```
CYP7A1     --------------------------------------------------MMTISLIWG------------IAMVVCCCIWVIFDRRRRKAGEPPL
CYP7B1     -----------------------------------------MAGEVSAATGRFSLERLGLPGLALAAALLLLALCLLVRRTRRPGEPPL
CYP8A1     ----------------------------------MSWAVVFG----------------LLAALLLLLLLT-RRRTRRPGEPPL
CYP8B1     ----------------------------MVLWGLLGA---------------LLMVMVGWLCLPGLLRQRRPQEPPL
CYP51A1    ------------------------------MDWDYYT-LLKTS--------------VAIIIVFVVAKLITSSKSKKKTSVVPLPPV
CYP51A2    ------------------------------MELDSENKLLKTG-------------LVIVATLVIAKLIFSFFTSD-SKKKRLPPT
CYP26A1    -----------------------------MGLPALLASALCTFVLPLLLFLAALKLWDLYCVSSRDRSCALPLPP
CYP26C1    ----------------------------MFPWGLSCLSVLGAAGTALLCAGLLLSLAQHLWTLRWMLSRDRASTLPLPK
CYP716A1   ------------------------------MYMAIMIILFLSSILLSLLLLLRKHLSHFSYPNLPP
CYP725A1   ---------------------MDSFIFLRSIGTKFGQLESSPAILSLTLAPILAIILLLLFRYNHRSSVKLPP
CYP718     ---------------------MVLEPNFVLSWVFLCIAATISSTLFFFRKKHHRFITKKIQKKKKLLP
CYP90A1    ------------------------------MAFTAFLLLLSSIAAGFLLLLLRRTRYR--RMGLPP
CYP90B1    -----------------------------MFETEHHTLLPLLLLLPSLLSLLLFLILLKRRNRKTRFNLPP
CYP724A1   ----------------------------MLVLSIFLSLGLFFLSILILYISISKKNETNDHHSSLT
CYP720A1   -----------------------MAESAGESYRLLSVSSSTTFLAFIIIFLLAGIARRKRRAPHRLPP
CYP85A1    -----------------------------MGAMMVMMGLLLIIVSLCSALLRWNQMRYTKNGLPP
CYP87A2    ------------------------------MW--ALLIWVSLLLISITHWVYSWRNPKCRGKLPP
CYP708A1   ------------------------MNNLISLDIMKEMWGVALSFVIALVVVKISLWLYRWANPNCSGKLPP
CYP702A1   ----------------------------MVEVYELLTVMVSLIVVKLFHWIYQSKNPKPNEKLPP
CYP88A3    ----------------------MAETTSWIPVWFPLMVLGCFGLNWLVRKVNVWLYESSLGENRHYLPP
CYP88B1    ----------------------MDFYNLALFFIALILGIFTFYAILMRINGWYYAIKFCSNKYNIPN
CYP3A1     -----------------------MDLLSALT------LETWVLLAVVLVLLYGFGTRTHGLFKKQGIP
CYP5A1     ----------------------MEVLGFLSPELNGPMVTMALAVVLLALLKWYSTSAFSRLEKLGIR
CYP6A2     ---------------------------MFVLIYLLIAISSLLAYLYHRNFNYWNRRGVP
CYP6B4     -----------------------------MLTIFIVTATLFAILYFYFTRNFNYWKDRNVV
CYP28A1    ----------------------------MLEITLILVLLLLGLFYVFMTWNFGYWRKRKVP
CYP28C1    ----------------------------MFGSLLLGIATLLGAIYAFLVSNFGHWRRRGVT
CYP13A2    ----------------------------MSLGFVLAVTFSIFLGILTYYLWIWTYWMRKGVK
CYP13B1    -----------------------------MGAIIVLVVLFATIAG---YFKWIHTYWRRRGIS
CYP72A8    --------------------MSDTKISAVAVAAAVVVVTTVTVWIWKGLNVAWLRPKKNEAYLKRQGLS
CYP72B1    --------------------MEEESSSWFIPKVLVLSVILSLVIVKGMSLLWWRPRKIEEHFSKQGIR
CYP721A1   -------------------MAVFFILVLVFFFLVFRFIYSNIWVPWRIQSHFKKQSVT
CYP709A1   -------------------MLLTILKSLLVIFVTTILRVLYDTISCYWLTPRRIKKIMEQQGVT
CYP709B1   -------------------MGLVIFLALIVLILIIGLRIFKAFMILVWH-PFVLTRRLKNQGIS
CYP715A1   ------------------MEFFEMSRVWYIFFKVFVVVICLMFLKLFLRCWIWPVRAQKKLRGNGFV
CYP714A1   ------------------MENFMVEMAKTISWIVVIGVLGLGIRVYGKVMAEQWRMRRKLTMQGVK
CYP4C3     -----------------MSSKVITSLMAESILLSKVGQVISGYSPITVFLLGSILIFLVVYNKRRSRLVKYIEKIP
CYP31A2    ----------------------MGVIIP-----AVLLAMATVIAWLLYKHLR--MRQVLKHLN
CYP37A1    -----------------------MGIAVYLLALVVIYVVFNLSKILKFVKERMRLYHLMSKID
CYP37B1    -----------------------MHFLNIATIFLITIFLFYYKLIYNFIRDRLRIYKYMRKFD
CYP32A1    -----------------------MIIVISIVIGYVIYLVVVNFQQILELWRINRKCAQNLSMVN
CYP29A2    -------------------------MTIFIPISIAIILAYLATWIPTLLKYKRHWQYGSKLP
CYP86A1    ------------------------MEALNSILTGYAVAALSVYALWFYFLSRRLTGPK
CYP86B1    --------------MNFNSSYNLTFNDVFFSSSSSSSDPLVSRRLFLLRDVQILELLLIAIFVFVAIHALRQKKYQGLP
CYP96A1    ------------------------------MALITLLEVSISLLFFSFLYGYFLISKKPHRSFLT
CYP96C1    -----------------------------MALASIEKVATGLICFILLIFSLKRIGHPR-----
CYP94A1    ------------------------------MFQFHLEVLLPYLLPLLLLILPTTIFFLTKPNNKVSSTSTNN
CYP94B1    ------------------------------MEMLNAIILILFPIIGFVLIFSFPTKTLKAKTASPSN
CYP704A1   ------------------------------MAIIVVTTIFILLSFALYLTIRIFTGKSRND----
CYP704B1   -----------------------------MSLCLVIACMVTS----WIFLHRWGQRNKSG----
CYP97A3    MAFPLSYTPTITVKP-VTYSRRSNFVVFSSSSSNGRDPLEENSVPNGVKSLEKLQEEKRRAELSARIASGAFTVRKSSFPSTVKNGLSKIGIPSNVLDFMF
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CYP97B3   MAFPAAATYPTHFQGGALHLGRTDHCLFG-----FYPQTISSVNS-----------RRASVSIKCQS--------TEPKTNGN------ILDNASNLLT
CYP1A1    ------------------------------------------------MLFPISMSATEFLLASVIFCLVFWVIRA--------SRPQVPK
CYP1B1    ---------------------------------------MATSLSADSPQQLSSLSTQQTILLLLVSVLAIVHLGQWL--------LRQWRRK
CYP17A1   ------------------------------------------------MWELVTLLGLILAYLFWPRQGS--------SGTKYPK
CYP19A1   ------------------------------------------------MWLLLAVFLLTLAYLFWPKTKH--------SGAKYPR
CYP2A7    ------------------------------------------------MLASGLLLVALLACLTVMVLMSVWQQRK--------SRGKLPP
CYP2M1    ----------------------------------------------MDVLHILQTNFVSIIIGFVVIILLWMNRGKQ--------SNSRLPP
CYP33A1   -------------------------------------------------MIFFLLLTAFVLYLFNEFYW--------KRRGLPP
CYP33C1   -------------------------------------------------MIIILLLTFLTIYFVYELYW--------KRRNFPP
CYP33B1   -------------------------------------------------MILIFFALCTLFFLIHQYLW--------RRRGLPP
CYP23A1   ------------------------------MPSLRNAILLTIATTFLYFRIMRTLNFDNYMATYIYFLTCITLYAIYELNY--------KRRRLPN
CYP35A1   -------------------------------------------------MFLVLIFLALSCWLIIRQYQ--------KVSRLPP
CYP35B1   -------------------------------------------------MIFVLLLTTFLAVLIIRQYQ--------KARKLPP
CYP34A1   -------------------------------------------------MFLVLLFFTIISLALAHQWR--------ARKQLPR
CYP71A12  ----------------------------------------MEMILMVSLCLTTLITLFLLKQFLKRTANKVN----------LPPS
CYP71C1   --------------------------------MALEAGYDYLHVAVVQCTPTQAAAVLGVLLLLAIRLAAAARSSSATSPKWKQHRLPPT
CYP71D11  ----------------------------------------------------VALMILRKNLKK------PDSIPNIPPG
CYP726A1  --------------------------------------------MEQKNLSFPSILISFLLVLILVVVMR------LWKKQNPPPG
CYP71K1   ---------------------------------------------MAELPLYLLLLALLVAVPFLCLTRWSLRHGGGGGGRLPPS
CYP99A1   -------------------------------------------RLISAVILAVCSLISRR---KPSPGSKKKRPPG
CYP71E1   ----------------------------------MATTATPQLLGGSVPQQWQTCLLVLLPVLLVSYYLLTSRSRNRSRSGKLGGAPRLPPG
CYP71N1   --------------------------------------------MALPPLLLSPLPSLLVVLALLSSLLLAGRKARGGSATWKLPPG
CYP71B2   --------------------------------------------MTILLCFFLVSLLTIVSSIFLKQNK---TSKFNLPPS
CYP83A1   ---------------------------------------MEDIIIGVVALAAVLLFFLYQKPKTKRYKLPPG
CYP83B1   -----------------------------------------MDLLLIIAGLVAAAAFFFLRSTTKKSLRLPPG
CYP83E1   --------------------------------------------MLPMLLLLVLCLTLPLLMFFHKHKTN-TNNPPG
CYP93B1   -----------------------------------------MEPQLVAVSVLVSALICYFFFRPYFHRYGKNL-----PPS
CYP93C17  -----------------------------------------MLVEIALALLALALFLQFRPTPTAKSKALRHLPNPPS
CYP93A1   ------------------------------------------MAYQVLLICLVSTIVFAYILWRKQSKKNL-----PPS
CYP705A1  ----------------------------------------MDAIVVDSQNCFIIILLCSFSLISYFVFFKKPK---VNFDLLPS
CYP712A1  ----------------------------------------MDLKLNTKLIILITSLAFPFMLYALFKWFLKEQGSLAATKLPQS
CYP75A1   -----------------------------------------MVLLSELAAATLIFLTTHIFISTLLSI--------TNGRRLPP
CYP75B1   -----------------------------------------MATLFLTILLATVLFLILRIFSHRRNRS--------HNN-RLPP
CYP92A2   ------------------------------------------MEGTNLTTYAAVFLGTLFLLFLSKLLR---------QRKLNLPP
CYP84A1   --------------------------------MESSISQTLSKLSDPTTSLVIVVSLFIFISFITR--------RRRPPYPP
CYP703A2  ------------------------------------------MILVLASLFAVLILNVLLWRWLKASA--------CKAQRLPP
CYP98A3   -----------------------------------------MSWFLIAVATIAAVVSYKLIQRLR------------YKFPP
CYP706A1  -------------------------------METASSNFSLSQILNIEEPYSSVMLGVAALLAVVCYFWIQGKSKS--------KNGPPLPP
CYP81D1   ------------------------------------------MEETNIRVVLYSIFSLIFLIISFKFLKP--------KKQNLPPS
CYP81E6   -------------------------------------------MDIISFLYYSLFYVALFAIIKLFLGS--------RKFKNLPP
CYP81B1   ------------------------------------------MEIPYLLTTTLLLLFTTLYLLLRR--------RSSTLPPT
CYP82A2   -----------------------------------------MELVLNSTTIGVGVVSLILLLYLFLRG----GSWKSGEEGPPT
CYP82B1   ----------------------------------MEKPILLQLQAGILGLLALICFLYYVIKVSLSTRNCNQLVKHPPE
CYP76A2   -----------------------------------------MEWEWSYVFFSAIIILPAFILFFSQKNTT-------KSSYKFPP
CYP76G1   -----------------------------------------MINQLTKNELIGLFTSIAVLIYVTCLFYTK-------RCRTRLPP
CYP76E1   -----------------------------------------MDHQTLLLVITFVSATILIFFLRKSNQT-------QNSTKLPP
CYP76F2   -----------------------------------------MELLSCLLCFLAAWTSIYIMFSARRGRK-------HAAHKLPP
CYP76C1   ----------------------------------MDIISGQALLLLFCFILSCFLIFTTTRSGRIS------RGATALPP
CYP76B1   -------------------------------------MDFLIIVSTLLLSYILIWVLGVGKP----------KNLPP
CYP80A1   -----------------------------------------MDYIVGFVSISLVALLYFLLFKP--------------KHTNLPP
CYP79A1   ---------------------------MATMEVEAAAATVLAAPLLSSSAILKLLLLFVVTLSYLARALRRPRKSTTKCSSTTCASPPAGVGNPPLPP
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CYP79B2    --------------------------------MNTFTSNSSDLTTTATETSSFSTLYLLSTLQAFVAITLVMLLKKLMTDPNK---------KKPYLPP
CYP79D1    ----------------------------MAMNVSTTIGLLNATSFASSSSINTVKILFVTLFISIVSTIVKLQFTKSAANK------EGSKKLPLPP
CYP79E1    ----------------------------MELITILPSVLPN-IHSTATVLFLLLLLTTALSFLFLFKQHLTKLTKFTSKS--------KSTTLPP
CYP79C1    -------------------------------MDYYLNN-VIFSVVVTFSITLNIVFLIKSVVAR---FLGRR--------KKLPP
CYP79F1    ----------------------------------MMSFTTSLPYPFHILLVFILSMASITLLGRILSRPTKTKDRS----------CQLPP
CYP77A6    -----------------------------------MSILSFPHTFFNISPSLFYTILISSLVLLILTRRSAKSKIVKLPP
CYP77B1    -------------------------------------MDLTDVIIFLFALYFINLWWRRYFSAGSSQCSLN-IPP
CYP89A2    --------------------------------------MEIWLLILASLSGSLLLHLLLRRRNSSSPPLPP
CYP27A1    ---------------------MAVLSRMRLRWALLDTRVMGHGLCPQGARAKAAIPAALRDHESTEGPGTGQDRPRLRSLAELP
CYP27B1    -------------------------MTQTLKYASRVFHRVRWAPELGASLGYREYHSARRSLADIP
CYP11A1    ------------------------MLARGLPFRSALVKACPPLLNTGREGWGHHRVGTGEGAGISTRTPRPYSEIP
CYP11B1    -----------------------MAFRLKSDVRLAGSWLCLRGARALGTRAVTASKAS------VLPFEVIP
CYP12A1    -------------------MIKYKQYSRAIVALRQRGAQQYSTNVTNASQPDVKATTTTTISPEWQEAKPFEEMP
CYP12C1    --------------------MLRLTVKHGLRANSQLAATRNPDASSYVQQLES-EWEGAKPFTELP
CYP74A     ----------------------MASISTPFPISLHPKTVRSKPLKFRVLTRPIKASGSETPDLTVATRTGSKDLPIRNIP
CYP74C1    ----------------------------------------------------MASSSPELPLKPIP
CYP74D1    ----------------------------------------------------MSSYSELSNLPIREIP
CYP74B2    -----------------------------------MLLRTMAATSPRPPPSTSLTSQQPPSPPSQLPLRTMP
CYP24A1    --------------------------MSCPIDKRRTLIAFLRRLRDLGQPPRSVTSKASASRAPKEVPLCPLMTDGETRNVTSLP
CYP10      -----------------------------MAIMKKFIHHSLKQLIKPNLTSTKRVVSTSPRKEQGVAAISLEPS
CYP9A1     ---------------------------------MILLLTWLVVIITAVLLYFRSVYSQLSKQGVN
CYP9B1     ----------------------------MSFVEICLVLATIGLLLFKWSTGTFKAFEGRNLY
CYP14A2    -------------------------------MSILIVAFLVSITVYIAYFYWKVSKYPK
CYP21A1    ---------------------------MLLPGLLLLLLLLLAGTRWLWGQWKLWKLRLPL
CYP36A1    ------------------------------MLFAQLVILVIIVMLFLCRFANKLRGLPP
CYP45A1    ----------------------------MITVVLVAVLAVLLTHFLWRRKNHFQLLARNGIP
CYP18A1    -------------------------------MVFLGLLALVTLLQWLVRNYRELRKLPP
CYP707A1   --------------------------------MDISALFLTLFAGSLFLYFLRCLISQRRFGSSKLPLPP
CYP722A1   --------------------------------MEHLCLCLVLCAAMLTLGKFLKIMFQDRKKSTAGVPP
CYP25A1    --------------------------------MALLILTSILILLVSFIIYILFARREQFKLREKIGLT
CYP73A5    --------------------------------MDLLLLEKSLIAVFVAVILATVISKLRGKKLKLPP
CYP78A6    -------------------------MATKLESSLIFALLSKCSVLSQTNLAFSLLAVTIIWLAISLFLWTYPGGPAWGKYLFGR
CYP4A4     -------------------------MSVSALSPTRLPGSLSGLLQVAALLGLLLLLLKAAQLYLHRQWLLRALQQFP
CYP719     ---------------------------MEMNPLLVCATVAIVFATTTIIRILFSSSSLPQMKWPS
CYP44A1    -----------------------------------MRRSIRNLAENVEKCPYSPTSSPNTPPRTFSEIP
CYP302A1   ----------------------------MLTKLLKISCTSRQCTFAKPYQAIPGPR
CYP22A1    ------------------------MHLENRVLSSVLDYASKFYKRMSSLVFFSANSIQVQMNISQSSWIKCRDWMAF
CYP52A1    ---------------------MSSSPSIAQEFLATITPYVEYCQENYTKWYYFIPLVILSLNLISMLHTKYLERKFKA
CYP701A3   ------------------------MAFFSMISILLGFVISSFIFIFFFKKLLSFSRKNMSEVSTLPSVP
CYP315A1   -----------------------MTEKRERPGPLRWLRHLLDQLLVRILSLSLFRSRCDPPPLQRFPATELPPAVAAKYVPIP
CYP39A1    ----------------------------MELISPTVIIILGCLALFLLLQRKNLRRPPC
CYP711A1   --------------------MKTQHQWWEVLDPFLTQHEALIAFLTFAAVVIVIYLYRPSWSVCNVP
CYP46A1    ----------------------------MSPGLLLLGSAVLLAFGLCCTFVHRARSRYEHIPG
CYP43A1    ----------------------------MILLILLPVAIFTYVFLRNFKLYYTLHKCGLNPRFDIF
CYP59A1    ------------------------------MPSFSLLTGHFGALKQTIDGMPP
CYP710A1   ----------------------MVFSVSIFASLAPYLISAFLLFLLVEQLSYLFKKRNIPG
CYP56A1    -------------------------MELLKLLCLILFLTLSYVAFAIIVPPLNFPK
CYP57A1    ----------------------MLVDTGLGLISELQAKLGWAVLLQIVPITIVAYNLLWFIYASFFSSL
CYP53A1    -----------------------MLALLLSPYGAYLGLALLVLYYLLPYLKRAHLRDI
CYP58A1    ----------------------MAVLNWASSRAATLSPCPRTAALVVITTWLLYAIGLAVYRLYFHPL
CYP20A1    ----------------------------MLDFAIFAVTLLALVGAVLYLYPASRQAAGIPG
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CYP38A1    ---------------------------------------------------------------MLDFVIFAITAVAGLIGILLFFYFSRSTETKPVS
CYP54A1    -------------------------------------------------------------MALTQLAHSASALLPLVLPSIAAILAFAIFQRYFAPN
CYP55A1    --------------------------------------------------------------MASGAPSFPFSRASGPEPPAEFAKLRATNP
CYP727A1   --------------------------------------------------MASPCEHHVPYTLLGALLSGGGPHAAACGGAAFLRDYAERGTNALLWAALLAV
consensus                                                                     .   .   .                          .
           1........10........20........30........40........50........60........70........80........90.........
