

Data S4. Amino acid sequences of putative PLP-dependent enzymes encoded by *Echinacea purpurea* contigs assembled from the sequenced transcriptome

| PLP Clade     | Locus ID                              | AA length | Full-length sequence ? | Missing sequence  | aa sequence  |
|---------------|---------------------------------------|-----------|------------------------|-------------------|--|
| A             | >epa_locus_11279                      | 503       | yes                    | none              | MGSYFSEFNPTKSLDSKEVEHLNPEDFRAKHAQVVDIADFYKNIENYFASQVQPGYLRTMPQAPDKPESLDAILKDVENDIIPGITQVHMFNYGYPFASISSAFLGEMLCACFNANGFSWASPALTELEVMVMDWFVMLRLPKCFMFGSGTGGVQVQATTEAVLVTILGARDVRLSKIGHGHAAGLVVYGSQAHSYMNKQKCIAGIHPQNIIRSIPARLEDEFALSPDLRKFLEADVEAGLIPFLCLTGTVSTTAVDNINDLALANKYNIWVHDVAAGGNACICPEYRHFLDGIEKVDLSLSPHKWLLCYAELCCLYVKNPSCVNTSLRTPNRYLYKSETSDSVYSKDWQVGTSSRRFSLRLLYFVLRYSYVESLQSHIRSHIQYAITFERLRSKDGREFLVRPFRSLVCFRLKQLNGYDASYTELLNRKLLBQVNSTGHALLTHSVGGYLLRFRVVGSTLTERHVIRKTEWVKKELTNAILLTEV |
| A             | >epa_locus_8034                       | 433       | yes                    | none              | MPKTPDDLPPDFDTILRDVQNDIIPGVTHWQSNFFGYFPASISSAFLGEMLCSCFNVGFNVAASPALTELEVMVMDVMSMLHLPKTFMFGSGGGVHLSTSTSEATLCTLAARDVRLKIGTERIGKLVVYGSQDTHSMFKVKCIAGIATHNIRAVPTCEDEFALSPDNQKVIADVEKGLVPLFLCLTVGTTSTTAVDPVKDLAEVANRYSIWVHDVAGYGNACICPEYRFLDGIKVDLSLSPHKWLLSYAECCLMKNFNLDLRLTEPEYLRNEYSSESVSYSYKDWQVGTARRFKSLRFLMFLRSYGVENLQNHIRAHVRMAITFERLVESDVKFEIVVPRFRALVCFRLKQLNGYDASYTELLNRKLLBQVNSTGHALLTHSVGGYLLRFRVVGSTLTERHVIRKTEWVKKELTNAILLTEV   |
| A             | >epa_locus_1048_iso_1_len_1193_ver_2  | 382       | yes                    | none              | MATCSFGDTLIVPRNAHISAFSAMVLSGVVPRYILPEYDSWDIACGITPSQVEHAINELNTEGRASVLIITSPYNGICSSLEISIQCHSHNIIPIVDEAHGAHLGPHPLRPSALQQVDSVQSTHTVCLSTQSSMLHMSGNIINERERICQCLQLTQTSYPSYLLSALDAAQAQISENPKTVFNKPIEATBAKSLIEKIPGIRIFDSTGLDPLRISVGVWDLGISGFQYDILDKDYGVAELVGTSLTFPNVLTGSRDDILRLVLGLRSLQTHNSTRVNIQPLTKNTSMKFSRPAFFASKKRVFEEISGRVCGELVCPYPPGIPLLMPGEVITTEVTYLIELKNNGGYIMGVDSTLSSIVVCS  |
| A             | >epa_locus_11903_iso_2_len_862_ver_2  | 189       | no                     | N- and C-terminii | MGGPHAHYVQTELAREVANLLGCTSSWAGPGLMDAATQALQAGKPVGGFKIGKEANEWTSNFHPYLSHTYLCRFFSARKHGLVDAVARSKRKTGCVLVLGGIGTLDEAFELALVQLERIGSALPVVFLMNYDSFYSKLLFLDVCEDWGTVSKGEVLSLKNNSSEALSLAQLGYDC  |
