

Supplementary Table S2. The amino acid sequences of PYR/PYLs from Arabidopsis and tomato used in phylogenetic tree construction.

>AtPYL1

MANSESSSSPVNEEENSQRISTLHHQTMPSDLTQDEFTQLSQSIAEFHTYQLGNGRCSSLLAQRIHAPPETVWSVVRFRDRPQIYKHFIKSCNVSEDFEMRVGCTRDVNVISGLPANTSRRERLDLLD
DDRRVTGFSITGGEHRLRNYKSVTTVHRFEKEEEEEERIWTVVLESYVVDVPEGNSEEDTRLFADTVIRLNLQKLASITEAMNRNNNNNNSSQVR

>AtPYL2

MSSSPAVKGLTDEEQKTLEPVIKTYHQFEPDPTTCTSLITQRIHAPASVWVPLIRRFDNPERYKHFVKRCRLISGDGDVGSVRETVISGLPASTSTERLEFVDDHRLVLSFRVVGGEHRLKNYKSVTS
VNEFLNQDSGKVYTVVLESYTVDIPEGNTEEDTKMFVDTVVKLNLQKLGVAATSAPMHDDE

>AtPYL3

MNLAPIHDPSSSSTTTSSSTPYGLTKDEFSTLDSIIRTHHTFPRSPNTCTSLIAHRVDAPAHAIWRFVRDFANPNKYKHFIKSCTRFVRDFANPNKYKHFIKSCIRVNGNGIKEIKVGTIREVSVVSGLP
ASTSVEILEVLDEEKRLSFRVLGGEHRLNNYRSVTSVNEFVVLEKDKKKRVYSVVLESYVDIPQGNTTEEDTRMFVDTVVKSNNLQNLAVISTASPT

>AtPYL4

MLAVHRPSSAVSDGDSVQIPMMIASFQKRFPSLSRDSTAARFHTHEVGPNQCCSAVIQEISAPISTVWSVVRFDNPQAYKHFLKSCSVIGGDGDNVGSRLRQVHVVSGLPAASSTERLDILDDER
HVISFSVVGGDHRLSNYRSVTTLHPSPISGTVVVESYVVDVPPGNTKEETCDFVDVIVRCNLQSLAKIAENTAAESKKKMSL

>AtPYL5

MRSPVQLQHGS DATNGFHTLQPHDQTDGPIKRVCLTRGMHVPEHVAMHHTHDVGPDQCCSSVVQMIHAPPESVWALVRRFDNPKVYKNFIRQCRIVQGDGLHVGDLREVMVVSGLPAVSS
TERLEILDEERHVISFSVVGGDHRLKNYRSVTTLHASDDEGTVVVESYVDVPPGNTTEEETLSFVDTIVRCNLQSLARSTNRQ

>AtPYL6

MPTSIQFQRSSTAAEAANATVRNYPHHHQKQVQKVSLTRGMADVPEHVELSHTHVVGPSQCFSVVVQDVEAPVSTVWSILSRFEHPQAYKHFKSCHVWIGDGREVGSVREVRVVSGLPAAFS
LERLEIMDDDRHVISFSVVGGDHRLMNYKSVTTVHESEEDSDGKKRTRVVESYVVDVPAGNDKEETCSFADTIVRCNLQSLAKLAENTSKFS

>AtPYL7

MEMIGGDDTDTEMYGALVTAQSLRLRHLHHCRENQCTSVLVKYIQAPVHLVWVSLVRRFDQPQKYKPFISRCTVNGDPEIGCLREVNKSGLPATTSTERLEQLDDEEHILGINIIGGDHRLKNYSSI
LTVHPEMIDGRSGTMVMESFVVDVPQGNTKDDTCYFVESLIKCNLKSACVSERLAAQDITNSIATFCNASNGYREKNHTETNL

>AtPYL8

MEANGIENLTNPNQEREFIRHHKHVELVDNQCSSTLVKHINAPVHIVWVSLVRRFDQPQKYKPFISRCVVKGNMEIGTVREVDVKSGLPATRSTERLELLDDNEHILSIRIVGGDHRLKNYSSIISLHPE
TIEGRIGTLVIESFVVDVPEGNTKDETCYFVEALIKCNLKSADISERLAVQDTTESRV

>AtPYL9

MMDGVEGGTAMYGGLETVQYVRTHHQHLCRENQCTSALVKHIKAPLHLVWVSLVRRFDQPQKYKPFVSRCTVIGDPEIGSLREVNKSGLPATTSTERLELLDDEEHILGIKIIGGDHRLKNYSSILTV
HPEIIEGRAGTMVIESFVVDVPQGNTKDETCYFVEALIRCNLKSLADVSRERLASQDITQ

