

Supplementary Material

Inactivation of *Escherichia coli* Using Biogenic Silver Nanoparticles and Ultraviolet (UV) Radiation in Water Disinfection Processes

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Table S1. Analysis of capping proteins of biogenic silver nanoparticles using UPLC-MS/MS, shotgun techniques, and identified using the protein BLAST server (NCBI, <https://blast.ncbi.nlm.nih.gov>) [1]:

AgNP-FU Proteins	NCBI RefSeq	Molecular Weight (kDa)	Score	% coverage	Sequence
Predicted-glutamine amino-transferase [<i>Fusarium oxysporum</i>]		28.3	110	6	MKFLSTLAGALAFTTTSASAIHRNTERTCITPGAIPDLKGS DIRNVGVVLFQALDMI DVFGPLDPLQLVSLSVQQLNLHLIAETLDPVSTAPVAMNKFNSFWPTIPPTKTFAD DLDDLIVPGGPGARNPNLGAVTDYIAKMAPKVKILMTICTGSGIAARAGVLDGH LAATNKNAWATMKAMGPKVNWVSPARFVIDGKIWSSSGVTSGLDLIFAF IETFWGAQQS QR IASIIEHV PRAATDDPFSQHFNITPTEA QPCPKA
Malate dehydrogenase [<i>R. solanacearum</i>]		35.4	92	5	MAKAPMRVAV TGAAGQIGYA LLFRIAAGEM LGKDQPVILQ LLEIPDEKAQKALKGVMMEI EDCAFLLAG MEAHADPMTA FKDVDVALLVGARPRGPGMERKDLLSANAQIFTAQGKALNAVASRNVKVLVVG PANTNAYIAMKSAPDLPRENFTAMLRLDHNRLSQIAAKTGKPVSSIEKLFVWGN HSPTMYADYRYATIDGQSVKDMINDPVWNNDVFLPTVGKRGAAIIEARGLSSAAS AANA AIDHVR DWVLGSNGKIVTMGIPSNGDYEIPQDVMFGFPVTTANGKYEYVKG F EVDAYSREKI NITLKELEEE RAGVQHLLG
Hypothetical, Zn-peptidase [<i>F. graminearum</i>] (FG06655.1)	XP_011326283.1	53.9	89	5	MAPPQEALDF VDFVNASPTP YHAVQSASAR FEKAGFKLIR ERDSWASTLRPGGKYLLTRN ASTIVAFTIG RKWRPGNPVA IVGAHTDSPC LRLKPVSKKT NVGFLQIGVE TYGGGIWTSW FDRDLSIAGR VLVKEGDNFV QKLVKVDKPLVRIPTLAIHL HRQTNFDPNK ETELFPIAGL VAAELNKDVK EKSEEKKDDG EEDEEFKPLK VITERHHPQV LDVIAAEAGV EVSDIVDFEL VLYDTQKSCIGGLADEFIFS PRLDNLGMTY CSVEGLIESV KNESLEEDGTIRLTVCFDHEEIGSTSAQG ANSNLLPSVI

					RRLSVLPGNRDASSEGSYEAVHHEGEDATAYEQTLRSFLVSADMAHSVHPNYAG KYESS HQPAMNGGTV VKINANQRYA TNSPGIVLIE ECARTAGVPL QLFVVRNDSP CGSTIGPLA AALGMR TLDLGNPQLSMHSI RETGGTADVG YGIRLFREFF EKYGSLEPKI LID
Hypothetical, dehydrogenase [F. graminearum and F. oxysporum] (FG02461.1)	XP_011318385.1	35.2	75	6	MFAASRIQRRAFSATARDLS KVTVLGAAGG IGQPLSLLK MNPR VTDLALYDIR GGPGVA ADISHVNTKS SVKGYEPNAA GLKEALSGAEVVLIPAGVPRKPGMTR DDLFN TNASIVR DLAKAAAEAAPKAKLLIIS NPV NSTVPIVKEV YKAAGVYNPK TLFGVTTLDV VRASRFVSEI KGTDPKDENI TVVGGHSGVT IVPLFSQSNH PDLSSNAELV KRVQFGGDEV VKAKDGAGSA TLSMAMAGAR MADSVLRAVQ GEKGVKEPAF VESPLYKDQG IEFFSSQVEL GPEGVEKIHPLGKLDANEK LVDAALVDLK KNIKGVAFV ASNPPK
2-Methylcitrate synthase [F. graminearum PH-1]	XP_011315788.1	52.0	74	4	MALNLTTSRR ALSSLKPLTR AAFVGARGYA TAEPDLKATL REAIPAKRELLKKVKAHSNK VLGEVKVENT LGGMRGLKAM VWEGSVLDANEGIRFHGRTIKDCQKELPKG KTGTEMLPEA MFWLLLTGQVPSVNQVRGFSRELAEKAQIPEFVSKMLNDFPKDLHPMTQFAMAVS ALNYESKFAKAYEQGINKADYWEPTFDDCISLLAK LPTIAAKIYQ NAYRGGGALP AEVDLEQDWS YNFAAMLGKG GKENENFQDL LRLYLALHGD HEGGNVSAHA THLVGSALSD PFLSYSAGLQGLAGPLHGLA AQEVLRWIIQ MKEAIPSNYT EQDVNDYLWS TLNSGR VVPG YGHAVLR KPDPRFEALMDYA AARPEIANDPVFQLVEKNSR IAEVLKKGKTKNPYPNVD SSSGVLFHHYGFHETLYYTA TFGVSR GLGPLAQLIWDR AL GLPIERPCKSI NLEGILKQVE GQ

Hypothetical protein FGSG_02204.1 [<i>F. graminearum</i> PH-1] Serine carboxy peptidase	XP_011318096.1	59.6	69	2	<p>MARGWFFVNCA AVLLALTAGV DAYTVPALSA RAKDSGPKAV</p> <p>NISVPVDHFNHNETIYEPHSD KKFPLRYWFD AQYYRKGGPV IILASGETSG</p> <p>EDRIPFLEHG ILQMLANATG GIGVILEHRY YGTSFPVPDL KPENMRFLST</p> <p>EQALADTAYFAQHVEFPDME EHNLTASTTP YIIYGGSYAG AFAAFARKIY</p> <p>PDLFWGGISS SGVTEAIVDY WQYFEAARLF APGDCAKVTQ KLTHAVDNIL</p> <p>LGDDKEEKKQLKIAFGLLGL RDDDFAMTIS QGIGGLQSN</p> <p>WDPASDSSSFLYCGSVSSD DILFASTRPLAPYVKKWLIS AGYKKQLKYM</p> <p>TNRFLNYIGY IRSNVESDKSGRCDGKTLQ CYSIRGSMND TKLDPNNMSR</p> <p>QWTYQTCTQW GYWQTGSGAP KDQLPMVSRLLIDVEYNTIPC</p> <p>REEFNITTPPNVESINKLGG FNFSYPRVAFIDGEYDPWRA ATPHAIGLPE</p> <p>RESTASEPFILIPYGVHHWDENGLAPGSEEIGLPPPAVKQAQQDIIDFTKAWLEDWE</p> <p>KEK GGATADL</p>
Hypothetical protein LOC100191904 Dehydrogenase [<i>F. fujikuroi</i>]	CAM90598.1	35.7	67	8	<p>MSSPHFSKVLVFGATGEVGS AVALEAHALG AHVSIALRDT</p> <p>TKTNEWISPSQERAADLQRI SADLTDPDSL KRAVHDTGAQ AAFIYAVRSK</p> <p>DALRGAIAAL RDAGIQYVVF LSTSQVRTAG TTKGDIRSIK PDHFIPWQHA</p> <p>QVEIALEELEVPAAVRAGF FASNPLRIYL DRSSEPKQVN LLAPVPHDP</p> <p>IDPKDIGRAA AAVLVNPRLYASGYQGEPKK DVVYLSGPAL LSQTEQWEII</p> <p>NRELVVAGKPEVKVNHITVE QYLENLAKLH VPDVVAKSLA</p> <p>KSMVETRALLYAPEDYEKSRG NVELLTGRKATSFDEFVKRE IPRYFD</p>
Malate dehydrogenase [<i>F. moniliforme</i> and <i>F. verticillioides</i>]		35.4	85	7	<p>MAKAPMRVAVTGAAGQIGYA LLFRIAAGEM LGKDQPVILQ</p> <p>LLEIPDEKAQKALKGVMMEI EDCAFPLLAG MEAHADPMTA FKDVDVALLV</p> <p>GARPRGPGME RKDLLSANAQ IFTAQGKALN AVASRNVKVL VVGNPANTNA</p> <p>YIAMKSAPDLPRENFTAMLR LDHNRALSQIAAKTGKPVSS IEKLFVWGNH</p> <p>SPTMYADYRY ATIDGQSVKD MINDPVWNND VFLPTVGKRGAAIIEARGLS</p>

