**Additional file 9:**

Protein sequences of Cytochrome P450 genes identified in *S. oryzae* genome

>SoG\_00091.T1

MKRGESLALIRTWHQEYGKTFKVQLGRPRVITIEPKNVQTVLALKFKDFELGERNKALSP

LLGQGIFASDGQVWEHSRALLRPNFVRTQIADMHVYERHVSNLIKRIPKDGSTVDLQTLF

FQMTIDSATEFLFGESIDSLGAGDSQPKFARDFNLSQEGLAIRTRLGPLMFLHKDRAFSE

ATVEARRFVDQFVQRAVEYRASHSKEAGASDASEEGYVFLYELSKRTADRKMLTDQLLNV

LLAGRDTTASLLSITCFTLARRRDVWDKLREEVLALGDKTPSFEDLKSMKYLNWVLNETL

RLYPVVPLNSRTAVRDTFLPTGGGPDGKHPTFVPKGVDVVYSVYSMHRLPEVYGPDADEY

RPERWATVKPGWAYLPFNGGPRICPGQQFALTEACYTMVQIVRHFKSMESRDDRPFVEGL

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>SoG\_00504.T1

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FKDSDRHLKAKNNNSGYFLGELLGKCVGLVSQNEWKQMRSVCEVPFVRSKSVTYIQQMER

RTDRHFRQLWKTSNLSESVIDPAQDLKMLPFWIVAEILYGNLTADMEAQLAELAPLRESL

FQYFLKGGVTRYEWSKYLPTAANRHLSEFKSRWAAFNRQARTGAHPNTPIASYYSAIDEG

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NEYWGEDSQTYRPERFLERSAVKDRYNFWRFGFGPRQCMGKFVADMMIRVLLVHLVENYD

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>SoG\_00521.T1

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PMAQDVASGGQRQLFMSYGPRWRQLRKHTHALLNLNASIKYMPIQDFESKQVLRDLLDNP

KEFYTINRRYSTSVIMLVTYGHRVPNFDDPLIKKIYTVLDNVTYITAFGAHVVDAFPSLA

SWPQWLFGNWRKKAIKIFEHDSKIYLDLWNRLRREVDNGTARQCFCKDFYLNDPSKNGID

DLQAAYACAGMIEAGSETTATALNNWVLCMLLFPDTFKKVQEEVDRVVGKDRLPQWEDEP

QLPYLRAMIKELMRYRPGNKFGMHHATSEDDWYDGMFIPKGSWAILNWWAIHHDPTIHPN

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>SoG\_00528.T1

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RDKEAHARKRRVLSNAFSDSATKEMQRYILNNIRTFCEQIGSMAGSSSEKKGWTAPKAMS

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RWTAGAENPLSASFERRTTADEVSLASSAFCPFSIGPRGCIGKNLAYVEMTITLARTIFL

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>SoG\_00604.T1

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EKGAQLSWTLYSYHRQRDVWGEDAEEFRPERWLGEGAMRFGWHYTPFNAGPRICLGQQFA

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>SoG\_01004.T1

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>SoG\_01096.T1

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>SoG\_01168.T1

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AVALFELAKKPEYLQKLYEALAKHISESSSEEILHDQIANIDLLTGVINEALRLYPPNPS

HPTRVTPPEGAMIAGKFIPGGTQVFTPQYVIGRDERIYPQANEFIPERWYSSPELVTDLK

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>SoG\_01175.T1

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DIIGVAGLGRQLNAVEKKQDPLTSIYERLLNPTREMIVYSAACIAFGYDRVKLLPWKMNK

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>SoG\_01277.T1

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LVKKGTRLILPAWGMNRYAKYWGPDAEEFRPERWLSGGSSDPSQPNECNDITEKTKAPTK

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>SoG\_01665.T1

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AKFLHLEKQSNLSYARGIPDVELSTRSPADTQRRPREGVSATKDLSTPERPPGIRTLKEE

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>SoG\_01788.T1

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>SoG\_02377.T1

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NSTYKNGTKVPDHEIAHMMIALLMAGQHSSSSTGSWIMLRLAQNPHVIEELYQEQVKALG

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TRREA

>SoG\_02481.T1

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REDARQRRTKAFEHASGATAERFQNPLWQLTELVTPGGFKLRRSLSIIRSQGKQIVSRAV

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>SoG\_02632.T1

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TFLHELVNATRDRKALRDQIMAVLLAGRDTTASTLSWAIYELGRNPAAMRKLRREIVDMV

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>SoG\_02715.T1

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>SoG\_03005.T1

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>SoG\_03048.T1

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>SoG\_03059.T1

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>SoG\_03504.T1

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>SoG\_03551.T1

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>SoG\_04044.T1

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>SoG\_04125.T1

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>SoG\_04186.T1