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CYP7A1     ENGLIPYLGCALKFGSN------PLEFLRANQRK--------HGH--------------------VFTCKLMGKYVHFITNSLS---------------
CYP7B1     IKGWLPYLGVVLNLRKD------PLRFMKTLQKQ--------HGD--------------------TFTVLLGGKYITFILDPFQ---------------
CYP8A1     DLGSIPWLGHALEFGKD------AAGFLTRMKEK--------HGD--------------------IFTVLVGGRHVTVLLDPHS---------------
CYP8B1     DKGSIPWLGHAMTFRKN------MLEFLKHMRSK--------HGD--------------------VFTVQLGGQYFTFVMDPVS---------------
CYP51A1    LQAWPPFIGSLIRFMKG------PIVLLREEYPK--------LGS--------------------VFTVKLLHKNITFLIGPEV---------------
CYP51A2    LKAWPPLVGSLIKFLKG------PIIMLREEYPK--------LGS--------------------VFTVNLVHKKITFLIGPEV---------------
CYP26A1    GTMGFPFFGETLQMVLQ------RRKFLQMKRRK--------YGF--------------------IYKTHLFGRPTVRVMGADN---------------
CYP26C1    GSMGWPFFGETLHWLVQ------GSRFHSSRRER--------YGT--------------------VFKTHLLGRPVIRVSGAEN---------------
CYP716A1   GNTGLPLIGESFSFLSAGRQG-HPEKFITDRVRR-------FSSSS-----------------SCVFKTHLFGSPTAVVTGASG---------------
CYP725A1   GKLGFPLIGETIQLLRTLRSE-TPQKFFDDRLKK-------FGP--------------------VYMTSLIGHPTVVLCGPAG---------------
CYP718     GEMGLPWIGETMDFYKAQKSNRVFEDFVNPRIIK-------HGN--------------------IFKTRIMGSPTIVVNGAEA---------------
CYP90A1    GSLGLPLIGETFQLIGAYKTE-NPEPFIDERVAR-------YG--------------------SVFMTHLFGEPTIFSADPET---------------
CYP90B1    GKSGWPFLGETIGYLKPYTAT-TLGDFMQQHVSK-------YG--------------------KIYRSNLFGEPTIVSADAGL---------------
CYP724A1   GSMGWPFIGETISFFKPHRSD-SIGTFLQQRVSR-------YG--------------------KVFKSNICGGKAVVSCDQEL---------------
CYP720A1   GSRGWPLIGDTFAWLNAVAGS-HPSSFVEKQIKK-------YG--------------------RIFSCSLFGKWAVVSADPDF---------------
CYP85A1    GTMGWPIFGETTEFLKQGP------NFMRNQRLR-------YG--------------------SFFKSHLLGCPTLISMDSEV---------------
CYP87A2    GSMGFPLLGESIQFFKPNKTS-DIPPFIKERVKK-------YG--------------------PIFKTNLVGRPVIVSTDADL---------------
CYP708A1   GSMGFPVIGETVEFFKPYSFN-EIHPFVKKRMFK-------HGG--------------------SLFRTNILGSKTIVSTDPEV---------------
CYP702A1   GSMGFPIIGETFEFMKPHDAF-QFPTFIKERIIR-------YG--------------------PIFRTSLFGAKVIISTDIEL---------------
CYP88A3    GDLGWPFIGNMLSFLRAFKTS-DPDSFTRTLIKR-------YGP-------------------KGIYKAHMFGNPSIIVTTSDT---------------
CYP88B1    GYMGLPYFCNTLSYFKASMCG-DPKSFIDFFATR-------FGE--------------------GGMYRAYIFGKPTIMVTKPEI---------------
CYP3A1     GPKPLPFFGTVLNYYMGLW-----------KFDVECHKKYG----------------KIWGLFDGQMPLFAITDTEM---------------
CYP5A1     HPKPSPFIGNLTFFRQGFW-----------ESHMELRKQYG----------------PLSGYYLGRRMIVVISDPDM---------------
CYP6A2     HDAPHPLYGNMVG-FRKNR--------------VMHDFFYDYYNKYRKSG----------FPFVGFYFLHKPAAFIVDTQL---------------
CYP6B4     GPEPTVFFGNIMESVIRRK--------------HLIMIYKDIYEAFPKE----------KVVGIYRMTTPCLLLRDLDV---------------
CYP28A1    GPKPHCFTGNYPHMYNMKR--------------HSVYDLNDIYSEYEHK----------FDAVGIYGARSPQLLVISPQV---------------
CYP28C1    EPRALPLFGSFPNMIWPRQ--------------HFTMDMRDIYMHYRNT----------HSYVGCYLLRAPKLLVLEPRL---------------
CYP13A2    GPRGRPFVGVLDVLLEHET--------------PGLIKLGEWTKKYGKV---------------YGYTDGTQRTLVVADPAM---------------
CYP13B1    GPEGLPFIGNYYDLADVNK--------------PRGYLIHKWTQKFGKV-------------FGYYEGAVPVLVVSDMDM---------------
CYP72A8    GTPFTFLVGDIKREASMVEQEKSRPIN------LTDDYTHRVMPLIQQTVKDH---------GKTSYMWMGPIASVIVTKPEH---------------
CYP72B1    GPPYHFFIGNVKELVGMMLKASSHPMP------FSHNILPRVLSFYHHWRKIY---------GATFLVWFGPTFRLTVADPDL---------------
CYP721A1   GPSYRIFSCNSGEVSRLTAEAKSKPIPSGR---NPHEFVHRVAPHYHEWSRVY---------GKTFLYWFGSKPVVATSDPRL---------------
CYP709A1   GPKPRPLTGNILEISAMVSQSASKDCDS-----IHHDIVGRLLPHYVAWSKQY---------GKRFIVWNGTDPRLCLTETEL---------------
CYP709B1   GPNYRIFYGNLSEIKKMKRESHLSILDP-----SSNDIFPRILPHYQKWMSQY---------GETFLYWNGTEPRICISDPEL---------------
CYP715A1   GPAPSFPFGNLNDMKKLKMASVVVDNSKSST-IINHDIHSIALPHFARWQQEY---------GKVFVYWLGIEPFVYVADPEF---------------
CYP714A1   GPPPSLFRGNVPEMQKIQSQIMSNSKHYSGDNIIAHDYTSSLFPYLDHWRKQY---------GRVYTYSTGVKQHLYMNHPEL---------------
CYP4C3     GPAAMPFLGNAIEM-NVDHDEL-------------FNRVIGMQKLWGTRIG--------------INRVWQGTAPRVLLFEPET---------------
CYP31A2    QPRSYPIVGHGLIT-KPDPEGF-------------MNQVIGMGYLYPDPR--------------MCLLWIGPFPCLMLYSADL---------------
CYP37A1    GPLALPLLGTTFQF-KMDPVEF-------------ALQLYNWGLEYSTKGS-----------SLAAFWMGPYPMVIVLTPEANKVQTRNMSGAQNFHI
CYP37B1    GPYSFPIIGTLYMVNIFDISKF-------------TTQSMELAQYYCQKGC-----------GTIGLWLGPVPLIAVINPQH---------------
CYP32A1    GPPALPLVGSAHLF-KWNPYAF-------------TFQMEGWAQKYLFGRAKYGEIAAPNNEVDGIMLLWIGPVPIVFLGTSEC---------------
CYP29A2    GPPAHPIFGNLGPIVGKKTEDL-------------PSVFINWAAEQRDQGHS-----------VMRVMILGKVYAWPLNGKAA---------------
CYP86A1    VLPFVGSLP-YLIANRSRIHDW-------------IADNLRATGGTYQTCTM-----------VIPFVAKAQGFYTVTCHPKN---------------
CYP86B1    VWPFLGMLPSLAFGLRGNIYEW-------------LSDVLCLQNGTFQFR-------------GPWFSSLN--STITCDPRN---------------
CYP96A1    NWPFLGMLPGLLVEIP-RVYDF-------------VTELLEASNLTYPFKG-------------PCFGGLD--MLITVDPAN---------------
CYP96C1    DWALVGILSVWFPSLG-HIYEK-------------LAKSLAKNDKTFVLKG------------SFLSKQD--VIFTCDPAN---------------
CYP94A1    NIITLPKSYPLIGSYLSFRKNL-------------HRRIQWLSDIVQISPSA----------TFQLDGTLGKRQIITGNPST---------------
CYP94B1    -----PTSYQLIGSILSFNKNR-------------HRLLQWYTDLLRLSPSQ----------TITVDLLFGRRTIITANPEN---------------
CYP704A1   -----KRYTPVHATIFDLFFHS-------------HKLYDYETEIARTKPTF----------RFLSPGQS---EIFTADPRN---------------
CYP704B1   -----PKTWPLVGAAIEQLTNF-------------DRMHDWLVEYLYNSRTV----------VVPMPFTT---YTYIADPIN---------------
CYP97A3    DWTGSDQDYPKVPEAKGSIQAV-------------RNEAFFIPLYELFLTYG----------GIFRLTFGPKSFLIVSDPSI---------------
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CYP97B3    NFLSGG-SLGSMPTAEGSVSDL-------------FGKPLFLSLYDWFLEHG-----------GIYKLAFGPKAFVVISDPII----------------
CYP1A1     GLKNPPGPWGWPLIGHMLTLGKNPHLALSRMSQQYGDVLQIRIGSTP--------------VVVLSGL--DTIRQALVRQGDD----------------
CYP1B1     PWSSPPGPFPWPLIGNAASVGRASHLYFARLARRYGDVFQIRLGSCP--------------VVVLNGE--SAIHQALVQQGGV----------------
CYP17A1    SLPSLPVVGSLPFLPKSGHM----HVNFFKLQKKYGSIYSFRLGSTT--------------TVVIGHH--QLARELLIKKGKE----------------
CYP19A1    SLPSLPLVGSLPFLPRRGQQ----HKNFFKLQEKYGPIYSFRLGSKT--------------TVMIGHH--QLAREVLLKKGKE----------------
CYP2A7     GPTPLPFIGNYLQLNTE-----HICDSIMKFSECYGPVFTIHLGPRR--------------VVVLCGH--DAVREALVDQAEE----------------
CYP2M1     GPAPIPLLGNLLRMDVK-----APYKLYMELSKKYGSVFTVWLGSKP--------------VVVISGY--QAIKDAFVTQGEE----------------
CYP33A1    GPIPLPIIGNMIELFSY----PPPTAAYDAWTKKFGKIYTVWMGTD--------------PAVIITGY--KELKDTFVNDGHS----------------
CYP33C1    GPCPLPVFGNLLSIANP----PPGYKAFERWTKKYGDVYTFWIGNT--------------PHIMINTW--DKIKETFIRDADT----------------
CYP33B1    GPTPIPIFGNLFQLSGSE---APGISIFQKWKDQYGPIFTFYMGIATIEKKNDYKKFSGPVPFVVLTDY--QDIKETVIKDGDT----------------
CYP23A1    GPVPWLVAGNMPSFINV----NNVDVLFQSWKQQYGGIFTVWIGPIP--------------LVMVSDL--PTIKKYFIQHADS----------------
CYP35A1    GP-------------------------KYGNIFTLWVGPVP--------------HVSICDY--ETSHEVFVKGANK----------------
CYP35B1    GPVSLPLIGNIHQLVYHIWNEKGVVPAFDLFRKKYGDVFTIWLGPIP--------------HVSICNY--ETSQEVFVKNGNK----------------
CYP34A1    GPYPLPLIGNLHQLLYYCWKNGGLVEGYAEIQKSFGKVYTLWIGPLP--------------TVFIADF--EVAHETHVKRAHE----------------
CYP71A12   P-WRLPLIGNLHQLSLHP----HRSLHSLSLRYGP--LMLLHFGR--------------VPILVVSS--GEAAQEVLKTHDLK----------------
CYP71C1    PPGKLPIIGHLHLIGSHP----HVSFRDLHAKYGHNGLMLVQVGA--------------VPTIVVST--PQAAEAVLRTHDHV----------------
CYP71D11   P-WKLPIIGSIPHLVGS---PPHRKLRDLAKKYGP--LMHLQLGE--------------VIFIIVSS--AEYAKEVMKTHDVT----------------
CYP726A1   P-WKFPIIGNLPHLLLTS-DLGHERFRALAQIYGP--VMSLQIGQ--------------VSAVVISS--AEAAKEVMKTQADA----------------
CYP71K1    P-WALPVIGHLHHVAGA---LPHRAMRDLARRHGP--LMLLRLCE--------------LRVVVACT--AEAAREVTKTHDLA----------------
CYP99A1    P-WRLPLIGNLLHLATS---QPHVALRDLAMKHGP--VMYLRLGQ--------------VDAVVISS--PAAAQEVLRDKDTT----------------
CYP71E1    P-AQLPILGNLHLLG-PL---PHKNLERLARRYGP--VMQLRLGT--------------VPTVVSS--AEAAREVLKVHDVD----------------
CYP71N1    P-PKLPVIGHLHLLGSSL---LHRSLWELSKKHGP--LMHLKFGR--------------VPVVVSS--PEMAKEVLKTHDLE----------------
CYP71B2    P-SSLPIIGNLHHLA-GL---PHRCFHKLSIKYGP--LVFLRLGS--------------VPVVVSS--SEAAEAVLKTNDLE----------------
CYP83A1    P-SPLPVIGNLLQLQKLN---PQRFFAGWAKKYGP--ILSYRIGS--------------RTMVVISS--AELAKEVLLKTQDVN----------------
CYP83B1    P-KGLPIIGNLHQMEKFN---PQHFLFRLSKLYGP--IFTMKIGG--------------RRLAVISS--AELAKELLKTQDLN----------------
CYP83E1    P-KGLPIIGNLLQLDISN---LHLQFSQFSKIYGP--LFSLQLGL--------------RPAIVVSS--AEIAKEVFKNNDHV----------------
CYP93B1    PFFRLPIIG--HMHMLG--PLLHQSFHNLSHRYGP--LFSLNFGS--------------VLCVVAST--PHFAKQLLQTNELA----------------
CYP93C17   PKPRLPFVG--HLHLLDQ-PLLHNSLIKLGEKYGP--LYTLYFGS--------------MPTVVAST--PELFKLFLQTHEATS----------------
CYP93A1    PK-ALPIIG--HLHLVS--PIPHQDFYKLSTRHGP--IMQLFLGS--------------VPCVVAST--AEAAKEFLKTHEINF----------------
CYP705A1   PP-SLPIIG--HLHLLLS-TLIHKSLQKLSSKYGP--LLHLRIFN--------------IPFILVSS--DSLAYEIFRDHDVN----------------
CYP712A1   PP-ALPFIG--HLHLIG--KVLPVSFQSLAHKYGP--LMEIRLGA--------------SKCVVVSS--SSVAREIFKEQELN----------------
CYP75A1    GPRGWPVIGALPLLGA----MPHVSLAKMAKK--YGAIMYLKVGT--------------CGMVVAST--PDAAKAFLKTLDLN----------------
CYP75B1    GPNPWPIIGNLPHMGT----KPHRTLSAMVTT--YGPILHLRLGF--------------VDVVVAAS--KSVAEQFLKIHDAN----------------
CYP92A2    GPKPWPIIGNLNLIGN----LPYRSIHELSLK--YGPVMQLQFGS--------------FPVVVGSS--VEMAKIFLKSMDIN----------------
CYP84A1    GPRGWPIIGNMLMMDQ----LTHRGLANLAKK--YGGLCHLRMGF--------------LHMYAVSS--PEVARQVLQVQDSV----------------
CYP703A2   GPPRLPILGNLLQLGP----LPHRDLASLCDK--YGPLVYLRLGN--------------VDAITTND--PDTIREILLRQDDV----------------
CYP98A3    GPSPKPIVGNLYDIKP----VRFRCYYEWAQS--YGPIISVWIGS--------------ILNVVSS--AELAKEVLKEHQK----------------
CYP706A1   GPWPLPIVGNLPFLNSD---VLHTQFQALTLK--HGPLMKIHLGS--------------KLAIVVSS--PDMAREVLKTHDIT----------------
CYP81D1    PPGWLPIIGHLRLLKPPI-HRTLRSFSETLDHNDGGGVMSLRLGS--------------RLVYVVSSH-KVAAEECFGKNDVV----------------
CYP81E6    GPTSLPIIGNLHHLKRPL-HRTFRALSEKY-----GDVFSLWFGN--------------RLVVVSS--FADVQECFTKNDVV----------------
CYP81B1    IFPSLPIIGHLYLLKPPL-YRTLAKLSAKH-----GQILRLQLGF--------------RRVLIVSS--PSAAEECFTKNDIV----------------
CYP82A2    VAGAWPIIGHLPLLLGS--KTPHKTLGDLADK--YGPIFSIKIGA--------------KNAVVVSN--WEMAKECYTTNDIA----------------
CYP82B1    AAGSWPIIGHLPQLVGSG-KPLFRVLGDMADK--FGPIFMWRFGV--------------YPTLVVST--WEMAKECFTSNDKF----------------
CYP76A2    GPPGLPIFGNMFELG----TEPYKKMAVLRQK--YGPVLWLKLGS--------------TYTMVVQT--AQASEELFKNHDIS----------------
CYP76G1    GPNPWPVIGNIFQLAG----LPPHDSLTKLSRR--HGPIMTLRIGS--------------MLTVVISS--SEVAREIFKKHDAA----------------
CYP76E1    GPYPLPIIGNILELG----KNPHKALTKLSKI--YGPIMTLKLGS--------------ITTIVISS--PQVAKQVLHDNSQI----------------
CYP76F2    GPVPLPIIGSLLNLG----NRPHESLANLAKT--YGPIMTLKLGY--------------VTTIVISS--APMAKEVLQKQDLS----------------
CYP76C1    GPPRLPIIGNIHLVG----KHPHRSFAELSKT--YGPVMSLKLGS--------------LNTVVIAS--PEAAREVLRTHDQI----------------
CYP76B1    GPTRLPIIGNLHLLG----ALPHQSLAKLAKI--HGPIMSLQLGQ--------------ITTLVISS--ATAAEEVLKKQDLA----------------
CYP80A1    SPPAWPIVGHLPDLISKNSPPFLDYMSNIAQK--YGPLIHLKFGL--------------HSSIFAST--KEAAMEVLQTNDKV----------------
CYP79A1    GPVPWPVVGNLPEMLLNK---PAFRWIHQMMREMGTDIACVKLGG--------------VHVVSITCP--EIAREVLRKQDAN----------------
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CYP79B2    GPTGWPIIGMIPTMLKSR---PVFRWLHSIMKQLNTEIACVKLGN---------------THVITVTCP--KIAREILKQQDAL----------------
CYP79D1    GPTPWPLIGNIPEMIRYR---PTFRWIHQLMKDMNTDICLIRFGRTF------------TNFVPISCP--VLAREILKKNDAI----------------
CYP79E1    GPRPWPIVGSLVSMYMNR---PSFRWILAQMEGR--RIGCIRLGG------------VHVVPVNCPFTEIAREFLKVHDAD----------------
CYP79C1    CPRGFPIIGNLVGMLKNR---PTSKWIVRVMNDMKTDIACFRFGR------------VHVIVITSD--VIAREVVREKDAV----------------
CYP79F1    GPPGWPILGNLPELFMTR---PRSKYFRLAMKELKTDIACFNFAG------------IRAITINSD--EIAREAFRERDAD----------------
CYP77A6    GPPGWPVVGNLFQFARSG---KQFYEYVDDVRKKYGPIYTLRMGS------------RTMIIISD--SALVHDVLIQRGPMF----------------
CYP77B1    GPKGWPLVGNLLQVIFQR---RHFVFLMRDLRKKYGPIFTMQMGQ------------RTMIIITD--EKLIHEALVQRGPTF----------------
CYP89A2    DPNFLPFLGTLQWLREGL---GGLESYLRSVHHRLGPIVTLRITS------------RPAIFVAD--RSLTHEALVLNGAVY----------------
CYP27A1    GPGTLR--FLFQLFLRGYVLHLHELQALNKAKYGPMWTTT--FGTRT-------------NVNLASAPLLEQVMRQEGKYP----------------
CYP27B1    GPSTPS--FLAELFCKGGLSRLHELQVQGAAHFGPVWLAS--FGTVR-------------TVYVAAPALVEELLRQEGPRP----------------
CYP11A1    SPGDNGWINLYHFWRKKGSQRIHFHHIENFQKYGPIYREK--LGNLE-------------SVYIIHPEGVAHLFKFEGSYP----------------
CYP11B1    QHQGNKRQRVLQFWKEQNHDDLHLEMHQTFQELGPIFRCD--VGSTR-------------IVAVMLPEDCARLHQAESPYP----------------
CYP12A1    SMNSWPIIKNMLPWGKYGKMEPTQFLMALRDDMGPIVRTAAFMGRPP-------------TVITHNPHDFEMVFRNEGIWP----------------
CYP12C1    GPTRWQLFRGFQKGGEYHQLGMDDVMRLYKKQFGDICLIPGLFGMPS-------------TVFTFNVETFEKVYRTEGQWP----------------
CYP74A     GNYGLPIVGPIKDRWDYFYDQGAEEFFKSRIRKYNSTVYRVNMPPGA--------------FIAENPQVVALLDGK----------------
CYP74C1    GGYGFPFLGPIKDRYDYFYFQGRDEFFRSRITKYNSTVFHANMPPGP--------------FISSDSRVVVLLDAL----------------
CYP74D1    GDYGFPIISAIKDRYDYFYNQGEDAWFHNKAEKYKSTVVKINMAPGP--------------FTSNDYKLVAFLDAN----------------
CYP74B2    GSYGWPLVGPLSDRLD---FQGPDKFFRTRAEKYKSTVFRTNIPPTFP--------------FFGNVNPNIVAVLDVK----------------
CYP24A1    GPTNWPLLGSLLEIFWKG-GLKKQHDTLAEYHKKYGQIFRMKLGSFDS-------------VHLGSPSLLEALYRTESAHP----------------
CYP10      EMAQCPFRKSIDTFTETTNAVKAPGMTEVQPFERIPGPKGLPIVGTLFDYFKK-------DGPKFSKMFEVYRQRALEFGNIYYEKVGHFHCVVISSPG
CYP9A1     HLPTIPVFGNLMWMVMKQEHFVDTLGRCVKAFPDD-------------------------KIVGHYDMVSPILVVLDVDT----------------
CYP9B1     FEKPYPFLGNMAASALQKASFQKQISEFYNRTRHHKLVGLFNLRTP---------------MIQINDPQLIKKICVKDFDH----------------
CYP14A2    GPFPLPFIGNILQIPSEN-----IQEYLDDLSKTYGPCFTLWTPLP---------------AIVLTDYEHVKEAFVTQGDA----------------
CYP21A1    APGFLHFLQPNLPVYLFG-----------------LAQKLGP-------------------IYRIRLGLQDVVVLNSNKT----------------
CYP36A1    GPTPWPFIGNTFQVPEDR-----IDLIINEFKKKYGGIFTLWLPFP--------------TIVICDYDMLKRNIVKNGES----------------
CYP45A1    TPKYHWLLGHMEQTFYSPGKRSVVEVKHEWLQLYG----------------------KVCGFYSGAIPRVLVADLDM----------------
CYP18A1    GPWGLPVIGYLLFMGSEK------HTRFMELAKQYGSLFSTRLGS---------------QLTVVMSDYKMIRECFRREEFT----------------
CYP707A1   GTMGWPYVCETFQLYSQDPNVFFQSKQKRYG-----------------------------SVFKTHVLGCPCVMISSPEA----------------
CYP722A1   GSDGFPVIGETLQFMLSVNSGKGFYEFVRSRRIRYGSCFRTSLFG--------------ETHVFLSTTES----------------------
CYP25A1    GPEPHWFMGNLKQIVDRKEKLGYDDSNKWFNELHKQYGETFGIYFG-------------AQMNIVLSNEEDIKEVFIKNFSN----------------
CYP73A5    GPIPIPIFGNWLQVGDDLN-----HRNLVDYAKKFGDLFLLRMGQRN---------------LVVVSSPDLTKEVLHTQGVEFG-------------
CYP78A6    LISGSYKTGNVIPGPKGFPLVGSMSLMSSTLAHRRIADAAEKFGAKR----------------LMAFSLGETRVIVTCNPDVAK-------------E
CYP4A4     CPPFHWLLGHSREFQNDQELERIQKWVEKFPG-----------------------------ACPWWLSGNKARLLVYDPDY----------------
CYP719     GPRKLPIIGNLHQLGDDVLHVALAKLAKVHGSVMTIWIGSWR--------------------PVIVISDIEKAWEVLVNKSAD----------------
CYP44A1    GPREIPVIGNIGYFKYAVKSDAKTIENYNQHLEEMYKKYGKIVKENLGFG----------RKYVVHIFDPADVQTVLAADGKTP--------------
CYP302A1   GPFGMGNLYNYLPGIGSYSWLRLHQAGQDKYEKYGAIVRETIVPGQD---------------IVWLYDPKDIALLLNERDCP----------------
CYP22A1    ALSHHIIMGIYLLILRNFLPQVVPDFEWQHYFMRVFIVHIIYIIISYFIRITRYP-----PGPPPMAVFGNSPFVNILTPEQTFLEYREIYGPIFTLHLS
CYP52A1    KPLAVYVQDYTFCLITPLVLIYYKSKGTVMQFACDLWDKNLIVSDPK--------------AKTIGLKILGIPLIETKDPEN----------------
CYP701A3   VVPGFPVIGNLLQLKEKK-----PHKTFTRWSEIYGPIYSIKMGSSS--------------LIVLNSTETAKEAMVTRFSS----------------
CYP315A1   RVKGLPVVGTLVDLIAAGGATHLHKYIDARHKQYGPIFRERLGGTQD--------------AVFVSSANLMRGVFQHEGQYP----------------
CYP39A1    IKGWIPWIGVGFEFGKAPLEFIEKARIKYG----------------------------PIFTVFAMGNRMTFVTEEEG----------------
CYP711A1   GPTAMPLVGHLPLMAKYG------PDVFSVLAKQYGPIFRFQMGRQP--------------LIIIAEAELCREVGIKKFKD----------------
CYP46A1    PPRPSFLLGHLPCFWKKDEVGGRVLQDVFLDWAKKYGPVVRVNVFHKT--------------SVIVTSPESVKKFLMSTKYNK--------------
CYP43A1    GIKGLLWLDSSAAHENFTRMCSMIGDQTFSVLRG---------------------------ATPVVITSNVDLIHAISTEH----------------
CYP59A1    NATLHSIMLKLSQKFRSG-----------------------------------------MFYINMWPFSGTWLVVATPSG-----------AA
CYP710A1   PFFVPPIIGNAVALVRDPTSFWDKQSSTANISG----------------------------LSANYLIGKFIVYIRDTELS-----------HQ
CYP56A1    NIPTIPFYVVFLPVIFPIDQTELYDLYIRESMEKYGAVKFFFGSRWN--------------ILVSRSEYLAQIFKDEDTFAK----------------
CYP57A1    RKIPGPFLARISRVWEMKKTATGNIHEIMMDLHRRHGAIVRIGPR--------------RYDFDTMEALKIIYRIG----------------
CYP53A1    PAPGLAAFTNFWLLLQTRRGHRFVVVDNAHKKYGKLVRIAPRHTS--------------IADDGAIQAVYGHG----------------
CYP58A1    ARFPGRKMAAVTTWYEFYYDFWYGGKYIFEIEKMHKEFGPIVRIN---------------PHELSIHDPEYYNELYVGSSKR----------------
CYP20A1    ITPTEEKDGNLPDIVNSG----SLHEFLVNLHERYGPVVSFWFGR--------------------RLVVSLGTVDVLKQHINP----------------
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CYP38A1     SASPTSTIPRWSAPPADIEKGDLDVMMKKHGSLHQFLLHLHDNGKTP-----------------VTSFWWGKTHVVSFCSPQAFK--------------
CYP54A1     PLSNLPIVGEEYHGYEKKRQAYLTKAKDLYLEGYTKFKHG----------------------LFRIVTPNRNSVIVVSPRF---------------
CYP55A1     VSQVKLFDGSLAWLVTKH--------------------------------------------KDVCFVATSEKLSKVRTRQG--------------
CYP727A1    TWLLVLRLAALLRLWALGARLPGPPAFPADPGLAAGDITGYLSKLHG-------------SYGPVVRLWLGPSQLLVSVKDSR--------------V
consensus   .    .... . .                        .   .              .        ..
            101......110......120.......130.......140.......150.......160.......170.......180.......190........