					SAASAANAIDHVRDWVLGS NGKIVTMGIP SNGDYEIPQD VMFGFPVTTANGKYEVVKGF EVDAYSREKINITLKELEE RAGVQHLLG
Putative glucoamylase GMY1 [<i>F. verticillioides</i> and <i>F. graminearum</i>]	ABY89280.1	68.7	84	1	MYFVSSAFLGSLVQLQNVLG RPTFDERSLL QERQSSVDSF IKSESSIAIEQLLCNIGSDG CNSKNVATGI VIASPDQTDP DYFYTWTRDAALVFKYVVDV FINQYDAGLQRKIQEYIASQ AKLQGVSNPS GSLSDGSLG EAKFNVDMSAFTGGWGRPQR DGPALRATAM ITYANWLIAN GYTSTANDIV WPVVRNDLNY VAQYWNQTGF DLWEEVKGSS FFTTGSQYRGAALAKKLGKS GDNYSNIAPQALCFLQTYWI SSGKYVDSNI NVNDGRTGKD ANSILSSIHN FDPALNCDPA TFQPCSDKALANHKAVTDSF RSWNINKGIS QGSAVAVGRY VEDVYYNGNPWYLATLAAAE QLYDAIYVWKQQGSITVSDV SLSFFKDLVS SVSTGTYSAD SATFKSITDAVSKYADGYVA IVAKYVGTGDGHLAEQFDKND GHPLSATDLTWSYAAFLSAA DRRAGVIPPS WAGSVAAPVN QCGTNTVAGS YSSATATSFP ASQTPKGGVP TPTGTQTSTS TSTSTSSST GTSCPTATSV AVTFQEVVTTNFGDTIKIVG NIAALGNWDTSKAVALSASD YTASNPVWKATISLTAGQSI QYKYINVKKD GSLTWEKDPN RTYAVPKTCATTATKSDKWQ S
Hypothetical protein LOC100191904 Reductase [<i>Botryotinia</i> <i>fuckeliana</i>]		35.7	69	8	MSSPHFSKVL VFGATGEVGS AVALEAHALG AHVSIALRDT TKTNEWISPSQERAADLQRI SADLTDPDSL KRAVHDTGAQ AAFIYAVRSK DALRGAIAAL RDAGIQYVVV LSTSQVRTAG TTKGDIRSIK PDHFIPWQHA QVEIALEELEVPHAAVRAGF FASNPLRIYL DRSSEPKQVN LLAPEVPHDP IDPKDIGRAA AAVLVNPRLY ASGYQGEPKK DVVYLSGPAL LSQTEQWEII NRELVVAGKPEVKVNHITVE QYLENLAKLH VPDVVAKSLA KSMVETRALYAPEDYEKSRG NVELLTGRKATSFDEFVKRE IPRYFD

NAD(P) ⁺ -specific glutamate dehydrogenase [<i>F. graminearum</i> , <i>F. oxysporum</i> and <i>F. oxysporum f.</i> <i>sp. lycopersici</i> 4287]	XP_018234470.1	48.8	62	4	<p>MSHLPQEPEF EQAYGELASA LENSSEFNEH PEYRTALAVA AIPERVIQFRVWVNDKGNL QVNRGYRVQFNGALGPYKGG LRFHPSVNLS ILKFLGFEQI 101 FKNALTGLNM GGGKGGADFD PKGKSDAEIR RFCQAFMTEL SKHIGAETDVPAGDIGVGR EIGYLFGAYR KFANRWEGVL TGKGLSWGGS LIRPEATGYG LVYYVEYMLK HANRGTFEKG RVALSGSGNV AQYAALKIIE LGGSVVSLSDSKGALVAKEG SSFTPEQIHN IAALKIKHQA LTTFEHGDQFTWIEGARPWVHVKGVDIALP SATQNEVSKE EAQALVDAGA FIVAEGSNMG CTAEAIDVFEAHRKEKGAEA LWYAPGKASN CCGVAVSGLE MAQNSQRIQW TEKEVDDRLK AIMKDAFVAG LETAQKYVEA KEGELPSLIA GSNIAGFIKV AEAMHDQGDWF</p>
Porin [<i>Ralstonia</i> <i>pickettii</i>]	WP_012763112.1	39.3	152	16	<p>MKMKLFAAAVAALAAGGAYA QSSVTLYGVV DAGLTYANKV PNGNGGGSSRVGLDSGGLSG SRWGLRGVED LGGGLKGIFN LESGFTIDDG KSAQGGRLFG RNAYVGLQGQWGQLTLGRQQ NLLYDFSLIY DPMIAASRYG LANQDAFFSGRADNAVKEYG TFGGLSVSAL YSFNRDNEQ PGLPKLGREW SLGANYAGGP FSVGAVYDQS NQTTIATADN KEQRATIAGT YAFGPAKLYA GYRWYHANFATVAGNGNLRS NLYWLGAGYQ ATPALTLTGT AYYQQFKNSN AGNPSWLFVVG TDYALSKRTDAYFNLAYAKN SSGSGLGVN LNKTDSYAGT TLGSTNFGNQNVYSSPAAGN ANQFGATVGI RHKF</p>
ADP, ATP carrier protein [<i>F. oxysporum f.</i> <i>sp. lycopersici</i> 4287]	XP_018243474.1	33.6	113	7	<p>MSEQPQKVLG MPPFVADFLM GGVSAAVSKT AAAPIERVKL LIQNQDEMLKTGRLDRKYNG IGDCFKRTMA DEGVMSLWRG NTANVIRYFTQALNFAFRDKFKKMFYKK DKDGYALWMA GNLASGGAAG ATSLLFVYSL DYARTRLANDAKNAKSGGDR QFNGLVDVYK KTLASDGIAG LYRGFMPSVA GIIVYRGLYF GMYDSIKPVV LTGPLANNFL ASFALGWIVTTGAGIASYPL DTIRRRMMMTSGEAVKYKNT LDAARQIVAK EGVKSLEFKGA GANILRGVAG AGVLSIYDQL QVLLFGKAFK</p>

ATP synthase beta chain, mitochondrial precursor [<i>Neurospora</i> <i>crassa</i> and <i>F. oxysporum</i> f. <i>sp. cubense</i> race 4]	XP_963253.2; EMT62383.1	55.5	112	6	<p>MFKSGISAF A RTARPSFAAA SRRAVRPAAL NLRAPALSRF</p> <p>ASSAGVGDGKIYQVIGAVVD VKFDTDKLPP ILNALETQNN GQKLVLVEVSQ</p> <p>HLGENVVRCI AMDGTEGLVR GAKASDTGAP ITIPVGPATL GRIINVTGDP</p> <p>IDERGPIKTDKFRPIHAEAP EFVEQSTTAE ILVTGIKVVD LLAPYARGGK</p> <p>IGLFGGAGVG KTVFIQELIN NIAKAHGGYS VFTGVGERTR EGNDLYHEMQ</p> <p>ETSVIQLDGD SKVALVFGQM NEPPGARARV ALTGLTIAEY FRDEEGQDVL</p> <p>LFIDNIFRFT QAGSEVSALL GRIPSAVGYQ PTLAVDMGQM QERITTTTKG</p> <p>SITSVQAVYVPADDLTDPAP ATTFAHLDAT TVLSRGISEL GIYPAVDPLD</p> <p>SKSRMLDPRI VGQEHYETAT RVQQILQEYK SLQDIILG MDELSEADKL</p> <p>TVERARKIQRFLSQPFTVAQ VFTGIEGKLV DLKDTIASFK</p> <p>AILAGEGDDLPEGAFYMGVD FASARAKGEK ILAELEGQA</p>
Mitochondrial outer membrane protein porin [<i>F. graminearum</i>]	PCD31551.1	37.1	87	3	<p>MSVPAFSDIA KPANDLLNKD FYHLSATTFE FKDTAPNGVA</p> <p>FKVTGKSSHEKATSAAIEGK YTDKPTGTTS PSSSSTLSQ SPSPSPPPVS</p> <p>NPRRKQNLPS LSVSRILGPK SGWPIGFATF VRPGFAQLLM FYSRTGLTLT</p> <p>QTWNTANALDTKIEVADSLA KGLKLEGLFN FLPATAAKGA KFNLFHKQPG</p> <p>FHGRAFFDLL KGPVANVDV VGHEGFLAGA SAGYDANKAA LTAYSAAVGY</p> <p>AAPQYSAAITASDNLSVFAA SYHVKVNSQV EAGAKATWNS KTGNVAGLEV</p> <p>ASKYRIDPVS FTKVKINDRG IAALAYNVLL REGVTLGLGG SFDTQKLDQA</p> <p>THKLGASFTFEG</p>

