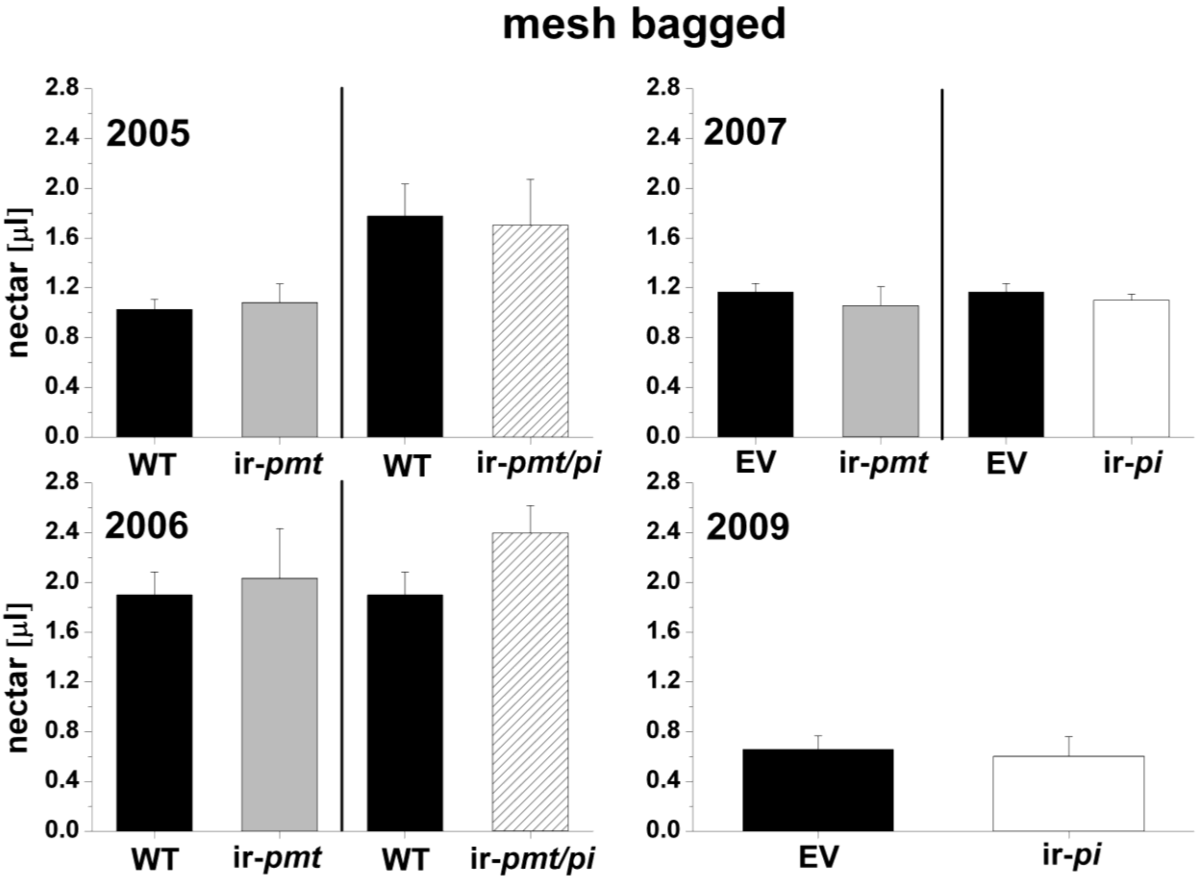
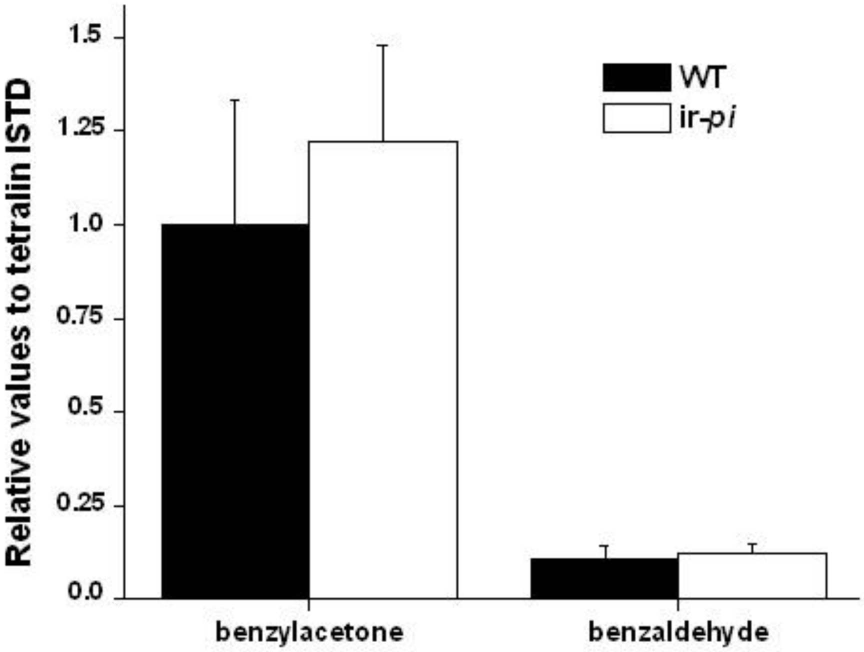
SUPPLEMENTAL FIGURES

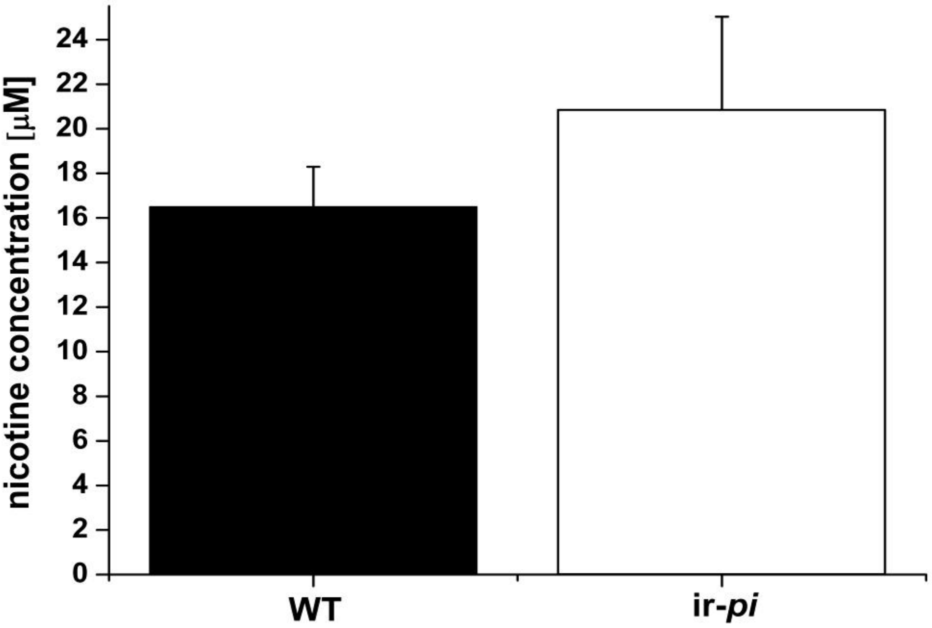


Supplemental Figure S1: Standing nectar volume from flowers of WT, EV, ir-*pmt*, ir-*pmt/pi* and ir-*pi* plants which were mesh bagged to exclude native floral visitors during the 2005, 2006, 2007, and 2009 field seasons (related to Figure 1).

Mean (±SE) standing nectar volume in flowers of *N. attenuata* wild-type plants (WT) or empty-vector plants (EV), and plants silenced in proteinase inhibitors (ir-*pi*), nicotine (ir-*pmt*) or both proteinase inhibitors and nicotine (ir-*pmt*/*pi*) production. Nectar volume was measured between 6:00 and 7:30 a.m. in flowers that had opened for the first time the previous night. No significant differences were determined (Student´s t-test, p>0.05). Different nectar volumes between the experiments are caused by different environmental conditions on the different days experiments were conducted.

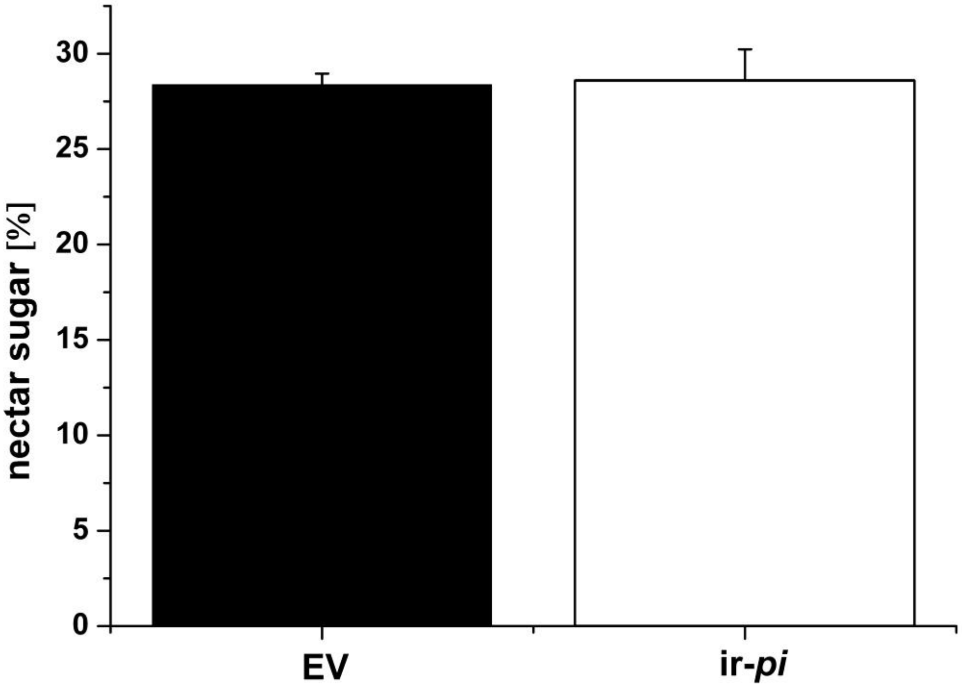


Supplemental Figure S2: Volatile organic compounds (VOCs) released from individual flowers of plants growing in the field plot at Lytle Ranch Preserve (Utah) from WT and ir-*pi* *N. attenuata* plants. Values are mean (± SE) peak areas in relation to the internal standard tetralin, of six to seven individual flowers from different plants for the two most abundant floral VOCs released from flowers during the night. All other minor floral VOC constituents (α-pinene, β-pinene, D-limonene, ethylbenzoate, benzylalcohol and β-myrcene) trapped also did not differ significantly between the two genotypes (Student´s t-test; $p>0.05$).