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CYP7A1     -YHKVLCHG-KYFDWKKFHYT-----TSAKAFGHRSIDPNDCNTTENINNTFTKTLQGDALHSLSEAMMQNLQFVLRPPD-------------LPK----
CYP7B1     -YQLVIKNH-KQLSFRVFSNK-----LLEKAFSISQLQKN--HDMNDELHLCYQFLQGKSLDILLESMMQNLKQVFEP---------------QL----
CYP8A1     -YDAVVWEPRSRLDFHAYAVF-----LMERIFDVQLPHYN----PGDEKSKMKPTLLHKELQALTDAMYTNLRTVLLG-------------DTV----
CYP8B1     -FGPILKDGQRKLDFVEYAKG-----LVLKVFGYQSIEGD----HRMIHLASTKHLMGHGLEELNKAMLDSLSLVMLGPE-------------GRS----
CYP51A1    -SSHFFNAYESELSQKEIYKF-----NVP-TFGPGVVFDVDYPVRMEQFRFFSSALKGQQLRGYVDQMTKETEDYFSK-------------------
CYP51A2    -SAHFFKASESDLSQQEVYQF-----NVP-TFGPGVVFDVDYSVRQEQFRFFTEALRVNKLKGYVDMMVTEAEDYFSK-------------------
CYP26A1    -VRRILLGEHRLVSVHWPASV-----RTILGAGCLSNLHD--SSHKQRKKVIMQAFSREALQCYVLVIAEEVSSCLEQ----------------------
CYP26C1    -VRTILLGEHRLVRSQWPQSA-----HILLGSHTLLGAVG--EPHRRRRKVLARVFSRAALERYVPRLQGALRHEVRS----------------------
CYP716A1   -NKFLFTNENKLVVSWWPDSV-----NKIFP-SSMQTSSK--EEARKLRMLLSQFMKPEALRRYVGVMDEIAQRHFET--------------------
CYP725A1   -NKLVLSNEDKLVEMEGPKSF-----MKLIGEDSIVAKRG--EDHRILRTALARFLGAQALQNYLGRMSSEIGHHFNE--------------------
CYP718     -NRLILSNEFSLVVSSWPSSS-----VQLMGMNCIMAKQG--EKHRVLRGIVANSLSYIGLESLIPKLCDTVKFHHET--------------------
CYP90A1    -NRFVLQNEGKLFECSYPASI-----CNLLGKHSLLLMKG--SLHKRMHSLTMSFANSSIIKDHLMLDIDRLVRFNLD--------------------
CYP90B1    -NRFILQNEGRLFECSYPRSI-----GGILGKWSMLVLVG--DMHRDMRSISLNFLSHARLRTILLKDVERHTLFVLD--------------------
CYP724A1   -NMFILQNEGKLFTSDYPKAM-----HDILGKYSLLLATG--EIHRKLKNVIISFINLTKSKPDFLHCAENLSISILK--------------------
CYP720A1   -NRFIMQNEGKLFQSSYPKSF-----RDLVGKDGVITVHG--DQQRRLHSIASSMMRHDQLKTHFLEVIPVVMLQTLS--------------------
CYP85A1    -NRYILKNESKGLVPGYPQSM-----LDILGTCNMAAVHG--SSHRLMRGSLLSLISSTMMRDHILPKVDHFMRSYLD--------------------
CYP87A2    -SYFVFNQEGRCFQSWYPDTF-----THIFGKKNVGSLHG--FMYKYLKNMVLTLFGHDGLKK-MLPQVEMTANKRLE--------------------
CYP708A1   -NFEILKQENRCFIMSYPEAL-----VRIFGKDNLFFKQGK-DFHRYMRHIALQLLGPECLKQRFIQQIDIATSEHLK--------------------
CYP702A1   -NMEIAKTN---HAPGLTKSI-----AQLFGENNLFFQSK--ESHKHVRNLTFQLLGSQGLKLSVMQDIDLLTRTHME--------------------
CYP88A3    -CRRVLTDDDA-FKPGWPTST-----MELIGRKSFVGISF--EEHKRLRRLTAAPVNGHEALSTYIPYIEENVITVLD--------------------
CYP88B1    -IRKVLMDEEY-LERGLPNYM-----KKLIG----LTTSI--EEDKYFRRLTAP-VKSHGLLSDYFDYIDKTVSSTLE--------------------
CYP3A1     IKNVLVKECFSVFTNRRDFGPV-------GIMGKAISVS-KDEEWKRYRALLSPTFTSGRLKEMFPVIEQYGDILVKYLR--QEKGKP-----------
CYP5A1     IKQVLAEKFSNFTNRMATGLES-------KPVADSILFL-RDKRWEEVRSVLTSAFSPKKLNKLTPLISQACDLLLAHLERYAESGDA-----------
CYP6A2     AKNILIKDFSNFADRGQFHNG-----RDDPLTQHLFNL-DCKKWKDMRQRLTPTFTSGKMKFMFPTVIKVSEEFVKVITEQVPAAQNGAV---------
CYP6B4     IKHVMIKDFDLFNDRGVEFS--------EEGLGLNIFHA-DGDRWRVLRQCFTPLFTSGKLKNMLNLMSDRGDKFIKMVEKFCDKEPE----------
CYP28A1    ARRVFVSDFRHFHDNEISLMVD---EKSDFIMANNPFSQ-IGDEWKQRRADITPGLTMGRIKTVYPVTQEVCQKMTDWLRKQIRLPPSGG---------
CYP28C1    VYEIYVSAFSHFENNDASKMVD---IAKDRLVALNPFVL-EGEEWRHQRAVFSTLLTNGRIRTTHAIMQRVCLDLCQFI--AIKSAGGKD---------
CYP13A2    VHEIFVKQFDNFYGRK-LNPIQGNPEK---EQRVHLLAA-QGYRWKRLRTISSQSFSNASLKKMKRTVEDS---ALELLRHIEKQTAGGEQ---------
CYP13B1    LQELFLKKFDNFYARKSTNHIHGNLECSKSEPRINLFTS-RGARWKRLRALASPGFSVKALKQVHDVMEDS---AINMVDLMAKHEDG-KP---------
CYP72A8    IKDVLNRVYD---FPKPPVHPI-----VELFAT-GVALY-EGEKWSKHRKIINPSFHLEKLKIMIPAFYESCSEMISKWEKLVTE---QGSS-------
CYP72B1    IREIFSKSEF---YEKNEAHPL-----VKQLEGDGLLSL-KGEKWAHHRKIISPTFHMENLKLLVPVVLKSVTDMVDKWSDKLSE---NGE--------
CYP721A1   IREALTTGGS---FDRIGHNPL-----SKLLYAQGLPGL-RGDQWAFHRRIAKQAFTMEKLKRWVPQMVTSTMMLMEKWEDMRN----GGEE-------
CYP709A1   IKELLMKHNG-VSGRSWLQQQG-----TKNFIGRGLLMA-NGQDWHHQRHLAAPAFTGERLKGYARHMVECTSKLVERLRKEVGEGANEV---------
CYP709B1   AKTMLSNKLG-FFVKSKARPEA-----VKLVGSKGLVFI-EGADWVRHRRILNPAFSIDRLKIMTTVMVDCTLKMLEEWRKESTKEETEHPK-------
CYP715A1   LSVMSKGVLGKSWGKPNVFKKD-----REPMFGTGLVMV-EGDDWTRHRHIITPAFAPLNLKVMTNMMVESVSNMLDRWGIQINSGNPEF---------
CYP714A1   VKELNQANTLN-LGKVSYVTKR-----LKSILGRGVITS-NGPHWAHQRRIIAPEFFLDKVKGMVGLVVESAMPMLSKWEEMMKRE--GEMV-------
CYP4C3     VEPILNS--QKFVNKSHDYDYL------HPWLGEGLLTS-TDRKWHSRRKILTPAFHFKILDDFIDVFNEQSAVLARKLAVEVG---SE----------
CYP31A2    VEPIFSS--TKHLNKGFAYVLL------EPWLGISILTS-QKEQWRPKRKLLTPTFHYDILKDFLPIFNEQSKILVQKLCCLGA---DE----------
CYP37A1    FQKVLES--NALINKSSEYDIF------LPWLGTGLLLA-SGEKWRGRRKMMTPSFHFNVLIDFQVVFNSQSMILLEQIENAAKKTDDS----------
CYP37B1    AKEILES--NEVITKAEEYDIL------FPWLGTGLLTS-TCSKWRQRRKMLTPAFHFKVLNDFLSVHDYQAKVFLEQIKPYADSGKE-----------
CYP32A1    IRPVLES--NTNISKPSQYDKM------SEWIGTGLLTS-THEKWFHRRKMLTPTFHFTIIQDYFPVFVRNAEVLADAVELHVD---GD----------
CYP29A2    -AAIIDS--TTETNKGDDYRFF------DPWLGGGLLLEGYCERWKSHRKMLTPAFHFAKLGGYFEVFNNESKILIDLLSDFSAS--GE----------
CYP86A1    VEHILKTRFDNYPKGPMWRAAF------HDLLGQGIFNS-DGDTWLMQRKTAALEFTTRTLRQAMARWVNGTIKNRLWLILDRAVQNNK----------
CYP86B1    VEHLLKNRFSVFPKGSYFRDNL------RDLLGDGIFNA-DDETWQRQRKTASIEFHSAKFRQLTTQSLFELVHKRLLPVLETSVKSSS----------
CYP96A1    IHHIMSSNFANYPKGTEFKK-I------FDVLGDGIFNA-DSELWKDLRKSAQSMMTHQDFQRFTLRTIMSKLEKGLVPLLDYVAEKKQ----------
CYP96C1    MHHVMSTNFSNYPKGPENRN-V------FDVYGEMLFTA-DHEKWKSHRKVTNAYFHDQRFNGFSQKVNKEVIEKELFPFLDHAAEEAL----------
CYP94A1    VQHILKNQFSNYQKGTTFTNTL------SDFLGTGIFNT-NGPNWKFQRQVASHEFNTKSIRNFVEHIVDTELTNRLIPILTSSTQTNN----------
CYP94B1    VEHILKTNFYNFPKGKPFTDLL------GDLLGGGIFNS-DCELWSSQRKLASHEFTMRSLREFTFEILREEVQNRLIPVLSSAVDCGE----------
CYP704A1   VEHILKTRFHNYSKGPVGTVNL------ADLLGHGIFAV-DGEKWKQQRKLVSFEFSTRVLRNFSYSVFRTSAS-KLVGFIAEFALSGK----------
CYP704B1   VEYVLKTNFSNYPK---------------VLLGDGIFNS-DGELWRKQRKTASFEFASKNLRDFSTVVFKEYSL-KLFTILSQASFKEQ----------
CYP97A3    AKHILKDNAKAYSKG-ILAEIL------DFVMGKGLIPA-DGEIWRRRRRAIVPALHQKYVAAMIS--LFGEASDRLCQKLDAAALKGE----------
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CYP97B3     ARHVLRENAFSYDKG-VLAEIL------EPIMGKGLIPA-DLDTWKLRRRAITPAFHKLYLEAMVK--VFSDCSEKMILKSEKLIREKETSSGEDT----
CYP1A1      FKGRPDLYTFTLISNG---------------QSMSFSPDSCPVWAARRRLAQNGLKSFSIASDPASSTSCYLEEHVSKEAEVL---------------
CYP1B1      FADRPPFASFRVVSGG---------------RSLAFGHYS-ERWKERRAAYGTMRAFSTR---HPRSRGLLEGHALGEAREL---------------
CYP17A1     FSGRPLTTTVALLSDN---------------GKGIAFADSSATWQLHRRLVLSSFSLFRDG-------EQKLENIICQELSAL---------------
CYP19A1     FSGRPKVATLDILSDN---------------QKGIAFADHCAHWQLHRKLALNAFALFKDG-------NLKLEKIINQEANVL---------------
CYP2A7      FSGRGEQATFEWVFKG-------------------YGVAFSNCERAKQLLRFAIATLRDFGVG-------KRGIEERIQEESGFL---------------
CYP2M1      FSGRANYPVIMTVSKG-------------------YGVLVSSCKRSKDLRRFSLMTLKTFGMG-------RRSIEERVQEEAKML---------------
CYP33A1     YLDKMIYSKLNTSL---------------RGGDYGVIDTNCNTWKEHRKFALHTLRDFGMG-------KEAMEASIQLEVDKI---------------
CYP33C1     YTNKVVLPMVTLS----------------RGGEYGIIDSNCAMWREHRRFALSTMRDFGLG-------KNLMQENILMEVQDV---------------
CYP33B1     YADKYLSPEFNKYFREMQFTKLLFQYCFPNLGGEYGIMDISCDRWKEHRKFAVLQLRELGVG-------KPLMESKILIEAEEL---------------
CYP23A1     FSNRWRNFVTDSIME---------------GSNGIVQIDCNKWREQRRFALHTLRDFGVG-------KPLMEQMITLEVTSL---------------
CYP35A1     YADIAHAPLFRELRQE-----------------MGVLVTNCSHWSTMKRFALHTFRDMGVG-------KDLMETRIMEELDAR---------------
CYP35B1     YKDRFLPPVYLHVSNN-----------------LGLFTANGPVCAEMRKFTLLAFRNMGVG-------RDLMEQRILDELNTRYLWGFELFLVQKKFCR
CYP34A1     FGTRYAPGLMNYNRYE-----------------RGVVASNGEFFQEHSRFVLSTFRNFASG-------RNIMEERIMDEYRYR---------------
CYP71A12    FANRPRSKAVHGLMNGGRD--------------VVFGP-YGEYWRQMKSVCI--LNLLTNKM--VASFEKIREEELNEMIKKLEKASSSS---------
CYP71C1     LASRPRNPVADIIRYNSTD--------------VAFAP-YGVYWRTARKVVN--THLLSAKM--VFSKRREREEEVRLVVARIRDAAEASP-------
CYP71D11    FASRPRSLFTDIVFYGSTD--------------IGFSP-YGDYWRQVRKICN--VELLSMKR--VQSLWPIREEEVKNLIQRIASEEGS---------
CYP726A1    FAQRPIVLDAQIVFYNRKD--------------VLFAS-YGDHWRQMKKIWI--LEFLSAKK--VQSSRLIREEEMEDAITFLRSKAGS---------
CYP71K1     FATRPITPTGKVLMADSVG--------------VVFAP-YGDGWRTLRRICT--LELLSARR--VRSFRAVREEEVGRLLRAVAAAAAVAALTTP----
CYP99A1     FASRPSLLVADIILYGSMD--------------MSFAP-YGGNWRMLRKLCM--SELLNTHK--VRQLAAVRDSETLSLVRKVVYAAGAGGGGRGQR--
CYP71E1     CCSRPASPGPKRLSYDLKN--------------VGFAP-YGEYWREMRKLFA--LELLSMRR--VKAACYAREQEMDRLVADLDRAAAS---------
CYP71N1     CCSRPSLLSFSKFSYGLSD--------------VAFIP-YGERWRQLRKLCT--VELLSTRK--INSFRDIRKEEMERVTKLICSHVRA---------
CYP71B2     CCSRPKTVGSGKLSYGFKD--------------ITFAP-YGEYWREVRKLAV--IELFSSKK--VQSFRYIREEEVDFVVKKVSESALK---------
CYP83A1     FADRPPHRGHEFISYGRRD--------------MALNH-YTPYYREIRKMGM--NHLFSPTR--VATFKHVREEEARRMMDKINKAADK---------
CYP83B1     FTARPLLKGQQTMSYQGRE--------------LGFGQ-YTAYYREMRKMCM--VNLFSPNR--VASFRPVREEECQRMMDKIYKAADQ---------
CYP83E1     FSNRPISYGQNILSYNGSE--------------IVFAP-YGDFWREIRKICA--IHIFSSKR--VSYYSSIRIFEVKKMIKNISVHADS---------
CYP93B1     FNCRIESTAVKKLTYESS---------------LAFAP-YGDYWRFIKKLSM--NELLGSRS--INNFQHLRAQETHQLLRLLSNRARA---------
CYP93C17    FSTRFQTSAIRRLTYDNS---------------VAMVP-FAPYWKFIRKVIM--NDLLNATT--VNKLRPLRSQEIRKVLKAMAQSAES---------
CYP93A1     SNRPGQNVAVKGLAYDSQDFL------------FAFAP-FGPYWKFMKKLCM--SELLSGRM--MDQFLPVRQQETKRFISRVFRKGVA---------
CYP705A1    VSSRGVGAIDESLAYGSSG--------------FIQAP-YGDYWKFMKKLIA--TKLLGPQP--LVRSQDFRSEELERFYKRLFDKAMK---------
CYP712A1    FSSRPEFGSAEYFKYRGSR--------------FVLAQ-YGDYWRFMKKLCM--TKLLAVPQ--LEKFADIREEEKLKLVDSVAKCCRE---------
CYP75A1     FSNRPPNAGATHLAYGAQD--------------MVFAH-YGPRWKLLRKLSN--LHMLGGKA--LENWANVRANELGHMLKSMFDMSRE---------
CYP75B1     FASRPPNSGAKHMAYNYQD--------------LVFAP-YGHRWRLLRKISS--VHLFSAKA--LEDFKHVRQEEVGTLTRELVRVG-----------
CYP92A2     FVGRPKTAAGKYTTYNYSD--------------ITWSP-YGPYWRQARRMCL--TELFSTKC--LDSYEYIRAEELHSLLHNLNKIS-----------
CYP84A1     FSNRPATIAISYLTYDRAD--------------MAFAH-YGPFWRQMRKVCV--MKVFSRKR--AESWASVRDEVDKMVRSVSCNVG-----------
CYP703A2    FSSRPKTLAAVHLAYGCGD--------------VALAP-MGPHWKRMRRICM--EHLLTTKR--LESFTTQRAEEARYLIRDVFKRSET---------
CYP98A3     LADRHRNRSTEAFSRNGQD--------------LIWAD-YGPHYVKVRKVCT--LELFTPKR--LESLRPIREDEVTAMVESVFRDCNLPENR------
CYP706A1    FANHDLPEVGKINTYGGED--------------ILWSP-YGTHWRRLRKLCV--MKMFTTPT--LEASYSTRREETRQTIVHMSEMARE---------
CYP81D1     LANRPQVIIGKHVGYNNAN--------------MIAAP-YGDHWRNLRRLCT--IEIFSTHR--LNCFLYVRTDEVRRLISRLSRLAGTK---------
CYP81E6     LANRPRFLSGKYIFYNYTT--------------LGSTS-YGEHWRNLRRITS--LDVLSNHR--INSFSPIRRDETTRLIRKLAEDSAKN---------
CYP81B1     FANRPKMLFGKIIGVNYTS--------------LAWSP-YGDNWRNLRRIAS--IEILSIHR--LNEFHDIRVEETRLLIQKLLSACNSG---------
CYP82A2     VSSLPDLISANLLCYNRSM--------------IVVAP-YGPYWRQLRKILM--SEFLSPSR--VEQLHHVRVSEVQSSITELFRDWRSNKNVQS----
CYP82B1     LASRPPSAASSYMTYDHAM--------------FGFSF-YGPYWREIRKIST--LHLLSHRR--LELLKHVPHTEIHNFIKGLFGIWKDHQKQQQPTGR
CYP76A2     FANRVIPDVNQAHSYYQGS--------------LAIAP-YGPFWRFQRICT--IEMFVHKK--ISETEPVRRKCVDNMLKWIEKEANSAEK-------
CYP76G1     LAGRKIYEAMKGGKSSDGS--------------LITAQ-YGAYWRMLRRLCT--TQFFVTRR--LDAMSDVRSRCVDQMLRFVEEGGQNGTK-------
CYP76E1     FSNRTVPHAITAVDHDKFS--------------VGWVP-TLNLWKKLRKNCA--TKVFSTKM--LDSTKILRQQKLQELLDYVNEKSHN---------
CYP76F2     FCNRSIPDAIRAAKHNQLS--------------MAWIP-VSTTWRALRRTCN--SHLFTSQK--LDSNTHLRHQKVQELLANVEQSCQA---------
CYP76C1     LSARSPTNAVRSINHQDAS--------------LVWLPSSSARWRLLRRLSV--TQLLSPQR--IEATKALRMNKVKELVSFISESSDR---------
CYP76B1     FSTRNVPDAVRAYNHERHS--------------ISFLH-VCTEWRTLRRIVS--SNIFSNSS--LEAKQHLRSKKVEELIAYCRKAALS---------
CYP80A1     LSGRQPLPCFRIKPHIDYS--------------ILWSD-SNSYWKKGRKILH--TEIFSQKM--LQAQEKNRERVAGNLVNFIMTKVGD---------
CYP79A1     FISRPLTFASETFSGGYRN--------------AVLSP-YGDQWKKMRRVLT--SEIICPSR--HAWLHDKRTDEADNLTRYVYNLATKAATGD-----
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CYP79B2    FASRPLTYAQKILSNGYKT--------------CVITP-FGDQFKKMRKVVM--TELVCPAR--HRWLHQKRSEENDHLTAWVYNMVKNSGS-------
CYP79D1    FSNRPKTLSAKSMSGGYLT--------------TIVVP-YNDQWKKMRKILTSFTEIISPAR--HKWLHDKRAEEADNLVFYIHNQFKANKN-------
CYP79E1    FASRPVTVVTRYSSRGFRS--------------IAVVP-LGEQWKKMRVVA--SEIINAKRLFTQWQLGLRTEEADNIMRYITYQCNTSGDTNG----
CYP79C1    FADRPDSYSAEYISGGYNG--------------VVFDE-YGERQMKMKKVMS--SELMSTKA--LNLLLKVRNLESDNLLAYVHNLYNKDESKTKHG--
CYP79F1    LADRPQLFIMETIGDNYKS--------------MGISP-YGEQFMKMKRVIT--TEIMSVKT--LKMLEAARTIEADNLIAYVHSMYQRSE-------
CYP77A6    ATRPTENPTRTIFSSNTFT--------------VNASAYGPVWRSLRKNMV--QNMLSSIR--FREFGSLRQSAMDKLVERIKSEAKDND-------
CYP77B1    ASRPPDSPIRLMFSVGKCA--------------INSAEYGSLWRTLRRNFV--TELVTAPR--VKQCSWIRSWAMQNHMKRIKTENVEK---------
CYP89A2    ADRPP--PAVISKIVDEHN--------------ISSGSYGATWRLLRRNIT--SEILHPSR--VRSYSHARHWVLEILFERFRNHGGEE---------
CYP27A1    IRDSMEQWKEHRDHKGL----------------SYGIFITQGQQWYHLRHSLNQRIVKPAEAALYTDALNEVISDFIARLDQVR-TESAS---------
CYP27B1    ERCSFSPWTEHRRCRQR----------------ACGLLTAEGEEWQRLRSLLAPLLLRPQAAARYAGTLNNVVCDLVRRLRRQRGRGTGP---------
CYP11A1    QRYDIPPWLAYHRYYQK----------------PIGVLFKKSGAWKKDRVVLNTEVMAPEAIKNFIPLLNPVSQDFVSLLHKRIKQQGS-----------
CYP11B1    HRMHLEPWMAYREHRRQ----------------NLGVFLLNGPEWLSNRRWLNPNVLSPKAVQNLLPMVDTVARDFSEALKQKVLQSAQ-----------
CYP12A1    IRPGGDAQMYHRTVLREDFFQ-----------GVTGLVSVNGEKWGNFRSTVNPVLMQPKNVRLYLNKMAQVNDEFMARIRQIRDPETL-----------
CYP12C1    VRGGAEPVIHYRNKRKDEFFK-----------NCMGLFG-NGAEWGKNRSAVNPVLMQHRNVAIYLKPMQRVNRQFVNRIREIRDKESQ-----------
CYP74A     --SFPVLFDVDKVEKKDLFTG------------TYMPSTELTGGYRILSYLDPSEPKHEKLKNLLFFLLKSSRNRIFPEFQATYSELFDS----------
CYP74C1    --SFPILFDTTKVEKRNILDG------------TYMPSLSFTGGIRTCAYLDPSETEHTVLKRLFLSFLASHHDRFIPLFRSSLSEMFVK----------
CYP74D1    --SFVCMFDNSLIDKTDTLGG------------TFKPGKEYYGGYRPVAFIDTKDPNHAALKGYILSSFAKRHNLFIPLFRNTLSDHLFN----------
CYP74B2    --SFSHLFDMDLVDKRDVLIG------------DFRPSLGFYGGVRVGVYLDTTEPKHAQIKGFAMETLKRSSKVWLQELRSNLNIFWGT----------
CYP24A1    --QRLEIKPWKAYRDHRNEAYG-----------LMILEGQEWQRVRSAFQKKLMKPVEIMKLDKKINEVLADFLERMDELCDERGR-----------
CYP10      EYSRLVHAERQYPNRREMVPIAYYR---KQKGFDLGVVNSQGEEWYRQRTVVSKKMLKLAEVSNFSTQMGEVSDDFVKRLSHVRDSHGEIP---------
CYP9A1     VKRITVKDFEHFVDRRSFTSSFDP-------IFGRGLLLLHGDEWKAMRSTMSPAFTSSKMRLMVPFMEEIALEMIRVLRGKIKDSGKP-----------
CYP9B1     ---FPNHQTLNIPNERLVN--------------DMLNVMRDQHWRNMRSVLTPVFTSAKMRNMFTLMNESFAQCLEHLKSSQPIAAGEN-----------
CYP14A2    FIYRADRPPETLLQPHLNTG-------------VLFSNGDNWRFQRRTALKILRDFGLGRNLMEEQVMRSVHEMLAQLERIADKKN-----------
CYP21A1    IEEALIQKWVDFAGRPQILDGKMN--------FDLSMGDYSLTWKAHKKLSRSALVLGMRDSMEPLVEQLTQEFCERMRAQAG---------------
CYP36A1    FSGRPDTFIMDMLVQGNYG-------------LFFMENNWWKAQRRFTTHIFRSLGVGQAGTQDTIASLASGLVEKIDGQKD-------------
CYP45A1    LKHILVKDINNFVNRSFFGTDK----------KMLIFLRDQQWKDVRRIMTPVFSSAKMKKMMPLMGGCVEELMDMYETAADSG-------------
CYP18A1    --GRPDTPFMQTLNG------------------YGIINSTGKLWKDQRRFLHDKLRQFGMTYMGNGKQQMQKRIMTEVHEFIGHLHASDG---------
CYP707A1   -AKFVLVTKSHLFKPTFPASKE-------RMLGKQAIFFHQGDYHAKLRKLVLRAFMPESIRNNMVPDIESIAQDSLRSWEG------------------
CYP722A1   -ARLVLNNDSGMFTKRYIKSIG-------ELVGDRSLLCAPQHHHKILRSRLINLFSKRSTALMVRHFDELVVDALGGWEHRG-----------------
CYP25A1    FSDRIVPPIFDSNQLNQS--------------LLQNTYATGWKHTRSAIAPIFSTGKMKAMQETIHSKVDLFLDILREKASSG--------------
CYP73A5    --SRTRNVVFDIFTGKGQD-------------MVFTVYGEHWRKMRRIMTVPFFTNKVVQQNREGWEFEAASVVEDVKKNPDSATKG----------
CYP78A6    ILNSPVFADRPVKESAYSLMFN----------RAIGFAPHGVYWRTLRRIASNHLFSTKQIRRAETQRRVISSQMVEFLEKQSSN-------------
CYP4A4     LKVILGRSDPKAPRNYKLMTPWIG---------YGLLLLDGQTWFQHRRMLTPAFHYDILKPYVGLMVDSVQIMLDRWEQLISQD-------------
CYP719     YGARDMPEITKIASASWHT--------------ISTSDAGSFWQNVRKGLQSGAMGPLNVAAQNQYQERDMKRLIKAMSDEAANNNG-----------
CYP44A1    FIVPLQETTQKYREMKGMN-------------PGLGNLNGPEWYRLRSSVQHAMMRPQSVQTYLPFSQIVSNDLVCHVADQQKRFG-----------
CYP302A1   -QRRSHLALAQYRKSRPDVYKT-----------TGLLPTNGPEWWRIRAQVQKELSAPKSVRNFVRQVDGVTKEFIRFLQESRNG-------------
CYP22A1    QPTIILAEYKTIQEALVKNGQQ-----TSGRSSAESFVLFTGDRLNGDGVILAMRQKWKDMRHEISRFMNKWYGAPMDELVLHHTRCLEQELAKIAET--
CYP52A1    VKAILATQFNDFSLGTRHDFLYS--------LLGDGIFTLDGAGWKHSRTMLRPQFAREQVSHVKLLEPHMQVLFKHIRKHHG----------------
CYP701A3   ISTRKLSNALTVLTCDKS--------------MVATSDYDDFHKLVKRCLLNGLLGANAQKRKRHYRDALIENVSSKLHAHARDHPQE-----------
CYP315A1   --QHPLPDAWTLYNQQHACQRG-----------LFFMEGAEWLHNRRILNRLLLNGNLNWMDVHIESCTRRMVDQWKRRTAEAAAIPLAESGE----
CYP39A1    -INVFLKSKKVDFELAVQNIVYR--------TASIPKNVFLALHEKLYIMLKGKMGTVNLHQFTGQLTEELHEQLENLGTHG----------------
CYP711A1   LPNRSIPSPISASPLHKKG--------------LFFTRDKRWSKMRNTILSLYQPSHLTSLIPTMHSFITSATHNLDSKPR----------------
CYP46A1    -DSKMYRALQTVFGERLFGQG------------LVSECNYERWHKQRRVIDLAFSRSSLVSLMETFNEKAEQLVEILEAKADG-----------
CYP43A1    -FDCFHSRIPEILSDDPITSDN-----------IHMFAAKGERWKRLRTLTSYGLSTVKLKLLFPTMDTCVSEFMDHVNSLSDGQSVVIN---------
CYP59A1    QIQSLNLSKPNILRRPLETITG-----------GPSLMSMHGETWKRWRALFNPGFNPNYLIGLAPLIADEVVVFCEQLRQKARTG-----------
CYP710A1   IFSNVRPDAFHLIGHPFGKKLFG----------DHNLIYMFGEDHKSVRRQLAPNFTPKALSTYSALQQLVILRHLRQWEGSTSGGSR----------
CYP56A1    SGNQKKIPYSALAAYTGDN--------------VISAYGAVWRNYRNAVTNGLQHFDDAPIFKNAKILCTLIKNRLLEGQTS--------------
CYP57A1    -NALPKADYYKPFGLPSFPN-------------LFDEQNPARHSAIKKQVASLYTMTALLSYEEGVDGQTAILKEQLQRFCDQK-------------
CYP53A1    -NGFLKSDFYDAFVSIHRG--------------LFNTRDRAEHTRKRKTVSHTFSMKSIGQFEQYIHGNIELFVKQWNRMADTQRNPKTG--------
CYP58A1    -RTNFWPLFQGCTDDTDVN-------------HFMTIDHDLHRQRRKPFDPFFSRMAINIRYWPMLAEKASFLESRIRECKGQGK------------
CYP20A1    --NKTLDPFETMLKSLLRYQ-------------SDSGNVSENHMRKKLYENGVTNCLRINFALLIKLSEELLDKWLSYPESQ-------------
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CYP38A1    ESAVFVNRPVELFVGFEPLITP------------FSIQYANDEDWVQRSKCLYHTLKGDDLKSYFHHFVQIAQEEESLWSSYTSDK-------------
CYP54A1    -LDELKKLPDDVVSFDAANDDS------------MHTKYTLIPTHEPILPHTIKTSLTPSLPRLNPQLSEEVQAFSQEIAPLMSSSPSD-----------
CYP55A1    ---FPELSASGKQAAKAKP---------------TFVDMDPPEHMHQRSMVEPTFTPEAVKNLQPYIQRTVDDLLEQMKQKGCAN-------------
CYP727A1   IKELLTKAEDKLPLTGKTYNLACG---------KLGLFISSFEKVKSRRESLKSFLDEKLSVGTGGSSFKIIQIVLDRVDSIMAR-------------
consensus                                        .      .  .. ....      .    .     .   .