6-Phospho gluconate dehydrogenase, decarboxylase 1 [<i>Aspergillus niger</i> CBS 513.88]	XP_001394208.2	54.1	87	4	MADQAVADFG LIGLAVMGQN LILNAADHGF TVCAYNRTTS KVDRFLENEAKGKPIVGAHS VEEFCAKLKR PRRIMLLVMA GKPVDQFIES LLPHLEKEDI IIDGGNSHFP DSNRRTKYLA EKGIRFVGS G VSGGEEGARY GPSLMPGGNEEAWPYIKDVF QSISAKSDGE ACCDWVGDEG AGHFVKMVHN GIEYGDMQLI CEAYDILKRG LGLPAKEIAD VFAKWNKGVL DSFLIEITRD VLYFNDNDGTPLVEKILDKA GQKGTGKWT AINALDLGMPV TLIGEAVFSR CLSALKDERI RASSLLDGPT PEFTGDKQAF IDDL EQALYA SKIISYAQGF MLIQEAAREYGWKL NKPSIA LMWRGGCIIR SVFLKDITNA YRKNPDLENL LFDEFFNTAI KKAQSGWRNV VSKGALWGIP TPAFSTALS F YDGYRTRDLP ANLLQAQRDYFGAHTFRIKP EHANETYPEG KDIHVNW TGR GGNVSASTYI A
Predicted protein Glutamin amidotransferase [<i>F. oxysporum</i>]		28.3	84	6	MKFLSTLAGA LAFTTTSASA IAHRNTERTC ITPGAIPDLK GSDIRNVGVVLFQALDMIDV FGPLDPLQLV SLSVQQNLNH LIAETLDPVS TAPVAMNKFN SSFWPTIPPT KTFADDLDLD LLIVPGGPGA RNP NLGAVTD YIAKMAPKV KILMTICTGSG IAARAGVLDG HLAATNKNAW ATMKAMGPKV NWVSPARFVI DGKIWSSSGV TSGLDLIFAF IETFWGAQQS QR IASIIIEHV PRAATDDPF SQHFNITPTEA QPCPKA IASIIIEHVPR
Quinase, HSP70 actin [<i>F. graminearum</i> and <i>F. oxysporum</i>]	XP_018238735.1	85.9	82	4	MSVVGIDFGT LKTVIAIARN RGV DVVTNEV SNRATPSLVG FGPKSRYLG EAAKTQEISNL KNTVSSLKRL AGRSFNDPDI QVEQQYVTAP LVDVNGQVGA EVNYLGKKEH FTATQLV GMY LSKIKQTAGA ELKLPVQDVC MSVPPWFTDVQRRALIDA AE IAGLRVLR LI NDGTAAALGW GITKLDLPAP EEPARRVCFI DIGHSSYTVS IVEFKKGELA VKATTWDKDF GGRDFDRALV EHLAKEFKGKYKVDIMTHGR ALARTIAAAE KTKKILSANQ QAPVNIESLM NDIDASAMIT RQEF EAMIEP LLQRTHHPLE EALAQA KLT K DDIDIIEVVG GGSRVPALKERIQAFFGKTL SFTLNAD EAL ARGSAFSCAI LSPVFRVRDF AVQDIISYPI EFGWEKAPDI PDEDTSLTVF NKG NVMPSTK ILTFYRKQPF

					<p>DLEARYAQPELLPGKTNPWI GRFSVKNVKA DGKDDFMICK LKARVNIHGV LNVETGYVVE EEEVEEEVNE DPDVSLPAPP MASSSPDSV STSSASVGD DSRAYPVKRQRLNDDDDKL LCSAAVDEN LEPSTYENRS LTYTSHKAME TDKDAPKKTR KVKKQVRKGD LPISTGSASL DDSTKASLE KESAMVMEDK LVADTEKKNELEAYIDLR AKLDEQYSEF ASDEEKETIK AKLEATEDWL YEDGEDTTKG VYVAKIDEIR AMAGPIVQRH FEKVEAERQA ALEKAEAERA AKKAEEDARKAQDAEKATAD QEMKDADAQD AEGTADPQ</p>
Putative histone H2B protein [<i>Phaeoacremoniu</i> <i>m minimum</i> UCRPA7]	XP_007912731.1	14.8	89	11	<p>MPPKAADKKP AAKAPVASKA PEKKDAGKKT ASTGEKKKRT KARRETYSSYIKVLKQVHP DTGISNRAMS ILNSFVNDIF ERVATEASKL AAYNKKSTIS SREIQTSVRL ILPGELAKHA VSEGTKAVTK YSSSTK</p>
Integral membrane protein [<i>Pyrenophora</i> <i>tritici-repentis</i> Pt- 1C-BFP]	XP_001933871.1	47.8	82	2	<p>MLGTPLNCEL GEGEVVVNND LRISFHRTIR VPDNDQKSFL PPDLGAYPLKPIQAYSKKMP TEMTSKGGLF FPMYQSEAMW INFECRKSQH YIIKIYVGGV NAISGEAAVE DAGTKLRRQA KLARQHANVD AASSLQDYII VPGQKWLDGIAEADGSVRQF VAMPFSGSYS VESQVTGKDA AGGIQFEITP YKPPQVASNT QRSANGHQKS FSIFVKTLTG KHITLSVWKE DTISMIKDMI QVKEGIPLSQQRLIFNGKQL EDGRTLADYG IENEFTIVLV LNLRGGGTGP PLEMAVAAGG KIKQGIVADK LADHWQSART TVLNVQILNS AVYRTVTGED PPTMPIDAKTYARHGLPFYD LYEEQSGISG DFSMIKSIGQ IDHKEDDTAT PKIVKIGEA QLRVGLTNP NGPLRGFRTA SDLKKEYEGF HVVQF</p>

Rs15_podan 40s ribosomal protein s15 (s12) [<i>F. graminearum</i> and <i>F.</i> <i>oxysporum</i>]	XP_009251452.1	17.5	78	10	MADEYDAEQA AELKRKRAFR KFSYRGIDLD QLDDLSSDQL RDVVHARARRRINRGLKRRP MGLIKLRKA KQEAQPNEKP DLVKTHLRDM IVVPEMIGSV IGIYSGKEFN QVEIKPEMVG HYLAEFSISY KPVKHGRPGI GATHSSRFIPLK
Nucleoside diphosphate kinase [<i>F. graminearum</i> PH-1]	XP_011324585.1	25.9	60	7	MVAEEPQRK DPAVSGKENS KQRRRTAEN LAPPFFALLF ALLAFYILFSPSSSLSPV PVCHSTISS VSSQVIPDK NIAKMSSSEQ TFIAIKPDGV QRGLVGPIIS RFENRGFKLA AIKLMTPGKE HLEKHYADLA GKPFFAGLIEYMNSGPICAM VWEGRDAVKT GRSILGATNP LASSPGTIRG DYAIDVGRNV CHGSDSVENA QKEIALWFKE GEVVSWSAQ FNWVYEKA

AgNP-OR Proteins	NCBI RefSeq	Molecular Weight (kDa)	Score	% coverage	Sequence
DNA polymerase epsilon catalytic A-like isoform X1 [Citrus sinensis]	XP_006471371.1	253.8	50.5	0.5%	MDRRRWDRQDGRRTKKQKLIRSAEEEELEAKLGYDLFSEGDKRL GWLLTFASSSLEDEDTRKVYSCIDLYFVSQDGSTFKSKYKFRP YFYAATKEKMEMDVEAYLRRRYESQIADIEILEKEDLDLKNHL SGLHKSYLKISFDTVQQLMDVKKDLLQVVERNQAKFDAAEAYE SILTGKREQRPQDFLDCIVDLREYDVPYHIRFAIDNDVRCGQW YDVSVSSTGPLLEKRVDLLQRAEVHVCAFDIETTKLPLKFPDA DYDIIMMISYMLDGQGYLIINRECVGEDIEDLEYTPKPEFEGY FKVTNVNNEIELLRLWFAHMQEVKPGIYVTYNGDYFDWPFLET RAAHHGFKMSEELGFQCDKNQGECRAKFACHLDCFAWVKRDSY LPQGSQGLKAVTKAKLGYDPLEVNPEDMVRFAKEKPQMMA SYS VSDAVATYYLYMTYVHPFIFSLATIIPMSPDEVLRKGSGLTCE MLLMVQAYKANVICPNKHQSDPEKFYRNHLESETYIGGHVEC LESGVFRSDLPTSFKLDPSAYEQLLNNLDRDLQYAIKVEGKMD LESVSNYDEVKNAIMEKLLRLQEPIREECPLIYHLDVAAMYP NIILTNR LQPPSIVTDEVCTACDFNRPGKTC LRKLEWVWRGEI FMGKRSDYYHLKKQIESEFVDGTNGHLSKSFLDLPKMEQQSRL KDRLKKYCQKAYKRVLDKPVTELREAGICMRENSFYVDTVRSF RDRRYEYKGLNKVWKGKLSEAKASGNSIKIQEAQDMVVLYDSL QLAHKCILNSFYGYVMRKGARWYSMEMAGVVITYTGAKIIQNAR

LLIEKIGKPLELDTDGIWCVLPGSFPENFTFKTKDLKKKLTIS
YPCVMLNVDVARNNTNDQYQTLVDPVSKTYETHSECSIEFEVD
GPYKAMILPASKEEGILIKKRYAVFNDDGTLAELKGFEIKRRG
ELKLIKVFQAELFDKFLHGSTIEECYSAVAANRWLDLLDNQ
GKDIADSELIDYISESSTMSKSLADYGEQKSCAVTTARRLSDF
LGDTMVKDKGLRCQYIVACEPQGTPVSERAVPVAIFETDAEIM
KFYLRKWCKTSSDVGIRSIVDWSYKQRLSSAIQK**IITIPAAM**
QKVSNPVPRVVHPDWLYKKVREKEDKFRQRKLVDIFSSLKKDD
FLNKTCAETNLMDENVEDLEDFPKKRNSVNGPRPIVRCFEVNNEQKTVKTTDQV
DSLRQQLEPSEVSDQQPSSQNAIDTENIDRIVDYKGWLELKKRWKDNLDRKKQK
LGSLRASHQANGVSESLGDMINHKEAQRRTGVGSYFRRQETAMTRC
HWQIIQLVPSSQSGVFLAWVVVEGIMVRIPITVPRLYLNSKD
PIVEKFPGRRVNKTLPHGRRSFNLIEVMIDEDQFRKESKKLAA
LLADPEVEGIYETKVPPEFNAILQIGCVCKVDKSTKKRNTQDG
WNLSELHMKTTAECPYLEQSVSFFYLYHSISDVRAIYIGYFPT
SRTVTVVVSPHQHRELSPSILEKQFREACRTLSTELPPGVRI
TFKVEYVGYVKDAEKILQRAISEYRHEHYGPTVAVIECPNSHS
LRLGLRVLNDFPCVSIPPNARDSKYQVLGWQQNAAKIGMQRCA
ASSQWFNERISLARYAHVPLGNFEPDWLMFTADVFFSRALHDQ
QQILWISDDGVPDLGGTSEEDCFADDEVHQPVLTYPGAYRKVS
VELKIHHL SVNALLKSNQVNEMEGGGLFGFDQDMNSGPYNNEL
CGFDETTSSAPAFRVLKQLIQRCLTDAVTSGNVFADAILQHLY
RWLCSPHSLKHDPVLHRILHKVMQKVFAMLLAEFRKLGAIIIF
ANFSKVIIDTGKFDLSAAKAYCDSLLKALQTRELFIEWIELEPV
HFWHSLLFMDQYNYGGIPARADESLDDDSQVDIVSSWNIAEYL
PKEIQDHFVLVSEFMYIPWKHAQKLAASRASLQEGSSCTPSI
TVAAAENFESHIVQYVKGEISSYFTGKLLSIVRDAIHHMKKMN
NDQHNSPGVMQTAANIHKVDAPLEFIKHVCAAFALDQNVQHDV

