

Table S2. Protein sequences of LOV domains and full length proteins. Uniprot identifiers or genomic position are given in parentheses.

Name	Sequence
AtPH1 (O48963)	MEPTEKPSTKPSRRTLPRDTRGSLEVFNPSTQLTRPDNPVFRPEPP AWQNLS DPRGTSPQPRPQQEPAPSNPVRSDQEIAVTT SWMALKDP SPETISKKTITAEKPQKSAVA AEQRAAEWGLVLKTDTKTGKPGVG VRNSGGTENDPNGKKTTSQRNSQNSCRSSGEMSDGDVPGGRSGI PRVSEDLKDALSTFQQTFVVS DATKPDYPIMYASAGFFNMTGYTSK E VVGRNCRFLQGS GTDADELAKIRETLAAGNNYCGRILNYKKDGTS FWNLLTIAPIKDESGKVLKFIGMQVEVSKHTEGAKEKALRPNGLPES LIRYDARQKDMATNSVTELVEAVKRPRALSESTNLHPFMTKSESE LPKKPARRMSENVVPSGRRNSGGRRNSMQRINEIPEKKS RKSSL SFMGIKKKSESLDESIDDGFIEYGEEDDEISDRDERPESVDDKVRQK EMRKGIDLATTLERIEKNFVITDPRLPDNPIIFASDSFLELTEYSREEIL GRNCRFLQGPETDLTTVKKIRNAIDNQTEVTVQLIN YTKSGKKFWNI FHLQPMRDQKGEVQYFIGVQLDGSKHVEPV RNVIEETAVKEGEDLV KKTAVNIDEAVRELPDANMTPEDLWANHSKV VHCCKPHRKDSPPWIA IQKVLESGEPIGLKHF KPVKPLGSGDTGSVHLVELVGT DQLFAMKA MDKAVMLNRNKVHRARAEREILDLLDHPFLPALYASFQTKTHICLITD YYPGGELFMLLDRQPRKVLKEDAVRFYAAQVVVALEYLHCQGIIYR DLKPENVLIQNGDISL SDFDL SCLT SCKPQLLIP SIDEKKKKKQQKS QQTPIFMAEPMRASNSFVGT E EYIAPEIISGAGHTSAVDWWALGILM YEMLYGYTPFRGKTRQKTFTNVLQKDLKFPASIPASLQVKQLIFRLL QRDPKKRLGCFEGANEVKQHSFFKGINWALIRCTNPPELETPIFSGE AENGEKVVDPELEDLQTNVF
AtPH1-LOV2	ESVDDKVRQKEMRKGIDLATTLERIEKNFVITDPRLPDNPIIFASDSFL ELTEYSREEILGRNCRFLQGPETDLTTVKKIRNAIDNQTEVTVQLIN Y TKSGKKFWNIFHLQPMRDQKGEVQYFIGVQLDGSKHVEPVR
AtPH2 (P93025)	MERPRAPPSPLNDAESLSERRSLEIFNPSSGKETHGSTSSSSK PPL DGNNKGSSSKWMEFQDSAKITERTA EWGLSAVKPDSGDDGISFKL SSEVERSKNMSRRSSEESTSSES GAFPRVSQELKTALSTLQQTFVV SDATQPHCPIVYASSGFFTMTGYSSKEIVGRNCRFLQGPDTDKNEV AKIRDCVKNKGSYCGRLLNYKKDGTPFWNLLTVTPIKDDQGNTIKFI GMQVEVSKYTEGVNDKALRPNGLSKSLIRYDARQKEKALDSITEVV QTIRHRKSQVQESVSNDTMVKPDSSTTPTPGRQTRQSDEASKSFR

