

Peptides sequences of identified proteins by MALDI-TOF/TOF

Spot	Protein name	Species (number accession) <sup>a</sup>	Sequence of peptides matched (ion score) <sup>b</sup>
2105	Oxygen-evolving enhancer protein 2, chloroplast precursor (OEE2)	<i>Pisum sativum</i> (gil131390)	AKTNTDYLPLYNGDGFK TNTDYLPLYNGDGFK LLVPAKWNPFSK WNPSKER EREFPGQVLR <b>EFPGQVLR (45)</b> YEDNFDATSNVSVLVQTTDDK SITDYGSPPEEFLSK VDYLLGK QYYNISVLTR TADGDEGGKHQLITATVK KFVEDTASSFSVA
3301	Oxygen-evolving enhancer protein 1, chloroplast precursor (OEE1)	<i>Pisum sativum</i> (gil131384)	GSSFDPK VPFLFTIK LTFDEIQSK <b>NTPLAFQNTK (55)</b> <b>RLTFDEIQSK (38)</b> LCLEPTSFTVK KLCLEPTSFTVK <b>GASTGYDNAVALPAGGR (49)</b> QLVASGKPDSPSSEFLVPSYR GASTGYDNAVALPAGGRGDEEELGK GTGTANQCPTIDGGVDSFSFKPGK
3305	Oxygen-evolving enhancer protein 1, chloroplast precursor (OEE1)	<i>Pisum sativum</i> (gil131384)	GSSFDPK <b>VPFLFTIK (46)</b> GSSFDPKGR LTFDEIQSK NTPLAFQNTK <b>RLTFDEIQSK (20)</b> LCLEPTSFTVK KLCLEPTSFTVK GASTGYDNAVALPAGGR DGIDYAAVTVQLPGER QLVASGKPDSPSSEFLVPSYR FEEKDGIDYAAVTVQLPGER GTGTANQCPTIDGGVDSFSFKPGK GTGTANQCPTIDGGVDSFSFKPGKYNK
5202	Light harvesting protein	<i>Pisum sativum</i> (gil309673)	<b>QYFLGLEK (37)</b> WLAYGEVINGR FQDWAKPGSMGK QGGVDRPLWFASK FAMLGAVGAIAPPEYLK
7501	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit	<i>Polypodium furfuraceum</i> (gil42541540)	EGNDIIR NHGMHFR AMHAVIDR SQAETGEIK DTDILAAFR DNGLLLHIHR

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			EVTLGFVDLLR
			DRFLFVAEALFK
			MSGGDHIHAGTVVGK
			DDENVNSQPFMR
			IPPAYSKTFMGPPHGIQVER
			DTDILAAFRMTPQPGVPAEEAR
5413	Fructose-bisphosphate aldolase 2, chloroplast	<i>Pisum sativum</i> (gil461501)	TFEVAQK
			ALQNTALK
			SNSLAQLGK
			GSYADELVK
			<b>AAQEALLFR (33)</b>
			<b>SAAYYQQGAR (32)</b>
			YIGDGESEEAkk
			<b>VAEYTLNLLHR (58)</b>
			LDSIGLENTEANR
			TVVSIPNGPSALAVK
			VAEYTLNLLHRR
			SPNPWHVSFSYAR
			RLDSIGLENTEANR
7508	Fructose-bisphosphate aldolase, cytoplasmic isozyme 2	<i>Pisum sativum</i> (gil1168410)	CAAITER
			<b>YYEAGAR (10)</b>
			ALQQSTLK
			AAQDALLTR
			VAPEVIAEHTVR
			AKANSEATLGTYK
			GILAADESTGTIGKR
			GASNLGAGASESLHVK
			YHDELIANAAYIGTPGK
			SKYHDELIANAAYIGTPGK
			TAAGKPFVDVLNEAGVLPGIK
			<b>IGANEPSEHSIHENAYGLAR (90)</b>
			GTVELAGTDGETTTQGLDGLGAR
			VDKGTVELAGTDGETTTQGLDGLGAR
			ALSDHHVILEGTLKPNMVTGSDAPK
6408	Malate dehydrogenase	<i>Glycine max</i> (gil3193222)	TLCTAIAK
			AKTFYAGK
			AGTYDEKR
			LFGVTTLDVVR
			<b>DDLFNINAGIVK (71)</b>
			RLFGVTTLDVVR
			AIFDDDVIETLTK
			<b>ALEGADVVIIPAGVPR (39)</b>
7311	Malate dehydrogenase	<i>Pisum sativum</i> (gil37725953)	TLCEGVAK
			AGTYDPKR
			TELAGSIQK
			AKTELAGSIQK
			FANSCLHGLK
			<b>LLGVTTLDVVR (11)</b>
			IQNGGTEVVEAK
			KPGMTRDDLK
			RLLGVTTLDVVR
			DDLKINAGIVR