LVMRKNLLKYVRVREFAPEAEFRDPCPSFILPNVICSYCND CR
DLDLCRDMALLAQDWHCAMPQCGQPYDREVMENALLQIVRQRE
RLYHLQDLVCIRC NQVKA AHLAEQCACAGSFRCKEDASDFRSM
MQIFLNIANRQGFQLLQECTSWILEVQ

Thyroid adenoma- associated protein homolog [<i>C. sinensis</i>]	XP_006482571.1	249.5	69.8	0.5%	<p>MSAKWRALQHRHRYTYSAVVFPTSLTESLTQIPSSQNSSFSKF HNAFRELVSLNSIYAQVNHAKKFASSFIELLSSANAADEWVL SKATRVYLEVMFLENSLPLHRTLVSALAKERKFQALIVSCFRD LCDEYGGGGRASDQNKRFCVSRVLSVMSLPKLGYLMDVIQDC AVLVAWDVLGLNGVVLETQEWARPSPIVMEQCQEALSCLYYL LQRCLDKFKGLSGQKESIMEMIFVVLISILKSTAFSRDCYVAA GVALCAALQVCLGPQELGLFLIEGIFYQKTCFSSEKSKSEFE DALQVCFRKTPTFNGDVCSEIHNFVLSRLCLIRGILTAVSRNV LNALFFVSKEDLSNGSENGDDSAKTILYNGILPELCSYCNPT DSHFNFHALTVLQICLQQIKTSILANLTNVSFDDYDPIPEDMGT RILRIIWNLEDPLSQTQVHLVFDLFDISSLRWVDVGSR IKSFLQKIASDLLCLGPRCKGRYVPLALLTKRLGAKTLLGMSP DLLSEIVNAYIDDDVCSAATSFLKCFLECLRDECWSSNGISRG YAVYRGHCLPPFLYGLASGVSKLRSNLNTYALPVLLDMDVDGI FPMLAFVSVPSEEENGLSYPELDCSSIELKVEQQVAVFVSLL KVSRLALAEGDIDLWKNSSVLRTGSKFVTEGSNLYALVCIKG INFKVLVDWLVLALTHADELLRVDAAESLFLNPKTASLPShLE LTLMKEAVPLNMRSCTAFQMKWTSLFRKFFSRVRTALERQFK QGSWRPVVSCENS DRTLINGTDTVSKAENLFKFMRWLSCFLF FSCYPSAPYKRKIMAMELILTMMNIWSIAPPQEKLDVSLESS LYPYNKGITAPNSTLLLVGSIIDSWDRLRESSFRILLHFPSP PGISSEGMVQKVITWSKKLVCSPRVRES DAGALALRLIFRKYV LDLGWIVRASVNVVCLHPQPQQLKGEQICKSSAPVVEYIKSL IDWLEVAVKEGERDLESCENSFVHGILLALRYTFEELDWN AVLSGYSEMKALEKLELVMRITSLALWVVSADAWCLPEDMD DMIIDNLLLDVPEEMDEPLRSLEDEEKNKPAQDVRTSEQVV MVG CWLAMKEV SLL LGTIIRKIPLINSSSDTVDSGSGTSDAA</p>
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DDLMTMSDAMLDLKQLEKIGNHFLEVLLKMKHNGAIDKTRAGFTALCNRL LCS
NDLRLCRLTESWMEQLMERTVAKGQIVDDLRRSAGIPAAFIALFLAEPEGAPKKLL
PQALRWLIDVANRSLDLIENKGAKTTMCEFHSNQETESAVPPDIY
ATWNSSKIRDEGVVPTVHAFNILRAAFNDTNLAADTSAFSAEA
LIISIRSFSPYWEIRNSACLAYTALIRRM LGFLNVQKRESAR
RALTGLEFFHRYPSLHPFIFNELRVITELLGNASSGQSASNLA
NVVHPSLCPMLILLCRLKPSALAGESGDDLDPFLFMPFIRRC S
TQSNLKVRVLASRAL TGLVPNEKLPDVLLNIASELLCVEDQNE
AAPVSSLRGTHRASFNLIHGILLQLGSLLDANC RNLVDFS KKD
QILGDLIKILGNCSWIANPKMCPILNASFLKVLDHVLSIAR
TCHTSKSFSTVRNLLLELSTDCLDVDASYGLTYDPTITELRK
KAANSYFSCVFQASEESGEEVLQLPQRCS PVDSTSSKIPDMEN
TFSGLLERLVRSLSDSSYEVRLSTLKWLLKFLKSTESDREVCE
LSSYEIKSIQNWTKNNLQATLMSRLELEKNPRCTNYVLRL LFT
WNLLQFQKLGSNVCTETIFVGSVDCDSVFQFWDRLMSSYELTR
HAKIKESLINCMAICIRRFANLFTSSILVDARKKTIEISESDH
LGRSAHLFACITAFVNIINRHSSSSEPVNMRKAATGSIVASGL
LEQADLIGSYVSNHQIPSENSSLHFEPQEAGNMYAHQVLVIWF
TCIKLEDEDDGIRQRLAIDVQKCFSLKRFGSSSHGVPNQVEK
VIELSFEHLSSIFGCWIEYFDYLCQWVLVAASHVVSGGDLVRR
VFDKEIDNHHEEKLLISQICCSQLEKIPILKSWVADSLNKDHA
RNYLLGWRQRFHQLM SFAKDHGRKYEGVDWIGGVGNHKDAFL
PLYANLLGFYALSICIFKVEAEDEMHLSDVVELGRIISPFLR
NPLVGNLYLLVVKLHEKQTGATADHTVEFRADMIWDGFDPYFL LR

Probable disease	XP_006465371.1	102.9	38.4	1%	
resistance					
protein					
At5g63020					
[C. sinensis]					
					MGNLLSSFLSSPESFRSILSYVGGEAKYVWALQVNLDALQAEL
					DKLIRTKDDLLNKVELVEQQQPRARRTNQVKGWLQRVQETVTK
					VVDLQNVRDQELDRLCLGGFCSKDLASSYFGKKVVTLTEQVI
					LLKNERGEIKDIAEMVPEDA AVELALERTVVGQESMLDQVLRC
					ITDQETNRGIGLYGTGGVGKTTLLKQVNNKFCIEQRQHDFDV
					VIWGVVSREPCLDKIQDAIGKRIGLSAESWMDKSLEEKALDIS
					NILSRKKFVLLDDIWQPIDLTELGIPQLSLNVSSKVVFTTRS
					LDVCGSMEADEKIEVKCLVHDEAWRLFQEKVGEATLRCHSDIL
					ELAQTLARECCGLPLALKTIGRAMAYKKNPDEWKYATKVLSTS
					PEKFSGMEENVFARLKFSYDSLPNYIIRSCFLYCSLFPEDYEV
					YKGDLDIDYWISEGFVDAFDEGYTIIGDLLRACLLEEVDNDNHVK
					MHDVIRDMALWIACKIDKEEENFLVHAGALLTEAPKIKDWEGF
					KRISLMENNITSLSAIPNCPLRRTLLLYRNRISMITDGFFQFM
					PSLKVLNLGFNIFLNKLP SGLSSLISLEHLDLSFTVIRELPEE
					MKALVNLRYLNLEYVYLNRLPLQLLCNFTKLQALRMLGCSNYS
					GEEEDRVFFKDAEPFMKELLCLENLDLLSFTFDSWHAFETFLT
					FQKLLSCTESLELTKLYTPMSLNVLPLAYMKHLKNFLIQNCAF
					EELKIENAVEIQNLVQRGFRSLHTVCISDCSRLKELTWLVFAP
					NLKNIDVQNCNNMEEIISPGKLSEVSEIKERQNFLAELKFLCL
					KDLENLESIYFDPLFPQLKEIEVTGCPKCLKLPLDSTRAMGH
					KIVVKGNIEWWVELQWEDRVTQRVFSTCFDPMEIVF