           201......210.......220.......230.......240.......250.......260.......270.......280.......290........
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CYP7A1     ------------------------------------------SKSDAWVTEGMYAFCYRVMFEAGYLTLFGRDTS------KPDTQRVLILNNLNSFKQFDQV
CYP7B1     ------------------------------------------LKTTSWDTAELYPFCSSIIFEITFTTIYGKVIV------CDNNKFISELR--DDFLKFDDK
CYP8A1     ------------------------------------------EAGSGWHEMGLLEFSYGFLLRAGYLTQYGVEAPPH-TQESQAQDRVHSADVFHTFRQLDLL
CYP8B1     ------------------------------------------PDASRWHEDGLFHFCYGVMFKAGYLSLFGHTS-------DKRQDLLQAEEIFIKFRRFDLL
CYP51A1    ------------------------------------------WGESGEVDLKAELERLITLTASRCLLGREVR----DQLFDDVAPLFHDLDKGMQPISVI
CYP51A2    ------------------------------------------WGESGEVDIKVELERLIILTASRCLLGREVR----DQLFDDVSALFHDLDNGMLPISVL
CYP26A1    ------------------------------------------WLSCGERGLLVYPEVKRLMFRIAMRILLGCEPGPAGGGEDEQQLVEAFEEMTRNLFSLPID
CYP26C1    ------------------------------------------WCAAG-GPVSVYDASKALTFRMAARILLGLRLDEAQCAT----LARTFEQLVENLFSLPLD
CYP716A1   ------------------------------------------EWANQ-DQVIVFPLTKKFTFSIACRSFLSME-----DPARVRQLEEQFNTVAVGIFSIPID
CYP725A1   ------------------------------------------KWKGK-DEVKVLPLVRGLIFSIASTLFFDVN-----DGHQQKQLHHLLETILVGSLSVPLD
CYP718     ------------------------------------------EWRGK-EEISLYRSAKVLTFTVVFECLYGIK-----VEIG---MLEVFERVLEGVFALPVE
CYP90A1    ------------------------------------------SWS---SRVLLMEEAKKITFELTVKQLMSFDPGE-----WSESLRKEYLLVIEGFFSLPLP
CYP90B1    ------------------------------------------SWQQN-SIFSAQDEAKKFTFNLMAKHIMSMDPGEE----ETEQLKKEYVTFMKGVVSAPLN
CYP724A1   ------------------------------------------SWKNC-REVEFHKEVKIFTLSVMVNQLLSIKPEDP----ARLYVLQDFLSYMKGFISLPIP
CYP720A1   ------------------------------------------NFKDG-EVVLLQDICRKVAIHLMVNQLLGVSSES-----EVDEMSQLFSDFVDGCLSVPID
CYP85A1    ------------------------------------------QWNEL-EVIDIQDKTKHMAFLSSLTQIAGN-LRKP----FVEEFKTAFFKLVVGTLSVPID
CYP87A2    ------------------------------------------LWSNQ-DSVELKDATASMIFDLTAKKLISHDPDK-----SSENLRANFVAFIQGLISFPFD
CYP708A1   ------------------------------------------SVSFQ-GVVDVKDTSGRLILEQMILMIISNIKPE-----TKSKLIESFRDFSFDLVRSPFD
CYP702A1   ------------------------------------------EGARR-GCLDVKEISSKILIECLAKKVTGDMEPE-----AAKELALCWRCFPSGWFRFPLN
CYP88A3    ------------------------------------------KWTKMGE-FEFLTHLRKLTFRIIMYIFLSSES-----ENVMDALEREYTALNYGVRAMAVN
CYP88B1    ------------------------------------------KYATTEEPVEFLHKMHKLTFEVFMRLLIGDEVN----QELFDEMFEEITAVISGVHNLPIN
CYP3A1     ------------------------------------------VPVKEVFGAYSMDVITSTSFGVNVDSLNNPKDPFVEKAKKLLRIDFFDPLFLS
CYP5A1     ------------------------------------------FDIQRCYCCYTTDVVASVAFGTQVNSSEEPEHPFVKHCRRFFAFSVPRLILVL
CYP6A2     ------------------------------------------LEIKELMARFTTDVIGTCRFGIECNTLRTPVSDFRTMGQKVFTDMRHGKLLTM
CYP6B4     ------------------------------------------QQIIPLVRKFTMASITTCAFGMELD--EEMIETLDKLDSLIFTTSYG----NE
CYP28A1    ------------------------------------------IDAKDMSLRFTSEMVTDCVLGLKAESFSDKPTPIMGYIKDLFAQSWTFIIYFV
CYP28C1    ------------------------------------------LDCIDLGLRFTGESLFDCVLGIQARTFTDNPLPVVRQNHEMSAENRGLAIAGA
CYP13A2    ------------------------------------------IDMLRFYQEYTMDVIGRFAMGQTDSMMFKNPIVNVVREIFCGSRKNL-MLICQ
CYP13B1    ------------------------------------------FNIHAYFQEFTYDVISRLAMGQPNSELFNNSGVEIVKSIFMRTHRVLPWYFTV
CYP72A8    ------------------------------------------NEIDVWPYLGDLTSDVISRTAFGSSYEEGKRIFELQEEQGRRVLKALELAFIPGM
CYP72B1    ------------------------------------------VEVDVYEWFQILTEDVISRTAFGSSYEDGRAVFRLQAQQMLLCAEAFQKVFIPGY
CYP721A1   ------------------------------------------IELEVHKEMHNLSAEMLSRTAFGNSVEEGKGIFELQERMMRLFYLVRWSVYIPGF
CYP709A1   ------------------------------------------EIGEEMHKLTADIISRTKFGSSFEKGKELFNHLTVLQRRCAQATRHLCFPGS
CYP709B1   ------------------------------------------IKKEMNEEFQRLTADIIATSAFGSSYVEGIEVFRSQMELKRCYTTSLNQVSIPGT
CYP715A1   ------------------------------------------DMESEIIGTAGEIIAKTSFGVTGENGTQVLKNLRAVQFALFNSNRYVGVPFS
CYP714A1   ------------------------------------------CDIIVDEDLRAASADVISRACFGSSFSKGKEIFSKLRCLQKAITHNNILFSLNGF
CYP4C3     ------------------------------------------AFNLFPYVTLCTLDIVCETAMG---RRIYAQSNSESEYVKAVYGIGSIVQSRQA
CYP31A2    ------------------------------------------EVDVLSVITLCTLDIICETSMG---KAIGAQLAENNEYVWAVHTINKLISKRTN
CYP37A1    ------------------------------------------TIDAFPYIKRCALDIICETAMG---TTVSAQTNHTHPYVVAVNEMNSLAFKYQR
CYP37B1    ------------------------------------------VDLFPYIKRLALDVICDTSMG---VTIDAQNNHDHQYVESVRLLSEYAFEWIL
CYP32A1    ------------------------------------------YFDAFPYFKRCTLDIICETAMG---IQVNAQLGHNNEYVHAVKRISEIVWNHMK
CYP29A2    ------------------------------------------TVDIFPYVKRCALDIISETAMG---IKIDAQINHDHKYVQAVEGYNKIGVLVSF
CYP86A1    ------------------------------------------PVDLQDLFLRLTFDNICGLTFGKDPETLSLDLPDN-PFSVAFDTATEATLKRLL
CYP86B1    ------------------------------------------PIDLQDVLLRLTFDNVCMIAFGVDPGCLGPDQPVI-PFAKAFEDATEAAVVRFV
CYP96A1    ------------------------------------------VVDLQDVFQRFTFDTSFVLATGVDPGCLSTEMPQI-EFARALDEAEEAIFFRHV
CYP96C1    ------------------------------------------VFDLQDVFQRLMLDSSSILTTGQNHRSLRVGLPYD-ETLEAINIANYQIFVRHI
CYP94A1    ------------------------------------------ILDFQDILQRFTFDNICNIAFGYDPEYLTPSTNRS-KFAEAYEDATEISSKRFR
CYP94B1    ------------------------------------------TVDFQEVLKRFAFDVVCKVSLGWDPDCLDLTRPVP-ELVKAFDVAAEISARRAT
CYP704A1   ------------------------------------------SFDFQDMLMKCTLDSIFKVGFGVELGCLDGFSKEGEEFMKAFDEGNGATSSRVT
CYP704B1   ------------------------------------------QVDMQELLMRMTLDSICKVGFGVEIGTLAPELPEN-HFAKAFDTANIIVTLRFI
CYP97A3    ------------------------------------------EVEMESLFSRLTLDIIGKAVFNYDFDSLTNDTGVIEAVYTVLREAEDRSVSPIP
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CYP97B3    ---------------------------------IELDLEAEFSSLALDIIGLSVFNYDFGSVTKESPVIKAVYGTLFEAEHRSTFYFP
CYP1A1     --------------------------------ISTLQELMAGPGHFNPYRYVVVSVTNVICAICFGRRYDHNH-----------QELLSLVNLNNNFG
CYP1B1     --------------------------------VAVLVRRCAGGACLDPTQPIIVAVANVMSAVCFGCRYNHDD-----------AEFLELLSHNEEFG
CYP17A1    -------------------------------CDFLATCDG--QVKDLSSSIFMTVVNIICMICFSVSYKEGD-----------MELVTIRRFTTGFV
CYP19A1    -------------------------------CDFLATQHG--EAIDLSEPLSLAVTNIISFICFNFSFKNED-----------PALKAIQNVNDGIL
CYP2A7     ------------------------------IEAIR---STHGANIDPTFFLSRTVSNVISSIVFGDRFDYED-----------KEFLSLLSMMLGIF
CYP2M1     ------------------------------VKAFG---EYRDSVVNPKELLCNCVGNVICSIVFGHRFENDD-----------PMFQLIQKAVDAYF
CYP33A1    ------------------------------DEELK---KVEGKEVNIQEHFDLAIGNIINQFLFGNRFKDS-----------SKFNELKKLLDLFF
CYP33C1    ------------------------------FARLD---AKLGSETDVPEVFDHAVANVVNQLLFGYRFMGPKE----------NEYQELKHIIDSPA
CYP33B1    ------------------------------IKKLKT-AEILNEDFLLQSELDVAVGSVINQFLFGYRFDRSKL---------FEFTRIKTLVNNFM
CYP23A1    ------------------------------MNHMEKSCGLDGKELHLCPSIAVCVGNIINNMLFGLRFNQDN----------SYMHRLHQLLDDQS
CYP35A1    ------------------------------CADTDKSATDGVTVAQAGDFFDLTVGSIINSILVGKRFEEHNK---------DDFLKIKEAMGAAF
CYP35B1    TFRRIFKYREKFLNSQFPVQNFEKSVSSFRRFSCAEIDADAVNGKTIVHTTEFFDLTVGSVINSLLVGKRFEAEDK---------DDFLEIKRLMAEAA
CYP34A1    ----------------------FEDFASSNGICNKERKIFETWARPFFDLLTGSVINKILINERFEQNDP-----------E-FEKLVSRLAKGF
CYP71A12   ----------------------------SSENLSELFVTLPSDVTSRIALGRKHSED-----------ETARDLKKRVRQIM
CYP71C1    ----------------------------GTALDMTELLGGYASDFVCRAVLGESHRKQ-----------GRNKLFRELTETSA
CYP71D11   ----------------------------VVNLSQAIDSLIFTITSRSAFGKRYMEQ-------------EEFISCVREVM
CYP726A1   ----------------------------PVNITKIIYGIIISIMIRTSVGN-CKQK--------------ERLLSVADAVN
CYP71K1    ---------------------------GATAAVNLSERISAYVADSAVRAVIGSRFKNR--------------AAFLRMLERRM
CYP99A1    ----------------------------GEAPVVNLGRLVLSCSMAITGRATLGKLCG----------------DEIMSVVDVAV
CYP71E1    ----------------------------KASIVLNDHVFALTDGIIGTVAFGNIYASK-QF---------AHKERFQHVLDDAM
CYP71N1    ----------------------------SSMVNLSELLLSLSCNMTCRSAFGSGFDD------------GGDIQLHDMLREAQ
CYP71B2    ----------------------------QSPVDLSKTFFSLTASIICRVALGQNFNESGFV---------IDQDRIEELVTESA
CYP83A1    ----------------------------SEVVDISELMLTFTNSVVCRQAFGKKYNED--G---------EEMKRFIKILYGTQ
CYP83B1    ----------------------------SGTVDLSELLLSFTNCVVCRQAFGKRYNEY--G---------TEMKRFIDILYETQ
CYP83E1    ----------------------------SNVTNLSELLISLSSTIICRTAFGKSYEDD--G---------IEKSRFHGLLHEFQ
CYP93B1    ----------------------------FEAVNITEELLKLTNNVISIMMVG------------------EAEEARDVVRDVT
CYP93C17   ----------------------------QKPLNVTEELLKWTNSTISRMMLG------------------EAEHVKDIVREVL
CYP93A1    ----------------------------GEAVDFGDELMTLSNNIVSRMTLSQKTSEN--D----------NQAEEMKKLVSNIA
CYP705A1   ----------------------------KESVMIHKEASRFVNNSLYKMCTGRSFSVE--N---------NEVERIMELTADLG
CYP712A1   ----------------------------GLPCDLSSQFIKYTNNVICRMAMSTRCSGT--D---------NEAEEIRELVKKSL
CYP75A1    ----------------------------GERVVAEMLTFAMANMIGQVILSKRVF--VNK------GVEVN--EFKDMVVELM
CYP75B1    ----------------------------TKPVNLGQLVNMCVVNALGREMIGRRLFG-ADA------DHKAD--EFRSMVTEMM
CYP92A2    ----------------------------GKPIVLKDYLTTLSLNVISRMVLGKRYLD-ESE------NSFVNPEEFKKMLDELF
CYP84A1    ---------------------------KPINVGEQIFALTRNITYRAAFG--------S------ACEKGQDEFIRILQEFS
CYP703A2   ----------------------------GKPINLKEVLGAFSMNNVTRMLLGKQFFGPGSL------VSPKEAQEFLHITHKLF
CYP98A3    ----------------------------AKGLQLRKYLGAVAFNNITRLAFGKRFMNAEGV------VDEQG-LEFKAIVSNGL
CYP706A1   ----------------------------GSPVNLGEQIFLSIFNVVTRMMWGATVEGDE--------RTSLG-NELKTLISDIS
CYP81D1    ----------------------------KTVVELKPMLMDLTFNNIMRMMTGKRYYGEET-------TDEEEAKRVRKLVADVG
CYP81E6    ----------------------------FSEVELTSRFFDMTFNNIMRMISGKRYYGEDCDM-----TELQEASEFRDMVTELL
CYP81B1    ----------------------------SSQVTMKFSFYELTLNVMMRMISGKRYFGGDNP------ELEEEGKRFRDMLDETF
CYP82A2    ----------------------------GFATVELKQWFSLLVFNMILRMVCGKRYFSASTS----DDEKAN---RCVKAVDEFV
CYP82B1    E---------------------------DRDSVMLEMSQLFGYLTLNVVLSLVVGKRVCNYHADGHLDDGEEAGQGQKLHQTITDFF
CYP76A2    ----------------------------GSGIEVTRFVFLASFNMLGNLILSKDLADLES-----------EEASEFFIAMKRIN
CYP76G1    ----------------------------T--IDVGRYFFLMAFNLIGNLMFSRDLLDPDS---------KRGSEFFYHTGKVM
CYP76E1    ----------------------------GEVFDIGETVFINVLNSISNTLFSMDLAHSTPD--------EKSQEFKTIIWGIM
CYP76F2    ----------------------------GGPVDIGQEAFRTSLNLLLSNTIFSVDLVDPIS--------ETAQEFKELVRGVM
CYP76C1    ----------------------------EESVDISRVAFITTLNIISNILFSVDLGSYNAK---------ASINGVQDTVISVM
CYP76B1    ----------------------------NENVHIGRAAFRTSLNLLLSNTIFSKDLTDPYE---------DSGKEFREVITNIM
CYP80A1    ----------------------------VVELRSWLFGCALNVLGHVVFSKDVFEYSDQ---------SDEVGMDKLIHGML
CYP79A1    ----------------------------VAVDVRHVARHYCGNVIRRLMFNRRYFGE----PQADGGPGPMEVLHMDAVFTSL
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CYP79B2    ------------------------------------------------VDFRFMTRHYCGNAIKKLMFGTRTFSKN---TAPDGGPTVEDVEHMEAMFEAL
CYP79D1    ------------------------------------------------VNLRTATRHYGGNVIRKMVFSKRYFTFGK--GMPDGGPGPEEIEHIDAVFTAL
CYP79E1    ------------------------------------------------AIIDVRFALRHYCANVIRRMLFGKRYFGSFT--GGEGGGPGKEEIEHVDATFDVL
CYP79C1    ------------------------------------------------AVVNVRDIVCTHTHNVKMRLLFGRRHFKET----TMDGSLGLMEKEHFDAIFAAL
CYP79F1    -----------------------------------------------TVDVRELSRVYGYAVTMRMLFGRRHVTKENV-FSDDGRLGNAEKHHLEVIFNTL
CYP77A6    -----------------------------------------------GLVWVLRNARFAAFCILLEMCFGIEMDEE------------SILNMDQVMKKVL
CYP77B1    -----------------------------------------------GFVEVMSQCRLTICSILICLCFGAKISEE------------KIKNIENVLKDVM
CYP89A2    ----------------------------------------------PIVLIHHLHYAMFALLVLMCFGDKLDEK------------QIKEVEFIQRLQL
CYP27A1    --------------------------------------------GDQVPDVANLLYHLALEAICYILFEKRVGCLEPS----------IPEDTATFIRSVG
CYP27B1    --------------------------------------------PALVRDVAGEFYKFGLEGIAAVLLGSRLGCLEAQ---------VPPDTETFIRAVG
CYP11A1    --------------------------------------------GKFVGDIKEDLFRFAFESITNVMFGERLGMLEDT----------VDTEAQKFIDAVY
CYP11B1    --------------------------------------------GSLTMDMQPDIHKYTVEVSNFALFGERLGLFGCN----------PSSQSLKFIHALE
CYP12A1    ---------------------------------------------EVPASFQEEMNRWTLESVSVVALDKQLGLITTN----------RDNPDLKKLIGLL
CYP12C1    ---------------------------------------------EVPGDFMNTINHLTFESVATVALDRELGLLREA----------NPPPEASKLFKNI
CYP74A     --------------------------------------------LEKEAFPLRESGFRRFQRRNRLLFLGSSFLRDE--SRRYKLKADAPGLITKWVLF
CYP74C1    --------------------------------------------LEDKLADKNKIADFNSISDAVSFDYVFRLFSDG--TPDSTLAADGPGMFDLWLGL
CYP74D1    --------------------------------------------NLEKQVTEQGKADFNALLPTMTFDFIFRLLCDQKNPSDTVLGAQGPEHLRKWLFP
CYP74B2    --------------------------------------------IESEIS-KNGAASYIFPLQRCIFSFLCASLAGVDASVSPDIAENGWKTINTWLAL
CYP24A1    --------------------------------------------IPDLYSELNKWSFESICLVLYEKRFGLLQKETEEEALTFITAIKTMMSTFGKMM
CYP10      -------------------------------------------ALERELFKWAMESIGTFLFEERIGCLGQETSPMAQTFIANLEGFFKTLQPLM
CYP9A1     -------------------------------------------YIDVEAKSMMTRYANDVIASCAFGLKVNSQASDHEFYVNSQAITKFKFSAFLKVLF
CYP9B1     -------------------------------------------AFELDMKVLCNKLSNDVIATTAFGLKVNSFDDPENEFHTIGKTLAFSRGLPFLKFM
CYP14A2    --------------------------------------------VDMFWPIQLCVGNVINESLFSYHYKYEDSK--------KFETFVKVLDKHL
CYP21A1    --------------------------------------------ASVAIHKEFSLLTCSIISCLTFGDKQDSTLLN--ATHSCVRDLLKAWNHWSVQIL
CYP36A1    --------------------------------------------KPIELRPLLVHVVGNVIHKHLFGFTREWNETEILDFHVAINDVLEHFTSPKTQLL
CYP45A1    --------------------------------------------QPIDMMEAFQCLTMDVINRCAITLDINCIKNPKNEVLAFMRKYVSQPIPCIFKFI
CYP18A1    --------------------------------------------QPVDMSPVISVAVSNVICSLMMSTRFSIDDPKFRRFNFLIEEGMRLFGEIHTVDY
CYP707A1   ---------------------------------------------TMINTYQEMKTYTFNVALLSIFGKDEVLYR-----------EDLKRCYYILEKGY
CYP722A1   ---------------------------------------------TVVLLTDLLQITFKAMCKMLVSLEKEEELG----------SMQRDVGFVCEAML
CYP25A1    ---------------------------------------------QKWDIYEDFQGLTLDVIGKCAFAIDSNCQRDRNDVFYVNARKFIANIDIRHSKVI
CYP73A5    ----------------------------------------------IVLRKRLQLMMYNNMFRIMFDRRFESEDDPLFLRLKALNGERSRLAQSFEYNY
CYP78A6    --------------------------------------------EPCFVRELLKTASLNNMMCSVFGQEYELEKN------------HVELREMVEEGY
CYP4A4     --------------------------------------------SSLEIFQHVSLMTLDTIMKCAFSYQGSVQLDRNSHSYIQAINDLNNLVFYRARNV
CYP719     --------------------------------------------IVKPLDHIKKNTVRLLTRLIFGQAFDDN-----------KFIESMHYEIEDII
CYP44A1    ---------------------------------------------LVDMQKVAGRWSLESAGQILFEKSLGSLGNR-SEWADGLIELNKKIFQLSAKMR
CYP302A1   --------------------------------------------GAIDMLPKLTRLNLELTCLLTFGARLQSFTAQEQDPRSRSTRLMDAAETTNSCIL
CYP22A1    --------------------------------------------KSLIDLRDPLAGAIANVIQQITIGRNYMYQDQEFQTQLRDINAVVKEIMTAEVFFV
CYP52A1    --------------------------------------------QTFDIQELFFRLTVDSATEFLLGESAESLRDE--SVGLTPTTKDFDGRNEFADAF
CYP701A3   -------------------------------------------PVNFRAIFEHELFGVALKQAFGKDVESIYVKELGVTLSKDEIFKVLVHDMMEGA
CYP315A1   ------------------------------------------IRSYELPLLEQQLYRWSIEVLCCIMFGTSVLTCPKIQSSLDYFTQIVHKVFEHSSRLMT
CYP39A1    ---------------------------------------------TMDLNNLVRHLLYPVTVNMLFNKSLFSTN------------KKKIKEFHQYFQ
CYP711A1   --------------------------------------------DIVFSNLFLKLTTDIIGQAAFGVDFGLSGKKPIKDVEVTDFINQHVYSTTQLKM
CYP46A1    --------------------------------------------QTPVSMQDMLTYTAMDILAKAAFGMETSMLLGAQKPLSQAVKLMLEGITASRNTLA
CYP43A1    ----------------------------------------------HSHSLFQNHTSYVLARKAFGNFAELQKSTAEKIAYIFPETKLIFKNSFVGHF
CYP59A1    --------------------------------------------TVFQLEPLTLRLTVDTICSVTLYVVTPVGRWPFLTPDLEIHSSTTKLRTTPLPQR
CYP710A1   --------------------------------------------PVSLRQLVRELNLETSQTVFVGPYLDKEAKN------RFRTDYNLFNLGSMALP
CYP56A1    ---------------------------------------------IPMGPLSQRMALDNISQVALGFDFGALTHEKN------AFHEHLIRIKKQIFH
CYP57A1    --------------------------------------------QVIDLPRFLQYYAFDVIGVITVGKSMGMMESNSDTNGACSALDGMWHYASMMAYI
CYP53A1    --------------------------------------------FASLDALNWFNYLAFDIIGDLAFGAPFGMLDKGKDFAEMRKTPDSPPSYVQAVEVL
CYP58A1    --------------------------------------------AVRLDRAFSAFSADCIERICTDDLEPGDGFLDQPDFGPEWYDGMLGLIRNAPIL
CYP20A1    --------------------------------------------HVPLCQHMLGFAMKSVTQMVMGSTFEDEQ----------EVIRFQKNHGTVWS
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CYP38A1    -------------------------------------------------EVSLTKEVFPMTIKGIARTCFGDIFKDE---------------NELSKMAESYH
CYP54A1    -------------------------------------------------WAPININSKLLRIVAKVSGRVFIGPELCHDERYLEAAVGYTVSVMEAQRAVERMNP
CYP55A1    -------------------------------------------------GPVDLVKEFALPVPSYIIYTLLGVPFN----------------DLEYLTQQNAIR
CYP727A1   -------------------------------------------------DFLDCRYFSQHMAFNIVGSALFGDAFFDWSDASAYEELMMTVAKDACFWASYAVP
consensus                                                   ...   .   .    ..  ....