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RESALHRAFLRTLKQQVAANKAPDCFGTELVKIQDHEDINDEKAVNILAMLIGAGADTTS

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SSLP

>SoG\_04293.T1

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>SoG\_04315.T1

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>SoG\_04319.T1

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>SoG\_04368.T1

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>SoG\_04488.T1

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>SoG\_04568.T1

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>SoG\_04594.T1

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>SoG\_04596.T1

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>SoG\_04763.T1

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>SoG\_04897.T1

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>SoG\_05073.T1

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>SoG\_05129.T1

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>SoG\_05347.T1

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>SoG\_05369.T1

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>SoG\_05747.T1

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RTQELR

>SoG\_05762.T1

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>SoG\_05850.T1

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>SoG\_06046.T1

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>SoG\_06058.T1

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>SoG\_06071.T1

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>SoG\_06094.T1

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>SoG\_06212.T1

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>SoG\_06398.T1

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>SoG\_06439.T1

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>SoG\_06454.T1

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ENE

>SoG\_06475.T1

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>SoG\_06480.T1

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>SoG\_06758.T1

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>SoG\_06973.T1

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>SoG\_07000.T1

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>SoG\_07113.T1

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>SoG\_07127.T1

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>SoG\_07427.T1

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>SoG\_07442.T1

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>SoG\_07443.T1

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>SoG\_07445.T1

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>SoG\_07787.T1

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>SoG\_07873.T1

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>SoG\_07890.T1

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>SoG\_07892.T1

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>SoG\_08028.T1

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>SoG\_08153.T1

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>SoG\_08286.T1

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>SoG\_08311.T1

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>SoG\_08779.T1

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>SoG\_08804.T1

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>SoG\_08843.T1

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>SoG\_08956.T1

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>SoG\_08983.T1

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>SoG\_09024.T1

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>SoG\_09219.T1

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FIWQIEDMHRKYGPCVRINPYEVHIIDPEFYDELYVSHKKLDKYRWWTNLAGADGSSFST

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MDVICDYSFANDRKYLDEPDFKLLWKQTIIGAFEGGAMGRQFPWMLPLMKKLPRSMVSAM

DASVGHLLNWQDGVKVQVQPIIDGTDELSRKGDTSRTIFHTLRDSDLPAHEKSLQRLCDE

GEILTGAGSETTAQTLTRIMFYVSQVPEVLTKLRAELDQIMSEQDSIPDIAELQALPYLS

AVIKEGLRLSYGVTTRLPRVCHEDIVYRDLVIPAGTPVSQTPYFILMHPDIFPEPKRFRP

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ICYHDFFVAVASLESKGVRATLTQRKLSC