Probable inactive receptor kinase At2g26730	XP_015384636.1	68.5	55.1	2%	<p>MRGSKLFLFLEGLICIAILPRLFTGCVGGELSESESEFFKFISA VDSQNVLRIGWNGNLPHPCSYNLKGICNLHATSIVGIRLENM NLSGIIDAESLCKLRHLRVVSLAKNLIQGRIPNSISNCRRITY LNLSSNLLSGAVPLALTKLKHLKTLDISNNHFACTSPDNFKQE IKYFDKYVVTSSSEINRASTVEARGLEDTPPPSVHNMSEHGE KRHWFRNWMTHIPLAAGIGLVVLIAYCMGKKSQAQIARDREILK ALQDSPSKSPPRVMDIEEVRPEVRRSELVFFVNENEKFKLDDL LEATADLRSTICSSLFMVRLKNSAVYAVKRLKKLQVSMDEFS QTMRQIGNLKHPNPLVLCYNSTNEEKLLVYKYQSNGLSLLSL EAYIEGKRDFPWKLRLSIATGIAKGLDFIYQKSNEEKTIHPGN LKLSNILLNENEDPLISECGYSKFLDPKKTCLFSSNGYTAPEK TVSEQGDVFSFGVILLELLTGKTVEKTGIDLPKWVKAMVREEW TGEVFDKEVAKAGRQWAFPLLNVALKCVSNPDDRPTMAEVLE RIEEVVNGNDERDRDHSNSSFSSMESIPHDSCLLHTVIQENWD TPRSSY</p>
Squamous cell carcinoma antigen recognized by T- cells 3-like [C. sinensis]	XP_015383384.1	113.4	53.0	0.5%	<p>MEPKEETLATIPEEEEDGDTVIPDVENNPKPTTKDNSSDSSDG SDSDSDSDSDSDSDSEDAKQSMELQTLQYQLSNEPSNYDTHV QYIKVLRKMGIEIKLRQAREAMNEIFPLTPAMWQEWARDEASI STGPEALLGVEKIYERGVSDYLSVPLWCDYLFVQYEDPSIRA FLPDGISKARNLFERAITAAGLHVSEGSNRETKKMEPKEETLA TIPEEEEDGDTVIPDVENNPKPTTKDNSSDSDASDSDSDSDS ESEDEAKQSMELQTLQYQLSNEPSNYDTHVQYIKVLRKMGIEI KLRQAREAMNEIFPLTPAMWQEWARDEASISAGPEALLGVEKI YERGVSDYLHMTSIPRPLLLVLQEKEKQVQRIRSFHRQLSVP LANSSATLLAYKSWEVEQGAVLDVESSNLDGDSNNVALAYQKA</p>

					LEMCNARAHLEEQISRQDLSDEKFQQYMIYLKYEQSSGDPGR VQLLYERAITDFPVSSDLWLDYTQYLDKTLKVGNNVRDVYSRA TKNCPWVGELWVRSLSLERSRASEEEISTVFEKSLLCAFSTF EEYLDLFLTRIDGLRRRILFSGEVEGVLDYSLIRETFQRASDY LSEQMKNTDGLRLYAYWAHLEQSMGKDMVSARGVWERLLKIS GAMLEAWQSYISMEIELGHINEARSIYKRCYSKRFTGTGSEDI CHAWLRFEREYGTLEDFDHSVQKVTPRLEELQLFRSQQESKSL PESADQKEHSVKKTGREKRKSDLNISYEQSPAKRQKNAPQKPK KVHDKKQQVQNLAENEGRETKQTVEEQPKEQPIKDAVPGR KGFTDECTAFLSNINLKATYEDLRRFFSDVGGVSSIRILHDKF TGKSRGLAYVDFIDDEHLAAAVAKNKQMFLGKKLSIARSNPKQ RKDSSGERAPTEQAQSHQQTGNAGTSASKESSIETSKQSRGRG DSVQLKGKNTFAVPRNVRPLGFPAIKPKTEEGEDLKPKSNDEF RKMFIKKD
MYB transcription factor [C. sinensis]	AMH40451.1	36.6	67.4	4%	MGRAPCCEKIGLKKGRWTAEEDEILTKYIRANGECSWRSLPKN AGLLRCGKSCRLRWINYLRADLKRGNITAE EEEE TIVKLHSSLG NRWSLIAAQLPGRTDNEIKNYWNSHLSRKTFSTGPADDPLTS DDLSNNGIKLAGGCKQRKGRTSKVNSKKHKLALASIGMPKTKR GTISEVLDQQVTADENKSSIGQVSCMASDEFFCGEASSDQASG LCLSKDIESEVLGPYEWLDSEIKRVNSNLNREKASAEDEVKRD QDKMAKSAEKESVFWGSNEDELLYTFDPTMMNCSGFDEEWLDF DWAAGGAECHNQCELRDGD DD KLLCWLWD SG N GE GCQ

Protein	XP_006488076.1	84.1	31.2	1%	
ENHANCED					MDNSQITSQGRMEGWLHLIRSNRIGLQYSRKRYFLEDHFLKS
DISEASE					FKSVPHSKNEDPVRSIIIDSCIRVTDNGRESIHRKVFFIFTLY
RESISTANCE 2					NTSNHNDQLKLGASSPEEAAKWIHSLQEAAALKGGPHQGVGDHI
[C. sinensis]					GCPNSPWESFRLSGSSRASHTKSIDWTLCSGTHMEQVTADVIA
					PSPWTIFGCQNGLRLFKEGKDRGSRGKWDDHPAIMAVGVVDGT
					SEAIQTLMSLGASRSVWDFCFYRGCVVEHLDGHTDIIHKQLY
					SDWLPWGMKRRDLLRRYWRREDDGTYVILYHSVFHKKCPRQK
					GSVRACKSGGYVITPMNHGKKSVMKMLAIDWKCWRSYLQPS
					SARSITIRMLGRVAALRELFRAKQGNYSPEFLSGELTRNMRM
					HQTDGNMVQMPTEDGNSKENTSEEVDQVSSEHASLVGLNDAAD
					EFFDVPEPSDYDDSENGWTSDFGPEMNSQDTRHPKISTAAGFV
					RKLHDLAVQKRGYVDLQGTAKEDNFSCCYGTTLQKDPTCTLPC
					SWTSTDPTFLIRGKNYLQDRHKVKAKGTLMQMVAADWLKSDK
					REDDLGGRPGGIVQKYAEQGGPEFFFIINIQVPGSTTYSALY
					YMMTPVKDAPLLESFINGDDAYRNSRFKLIPYISEGSWIVKQ
					SVGKKACLIGQALEINYFHGKNYLELGVDIGSSTVARGVVSLV
					LGYLNNLVIEMAFLIQANTEELPEFLLGTCRLNHLDAAKAVL
					LKPSSRLSSSSQGPVRN

Hypothetical protein CISIN_1g001123 1mg, partial [<i>C. sinensis</i>]	KDO77096.1	64.2	57.9	1.5%	DLWSGSEGGGIKWPWEAIEKALSLKPEERHTAALIVERSYID LRSHLSVNGFSSILTS DIKNLLSDHSRAKVWSAGFLSFALWDA RTRELLKVFNIDGQIENRVDMSELLPDFAMEDEFKTKIVTSSKK DKAQSSFQFFQSRNAIMGAADAVRRVA AKGGFGDDNRRTEAL TTSIDGMIWTGGANGLLLQWDPNGNRLQDFQYLPFAVQCLCTF GSQIWVGYMNGIVQVLDLEGNLLGGWVAHSSPVIKMAVGAGYI FTLANHGGIRGWNVTSPGPLDSILCKELAGKEFLYTRMENLKI LAGTWNVGQGRASQDALISWLGSASDVGIVVVG LQEVMGAG FLAMSAKETVGLEGS AVGHWWLDMIGKILDDGSTFERVGS RQLAGLLIAVWVRK NLKDYVG DVDA AVPCGF GRAIGNKGAVGLRVRVYDRIMCFVNCHFAAHLEAV NRRNADFDHVYRTMTFCRPSN LCSAAAAGASSVVQMLRSTNPLSGLTVEGVPELSEADMVIFLG DFNRYRLDGITYDEARDFISQRCFDWLRERDQLRAEMEAGNVFQ GMREADIKFPPTYKFEKHLA GLAGTL
Oleosin 18.2 kDa [<i>C. sinensis</i>]	XP_006470260.1	17.1	46.9	7%	MAERDRPQPHQLQVHPQQHSLIGQRGAAGGGPSASKVLAVL AMLPLGGTFLALAGVTLTGTHGLCVTTPLFIIFSPVIVPAAI VLALAVTGFLTSGAFGLTALSSLSWVLSILWQKTGSVP EMADQ AKKRVAGIADYVGQKTKEVGQDIQSKVHEAGGKTGR T