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			AGAGSATLSMAYAAK
			<b>ANTFVAEVLGVDPR (47)</b>
			VAILGAAGGIGQPLSLLLK
			<b>GGAEIYQLGPLNEYER (53)</b>
5504	Glutamate-ammonia ligase (EC 6.3.1.2) 3A, cytosolic	<i>Pisum sativum</i> (gil2129882)	DIVDAHYK
			<b>QGPYYCGIGADK (33)</b>
			EHIAAYGEGNER
			TLPGPVSDPAKLPK
			<b>HKEHIAAYGEGNER (31)</b>
			QGPYYCGIGADKAYGR
5408	Pyridoxal-5-phosphate- dependent enzyme, beta subunit	<i>Medicago truncatula</i> (gil92876186)	YLSTVLFQK
			IQGIGAGFVPR
			FAISPRSISTR
			AFGAELVLTAAK
			LIGVVFPSFGER
			IGYSMILDAEKK
			LILTMPASMSLER
			<b>IREECENMQPEP (16)</b>
			IHFETTGPFIWEDTR
2307	DNA-binding protein	<i>Arabidopsis thaliana</i> (gil601843)	AENRAQK
			AAVEAQLR
			AEEQKTSK
			KAAVEAQLR
			AAVEAQLRK
			IHNPPPVESK
			VAAIHKLAEEK
			DVILADLEKEK
			VDVESPVLAPAK
			GEELLEAEEMGAKYR
3103	Glycine-rich RNA binding protein	<i>Medicago sativa</i> (gil6273331)	IINDRETGR
			<b>AFSQYGEIVDSK (58)</b>
6505	Far-red impaired response protein	<i>Oryza sativa</i> (gil42407459)	EKGFSVR
			MYNLRK
			SDIASVQK
			RISYAQK
			SCAIYLR
			YMQARQK
			DMYNFFVR
			DAMSKDVIQR
			SESLNSKLHR
			VAEDNQWLGR
			SNQRSESLNSK
			RLFWADPQSR
			SEEDGFIFYNR
			HTSVFIWICSIHK
			FKSEEDGFIFYNR
			MHTSVFIWICSIHKFK
4508	Elongation factor Tu, chloroplast precursor (EF- Tu)	<i>Pisum sativum</i> (gil6015084)	YIPIPQR
			FSAIVYVLK
			GTVATGRIER
			<b>VGDVVDLVGLR (47)</b>

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			YDEIDAAPEER
			NTTGTGVEMFQK
			<b>KYDEIDAAPEER (91)</b>
			VTSIMNDKDEESK
			ILDDAMAGDNVGLLLR
			HYAHVDCPGHADYVK
			GITINTATVEYETETR
			KKPHLNIGTIGHVDHGK
			HSPFFAGYRPFQYMR
6305	Retrotransposon protein, putative, unclassified	<i>Oryza sativa</i> (gil110288963)	TKIFSULK
			HRTWTTMR
			KIWEGGSSDK
			SMLEQQTSGK
			YWWSNQEK
			IDIRKPLMR
			TSGSRFQVQR
			GAVMAALNMQR
			SAGGGDEGEKPTK
			AMKLPLGLMTK
			CVSTVTYRIR
			INTDGAYSSNMK
			ALEDGPWMFNK
			INTDGAYSSNMK
			ALEDGPWMFNK
			MKAQSAMDEFR
			YNEDAGHLFFK
			DLVVMIDLDETK
			RALEDGPWMFNK
			SAVMFSPNTSSLEK
			AMFPAARVINGDPR
			ANLHHRGMDVDTR
			ASRNGCPGVSNWESGDDDFWK
			EVGEFMTMDLEEDGSAVGQFLRIK
6506	Reverse transcriptase	<i>Oryza sativa</i> (gil20279456)	EALDAIGDLK
			HRTWTTMR
			KIWEGGSSDK
			YWWSNQEK
			IDIRKPLMR
			GAVMAALNMQR
			SAGGGDEGEKPTK
			AMKLPLGLMTK
			CVSTVTYRIR
			ALEDGPWMFNK
			ANKSMGIHQIK
			YNEDAGHLFFK
			YLGLPVFVGRSR
			MANKSMGIHQIK
			RALEDGPWMFNK
			GTQGEDEVTSPLKK
			SAVMFSPNTSSLEK
			ANLHHRGMDVDTR
			DKSAVMFSPNTSSLEK