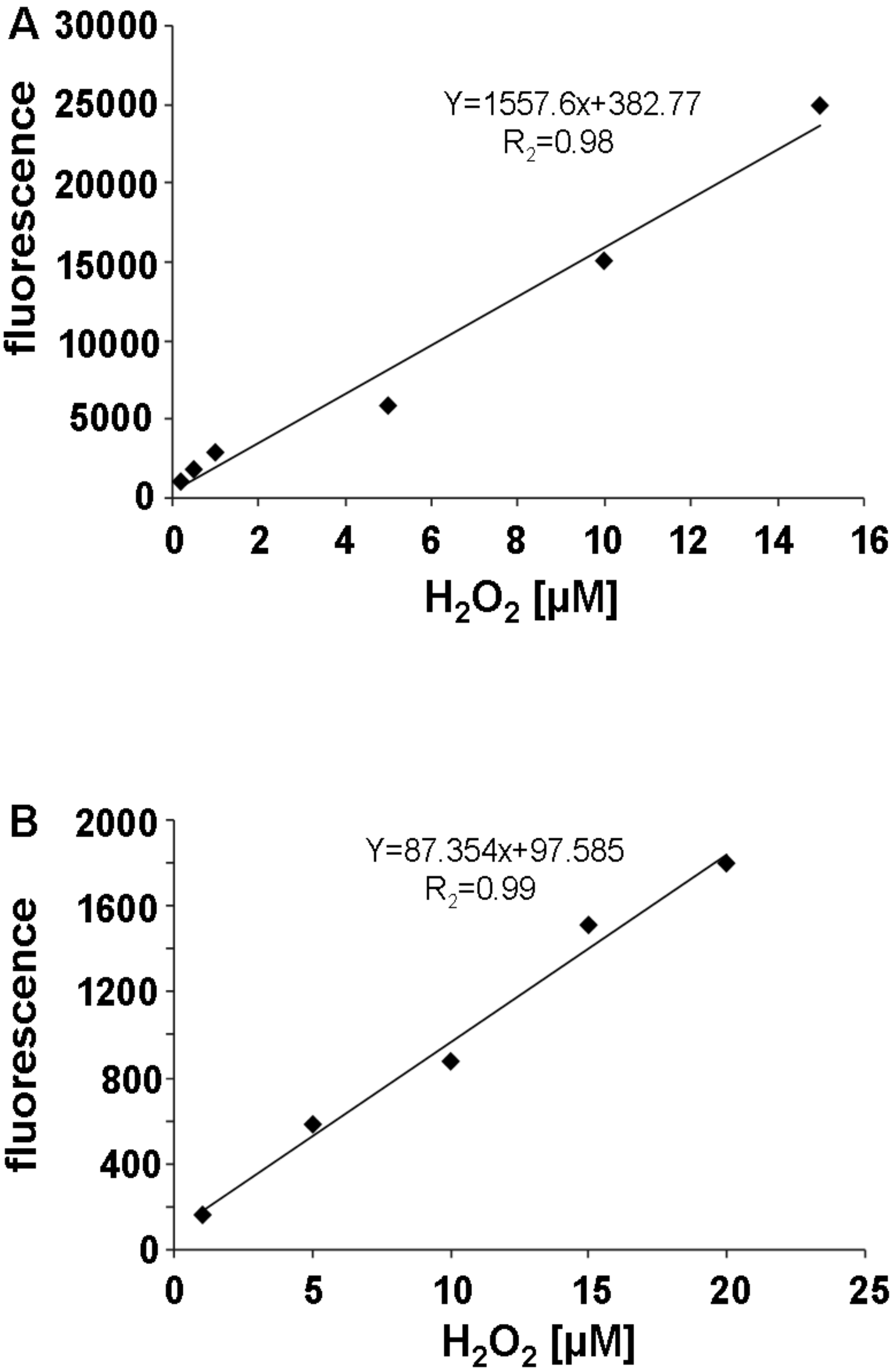
Supplemental Figure S3: Nicotine concentration in nectar

Mean (±SE) concentration of nicotine in nectar of flowers from *N. attenuata* wild-type plants (WT) and plants silenced in proteinase inhibitors (ir-*pi*) did not differ (Student´s t-test; $p>0.05$). Nicotine was measured with a Bruker-MicroToF LC-MS in relation to internal standard (nicotine-D_3).



Supplemental Figure S4: Nectar sugar concentration in field-grown plants

Mean (±SE) nectar sugar concentration in *N. attenuata* empty-vector plants (EV), and plants silenced in proteinase inhibitors (ir-*pi*). Nectar sugar concentration was measured from mesh-bagged flowers that had opened the previous night between 6:00 p.m. and 7:30 a.m. in 2007 field season. No differences between the lines were found (Student´s t-test; p>0.05).



Supplemental Figure S5: Hydrogen peroxide standard curves using (A) amplex red hydrogen peroxide/peroxidase assay, (B) luminol chemiluminescence assay.

Supplemental Table I. Protein spots identified with LC-MS/MS

Mass spectrometric identification of protein spots with differential accumulation after silencing TPI in *N. attenuata* , using fragment spectral searches in UniProt non-redundant (<= 100%) databases (www.uniprot.org), and MS-Blast similarity search from the generated *de novo* peptide sequences.

Spot N°	Accession N°	Name of protein	Protein identification data	
			Peptide Sequence	Protein sequence
1	Q01M83	H0622G10.1 protein From: *Oryza sativa*	Pep1:(-)LESPLVDLELR(-) Pep2:(-)AEVVSLNLGLQK(-) Pep3:(-)EAVVSLNGLLQK(-) Pep4:(-)EAVVSLNLGLQK(-) Pep5:(-)TVSPATLNSR(-) Pep6:(-)ASCGGTACVNSFGD EQLAVDMLADK(-) Pep7:(-)NAYWTLELYYGTTK NDTKYLAGQ(-) Pep8:(-)NAYWTLELRLNTTK NDTKYLAGQ(-) Pep9:(-)NAYWTLELRNLTTK NDTKYLAGQ(-)	METVAAASYTRGAATRSPACCAAMSFS QSYRPKAARPPSTFYGESLRVNTARSL PSGRQSKAASRAALSTRCEIGDSLEEF LTKATPDKNLIRLLICMGEAMRTISFK VRTASCGGTACVNSFGDEQLAVDMLAD KLLFEALEYSHVCKYACSEEVPELQDM GGPVDGGFSVAFDPLDGSSIVDTNFTV GTIFGVWPGDKLTGVTGGDQVAAAMGI YGPRTTYIIALKDCPGTHEFLLLDEGK WQHVKDTTTIGEGKMFSPGNLRATFDN PEYDKLINYYVKEKYTLRYTGGMVPDV NQIIVKEKGIFTNVTSPTAKAKLRLLF EVAPLGFLIEKAGGYSSDGKQSVLDKV INNLDERTQVAYGSKNEIIRFEETLYG SSRLTAGATVGAAA
2	Q8WJ47	Ribulose bisphosphate carboxylase large chain From: *Polysiphonia japonica*	Pep1:(-)AEVVSLNGLLQK(-) Pep2:(-)AEVVSNLGLLQK(-) Pep3:(-)VATVSLPR(-) Pep4:(-)LSSPATLNSR(-) Pep5:(-)SLSPATLNSR(-) Pep6:(-)TVSPATLNSR(-) Pep7:(-)VPGVSLPR(-) Pep8:(-)GHYMNITAATMEE MYER(-) Pep9:(-)WNSTNSLSGSHSLG GSTYGFSH(-) Pep10:(-)WNSTGGSLSAPLS LGGSTYGFSH(-) Pep11:(-)WNSTNSLSAPLSLG GSTYGFSH(-)	WTVVWTDLLTACDLYRAKAYKVDAVPN TSDQYFAYIAYDIDLFEEGSIANLTAS IIGNVFGFKAVKALRLEDMRXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXNR SIAATGEVKGHYMNITAATMEEMYERA EFGKQIGTIIVMIDLVIGYTAIQTMAV WARKNDMILHLHRAGNSTYSRQKIHGM NFRVICKWMRMAGVDHIHAGTVVGKLE GDPLMIKGFYNTLLETHLDINLPQGIF FQQDWESLRKVAPVASGGIHCGQMHQL LDYLGNDVVLQFGGGTIGHPDGIQAGA TANRVALESMVIARNEGRDYVAEGPQI LRDAAKTCGP
3	Q84UV8	Nectarin-II From: *Nicotiana langsdorffii* × *Nicotiana sanderae*	Pep1:(-)AEVVSNLGLLQK(-) Pep2:(-)EAVVSLNGLLQK(-) Pep3:(-)EAVVSNLGLLQK(-) Pep4:(-)TLLDLDGWK(-) Pep5:(-)VATVTVPR(-) Pep6:(-)TLLDTPSWK(-) Pep7:(-)VATVSLPR(-) Pep8:(-)ALGTLDLPNQK(-) Pep9:(-)LAGTLDLPNQK(-)	MRMAAITKMLFISFLFLSSVFLARSGE VDDESEFSYDEKSENGPANWGNIRPDW KECSGKLQSPIDIFDLRAEVVSNLRIL QKDYKPSNATLLNRGHDIMLRLDDGGY LKINETQYQLKQLHWHTPSEHTINGER FNLEAHLVHESNNGKFVVIGIVYEIGL WPDPFLSMIENDLKVPANKKGIERGIG IIDPNQIKLDGKKYFRYIGSLTTPPCT EGVVWIIDRKVKTVTRRQIKLLQEAVH DGFETNARPTQPENERYINSTYHSFGI EKQQ

Spot N°	Accession N°	Name of protein	Protein identification data	
			Peptide Sequence	**Protein sequence**
5	AAO85482.1	Nectarin-II From: *Nicotiana langsdorffii* × *Nicotiana sanderae*	Pep1:(-)EAVVSNLGLLQK(-) Pep2:(-)AEVVSLNGLLQK(-) Pep3:(-)EAVVSLNGLLQK(-) Pep4:(-)LESPLQLNTLR(-) Pep5:(-)ALGTLDPNQLK(-) Pep6:(-)LAGTLDPNQLK(-) Pep7:(-)LESPLQVQTLR(-) Pep8:(-)NETLQYELPVPNETQLPHGQ(-) Pep9:(-)NETLQYELPVPNETKLPHGQ(-) Pep10:(-)NETGALYELPVPNETQLPHGQ(-) Pep11:(-)LESPLNLQTLR(-)	MRMAAITKMLFISFLFLSSVFLARS GEVDDESEFSYDEKSENGPANWGNI RPDWKECSGKLQSPIDIFDLRAEVV SNLRILQKDYKPSNATLLNRGHDIM LRLDDGGYLKINETQYQLKQLHWHT PSEHTINGERFNLEAHLVHESNNGK FVVIGIVYEIGLWPDPFLSMIENDL KVPANKKGIERGIGIIDPNQIKLDG KKYFRYIGSLTTPPCTEGVVWIIDR KVKTVTRRQIKLLQEAVHDGFETNA RPTQPENERYINSTYHSFGIEKQQ
32	Q84UV8	Nectarin-II From: *Nicotiana langsdorffii* × *Nicotiana sanderae*	Pep1:(-)KNGVSNLGLLQK(-) Pep2:(-)NKGVSNLGLLQK(-) Pep3:(-)ALGTLDPNQLK(-) Pep4:(-)LAGTLDPNQLK(-) Pep5:(-)LAGTLDPGGQLK(-) Pep6:(-)LESPLAKQELR(-) Pep7:(-)NPDLEYGALPTALGTLDPNQLK (-) Pep8:(-)LESPLANLLDAK(-) Pep9:(-)EASPATLNSR(-)	MRMAAITKMLFISFLFLSSVFLARS GEVDDESEFSYDEKSENGPANWGNI RPDWKECSGKLQSPIDIFDLRAEVV SNLRILQKDYKPSNATLLNRGHDIM LRLDDGGYLKINETQYQLKQLHWHT PSEHTINGERFNLEAHLVHESNNGK FVVIGIVYEIGLWPDPFLSMIENDL KVPANKKGIERGIGIIDPNQIKLDG KKYFRYIGSLTTPPCTEGVVWIIDR KVKTVTRRQIKLLQEAVHDGFETNA RPTQPENERYINSTYHSFGIEKQQ
35	Q84UV8	Nectarin-II From: *Nicotiana langsdorffii* × *Nicotiana sanderae*	Pep1:(-)AEVVSLVANLQK(-) Pep2:(-)EAVVSLNLGLQK(-) Pep3:(-)EAVVSLVANLQK(-) Pep4:(-)TVSPATLNSR(-) Pep5:(-)VGPVSLPR(-) Pep6:(-)VPGVSLPR(-) Pep7:(-)GSFEVPDQLPTLNETQYQLK(-) Pep8:(-)GSFEVPNELPTLNETQYQLK(-) Pep9:(-)SGFEVPNELPTLNETQYQLK(-)	MRMAAITKMLFISFLFLSSVFLARS GEVDDESEFSYDEKSENGPANWGNI RPDWKECSGKLQSPIDIFDLRAEVV SNLRILQKDYKPSNATLLNRGHDIM LRLDDGGYLKINETQYQLKQLHWHT PSEHTINGERFNLEAHLVHESNNGK FVVIGIVYEIGLWPDPFLSMIENDL KVPANKKGIERGIGIIDPNQIKLDG KKYFRYIGSLTTPPCTEGVVWIIDR KVKTVTRRQIKLLQEAVHDGFETNA RPTQPENERYINSTYHSFGIEKQQ