| A             | >epa_locus_46833_iso_1_len_333_ver_2  | 112       | no                     | N- and C-terminii | LLDKIGREFAPKLVVYCSQDTHCSFQKSAKIVGINPENIREVLTSSKSNFQLSPKLLDEMIKDI EAGLVPMYICATVGTSTMTMVDPLGLCEVSRABNMVHVDAAAYAG   |
| A             | >epa_locus_520_iso_6_len_1004_ver_2   | 264       | no                     | N-terminus        | MPSLATVAAMAALAPPSTAGPEILPDDLPSLVNTPSHSNALYKVDWGAPYFVSNSSGNVTRPHGDATMDHQEIDLKLVKASDSKSNGLDLQLPLIRFDPVILKRNLECLQAANFVAVKSESYSYHYGVVPCNQRFLVEDIVRFGSPFRFLEAGSKPELLLAMSCCLCKGSESLVLCNGFKVDIYISLALIAKRLSNLNVILVLEQEEELSDVIDISLKLGVRFVIGVRAKLRTRHSGHFGTSGEKGX  |
| A             | >epa_locus_67189_iso_1_len_357_ver_2  | 120       | no                     | N- and C-terminii | YLLGMLGGAYEALGGVHNLFGGSPVHVVSQNGPQGFVTRAVPFGPSCDDVLRVMQYEPMLFQTLKRIIEEFDAGDSSSLALANDLACSFNNMXYLAASASCLTASTAGSGGX   |
| B             | >epa_locus_952                        | 484       | yes                    | none              | MAGSIDVMLRELNLSVESLPDDFPTAVIKDPLRVASECSGMNGEKLINGKEHREILGRNVHTSCLVTEPDDDDDEVTEGAEQAASVLYARYSKLLERTKHLGYPYMLFDYAGLSQLHFSINLNDPFIENSVGHRSQFVGLDWARLEWELEKNEYGYITNGCTGNLHGILVGREVFDGILVASCESHYFCAARMYMDKCEKXVTUSGIEDCEDFRKLSLHKDPAININIGTIVKGAVDLVLKTLLEESGTHDRFYHCDGALGMLMPPVLPKAPYSFKKPGVSGVSKHGFQCPMQVQITREHINAPFKLELARSLDATINGSRNHAPLWYTLNRKYGRFQVQKCLRNAHYLRHGLTASIGAMLNLSVTVFPERQDEFTRKWLQACQGNIAHVVMNPIITDKLDFVNELEKRVVYKDGKRPKPCVASEIGKANCELHK  |
| between B & C | >epa_locus_10511_iso_1_len_1803_ver_2 | 494       | yes                    | none              | MVLSRTGSDSDASHSTFASRYRASLPFRKMPDINSIPKEAAFQIINDELMDGNPRLNLSFVTTWMEPECDKLIMASINKNYVDMDEYVTTQLNRCVNMIAIRFNAPLGESETAVGVGTGSSEAMLAGLAFKRWQTKMALKGPKWDPKINIVTGANVQVCEKFAFDFEVELKREGVYMDPEKAVEMVDENTICVAAILGSLNGYFEDVKRNLNLLKNAETGWDPIHVDAAAGSFIAPLPELEWDFRFLPVSINVSGHYGLVYAGVWIRNWDKDDPEPIFHNIYGAQDPFTLMSKGSQIAIYHQQLRGLFGKINMENCENAMVLEKLEKTRFOIVSKDNGVPLVAFSLKDHSEHNEFISOMLRRFVWIPVATMPDQAHTLVRVWREDFRSLAERLVDITKVLHEDTLAPRVNAKTEICEKEGINKLEMQKRTNAWKTIVANKKNTGVC   |
| between B & C | >epa_locus_1300_iso_7_len_829_ver_2   | 223       | no                     | C-terminus        | MVLSRTVQAASDASHSTFASRYRASLPFRKMPDINSIPKEAAFQIINDELMDGNPRLNLSFVTTWMEPECDKLIMASINKNYVDMDEYVTTQLNRCVNMIAIRFNAPLGESETAVGVGTGSSEAMLAGLAFKRWQTKMALKGPKWDPKINIVTGANVQVCEKFAFDFEVELKREGVYMDPEKAVEMVDENTICVAAILGSLNGYFEDVK  |
| between B & C | >epa_locus_11730_iso_4_len_1115_ver_2 | 352       | no                     | N-terminus        | HNGHSPCCRFGLDPTYICPISVFLKILKDLIEMGELAAEKHAKYILTEVEKSDSIESVMEHLRINAGYWLTLTDLGLAAVDQETISVWMSQHESGGFGGNEGHDPHLLYSIAQLANFKIETLDIEQYNTYALQNEEDGSGDKWGEIDTRFSYVAICSLALKQHINNEKAVYIISCKNHDDGFGCTPGAESHAGQIFCGALAITGSLHYVDKDLGWLCEQRQVSGGLGRPEKIPDVCYSWVSSLIIDRVHWDKELKVLFDLQCKENGGISDRPDAVDVHTFYGVAGLSLEYPLGAIKADAPALPVDVINRIFLH  |