           301......310.......320.......330.......340.......350.......360.......370.......380.......390........
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CYP7A1    FPALVAG-LPIHLFKAAHKAREQLAEGLK---HENLSVRDQVSELIRLRMFLNDTLS----------------------------------------
CYP7B1    FAYLVSN-IPIELLGNVKSIREKIIKCFS---SEKLAKMQGWSEVFQSRQDVLEKYY----------------------------------------
CYP8A1    LPKLARGSLSAGDKDRVGKVKGRLWKLLS---PTRLASRAHRSRWLESYLLHLEEMG----------------------------------------
CYP8B1    FPRFVYSLLGPREWREVGRLQQLFHELLS---VKHNPEKDGMSNWIGHMLQYLSEQG----------------------------------------
CYP51A1   FPKLPIPAHNCRD-RARGKIAKIFSNIIA---TRKRSGDKSENDMLQCFIDSKYKDGR---------------------------------------
CYP51A2   FPYLPIPAHRRRD-RAREKLSEIFAKIIG---SRKRSG-KTENDMLQCFIESKYKDGR---------------------------------------
CYP26A1   VPFSGLYRGVKARNLIHARIEENIRAKIR--RLQATEPDGGCKDALQLLIEHSWERGE---------------------------------------
CYP26C1   VPFSGLRKGIRARDQLHRHLEGAISEKLH--EDKAAEPG----DALDLIIHSARELGH---------------------------------------
CYP716A1  LPGTRFNRAIKASRLLRKEVSAIVRQRKE--ELKAGKALEE-HDILSHMLMNIGETK---------------------------------------
CYP725A1  FPGTRYRKGLQARLKLDEILSSLIKRRRR--DLRSGIASDD-QDLLSVLLTFRDEKGN---------------------------------------
CYP718    FPCSKFARAKKARLEIETFLVGKVREKRR--EMEKEGAEKP-NTTLFSRLVEELIKG---------------------------------------
CYP90A1   LFSTTYRKAIQARRKVAEALTVVVMKR----REEEEEGAERKKDMLAALLAADDG----------------------------------------
CYP90B1   LPGTAYHKALQSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKH-------------------------
CYP724A1  LPGTGYTNAIKARKRLSARVMGMIKERE---REEEDMNNAIREEDFLDSIISNED----------------------------------------
CYP720A1  LPGFTYNKAMKARKEIIRKINKTIEKR-----LQNKAASDTAGNGVLGRLLEEES---------------------------------------
CYP85A1   LPGTNYRCGIQARNNIDRLLRELMQERR--------DSGETFTDMLGYLMKKEGNR---------------------------------------
CYP87A2   --IPGTAYHKCLQG--RAKAMKMLRNMLQERRENPRKNPS---DFFDYVIEEIQKEG---------------------------------------
CYP708A1  PSFWNALYNGLMVRSARSNVMKMLKRMFKERREEATSDDSKYGDFMETMIYEVEKEG--------------------------------------
CYP702A1  ----------LPGTGVYKMMKARKRMLHLLKETILKKRAS-GEELGEFFKIIFEGA--------------------------------------
CYP88A3   IPGFAYHRALKARKTLVAAFQSIVTERRNQRKQNILSNKKDMLDNLLN--VKDEDGK---------------------------------------
CYP88B1   LPGFAYHKGLKARKVLXEVFKKLIDERREAMKDGKSMPKANIIDMLLSNNNQDYEAN--------------------------------------
CYP3A1    VVLFPFLTPVYEMLNICMFP----KDSIEFFKKFVYRMKETR----LDS-----------------------------VQKHRVDFLQLMMNAHNDSK
CYP5A1    ILSFPSIMVPLARILPNKKR----DEVNGFFNKLIRNVIALRD---QQA-----------------------------AEERRQDFLQMVLDLRHSAP
CYP6A2    FVFSFPKLASRLRMRMMPED----VHQFFMRLVNDTIALRER-----------------------------------ENFKRNDFMNLLIELKQK--
CYP6B4    IDMMYPGILKKLNSSIFSKM------IAPFFDNLTKTIIEQRGG--------------------------------KPTNRKDLMDLILELRQKKA
CYP28A1   LVSTLPALRHVFKLRFVPLR------IENFFVNLMQTAIDARRQQLAAG-----------------------------KQFERVDFLDYILHLGKK--
CYP28C1   VHGLFPNLPRWLRPKVFPRS------HDRFYGQMISEALRLRRS---------------------------------KHQERNDFINHLLEMQRE--
CYP13A2   VFPPIGQFIRDLTFKFPRIP---AFKLYSIMQDVVAARIAQRE-REKGA----------------------------ESGEPQDFIDLFLDARSDDV
CYP13B1   LFPQFEHLVKRMFYNHAAVQGGDIEKLLLICKKTVESRIQEREENAKLG----------------------------FENAENDFIDMFLNYYSEQV
CYP72A8   RFLPTKNNLRMRQINKEVKS--------RLREIIMKRQR------GMDT-----------------------------GEAPKNDLLGILLESNSGD-
CYP72B1   RFFPTRGNLKSWKLDKEIRK--------SLLKLIERRRQNAIDGEGEEC---------------------------KEPAAKDLLGLMIQAKN---
CYP721A1  RFFPSKTNREIWRIEKQIRV--------SILKLIENNKT------AVEK-----------------------------SGTLLQAFMSPYTNQNGQE-
CYP709A1  RFLPSKYNREIKSLKKEVER--------LLIEIIQSRRDC----AEMGR----------------------------SSTHGDDLLGLLLNEMDIDK
CYP709B1  QYLPTPSNIRVWKLERKMDN--------SIKRIISSR---------LQS-----------------------------KSDYGDDLLGILLKAYNTE-
CYP715A1  NILSYKQTVKAKGLGHEIDG--------LLLSFINKRK------ISLAE----------------------------GDDQGHDLLGMLLKADQKG-
CYP714A1  TDVVFGTKKHGNGKIDELER--------HIESLIWETVKE----REREC----------------------------VGDHKKDLMQLILEGARSSC
CYP4C3    KI--WLQSDFIFSLTAEYKLHQSYINTLHGFSNMVIRERKAELAILQENN---------NNNNNNAPDAYD-------DVGKKKRLAFLDLLIDASKEGT
CYP31A2   ----------NPLITEDGRTHEKCLRILHDFTKKVIVERK---EALQEN--------------------------DYKMEGRLAFLDLLLEMVKSG-
CYP37A1   MP--WLWIKPIRQLIGYEADFQRNLDIVTSFTKKVIDRKLREHD-------------ETDGMVVVE-----------EESKKKAFLDMLIEK-KEEG
CYP37B1   RP--WLRLKPLWYLTGPGHEYDRHLKIVTDFTKTVIKEKWEEFQ--------------KFHVDPVVK-----------TDKRSMAFLDLLLEL-RNEG
CYP32A1   FP--WLWLKPIWYLTGLGFEFDRNVRMTNNFVRKVDAADFKIENQKNYYYLGIVLPEAFKINFQVIQERKELLNEDGNEASEKKRKAFLDLLLTIQKEEG
CYP29A2   NP--HLKNQFIFWATGYKAQYDDYLSTLKSMTEKVIKERRAAHDSGEVEK-------------------------ETSKRMMNFLDLMLSMEESN-
CYP86A1   YT-GFLWRIQKAMGIGSEDKLKKSLEVVETYMNDAIDARKN---------------------------------SPSDDLLSRFLKKRD---
CYP86B1   MP-TCVWKFMRYLDIGTEKKLKESIKGVDDFADEVIRTRKKELSLE--G----------------------------ETTKRSDLLTVFMGLRD---
CYP96A1   KP-EIVWKMQRFIGFGDELKMKKAHSTFDRVCSKCIASKRDEITNGVIN--------------------------IDSSSKDLLMCYMNVDTICH
CYP96C1   LP-AKIWKFQKWLGIMGEKKIKKAWRILDDISVEYMNRRKKEISS-------------------------------TISSQEDMDVVKFSEE---D
CYP94A1   LPLPIIWKIKKYFNIGSEKRLKEAVTEVRSFAKKLVREKKRELEEK------------------------------SSLETEDMLSRFLSSGHSD-
CYP94B1   EPVYAVWKVKRFLNVGSEKRLREAIKTVHLSVSEIIRAKKKSLDIGG----------------------------DVSDKQDLLSRFLAAGHG--
CYP704A1  DP---FWKLKCFLNIGSESRLKKSIAIIDKFVYSLITTKRKELSKEQ----------------------------NTSVREDILSKFLLESEKDP
CYP704B1  DP---LWKMKKFLNIGSEALLGKSIKVVNDFTYSVIRRRKAELLEAQ-----------------------------VKHDILSRFIEISDDPD
CYP97A3   VWDIPIWKDISPRQRKVATSLKLINDTLDDLIATCKRMVEEEELQFHEE--------------------------YMNERDPSILHFLLAS----
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CYP97B3    YWNFPPARWIVPRQRKFQSDLKIINDCLDGLIQNAKETRQETDVEKLQER-----------------------------DYTNLKDASLLRFLVDMR---
CYP1A1     EVVGSGNPADFIP----------ILRYLPNPS---LNAFKDLNEKFYSFMQKMVKEHYKTFEKG-HIR------------DITDSLIEHCQEKQLDEN
CYP1B1     RTVGAGSLVDVMP----------WLQLFPNPVRTIFREFEQINRNFSNFVLDKFLRHRESLVPGAAPR------------DMMDAFILSAEKKATGDP
CYP17A1    NSLSDDNLVDIFP----------WLKIFPNKTLEMIRKYTEIRGAMLSKILKECKEKFRSDSVSNLID------------LLIQAKVNENNNNSSLDQ
CYP19A1    EVLSKEVLLDIFP----------VLKIFPSKAMEKMKGCVQTRNELLNEILEKCQENFSSDSITNLLH------------ILIQAKVNADNNNAGPDQ
CYP2A7     QFTSTSTGQLYEM----------FSSLMKHLPGPQQQ--AFKLLLGLEDFIAKKVEHNQRTLDPNS-------------PQDFIDSFLIHMQEEE
CYP2M1     NVLSSPIGAMYNM----------FPRIVWCFPGNHHE--MFAIVNKAKVYIQEQAEIRLKTLNISE-------------PQDFIEAFLVKMLEEK
CYP33A1    EVQGSLRVYFAYT----------VDFLPQWMVELLTP-DVSRVRDGIYQFFDEQIEEHRQEIDFETSD------------SK--DYVETFMKEQKKRE
CYP33C1    EIFGKLHIFLAMN----------IPIFAKLLPESLYEGPIKTFRDTTLAFFNKQIEAHRHRIDFEDLN------------SESTDFVETFLKEQRRE
CYP33B1    EEVGKPLGVLAFT----------CHGIPSFLVKLMVS-GIEEQKRELFRFLRKQIDGAKSQINYEEEH------------NE--DFVEAYLRKKFQRE
CYP23A1    HTVMQPIMGAYIA----------FPVTSKIPIINGEWNRLMGIKNELLEFLETQIEGHRMNWKDEMIE------------QEPEDLTYAYMIEVEKRK
CYP35A1    EVFSPFDMAVPVW----------FLRT-FFRSRYDMMMTTQNTAKRFAAAEAVKSIETLKT----------------------------------
CYP35B1    DLFTMFDLVVPVW----------FLKS-FFPSRFERVVAIFEKALNYLSREALARYEKLKTGEYSVNA------------EDPQQDFVEAYLAKMEQER
CYP34A1    ENTGFLDIFCPVR----------ILESRFLKWRQDTIFEPFNYILELNKKSIARRVAQLKADEHVLS------------DDPDDFLDAYLLKMQKDK
CYP71A12   ELLGEFPIGDYVP-----ALAW-IDRIN-GFNARIKEV--SQGFSDLMDKVVQEHLEAG-----NHK------------------EDFVDILLSIESEK-
CYP71C1    ALLGGFNVEDYFP-----KLAD-VDLFLRIICAKAKSV--SKRWDSLFNELLSEYALSGGKQGDHNS------------------EDFVHLLLSLQKD--
CYP71D11   KLAGGFNIADLFP-----SAK--WLENLTRMRSKFEYL--HQKMDRILETIIDDHKANSRTKEGQVEG--------------GEEDLIDVLLKYENSS-
CYP726A1   EAATSFGTADAFP-----TWK--LLHYIIGAESKPRRL--HQEIDDILEEILNEHKANKPFEA---------------------DNLMDVLLNLQKN--
CYP71K1    KLLPAQCLPDLFP-----SSR--AAMLVSRMPRRMKRE--RQEMMDFIDDIFQEHHESRAAAG-------------------AEEDLLDVLLRIQSQD-
CYP99A1    LYGSGFCAGDLFP-----SLW--FVDVVTGLTRRLWTA--RRRLDAIFDRILAECEARQRQEEKMT----------------GDDGFLGVLLRIRDDDG
CYP71E1    DMMASFSAEDFFP-----NAAGRLADRLSGFLARRERI--FNELDVFFEKVIDQHMDPARPVPDNG------------------GDLVDVLINLCKE--
CYP71N1    EELSGLFLSDYLP-----LLG--WVDRLSGMRSRLERA--FLKLDSIYQRRIDYHQDRLRQQGKED------------------GDVLDALLRMQKD--
CYP71B2    EALGTFTFSDFFP-----GGLGRFVDWLFQRHKKINKV--FKELDAFYQHVIDDHLKPEGRKNQDI------------------VTLILDMIDKQED--
CYP83A1    SVLGKIFFSDFFP-----YCG--FLDDLSGLTAYMKEC--FERQDTYIQEVVNETLDPKR-VKPET------------------ESMIDLLMGIYKE--
CYP83B1    ALLGTLFFSDLFP-----YFG--FLDNLTGLSARLKKA--FKELDTYLQELLDETLDPNR-PKQET------------------ESFIDLLMQIYKD--
CYP83E1    ALLAASFFADYIP-----FTG--WIDKLRGLHGRVDRN--FKEFDEFYQEIIDEHLDPNREQITDE------------------EDIVDVLLELKKK--
CYP93B1    EIFGEFNVSDFIW-LFKKMDLQGFGKRIEDLFQRFDTL--VERIISKREQTRKDRRRNGKKGEQGSGD-------------GIRDFLDILLDCTEDE-
CYP93C17   KIFGEYSLTDFIW-PLKKLRVGQYEKRIDEIFNKFDPV--IEKVIKKRQEIIK--RRKERNGELEEGE-------------QSVVFLDTLLEYAADE-
CYP93A1    ELMGKFNVSDFIW-YLKPFDLQGFNRKIKETRDRFDVV--VDGIIKQRQEERR------KNKETGTAK-------------QFKDMLDVLLDMHEDE-
CYP705A1   ALSQKFFVSKMFRKLLEKLGISLFKTEIMVVSRRFSEL--VERILIEYEEKMD-----------GHQG-------------T--QFMDALLAAYRDE-
CYP712A1   ELAGKISVGDVLG-PLKVMDFSGNGKKLVAVMEKYDLL--VERIMKEREAKAK----------KKDG-------------TRKDILDILLETYRDP-
CYP75A1    TTAGYFNIGDFIP--------CLAWMDLQGIEKGMKRL--HKKFDALLTKMFDEHKAT------------------SYERKGKPDFLDCVME------
CYP75B1    ALAGVFNIGDFVP--------SLDWLDLQGVAGKMKRL--HKRFDAFLSSILKEHEMN------------------GQDQK-HTDMLSTLIS------
CYP92A2    LLNGVLNIGDSIP--------WIDFMDLQGYVKRMKVV--SKKFDKFLEHVIDEHNIRRN------------------GVENYVAKDMEDVLLQ------
CYP84A1    KLFGAFNVADFIP--------YFGWIDPQGINKRLVKA--RNDLDGFIDDIIDEHMKKKE------------------NQNAVDDGDVVDTDMVDDLLAF
CYP703A2   WLLGVIYLGDYLP--------FWRWVDPSGCEKEMRDV--EKRVDEFHTKIIDEHRRAKLE----------------DEDKNGDMDFVDVLLS------
CYP98A3    KLGASLSIAEHIP--------WLR-WMFPADEKAFAEH--GARRDRLTRAIMEEHTLARQ------------------KSSGAKQHFVDALLT------
CYP706A1   DIEGIQNYSDFFP--------LFSRFDFQGLVKQMKGH--VKKLDLLFDRVMESHVKMVG------------------KKSEEEEDFLQYLLR------
CYP81D1    ANTSSGNAVDYVP--------ILRL--FSSYENRVKKL--GEETDKFLQGLIDDKRGQ----------------------QETGTTMIDHLLV------
CYP81E6    QLSGANNKADFMP--------ILRLVDFEGLEKRVKGI--SSKTDRFLRGLLQEHRDKK---------------------QRTANTMIDHLLT------
CYP81B1    VLAGASNVGDYLP--------VLSWLGVKGLEKKLIKL--QEKRDVFFQGLIDQLRKSKGTED----------------VNKKKTMIELLLS------
CYP82A2    RLAATFTVGDAIP--------YLRWFDFGGYENDMRET--GKELDEIIGEWLDEHRQKRKMG-----------------ENVQDLMSVLLS------
CYP82B1    KLSGVSVASDALP--------LLGLFDLGGKKESMKRV--AKEMDFFAERWLQDKKLSLSLSSETNNKQ-N-------DAGEGDGDDFMDVLMS------
CYP76A2    EWSGIANVSDIFP--------FLKKFDLQSLRKKMARD--MGKAVEIMSMFLKEREE--ERKKG---------------TEKGKDFLDVLLEFQGTG-
CYP76G1    EFAGKPNVADFFP--------LLRFLDPQGIRRKTQFH--VEKAFEIAGEFIRERTEVREREKS---------------DEKTKDYLDVLLEFRGGDG
CYP76E1    EEAGKPNISDFFP--------ILRPLDPQGLYARMTNH--MKKLCEIFDGIIEERICLKDSKGD---------------YEVCNDVLDSLLNINIGE-
CYP76F2    EEAGKPNLVYYFP--------VLRQIDPQGIRRRLTIY--FGRMIEIFDRMIKQRLQLRKIQG-----------------SIASSDVLDVLLNISE-D-
CYP76C1    DAAGTPDAANYFP--------FLRFLDLQGNVKTFKVC--TERLVRVFRGFIDAKIAEKSSQNNP--------------KDVSKNDFVDNLLDYKG---
CYP76B1    VDSAKTNLVDVFP--------VLKKIDPQGIKRGMARH--FSKVLGIFDQLIEERMRTGRFEQG---------------DVLDVCLKMMQ-D-
CYP80A1    MTGGDFDVASYFP--------VLARFDLHGLKRKMDEQ--FKLLIKIWEGEVLARRANRNPEPK---------------DMLDVLI-------
CYP79A1    GLLYAFCVSDYLP--------WLRGLDLDGHEKIVKEA--NVAVNRLHDTVIDDRWRQWKSG-----------------ERQEMEDFLDVLITLKDAQ-
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CYP79B2    GFTFAFCISDYLP--------MLTGLDLNGHEKIMRES--SAIMDKYHDPIIDERIKMWREG-----------------KRTQIEDFLDIFISIKDEQ-
CYP79D1    KYLYGFCISDFLP--------FLLGLDLDGQEKFVLDANKTIFTRDYQNPLIDERIQQWKSG---------------ERKEMEDLLDVFITLKDSD-
CYP79E1    GLIYAFNAADYVS--------WLKFLDLHGQEKKVKKAIDVVNKYFTHDSVIESRRERKVEGR--------------EDKDPEDLLDVLLSLKDSN-
CYP79C1    DCFFSFYVADYYP--------FLRGWNLQGEEAELREA--VDVIARYNKMIIDEKIELWRGQNKDYNRAET-------KNDVPMIKDWLDILFTLKDEN-
CYP79F1    NCLPSFSPADYVER-------WLRGWNVDGQEKRVTEN--CNIVRSYNNPIIDERVQLWR---------E-------EGGKAAVEDWLDTFITLKDQN-
CYP77A6    ITLNPR-LDDYLP--------ILAPFYSKE-RARALEVRCEQVDFIVKLIERRR---RAIQKPGTDK----------TASS-FSYLDTLFDLKTEG-
CYP77B1    LITSPT-LPDFLP---------VFTPLFRRQ-VREARELRKTQLECLVPLIRNNRRKFVDAKENPNEEM----------VSPIGAAYVDSLFRLNLIE-
CYP89A2    LSLTKFNIFNIWP---------KFTKLILRKRWQEFLQIRRQQRDVLLPLIRARRKIVEERKRSEQED----------KKDYVQSYVDTLLDLELPE-
CYP27A1    LMFKNSVYVTFLP---------KWSRPLLP-FWKRYMNNWDNIFSFGEKMIHQKVQEIEAQLQAAGPD-----------GVQVSGYLHFLLTKE----
CYP27B1    SVFVSTLLTMAMP---------HWLRHLVPGPWGRLCRDWDQMFAFAQRHVERREAEAAMRNGGQPEK-----------DLESGAHLTHFLFRE----
CYP11A1    KMFHTSVPLLNLPP--------ELYRLFRTKTWRDHVAAWDTIFNKAEKYTEIFYQDLRQKT-----E----------FRNYPGILYHLLKSE----
CYP11B1    AVFKTTTQLMFLPR--------SLSRWMRSQAWKEHFEAWDYISEYAENRIQKKYEELARG-----------------CSQYNSIVANLMLQG----
CYP12A1    NDFFELGQKIEFGL--------PFWKYIKTPTFKLFMKTLDGLLEIGNKYVNEAIDRLEAERQSGVPE-----------KPENEKSVLEKLIKI----
CYP12C1    EVLMDSFFDLGVRP--------SLYRYIPTPTYKKFSRAMDEIFDTCSMYVNQAIERIDRKSSQGD-------------SNDHKSVLEQLLQI----
CYP74A     NLHP-LLSIGLP---RVIEEPLIHTFSLPPALVKSDYQRLY-EFLRIRGEILVEADK-------------------------------------
CYP74C1    QLAP-LASIGLPKIFSVFEDLIIHTIPLPFFPVKSRYRKLYKAFYSSSGSFLDEAEK-------------------------------------
CYP74D1    QLIPSLSAKKLP---NIIEDMLFHNFLIPFGFIKSDYNKLVDAFSKSAVSMLDEAEK----------------------------------
CYP74B2    QVIPTAKLGVVP---QPLEEILLHTWPYPSLLIAGNYKKLYNFIDENAGDCLRLGQEE---------------------------------
CYP24A1    VTPVELHKRLNTKVWQAHTLAWDTIFKSVKPCIDNRLQRYSQQPGADFLCDIYQQD----------------------------------
CYP10      YNLPTYKLWSTKLWKQFENYSDNVIDIGRSLVEKKWHPCKMEVTQNLHLISYLVNNG----------------------------------
CYP9A1     FRCLPSVAQKLKMSLVPRECSDYFSNVVLTTMKDREKNKVVRNDLININLMEVKKGQLTHEKDDADADAG-------------FATVEESHIGRKQHN-
CYP9B1     MCLLAPKVFNFFKLTIFDSTNVEYFVRLVVDAMQYREKHNITRPDMIQLLMEAKKESK--------------------------------
CYP14A2    KTVQGKTIFLMSAFPWLKHFPVIGELGYHRIKKNIQSYQEFINDEVTSQIKHYDGESE-------------------PENFVHAYMQQMKQSG