Uncharacterized protein LOC102613021 isoform X1 [<i>C. sinensis</i>]	XP_006468109.1	267.3	34.6	0.5%	MTDKNPSRRELLDRWRGIEEEEELDDGNDPLKRRRIDGLKEKW FADAFNFLIGLPEKNHIWCGSWDIMGPYLELFYNYFKDECHDS PLRLLWKRISGEMQHCIQCVSQHHQAQEMYSMEYESGVIGPLL DVLRLSDEERVTKYLREINARLAHQEYYPQIDNNQVICIMYEV LMFPVLLDDQSLFTEFETFIEAVDNMHELALDGHQLFPGVFAL FFFNRRVRTIGRRLARSMGKLRRATDLEPMQPLLKKFIGFLET EVLTSFKTSRPRARLKRLPIWLGITSLLEFLEPPALEEGILE RYPIFFDTVLNHISGDSPEFSHAVSCLRELFKMLGYKLWLRST LSPSVMRNTLLGQC FHTRSEKIHKDIFDLFPPFLQSLEALQDG EHEKQRRHFLYFLLYQVPVSSNFSVLTAQMACKISLLIHRGY KMNPPCPPFECAHMGWGPFLVSSLDSSLHSSLRQPAFDLIQTI IVSDAAALVTSVLKSARPLRTETIISVEMNEDEDDLKFPFDPD VDEKDDNSSWNEFTAQSRITSQEFRVWMCIPMLWIDVLVDINP SVLPVSFSKVVFWARSHFSIVEPEISAEMALDVRAWLSSSATE ISSTFGWKAPTGCDDGGAGKVSKNSMEVSTMCLPLIRAFKRLT AHFIVQIGQGELRKQWTWEPRMGESLILSLVDPNDNVRRQFGKC ILEQVSNTRGLASGLKFLSSSTSSLSTIFLGLKHALKLVQLDS VLLKFQSLHHFFVLRKIFEEGHLPKCDLLKSSSGHSSITMFS SQGGFLRQPQFESFDANTGCSSNIDLKLWEKFHYTLSEITWPS VKRCLQEGKTFLDYSLCQMT CIRVLEILPVVFGKVCPLLAELS GYSATTMQNVFDFKWLHDLVDWGKSQLKVIVYWKRTITCLLN LLKDSCSGTSLLT VSSIENLISSDHLDMDGLVEKVSLLCVSL KESSRNSGKTLMSMAHFPEDLSVERKSATLDIRPFPVKDMDVE ILDSETIASKSKDNLIVVSDDETEKEPSVDQGLLSDFKSRQCV VVSKTGAPISDKRASQTESLKNRVSILDSSKDLLDGSGPASP QVLDES VGKSLNSLDSKVVDGKKKESNSKFNASDSLFSQNRVG LRNKPVESSEFKNVNQASTNVVAKPTNKLLKELVCDVENDPLE
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SSFKSGKHQQTYLTKSGPFVPKRQVIQLK
SPFENRCGLHRMETGVKRFGPPKLDDWYKPILEIDYFATVGLA
SSREDENRVHCKLKEVPVCFQSPEQFVSIFRPLVLEEFKAQLH
SSFLEMSSWEDMYYGSLSVLSVERVDDFHLVRFVHDDNDSVTS
KIFSENDLVLLTRVSPQKTPHDVHVMVGKVERRERDNNRRSSIL
LIRFYLQNGSVRLNQARRNLLERSKWHATLIMSITPQLREFHA
LSSLKSIPLLPILNPVNVSRGYNESREPDLGKLSQLQQILKT
SFNESQLQAISVAIGLSSSWKKDCELSLIQGPPGTGKTRTIVA
IVSALLATRTSPKSHLKQNYSSCINSRPKIGQSAAIARAWQDA
ALARQINEDSERDKKSSSESVRARVLICAQSNAAVDELVSRI
KEGLYGSDGKTYKPYLVRVGNVKTVHPNSLPFFIDTLVDHRLA
EERMHLTDPKNEFCTRSSTLRNLEKLVDRIFFEAKRANTKD
GNSDPKNMLDDEVHKGDDVKLSDVELEAKLRKLYEQKKQIYRE
LGAAQVQEKKSYETKALKHKLRSILKEAIEIVTTLSGCGGD
LYGVCSESVSGFKFGNPSENTLFDVVIDEAAQALEPATLIPL
QLLSYGTRCVMVGDPKQLPATVLSNVASKFLYECMFERLQR
AGHPVVMLTKQYRMHPDICRFP SLHFYENKLLNGEEMSRKSAP
FHVTGGLGPYVFYDISDGQELRGKNAGAFSLYNEHEVDAAVEL
LRFKRKRYLSEFVGGRIGIITPYKSQLGLLRSQFSNAFGSSVT
SDIEFNTVDGFQGREVDILILSTVRAADSSSASSGRSSSIGF
VADVRRMNVALTRARLSLWILGNARTLQMNYNWAALVKDAKER
NLVISIKKPYASMFKSMFKSSLRKNHSELQDDHLSQLKHITEK
HGD TNQFVKQIGRKS RAGVETKTRDIDHMAQC NKAVARDNDTV
SAKREDLQTSRRRARDQSDLPKTDHPSAAANGQSRTSKSVKSA
VLGEHVL DSETRGEESGKKKFSSSNTLTDQKKDEYSKSKLDQS
APLDQQKDKYSKGKSDHSGHEAGNSHKHSKFKVSKGSSKSFEQ
DRSLKKLK **GSDPSTGGSQK**EQEANDQGRNPNSVGS SDALIAKR

KQQREAVDAILYSSLISSKKPEPVKPAPTKRSLSPSTSIAGGGI
RPPKRKKVPAASSESALQDQ

Uncharacterized XP_006488053.1 79.7 26.1 1%
protein
LOC102616627
[*C. sinensis*]

MSHPQQLRRALNQPLEPDHHESSFLSSHAKASQTSATASSTT
SRCSSFASKSASYSSNQHQYSSFHHQNLFACTSCIRLNVFSTSS
KRWSAWFKLHCPGSFMASQQTRLNFMPLDIARRKKISRQKK
EELQREVSMLQKMLEQEETLHEILERIHNGQDGSAISIPNLP
PKVKELLAELALVEGEIKRLEGQISQLQLGLKHEQEVTKETKS
KQWQLGSLGNLQGHSTYMANISSPLINKVGNEKVAFETKALHF
ISKAIKGDYNLSDFSVNEKKMGNSKVVFVDQKENQFQQQQEVK
FQDRVPRKSGMIKPASPLRDPRHPTPKPRERNAAEISFDLPPK
SLSNSILLEESIQNWQPNKLSSESIMKCLNFIYVRLRLTSRAIE
LEKAGPISRSMHSSITSRSFRADTSLNSKSSIVLQKDSRQQDP
YGIFDMEESIPRDIGPYKNLVIFSSSSMDPKCISSSSSVPLIR

KLRILMNNLQTVDLKALTYQQKLAFWINMFNACIMHGFLQYGV
 PNSPEKLIALMNKATLSIGGSTINAQAIEHYILRGQESSNLKE
 VDQKAGEKDEKEAIVRKLYGLESTDPNVTFALCYGTRSSPAVR
 IYTADGVIAELEKSKLEYLQASVVVTNTRKIAFPELLFRNMLD
 FAMDIDTLVEWVCHQLPTSGSLRKSMVDCFRHQGHNGKISIT
 VEKIPYDFEFQYLLAI

Uncharacterized protein
 LOC107177306
 [C. sinensis]

MMKIPYADHFPGHITSMCKLDVIVNAIREKLTRQQQLQLFK**DNI**
FGHFLRCRSYPFSGVIVHNLLLRQVSHGDGNDKDDLWFQVGDH
 LIRLSIGEWCLVTGLCCGEKVFLTKHKTKHRLLNKYFGGRNRD
 INLGQFEEIFMNLHFKTMNDTDALKIAMFYFADRVLHGRKDKH
 QINFNLLNEVDDINHFRSIPWGRLSWETIYKSIDNVLNGKAKK
 FKKASAENPLHRIEKYNFYGFTSAVHAWIFEAIEGLPLEWVEK IRRKASFIPPPKT

Phospholipase A1-Sigma 3,
 chloroplastic
 [C. sinensis]

MAPNLLSFSSPKGVFPFLPQQYRYYNKKAKTSLLYLNNLTNVS
 SLNSKNLLKCSSVSNLSTPPLDETAFDHQQEEEEQEQQEKEK
 ELHEMWKAIQGCNDWQGLDPMNCHLRKEIIRYGEFSQACYDS
 FDFDPHSKYCGTCKYSAASFFKKLDMADSGYQISRYLYATSNI
 NLPKFFQKSRLSSVWSTYANWMGYIAVTTDEEEKRLGRRDIV
 VAWRGTVTYIEWIYDLKDILHTANFGSDPSIKIELGFHDLYTK
 KEQSCNYCTFSAREQVLAIEIKRLIEYEGEEISITFTGHSLGA
 ALAIVSAYDVAELGLNIVNDGESSSTKKIPITVYSFAGPRVG
 NLKFKERCEDELGVKVLRVVNVHDKVPTVPILANEKFQFQKHF

					EEATKFPWSYAHVGVELALDHTNSPFLKNTKDFGCAHNLEALL HLLDGYCGKENQFCLETTKRDIALVNKSCDFLKSEYEVPPHWR QDENKGMVRNTDGRWVLPERPRLALPEDTAHHLQKVLKNIAN SNNNNNSNSANNSSQLEAI
Hypothetical protein CISIN_1g015135 mg [<i>C. sinensis</i>]	KDO69165.1	44.9	43.5	3%	MAGICCGVVGSEPAVSVEQSSRASRRRRLRPFNLVADVAV LPPSENVVRKRKKLELYTTLTAAHARENTEQNCEKDSERGRV NKEELVGNNEAADDLVNDNPKFGMTSVCGRRRDMEDTVSIHPS FCKQNCAHFYGVFDGHGCSHVAMKCKDRLHDILREEIESCNV EESVKWKQTMQASFGKMDKEVQDWSVSSKISNCRCELQTPQCD AVGSTAVVAVVTPEKLIVSNCGDSRAVLCRNGVAVPLSNDHKP DRPDELLRIEAAGGRVIYWDGPRVLGVLAMSRAIGDNYLKPYP ISEPEVTVTERTAEDDECLILASDGLWDVVSNETACSVVRTCFR AQKAAAAASPSPGSEVAVSQSSDKACLDASILLTKLALAR RSSDNVSVVVVDLRRIKSQKQGLSS
Hypothetical protein CISIN_1g016141 mg [<i>C. sinensis</i>]	KDO70337.1	43.1	33.3	2.5%	MGNAVGCVSAGVKAPKKASSYGFPFPLFSSFHGRPRNALQSS SSSSRNKKQKRERIQVDEGSAITSEQALPAALPFHSDQTSSSI PFSRSTSVVHPSLGSKKQSFQRSSSARRRSNNDPLIKRPHQLV NQEPKIESPETSHFVLVHGGGFGAWCWYKTMTLKESGFKVDA VDLTGSGVSSCDTNSITSLEQYVKPLIDTFNELGNEEKVILVG HDFGGACISYVMELFPSKVAKAVFIAATMLTSGQSALDTISQQ