| between B & C | >epa_locus_1300_iso_6_len_1162_ver_2  | 138       | no                     | C-terminus        | MASVASSTFMPSSLKHPNQTLTRASNFAVSLAINGKFPFLKSSAPSRFVCAATPVDKVCNIVRKLQVLPVGTGVSFKATGADSLDTEVIMGLGEEFGISVFEESAQTATVQDAADLEKLVSK   |
| between B & C | >epa_locus_9434_iso_2_len_1717_ver_2  | 399       | no                     | internal          | SSNFKRKPHTVPRVAFASFSKREFKLTAKVQTSNGEQYHRQIGEDALVMDWTENQCCIQDKGGDDLVCNADGCPVHMCMGCEAFHDDVGNFYCYVYQYAAEASLRQSMVLTAKALSTLEADMRDNDHOEPPVEMANEKDDISKDELAVENHGVLENDCEPHTDTPPEKTEVNLNNEGAHVAHQNEGVHEVNVQNEGVREVDVNTCRMVYKPNDSHYSKMKMVDHQTNGECTCKVQDQAKRSRADIWLTIDEQYCSCKRTSDVAXXXXXXSEKSVAFNKRKPEVPMKHEVKKSGSLMSIDRSTGGRLVTEQEEELMKEGQVSVFTKKNLWKILLEGHRVHFSRAPSOLDKWRIAKHNST   |
| between B & C | >epa_locus_16161_iso_1_len_786_ver_2  | 155       | no                     | N-terminus        | GRGGDMLYEDYGAIVSELGTRITVNLGTRDRLVRLVSLGQLHQRNLLGQVNERDFTDVIKSSIGTSSGMRLSPREAFKASKVYFNESVGIKCGELVCPYPPGVPILIPVEITAEVLSLVVKNNGGFGVGAADSSLTVVCS   |
| between B & C | >epa_70148                            | 163       | no                     | N- and C-terminii | MGLVSKAVFDGGCHVIGVPIKMLPKEIGSDIGSEVYKPVANMHQRKAEMARQADAFIALPGYGLTELEEVITVAQLGHKHPVGLLVNDDGYNSLSDIKAVDEGFTVTPDASRIVSTPAHELLELEVPEVNTVQKSSVTEQQLSYVSKSEIAR   |
| between B & C | >epa_locus_238_iso_1_len_972_ver_2    | 193       | no                     | N- and C-terminii | ISVPHRGCDTATPGLMIRKTRILLRCDLRSQVGLIMEGGSSSKRFRICVCGSHGRREVFVAATELGDLEKRRMNLVYGGSGVLMGMIAQRVFDGGRCGLIPIIKVIMESVSEVGEVRVNSDMHERKAEMARESDAFIALPGYGLTELEEVITVAQLGHKHPVGLLVNDDGYNSLSDIKAVDEGFTVTPDASRIVSTPAHELLELEVPEVNTVQKSSVTEQQLSYVSKSEIAR   |
| between B & C | >epa_locus_10674_iso_1_len_795_ver_2  | 216       | no                     | N- and C-terminii | MLETGKSRFRKRCVCGSPKPSYQAEALGKELVERRIDLYGGSGVLMGLVQAVHGGRRHVLGVIPRTLMPEITGETVGEKAVADMHERKAEMARQADAFIALPGYGLTELEEVITVAQLGHKHPVGLLVNDDGYNSLSDIKAVDEGFTVTPDASRIVSTPAHELLELEVPEVNTVQKSSVTEQQLSYVSKSEIAR   |
| between B & C | >epa_locus_10172_iso_4_len_952_ver_2  | 213       | no                     | N- and C-terminii | MEGSSSKRFRICVCGSPKPSYQAEALGKELVERRIDLYGGSGVLMGLVQAVHGGRRHVLGVIPRTLMPEITGETVGEKAVADMHERKAEMARQADAFIALPGYGLTELEEVITVAQLGHKHPVGLLVNDDGYNSLSDIKAVDEGFTVTPDASRIVSTPAHELLELEVPEVNTVQKSSVTEQQLSYVSKSEIAR  |