CYP21A1    DIIPFLRFFPNPGLWKLKQFQESRDHIVMQELKRHKDSLVAGQWKDMIDYMLQGVEKQRDARD---------------------------
CYP36A1    DAWPWLAYLDKPLSLGIPRTTRANDAIIQNLEQALAKHKTGINYDEEPSSYMDAFLKEMKIRAAEN------------------------
CYP45A1    VAFPMLYDLIRLLIPENKRNNITFIEEHLTKVVKQRREQTQATVVDGLQLLVDAADANVDAS-------------------------
CYP18A1    IPTMQCFPSISTAKNKIAQNRAEMQRFYQDVIDDHKRSFDPNNIRDLVDFYLCEIEKAKAEGTDAELFD-------------------
CYP707A1   NSMPVNLPGTLFHKSMKARKELSQILARILSERRQNGSSHNDLLGSFMGDK-----------------------------
CYP722A1   AFPLNLPWTRFHKGIMARGRVMEMLEKIIRERRNEINSHNNHHEDFLQQLLAVDNDTP---------------------
CYP25A1    AASFILPELAPLWRALYKYTPLADAEIPLVEGLSNVTPFLLENFCSFSLILTKIFSYERRRGGE----------------GSDSVDLLKLLLNREDDKS
CYP73A5    GDFIPILRPFLRGYLKICQDVKDRRIALFKKYFVDERKQIASSKPTGSEGLKCAIDHILEAEQ-----------------------
CYP78A6    DLLGTLNWTDHLP---------WLSEFDPQRLRSRCSTLVPKVNRFVSRIISEHRNQTG--------------------DLPRDFVDVLLSLHGSD-
CYP4A4     FHQSDFLYRLSPEGRLFHRACQLAHEHTDRVIQQRKAQLQQEGELEKVRRKRR-----------------------------LDFLDVLLFAKMENG
CYP719     RISGYARLAEAFYYAKYLPSHKKAEREAFLVKCRVEELVRPLLSSKPPTNSYLYFLLS----------------------------
CYP44A1    LGLPIFRLFSTPSWRKMVDLEDQFYSEVDRLMDDALDKLKVNDSDSKDMRFASYLINR--------------------------
CYP302A1   PTDQGLQLWRFLETPSFRKLSQAQSYMESVALELVEENVRNGSVGSSLISAYVKNPE---------------------
CYP22A1    NCYPWLRYLPEGILRKWTNYKRSGFRLQQWFRTILEEHHVNRHQGDFMSHMIDLQESK------------------------
CYP52A1    NYSQTNQAYRFLLQQMYWILNGSEFRKSIAIVHKFADHYVQKALELTDEDLEKKEGYVFLFELAK-------------------
CYP701A3   IDVDWRDFFPYLKWIPNKSFEARIQQKHKRRLAVMNALIQDRLKQNGSESDDDCYLNFLMS-----------------------
CYP315A1   FPPRLAQILRLPIWRDFEANVDEVLREGAAIIDHCIRVQEDQRRPHDEALYHRLQAAD--------------------------
CYP39A1    VYDEDFEYGSQLPECLLRNWSKSKKWFLELFEKNIPDIKACKSAKDNSMTLLQATLD-------------------------
CYP711A1   DLSGSLSIILGLLIPILQEPFRQVLKRIPGTMDWRVEKTNARLSGQLNEIVSKRAKEAETDS--------------------KDFLSLILKARESDP
CYP46A1    KFLPGKRKQLREVRESIRFLRQVGRDWVQRRREALKRGEEVPADILTQILKAEEG---------------------------
CYP43A1    LKSATQQKFLDYLLHLISNFQSRKNVDNNNGICCTENDHYSLLGFFFEHHNEKKLIEKAEGQIDMKKVK-----------------
CYP59A1    CNGRSNGPRLELPSTPLRRYLTVRPLVMWYNNRLMNRFIDQEVDRAYREQSGRQSKSVISLALRDYMKE-------------------
CYP710A1   IDLPGFAFGEARRAVKRLGETLGICAGKSKARMAAGEEPACLIDFWMQAIVAENPQPP--------------------------
CYP56A1    PFFLTFPFLDVLPIPSRKKAFKDVVSFRELLVKRVQDELVNNYKFEQTTFAASDLIRAHN----------------------
CYP57A1    PNMHAWWLRLSSLLPIEVPIKGLTEYVERRIIQYRLKAAEFGDDAALKGENNFLAKLLLME--------------------
CYP53A1    NRRGEVSATLGCYPALKPFAKYLPDSFFRDGIQAVEDLAGIAVARVNERLRPEVMANN-----------------TRVDLLARLMEGKDSNG
CYP58A1    TKFPKALSSLRYVPPRLLLWLFPQGRIANKYDARTRTQIHKAVTKQHLSKDTTTNSEHTTLFRALAQSD-------------------
CYP20A1    EIGKGFLDGSLDKSTTRKKQYEDALMQLESILKKIKERKGRNFSQHIFIDSLVQG--------------------------
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CYP38A1    VCWRTMEEGVPEAGSKRETEFLKHRRVLEDIIRRIIQERKEGEDLQELPFIDSMLQN-------------------------------------
CYP54A1    WVRPIAAWRLKEVRKLAQMERDATAFLRPVVEARREKQRKGEEKDNDMLQWLMDSADQGQGKQHG--------------------------------
CYP55A1    TNGSSTAREASAAN-----------QELLDYLAILVEQRLVEPKDDIISKLCTEQVKP---------------------------------------
CYP727A1   PFWKPDYRRYRTLCARLKLLTQGIVAKSRNQNGVLSLIDLSSCQRSERMIKDPCRGFSLLDG--------------------VISSRCLNEAAEG-
consensus                             .                                                              .  .
           401......410.......420.......430.......440.......450.......460.......470.......480.......490.......
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CYP7A1    --------------------------------------------TFDDMEKAKTHLAILWASQ--ANTIPATFWSLFQMIRSPDALRAASEEVNGALQSAGQKLSSE--
CYP7B1    --------------------------------------------VHEDLEIGAHHLGFLWASV--ANTIPTMFWAMYYLLRHPEAMAAVRDEIDHLLQSTGQKKGS---
CYP8A1    --------------------------------------------VSEEMQA-RALVLQLWATQ--GNMGPAAFWLLLFLLKNPEALAAVRGELETVLLGAEQPISQ---
CYP8B1    --------------------------------------------VAPAMQD-KFNFMMLWASQ--GNTGPASFWALIYLLKHPEAMRAVKEEATRVLGEPRLEAKQ---
CYP51A1   --------------------------------------------ETTESEVTGLLIAGLFAGQ--HTSSITATWTGAYLIQNKHWWSAALDEQKKLIGKHGDKIDY---
CYP51A2   --------------------------------------------QTTESEVTGLLIAALFAGQ--HTSSITSTWTGAYLMRYKEYFSAALDEQKNLIAKHGDKIDH---
CYP26A1   --------------------------------------------RLDMQALKQSSTELLFGGH--ETTASAATSLITYLGLYPHVLQKVREEIKSKGLLCKS-------
CYP26C1   --------------------------------------------EPSMQELKESAVELLFAAF--FTTASASTSLVLLLLQHPAAIAKIREELVAQGLGRACGCAPGAA
CYP716A1  -----------------------------------------DEDLADKIIGLLIGGH--DTASIVCTFVVNYLAEFPHVYQRVLQEQKEILKEKKE-------
CYP725A1  --------------------------------------------SLTDQGILDNFSAMFHASY--DTTVAPMALIFKLLYSNPEYHEKVFQEQLEIIGNKKE-------
CYP718    --------------------------------------------VITEEEVVDNMVLLVFAAH--DTTSYAMSMTFKMLAQHPTCRDTLLQEHAQIKANKGE-------
CYP90A1   ---------------------------------------------FSDEEIVDFLVALLVAGY--ETTSTIMTLAVKFLTETPLALAQLKEEHEKIRAMKSDS------
CYP90B1   --------------------------------------------SNLSTEQILDLILSLLFAGH--ETTSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELG-----
CYP724A1  -------------------------------------------LNYEEKVSIVLDILLGGF--ETSATTLSLVVYFLAKSPNLLHKLKEEHAAIRAKKGDG-----
CYP720A1  -------------------------------------------LPNESMADFIINLLFAGN--ETTISKTMLFAVYFLTHCPKAMTQLLEEHDRLAGG---------
CYP85A1   --------------------------------------------YPLTDEEIRDQVVTILYSGY--ETVSTTSMMALKYLHDHPKALQELRAEHLAFRERKQD------
CYP87A2   --------------------------------------------TILTEEIALDLMFVLLFASF--ETTSLALTLAIKFLSDDPEVLKRLTEEHETILRNNREDA------
CYP708A1  --------------------------------------------DTINEERSVELILSLLIASY--ETTSTMTALTVKFIAENPKVLMELKREHETILQNRADK------
CYP702A1  --------------------------------------------ETMSVDNAIEYIYTLFLLAN--ETTPRILAATIKLISDNPKVMKELHREHEGIVRGKTEK------
CYP88A3   ---------------------------------------------TLDDEEIIDVLLMYLNAGH--ESSGHTIMWATVFLQEHPEVLQRAKAEQEMILKSRPEG------
CYP88B1   --------------------------------------------MLSDKKIIEILVLFSFAGF--EPVALMSVKAIFHLQKHPHFLEKAKEEQEEIVKRRASS------
CYP3A1    -----------------------------------DKESHTALSDMEITAQSIIFIFAGY--EPTSSTNTLSFVLHSLATHPDTQKKLQEEIDRALPNKA--------
CYP5A1    SVGVENFDIVRQAFSSAKGCPADPSQPHLPRPLSKPLTVDEVVGQAFLFLIAGY--EIITNTLSFVTYLLATNPDCQEKLLREVDIDFSKKHP--------
CYP6A2    ---GRVTLD--------------------NGEVIEGMDIGELAAQVFVFYVAGF--ETSSSTMSYCLYELAQNQDIQDRLRNEIQTVLEEQE--------
CYP6B4    IEPMKKTHD-------------------EQVTTLELTDSVIAAQTFIFYAAGY--ETSASTMSFLLFELAENPDIQEKVIAEVDETLKRHN--------
CYP28A1   -----------------------------KNLDTRHLTAHTMTFLLDGF--ETTA-LYDSCALVLSRDQEAQQKLREELEAHLDD-K--------
CYP28C1   -----------------------------LDLSEEDMASHAMTFMFDGL--DTTSNSIAHCLLLLGRNPDCQRRLYEELQLVNPG-G-------
CYP13A2   DFSAEAREDFSKR----------------NLKITKELSADEVVGQCFLFLIGGF--DTTALSLSYVTYLLAVNPKIQEKVIEEIAREFGT----------
CYP13B1   EDIEFG-----------------------STVEKKVTAEDVIGACFVFLLAGF--DTTANSLAYASYLLAKHPEKMKLAQEEVDTVVGS----------
CYP72A8   -----------------------------HGMSIEDVVEECRLFHFAGQ--ETTAVLLVWTMIMLSHHQKWQDQAREEILKVIGKN---------
CYP72B1   -----------------------------VTVQDIVEECKSFFFAGK--QTTSNLLTWTTILLSMHPEWQAKARDEVLRVCGSR---------
CYP721A1  ----------------------------EKLGIEEVTDECKTFYFAAK--ETTANLMTFVLVLLAMNQEWQNIAREEVICVLGQT---------
CYP709A1  N----------------------------NNNNNNNLQLIMDECKTFFFAGH--ETTALLLTWTTMLLADNPTWQEKVREEVREVFGRN---------
CYP709B1  -----------------------------GKERKMSIEEIIHECRTFFFGGH--ETTSNLLAWTTMLLSLHQDWQEKLREEIFKECGKE---------
CYP715A1  ----------------------------NFTAKELVDECKTFFFAGH--ETTIALALTWTFMLLAIHPEWQDTIREEIREVIGDS---------
CYP714A1  DG---------------------------NLEDKTQSYKSFVVDNCKSIYFAGH--ETSAVAVSWCLMLLALNPSWQTRIRDEVFLHCKN---------
CYP4C3    -----------------------------VLSNEDIREEVDTFMFEGH--DTTSAAISWTLFLLGCHPEYQERVVEELDSIFGDDKETP-----
CYP31A2   -----------------------------QMDETDVQAEVDTFMFEGH--DTTSTGLMWAIHLLGNHPEVQRKVQAELDEVMGDDED-------
CYP37A1   -----------------------------GLGYEDIREEVDTFMFEGH--DTTSAGIGWSLWCLANCPEYQKKCHEELDEIFEGTSRE-------
CYP37B1   -----------------------------LMNEDDIREEVDTFMFEGH--DTTSASMGWTLWCLAHNPEFQEKVIQEVDGIFGTSDRD------
CYP32A1   -----------------------------TLSDEDIREEVDTFMFEGH--DTTSSGIGFTILWLGFYPECQKKLQKELDEVFGFETNQP-----
CYP29A2   -----------------------------QLTSEDIRQEVDTFMFAGH--DTTTSSTSWACWNLAHNPNVQEKVYKEMIEVFGDDPNTD-----
CYP86A1   -----------------------------VNGNVLPTDVLQRIALNFVLAGR--DTSSVALSWFFWLVMNNREVETKIVNELSMVLKETR--G----
CYP86B1   -----------------------------EKGESFSDKFLRDICVNFILAGR--DTSSVALSWFFWLLEKNPEVEEKIMVEMCKILRQRDDHG-----
CYP96A1   TT---------------------------KYKLLNPSDDKFLRDMILSFMLAGR--DTTSSALTWFFWLLSKNPKAITKIRQEINTQLSPRT--------
CYP96C1   HV---------------------------VLKSVDASDN-LLRDTVKGILLAGT--DTTATVLSWFFWLILKNPRVEQKIREEIELYLKQKN--------
CYP94A1   ---------------------------------EDFVADIVISFILAGK--DTTSAALTWFFWLLWKNPRVEEEIVNELSKK-----------
CYP94B1   ---------------------------------EEAVRDSVISFIMAGR--DTTSAAMTWLFWLLSQNDDVETKILDELRNK-----------
CYP704A1  -----------------------------ENMNDKYLRDIILNVMVAGK--DTTAASLSWFLYMLCKNPLVQEKIVQEIRDVTSSHEKTT-----
CYP704B1  -----------------------------SKETEKSLRDIVLNFVIAGR--DTTATTLTWAIYMIMMNENVAEKLYSELQELEKESAEATNTSLH
CYP97A3   -----------------------------GDDVSSKQLRDDLMTMLIAGH--ETSAAVLTWTFYLLTTEPSVVAKLQEEVDSVIGDRF--------
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CYP97B3    --------------------------------------------GVDIDDRQLRDDLMTMLIAGH--ETTAAVLTWAVFLLSQNPEKIRKAQAEIDAVLGQGP--------
CYP1A1     AN----------------------------------------VQLLSDEKIINIVLDLFGAGF--DTVTTAISWSLMYLVMNPRVQRKIQEELDTVIGR-SRRPRLS--
CYP1B1     GDSP------------------------------------SGLDLEDVPATITDIFGASQ--DTLSTALLWLLILFTRYPDVQARVQAELDQVVGR-DRLPCMS--
CYP17A1    DS-------------------------------------NLFSDKHILTTLGDIFGAGV--ETSSSVVLWVIAFLLHNPQVKKKIQEEIDHNVGF-SRTPTFS--
CYP19A1    DS-------------------------------------KLLSNRHMLATIGDIFGAGV--ETTSVIKWIVAYLLHHPSLKKRIQDDIDQIIGF-NRTPTIS--
CYP2A7     KNPN--------------------------------TEFYLKNLMMSTLNLFIAGT--ETVSTTLRYGFLLLMKHPEVEAKVHEEIDRVIGK-NRQPKFE--
CYP2M1     DDPN--------------------------------TEFNNGNMVMTAWSLFAAGT--ETTSSTLRQSFLMMIKYPHIQESVQKEIDEVIG--SRVPTVD--
CYP33A1    AEG------------------------------DFASFSNEQLKNMCFDMWVAGM--HTTNTMGFLTAFALNNMDAQRKMQKELTEVIG--DRVVTMK--
CYP33C1    SEANS----------------------------KNLNFSNIQLLNVCIDLWFAGL--NTTTNTITWAISYVLHHPEVQDKIHEELDKVIGS-DRLITTA--
CYP33B1    QKN------------------------------DFDSYCDSQLENVCFDIWAAGF--DTLTNTVGFLIAYAINYPEMQMLIHQEIDNYLAHHSRLLTLA--
CYP23A1    RNGE-----------------------------DVGFFDDQQLKMLLLDLFFAGM--ETTVTTLKWAFLLMAKNQKVQKNVQAELDSIGQP---MIEIQ--
CYP35A1    ----------------------------------MIIDLWMTGQ--ETTTTLISGFTQLLLHPEVMVKAREEILKITENGSRHLSLT--
CYP35B1    LRDS--------------------------DTPYTMECLKFVIGDLWLAGQ--DTTSTTLVAGFNHLVKNPEIVRKCREEILRITENGSRPLQLK--
CYP34A1    NEGL--------------------------ETTFTLENLAVDMYDLWLGGQ--ETTSTTLNWACACLLNRPDVITTAREELIRVTG-GHRSLSLI--
CYP71A12   ---------------------------SIGFQAQRDDIKFMI-LDMFIGGT--STSSTLLEWIMTELIRNPNVMKKLQDEIRSTIRPHG-SYIKEK-
CYP71C1    ---------------------------YGLTTDNIKGIL-VNMFEAAI--ETSFLVLEYSMSELMNNRHVLAKLQKEVR-TATPDG-RMVMEE-
CYP71D11   ---------------------------TDQDFHLTIRNIKAIL-FDIFIAGS--ETSATTINWTMAEMMKDPILLKKAQDEVREIFQ--RRGKVDET-
CYP726A1   ---------------------------GNVPVPVTNESIKASV-LQMFTAGS--ETTSKATEWVMAELMKNPTELRKAQEEVRQVFG--EMGKVDES-
CYP71K1    ---------------------------KTNPALTNDNIKTVI-IDMFVASS--ETAATSLQWTMSELMRNPRVMRKAQDEVRRALAIAGQDGVTEE-
CYP99A1    ---------------------------EPETGGISTTSIKAIL-FDMLAGGT--ETTSSAAEWIMSELMRKPEAMAKAQAEVRGALDGKSPE-DHEG-
CYP71E1    ---------------------------HDGTLRFTRDHVKAIV-LDTFIGAI--DTSSVTILWAMSELMRKPQVLRKAQAEVRAAVGDDKPRVNSE--
CYP71N1    ---------------------------EEG---LTEDHIKGVL-MDIFIAGT--DTSSATVEWAMAELIRQPELMKRAQDEVRRCVGS-KGEVEES--
CYP71B2    ---------------------------SDS-FKLNMDNLKAIV-MDVFLAGI--DTSAVTMIWAMTELIRNPRVMKKAQESIRTTLGLKKERITEE-
CYP83A1    ---------------------------QPFASEFTVDNVKAVI-LDIVVAGT--DTAAAAVVWGMTYLMKYPQVLKKAQAEVREYMKEKGSTFVTED-
CYP83B1    ---------------------------QPFSIKFTHENVKAMI-LDIVVPGT--DTAAAVVWAMTYLIKYPEAMKKAQDEVRSVIGDKG--YVSEE-
CYP83E1    ---------------------------RSFSFDINFDHIKGIL-TDMLVAAT--DTTSAASVWAMTALIKNPRVMSKVKGEIRNLGVKKD--FLYED-
CYP93B1    ---------------------------NSEIKIQRVHIKALI-MDFFTAGT--DTTAISTEWALVELVKKPSVLQKVREEIDNVVGKDR--LVEES-
CYP93C17   ---------------------------NMEIKITKEQIKGLV-VDFFSAGT--DSTAVATDWALAELINNPRVLKKAREEVDSVVGKDR--LVDES-
CYP93A1    ---------------------------NAEIKLDKKNIKAFI-MDIFVAGT--DTSAVSIEWAMAELINNPDVLEKARQEIDAVVGKSR--MVEES-
CYP705A1   ---------------------------NTEYKITRSHIKSLLTVEFFIGAA--DASSIAIQWAMADIINNREILEKLREEIDSVVGKTR--LVQET-
CYP712A1   ---------------------------TAEMKITRNDMKSFL-LDVFMAGT--DTSAAAMQWAMGQLINHPQAFNKLREEINNVVGSKR--LVKES-
CYP75A1    -------NRD----------------NSEGERLSTTNIKALLLNLFTAGT--DTSSSAIEWALAEMMKNPAILKKAQGEMDQVIGN-NRRLLES--
CYP75B1    -------LKGTD--------------LDGDGGSLTDTEIKALLLNMFTAGT--DTSASTVDWAIAELIRHPDIMVKAQEELDIVVGR-DRPVNES--
CYP92A2    -------LADD---------------PKLEVKLERHGVKAFTQDMLAGGT--ESSAVTVEWAISELSKKPEIFKKATEELDRVIGQ-NRWVQEK--
CYP84A1    YSEEAKLVSETA-------------DLQNSIKLTRDNIKAIIMDVMFGGT--ETVASAIEWALTELLRSPEDLKRVQQELAEVVGL-DRRVEES--
CYP703A2   -------LPGE---------------NGKAHMEDVEIKALIQDMIAAT--DTSAVTNEWAMAEAIKQPRVMRKIQEELDNVVGS-NRMVDES--
CYP98A3    ----------LK---------DQYD---LSEDTIIGLLWDMITAGM--DTTAITAEWAMAEMIKNPRVQQKVQEEFDRVVGL-DRILTEA--
CYP706A1   ----------VK---------DDDEKAPLSMTHVKSLLMDMVLGGV--DTSVNASEFAMAEIVSRPEVLNKIRLELDQVVGK-DNIVEES--
CYP81D1    ------LQKSD--------------IEYYTDQIIKGIILIMVIAGT--NTSAVTLEWALSNLLNHPDVISKARDEIDNRVGL-DRLIEEA--
CYP81E6    ------LQESQ--------------PEYYTDQIIKGLALAMLLAGT--DSSAVTLEWSMCNVLNYPEVLEKIKAELDTHVGQ-DRLVDES--
CYP81B1    ------LQETE--------------PEYYTDAMIRSFVLVLLAAGS--DTSAGTMEWVMSLLLNHPQVLKKAQNEIDSVIGK-NCLVDES--
CYP82A2    ------LLEG---------------KTIEGMNVDIVIKSFVLTVIQAGT--EASITTLIWATSLILNNPSVLEKLKAELDIQVGK-ERYICES--
