCYPLKLI KAGVNGSVV TEKVLSNDF KPGYNAATGQ YEDLMAAGII
451 DPTKVVRCCLEHAASVAKTF LTSDVVVEI KEPEAAPLAN PMDNSGFGY

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Spot 15. Predicted protein; gi|326523629; BAJ92985; Score: 3733; [Hordeum vulgare subsp. vulgare].

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1  MAFSPATTAA ATAAGAITFT SGRVASSPPS SLSSPFLPRA AGAIVARRGR
51  AGARAASAVP VRAQAAGAAK KKVLVVNTNS GGHAVIGFYF AKALLAAGHD
101 VTLTLTVGDEA SDKMKKPPFS RFSELTSA GA KTVWGDPA DV GAAVGAASFD
151 VVLDNNGKDL DAVKPVADWA KAAGVGQFLF ISSAGIYLQT DEPPHVEGDA
201 VKESAGHVG V EKYIAAEFGS WASFRPQYMT GSGNNKDCEE WFFDRVVRKR
251 PVPIPGSGMQ LTNISHARDL GSMLTLAVEN PDAAAGKIFN CVSDRGVTLD
301 GLAKMCAAAA GATVEIVHYD PAAVGVDAAK AAFPFRNMHFY AEPRAAKEVL
351 GWTSTTNLPE DLKERFAEYA SSGRGEKAMT FDLDDKILAA VGAAPVSVAA
401

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Blast

Any recognized protein with high homology.

Spot 16. Ferredoxin-NADP(H)oxidoreductase; gi|20302473; CAD30025; Score: 1976; [Triticum aestivum].

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1  MAAQLTAALP SYSPATTKAA AGGSSPSSH F LAYPSRPRNV RINGVRAQVST
51  TEPTAEAPAP APAKPVKISK KQDEGVVTNK YRPKEPYVGR CLLNTRLTGD
101 NAPGETWHMV FSTEGEVPYR EGQSIGVIAD GEDKNGKPHK LRLYSIASSA
151 LGDFGDSKTV SLCVKRLVYT NDAGEVVKG V CSNFLCDLKP GSEVKITGPV
201 GKKMLMPKDP NATIIMLATG TGIAPFRSFL WKMFFEEHED YKFNGLAWLF
251 LGVPTSDTLL YKEEFKMEVE IGGENFR LDF AVSREQTNA A GEMMYIQTRM
301 A EYKEELWEM LKKDNTYVYM CGLKGMEKGI DDIMVDLAAK DGIDWIDYKK
351 QLKKAEQWNV EVY

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Spot 17. Predicted protein; gi|326500884; BAJ95108; Score: 1011; [Hordeum vulgare subsp. vulgare].

```

1  MAATYCA YPA ASAAAAANLT RRRPQTLNSP GALPAVRKPS RQPPSFLSFR
51  RPNALPPLR VAGADPQIVN GEDFPPMNDL IRLYKKAFLD GNEDVVSDIE
101 KAITSMEERER SKAASQFDSI TAEITSGKNK FLRLNADLEN FRKQTEKDRA
151 KFTSNIQVEL VQSLPLVDS FEKTNVEVTL BTEKEQKIST SYQGIYKQLV
201 ETLKSLGVGV VETVGKPFDP VVHEAIAREE STEFKAGIVS HEVHRGFLLR
251 ERVLRPAAVK VSTGPGDQNT SSTTSEEPVE DTKEDAAV

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Blast

Any recognized protein with high homology.

Spot 18. cp31BHv (nucleic acid-binding protein); gi|3550483; CAA11893; Score: 1081; [Hordeum vulgare subsp. vulgare].

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1  MATSAMTLAM SAATEASLFH PAFAAQHKLA PASASLPLIF SRAPLLRSTR
51  PRVPLTPLVT SSDAAEAGLD WADAEAEET VTEEEPVVAA SGGDAGYTAE
101 PPEEAKVYVG NLPYD VDSER LAQLFDQAGV VEVAEVIYNK ESGQSRGFGF
151 VTMSTIEEAD KAIETFNRYN ISGRLLNVNR AAQRGSRVER PPRQFASSFR
201 AYVGNLPWQA EDSRLVQMFS EHGEVVNATI VYDRETGRSR GFGFVTMASK
251 EDLDSAISAL DGQEMDGRPL RVNVAAERPQ RGF

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Spot 19. cp31BHv (nucleic acid-binding protein); gi|3550483; CAA11893; Score: 1170; [Hordeum vulgare subsp. vulgare].

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1  MATSAMTLAM SAATEASLFH PAFAAQHKLA PASASLPLIF SRAPLLRSTR
51  PRVPLTPLVT SSDAAEAGLD WADAEAEET VTEEEPVVAA SGGDAGYTAE
101 PPEEAKVYVG NLPYD VDSER LAQLFDQAGV VEVAEVIYNK ESGQSRGFGF
151 VTMSTIEEAD KAIETFNRYN ISGRLLNVNR AAQRGSRVER PPRQFASSFR
201 AYVGNLPWQA EDSRLVQMFS EHGEVVNATI VYDRETGRSR GFGFVTMASK
251 EDLDSAISAL DGQEMDGRPL RVNVAAERPQ RGF

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Spot 20. Predicted protein; gi|326504940; BAK06761; Score: 3114; [Hordeum vulgare subsp. vulgare].