| between B & C | >epa_locus_55012_iso_1_len_661_ver_2  | 210       | no                     | N- and C-terminii | MERDESISKSRFRKRCVCGSPKPSYQAEALGKELVERRIDLYGGSGVLMGLVQAVHGGRRHVLGVIPRTLMPEITGETVGEKAVADMHERKAEMARQADAFIALPGYGLTELEEVITVAQLGHKHPVGLLVNDDGYNSLSDIKAVDEGFTVTPDASRIVSTPAHELLELEVPEVNTVQKSSVTEQQLSYVSKSEIAR  |
| between B & C | >epa_locus_39195_iso_1_len_799_ver_2  | 222       | no                     | N- and C-terminii | HLGSLTKVDFRDAVLMVNYIEDRSQFIEDFLNIGGLGIDYHTGAVLPTPRDITDRELVRNRLNIEPGRSLIANTCCFNVRVGTGKVTNGFVIDGSMALIRPSLYGAYQHIELVSPSPNAIEFTDVGVPVGCESADFLGKDRPLTPAKGAGLVHDAGAYCMSASTYLNKMRPEVYVEEDGVSIRKIHGEMFEDHRRFFEGEL  |
| between B & C | >epa_locus_13914_iso_2_len_1717_ver_2 | 401       | yes                    | none              | MEAVEKRPFFLYSKPQTRVYEAKEALGSLIIGYAIKANNFNVLQHLRRGCGAVLSGNELRALRAGFPTRCVFNGNKLLEDLVAQEGVFNIDSEFLDNIIVSAARIAGKVNLRINPDDVQPHYVATGNSKFGIRNEKQWFLDAVKSYPDELKLVGAHCHLGGITSTIKVDIFRDAAMAVKFIIDIRAQGFDSYSLNIGGLGIDYHTGTVLPTPRDITDRELVRNRLNIEPGRSLIANTCCFNVRVGTGKVTNGFVIDGSMALIRPSLYGAYQHIELVSPSPNAIEFTDVGVPVGCESADFLGKDRPLTPAKGAGLVHDAGAYCMSASTYLNKMRPEVYVEEDGVSIRKIHGEMFEDHRRFFEGEL   |
| between B & C | >epa_locus_1367_iso_26_len_1136_ver_2 | 380       | no                     | N-terminus        | KSVRFEAEVAMTALGFSGKEKASGNGCNMTSGTESILLAVKSSRDYMRKKNITRPEMIIPEASHSAYDKACQYFKILRVPVNEFQADIKAIKHNKINTMIVGSAFPGPHIDIEELAVRAGYICHLVCLGGVFLPARKLPPDFPVTGVSISADVHYGLAPKGSIVLYRNIHERKHQFVAVTEWGGVYSPGASRPGNVIAGAWAAMISLQEGEYHREIMESKRIQGVREISELFIWRPDMTIVAFSGNVIDIEFVNDLSSKGWHLNPLQRNSHICVTLQHPVDFDKLSDVQVTKKPNPGLINGLAPIYSAGIQDRGMVCELLDFMNTCXDYX   |
| between B & C | >epa_locus_18053_iso_1_len_410_ver_2  | 137       | no                     | N- and C-terminii | LVFEAVASSHDSQFQSPPEIEYEEQLTDDARADRYNLYAAAVHGEYENCLLYAEQLKRCQVEQFKESLTMELQAALVGLCELVSKAIGVDSVRTYHNVLSVFTSPDFWIGQLFPVPIHRLDERPAVRGX  |
| C             | >epa_locus_3096                       | 488       | yes                    | none              | MENGLDKAMDAEQRENGHKMVDIADYKNIETFPVLSQVEPGYQLKLLPDSAPVQESLQAVLQEVETKILPGVTHWQSPDYFAYFNSNSVAGFLGEMLSAGINMVGFSWIASPAATEMELMIDLWANLLKPNHLSRPGGGAIGCTASEALLVLLAARDKILKEVGDALGKLVVAGVSDQTHSSLQKACQIAGHPENIRLKTDTCNELYSPELSDAISHDVAGSLIPLFLCATVGTSTTAVDPLHALGKTKYKGIWFDVDAAGSACICPEYRHHLLGIEEADSFMMCHKWFLNFDPSALWIKDRNALIQSLTNPFLKKNASQGGTVIDYKDWQIPLGRFRSLKMLWVLRLLYGVESLQSYINRHLKLAQGFEDLV AQDTRFEIVATRTFSLVCFRLHANKPEEYVKNLHNDLDAVNSSGKIPIDSHVLSGKYYLRFVVGAPLTERHIIIAAWLKQEAASSLLEN                        |