>AtPYL10

MNGDETKKVESEYIKKHRRHELVEQCSSTLVKHIAKAPLHLVWSIVRRFDEPQKYKPFISRCVVQGKKLEVGSVREVDLKSGLPATKSTEVLEILDDNEHILGIRIVGGDHRLKNYSSTISLHSETIDGKT
GTLAIESFVVDVPEGNTKEETCFFVEALIQCNLNSLADVTERLQAESMEKKI

>AtPYL11

MKTSQEQHVCGSTVVQTINAPLPLVWSILRRFDNPKTFKHFKVTCKLRSGDGGEGSVRETVVSDLPASFSLERLDELDDESHVMVISIIGGDHRLVNYQSKTTVFVAAEEKTVVVESYVVDVPEG
NTEETTLFADTIVGCNLRSLAKLSEKMMELT

>AtPYL12

MKTSQEQHVCGSTVVQTINAPLPLVWSILRRFDNPKTFKHFKVTCKLRSGDGGEGSVRETVVSDLPASFSLERLDELDDESHVMVISIIGGDHRLVNYQSKTTVFVAAEEKTVVVESYVVDVPEG
NTEETTLFADTIVGCNLRSLAKLSEKMMELT

>AtPYL13

MESSKQKRCRSSVETIEAPLPLVWSILRSFDKPQAYQRFVKSCTMRSGGGGGKGGEGKGSVRDVTLVSGFPADFSTERLEELDDESHVMVSIIGGNHRLVNYKSKTKVVASPEDMAKKTVVVES
YVVDVPEGTSEEDTIFFVDNIIRYNLTSLAKLTKKMMK

>AtPYR1

MPSELTPEERSELKNSIAEFHTYQLDPGSCSSLHAQRIHAPPELVWSIVRRFDKPQTYKHFIKSCSVEQNFEMRVGCTRDVIVISGLPANTSTERLDILDDERRVTGFSIIGGEHRLTNYKSVTTVHRFEK
ENRIWTVVLESYVVDMPGENSEDDTRMFADTVVKLNQKLATVAEAMARNSGDGSGSQVT

>SIPYR1.1 Solyc06g061180

MEQSDNSTTHVHQEAEEEPNPTHQFMLPPGLTPEESDELKSSVTDHFSYQVNSSQCSSLAQRIHAPPHVWPVRRFEKPQIYKHFIKSCSVAENFSMVVGATRDVNVISGLPANTSTERLDLLD
DEKYVTGFSIIGGEHRLKNYRSVTSVHGFERHGRIWTVVLESYVVDVPEGNTEEDTRLFADTVVKLNQKLASVAEAIALGGNGEIS

>SIPYR1.2 Solyc08g076960

MDNKPETSLDNVPVHQRSEPGSETGSSLSTITTHHLTVPPGLTPEEFQELSSSIAEFHSYRINPGQCSSLAQRIHAPVETVWTVRRFDKPQTYKHFIKSCSVGEDFRMTVGSTRDVTVISGLPAATST
ERLDILDDDRHVTGFSIIGGEHRLRNYSVTTVHGFERDGEIWTVVLESYVVDVPEGNTEEDTRLFADTVVKLNQKLASVTETLAREAGNGSVNSRDASHR

>SIPYL2.1 Solyc08g065410

MRIEAPANVWPVRRFDNPQYKHFISCKMTGDGGVGSIREVSVVSGIPASTSTERLEILDDEKHILSFKVVGGEHRLNNYKSVTSVNEFEKNGKAYTIVLESYVDIPQGNTGEDTKMFTD TVVKL
NLQKLGVVAMAAMHGHE

>SIPYL2.2 Solyc12g095970

MDGDRQLLV PQGLTQEEFVELEPLIRNYHTFEDLPNTCTSLVTQRIDAPVDVWPVRRFDNPEKYKHFIKSCRIVSGDGGVGSIREVTVVSGIPASTSTERLEILDDEKHILSFVVGGEHRLTNYKSV
TSVNEFKKNGKIY TIVLESYVDIPEGNTGEDTKMFTD TVVKLNQKLALVAMSTMHGHE

>SIPYL4.1 Solyc06g050500

MPSSLQLHRINPTTATLAVKQPQLSQATTWFSPVSTSPDNVLHHHTHVVGPNQCCSAVLQSIAPIDTVWSLVRFDNPQAYKHFLKSCHVIVGDGDVGTLEVRVVSGLPAGSSTERLEILDD
EKHVLSFSVVGGDHRLNNYRSVTTLHRAAEEGSTVVVESYVVDVPQGNTKEETCVFVD TIVRCNLQSLAQIAQNLA KTSKNHDEDPQLKIHRLVDFVDCVKGSCKCLNVLLWYIMVCCVFCITT
HFVTITYILLNIFKVLTVKDIFLSS