Spot N°	Accession N°	Name of protein	Protein identification data	
			Peptide Sequence	Protein sequence
37	Q9LDB9	Zeaxanthin epoxidase From: *Arabidopsis thaliana*	Pep1:(-)MQWYAFHEEPAG GADAPNGMK(-) Pep2:(-)AEVVSLNGLLQK(-) Pep3:(-)EAVVSLNGLLQK(-) Pep4:(-)EAVVSNLGLLQK(-) Pep5:(-)SLSPAFLDVP(-) Pep6:(-)VTSPAFLDVP(-) Pep7:(-)QEFIAHLRR(-)	MGSTPFCYSINPSPSKLDFTRTHVFSP VSKQFYLDLSSFSGKPGGVSGFRSRRA LLGVKAATALVEKEEKREAVTDKKKKS RVLVAGGGIGGLVFALAAKKKGFDVLV FEKDLSAMRGEGKYRGPIQIQSNALAA LEAIDIEVAEQVMEAGCITGDRINGLV DGISGTWYVKFDTFTPAGVTGLPVTRV ISRMTLQQILARAVGEDVIRNESNVVD FEDSGDKVTVVLENGQRYEGDLLVGAD GIWSKVRNNLFGRSEATYSGYTCYTGI ADFIPADIESVGYRVFLGHKQYFVSSD VGGGKMQWYAFHEEPAGGADAPNGMKK RLFEIFDGWCDNVLDLLHATEEEAILR RDIYDRSPGFTWGKGRVTLLGDSIHAM QPNMGQGGCMAIEDSFQLALELDEAWK QSVETTTPVDVVSSLKRYEESRRLRVA IIHAMARMAAIMASTYKAYLGVGLGPL SFLTKFRVPHPGRVGGRFFVD
38	AAO85482.1	Nectarin-III (Containing Nectarin II) From: *Nicotiana langsdorffii* × *Nicotiana sanderae*	Pep1:(-)TWVLVPR(-) Pep2:(-)LESPLDLDLLR(-) Pep3:(-)LESPLDLEVLR(-) Pep4:(-)LESPLDLLDLR(-) Pep5:(-)AVPTNTGLLR(-) Pep6:(-)EAVVSLNGLLGAK(-) Pep7:(-)EAVVSLNGLLQK(-) Pep8:(-)EAVVSNLGLLQK(-) Pep9:(-)ALGTLDPNQLK(-) Pep10:(-)LAGTLDPNGALK(-) Pep11:(-)LAGTLDPNQLK(-) Pep12:(-)ANLLRVLLDQRAL TDAGYLGQATLLNR(-)	MRMAAITKMLFISFLFLSSVFLARSGE VDDESEFSYDEKSENGPANWGNIRPDW KECSGKLQSPIDIFDLRAEVVSNLRIL QKDYKPSNATLLNRGHDIMLRLDDGGY LKINETQYQLKQLHWHTPSEHTINGER FNLEAHLVHESNNGKFVVIGIVYEIGL WPDPFLSMIENDLKVPANKKGIERGIG IIDPNQIKLDGKKYFRYIGSLTTPPCT EGVVWIIDRKVKTVTRRQIKLLQEAVH DGFETNARPTQPENERYINSTYHSFGI EKQQ

Spot N°	Accession N°	Name of protein	Protein identification data	
			Peptide Sequence	Protein sequence
39	Q2RAV0	Calcium-dependent protein kinase From: *Oryza sativa*	Pep1:(-)LATVVPEK(-) Pep2:(-)VATVPVRT(-) Pep3:(-)ALGTLDPNQLK(-) Pep4:(-)TVSPATLNSR(-) Pep5:(-)AVAGDEAEPGTSKAAPPSR(-) Pep6:(-)NALLTLLLLNRRWDAGYQGLATLLNR(-) Pep7:(-)NALTLLLLLNRRWDAGYQGLATLLNR(-)	MGQCCTGGGKAVAGDEAEPGTSKAAPPSRGTSSKNGSAKQQPCSPAAKAAATEAAAAASSSKKPAGPIGEVLERPMEEVRTTYSIGKELGRGQFGVTHLCTHKATGEKLACKTIAKRKLANKEDVDDVRREVQIMHHLSGQPNIVDLRGAYEDKHNVHLVMELCAGGELFDRIIARGHYTERAAAALLRAIVGIVHTCHSMGVIHRDLKPENFLLLSKGDDAPLKATDFGLSVFFKEGEVFRDIVGSAYYIAPEVLKRKYGPEADIWSIGVMLYIFLAGVPPFWAESENAIFTAILRGQIDLASEPWPKISSGAKDLVRKMLNINPKERLTAFQVLNHPWIKEDGDAPDVPLDNVVLNRLKQFRAMNQFKKAALRIIAGCLSEEEIKGLKEMFKNIDKDNSGTITLEELKNGLAKQGTKFSDNEIEQLMEAADADGNGIIDYEEFVTATVHMNKMDREEHLYTAFQYFDKDNSGYITKEELEQALKEQGLYDANEIKDVITDADSNNDGRIDYSEFVAMMRKGSGCAEATNPKKKRRDLV
40	Q84UV8	Nectarin-II From: *Nicotiana langsdorffii* × *Nicotiana sanderae*	Pep1:(-)QAAKSIVANGLAR(-) Pep2:(-)LESPLDVELLR(-) Pep3:(-)LESPLDVLELR(-) Pep4:(-)LLYCQR(-) Pep5:(-)AMFEPLGPSYRGPR(-) Pep6:(-)LESPLQGSALLR(-) Pep7:(-)TVSPATLNSR(-) Pep8:(-)ALGTLDPNQLK(-) Pep9:(-)LAGTLDPNQLK(-) Pep10:(-)LASALDPNQLK(-) Pep11:(-)AEVVSLNGLLQK(-) Pep12:(-)EAVVSLNGLLGAK(-)	MRMAAITKMLFISFLFLSSVFLARSGEVDDESEFSYDEKSENGPANWGNIRPDWKECSGKLQSPIDIFDLRAEVVSNLRILQKDYKPSNATLLNRGHDIMLRLDDGGYLKINETQYQLKQLHWHTPSEHTINGERFNLEAHLVHESNNGKFVVIGIVYEIGLWPDPFLSMIENDLKVPANKKGIERGIGIIDPNQIKLDGKKYFRYIGSLTTPPCTEGVVWIIDRKVKTVTRRQIKLLQEAVHDGFETNARPTQPENERYINSTYHSFGIEKQQ
42	Q69KU5	Putative uncharacterized protein. From: *Oryza sativa*	Pep1:(-)MAAADTGGDGNGGPTTP(-) Pep2:(-)DHGGAAAEGRQDLGK(-) Pep3:(-)AEVVSLNLGLQK(-) Pep4:(-)EAVVSLNGLLQK(-) Pep5:(-)EAVVSLNLGLQK(-) Pep6:(-)TVSPATLNSR(-)	MARRLRARGQTTTGDGSASRWRAWGAADGEKGEGAVGILTEDGDGETTTGRWPAAEKMAATGTGGDGNGVPTTPDHGGAAAEGRQDLGKILERLGREIGDRSGEERWFETTTAVAELGSTAESGRLKTAAAGERGGARGGGVPEAERGNGVEAGLRHGAAKPTVVADWRGGGWSGGIGRPELAGKRWCTGARWGGV

Spot N°	Accession N°	Name of protein	Protein identification data	
			Peptide Sequence	**Protein sequence**
44	Q84UV8	Nectarin-II From: *Nicotiana langsdorffii* × *Nicotiana sanderae*	Pep1:(-)LESPLDVELLR(-) Pep2:(-)AKDQESYPK(-) Pep3:(-)AEVVSLNGLLQK(-) Pep4:(-)EAVVSLNGLLGAK(-) Pep5:(-)SLNNQFSATVFR(-) Pep6:(-)ALGTLDPNQLK(-) Pep7:(-)LAGTLDPNGALK(-) Pep8:(-)NALTNALNRGYKCTPSNATLLNR(-)	MRMAAITKMLFISFLFLSSVFLAR SGEVDDESEFSYDEKSENGPANWG NIRPDWKECSGKLQSPIDIFDLRA EVVSNLRILQKDYKPSNATLLNRG HDIMLRLDDGGYLKINETQYQLKQ LHWHTPSEHTINGERFNLEAHLVH ESNNGKFVVIGIVYEIGLWPDPFL SMIENDLKVPANKKGIERGIGIID PNQIKLDGKKYFRYIGSLTTPPCT EGVVWIIDRKVKTVTRRQIKLLQE AVHDGFETNARPTQPENERYINST YHSFGIEKQQ
54	Q9SM34	Germin-like protein From: *Triticum aestivum*	Pep1:(-)GMQLAQETIEKMTSR(-) Pep2:(-)LTPALNTLGLTLLR(-) Pep3:(-)ASDPPLSDDYLAK(-) Pep4:(-)TLPALNGLTLTLLR(-) Pep5:(-)TLPALNTLGLTLLR(-)	MASSSSFLLLAALLALVSWQATA SDPSPLQDFCVADMNSPVRVNGF VCKNPMEVNADDFFKAANLDKPK MPNKVGSNVTLINVMQIAGLNTL GISIARIDYAPLGQNPPHTHPRA TEILTVLEGTLYVGFVTSNQPAP NKNKFLSKVLNKGDVFVFPVGLI HFQFNPNPHQPAVAIAALSSQNP GAITIANAVFGSDPPISDDVLAK AFQVEKNTIDYLQAQFWENNHY
55	ACG47794.1	Germin-like protein From: *Zea mays*	Pep1:(-)PDPNSNLGGTK(-) Pep2:(-)PDPNSNVAGTK(-) Pep3:(-)PDPNSNVQTK(-) Pep4:(-)QVDLESADLDPR(-) Pep5:(-)PALNTLGKKSPR(-) Pep6:(-)LPANYDGLYSVAVDAR(-) Pep7:(-)MVLEDLR(-) Pep8:(-)VMLEDLR(-) Pep9:(-)VPYEDLR(-) Pep10:(-)ANGDLLVFVFPQGH(-) Pep11:(-)NAGDLLVFVFPQGH(-) Pep12:(-)NALGDLVFVFPQGH(-) Pep13:(-)MVLEELR(-) Pep14:(-)ASDPPLSDDYLAK(-) Pep15:(-)TGDPPLSDDYLAK(-) Pep16:(-)VMFEDKLR(-) Pep17:(-)LTPALNGLTLTLLR(-) Pep18:(-)TLPALNGLTLLTLR(-) Pep19:(-)TYLEDKLR(-)	MAASSYFLLAAFLAVVASHATAS DPSPLQDFCVADMHSPVKVNGFV CKDSMAVTADDFFKAANLDKARD TMKSKVGSNVTLINVIQLPGLNT LGISLARIDYAPLGENPPHTHPR ATEILTVLEGTLYVGFVTSNPNK LFAKVLNKGDVFVFPQGLIHFQF NPVYNKPAVAIAALSSQNPGVIT IANAVFGSKPPISDDVLAKAFQV EKGTIDWLQAQFWENNHY