CYP82B1    ------ILPDDD-------------DSLFTKYSRDTVIKATSLSMVVAAS--DTTSVSLTWALSLLLNNLQVLRKAQDELDTKVGR-DRHVEEK--
CYP76A2    ---------------------------KDEPAKLSEHEIKIFVLEMFLAGT--ETTSSSVEWALTELLRHPEAMAKVKTEISQAIEP-NRKFEDS--
CYP76G1    ---------------------------VDEEPSSFSSRDINVIVFEMFTAGT--DTTSTLEWALAELLHNPRTLTKLQTELRTYFKSSNQKLQEE--
CYP76E1    ---------------------------ATSELSRNEMVHLFLDLFVAGI--DTSSMIEWIIAELLRNPDKLTKVRKELCQTIGK-GETIEES--
CYP76F2    ---------------------------NSNEIERSHMEHLLLDLFAAGT--DTTSSTLEWAMAELLHNPETLLKARMELLQTIGQ-DKQVKES--
CYP76C1    ---------------------------DESELSISDIEHLLLDMFTAGT--DTSSSTLEWAMTELLKNPKTMAKAQAEIDCVIGQ-NGIVEES--
CYP76B1    ---------------------------NPNEFNHTNIKALFLDLFVAGT--DTTSITIEWAMTELLRKPHIMSKAKEELEKVIGK-GSIVKED--
CYP80A1    ---------------------------ANDFNEHQINAMFMETFGPGS--DTNSNIIEWALAQLIKNPDKLAKLREELDRVVGR-SSTVKES--
CYP79A1    ---------------------------GNPLLTIEEVKAQSQDITFAAV--DNPSNAVEWALAEMVNNPEVMAKAMEELDRVVGR--ERLVQES-
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CYP79B2   -------------------------------------GNPLLTADEIKPTIKELVMAAP--DNPSNAVEWAMAEMVNKPEILRKAMEEIDRVVGK--ERLVQES-
CYP79D1   -------------------------------------GNPLLTPDEIKNQIAEIMIATVFTDNPSNAIEWAMGEMLNQPEILKKATEELDRVVGK--DRLVQES-
CYP79E1   -------------------------------------GKPLLDVEEIKAQIADLTYATVDNFTPSNAVEWALAEMLNNPDILQKATDEVDQVVGR--HRLVQES-
CYP79C1   -------------------------------------GKPLLTPQEIT-HLSDLDVVGI--DNAVNVIEWTLAEMLNQREILEKAVEEIDMVVGK--ERLVQES-
CYP79F1   -------------------------------------GKYLVTPDEIKAQCVEFCIAAI--DNPANNMEWTLGEMLKNPEILRKALKELDEVVGR--DRLVQES-
CYP77A6   -------------------------------------RITTPSNEELVSLCSEFLNGGT--DTIGTAIEWGIAQLIVNPEIQSRLYDEIKSTVG--DREVEEK--
CYP77B1   -------------------------------------RGGELGDEEIVTLCSEIVSAGT--DTSATTLEWALFHLVTDQNIQEKLYEEVVGVVGK-NGVVEED--
CYP89A2   -------------------------------------ENRKLNEEDIMNLCSEFLTAGT--DTTATALQWIMANLVKYPEIQERLHEEIKSVVGEEAKEVEEE--
CYP27A1   ----------------------------------LLSPQETVGTFPELILAGV--DTISNTLTWALYHLSKNPEIQEALHKEVTGVVPFG--KVPQNK-
CYP27B1   ----------------------------------ELPAQSILGNVTELLLAGV--DTVSNTLSWALYELSRHPEVQTALHSEITAALSPGSSAYPSAT-
CYP11A1   ----------------------------------KMLLEDVKANITEMLAGGV--DTTSMTLQWHLYEMARSLNVQEMLRKEVLNARRQAEGDISK---
CYP11B1   ----------------------------------NLPLRAMKANIMDLVAGSV--DTTALPLMMTLFELARNPTVQQALRQESMATEPNIYENPQR---
CYP12A1   ----------------------------------DRKIATVMA--IDMILAGV--DTTSTTFTALLLCLAKNPEKQEKLREEIRQILPRKDSQFEPS--
CYP12C1   ----------------------------------DRKLAVVMA--MDMLMGGV--DTTSTAISGILLNLAKNPEKQQRLREEVLSKLTSLHSEFTVE--
CYP74A    ----------------------------------LGISREEATHNLLFATSFNTWGGMKILFPNMVKRIGPGGHQVHNRLAEEIRSVIKSNGGELTMGA-
CYP74C1   ----------------------------------QGIDREKACHNLVFLAGFNAYGGMKVLFPTILKWVGTGGEDLHRKLAEEVRTTVKEEGG-LTFSA-
CYP74D1   ----------------------------------LGIKREEAVQNILFLVGINMFAGLNAFFPHLFRFVGEAGASLHTQLAKEIRSVIKEEGGAITLSA-
CYP74B2   ----------------------------------FGLTRDEAIQNLLFVLGFNAYGGFSVFLPSLIGRITGDNSGLQERIRTEVRRVCG-SGSDLNFKT-
CYP24A1   ----------------------------------HLSKKELYAAVTELQLAAV--ETIANSLMWILYNLSRNPQAQRRLLQEVQSVLPDNQTPR-----
CYP10     ----------------------------------SMSTKEVTGLIVDLMLAAV--ETISSATVWCLYNLAKNPQVQEKLFQEITEAQAKNNGTISAED-
CYP9A1    ----------------------------------YEWTDSDLIAQCAALFLFAGF--DTVSTSMSFLLYELAVNPDVQDRLLQEIREYDEKNHGKIDYN--
CYP9B1    ----------------------------------DNWTDDEIVAQCFIFFFAAFE--NNSNLICTTAYELRNLDIQERLYEEVKETQEALKGAPLTYD-
CYP14A2   ----------------------------------NPNLDMNNLCASVIDFWLAGM--ETISNSLRWHLAFMMKYPEIQDKVRKEILDNVGTARLPSMSDK-
CYP21A1   ----------------------------------PGQLHERHVHMSVVDLFVGGT--ETTAATLSWAVAFLLHHPEIQKRLQEELDLKLAPSSQLLYKN--
CYP36A1   ----------------------------------ALEDGFTEKQLIVAIYDLYSAGM--ETIIVLRFAFLYLVNNPETQKRIHEELDRNVGRERQVVMDDQ-
CYP45A1   ----------------------------------KTKLTDEEVVDNAFLFLLAGF--ETTSTALTYTSYLLALNPDIQEKIFQEVEEVVGLERAPSYED--
CYP18A1   ----------------------------------GKNHEEQLVQVIIDLFSAGM--ETIKTTLLWINVFMLRNPKEMRRVQDELDQVVGRHRLPTIED--
CYP707A1  ----------------------------------EELTDEQIADNIIGVIFAAR--DTTASVMSWILKYLAENPNVLEAVTEEQMAIRKDKEEGESLTWG
CYP722A1  ----------------------------------QLTDAEIKDNILTMIIAGQ--DTTASALTWMVKYLGENQKVLDILIEEQSQITKKASNKPFLEL-
CYP25A1   ----------------------------------KPMTKQEVIENCFAFLLAGY--ETTSTAMTYCSYLLSKYPNVQQKLYEEIMEAKENGGLTYDS---
CYP73A5   ----------------------------------KGEINEDNVLYIVENINVAAI--ETTLWSIEWGIAELVNHPEIQSKLRNELDTVLGPGVQVTEP---
CYP78A6   ----------------------------------KLSDPDIIAVLWEMIFRGT--DTVAVLIEWILARMVLHPDMQSTVQNELDQVVGKSRALDESD--
CYP4A4    ----------------------------------SSLSDQDLRAEVDTFMFEGH--DTTASGVSWIFYALATHPEHQRCREEIQGLLGDGASITWEH--
CYP719    ----------------------------------QNFEEEVIIFCIFELYLLGV--DSTSSTTTWALAYLIREQGAQEKLYQDIRMTLGDVDLVKIED--
CYP44A1   ----------------------------------KELNRRDVKVILLSMFSDGLS--TTAPMLIYNLYNLATHPEALKEIQKEIKEDPAS----------
CYP302A1  ----------------------------------LDRSDVVGTAADLLLAGI--DTTSYASAFLLYHIARNPEVQQKLHEEARRVLPSAKDELSMD--
CYP22A1   ----------------------------------QEQFRDLSIILTCGDMWTGGM--ETTVTTLRWGIIYLLNNPEVQAKCQMEILDVFGNDIPDMG----
CYP52A1   ----------------------------------QTRDPKVLRDQLLNILVAGR--DTTAGLLSFLFFELSRNPEIFAKLREEIENKFGLGQDARVEEIS
CYP701A3  ----------------------------------EAKTLTKEQIAILVWETIIETA--DTTLVTTEWAIYELAKHPSVQDRLCKEIQNVCGGEKFKEE----
CYP315A1  ----------------------------------VPGDMIKRIFVDLVIAAG--DTIAFSSQWALFALSKEPRLQQRLAKERATNDSR----------
CYP39A1   ----------------------------------IVETETSKENSPNYGLLLLWASLSNAVPVAFWTLAYVLSHPDIHKAIMEGISSVFGKAGKDKIKVS-
CYP711A1  ----------------------------------FAKNIFTSDYISAVTYEHLLAGS--ATTAFTLSSVLYLVSGHLDVEKRLLQEIDGFGNRDLIPTAHD--
CYP46A1   ----------------------------------AQDDEGLLDNFVTFFIAGH--ETSANHLAFTVMELSRQPEIVARLQAEVDEVIGSKRYLDFED--
CYP43A1   ----------------------------------VEKSISYEEITAQCKFISVAGF--DTISNTLTLLFNFLANNPDVQDKIYEAEIKNQPEQISFETVS--
CYP59A1   ----------------------------------KDGSLEDFKRRVAPQLRVFLAGR--DTTSSTLLYAFYLLSRHPEALAKVRLEHDQVFGPYHQQVHEKIH
CYP710A1  ----------------------------------HSGDEEIGGLLFDFLFAAQ--DASTSSLLWAVTLLDSEPEVLNRVREEVAKIWSPESNALITVD-
CYP56A1   ----------------------------------NEIIDYKQLTDNIVIILVAGHE-NPQLLFNSSLYLLAKYSNEWQEKLRKEVNGITDPKG--------
CYP57A1   ----------------------------------KKGTVTPVETQQAVGLNIGAGSDTTANALSTILYYLYTNPRTLHTLREELERYVKDGPISFQQS--
CYP53A1   ----------------------------------EKLGRAELTAEALTQLIAGS--DTTSNTSCAILYWCMRTPGVIEKLHKALDEAIPQDVDVPTHA--
CYP58A1   ----------------------------------NLSPADKAEERLVREAKLIFLGGT--ISTGRTLSFVSYYILSRPDIKARLEDELRDVMATWPEVVPTWT-
CYP20A1   ----------------------------------NLNDQQILEDTMIFSLASC--MITAKLCTWAVCFLTTYEEIQKKLYEEIDQVLGKGPITS-----
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CYP38A1     ------------------------------------YDSEDKIIADAISFMVGGF--HTSGYMFTWMLWYLSSHPESQDRLRTEIERETGGERGDRLKEY-
CYP54A1     -----------------------------KWGEDTTTTRKLARLQLAISFAAIHTTTLVTTHAVYSLAADPKLQATLREEIQSVLQEHKGVFNTS--
CYP55A1     ------------------------------GNIDKSDAVQIAFLLLVAGN--ATMVNMIALGVATLAQHPDQLAQLKANPS----------------
CYP727A1    ------------------------------PLSSEEEICGNIMGLMLHGIS--TCANLIGNILTRLALYPNLQCQLHSEIVSGHSESSELKIDD--
consensus                                     .     .  .. ..:..  ...   .  .  .  .  ...  .. ...  ...
            501......510.......520.......530.......540.......550.......560.......570.......580.......590........
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CYP7A1     ----------------GNAIYLDQIQLNNLP--VLDSIIKEALRLS-SASLNIRTAKEDFTLHLEDG------SYNIRKDDIIALYPQLMHL-DPAIYPDP
CYP7B1     ----------------GFPIHLTREQLDSLI--CLESSIFEALRLS-SYSTTIRFVEEDLTLSSETG------DYCVRKGDLVAIFPPVLHG-DPEIFEAP
CYP8A1     -----------------MTTLPQKVLDSMP--VLDSVLSESLRLT-AAPFITREVVADLALPMADGR-----EFSLRRGDRLLLFPFLSPQKDPEIYTDP
CYP8B1     ------------------SFTVQLSALQHIP--VLDSVMEETLRLG-AAPTLYRVVQKDILLKMASGQ-----ECLLRQGDIVTLFPYLSVHMDPDIHPEP
CYP51A1    -----------------DVLSEMD--FLFRSAKEALRLHPPKILLLRTVHSDFTVTTREGK-----QYEIPKGHIVATSPAFANR-LPHVYKDP
CYP51A2    -----------------DILSEMD--VLYRCIKEALRLHPPLIMLMRASHSDFSVTARDGK-----TYDIPKGHIVATSPAFANR-LPHIFKDP
CYP26A1    ---------------NQDNKLDMETLEQLK--YIGCVIKETLRLNPPVPGGFRVALKTFELNG---------YQIPKGWNVIYSICDTHDVADIFTNKE
CYP26C1    GGS-----EGPPPDCGCEPDLSLAALGRLR--YVDCVVKEVLRLLPPVSGGYRTALRTFELDG---------YQIPKGWSVMYSIRDTHETAAVYRSPP
CYP716A1   ----------------KEGLRWEDIEKMR--YSWNVACEVMRIVPPLSGTFREAIDHFSFKG---------FYIPKGWKLYWSATATHMNPDYFPEPE
CYP725A1   ----------------GEEISWKDLKSMK--YTWQAVQESLRMYPPVFGIFRKAITDIHYDG---------YTIPKGWRVLCSPYTTHLREEYFPEPE
CYP718     ----------------GEYLTVEDVKKMK--YSWQVVRETMRLSPPIFGSFRKAVADIDYGG---------YTIPKGWKILWTTYGTHYNPEIFQDPM
CYP90A1    ----------------YSLEWSDYKSMP--FTQCVVNETLRVANIIGGVFRRAMTDVEIKG---------YKIPKGWKVFSSFRAVHLDPNHFKDAR
CYP90B1    ----------------ESELNWDDYKKMD--FTQCVINETLRLGNVVRFLHRKALKDVRYKG---------YDIPSGWKVLPVISAVHLDNSRYDQPN
CYP724A1   ----------------ELLNWEDYQKME--FTQCVISEALRCGNIVKTVHRKATHDIKFNE---------YVIPKGWKVFPIFTAVHLDPSLHENPF
CYP720A1   ----------------MLTWQDYKTMD--FTQCVIDETLRLGGIAIWLMREAKEDVSYQD---------YVIPKGCFVVPFLSAVHLDESYYKESL
CYP85A1    ----------------EPLGLEDVKSMK--FTRAVIYETSRLATIVNGVLRKTTRDLEINGG---------YLIPKGWRIYVYTREINYDANLYEDPL
CYP87A2    ----------------DSGLTWEEYKSMT--YTFQFINETARLANIVPAIFRKALRDIKFKD---------YTIPAGWAVMVCPPAVHLNPEMYKDPL
CYP708A1   ----------------ESGVTWKEYRSMMNFTHMVVINESLRLGSLSPAMFRKAVNDVEIKG---------YTIPAGWIVLVVPSLLHYDPQIYEQPC
CYP702A1   ----------------ETSITWEEYKSMT--FTQMVINESLRITSTAPTVFRIFDHEFQVGS---------YKIPAGWIFMGYP-NNHFNPKTYDDPL
CYP88A3    ----------------QKGLSLKETRKME--FLSQVVDETLRVITFSLTAFREAKTDVEMNG---------YLIPKGWKVLTWFRDVHIDPEVFPDPR
CYP88B1    ----------------NAGLSFDEIRQMT--FVSKIINETLRIATDQSVFLRDTSTTFNING---------YTIPKGWKFFAVVWNIHMNPDVYVQPK
CYP3A1     ----------------PP-TYDTVMEME--YLDMVLNETLRM--YPIGNRLERVCKKDVEING--------VFMPKGSVVMIPSYALHRDPQHWPE-P
CYP5A1     ----------------SPEHCSLQQGLP--YLDMVLSETLRM--YPPAFRFTREAARDCEVLG--------QRIPAGTVLEVAVGALHHDPKWPH-P
CYP6A2     ----------------GQLTYESIKAMT--YLNQVISETLRL--YTLVPHLE-RKALNDYVVP----GHEKLVIEKGTQVIIPACAYHRDEDLYPN-P
CYP6B4     ----------------GEITYDTLSEMT--YLTQVFHETLRK--YPVADILL-RNAKADYAVP----GTN-VTLKKGQTVVVSGFGIHYDPKYYPD-P
CYP28A1    ----------------GIIDFEKLNELP--FLDACVQESLRI--FPPAFMSN-KLCTEPIELP-NK-TGENFTVERGTTVVVPHYCFMMDEEFFPD-P
CYP28C1    ----------------YLPDLDALIDLP--YLSACFNESLRI--YPAGGWAS-KTCTKEYELRGSH-HSEPLKLRPGDHVMVPIYALHNDPDLYPE-P
CYP13A2    ----------------SEVEFEKLGRLK--YMDCVIKEALRL--YPLASISNSRKCMKTTTVN-------GVKIEAGVYVQMDTWSLHYDPELWGEDV
CYP13B1    ----------------ENVSYDDMTKLK--YLDAVVRESLRL--YPVAWFACSRECVKPTTLG-------DIYIDKGVKIEADVMSLHRSKEIWGENA
CYP72A8    ----------------NKPNFDALSRLK--TMSMILNEVLRL--YPPGILLGRTVEKETKLGED------MTLPGGAQVVIPVLMVHRDPELWGEDV
CYP72B1    ----------------DVPTKDHVVKLK--TLSMILNESLRL--YPPIVATIRRAKSDVKLGG-------YKIPCGTELLIPIIAVHHDQAIWGNDV
CYP721A1   ----------------GLPTLDILQDLK--TLSMIINETLRL--YPPAMTLNRDTLKRAKLGD--------LDIPAGTQLYLSVVAMHHDKETWGDDA
CYP709A1   ----------------GLPSVDQLSKLT--SLSKVINESLRL--YPPATLLPRMAFEDLKLGD--------LTIPKGLSIWIPVLAIHHSEELWGKDA
CYP709B1   ----------------KTPDSETFSKLK--LMNMVIMESLRL--YGPVSALAREASVNIKLGD--------LEIPKGTTVVIPLLKMHSDKTLWGSDA
CYP715A1   ----------------KIEYN-KLAGLK--KMSWVMNEVLRL--YPPAPNAQRQARNDIEVNG--------RVIPNGTNIWIDVVAMHHDVELWGDDV
CYP714A1   ----------------GIPDADSISNLK--TVTMVIQETLRL--YPPAAFVSREALEDTKLGN--------LVVPKGVCIWTLIPTLHRDPEIWGADA
CYP4C3     -----------------ATMKNLMDMR--YLECCIKDSLRL--FPSVPMMARMVGEDVNIGG--------KIVPAGTQAIIMTYALHRNPRVF-PKP
CYP31A2    -----------------VTIEHLSRMK--YLECALKEALRL--FPSVPIITRELSDDQVIGG--------VNIPKGVTFLLNLYLVHRDPAQW-KDP
CYP37A1    -----------------CSVEDLKKMK--YLEKCVKEALRM--RPSVPQMARSVEEEVEIDG--------KILPKGCSVMISPAFIQNNPRTF-PNH
CYP37B1    -----------------CTNDDLKQMK--YLEKCLKESLRM--YPSVPFFGRTVEQDVVING--------DFFPKGVRIIVMPLLLQRNPLIF-DNP
CYP32A1    -----------------PSMDDIKKCS--YLEKCIKESLRM--FPSVPLIARRLSEDVTINHP---SGQKIVLPAGLAACVSPIAAARDPRAW-PDP
CYP29A2    -----------------ITLENVNNLN--YLDIVLKESKRI--IAPVPALQRKLTNDLEIDG--------YIVPAGGNVTISPMVLHSNHHVF-KNP
CYP86A1    ----------NDQEKWTEEPLEFDEADRLV--YLKAALAETLRL--YPSVPQDFKYVVEHDVLP-------DGTFVPRGSTVTYSIYSIGRMKTIWGEDC
CYP86B1    ----------NAEKSDYEPVFGPEEIKKMD--YLQAALSEALRL--YPSVPVDHKEVQEDDVFP-------DGTMLKGDKVIYAIYAMRMEAIWGKDC
CYP96A1    ----------NDFDSFN-AQELNKLV--YVHGALCEALRL--YPPVPFQHKSPTKSDVLP-------SGHRVDASSKIVFCLYSLGRMKSVWGEDA
CYP96C1    ----------GEHGLYTNPEELNELM--YLHAAIYETMRL--YPAAPFTSRKSIQADVFP-------TGHQVNPNTTIVMAYYAVGRMKSIWGEDC
CYP94A1    ----------SEL-MVYDEVKEMV--YTHAALSESMRL--YPPVPMDSKEAVNDDVLP-------DGWVVKKGTIVTYHVYAMGRMKSLWGDDW
CYP94B1    ----------GSLGLGFEDLREMS--YTKACLCEAMRL--YPPVAWDSKHAANDDILP-------DGTPLKGDKVTYFPYGMGRMEKVWGKDW
CYP704A1   -----DVNGFIESVTEEA-------LAQMQ--YLHAALSETMRL--YPPVPEHMRCAENDDVLP-------DGHRVSKGDNIYYISYAMGRMTYIWGQDA
CYP704B1   QYDTEDFNSFNEKVTEFAGLLNYDSLGKLH--YLHAVITETLRL--YPAVPQDPKGVLEDDMLP-------NGTKVKAGGMVTYVPYSMGRMEYNWGSDA
CYP97A3    -----------------PTIQDMKKLK--YTTRVMNESLRL--YPQPPVLIRRSIDNDILG-------EYPIKRGEDIFISVWNLHRSPLHW-DDA
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CYP97B3    --------------------PTYESMKKLE--YIRLIVVEVLRL--FPQPPLLIRRTLKPETLPGGHKGEKEGHKVPKGTDIFISVYNLHRSPYFW-DNP
CYP1A1     ---------------------DRSHLP--YMEAFILETFRH--SSFVPFTIPHSTTRDTSLKG-------FYIPKGRCVFVNQWQINHDQKLW-VNP
CYP1B1     ---------------------DQPNLP--YVMAFLYESMRF--TSFLPVTLPHATTANTFVLG-------YYIPKNTVVFVNQWSVNHDPAKW-SNP
CYP17A1    ---------------------DRNHLL--MLEATIREVLRI--RPVAPILIPHKANTDSSIGE-------FAIDKDTNVLVNLWALHHNEQEW-DRP
CYP19A1    ---------------------DRNRLV--LLEATIREVLRI--RPVAPTLIPHKAVIDSSIGD-------LTIDKGTDVVVNLWALHHSEKEW-QHP
CYP2A7     ---------------------DRTKMP--YMEAVIHEIQRF--GDVIPMSLARRVKKDTKFRD-------FFLPKGTEVFPMLGSVLRDLRFF-SNP