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7313	50S ribosomal protein L1, chloroplast precursor (CL1)	<i>Pisum sativum</i> gil1350625	ASRNGCPGVSNWESGDDDFWK EVGEFMTMDLEEDGSAVGQFLRIK RFLEIQK <b>YNDQQLR (19)</b> GGFMEFDK VAVLTQGER FVETVEAHFR TKFVETVEAHFR <b>VAVLTQGERFDEAK (21)</b> GTGKPIKVAVLTQGER <b>NAGADLVGGEDLIEQIK (59)</b> GGFMEFDKLIASPDMMMPK
1104	Disease resistance response protein Pi49 (PR10)	<i>Pisum sativum</i> gil118933	AKGDGLFK LSAGPNGGSIK LTFVEDGETK GDAAPSEEQLK ALVTDADNLTTPK KLTFVEDGETK <b>SIEIVEGNGGAGTIK (76)</b> <b>ALEGYCLAHPDYN (66)</b> SIEIVEGNGGAGTIKK <b>YFTKGDAAPSEEQLK (88)</b> LTFVEDGETKHVLHK GVFNVEDEITSVVAPAILYK
2106	ABA-responsive protein ABR17	<i>Pisum sativum</i> (gil1703042)	AIEGYVLNPGY GDAALSDAVRDETK YHTKGDAALSDAVR LSILEDGKTNYVLHK EAQGVEIIEGNGGPGTIK VAFETIILAGSDGGSIVK GVFVFDDEYVSTVAPPK EAQGVEIIEGNGGPGTIKK
5204	Annexin -like protein	<i>Arabidopsis thaliana</i> (gil51969286)	NATQRSFIR FGSSINKFLK MGTDEWALTR DMLLALLGHDHA TAIKCLTYPEK ELDGELSGDFER VVMLWTLDPTR SFIRAVYAANYNK TSLEEDVAYHTSGNIR
6403	Heat shock protein binding	<i>Arabidopsis thaliana</i> (gil15231204)	VHAGAMGR DFMEIHK AIYDSTLR MAGTLVNSAGR VHAGAMGRSGR TARFYSGTAR RWETDQCW VYHPDASESDGRDFMEIHK
2304	Myosin class II heavy chain (ISS)	<i>Ostreococcus tauri</i> (gil116057040)	AGESATKR IADSDVAR STIEMRK

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			AEFERVK
			TLELTQAK
			GGVAEITIR
			EAAGKSEAR
			NNRGILLK
			ERSAELEK
			ESEKEDLK
			TQLALAAAER
			DTIETMRK
			EQRSLASPLR
			ELNVIIMAQIK
			EIANLRELNTR
			IEMEAGNSAAARR
			LRVMNSELLGSIK
			ELNAMLMKQLSAAR
			SMQANMALIVELESK
			IGIFGGACAMVSHIVR
3104	Myosin class II heavy chain (ISS)	<i>Ostreococcus tauri</i> (gil116057804)	ASRTQTR
			SLLAMQR
			WEYLVR
			ALRLQNR
			MILASRDK
			TAYSSLEK
			LEHEIAALR
			VEEMIALEK
			LEDELGELR
			SADLLTAEHK
			LEMQVKELK
			LSQLSNDHSK
			DQLNATKGER
			DLSSKSESER
			FFSVSKGFSR
			ERLAQEDFR
			VFDSERSGLR
			IGFLNSQLSAK
			THETEVALER
			IIESQNAVIAR
			LLILSANMQAR
			AYTAEKLV DAR
			RWQATSDTTVR
			IRCMEDAVER
			SKANSDAAFEHSR
			INELQALVASLEK
			AKVSDLES AFATAR
			SSEGANDDAVMQLK
			TKIDHLEAELATER
			VEEMIALEKQIGLLK
			DTDMLALREELASNGR
			IQALEDMVNDYQSSMHEAK
1707	Unknown protein	<i>Arabidopsis thaliana</i> gil15223730	ITEYHR
			SMVQAKR
			VVEKETK