Spot N°	Accession N°	Name of protein	Protein identification data	
			Peptide Sequence	Protein sequence
57	Q84PM0	Germin-like protein From: *Gossypioides kirkii*	Pep1:(-)LTPALNTLGLTLLR(-) Pep2:(-)TLPALNGLTLTLLR(-) Pep3:(-)MVKLATANR(-) Pep4:(-)LLNAGDVFVFPQGH(-)	PLQDFCVALNSTKHAVFVNGKLC KDPKLATADDFFFSGLDKPGNTS NAVGSRVTPVNVDQIPGLNTLSI SLVRIDYAPNGGQNPPHTHPRAT EILVVTKGTLYVGFITSNPDNRL FTKVLKTGDVFVFPVGLIQFQFN IGKTNAIAFAGLSSQNPGVITIA NAVFGSNPAINSEVLAKTFKLDK KMA
83	Q94EG3	Nectarin-I From: *Nicotiana langsdorffii* × *Nicotiana sanderae*	Pep1:(-)LTPALNTLGLTLLR(-) Pep2:(-)TLPALNGLTLTLLR(-) Pep3:(-)TLPALNTLGLTLLR(-) Pep4:(-)YPVEDLR(-) Pep5:(-)FLVEDLR(-) Pep6:(-)FVLEDLR(-) Pep7:(-)PYLEDKLR(-) Pep8:(K)GEVFVFPR(G) Pep9:(-)FLLEDKLR(-) Pep10:(-)LFLEDKLR(-)	MAAFGINSKIFQSMEMAILFLLA ISIDRYCFAADEDMLQDVCVADL HSKVKVNGFPCKTNFTAADFSSL AISKPGATNNKFGSVVTTANVEQ VPGLNTLGVSLARIDYAPGGINP PHTHPRASEMVFVMEGELDVGFI TTANVLVSKKIIKGEVFVFPRGL VHFQKNNGEVPAAVISAFNSQLP GTQSIPITLFGASPPVPDDVLAQ TFQINTEDVQQIKSKFAPVKKF
84	Q9SM34	Germin-like protein From: *Triticum aestivum*	Pep1:(-)ASDPPLSDDYLAK(-) Pep2:(-)LTPALNTLGLTLLR(-) Pep3:(-)TLPALNTLGLLTLR(-) Pep4:(-)TLPALNTLGLTLLR(-) Pep5:(-)MVLEDLR(-) Pep6:(-)VMLEDLR(-)	MASSSSFLLLAALLALVSWQATA SDPSPLQDFCVADMNSPVRVNGF VCKNPMEVNADDFFKAANLDKPK MPNKVGSNVTLINVMQIAGLNTL GISIARIDYAPLGQNPPHTHPRA TEILTVLEGTLYVGFVTSNQPAP NKNKFLSKVLNKGDVFVFPVGLI HFQFNPNPHQPAVAIAALSSQNP GAITIANAVFGSDPPISDDVLAK AFQVEKNTIDYLQAQFWENNHY
86	Q6YZB2	Germin-like protein From: *Oryza sativa*	Pep1:(-)KLLGVTTLDVAR(-) Pep2:(-)SGEVGLKVK(-) Pep3:(-)VLLEKAACK(-) Pep4:(-)KEATTAAVDVELR(-) Pep5:(-)EQLQSSSICPSR(-) Pep6:(-)LLNADGVFVFPQGH(-) Pep7:(-)LLNAGDVFVFPAGGH(-) Pep8:(-)MVLEDLR(-) Pep9:(-)VYPEDLR(-) Pep10:(-)AVSLYEDSK(-) Pep11:(-)SVALYEDSK(-) Pep12:(-)ASDPPLSDDYLAK(-) Pep13:(-)FGKVLVIDGK(-) Pep14:(-)MVLEDKLR(-) Pep15:(-)LTPALNTWLLLLK(-)	MASSSSFLLLAALLALVSWQAT ASDPSPLQDFCVADMNSPVRVN GFVCKNPMEVNADDFFKAANLD KPKMPNKVGSNVTLINVMQIAG LNTLGISIARIDYAPLGQNPPH THPRATEILTVLEGTLYVGFVT SNQPAPNKNKFLSKVLNKGDVF VFPVGLIHFQFNPNPHQPAVAI AALSSQNPGAITIANAVFGSDP PISDDVLAKAFQVEKNTIDYLQ AQFWENNHY

			Protein identification data	
Spot N°	**Accession N°**	**Name of protein**	**Peptide Sequence**	**Protein sequence**
89	AAB51582.1	Germin-like protein From: *Arabidopsis thaliana*	Pep1:(-)MSVEIPPSDDFRAMK(-) Pep2:(-)GGSPSSFSGLNMVSR(-) Pep3:(-)LSFKNSPENR(-) Pep4:(-)EQLQSSSICPSR(-) Pep5:(-)LTPALNTLGLTLLR(-) Pep6:(-)TLPALNTLGLLTLR(-) Pep7:(-)TLPALNTLGLTLLR(-) Pep8:(-)MVLEDLR(-) Pep9:(-)PYVEDLR(-) Pep10:(-)YPVEDLR(-) Pep11:(-)NSGGGGGHSGGTECIMGDSK(-) Pep12:(-)VLPNSASGGGLK(-) Pep13:(-)MVLEDKLR(-) Pep14:(-)TYKNDKLR(-) Pep15:(-)YTKNDKLR(-)	PKRVDAKDFFFSGLNMPGNTN NQVGSNVTTVNVDQIPGLNTM GISLVRIDYAPHGQNPPHTHP RGSEILVLVEGTLYVGFVSSN QDNNRLFAKVLHPGDVFVFPI GMIHFQVNVGKIPAVAFAGLS SQNAGVITIANTVFGSNPPIY PELLARAFQLDASVVKELQAK FGSI

Supplemental Table II. Protein spots identified with LC-MS/MS

Mass spectrometric identification of protein spots, common in WT and ir-*pi* *N. attenuata* nectar, in *N. attenuata* , using fragment spectral searches in UniProt non-redundant (<= 100%) databases (www.uniprot.org), and MS-Blast similarity search from the generated *de novo* peptide sequences.

Spot N°	Accession N°	Name of protein	Protein identification data	
			Peptide Sequence	Protein sequence
A	Q401N7	Aspartic proteinase From: *Triticum aestivum*	Pep1:(-)AEVVSNLGLLQK(-) Pep2:(-)EAVVSNLGLLQK(-) Pep3:(-)EAVVSNLLGLQK(-) Pep4:(-)ALGTLDPNQLK(-) Pep5:(-)LAGTLDPNQLK(-) Pep6:(-)TVSPATLNSR(-) Pep7:(-)VGEGTATQCISGFTAMDIPPPR(-)	VAKFDGILGLGFKEISVGKAVPVWYNM VEQGLISDPVFSFWLNRHADDEGEGGE IIFGGMDPKHYVGEHTYVPATQKGYWQ FDMGDVLVGGKSTGFCAGGCAAIADSG TSLLAGPTAIITEINEKIGAAGVVSQE CKTIVSQYGQQILDLLLAETQPKKVCS QVGLCTFDGTRGVSAGIRSVVDDEPVK SNGLHTDPMCSACEMAVVWMQNQLAQN KTQDLILDYVNQLCNRLPSPMGESAVD CASLGSMPDIEFTISGKKFALKPEEYI LKVGEGAAAQCISGFTAMDIPPPRGPL WILGDVFMGPYHTVFDYGKLRVGFAKA
B	Q5ZDT4	Putative HGA6 From: *Oryza sativa*	Pep1:(-)LESPLDAVKSPK(-) Pep2:(-)LESPLDVAKSPK(-) Pep3:(-)SGKGPLDAVKSPK(-) Pep4:(-)TVSPATLNSR(-) Pep5:(-)ALGTLDPNGALK(-) Pep6:(-)AEVVSLNGLLQK(-) Pep7:(-)EAVVSLNLGLQK(-) Pep8:(-)NAAGFMNASSDGSNQQQLDLDRDAMSR(-) Pep9:(-)HYQLFDSDSFGGTLRLGFSNEQNNGK(-) Pep10:(-)HYQLFDSDSFGGTLRLGFSNHFTTSP(-)	MEGGGKAGYSYGGHHHHQDAKLLKNLSR VEPRRFGLGLVAGFLIVTCAYFSTAKFD AIHIAMSTPAHLLLLLLTHLHAYLCISL LSPWILAVSSPAKNAAGFMNASSDGSNQ QQLDLDRDAMSREGSKAQVLDTDGDDKI SSLGPDLGHNASALEGKKKDETFAKDSG DASVSASTDEALAKDDDAIVGAVLPPLS SEEPTNITQDSVLEDEELKVQETAPATT NPSPEKSSNNGSSPSVVPSDPATLPVQQ IPPTQEAKDPPAQQIPAVPEAKVPPVQQ IPTFPVVKTEAAPRRKEWKPLCDLWSNR RIDWCELDGDVRVAGANGTVSLVAPPGP ADERTFRAESWHIKPYPRKADPNA
C	Q84UV8	Nectarin-II From: *Nicotiana langsdorffii* × *Nicotiana sanderae*	Pep1:(-)LESPLDVLQNR(-) Pep2:(-)FCNYHGSFDGDNYNIGSQMR(-) Pep3:(-)ELSPLDVLELR(-) Pep4:(-)LESPLDVLELR(-) Pep5:(-)TVSPATLNSR(-) Pep6:(-)AEVVSLNGLLQK(-) Pep7:(-)EAVVSNLGLLQK(-) Pep8:(-)LLVLVFWVHR(-) Pep9:(-)LLVVLFWVHR(-) Pep10:(-)ANEGLGFNSFSHLFLGYADDAGLSEDGK(-) Pep11:(-)NAEGLGFNSFSHLFLGYADDAGLSEDGK(-) Pep12:(-)HFSLGFNSEELLFLGFSPGMGLSEDGK(-) Pep13:(-)NALMLEGKKTCKDSWLCMRATLLGGR(-)	MRMAAITKMLFISFLFLSSVFLARSGE VDDESEFSYDEKSENGPANWGNIRPDW KECSGKLQSPIDIFDLRAEVVSNLRIL QKDYKPSNATLLNRGHDIMLRLDDGGY LKINETQYQLKQLHWHTPSEHTINGER FNLEAHLVHESNNGKFVVIGIVYEIGL WPDPFLSMIENDLKVPANKKGIERGIG IIDPNQIKLDGKKYFRYIGSLTTPPCT EGVVWIIDRKVKTVTRRQIKLLQEAVH DGFETNARPTQPENERYINSTYHSFGI 0EKQQ