	<p>TPGRVSTPTGSKLKSSNNRHEDLLRMEPEELMLSTEVIGQRDSWDL SDRERDIRQGIDLATTLERIEKNFVISDPRLPDNPIIFASDSFLELTEYS REEILGRNCRFLQGPETDQATVQKIRDAIRDQREITVQLINYTKSGKK FWNLFHLQPMRDQKGELQYFIGVQLDGSVDHVEPLQNRLSERTEMQ SSKLVKATATNVDEAVRELPDANTRPEDLWAAHASKPVYPLPHNKES TSWKAIKKIQASGETVGLHHFKPIKPLGSGDTGSVHLVELKGTGELY AMKAMEKTMMLNRNKAHRACIEREIIISLLDHPFLPTLYASFQTSTHV CLITDFCPGGELFALLDRQPMKILTEDSARFYAAEVVIGLEYLHCLGI VYRDLKPENILLKKGHIVLADFDLSFMTTCTPQLIIPAAPSKRRRSK SQPLPTFVAEPSTQSNSFVGTEEYIAPEIITGAGHTSAIDWWALGILL YEMLYGRTPFRGKNRQKTFANILHKDLTFPSSIPVSLVGRQLINTLLN RDPSSRLGSKGGANEIKQHAFRRGINWPLIRGMSPPLDAPLSIIEK DPNAKDIKWEDDGVLVNSTDLIDL</p>
AtPH2-LOV2	<p>DSWDLSDRERDIRQGIDLATTLERIEKNFVISDPRLPDNPIIFASDSFL ELTEYSREEILGRNCRFLQGPETDQATVQKIRDAIRDQREITVQLINY TKSGKKFWNLFHLQPMRDQKGELQYFIGVQLDGSVDHVEPLQ</p>
CrPH (A8IXU7)	<p>MAGVPAPASQLTKVLAGLRHTFVVADATLPDCPLVYASEGFYAMTG YGPDEVLGHNCRFLQGEGTDPKEVQKIRDAIKKGEACSVRLLNYRK DGTPFWNLLTVTPIKTPDGRVSKFVGVQVDVTSKTEGKALADNSGV PLLVKYDHRLRDNVARTIVDDVTIAVEKAEGVEPGQASAVAAAAPLG AKGPRGTAPKSFPRVALDLATTVERIQNFCISDPTLPDCPIVFASD AFLELTGYSREEVLGRNCRFLQGAGTDRGTVDQIRAAIKEGSELTV RILNYTKAGKAFWNMFTLAPMRDQDGHARFFVGVQVDVTAQSTSP DKAPVWNKTPEEEVAKAKMGAEAASSLISSALQGMAAPTANPWAAI SGVIMRRKPHKADDKAYQALLQLQERDGMKLMHFRRVKQLGAGD VGLVDLVQLQGSELKFAMKTLDFEMQERNKVARVLTESAILAAVD HPFLATLYCTIQTDTLHLHFVMEYCDGGELYGLLNSQPKKRLKEEHV RFYASEVLTALQYLHLLGYVYRDLKPENILLHHTGHVLLTDFDLSYSK GSTTPRIEKIGGAGAAGGSAPKSPKKSSSKSGGSSSSGSALQLENYL LLAEPSARANSFVGTEEYLAPEVINAAGHGPAAVDWWSLGILIFELL YGTTFRGARRDETFFENIISPLKFPSPKPAVSEECRDLEKLLVKDVG ARLGSRTGANEIKSHPWFKGINWALLRHQQPPYVPRRASKAAGGS STGGAAFDNY</p>
CrPH-LOV1	<p>AGLRHTFVVADATLPDCPLVYASEGFYAMTGYGPDEVLGHNCRFL QGEGTDPKEVQKIRDAIKKGEACSVRLLNYRKDGTPFWNLLTVTPIK</p>

	TPDGRVSKFVGVQVDVTSKTEGKALA
NcVV (Q9C3Y6)	MSHTVNSSTMNPWEVEAYQQYHYDPRTAPTANPLFFHTLYAPGGY DIMGYLIQIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYASEAFL YMTGYSNAEVLGRNCRFLQSPDGMVKPKSTRKYVDSNTINTMRKAI DRNAEVQVEVVNFKKNGQRFVNFLTMIPVRDETGEYRYSMGFQCE TE
NcVV-LOV	HTLYAPGGYDIMGWLIQIMNRPNPQVELGPVDTSCALILCDLKQKDT PIVYASEAFLYMTGYSNAEVLGRNCRFLQSPDGMVKPKSTRKYVDS NTINTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMIPVRDETGEY RYSMGFQCETE
NcWC1 (Q01371)	MNNNYGYSPLSPEELQHQMHHQHQQQQQQQQQQQQQQQQQQQQ QQQQQQQQQHQQHQQQKTNQHRNAGMMNTPPTTNQGNSTIHAS DVTMSGGSDSLDEIIQQNLDEMHRRRSVPQPYGGQTRRLSMFDYA NPNDGFSDYQLDNMSGNYGDMTGGMGMSGHSSPYAGQNIMAMS DHSGGYSHMSPNVMGNMMTYPNLNMYHSPPIENPYSSAGLDTIRT DFSMDMNMDSGSVSAASVHPTPGLNKQDDEMMEQGFGGGDD ANASHQAQQNMGGLTPAMTPAMTPAMTPGVSNFAQGMATPVSQD AASPATTFQSPSLSATTQTIRIGPPPPSVTNAPTAPFTSTPSGG GASQTKSIYSKSGFDMLRALWYVASRKDPKLLGAVDMSCAFVVC DVTLNDCPIIYVSDNFQNLTGYSRHEIVGRNCRFLQAPDGNVEAGTK REFVENNAVYTLKKTIAEGQEIQQLINRKGKPFLLNLLTMIPIPWD TEEIRYFIGFQIDLVECPDAIIGQEGNGPMQVNYTHSDIGQYIWPPT QKQLEPADGQTLGVDDVSTLLQQCNSKGVASDWHKQSWDKMLLE NADDVHVLSLKGLFLYLSPACKKVLEYDASDLVGTSLSSICHPSDIV PVTRELKEAQQHTPVNIVFRIRKNSGYTWFESHGTLFNEQGKGRK CIILVGRKRPVFALHRKDLELNGGIGDSEIWKVSTSGMFLFVSSNV RSLDLLPENLQGTSMQDLMRKESRAEFGRTIEKARKGKIASCKHE VQNKRGQVLQAYTTFYPGDGEGQRPTFLLAQTLLKASSRTLAPA TVTVMNSPGGVPLSPMKGIQTSDSNTLMGGMSKSGSSDSTGA MVSARSSAGPGQDAALDADNIFDELKTRCTSWQYELRQMEKVNR MLAEELAQLLSNKKKRKRKRRKGGGNMVRDCANCHTRNTPEWRRGP SGNRDLCNSCGLRWAKQTGRVSPRTSSRGGNGDSMSKKSNSPSH SSPLHREVGNDSPSTTTATKNPSLGRSSTTAPGTITTDSPAVASS ASGTGSTTIATSANSAASTVNALGPPATGPSGGSPAQHLPPHLQGT HLNAQAMQRVHQHKQHQQHQQQHQQQHQQQHQQQHQQLQQH