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			WMAWRK
			NENGSSRK
			TSTSGAMEK
			NEHEEKK
			QTKDGS LGK
			GVKEDEVV GK
			LDKEDTC GK
			KIHEHEER
			DLGVSGRY IK
			HSEDRNL IK
			EFGSDDDI AR
			SYEDWTHEK
			NETEQESTGL R
			IEEEKGLADSN K
			GKQGMTAENML R
			AELNTEEDSF KK
			QGMTAENMLRQR
			LESADEVDKMVE K
			NAEEEMQDKIDR
2701	Unnamed protein product	<i>Ostreococcus tauri</i> (gil116054844)	SDLMLQLK
			YQSAESR
			ESLEKIK
			EKINSTR
			KMEVADR
			LHSTLTAK
			ESLERTR
			DVSMLQ GK
			QLDMESDR
			VEISTLRTR
			VNHLTADLAK
			EFEEMNER
			QKYQSAESR
			RVQDETNSR
			QTWQNERVR
			DLLQQSITSID
			DVEGIMGTEAER
			EAFARLAAAASEK
			RAFEMEMADLK
3112	Hypothetical protein	<i>Oryza sativa</i> (gil50508931)	VFDHFR
			MSPLGRR
			EERVQMK
			KEIGSSSSR
			TAASASGRNR
			EEMEEERR
			VLHNGFSPSR
			SLENALEKAR
			ELEGANGKLVK
			RTVDMLAASVR
			TTRPSLLGVGGRK
			MLQMAEVWREER
			SRPGPSPPAYGGCAKR
3408	Hypothetical protein	<i>Medicago truncatula</i>	DEYAWK

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	MtrDRAFT_AC140774g5v1	(gil92870352)	VRYSAFK
			MSEVVQIER
			TASYMPLLR
			MSEVVQIERR
			VMITPMDSLDDLK
4306	Unknown protein	<i>Arabidopsis thaliana</i> (gil15238179)	HEVETLEAK
			MKMEDHIR
			TSICHVALQA
			LEESGELGNR
			DNTQTEENR
			LSMEIKDQK
			ELEMELVKK
			EFNEEMKSK
			MEEAKTEVEK
			GNRAVSETQFK
			TNQVSETQMLK
			LECREAQESLLK
			EKEFELLSLGEGK
			DNNMKHEVETLEAK
5416	Hypothetical protein	<i>Oryza sativa</i> (gil53793527)	KVLAEIAK
			KWDDWK
			AAETEASR
			AAELEARAK
			AELDAAWAR
			DFKILVQR
			LGPLPQATLR
			SVEAMVEVGR
			QLAMRPRAR
			EDALTERER
			RSVEAMVEVGR
			QLPGQLATRPR
			DLADREAAVTIR
			AERAELDAAWAR
			LAGEVGPGLWDAVSR
			TIADLQALDSSAGEVEALR
8201	Hypothetical protein	<i>Arabidopsis thaliana</i> (gil4467113)	QEATKSR
			NCSANLR
			EIAELKR
			HSDAERR
			AEIMTVGGR
			AELEQNQNL
			HEEDVVTEDR
			TSEAEKTELK
			ENNNGETIGSPR
			ANEELQRCLR
			AELETKQTELK
			FGPVLLEDFEK
			NAALAKAQMEIK
			NMMSGLDEASEK
			VISHARSSDSEK
			LRINSQFATLR
			QTL SMKDAYFK

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EERESVACLLK  
DDVVVKMEEK  
NMMSGLDEASEK  
EGNCYSLMEQLDQK  
EMLEESTKTQLLQEK  
KMMIIELEGEISSLSQK

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<sup>a</sup> Number accession from NCBI database.

<sup>b</sup> Sequences of the peptides matched. Fragmented peptides and ion score are given in boldface.