					MGSNDLMQQAQIFLYANGKQNPPTSIDLDRDLLFNRSAA KDVELALISMRIPIFAPVLEKLSVSDNYGSVPRFYIKTLQDC AIPVSVQEAMINSNPPELVFEIKGSDHAPFFSKPRALHRILVEISKITHR
Putative disease resistance protein RGA3 [C. sinensis]	XP_006492568.1	109.9	38.8	1%	MVDAIVSPLEKLISFSVKEVTQQVKLVKGVQDEVEKLTIHLQ MIHAVLNDAEQRQVKEKSVRLWLGRLKDVSYDIEDVLDEWITA RRKLQMKQNGHFPQKQVCSCSPASSIGFEKIILRPDIAVKIKE INEKLDAIATQKYIFKFVENGSNSTREPRGRAQSTSLIDEEEI CGRVDEKNELLSKLLCESSDSPKGLHIISIIGMGMGKTTLAQ LACNHEEVKRKFDKILWVCVSETFEEFRVAKAIVEALDGHESR LGEFQSLIKHIYESVAGMCFLLVLDDVDGNYMKWEFFHCL KNGLHRSKILVTTRKKSVASMMGSTNIISIKELTEEECRLLFN KIAFSDRPIEEREKLEQIGRKIANCKKGLPLAAKIIGSLMRSK ETEEEWRRILNSGLWKVEEIEKDILSSLLSYNDLPSKVKKCF SYCAIFPKDYNIEKDRILITLWMAQGYLDTEQDEEMESKGEEYF GILASRSFFQEFTKSYDNCIMQCKMHDMVHDFGQFISQNECLS MEISGLNAINSFDEKVRHLLLVGNGASFPVSTCGVKKMRSLI IDYSRYFHLYLNGKILERLFRESTSLRVLEFGDWARSLLQGP LTRIPRNIERLVHLRYLNLSNQSIRKLPDTLCELNYLQKLDIS CCCKLKELPQGIGKLINMRHLLNYGTISLRYMPVGIGRLTSLR TLDEFYVSGGGGIDGRKACRLESLSLELLQVCGIRRLGNVTD VGEAKRLELDKMKNLSCLKLLFNKEEGDGQRRKNEDDQLLEF LQPPPNLRKLLIGSYRGKTVFPPWMMSLTNLRSLDLDDCENCE KLPLGKLPSEKLSISFMCVSRVDNEILGIESDHHDSSSCS SSSVTIAFPKLSLTISWMLELEDWDYGIAGTGNAFISIMPR

LSSLTFDSCPCLKALPDHFHQTTTLQEFNIGWNCGLLEKRYRK
 GEGEDWHKISHIPNLEIGP

Hypothetical
 protein
 CISIN_1g038912
 mg, partial
 [C. sinensis]

MFRTSRISFLPDELLSEILARVGACSLDDLLNAGLSCKLFNEI
 TFDKYVLRQASIEKIPAMPWHKNYSFLEKCRDSGNPEALYKQG
 VVEFFSYSNLEAGVAYLDIATKSGHLGASYILGVIFLCKDDED
 DDNESNQKGMQHLDKVYRAKRLSQCRNKLQSITQTLWKNNYLK
 PKLNKCPSRKNHGLKVGWPCEVDDIEL

Hypothetical
 protein
 CISIN_1g037051
 2mg, partial
 [C. sinensis]

MRKLEHGELKATFPKIVFNPSFEDEEEKCMDITTVQRSTMSRLSPEETSDLTGSKERKA
 EPVRQNPTLPPPASVRLLTQPPPPPPPP PPSVNHPSQATLPPIR

Glyceraldehyde-
 3-phosphate-
 dehydrogenase
 GAPC1,

MAGDKKIKIGINGFGRIGRLVARVVLQRDDVELVAVNDPFIST
 DYMTYMFKYDSVHGQWKHNELKVKDEKTLFGEKPVAVFGRN
 PEEIPWAKTGAEYVVESTGVFTDKDKAAHLKGGAKKVVISAP
 SKDAPMFVVGVNEKEYKPELDIVSNASCTTNCLAPLAKVIHDK

cytosolic [C. <i>sinensis</i>]					FGIVEGLMTTVHSITATQKTVDGSPMKDWRGGR AASFN IIP SSTGAAK AVGKVLPALNGKLTGMSFRVPTVDVSVVDLTVR LEKEATYEEIKNAIKEESEGLKLGILGYTEEDVVSTDFVGDSR SSIFDAKAGIALSKNFVKLVSWYDNEWGYSSRVIDLIVHMAKT QA
Uncharacterized protein LOC102621728 isoform X4 [C. <i>sinensis</i>]	XP_015389051.1	16.3	34.1	7%	MANVESDSTPSVPKKENITPVG SKIAELNESRAELLNRIQGLK QDLQNWRSKLDTQVKIYRDELTDMKK TL SVEVEQLR SEFQELR STLQQQQDDVTASLRNLGLQDFSGDDKERKDDPNINGKDEEVH AIATPVEDNAKADDDK
Hypothetical protein CISIN_1g037790 mg [C. <i>sinensis</i>]	KDO60176.1	79.7	26.1	1%	MSHPQQLRRLALNQPLEPDHHESSFLSSHAKASQTSATASSTT SRCSSFASKSASYSSNQHQYSSFHHQNLFCTSCIRLNVFSTSS KRWSAWFKLHCPGSFMASQQTRLSFNMPLDIARRKKISRQQKK EELQR EV SMLQK MLEQEETLHEILERIHNGQDGS AISIPNFLP PKVKELLAELALVEGEIKRLEGQISQLQLGLKHEQEVTKETKS KQWQLGSLGNLQGHSTYMANISSPLINKVGNEKVAFETKALHF ISKAIKGDYNLSDFSVNEKKMGNSKVVFVDQKENQFQQQQEVK FQDRVPRKSGMIKPASPLRDPRHPTPKPRERNAAEISFDLPPK SLSNSILLEESIQNWQPNKLSSEIMKCLNFIYVRLLRTSRAIE LEKAGPISRSMHSSITSRSFRA DTSLNSKSSIVLQKDSRQQDP YGIFDMEESIPRDIGPYKNLVIFSSSSMDPKCISSSSSVPLIR KLRILMNNLQTVDLKALTYQQKLA FWINMFNACIMHGFLQYGV

PNSPEKLIALMNKATLSIGGSTINAQAIEHYILRGQESSNLKE
 VDQKAGEKDEKEAIVRKLYGLESTDPNVTFALCYGTRSSPAVR
 IYTADGVIAELEKSKLEYLQASVVVTNTRKIAFPELLFRNMLD
 FAMDIDTLVEWVCHQLPTSGSLRKSMVDCFRHQGHNNGKISIT
 VEKIPYDFEFQYLLAI

Penta
 tricopeptide
 repeat-
 containing
 protein
 At5g04780,
 mitochondrial-
 like
 [*C. sinensis*]

XP_006467747.1

105.9

48.4

1%

MIHKWNMKNFFENSLQKNLHQRIYLPFKKPFQKTHSKYIQ
 TATIISENPESTSNLNVTHDSNFTPTSIPYSKLLSQCTISK
 SVNLGKEIHAHLIRFGLLKDPKNKNNLINFYAKLQFFLYARKL
 VDESPEPDLVSWALISGYAQNGR**GEEAALAFQK**MHLLGLKCN
 EFTFPSVLKACTSKKDLFLGLQVHGIVVFTGFDSDEFVANSLV
 VMYAKCGNFIDSRRLFDAIPERSVVSWSLFCYVHCDFFLEEA
 VCFFKEMVLGIRPNEFSLSSMINACAGSGDSSLGRKIHGYSI
 KLGYSDFMFSANALVDMYAKVGNLEDAVAVFKDIEHPDIVSWN
 AVIAGCVLHEHNDWALKLFQQMKSSSEINPNMFTYTSALKACAG
 MELKELGRQLHCSLIKMEIKSDPIVGVGLVDMYAKCGSMDEAR
 MIFHLMPEKNLIAWNIVISGHLQNGGDMEAASLFPWMYREGVG
 FDQTTLSTVLKSVASFQAIGVCKQVHALSVKTADESDDYIVNS
 LIDAYGKCGHVEDAVQIFKESSAVDLVACTSMITAYAQFGLGE
 EALKLYLEMQDREINPDSFVCSSLLNACANLSAYEQGKQVHVH
 IIKFGFMSDTFAGNSLVNMYAKCGSIDDADRAFSEIPDRGIVS
 WSAMIGGLAQHGRGKEALQMFGQMLEDGVLPNHITLVSVLCAC
 NHAGLVAEAKHHFESMEKKFGIQPMQEHYACMIDILGRAGKFQEAMELVDTMPF
 QANASVWGALLGAARIYKNVEVGQHAAEMLFA
 IEPEKSSTHVLLSNIYASAGMWDNVAKVRRFMKDNKLKKEPGM