```

1 TGSQVVYSKY AGTEVEYNNS KHLIMKEDDI IGILESDDVK DMKPLNDRVL
51 IKVAEASDKT EAGLILTETT KEKPSIGTVV AVGPGLDDEE GNRQPLSVSP
101 GSTVLYSKYA GGEFKGTDGT NYIVLRVSDV MAELS

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Blast

Chaperonin; ACG41110.1; [Zea mays].

Spot 21. Predicted protein; gi|326490876; BAJ90105; Score: 348; [Hordeum vulgare subsp. vulgare].

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1 MALASTSPLA ATVARPKAPA SLTRCSRRL QRISQATTD RSGGGNASNT
51 SPAPPRWRVA VSAALAAAVV VAMPAHADLN KYEADQGEF GIGSAAQFGN
101 ADLKNTVHVN ENFRANFTS ADMRESDFSG STFNGAYMEK AVAFRANFTG
151 ADLSDTLMDR MVLNEANLTN AVLSRTVLTR SDLGGATIEG ADFSDAVIDL
201 PQKLALCKYA SGTNPITGVS TRKSLGCGNS RRNAYGSPSS PLLSAPPPKL
251 LDRDGFCDEA SGLCDAK

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Blast

Any recognized protein with high homology.

Spot 22. ES2A [gibberellic acid (GA3)inducible]; gi|929669; CAA55976; Score: 987; [Hordeum vulgare].

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1 MSSWLQEKSG EVVETTOVKA GEATKMASET GQSIQDRAVE AKDQTGSFLG
51 EKSEAVTKSA SETTEAAKKM GGEAMGKVSE TVQAGQDRAV EGKDQTASFL
101 GEKTEAVKKT ATETADAAKE KSTEAAQHVO DTAABYTKDT PVAPKENVFQ
151 KAGGNIVGAA TDAKDAVMNT LGMGGDK

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Spot 23. Predicted protein; gi|326504940; BAK06761; Score: 230; [Hordeum vulgare subsp. vulgare].

```

1 TGSQVVYSKY AGTEVEYNNS KHLIMKEDDI IGILESDDVK DMKPLNDRVL
51 IKVAEASDKT EAGLILTETT KEKPSIGTVV AVGPGLDDEE GNRQPLSVSP
101 GSTVLYSKYA GGEFKGTDGT NYIVLRVSDV MAELS

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Blast

Chaperonin; ACG41110.1; [Zea mays].

Spot 24. Os02g0622400; gi|115447377; NP_001047468; Score: 113; [Oryza sativa Japonica Group].

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1 MAETVFTPSL EGMKHVKSES SVILTKPFLD VCKQILPVLD KFGAAMALVK
51 SDIGGNITRL ENKYSSDPSK YEQLYSMVQE EVQNKTAQGS SSCTNGLLWL
101 TRAMDFLVEL FRNLLEHQDW TMSQACTDSY TKTLKKWHGW LASSSFTVAM
151 KLAPNREKFM EVISGTGDIK ADIEKFCTTF YPFLKENHDF LASVGLDDLK
201 AS

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Blast

glycolipid transfer protein-like; BAD22518.1; [Oryza sativa Japonica Group] >.

Spot 25. Unnamed protein product; gi|11587; CAA25265; Score: 708; [Hordeum vulgare].

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1 MSPQTETKAG VGFQAGVKDY KLTYTPEYE TKDIDILAAF RVSPQPGVPP
51 EEAGAAVAEE SSTGTWTTVW TDGLTSLDRY KGRCYHIEPV AGEDSQWICY
101 VAYPLDLFEE GSVTNMFTSI VGNVFGFKAL RALRLDLRI PPTYSKTPQG
151 PPHGIQVERD KLNKYGRPLL GCTIKPKLGL SAKNYGRACY ECLRGGLDFT
201 KDDENVNSQP FMRWRDRFVF CAEAIYKSQA ETGEIKGHYL NATAGTCEEM
251 IKRAVFAREL GVPIVMHDYL TGGFTANTTL AHYCRDNGLL LHIHRAMHAV
301 IDRQKNHGMH FRVLAKALRM SGGDHIHSGT VVGKLEGERE MTLGFVDLLR
351 DDFIEKDRAR GIFFTQDWVS MPGVIPVAGS GIHVWHMPAL TEIFGDDSVL
401 QFGGGTLGHP WGNAPGAAAN RVALEA

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Blast

ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit; YP_874661.1; Hordeum vulgare subsp.

Spot 26. Germin-like protein 1; gi|4239821; BAA74702; Score: 2249; [Oryza sativa].

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1 MAKAVMMLPV LLSFLLLPFS SMALTQDFCV ADLTCSDTFA GYPCKASVGA
51 GDFAYHGLAA AGNTSNLIKA AVTPAFVGQF PGVNGLGISA ARLDIAVGGV
101 VPLHTHPAAS ELLFVTQGTV AAGFITSSSN TVYTRTLYAG DIMVFPQGLL
151 HYQYNAGQSA AVALVGFSGP NPGQLINDYA LFANNLPSAI VEKVTFLDDA
201 QVKKLKSVLG GSG

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Spot 27. Predicted protein; gi|326500102; BAJ90886; Score: 161; [Hordeum vulgare subsp. vulgare].

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1 MSGVKKVADV AAKAGKAIDW DGMAMLVSE EARKEFANLR RTFEDVNHQL
51 QTKFSQEPQP IDWEYRKG I GSKVVDMYKE AYDSIEIPKY VDTVTPIYKP
101 KFDALLVELK EAETSLKES ERIEKEIAEM KEMKKKISTM TADEYFAKHP
151 ELKKKFDDM RNDYWG Y

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Blast

ATP synthase D chain, mitochondrial, putative; AAT40531.1; [Solanum demissum].

Spot 28. Eukaryotic translation initiation factor 5A1; gi|74048999; AAZ95171; Score: 447; [Triticum aestivum].

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1 MSDTDEHHFE SKADSGASKT YPQAGAIRK GGHIVIKARP CKVVEVSTSK
51 TGKHGHAKCH FVAIDIFNGK KLEDIVPSSH NCDVPHVDRQ DYQLIDITDD
101 GYVSLLETSG NTKDDLKLP T DDVLLGQIKT GFADGKDLIL SVMSAMGEEQ
151 ICAVKEIGGG K