>SoG\_09258.T1

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MFKSFHVGAPLTKLTRSLAARLTDIVEEGRMAIDEYIGCPTEWTAHPLTEQAFRTVTRTA

NRLLLGIDLARNEEFLQLSIEYTGILFGGANTIKKYPDYLKYFMLRWKTGLSSANKLAMK

HLVPIFKARVAERQRYADQNELDIWEKKVKKDDCVQWILDAAPPDELRNFKSLTHRMLHI

NIAAVHTSSNNFMSMMQVLSLMPELQQELREEILEVFERDGGWTKQTMTHLKKLDSFMVE

SGRLCGDSAVKLKRKVVKDFRLSDGTLLPKGLVIFVNSIPFLTDPAVVESPEKFDALRMY

RKRLEPGQENQNQWVMYSETNQTFGAGKHACPGRFFAANEIKSLLVLFLMRYEFRMSSGH

TLDDIYKGVWHNEARTARTDTVLEFRALRMDIPEALKFSF

>SoG\_09368.T1

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YPQWIPIMGFDIAMSMAKSLRDHTFLLWLRKLHETGPGTSKTFTIDFLGRHVIHTIEPEN

MKALSATVWKDFGVEPLRRNTGASMPFADKGVNTTDGHDWAFSRFLIKPYFLRDAFSNTD

RLKTHTDNLLSLIPLDGSTFDMQTLMQRWFLDTSSHFLFGESISCLLYPERAEIAWAMTD

VLRGLRLRLQMSKWLWMFRWKPWFDAIEVVHEFIDRQVDRAYEERAKSIATGSTKSEESS

NFGVGLKPERTDLLWSMVGNVPEDRARLRSEMLLLFVPNNDTTSIFISNVFWNLARFPAV

YAKVREEVLAVGEDTQLTYECLRGMKYLDAVLNESEHISSFRLPLFCSWRKRNQANQRFS

AHRLYPNGIMQVRYCIKDTTLPLGGGSDGKSPMLVRKGDVVQVNKSVMQRDKDIWGEDAD

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VMRAGPVNTRGVKIAVTPA

>SoG\_09369.T1

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LENSRKVTGTEHAFKGVQPNNAISIEQYLQTIDEMIFTNIEVTGSILAFMFGKLAEHQEY

QQRLHEEIEAQKSSEAFHIRNYLTLQTSLLHYLVLESIRLRPATWFSAPECITIDKVIGR

YKVPAKTPVVIDVRRLNTSALTWGPDSQDFRPERFSEISPNEYRYAYMKFGVISGKCLGK

HMAEILMKLAVVTVLEQYRIEHVEMNIGVKEGDLAFIKRN

>SoG\_09385.T1

MVAHQVLYAAYALIFYAVFKYLTATDVPKIKNLPEIPGVPVFGNLIQLGTDHARVAQKWA

KKYGPVFQTRLGNTVSISSFSCSTFFTSCHTWLTPFHFATQRVIFANSYDSVRHFWITHQ

SALISRPTFHTFHSVVSSSQGFTIGTSPWDESCKRRRKAAGTALNRPAVQSYMPILDLES

VVSIKELLEDCKGGTNDIDPTPYFARFALNTSLTLNYGFRIDGDVNNQLLQEITHVEREI

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>SoG\_09412.T1

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QIVLSTPVEPPKHLQIGTAHRPPHEGFLAGGNLSRVWPILTTATGITGAKMTLLEIINDN

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ATTRSVYGPKNPYEKEGVVDGFXNARDFEGGLIALAIGILPSIVAKKAIAGRDKVTAAIR

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>SoG\_09429.T1

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CALDIIGLVGLGRDFGAVADENNSLAKTYSLVMKPNRLAVLFALLRLVFPHWLVNLIPTQ

RNNVINSASQHIRGVCCDLVRDKKSRLEKGEQPDPDILSTALQGGGFTIEQTVDQAMTFL

AAGHETVASTMAWAIYALCRNPEAQAKLRDEVRWRLPSVDSGKGITSADIEAMPYLNAVC

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>SoG\_09512.T1

MIFLHPAFLAGIGLYVLGIFIVRRMSTPVTWLPGPAISRITGLYLKWQELRANRTLYVHA

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CVGKHLALAEMKTLLRDTYSKFSTTPDPSMRAESMVMSDQLISSRPLGQRCLLRFHPIGE

AETV

>SoG\_09546.T1

MLASSGGISHLLEVLADFGYARLGALWLLAILIYRLGYQLFFSPLRNIPGSLLSRLFASH

SVLKRVLAEGSRSVQKDYETYGDIYVNKPNGVSISNPRDIKTVLTSYEFRKTDIYQMLDI