MRGSKLFLFLEGICIAILPRLFTGCVGGELSESESSFFKFISA
VDSQNVLRIGWNGNLPHPCSYNLKGICNLHATSIVGIRLENM
NLSGIIDAESLCKLRHLRVVSLAKNLIQGRIPNSISNCRRLTY
LNLSSNLLSGAVPLALTCLKHLKTLDISNNHFAGTSPDNFKQE
IKYFDKYVVETSSSEINRASTVEARGLEDTPPPSVHNMSEHGE
KRHWFRNWMTIPLAAGIGLVVLIAYCMGKKSAAQIARDREILK
ALQDSPSKSPPRVMDIEEVRPEVRRSELVFFVNENEKFKLDDL
LEATADLRSQTICSSLFMVRLKNSAVYAVKRLKKLQVSMDEFS
QTMRQIGNLKHPNPLVLCYNSTNEEKLLVYKYSNGSLLSL
EAYIEGKRDFPWKLRLSIATGIAKGLDFIYQKSNEEKTI PHGN
LKLSNILLNENEDPLISECGYSKFLDPKKTCLFSSNGYTAPEK
TVSEQGDVFSFGVILLELLTGKTVEKTGIDLPKWVKAMVREEW
TGEVFDKEVAKAGRQWAFPLLNVALKCVSNSPDDRPTMAEVLE
RIEEVVNGNDERDRDHSNSSFSMESIPHDSCLLHTVIOENWDTPRSSY

Proline-rich protein 4-like [<i>C. sinensis</i>]	XP_006487410.1	55.8	598	1.5%	<p>MRILPGSRGALVCFLVPLLFAVSLCHAKDKAVEVVGTGECADC</p> <p>AQSNFKTSQAFSGLRVTIDCKSKNGEFKTRGTGELDEEGQFKV</p> <p>SLPEEIVEDGKLKDECYAQVHSSATPCPAYDGLESSKIVLKT</p> <p>KINGKHTFGLAKKLKFSPTVCASAFFWPHFKYPPLPKWSHPKF</p> <p>KLPHLKSFGHHPFPFPKSFPPKFKKPLPIPKFKKPLPIPK</p> <p>IPPVPFYKPKPIPKVIPPIPIYKPKPIPKVLPPPIPIYKL</p> <p>KPPIPKLLPIPIYKPKPIPKVLPPPIPIYKPKPIPKVLPP</p> <p>IPYKPKPIPKVLPPVPIYKPKPIPKLLPIPIYKPKPI</p> <p>PKLLPIPIYKPKPIPKVLPPPIPIYKPKPIPKVLPPPI</p> <p>YKPKPIPKVLPPPIPIFKPKPIPKVLPLVPTYKPKPIPK</p> <p>VLPLPIYKPKPIFKLLPLPKIPFPKPCPPLPKLPLP</p> <p>KIPPKYNDHPKFGKWRPLPLPLPLFPSHP</p>
Uncharacterized protein LOC102616407 [<i>C. sinensis</i>]	XP_006483435.1	28.3	26.5	3%	<p>MMVAMVKDEWVRAAMMDDSVVVELLVRLKKQTNHVVKSEAEAV</p> <p>AVPLRWGIRQRRSRSCDAVSMRRKDAADSANNMRSPTTP</p> <p>LSWSGGSGGAASPSATADEETSRHQTSAVRSKGTATNETTGN</p> <p>STKRSRKKKTFAQLKEEEGFLKERIHLNKELETLRATYIQS</p> <p>AKNENLKRIKLDLGLDSGKNSSESHVDNGLASSTFPSQSAIID</p> <p>LPRLEYCETHEVVPAAHSSLCLLPDLNMTPAEDDSASETYGMS</p>

Beta-hexosaminidase 2-like [<i>C. sinensis</i>]	XP_006492777.1	66.5	79.7	3.5%	MARAIIFISLSQLCLLSLQSDPINVWPKPRIFSWPKPEATSL AAEFKIQAPMQTQLSSAVDRYLKLIKSEHHHHLVRPSINISS PPLQTLNISVDNISVPLTHGVNESYSVTITSDENTAYLVASTV WGAMRGLETFSQLVWGNPSCVAVGIYVWDEPLFSHRGLLLDTS RNYEVDLILRTISAMSANKLNVFHHITDSHSFPLLLPSDPN LAAKGSYGEDYLYTPSDVKKIIEYGLDYGVRVVEIDTPGHSG SWAGAHPEIVSCANKFWWPAGTKWEDRLASEPGTGQLNPLHPK TFGVMINVLENVASIFFENFFHSGGDEILPACWKSDSLIQSFL STGGTLEVLEKFINFVFPFIVALDKTAIWEDVILDNEIKVD PSYLYPEYTIFQSWKNGTESTKKIVQAGYRVIVSSDYLYLDC GHGGFLGNDSLYDQPPEIQKAAGGGSWCSPFKTWQTVYNYDIT EGLTEEEKELVLGGEVALWSEQADGTVLDARLWPRTSAMAELWSGNRDETGKK RYAEATDRLNEWRRHMRVNRGIGAEPIQLWCL QNPGMCNTVHAYNSGDDEENVTLSTGSADFKGFADSS
Hypothetical protein CISIN_1g0011 [<i>C. sinensis</i>]	KDO77096.1	64.2	57.9	1.5%	DLWSGSEGGGIKWPEAIEKALSLKPEERHTAALIVERSYID LRSHLSVNGFSSILTSIDKNLLSDHSRAKVWSAGFLSFALWDA RTRELLKVFNDGQIENRVDMSELLPDFAMEDEFKTKIVTSSKK DKAQSSFGFFQSRNAIMGAADAVRRVAAGGGFGDDNRRTEAL TTSIDGMIWTGGANGLLLQWDPNGNRLQDFQYLPFAVQCLCTF GSQIWVGYMNGIVQVLDLEGNLLGGWVAHSSPVIKMAVGAGYI FTLANHGGIRGWNVTSPGPLDSILCKELAGKEFLYTRMENLKI LAGTWNVGQGRASQDALISWLGSAASDVGIVVVGLEQEVEMGAG FLAMSAKETVGLGSAVGHWWLDMIGKILDDGSTFERVGSRQ

					LAGLLIAVWVRKNLKDYVGDDVAAVPCGFGRAIGNKGAVGLR VRVYDRIMCFVNCHFAAHLEAVNRRNADFDHVYRTMTFCRPSN LCSAAAAGASSVVQMLRSTNPLSGLTVEGVPELSEADMVIFLG DFNYRLDGITYDEARDFISQRCFDWLRERDQLRAEMEAGNVFQ GMREADIKFPPTYKFEKHLAGLAGTL
Protein chromatin remodeling isoform X1 [C. sinensis]	XP_006465090.1	132.7	33.1	1%	MAEKSKPRSLNDSHYRLLQDLASPTNRSALSSFSEYEKPSV AKHLASSKLNDNASVKRLQFSDTTRFDSTLDDKKPVKVEAEVR TNDCSVLSRDHDHVESRSVIDEEKPKVKIEGRRRLCKVSSRD VDNTENRAVVDDEPNFSDITDFDSPLQSKTVSTMVNIESRAVI DDGPKFSDITVFDSPPKAKTVSENDNYKGGNEIRDILNDLSAR LEILSIDKRRVPKTVDPEDDFSRLVKNGDTGQGSKGNLPEYAS AESSFSLTSDLSDSSSGVTKDNVGGVVESVADEYEESKGDDVA DEEQETENVGIGLKRNEPRWVDNNLVSARESFESNLDGEEDGG SLGEVEGDEHLSRVHETKKHHQRQKKNPKRVHDGERFNGQSF VSGGREEYDDEDDCVIVSGKLVVNRPDRRDGKLNKSAHSGLVN VLDDYSDDSVLEDEGSITLSGPRSTYMLPGKIGNMLFPHQREG LRWLWSLHCQGKGGILGDDMGLGKTMQICGFLAGLFHSRLIKR ALVVAPKTLTSHWIKELTAVGLSAKIREYFGTCVKTRQYELQY VLQDKGVLLTTYDIVRNNSKSLRGSSFISDEAGDDDAIWYMI LDEGHLIKNPSTQRAKSLLEIPSAHRIISGTPIQNNLKLWA LFNFCCPELLGDNKWFKEKYELPILRGNDKHALDREKRIGSAV

AKELRERIQPYFLRRLKNEVFHEDDVTSSATLSKKNEMIVWLR
 LTSCQRQLYEAFNLSEIVLSAFDGSPLAALTILKKICDHPLLL
 TKRAAEDVLDGMSMLNPEDAALAEKLAMHIADVAEKDDFQEQ
 HDNISCKISFILSLLDKLIPEGHNVLFISQTRKMLNLIQESIG
 SKGYKFLRIDGTTKASDRVKIVNDFQEGDVAPIFLLTSQVGGL
 GLTLTKADRVIVVDPAWNPSTDNQSVDRAYRIGQKKDVVVYRL
 MTCGTVEEKIYRKQIFKGGLFKTATEHKEQIRYFSQQDLRELL
 SLPKQGFVSLTQQQLHEEHGDQHNMDSELEAHIQFLDTLGIA
 GVSHHSLLFSKTARVQVVQEEEEATRRKGTA FVGNSSSSYLVA
 RNVDGAEYAFNPRDIKLNKSSSPKNEAKLKESDIKERIKRLS
 QLISNKVTVERLPDKGTLQKQIAELNSELNLIKMEKRPEPGV
 IDLDDVTGKLQRGLFLTQQF

*Empty boxes = there are no registered NCBI Reference Sequences in the platform.

**Peptides in red = identified by MS.

Reference

1. Ballotin, D.; Fulaz, S.; Souza, M.L.; Corio, P.; Rodrigues, A.G.; Souza, A.O.; Marcato, P.G.; Gomes, A.F.; Gozzo, F.; Tasic, L. Elucidating protein involvement in the stabilization of the biogenic silver nanoparticles. *Nanoscale Res. Lett.* **2016**, *11*, 313.