Spot N°	Accession N°	Name of protein	Protein identification data	
			Peptide Sequence	**Protein sequence**
D	Q2KMD9	Glyceraldehyde-3-phosphate dehydrogenase From: *Nicotiana tabacum*	Pep1:(-)LEKEATYDDIK(-) Pep2:(-)LSSPAQLSSR(-) Pep3:(-)LSSPAVAASSR(-) Pep4:(-)ALGTLDPNQLK(-) Pep5:(-)LAGTLDPNGALK(-) Pep6:(-)LAGTLDPNQLK(-)	GLMTTVHSITATQKTVDGPSMK DWRGGRAASFNIIPSSTGAAKA VGKVLPVLNGKLTGMAFRVPTV DVSVVDLTVRLEKEATYDDIKA AIKEASQGKLKGILGYTEDDVV STDFVGDSRSSIFD
E	Q84UV8	Nectarin-II From: *Nicotiana langsdorffii* × *Nicotiana sanderae*	Pep1:(-)ELSPLDVLELR(-) Pep2:(-)LESPLDVELLR(-) Pep3:(-)LESPLDVLELR(-) Pep4:(-)AEVVSLVANLQK(-) Pep5:(-)EAVVSLVANLAGK(-) Pep6:(-)ALGTLDPNQLK(-) Pep7:(-)ALSALDPNQLK(-) Pep8:(-)LAGTLDPNQLK(-) Pep9:(-)NAAYTDLQLSVYHTN LETQYQLK(-) Pep10:(-)NASFNKSQLFTTHTR AETQYQLK(-) Pep11:(-)NASFLCLQLSVYH TARETQYQLK(-)	MRMAAITKMLFISFLFLSSVFL ARSGEVDDESEFSYDEKSENGP ANWGNIRPDWKECSGKLQSPID IFDLRAEVVSNLRILQKDYKPS NATLLNRGHDIMLRLDDGGYLK INETQYQLKQLHWHTPSEHTIN GERFNLEAHLVHESNNGKFVVI GIVYEIGLWPDPFLSMIENDLK VPANKKGIERGIGIIDPNQIKL DGKKYFRYIGSLTTPPCTEGVV WIIDRKVKTVTRRQIKLLQEAV HDGFETNARPTQPENERYINST YHSFGIEKQQ
F	Q84UV8	Nectarin-II From: *Nicotiana langsdorffii* × *Nicotiana sanderae*	Pep1:(-)EIQAGCSESLPGS SKSSWK(-) Pep2:(-)ELSPLDVELLR(-) Pep3:(-)LESPLDVELLR(-) Pep4:(-)AEVVSLNGLLQK(-) Pep5:(-)EAVVSLNGLLGAK(-) Pep6:(-)LESPLLTELLR(-) Pep7:(-)ALGTLDPNQLK(-) Pep8:(-)LAGTLDPNGALK(-) Pep9:(-)LAGTLDPNQLK(-)	MRMAAITKMLFISFLFLSSVFL ARSGEVDDESEFSYDEKSENGP ANWGNIRPDWKECSGKLQSPID IFDLRAEVVSNLRILQKDYKPS NATLLNRGHDIMLRLDDGGYLK INETQYQLKQLHWHTPSEHTIN GERFNLEAHLVHESNNGKFVVI GIVYEIGLWPDPFLSMIENDLK VPANKKGIERGIGIIDPNQIKL DGKKYFRYIGSLTTPPCTEGVV WIIDRKVKTVTRRQIKLLQEAV HDGFETNARPTQPENERYINST YHSFGIEKQQ

Spot N°	Accession N°	Name of protein	Protein identification data	
			Peptide Sequence	Protein sequence
G	Q84UV8	Nectarin-II From: *Nicotiana langsdorffii* × *Nicotiana sanderae*	Pep1:(-)LESPLSDLLLSP(-) Pep2:(-)LESPLFLALPSP(-) Pep3:(-)AEVVSNLGLLQK(-) Pep4:(-)EAVVSLVANLQK(-) Pep5:(-)ALGTLDPNQLK(-) Pep6:(-)LAGTLDPNGALK(-)	MRMAAITKMLFISFLFLSSVFLARSG EVDDESEFSYDEKSENGPANWGNIRP DWKECSGKLQSPIDIFDLRAEVVSNL RILQKDYKPSNATLLNRGHDIMLRLD DGGYLKINETQYQLKQLHWHTPSEHT INGERFNLEAHLVHESNNGKFVVIGI VYEIGLWPDPFLSMIENDLKVPANKK GIERGIGIIDPNQIKLDGKKYFRYIG SLTTPPCTEGVVWIIDRKVKTVTRRQ IKLLQEAVHDGFETNARPTQPENERY INSTYHSFGIEKQQ
H	Q84UV8	Nectarin-II From: *Nicotiana langsdorffii* × *Nicotiana sanderae*	Pep1:(-)NSSPAVESQK(-) Pep2:(-)LESPLQGDRLR(-) Pep3:(-)LESPLQGRDLR(-) Pep4:(-)LESPLDLLDLR(-) Pep5:(-)SNVVSNLLGAGLK(-) Pep6:(-)SNVVSVLLQANK(-) Pep7:(-)SNVVSVLQGAGLK(-) Pep8:(-)AEVVSLNGLLGAK(-) Pep9:(-)AEVVSLNGLLQK(-) Pep10:(-)AYIQQLETSR(-) Pep11:(-)ALGTLDPNQLK(-) Pep12:(-)LASALDPNQLK(-)	MRMAAITKMLFISFLFLSSVFLARSG EVDDESEFSYDEKSENGPANWGNIRP DWKECSGKLQSPIDIFDLRAEVVSNL RILQKDYKPSNATLLNRGHDIMLRLD DGGYLKINETQYQLKQLHWHTPSEHT INGERFNLEAHLVHESNNGKFVVIGI VYEIGLWPDPFLSMIENDLKVPANKK GIERGIGIIDPNQIKLDGKKYFRYIG SLTTPPCTEGVVWIIDRKVKTVTRRQ IKLLQEAVHDGFETNARPTQPENERY INSTYHSFGIEKQQ
I	Q84UV8	Nectarin-II From: *Nicotiana langsdorffii* × *Nicotiana sanderae*	Pep1:(-)AEVVSLNGLLQK(-) Pep2:(-)EAVVSNLGLLQK(-) Pep3:(-)NATAVEYELAYHNT LNETQYLAGK(-) Pep4:(-)NATAVEYELKGYHT LNETQYALGK(-) Pep5:(-)NAMRVRRTTCKDA NRHQWATLLNR(-) Pep6:(-)NAVRMRRTTCKDA NRHQWATLLNR(-)	MRMAAITKMLFISFLFLSSVFLARSG EVDDESEFSYDEKSENGPANWGNIRP DWKECSGKLQSPIDIFDLRAEVVSNL RILQKDYKPSNATLLNRGHDIMLRLD DGGYLKINETQYQLKQLHWHTPSEHT INGERFNLEAHLVHESNNGKFVVIGI VYEIGLWPDPFLSMIENDLKVPANKK GIERGIGIIDPNQIKLDGKKYFRYIG SLTTPPCTEGVVWIIDRKVKTVTRRQ IKLLQEAVHDGFETNARPTQPENERY INSTYHSFGIEKQQ

Spot N°	Accession N°	Name of protein	Protein identification data	
			Peptide Sequence	Protein sequence
J	Q94EG3	Nectarin-I From: *Nicotiana langsdorffii* × *Nicotiana sanderae*	Pep1:(-)NSSPAVSLGTN(-) Pep2:(-)SNSPAVSLTGN(-) Pep3:(-)NSSPAVNTTR(-) Pep4:(-)TLPALNTLLALSLR(-) Pep5:(-)TLPALNTLLTGLLR(-) Pep6:(-)TLPALNTLLTRLAV(-) Pep7:(-)VDGFPCK(D) Pep8:(K)GEVFVFPR(G) Pep9:(-)VATVLSPR(-) Pep10:(-)VATVSLPR(-) Pep11:(-)VGPVSLPR(-) Pep12:(-)VPGVSLPR(-) Pep13:(-)VPGLALVLRDFP(-) Pep14:(-)VPGLAVLLRDFP(-) Pep15:(R)GLVHFQK(N) Pep16:(-)VPGLNTLKLWR(-)	MAAFGINSKIFQSMEMAILFLLAISI DRYCFAADEDMLQDVCVADLHSKVKV NGFPCKTNFTAADFSSLAISKPGATN NKFGSVVTTANVEQVPGLNTLGVSLA RIDYAPGGINPPHTHPRASEMVFVME GELDVGFITTANVLVSKKIIKGEVFV FPRGLVHFQKNNGEVPAAVISAFNSQ LPGTQSIPITLFGASPPVPDDVLAQT FQINTEDVQQIKSKFAPVKKF
K	Q9LM03	Methionine synthase From: *Solanum tuberosum*	Pep1:(-)VDPALNTLLLATVR(-) Pep2:(-)DIFDSMAADR(-) Pep3:(-)LTPALNTLLLATVR(-) Pep4:(-)TLPALNTLLLATVR(-) Pep5:(R)IPSTDEIADR(I) Pep6:(R)IPSTEEIADR(I) Pep7:(K)VVEVNALAK(A) Pep8:(K)YLFAGVVDGR(N) Pep9:(K)GVTGFGFDLVR(G) Pep10:(-)FPRGIGR(-) Pep11:(R)GNASVPAMEMTK(W) Pep12:(-)TVSPATLNSR(-) Pep13:(K)ISEEDYVK(A) Pep14:(K)ISEEEYVK(A) Pep15:(K)YGAGIGPGVY DIHSPR(I)	MASHVVGYPRMGPKRELKFALESFWDG KSSAEDLKKVSADLRSSIWKQMSDAGI KYIPSNTFSYYDQVLDTTAMLGAVPSR YNWTGGEIEFGTYFSMARGNASVPAME MTKWFDTNYHFIVPELGPDVNFSYASH KAVNEYKEAKAQGVDTVPVLVGPVSYL LLSKPAKGVEKSFPLLSLLDKILPIYK EVIAELKAAGASWIQLDEPTLVLDLES HKLEAFTKAYADLESSLSGLNVLVETY FADVPAEAFKTLTALKGVTAFGFDLVR GTQTLELIKSSFPSGKYLFAGVVDGRN IWANDLAASLALLQSLEGVVGKDKLVA STSCSLLHTAVDLINETKLDDEIKSWL AFAAQKVVEVNALAKALSGAKDEAFFS ANAAAQASRKSSPRVTNEAVQKASAAL QGSDHRRATNVSARLDAQQKKLNLPIL PTTTIGSFPQTVELRRVRREYKAKKIS EEEYVKAITEEIKKVVDLQEELDIDVL VHGEPERNDMVEYFGEQLSGFAFTANG WVQSYGSRCVKPPIIYGDVSRPKPMTV FWSSKAQEMTKRPMKGMLTGPVTILNW SFVRNDQPRFETCYQIALAIKDEVEDL EKAGITVIQIDEAALREGLPLRKAEHA FYLNWAVHSFRITNVGIEDTTQIHTHM CYSNFNDIIHSIIDMDADVITIENSRS DEKLLSVFREGVKYGAGIGPGVYDIHS PRIPSTEEIADRVNKMLAVLDTNILWV NPDCGLKTRKYTEVKPALQNMVSAAKT IRTQLASAK