>SIPYL4.2 Solyc10g076410

MIPNPQKSSILLQRITSNNPCNCNKQSLHHHTPICTADIPDSVVKYHAHLVGPYQCCSAAIQRISAPVSTVWSVRRFDNPQAYKHFIKSCHLIDGDGNVGTLEVRVISGLPAVNSTERLEILDEE
RHVISFSVVGGDHRLANYKSVTTLHPEPFGNGTIVVESYVVDIPKGNTKDETCVFVD TIVKCNLLSLKQIAENLK

>SIPYL4.3 Solyc10g085310

MPPSSSDSSVLLQRISSNNTHDFAYKQSHHQLQRRMPIPCSTEV PDSVSR YHTHTVSPDQCCSAVIQRISAPVSTVWSVRRFDNPQAYKHFKSCHV VVGDDVGTLEVRVISGLPAASSTER
LEILDDERHVISFSVVGGDHRLANYRSVTTLHTEPSSGNEAAAAAASAETIVVESYVVDVPPGNTREETCVFVD TIVKCNLQSLSQIAQNSAR

>SIPYL6.1 Solyc02g076770

MDQIDIYSNPKCIRPIMLFTNQPKNSKALEEMIKLHHTHELSPKQCSSLVVKVIDAPLPLVWSLVRKFDKPQCYKNFISSCTLISGEGGVGSIREVNLVSGFPGKRSIERLDILDDDMHVSFVSVVDGD
HSFSNFKSIMTLHEDKVEEDHDIIGNYYKTVVIHSYVVDIPEISCRDDTCEVTDNILRWNLRLSLAWVAENMDTNDQVSSLDLNEKEITC

>SIPYL6.2 Solyc03g095780

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>SIPYL6.3 Solyc05g052420

MSISIIGGDHRLNNYRSVTTLHRAAADGGDGGRTVVVESYVVDVPQGNTKEETRVFIDTIVRCNLQWLQGQIAENLEKTKSN

>SIPYL6.4 Solyc09g015380

MPPKSSLLLRITTTTTSTSSKQRTPIPCTTQVPDSITSHHTSVSPNQCCSAVIQRISAPISTVWSVLRRFDNPQAYKHFKSCHVIGGDGKVGTVREVRVISGLPAANSMERLEILDEERHVISFSV
GGDHRLVNYSVTTLHSDQSSGTTIVVESYVVDIPHGNTTEETCVFVDTIVKCNLQSLAQIVENSNTTNLK

>SIPYL8.1 Solyc01g095700

MESQFIERYHSHQPSEHQCSSSLVKHIKAPVDIVWSLVRREFDQPQKYKPFISRCTVKGDLTIGSVREVNKSGLPATTSTERLELLDDEEHILGIRIVGGDHRLKNYSSVITVHPETLDGRPGTLVIESFV
VDVPEGNTKEETCYFVKALINCNLKSLADVSEAMAMQGGVLPVSVNWSSSNQIEI

>SIPYL8.2 Solyc03g007310

MNANGFCGVEKEYIRKHHIHEPKENQCSSLVKHIRAPVHLVWSLVRREFDQPQKYKPFISRCIVQGD LGIGSLREVDVKSGLPATTSTERLELLDDEEHILSVRIVGGDHRLKNYSSVISVHPEVIDGR
PGTLVLESFVVDVPEGNTKDETCYFVEALINCNLKSLADVSEALAVQDRTEPIDQV

>SIPYL9.1 Solyc08g082180

MVSIMNVDRKISSEDEYIRRHHRHDVRDNQCSSLVKHIKAPVHLVWSLVRREFDQPQRYKPFVSRIVQGDLEIGSVREVNKSGLPATTSKERLELLDDEHIFGVKIVGGDHRLKNYSSIITVHPK
VIDGRPGTMVVESFVVDVPDGNTKDETCYFVEALIRC NLKSLADVSEALAVQGHMEPIDRM

>SIPYL9.2 Solyc12g055990

MMNMEDEYIRRHHRHVLHDHNCSSSLVKRIKAPVNLVWSLVRREFDQPQRYKPFVSKCVVQGDLEIGSVRKVNVRSGLPATTSKERLELLDDEHIFGVKIVGGDHRLKNYSSIITVHPEVIDGRP
GTIVIESFVVDIPDGNTKDETCFFVEALIRC NLKSLADVSKRLAVQGHDPIDRI