```

Spot 29. RuBisCO large subunit-binding protein subunit beta, chloroplastic (60 kDa chaperonin subunit beta); gi|2493650; Q43831; Score: 1069; [Secale cereale].

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1 PQIVNDGVTV AREVELEDPV ENIGAKLVRQ AAKTNDLAG DGTTSVVL A
51 QGLIAEGVKV IAAGANPVQI TRGIEKTAKA LVLELKKMSK EVEDSELADV
101 AAVSAGNNYE IGMNIAEAMS KVGKGVVTL EGRSSNNL YVVEGMQFER
151 GYISPYFVTD SEKMTTEYEN CKLLLVDKKI TNARDLINVL EEAIRGQYPI
201 LIIAEDIEQE ALATLVVNKL RGLKICAIAK APGFGERKTQ YLDDIAILTG
251 GTVIRDEVGL TLDKADNTVL GTAAKVVLTK ESTTIVGDGS TQEEVTKRVA
301 QIKNLIEAAE QDYKEKLNE RIAKLAGGVA VIQVGAQTET ELKEKKLRVE
351 DALNATKA AV BEGIVVGGGC TLLRLAAKVD AIKDTLENDE QKVGAEIVRR
401 ALCYPLKLI A KNAGVNGSVV TEKVLSNDFN KPGYNAATGQ YEDLMAAGII
451 DPTKVVRCC L EHAASVAKTF LTSDVVVEI KEPEAAPLAN PMDNSGFGY

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Spot 30. Predicted protein; gi|326496140; BAJ90691; Score: 567;[Hordeum vulgare subsp. vulgare].

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  1 MAAATSSFAT LAVARPAAAA QRALLAAKAP SSALSLRGVG RVASPALSVS
 51 LQTRARFVAS ASAEPYAPEL QSKVTNKVYF DINIGNPVGK NVGRIVIGLY
101 GDDVPQTVEN FRALCTGEKG FGYKGSSFHR VIKDFMIQGG DFDKGNGTGG
151 KSIYGRIFKD ENFQLVHTGP GVLSMANAGP NINGSQFFIC TVKTPWLDGR
201 HVVFGQVLEG MDIVRMISS ETDRGDRPKK KVVISECGEL PVV

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Blast

cyclophilin-like protein; AAP44537.1; [Triticum aestivum].

Spot 31. Huntingtin interacting protein K; gi|195632082; ACG36699; Score: 142; [Zea mays].

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  1 MGAAGDEKAA MAASAAAAGA GAAEGEGAVD SKDLQQQSKA LDKLTDHVED
 51 RQLDSSRVQS AMAALASSKE ADWNAMRLRE KELAAVKINP ADVEIIASEL
101 ELDKKIAERT LREHKDAVA AVRFLLR

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