Spot N°	Accession N°	Name of protein	Protein identification data	
			Peptide Sequence	Protein sequence
L	Q94EG3	Nectarin-I From: *Nicotiana langsdorffii* × *Nicotiana sanderae*	Pep1:(-)NSSPAVSLGTN(-) Pep2:(-)SNSPAVSLTGN(-) Pep3:(-)NSSPAVNTTR(-) Pep4:(-)TLPALNTLLALSLR(-) Pep5:(-)TLPALNTLLTGLLR(-) Pep6:(-)TLPALNTLLTRLAV(-) Pep7:(-)VDGFPCK(D) Pep8:(K)GEVFVFPR(G) Pep9:(-)VATVLSPR(-) Pep10:(-)VATVSLPR(-) Pep11:(-)VGPVSLPR(-) Pep12:(-)VPGVSLPR(-) Pep13:(-)VPGLALVLRDFP(-) Pep14:(-)VPGLAVLLRDFP(-) Pep15:(R)GLVHFQK(N) Pep16:(-)VPGLNTLKLWR(-)	MRMAAITKMLFISFLFLSSVFLARSG EVDDESEFSYDEKSENGPANWGNIRP DWKECSGKLQSPIDIFDLRAEVVSNL RILQKDYKPSNATLLNRGHDIMLRLD DGGYLKINETQYQLKQLHWHTPSEHT INGERFNLEAHLVHESNNGKFVVIGI VYEIGLWPDPFLSMIENDLKVPANKK GIERGIGIIDPNQIKLDGKKYFRYIG SLTTPPCTEGVVWIIDRKVKTVTRRQ IKLLQEAVHDGFETNARPTQPENERY INSTYHSFGIEKQQ
M	Q94EG3	Nectarin-I From: *Nicotiana langsdorffii* × *Nicotiana sanderae*	Pep1:(-)DVPALNTLPKGSRK(-) Pep2:(-)LTPALNTPGKLSRK(-) Pep3:(-)TLPALNTPGKLSRK(-) Pep4:(-)TGHHVFPR(-) Pep5:(-)EGVFVFPR(-) Pep6:(-)GEVFVFPR(-) Pep7:(-)VPGLNTLGVTAVR(-) Pep8:(-)VPGLNTLGVTLGR(-) Pep9:(-)VPGLNTLGVTVAR(-) Pep10:(-)LENQKGHSPR(-)	MAAFGINSKIFQSMEMAILFLLAISI DRYCFAADEDMLQDVCVADLHSKVKV NGFPCKTNFTAADFSSLAISKPGATN NKFGSVVTTANVEQVPGLNTLGVSLA RIDYAPGGINPPHTHPRASEMVFVME GELDVGFITTANVLVSKKIIKGEVFV FPRGLVHFQKNNGEVPAAVISAFNSQ LPGTQSIPITLFGASPPVPDDVLAQT FQINTEDVQQIKSKFAPVKKF
N	Q9SM34	Germin-like protein From: *Triticum estivum*	Pep1:(-)DPPNSLGGSQK(-) Pep2:(-)PDPNSLGGSQK(-) Pep3:(-)PDPNSLGSGQK(-) Pep4:(-)ANYDGLYALATDAR(-) Pep5:(-)NAYDGLYALATDAR(-) Pep6:(-)NAYDGLYASVVDAR(-) Pep7:(-)DFLEDKLR(-) Pep8:(-)FDLEDKLR(-) Pep9:(-)LTPALNTLGLTLLR(-) Pep10:(-)TLPALNTLGLTLLR(-) Pep11:(-)TLPALNTLLGTLLR(-) Pep12:(-)ASDPPLSDDYLAK(-) Pep13:(-)SADPPLSDDYLAK(-) Pep14:(-)TGDPPLSDDYLAK(-) Pep15:(-)MVLEELR(-) Pep16:(-)APNLTLRKLQK(-) Pep17:(-)PNALTLRKLQK(-) Pep18:(-)DEASYLNVYSSCNGGR(-) Pep19:(-)FLLDELR(-) Pep20:(-)FVLEELR(-)	MASSSSFLLLAALLALVSWQATAS DPSPLQDFCVADMNSPVRVNGFVC KNPMEVNADDFFKAANLDKPKMPN KVGSNVTLINVMQIAGLNTLGISI ARIDYAPLGQNPPHTHPRATEILT VLEGTLYVGFVTSNQPAPNKNKFL SKVLNKGDVFVFPVGLIHFQFNPN PHQPAVAIAALSSQNPGAITIANA VFGSDPPISDDVLAKAFQVEKNTI DYLQAQFWENNHY

Spot N°	Accession N°	Name of protein	Protein identification data	
			Peptide Sequence	**Protein sequence**
O	Q2QXJ4	Germin-like protein From: *Oryza sativa*	Pep1: (-) PDPNSNSLQK (-) Pep2: (-) PDPNSSAGVQK (-) Pep3: (-) NTPALLGLTNTLLR (-) Pep4: (-) QSPALLGLTNTLLR (-) Pep5: (-) TNPALLGLTNTLLR (-) Pep6: (-) LPANYDGLHPPGVMAR (-) Pep7: (-) KSWDNTSIAAAAGSVMK (-) Pep8: (-) LPANYDGLYASVVDAR (-) Pep9: (-) LTPALNGLTLTLLR (-) Pep10: (-) TLPALNTLGLTLLR (-) Pep11: (-) FGLVVPNSSNLQK (-) Pep12: (-) GFVLVPNSSNLQK (-) Pep13: (-) YDGLYAATEVAR (-) Pep14: (-) LLNAGDVFVFPQGH (-) Pep15: (-) LLNQDVFVFPQGH (-) Pep16: (-) AFHISPR (-) Pep17: (-) MVLEDKLR (-) Pep18: (-) LYSAVPSSLLFASDPPLSDDYLAK (-) Pep19: (-) LYSAVPSTLVFASDPPLSDDYLAK (-) Pep20: (-) YDGLYAPGFVAR (-)	MASSNFFLPTALIALVATQAMAFDPS PLQDFCVADRNSPVRVNGFPCKDAKD VNVDDFFLEANLDKPMDTTKSKAGSN VTLINVMKLTGLNTLGISMARIDYAP KGQNPPHTHPRATEILTVFEGTLYVG FVTSNQANGENKLFTKTLNKGDVFVF PQGLIHFQFNPSYDKPAVAIAALSSQ NPGAITIANAVFGSNPPISDDVLAKA FQVDKKAVDWLQAQFWENNHN
P	ACG41245.1	Germin-like protein From: *Zea mays*	Pep1: (-) MVLEDKLR (-) Pep2: (-) NAYDGLYALATDAR (-) Pep3: (-) NAYDGLYASVVDAR (-) Pep4: (-) NPAADAAPAGGGGALPGLGPWPPQFSPLASSAGYAPSTDAR (-) Pep5: (-) NPTPSNPAGGGGALPGLGPWPPQFSPLASSAGYAPSTDAR (-) Pep6: (-) PALNTLLKAVEL (-) Pep7: (-) PALNTLLKNNAL (-) Pep8: (-) PYLEDKLR (-) Pep9: (-) PYLEKDLR (-) Pep10: (-) SLFASDPPLDSDLYAK (-) Pep11: (-) SLFASDPPLSDDLYAK (-) Pep12: (-) SLFASDPPLSVDEYAK (-) Pep13: (-) TLGPVNQSFPALNTLGLTLLR (-) Pep14: (-) TLNPRQAYPALNTLGLTLLR (-) Pep15: (-) TLPALNGLTLTLLR (-) Pep16: (-) TLPALNTLGLTLLR (-)	MASSLVLVAAALLALASSWQQA IAYDPSPLQDFCVADKNSPVRV NGFPCKDPMAVTPDDFFNAAMI IDKRRDTNNKVGSNVTNVNVES FPGLNTLGISLARIDYAPLGVN PPHIHPRATELLTVLEGTLYLG FVTSNPNRLFSKVVKKGDVFVF PKAMIHFQMNLDHDKPAAALSS LSSQNPGVITIASAVFGSKPPI SDDVLAKAFQVEKKLIDWLQSQ FWDTNY

Spot N°	Accession N°	Name of protein	Protein identification data	
			Peptide Sequence	**Protein sequence**
Q	Q9SM34	Germin-like protein From: *Triticum estivum*	Pep1: (-) EATVLSPR (-) Pep2: (-) NAGPCPANAAAASSALNPNAGFK (-) Pep3: (-) DDNHEILR (-) Pep4: (-) PALNTLLTLTPK (-) Pep5: (-) NAYDGLYASVVDNL (-) Pep6: (-) NAGPGSGPSAAAASSALNPNAGFK (-) Pep7: (-) PALNTLLTLGLR (-) Pep8: (-) ANYDGLYASVVDAR (-) Pep9: (-) MVLEDKLR (-) Pep10: (-) MVLEELR (-) Pep11: (-) MVLENGVK (-) Pep12: (-) LTPALNTLGLTLLR (-) Pep13: (-) ASDPPLSDDYLAK (-) Pep14: (-) TGDPPLSDDYLAK (-) Pep15: (-) TYLEDKLR (-) Pep16: (-) TYKNDKLR (-)	MASSSSFLLLAALLALVSWQATASDP SPLQDFCVADMNSPVRVNGFVCKNPM EVNADDFFKAANLDKPKMPNKVGSNV TLINVMQIAGLNTLGISIARIDYAPL GQNPPHTHPRATEILTVLEGTLYVGF VTSNQPAPNKNKFLSKVLNKGDVFVF PVGLIHFQFNPNPHQPAVAIAALSSQ NPGAITIANAVFGSDPPISDDVLAKA FQVEKNTIDYLQAQFWENNHY
S	Q9GEP9	Ribulose bisphosphate carboxylase From: *Primula palinuri*	Pep1: (-) DPPNSLGGNTK (-) Pep2: (-) PDPNSLGGNTK (-) Pep3: (-) PDPNSLGGSQK (-) Pep4: (-) NADPATPNGVASSALNPNQFK (-) Pep5: (-) NADPSVNPAAASSALNPNGAFK (-) Pep6: (-) RDGDLAAGNGK (-) Pep7: (-) ANYDGLYKEVDAR (-) Pep8: (-) NAYDGLYKDLDAR (-) Pep9: (-) LTPALNTLGLTLLR (-) Pep10: (-) TLPALNGLTLTLLR (-) Pep11: (-) GIYFTQDWVSL (-) Pep12: (-) MVLEDLR (-) Pep13: (-) NAYDGLYAPQVFR (-) Pep14: (-) EFRQQVQEDVK (-)	KAGVGFKAGVKGYKVTYYTPEYDPKD TDILAAFRVTPQPGVPPEEAGAAVAA ESSTGTWTTVWTDGLTNLDRYKGRCY HIEPVAGEENQFIAYVAYPLDLFEEG AVTNMFTSIVGNVFGFKALRALRLED LRIPPAYVKTFQGPPHGIQVERDKLN KYGRPLLGCTIKPKLGLSAINPGRAV YECLRGGLDFTKDDENVNSQPFMRWX DRFLFCAEALYKAQAETGEIKGHYLN LTAGTCEEMIKRAVFARELGVPIVMH DYLTGGFTANTSLSHYCRDNGLLLHI HRAMHAVIDRQKNHGIHFRVLAKXLR MSGGDHIHSGTVVGKLEGERXITLGL VDLLRDDYIEKDRSRGIYFTQDWVSL PGVLPVASGGIHVWHMPALTEIFGDD SVLQFGGGTLGHPWENAPGAVANRVA LEACVQARNEGRDLAAEGNEIIREAC KWSPELAAACEVWKEIKFEFEAMDTL

Spot N°	Accession N°	Name of protein	Protein identification data	
			Peptide Sequence	**Protein sequence**
T	A8QK89	Germin-like protein From: *Vitis vinifera*	Pep1: (-) GGVGKSTTAVNIAVALAK (-) Pep2: (-) ANYDGLYASNQAAR (-) Pep3: (-) GDFLSNYASNQAAR (-) Pep4: (-) LTPALNTLGLTLLR (-) Pep5: (-) TLPALNGLTLTLLR (-) Pep6: (-) TLPALNTLGLTLLR (-) Pep7: (-) FDLEDKLR (-) Pep8: (-) MVLEDLR (-) Pep9: (-) MVLEDKLR (-) Pep10: (-) ASDPPLSDDYLAK (-) Pep11: (-) TGDPPLSDDYLAK (-) Pep12: (-) VYLEDKLR (-) Pep13: (-) FVLEDLR (-) Pep14: (-) TYKNDKLR (-)	MALASSFASASDPSPLQDTCVAIDEP KNAVFVNGKFCKNPNLTVAEDFFSKG LNIPGNTSNLVGSSVTTVNVDVIPGL NTLGISLVRIDYAPYGQNPPHTHPRA TEILTVLEGTLLVGFVTSNPQNRLFS KVLNKGDVFVFPIGLIHFQFNIGHMN AVAIAGLSSQNPGVITIANAVFGSNP PINPDFLAKAFQLDKKVGEFLQARF
U	O24500	Glycolate oxidase From: *Arabidopsis thaliana*	Pep1: (-) VDLDPGFLNA (-) Pep2: (-) VPVFLDGGVRR (-) Pep3: (-) LTPALNTLGLTLLR (-) Pep4: (-) TLPALNGLTLTLLR (-) Pep5: (-) ELVKQQK (-) Pep6: (-) GVPVSLPR (-) Pep7: (-) VPGVSLPR (-) Pep8: (-) MVLEDLR (-) Pep9: (-) VMLEDLR (-) Pep10: (-) MVLEDKLR (-)	ATSSVEKIASTGPGIRFFQLYVYKNR KVVEQLVRKAEKAGFKAIALTVNTPR LGPKKSDIKNRFTLPPNLTLKNFEGL DLGKMDEANDSGLASYVAGQIDRTLS WKDIQWLQTITNMPILVKGVLTGEDA RIAIQAGAAGIIVSNHGARQLDYVPA TISALEEVVKATQGGVPVFLDGGVRR GTDVFKALALGTSGIFIGRPVVFALA AEGEAGVKKVLQMLRDEFELTMALSG CRSISEITRNHIVTEWDIPRHLPRL

Supplemental Table III. Alignment details of sequenced peptides (Query) with the identified proteins (Sbjct)

Only peptides with an alignment match above 50 % are presented in this table.