	QFNPPQSQPILLEGGSGFRGSGMEMTSIREEMGEHQGLSV
NcWC1-LOV	KSIYSKSGFDMLRALWYVASRKDPKLLGAVDMSCAFVVCDEVTLND CPIIYVSDNFQNLGTGYSRHEIVGRNCRFLQAPDGNVEAGTKREFVE NNAVYTLKKTIAEGQEIQQLINRKGKGFLLNLLTMIPIPWDTEEIRY FIGFQIDLVECPDAIIGQEGNGPMQVNYTHS
RsLP-LOV (NC_009428: 2302851-2303211)	AMDQKQFEKIRAVFDRSGVALTLVDMSLPEQPLVLANPPFLRMTGY TEGQILGFNCRFLQRGDENAQARADIRDALKGRELQVLRNYRAN DEPFDNLLFLHPVGGRPDAPDYFLGSQFELGRSGNSEEAAAAGHA GALTGELARIGTVAARLEMDSRRHLAQAAAALVRAWERRG
VfAU1 (A8QW55)	MNGLTPPLMFCSRSDPSSTSNINLDDVFADVFFNSNGELLDIDEID DFGDNTCPKSSMSVDDASSQVFQGHFLGNALSSIALSDSGDLST GIYESQGNASRGKSLRTKSSGSISSELTEAQKVERRERNREHAKRS RVRKKFLLESQQSVNELNHENNCLKESIREHLGPRGDSLIAQCSPE ADTLLTDNPSKANRILEDPDYSLVKALQMAQQNFVITDASLPDNPVY ASRGFLTGTGYSLDQILGRNCRFLQGPETDPRAVDKIRNAITKGVDT SVCLLNRYRQDGTTFWNLFFVAGLRDSKGNIVNYVGVQSKVSEDYAK LLVNEQNIEYKGVRTSNMLRRK
VfAU1-LOV	PDYSLVKALQMAQQNFVITDASLPDNPVYASRGFLTGTGYSLDQIL GRNCRFLQGPETDPRAVDKIRNAITKGVDTSVCLLNRYRQDGTTFWN LFFVAGLRDSKGNIVNYVGVQSKVSEDYAKLLVNEQNIEYKGVRTS NMLRRK
NgPA1 (K8Z861)	MTEEQKVERRERNREHAKRSRVRKKFLLESQKSVNALQEENDKL RGAIRSHLKEGADDLLKTCEVEVDESILASDPCSATKILDDPDYTLVK ALQTAQQNFVITDPTLPDNPVYASGGFLSLTGYQMDQILGRNCRFL QGPDTDPAAVDKIRRAIEDGTDGVSCLLNRYRADGSTFWNQFFIAAL RGADGNIVNYVGVQCKVSEEYASEVLKKEATSSTVAEASSKR
NgPA1-LOV	PDYTLVKALQTAQQNFVITDPTLPDNPVYASGGFLSLTGYQMDQIL GRNCRFLQGPDTDPAAVDKIRRAIEDGTDGVSCLLNRYRADGSTFW NQFFIAALRGADGNIVNYVGVQCKVSEEYASEVLKKEATSSTVAEAS SKR
OdPA1 (C5NSW6)	MTSKQQLPPPIFGVLGDEKQVARNGIISLVDIFDDFLFSGDRNQPS NTASSSSHAQESSESVGKDEENDYDSNDDEGDSDDGKRRKRSRTL PRNMTEEQKIERRERNREHAKRSRVRKKFLLESQHSVRALEEENE KLRNAIRENLQGEAEQLLTRCSCGGPSVIASDPNTATRLLDDPDYSL VKALQTAQQNFVISDPSIPDNPVYASQGFLTGTGYSLVSEVLGRNCR

	FLQGPETDPKAVEKVRKGLERGEDTTVLLNYRKDGSTFWNQLFIA ALRDGEGNVVNYLGVQCKVSEDYAKAFLKNEENEK
OdPA1-LOV	PDYSLVKALQTAQQNFVISDPSIPDNPIVYASQGFLTTLTG YALSEVLG RNCRFLQGPETDPKAVEKVRKGLERGEDTTVLLNYRKDGSTFWN QLFIAALRDGEGNVVNYLGVQCKVSEDYAKAFLKNEENEK