KGRPSIFTNRDPAQASQRRRQLGPFLNLGFLGRMEPLILKYSIVAIKNKWDALIDKAGGN

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>SoG\_09659.T1

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DVDSDPLTGNADPTNLVAPPPRARCYFVPRNEKALSAALGIGKTG

>SoG\_09761.T1

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EHSRKRKIVSNTFSAKSIGQFEPYIHHNLELFVKKWDEMAKHQATPDGTVHVDCLNWFNF

IAFDVIGDLAFGAPFGMLSTGADMAEVRSSPDSPPIYAPAVEILNRRGEVSGTLGCMPGL

IPIAKYLPDPFFSKGLAAVKDLAGIAIAQVRRRLDNPPPADRKDLLARLIEGRDENGQPL

GREELTAEALTQLIAGSDTTSNTSCALLYHAVRTPGVVDKLRAELDAAIPRDVTVPTFEQ

VKELPYLQNVINETMRHHSTSGIGLPRQVPPESPGVEILGRFYPGGTVLSVPTYSIHHST

DIWGPDADDFRPERWEKATERQKNAFIPFSYGPRACIGRNIAEMELKLIVSAWVRRYDVQ

LRQGEMETREGFLRKPVALEIGFKRRP

>SoG\_10141.T1

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FQKGVDHLFSMRDEAKHSATRTKVGPGYAGTFLVEEAIDRQLARMLRIIDEQYVVEPGEH

KPMDLAVITQFLALDIVGDMTFGKPFGFLDQGRDIYGWIEWNEGFFPVASTCATLPFLAS

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SEALVQVDSEPPPAPRVSLTSVFPFPSVAGTDSVAVALRMALLYILSTPRVYNKLVGELR

DAERAGLASTPIRDAEAKRLPYLQAVIREGMRIFASQTPLLNKTVPDGGDVIAGVWVPAG

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AA

>SoG\_10205.T1

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SAAHATVDMRHWFQCYAFDVIGMITYAKRLGFLDSGEDVGNVISALEDHLGYATIVGIFP

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KRTQDPENFTSFHVLSGCVSNMVAGSDTTAISLSAVLYYLLKNPICMQRLKDEVDKKTRD

GELSTNPTFKESQQMPYLQAVIKEALRLHPATGLPLERVVPEGGATISGQFFPKGTIVGL

NTWVTHRDPEVWGIDAEKFRPERWLDPDINKLGIMNRQWTPFGLGSRTCIGRHISMLEIC

KLIPRLIRDFTFQLDGPLQTGNWRTSDYWFVKPLNFKVKVHQTLMRLIDTEMTHSGALGE

>SoG\_10242.T1

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RAFVGLPLSRQEEWVEATVDYTAGVSRAWLVLRLIPWPIRFFVAPFLSQVKALKQQRAIN

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NEHKFQHATTGVDNINFGHGIWACPGRFFASAEIKVVLAYILRHYDVTLKPGEPKPKQQH

FGLAILPDPTAEVLFKARQ

>SoG\_10275.T1

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HVPQVVLDFDGFLSGLMKRYPEGIFSVKLVGKVHNFISRPSLATLLMNQPESVASSNWLH

LRLVYTVFGYRESDGEDLIRKTYDVYHVLSSTHSLNSMTETTVKTLNQNIADWVTFNSQP

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DNVSAFLKARLEVYRRERAPIRARAAIELGLLWAMNANSAPLVFWMLYEINRDPVLLEQI

REEMAPYMHAVQPRNDFGLAVWMAPELRNVDVDGLMEKCPLLKASYIETLRLYTGSYTIK

WMNEDAVLGKQSDAAGGGYLLRKGTYAHAAHDLHQLDPESYPDPHEWQPARHLKTVVGKG

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>SoG\_10310.T1

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ALGIDVATFGSIHNEAHRRRRAAINPFFSRKKVLELEGIVHDKADKLCRILNSDRAANKP

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EAFPDPEVFDPDRWTDPTTFHDRDRCLVPFSRGRRMCVGMNLAWCELYVTLGKLFHRFQH

LEAFDVSDEDMVYQEYFSAFHPPEKRKFRVVVRDD