Spot N°		Peptide alignment details
1	Pep6	

```
Score = 180 (91.1 bits)
Identities = 25/25 (100%), Positives = 25/25 (100%)
Query:     1 ASCGGTACVNSFGDEQLAVDMLADK 25
             ASCGGTACVNSFGDEQLAVDMLADK
Sbjct:   112 ASCGGTACVNSFGDEQLAVDMLADK 136
```

Spot N°		Peptide alignment details
2	Pep8	

```
Score = 142 (72.7 bits)
Identities = 17/17 (100%), Positives = 17/17 (100%)
Query:     1 GHYMNITAATMEEMYER 17
             GHYMNITAATMEEMYER
Sbjct:   172 GHYMNITAATMEEMYER 188
```

Spot N°		Peptide alignment details
3	Pep1	

```
Score = 63 (33.3 bits)
Identities = 10/12 (83%), Positives = 11/12 (91%)
Query:     2 AEVVSNLGLLQK 13
             AEVVSNL +LQK
Sbjct:    72 AEVVSNLRILQK 83
```

Spot N°		Peptide alignment details
5	Pep1	

```
Score = 49 (26.1 bits)
Identities = 8/10 (80%), Positives = 9/10 (90%)
Query:     4 VVSNLGLLQK 13
             VVSNL +LQK
Sbjct:    74 VVSNLRILQK 83
```

Spot N°		Peptide alignment details
	Pep5	

```
Score = 58 (30.5 bits)
Identities = 6/10 (60%), Positives = 9/10 (90%)
Query:     2 LGTLDPNQLK 12
             +G +DPNQ+K
Sbjct:   188 IGIIDPNQIK 197
```

Spot N° **Peptide alignment details**

32

Pep1

```
Score = 42 (22.9 bits)
Identities = 7/9 (77%), Positives = 8/9 (88%)
Query:     4 VSNLGLLQK 13
             VSNL +LQK
Sbjct:    75 VSNLRILQK 83
```

Pep3

```
Score = 58 (30.9 bits)
Identities = 6/10 (60%), Positives = 9/10 (90%)
Query:     2 LGTLDPNQLK 12
             +G +DPNQ+K
Sbjct:   188 IGIIDPNQIK 197
```

Pep7

```
Score = 66 (35.0 bits)
Identities = 8/9 (88%), Positives = 9/9 (100%)
Query:    12 LNETQYQLK 21
             +NETQYQLK
Sbjct:   111 INETQYQLK 119
```

35

Pep1

```
Score = 36 (19.6 bits)
Identities = 8/12 (66%), Positives = 8/12 (66%)
Query:     1 AEVVSLVANLQK 12
             AEVVS    LQK
Sbjct:    72 AEVVSNLRILQK 83
```

Pep9

```
Score = 66 (34.4 bits)
Identities = 8/9 (88%), Positives = 9/9 (100%)
Query:    12 LNETQYQLK 21
             +NETQYQLK
Sbjct:   111 INETQYQLK 119
```

37

Pep1

```
Score = 168 (84.9 bits)
Identities = 21/21 (100%), Positives = 21/21 (100%)
Query:     1 MQWYAFHEEPAGGADAPNGMK 21
             MQWYAFHEEPAGGADAPNGMK
Sbjct:   303 MQWYAFHEEPAGGADAPNGMK 323
```

Spot N° | **Peptide alignment details**

38

Pep4

```
Score = 56 (29.7 bits)
Identities = 7/11 (63%), Positives = 10/11 (90%)
Query:    1  LESPLDLLDLR 11
             L+SP+D+ DLR
Sbjct:    61 LQSPIDIFDLR 71
```

Pep8

```
Score = 49 (26.2 bits)
Identities = 8/10 (80%), Positives = 9/10 (90%)
Query:     3 VVSNLGLLQK 13
             VVSNL +LQK
Sbjct:    74 VVSNLRILQK 83
```

Pep9

```
Score = 58 (30.7 bits)
Identities = 6/10 (60%), Positives = 9/10 (90%)
Query:     2 LGTLDPNQLK 12
             +G +DPNQ+K
Sbjct:   188 IGIIDPNQIK 197
```

Pep12

```
Score = 39 (21.2 bits)
Identities = 6/6 (100%), Positives = 6/6 (100%)
Query:    28 ATLLNR 34
             ATLLNR
Sbjct:    90 ATLLNR 95
```

39

Pep5

```
Score = 131 (67.1 bits)
Identities = 19/19 (100%), Positives = 19/19 (100%)
Query:     1 AVAGDEAEPGTSKAAPPSR 19
             AVAGDEAEPGTSKAAPPSR
Sbjct:    11 AVAGDEAEPGTSKAAPPSR 29
```

Spot N°	Peptide alignment details	
40	Pep1	Score = 47 (25.2 bits) Identities = 6/11 (54%), Positives = 10/11 (90%) Query: 1 LESPLDVLELR 11 L+SP+D+ +LR Sbjct: 61 LQSPIDIFDLR 71
	Pep8	Score = 47 (25.2 bits) Identities = 6/11 (54%), Positives = 10/11 (90%) Query: 2 LESPLDVLELR 13 L+SP+D+ +LR Sbjct: 61 LQSPIDIFDLR 71
44	Pep1	Score = 35 (19.3 bits) Identities = 4/7 (57%), Positives = 7/7 (100%) Query: 1 LESPLDV 8 L+SP+D+ Sbjct: 61 LQSPIDI 67
	Pep3	Score = 38 (20.8 bits) Identities = 8/12 (66%), Positives = 9/12 (75%) Query: 1 AEVVSLNGLLQK 12 AEVVS +LQK Sbjct: 72 AEVVSNLRILQK 83
	Pep6	Score = 58 (30.8 bits) Identities = 6/10 (60%), Positives = 9/10 (90%) Query: 2 LGTLDPNQLK 11 +G +DPNQ+K Sbjct: 188 IGIIDPNQIK 197
	Pep8	Score = 61 (32.3 bits) Identities = 9/9 (100%), Positives = 9/9 (100%) Query: 15 PSNATLLNR 24 PSNATLLNR Sbjct: 87 PSNATLLNR 95

Spot N°		Peptide alignment details
54	Pep1	Score = 30 (16.6 bits) Identities = 3/4 (75%), Positives = 4/4 (100%) Query: 2 MQLA 6 MQ+A Sbjct: 84 MQIA 87
	Pep2	Score = 43 (23.0 bits) Identities = 6/10 (60%), Positives = 8/10 (80%) Query: 5 LNTLGLTLLR 15 LNTLG+ + R Sbjct: 89 LNTLGISIAR 98
	Pep3	Score = 68 (35.3 bits) Identities = 10/12 (83%), Positives = 11/12 (91%) Query: 2 SDPPLSDDYLAK 14 SDPP+SDD LAK Sbjct: 196 SDPPISDDVLAK 207
55	Pep5	Score = 37 (20.0 bits) Identities = 6/7 (85%), Positives = 6/7 (85%) Query: 1 PALNTLG 7 P LNTLG Sbjct: 88 PGLNTLG 94
	Pep10	Score = 54 (28.4 bits) Identities = 7/7 (100%), Positives = 7/7 (100%) Query: 6 VFVFPQG 13 VFVFPQG Sbjct: 149 VFVFPQG 155
	Pep14	Score = 54 (28.4 bits) Identities = 7/7 (100%), Positives = 7/7 (100%) Query: 2 VFVFPQG 9 VFVFPQG Sbjct: 149 VFVFPQG 155

Spot N° | **Peptide alignment details**

57

Pep1

```
Score = 55 (29.6 bits)
Identities = 8/12 (66%), Positives = 9/12 (75%)
Query:     3 PALNTLGLTLLR 14
             P LNTLG+ L R
Sbjct:    62 PGLNTLGISLVR 73
```

Pep3

```
Score = 33 (18.4 bits)
Identities = 5/6 (83%), Positives = 6/6 (100%)
Query:     3 KLATAN 9
             KLATA+
Sbjct:    27 KLATAD 32
```

Pep4

```
Score = 57 (30.6 bits)
 Identities = 8/10 (80%), Positives = 8/10 (80%)
Query:     2 LNAGDVFVFP 12
             L  GDVFVFP
Sbjct:   120 LKTGDVFVFP 129
```

83

Pep6

```
Score = 44 (23.3 bits)
Identities = 8/12 (66%), Positives = 8/12 (66%)
Query:     3 PALNTLGLTLLR 15
             P LNTLG  L R
Sbjct:    94 PGLNTLGVSLAR 105
```

Pep8

```
Score = 75 (38.4 bits)
Identities = 10/10 (100%), Positives = 10/10 (100%)
Query:     1 KGEVFVFPRG 11
             KGEVFVFPRG
Sbjct:   151 KGEVFVFPRG 160
```

84

Pep6

```
Score = 68 (35.0 bits)
Identities = 10/12 (83%), Positives = 11/12 (91%)
Query:     2 SDPPLSDDYLAK 14
             SDPP+SDD LAK
Sbjct:   196 SDPPISDDVLAK 207
```

Spot N° | **Peptide alignment details**

86

Pep7

```
Score = 60 (31.5 bits)
Identities = 9/10 (90%), Positives = 9/10 (90%)
Query:     2 LNAGDVFVFP 12
             LN GDVFVFP
Sbjct:   146 LNKGDVFVFP 155
```

Pep12

```
Score = 63 (33.0 bits)
Identities = 9/12 (75%), Positives = 11/12 (91%)
Query:     2 SDPPLSDDYLAK 14
             S+PP+SDD LAK
Sbjct:   194 SNPPISDDILAK 205
```

89

Pep2

```
Score = 45 (23.9 bits)
Identities = 6/6 (100%), Positives = 6/6 (100%)
Query:     7 FSGLNM 13
             FSGLNM
Sbjct:    11 FSGLNM 16
```

Pep5

```
Score = 50 (26.3 bits)
Identities = 7/12 (58%), Positives = 8/12 (66%)
Query:     2 PALNTLGLTLLR 14
             P LNT G+ L R
Sbjct:    37 PGLNTMGISLVR 48
```

A

Pep7

```
Score = 150 (76.7 bits)
Identities = 20/22 (90%), Positives = 20/22 (90%)
Query:    82 VGEGTATQCISGFTAMDIPPPR 103
             VGEG A QCISGFTAMDIPPPR
Sbjct:   456 VGEGAAAQCISGFTAMDIPPPR 477
```

B

Pep8

```
Score = 197 (101.2 bits)
Identities = 27/27 (100%), Positives = 27/27 (100%)
Query:    1  NAAGFMNASSDGSNQQQLDLDRDAMSR 27
             NAAGFMNASSDGSNQQQLDLDRDAMSR
Sbjct:    98 NAAGFMNASSDGSNQQQLDLDRDAMSR 124
```

Spot N° — **Peptide alignment details**

C — Pep4

```
Score = 47 (25.2 bits)
Identities = 6/11 (54%), Positives = 10/11 (90%)
Query:     1 LESPLDVLELR 11
             L+SP+D+ +LR
Sbjct:    61 LQSPIDIFDLR 71
```

C — Pep7

```
Score = 49 (26.2 bits)
Identities = 8/10 (80%), Positives = 9/10 (90%)
Query:     3 VVSNLGLLQK 13
             VVSNL +LQK
Sbjct:    74 VVSNLRILQK 83
```

C — Pep13

```
Score = 34 (18.7 bits)
Identities = 5/9 (55%), Positives = 7/9 (77%)
Query:     1 NALMLEGKK 9
             N + L+GKK
Sbjct:   194 NQIKLDGKK 202
```

D — Pep1

```
Score = 82 (42.9 bits)
Identities = 11/11 (100%), Positives = 11/11 (100%)
Query:     1 LEKEATYDDIK 11
             LEKEATYDDIK
Sbjct:    77 LEKEATYDDIK 87
```

Spot N°		Peptide alignment details
E	Pep3	Score = 47 (25.1 bits) Identities = 6/11 (54%), Positives = 10/11 (90%) Query: 1 LESPLDVLELR 13 L+SP+D+ +LR Sbjct: 61 LQSPIDIFDLR 71
	Pep4	Score = 36 (19.7 bits) Identities = 8/12 (66%), Positives = 8/12 (66%) Query: 1 AEVVSLVANLQK 12 AEVVS LQK Sbjct: 72 AEVVSNLRILQK 83
	Pep6	Score = 58 (30.6 bits) Identities = 6/10 (60%), Positives = 9/10 (90%) Query: 2 LGTLDPNQLK 12 +G +DPNQ+K Sbjct: 188 IGIIDPNQIK 197
F	Pep3	Score = 35 (19.2 bits) Identities = 4/7 (57%), Positives = 7/7 (100%) Query: 1 LESPLDV 7 L+SP+D+ Sbjct: 61 LQSPIDI 67
	Pep4	Score = 38 (20.7 bits) Identities = 8/12 (66%), Positives = 9/12 (75%) Query: 1 AEVVSLNGLLQK 12 AEVVS +LQK Sbjct: 72 AEVVSNLRILQK 83
	Pep7	Score = 58 (30.7 bits) Identities = 6/10 (60%), Positives = 9/10 (90%) Query: 2 LGTLDPNQLK 12 +G +DPNQ+K Sbjct: 188 IGIIDPNQIK 197

Spot N°		Peptide alignment details

G

Pep3

```
Score = 63 (33.4 bits)
Identities = 10/12 (83%), Positives = 11/12 (91%)
Query:     1 AEVVSNLGLLQK 12
             AEVVSNL +LQK
Sbjct:    72 AEVVSNLRILQK 83
```

Pep5

```
Score = 58 (30.9 bits)
Identities = 6/10 (60%), Positives = 9/10 (90%)
Query:     2 LGTLDPNQLK 12
             +G +DPNQ+K
Sbjct:   188 IGIIDPNQIK 19
```

H

Pep4

```
Score = 56 (29.8 bits)
Identities = 7/11 (63%), Positives = 10/11 (90%)
Query:     1 LESPLDLLDLR 11
             L+SP+D+ DLR
Sbjct:    61 LQSPIDIFDLR 71
```

Pep9

```
Score = 38 (20.8 bits)
Identities = 8/12 (66%), Positives = 9/12 (75%)
Query:     1 AEVVSLNGLLQK 12
             AEVVS   +LQK
Sbjct:    72 AEVVSNLRILQK 83
```

Pep11

```
Score = 58 (30.8 bits)
Identities = 6/10 (60%), Positives = 9/10 (90%)
Query:     2 LGTLDPNQLK 10
             +G +DPNQ+K
Sbjct:   188 IGIIDPNQIK 197
```

Spot N° — **Peptide alignment details**

I

Pep1

```
Score = 49 (26.1 bits)
Identities = 8/10 (80%), Positives = 9/10 (90%)
Query:     3 VVSNLGLLQK 10
             VVSNL +LQK
Sbjct:    74 VVSNLRILQK 83
```

Pep3

```
Score = 52 (27.6 bits)
Identities = 8/12 (66%), Positives = 9/12 (75%)
Query:    11 GYHTLNETQYAL 23
             GY  +NETQY L
Sbjct:   107 GYLKINETQYQL 118
```

J

Pep8

```
Score = 75 (39.6 bits)
Identities = 10/10 (100%), Positives = 10/10 (100%)
Query:     1 KGEVFVFPRG 11
             KGEVFVFPRG
Sbjct:   151 KGEVFVFPRG 160
```

Pep15

```
Score = 67 (35.5 bits)
Identities = 9/9 (100%), Positives = 9/9 (100%)
Query:     1 RGLVHFQKN 10
             RGLVHFQKN
Sbjct:   159 RGLVHFQKN 167
```

Spot N°		Peptide alignment details
K		

Pep6

```
Score = 85 (42.6 bits)
Identities = 11/12 (91%), Positives = 12/12 (100%)
Query:     1 RIPSTEEIADRI 12
             RIPSTEEIADR+
Sbjct:   704 RIPSTEEIADRV 715
```

Pep7

```
Score = 74 (37.4 bits)
Identities = 11/11 (100%), Positives = 11/11 (100%)
Query:     1 KVVEVNALAKA 11
             KVVEVNALAKA
Sbjct:   357 KVVEVNALAKA 367
```

Pep8

```
Score = 87 (43.6 bits)
Identities = 12/12 (100%), Positives = 12/12 (100%)
Query:     1 KYLFAGVVDGRN 12
             KYLFAGVVDGRN
Sbjct:   286 KYLFAGVVDGRN 297
```

Pep9

```
Score = 83 (41.7 bits)
Identities = 12/13 (92%), Positives = 12/13 (92%)
Query:     1 KGVTGFGFDLVRG 13
             KGVT FGFDLVRG
Sbjct:   259 KGVTAFGFDLVRG 271
```

Pep11

```
Score = 112 (55.6 bits)
Identities = 14/14 (100%), Positives = 14/14 (100%)
Query:     1 RGNASVPAMEMTKW 14
             RGNASVPAMEMTKW
Sbjct:    99 RGNASVPAMEMTKW 112
```

Pep14

```
Score = 75 (37.8 bits)
Identities = 10/10 (100%), Positives = 10/10 (100%)
Query:     1 KISEEEYVKA 10
             KISEEEYVKA
Sbjct:   457 KISEEEYVKA 466
```

Pep15

```
Score = 135 (66.7 bits)
Identities = 18/18 (100%), Positives = 18/18 (100%)
Query:     1 KYGAGIGPGVYDIHSPRI 18
             KYGAGIGPGVYDIHSPRI
Sbjct:   688 KYGAGIGPGVYDIHSPRI 705
```

Spot N°		Peptide alignment details

L

Pep7

```
Score = 49 (26.5 bits)
Identities = 6/7 (85%), Positives = 7/7 (100%)
Query:    1  VDGFPCK 7
             V+GFPCK
Sbjct:    52 VNGFPCK 58
```

Pep8

```
Score = 75 (39.6 bits)
Identities = 10/10 (100%), Positives = 10/10 (100%)
Query:    1  KGEVFVFPRG 10
             KGEVFVFPRG
Sbjct:   151 KGEVFVFPRG 160
```

Pep15

```
Score = 67 (35.5 bits)
Identities = 9/9 (100%), Positives = 9/9 (100%)
Query:     1 RGLVHFQKN 9
             RGLVHFQKN
Sbjct:   159 RGLVHFQKN 167
```

Pep16

```
Score = 46 (25.0 bits)
Identities = 7/7 (100%), Positives = 7/7 (100%)
Query:     1 VPGLNTL 7
             VPGLNTL
Sbjct:    93 VPGLNTL 99
```

M

Pep6

```
Score = 62 (33.3 bits)
Identities = 8/8 (100%), Positives = 8/8 (100%)
Query:     1 GEVFVFPR 8
             GEVFVFPR
Sbjct:   152 GEVFVFPR 159
```

Pep9

```
Score = 73 (38.9 bits)
Identities = 11/13 (84%), Positives = 11/13 (84%)
Query:     1 VPGLNTLGVTVAR 13
             VPGLNTLGV  AR
Sbjct:    93 VPGLNTLGVSLAR 105
```

Spot N° | **Peptide alignment details**

N

Pep9

```
Score = 43 (23.1 bits)
Identities = 6/10 (60%), Positives = 8/10 (80%)
Query:     5 LNTLGLTLLR 15
             LNTLG+ + R
Sbjct:    89 LNTLGISIAR 98
```

Pep12

```
Score = 68 (35.4 bits)
Identities = 10/12 (83%), Positives = 11/12 (91%)
Query:     1 SDPPLSDDYLAK 12
             SDPP+SDD LAK
Sbjct:   196 SDPPISDDVLAK 207
```

O

Pep14

```
Score = 74 (38.7 bits)
Identities = 11/12 (91%), Positives = 11/12 (91%)
Query:     2 LNAGDVFVFPQG 12
             LN GDVFVFPQG
Sbjct:   148 LNKGDVFVFPQG 159
```

Pep19

```
Score = 76 (39.7 bits)
Identities = 11/15 (73%), Positives = 13/15 (86%)
Query:    10 VFASDPPLSDDYLAK 25
             VF S+PP+SDD LAK
Sbjct:   193 VFGSNPPISDDVLAK 207
```

P

Pep13

```
Score = 65 (34.0 bits)
Identities = 10/15 (66%), Positives = 12/15 (80%)
Query:     6 QSFPALNTLGLTLLR 21
             +SFP LNTLG+ L R
Sbjct:    87 ESFPGLNTLGISLAR 101
```

Spot N°	Peptide alignment details	
Q	Pep12	Score = 43 (22.9 bits) Identities = 6/10 (60%), Positives = 8/10 (80%) Query: 5 LNTLGLTLLR 15 LNTLG+ + R Sbjct: 89 LNTLGISIAR 98
	Pep13	Score = 68 (35.2 bits) Identities = 10/12 (83%), Positives = 11/12 (91%) Query: 2 SDPPLSDDYLAK 14 SDPP+SDD LAK Sbjct: 196 SDPPISDDVLAK 207
S	Pep4	Score = 33 (18.1 bits) Identities = 4/5 (80%), Positives = 5/5 (100%) Query: 12 SALNP 17 SA+NP Sbjct: 174 SAINP 178
	Pep11	Score = 87 (44.9 bits) Identities = 11/11 (100%), Positives = 11/11 (100%) Query: 1 GIYFTQDWVSL 11 GIYFTQDWVSL Sbjct: 354 GIYFTQDWVSL 364
T	Pep1	Score = 39 (21.0 bits) Identities = 7/12 (58%), Positives = 8/12 (66%) Query: 3 VGKSTTAVNIAV 15 VG S T VN+ V Sbjct: 63 VGSSVTTVNVDV 74
	Pep4	Score = 55 (28.8 bits) Identities = 8/12 (66%), Positives = 9/12 (75%) Query: 3 PALNTLGLTLLR 15 P LNTLG+ L R Sbjct: 76 PGLNTLGISLVR 87
	Pep3	Score = 49 (25.9 bits) Identities = 7/12 (58%), Positives = 10/12 (83%) Query: 2 SDPPLSDDYLAK 14 S+PP+ D+LAK Sbjct: 180 SNPPINPDFLAK 191

Spot N°	Peptide alignment details
U	Pep4

```
Score = 79 (40.7 bits)
Identities = 11/11 (100%), Positives = 11/11 (100%)
Query:     1 VPVFLDGGVRR 11
             VPVFLDGGVRR
Sbjct:   172 VPVFLDGGVRR 18
```