CYP2M1     ---------------------DRVKMP--YTDAVIHEVQRY--MDLSPTSVPHKVMRDTEFYN-------YHIPEGTMVLPLLSSVLVDPKLF-KNP
CYP33A1    ---------------------DKLNLP--YTNAFINEAQRC--ANLVPMNLPHAVTRDVQLLG-------CTIPKGTTVIHQISSVMSDPEIF-EEP
CYP33C1    ---------------------DKNDLP--YFNASINESQRG--INILPLNLQHATTRDTVIDG-------FKIPKGTGVVAQISTVMNNEEVF-PDP
CYP33B1    ---------------------DKNALV--YFNAFANEAQRV--SNILPMNLPHALTRDVKLKG-------YHLKKGTGVIHQIANVMTDETIF-KDS
CYP23A1    ---------------------HRTRLP--YVQATINEIQRI--ANILPINLLRTVAEDIEIDG-------YNFKKGDLIIPQISILMNDPEIF-ENP
CYP35A1    ---------------------DRTSTP--YLNAMIGEIQRH--ASILNVSFWKINKELTYMGG-------HPVDAGALVTAQLSALHVNDTIF-KNP
CYP35B1    ---------------------DRAESH--YLNATTIAEIQRH--ASILNVNFWRLVHEPTTVQG-------HPVDSGSVICAQLGALHVNDDLF-KNP
CYP34A1    ---------------------DRRETP--YLSAVISEVQRF--ASILNMNLFRIIKEDTVVDG-------QPLRAGTAVTAHIAMIHVDEDLF-KNH
CYP71A12   ---------------------DVENMK--YLKAVIKEVFRV--HPPLPLILPRLLSEDVKVKG-------YNIAAGTEVIINAWAIQRDPAIWGPDA
CYP71C1    ---------------------DLSRMP--YLKATIKESMRI--HPPAPFLLPHFSTHDCEING-------YTIPAGTRVIVNAWALARDPTCWD-KA
CYP71D11   ------------------CIYELK--YLKAFINEVLRL--HPPG-PLVFRECRQACEING-------YHIPAKSTVLVNTFAIGTDSKYW-AEP
CYP726A1   ---------------------RFHDLK--FFKLVVKETLRL--HPPV-VLIPRECRETTRIDG-------YEIHPNTRIVVNAWAIGRDPNTW-SEP
CYP71K1    ---------------------SLRDLP--YLHLVIKESLRL--HPPVTMLLPRECRETCRVMG-------FDVPEGVMVLVNAWAIGRDPAHW-DSP
CYP99A1    ---------------------QMDKLS--YTRMVVKEGLRL--HPVLPLLLPRSCQETCDVGG-------FEVTKGTKVIVNAWALARSPERW-HDP
CYP71E1    ---------------------DAAKIP--YLKMVVKETLRL--HPPATLLVPRETMRDTTICG-------YDVPANTRVFVNAWAIGRDPASW-PAP
CYP71N1    ---------------------DLHQLH--FFKCVIKETMRL--HPPAPLLLPRETMQHFKLNG-------YDILPKTWMYVNAWAIGRDPNSW-GRP
CYP71B2    ---------------------DLGKVE--YLNHILKETFRL--HPALPFVVPRETMSHIKIQG-------YDIPPKTQIQLNVWTIGRDPKRW-NDP
CYP83A1    ---------------------DVKNLP--YFRALVKETLRI--EPVIPLLIPRACIQDTKIAG-------YDIPAGTTVNVNAWAVSRDEKEWGPNP
CYP83B1    ---------------------DIPNLP--YLKAVIKESLRL--EPVIPILLHRETIADAKIGG-------YDIPAKTIIQVNAWAVSRDTAAWGDNP
CYP83E1    ---------------------DIQNCP--YLKAVVKETLRL--HLPAPLLVPRESIENCTING-------YNIPAKTILYVNAWAIQRDPDIW-INP
CYP93B1    ---------------------DCPNLP--YLQAILKETFRL--HPPVPMVTR-RCVAECTVEN-------YVIPEDSLLFVNVWSIGRNPKFW-DNP
CYP93C17   ---------------------DIQNLP--YIRAIVKETFRM--HPPLPVVKR-KCVQECELNG-------YVIPEGALVLFNVWAVQRDPKYW-KTP
CYP93A1    ---------------------DIANLP--YLQAIVRETLRL--HPGGPLVVR-ESSKSAVVCG-------YDIPAKTRLFVNVWAIGRDPNHW-EKP
CYP705A1   ---------------------DLPNLP--YLQAVVKEGLRL--HPPTPLVVR-EFQEGCEIGG-------FFVPKNTTLIVNSYAMMRDPDSW-QDP
CYP712A1   ---------------------DVPNLP--YLRAVLRETLRL--HPSAPLIIR-ECAEDCQVNG-------CLVKSKTRVLVNVYAIMRDSELW-ADA
CYP75A1    ---------------------DIPNLP--YLRAICKETFRK--HPSTPLNLPRISNEPCIVDG-------YYIPKNTRLSVNIWAIGRDPEVW-ENP
CYP75B1    ---------------------DIAQLP--YLQAVIKENFRL--HPPTPLSLPHIASESCEING-------YHIPKGSTLLTNIWAIARDPDQW-SDP
CYP92A2    ---------------------DIPNLP--YIEAIVKETMRL--HPVAPMKATECR-ENSKVAG-------YDVQKGTRVLVSVWTIGRDPTLW-DEP
CYP84A1    ---------------------DIEKLT--YLKCTLKETLRM--HPPIPLLLHETA-EDTSIDG-------FFIPKKSRVMINAFAIGRDPTSW-TDP
CYP703A2   ---------------------DLVHLN--YLRCVVRETFRM--HPAGPFLIPHESVRATTING-------YYIPAKTRVFINTHGLGRNTKIW-DDV
CYP98A3    ---------------------DFSRLP--YLQCVVKESFRL--HPPTPLMLPHRSNADVKIGG-------YDIPKGSNVHVNVWAVARDPAVW-KNP
CYP706A1   ---------------------HLPKLP--YLQAVMKETLRL--HPTLPLLVPHRNSETSVVAG-------YTVPKDSKIFINVWAIHRDPKNW-DEP
CYP81D1    ---------------------DLSELP--YLKNIVLETLRL--HPATPLLVPHMASEDCKIGS-------YDMPRGTTLLVNAWAIHRDPNTW-DDP
CYP81E6    ---------------------DIPKLT--YLKNVINETLRL--YTPAPLLLPHSASDDCTIGG-------YKVPRDTIVLINAWALHRDPQLW-TEA
CYP81B1    ---------------------DIPNLP--YLRCIINETLRL--YPAGPLLVPHEASSDCVVGG-------YNVPRGTILIVNQWAIHHDPKVW-DEP
CYP82A2    ---------------------DLSKLT--YLQAVVKETLRL--YPPAPLSRPREFEEDCTIGG-------YTVKKGTRLITNLSKIHTDHNVW-SNP
CYP82B1    ---------------------DIDNLV--YLQAIVKETLRM--YPAGPLSVPHEAIEDCNVGG-------YHIKTGTRLLVNIWKLQRDPRVW-SNP
CYP76A2    ---------------------DIENLP--YMQAVLKESLRL--HPPLPFLIPRETIQDTKFMG-------YDVPKDTQVLVNAWAIGRDPECW-DDP
CYP76G1    ---------------------DLPNLP--YLSAVIMETLRL--HPPLPFLVPHKAMSTCHIFDQ------YTIPKETQVLVNVWAIGRDPKTW-IDP
CYP76E1    ---------------------HISKLP--FLQAVVKETFRL--HPPIPLLLPHKCDELVNILD-------FNVPKNAQVLVNVWAMGRDPAIW-DNP
CYP76F2    ---------------------DISRLP--YLQAVVKETFRL--HPAVPFLLPRRVEGDADIDG-------FAVPKNAQVLVNAWAIGRDPNTW-ENP
CYP76C1    ---------------------DISKLP--YLQAVVKETFRL--HTPVPLLIPRKAESDAEILG-------FMVLKDTQVLVNVWAIGRDPSVW-DNP
CYP76B1    ---------------------DVLRLP--YLSCIVKEVLRL--HPPSPLLLPRKVVTQVELSG-------YTIPAGTLVFVNAWAIGRDPTVW-DDS
CYP80A1    ---------------------HFSELP--YLQACVKETMRL--YPPISIMIPHRCMETCQVMG-------YTIPKGMDVHVNAHAIGRDPKDW-KDP
CYP79A1    ---------------------DIPKLN--YVKACIREAFRL--HPVAPFNVPHVALADTTIAG-------YRVPKGSHVILSRTGLGRNPRVW-DEP
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CYP79B2    ------------------------DIPKLN--YVKAILREAFRL--HPVAAFNLPHVALSDTTVAG-------YHIPKGSQVLLSRYGLGRNPKVW-ADP
CYP79D1    ------------------------DIPNLD--YVKACAREAFRLFTHPVAHFNVPHVAMEDTVIGD-------YFIPKGSWAVLSRYGLGRNPKTW-SDP
CYP79E1    ------------------------DFPNLP--YIRACAREALRLHPFTVAAFNLPHVSLRDTHVAG-------FFIPKGSHVLLSRVGLGRNPKVW-DNP
CYP79C1    ------------------------DVPNLN--YVKACCRETLRL--HPTNPFLVPHMARHDTTLAG-------YFIPKGSHILVSRPGVGRNPKTW-DEP
CYP79F1    ------------------------DIPNLN--YLKACCRETFRI--HPSAHYVPSHLARQDTTLGG-------YFIPKGSHIHVCRPGLGRNPKIW-KDP
CYP77A6    ------------------------DVDKMV--FLQAVVKEILRK--HPPTYFTLTHSVTEPTTVAG-------YDVPVGINVEFYLPGINEDPKLW-SDP
CYP77B1    ------------------------DVAKMP--YLEAIVKETLRR--HPPGHFLLSHAAVKDTELGG-------YDIPAGAYVEIYTAWVTENPDIW-SDP
CYP89A2    ------------------------DVEKMP--YLKAVVLEGLRR--HPPGHFLLPHSVTEDTVLGG-------YKVPKNGTINFMVAEIGRDPVEW-EEP
CYP27A1    ------------------------DFAHMP--LLKAVIKETLRL--YPVVPTNSRIITEKETEING------FLFPKNTQFVLCHYVVSRDPSVF-PEP
CYP27B1    ------------------------VLSQLP--LLKAVVKEVLRL--YPVVPGNSRVP-DKDIHVGD-------YIIPKNTLVTLCHYATSRDPAQF-PEP
CYP11A1    ------------------------MLQMVP--LLKASIKETLRL--HPISVTLQRYP-ESDLVLQD-------YLIPAKTLVQVAIYAMGRDPAFF-SNP
CYP11B1    ------------------------LRMELP--LLWAAIKETLRM--YPVGLFLERFL-TSPLVLQN-------YHIPAGTLVHLNLYSMGRNPEVF-LSP
CYP12A1    ------------------------SLNHIP--YTRACIKEALRM--YPLTLGNARIL-ANDTVLSG-------YRVPKGTLVSMISTGLLQDDNHY-TKA
CYP12C1    ------------------------DMKSLP--YLRAVIKESLRL--YPVTFGNARSA-GADVVLDG-------YRIPKGTKLLMTNSFLLKDDRLY-PRA
CYP74A     ------------------------IEKME--LTKSVVYECLRFEPPVTAQYGRAKKDLVIESHDAA------FKVKAGEMLYGYQPLATRDPKIF-DRA
CYP74C1    ------------------------LEKMS--LLKSVVYEALRIEPPVPFQYGKAKEDIVIQSHDSC------FKIKKGETIFGYQPFATKDPKIF-KDS
CYP74D1    ------------------------INKMS--LVKSVVYETLRLRPPVPLQYGKAKKEFMVQSHDAS------YKINKGQFVVGYQPMASRDPKIF-ANP
CYP74B2    ------------------------VNEME--LVKSVVYETMRFSPPVPLQFARARKDFQISSHDAV------FEVKKGELLCGYQPLVMRDANVF-DEP
CYP24A1    ----------------AEDLRNMP--YLKACLKESMRLT--PSVPFTTRTLDKPTVLG--------EYALPKGTVLTLNTQVLGSSEDNF-EDS
CYP10      ------------------------LCKLP--MVKAVVKETLRLY---PITYSTSRNIAEDMELGG-------YTIPAGTHVQANLYGMYRDPSLF-PEP
CYP9A1     ------------------------VVQSMT--YLDMVVSEGLRLWPPAAVVDRVCVKDYNIGRPNKK--ATKDLIIHTGQAVAISPWLFHRNPKFF-PEP
CYP9B1     ------------------------AAQEMT--YMDMVISESLRKWTLSAAADRLCAKDYTLTDDEG----TKLFEFKAGDNINIPICGLHWDERFF-PQP
CYP14A2    ------------------------PNMP--YTQAVIHVQRCS--NMIPILGTHTNRDDILLKG-------KKIPTGTLVFAQIWSVLKNDPVF-EES
CYP21A1    ------------------------RMQLP--LLMATIAEVLRLR--PVVPMALPHRATKASSISG-------YDIPKDTIIIPNIQGANLDEMVW-ELP
CYP36A1    ------------------------KHLP--YTCAFLQEVYRLG-YVLPVNFLRCTLTDVEDCEG-------YRLNAGTRVIAQFQSVHVDKKHF-PDP
CYP45A1    ------------------------LSKLV--YTEAVALESTRM--YPPVTGFITRQATQDWQYGP-------YTIPAGTEVEVPVWSIHHNPELY-PQP
CYP18A1    ------------------------LQYLP--ITESTILESMRR--SSIVPLATTHSPTRDVELNG-------YTIPAGSHVIPLINSVHMDPNLW-EKP
CYP707A1   ------------------------DTKKMP--LTSRVIQETLRV---ASILSFTFREAVEDVEYEG------YLIPKGWKVLPLFRNIHHSADIF-SNP
CYP722A1   ------------------------EDLSEMP--YASKMVKESLRM---ASVVPWFPRLVLQDCEMEG------YKIKKGWNINIDARSIHLDPTVY-SEP
CYP25A1    ------------------------IHNMK--YLDYVYKETLRC--YPPVIHFINRRCLADITIRG------QFYPKGSVVTCLPHTVHLNPENW-DSP
CYP73A5    ------------------------DLHKLP--YLQAVVKETLRLR--MAIPLLVPHMNLHDAKLAG------YDIPAESKILVNAWWLANNPNSW-KKP
CYP78A6    ------------------------LASLP--YLTAVVKEVLRLHPPGPLLSWARLAITDTIVDGR--------LVPAGTTAMVNMWAVSHDPHVW-VDP
CYP4A4     ------------------------LDQMP--YTTMCIKEALRL--YPPVPSVTRQLSKPVTFPDG-------RSLPKGVILFLSIYGLHYNPKVW-QNP
CYP719     ------------------------VNKLK--YLQGVVKETMRMK--PIAPLAIPHKTAKETTLMG-------TKVAKGTRIMVNLYALHHNQNIW-PDP
CYP44A1    ------------------------SKLT--FLRACIKETFRMF---PIGTEVSRVTQKNLILSG-------YEVPAGTAVDINTNVLMRHEVLFSDSP
CYP302A1   ------------------------ALRTDITYTRAVLKESLRLN---PIAVGVGRILNQDAIFSG------YFVPKGTTVVTQNMVACRLEQHF-QDP
CYP22A1    ------------------------KMNQTP--YVRATLSEIQRL--ANVLPWAIPHKTIEECNIGG------YDIPVNTEIIPALGAVLFDPNVF-ESP
CYP52A1    ------------------------FETLKSCEYLKAVINETLRIYPSVPHNFRVATRNTTLPRGGGEG-GLSPIAIKKGQVVMYTILATHRDKDIYGEDA
CYP701A3   ------------------------QLSQVP--YLNGVFHETLRK--YSPAPLVPIRYAHEDTQIGG------YHVPAGSEIAINIYGCNMDKKRW-ERP
CYP315A1   ------------------------LMHGLIKESLRLY---PVAPFIGRYLPQDAQLGG------HFIEKDTMVLLSLYTAGRDPSHF-EQP
CYP39A1    ------------------------EDDLENLLLIKWCVLETIRLK----APGVITRKVVKPVEILN-------YIIPSGDLLMLSPFWLHRNPKYF-PEP
CYP711A1   ------------------------LQHKFP--YLDQVIKEAMRFY---MVSPLVARETAKEVEIGG------YLLPKGTWVWLALGVLAKDPKNF-PEP
CYP46A1    ------------------------LGRLQ--YLSQVLKESLRLY---PPAWGTFRLLEEETLIDG------VRVPGNTPLLFSTYVMGRMDTYF-EDP
CYP43A1    ------------------------SLR--LLQNCIFETLRL--FPHASPLQTRICTEPFKIGK-------YQFLENVQIVVNPWGPHHDREIWGNDV
CYP59A1    ------------------QDAKLLNQLP--YTTAVLKETLRLFPPSASMREGGPGVEITDDNGQ-------VYPTAGCNVWTLTVALHHNSAHW-AEA
CYP710A1   ------------------------QLAEMK--YTRSVAREVIRYR--PPATMVPHVAAIDFPLTET-------YTIPKGTIVFPSVFDSSFQGFTE---P
CYP56A1    ------------------------LADLP--LLNAFLFEVVRMY--PPLSTIINRCTTKTCKLGA-------EIVIPKGVYVGYNNFGTSHDPKTWGTTA
CYP57A1    ------------------------QSMP--YLQAVIKEALRLH-PGVGTQLTRVVPKGGLVIEG-------QFFPEGTEVGVNGWALYHNKAIFGNDA
CYP53A1    ------------------------MVKDIP--YLQWVIWETMRIHSTSAMGLPREIPAGNPPVTISG------HTFYPGDVVSVPSYTIHRSKEIWGPDA
CYP58A1    ------------------------ELEKLP--YLQAVIKEALRNRLSYGFMRRLPRVSPDVAIQYK------EYTIPPGTPVGMSAYLMHSNPEVY-QDP
CYP20A1    ------------------------EKIEELR--YCRQVLCETVRTAKLTPVSARLQDIEGKIDK---------FIIPRETLVLYALGVVLQEXGTW-SSP
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CYP38A1    -----------------------------SLRADTFLRQVQDETIRLS---TLAPWAARYSDKKVTVCG-------YTIPAKTPMIHALGVGLKNKTVW-ENT
CYP54A1    -----------------------ALQAMK--KTDSFLKETMRFHPLGQTSFNRKVLRTFALSNGQ-------VIPKGSTIEVPNYAVSRDPEAY-PNP
CYP55A1    -----------------------------LAPQFVEELCRY--HTASALAIKRTAKEDVMIGD-------KLVRANEGIIASNQSANRDEEVFENPD
CYP727A1   ------------------------VLRMKFLLATVCESARL--LPAGPLLQRCSLQQDVNLSS------ITIPAGAILVIPLHLVQMEASTWGNDA
consensus                          ..  .  ..  .......*.  .      ..  .  . ..... ...  ... ... ..  .
           601......610.......620.......630.......640.......650.......660.......670.......680.......690.......
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CYP7A1     LTFKYDRYLDENKKAKTSFYSNG------------NKLKYFYMPFGSGATI-CPGRLFAVQEIKQFLILMLSYFELELVESHVKCPPLDQSRA------
CYP7B1     EEFRYDRFIEDGKK-KTTFFKRG------------KKLKCYLMPFGTGTSK-CPGRFFALMEIKQLLVILLTYFDLEIIDDKPIG--LNYSRL------
CYP8A1     EVFKYNRFLNPDGSEKKDFYKDG------------KRLKNYSLPWGAGHNQ-CLGKGYAVNSIKQFVFLVLTQFDLELITPDVDIPEFDLSRY------
CYP8B1     TTFKYDRFLNPNGSRKVDFYKAG------------QKIHHYTMPWGSGVSI-CPGRFFALSEMKLFVLLMVQYFDLELVDPNTPVPPIDPRRW------
CYP51A1    ENFDPDRFSKEREEDKAAGSCS-------------------YISLGAGRHE-CPGGSFAFLQIKAVWCHLLRNFELELVSP------FPEINW------
CYP51A2    DTYDPERFSPGREEDKAAGAFS-------------------YIAFGGGRHG-CLGEPFAYLQIKAIWSHLLRNFELELVSP------FPEIDW------
CYP26A1    E-FNPDRFIVPHPED----------------------ASRFSFIPFGGGLRS-CVGKEFAKILLKIFTVELARHCDWQLLN-GPPTMKTSPTV-------
CYP26C1    EGFDPERFGAAREDSRGA-------------------SSRLHYIPFGGGARS-CLGQELAQAVLQLLAVELVRTARWELATPAFPAMQTVPIV-------
CYP716A1   R-FEPNRFEGSG--P----------------------KPYTYVPFGGGPRM-CPGKEYARLEILIFMHNLVNRFKWEKVFPNENKIVVDPLP-------
CYP725A1   E-FRPSRFEDEGRHV----------------------TPYTYVPFGGGLRT-CPGWEFSKIEILLFVHHFVKNFSSYIPVDPNEKVLSDPLPP------
CYP718     S-FDPTRFDKPIQ------------------------AYTYLPFGGGPRL-CAGHQLAKISILVFMHFVVTGFDWSLVYP-DETISMDPLP-------
CYP90A1    T-FNPWRWQSNSVTTGPS-------------------NVFTPFGGGPRL-CPGYELARVALSVFLHRLVTGFSWVPAEQDKLVFFPTTRT-------
CYP90B1    L-FNPWRWQQQNNGASSSGSGSF-------------STWGNNYMPFGGGPRL-CAGSELAKLEMAVFIHHLVLKFNWELAEDDKPFAFPFVDF-------
CYP724A1   E-FNPMRWTDKAKMNKKT-------------------TAFGGGVRV-CPGGELGKLQIAFFLHHLVLSYRWKIKSDEMPIAHPYVEF-------
CYP720A1   S-FNPWRWLDPETQQKRN-------------------WRTSPFYCPFGGGTRF-CPGAELARLQIALFLHYFITTYKSVHVMLLKYVCLRL----------
CYP85A1    I-FNPWRWMKKSLESQNS-------------------CFVFGGGTRL-CPGKELGIVEISSFLHYFVTRYRWEEIGGDELMVFPRVFA-------
CYP87A2    V-FNPSRWEGSKVTNAS--------------------KHFMAFGGGMRF-CVGTDFTKLQMAAFLHSLVTKYRWEEIKGGNITRTPGLQF-------
CYP708A1   E-FNPWRWEGKELLSGS--------------------KTFMAFGGGARL-CAGAEFARLQMAIFLHHLVTTYDFSLIDKSYIIRAPLLRF-------
CYP702A1   V-FNPWRWEGKDLGAIVS-------------------RTYIPFGAGSRQ-CVGAEFAKLQMAIFIHHLS-RDRWSMKIGTTILRNFVLMF-------
CYP88A3    K-FDPARWDNGFVPKAG--------------------AFLPFGAGSHL-CPGNDLAKLEISIFLHHFLLKYQVKRSNPECPVMYLPHTR-------
CYP88B1    E-FNPSRWDD-IETKPG--------------------IFLPFSMGPKS-CPGSNLAKLQISVILHYYLLHYRVEQINPEARCYPPENCL-------
CYP3A1     EEFRPERFSKE----------------------NKGSIDPYVYLPFGNGPRN-CIGMRFKMLALTKVLQNFSFQPCKETQIPLKLSRQ--------
CYP5A1     ETFDPERFTAE----------------------AQRLQQPFTYLPFGAGPRS-CLGVQLGLLEIKLTLLHILRKRFEACPETQVPLQLESK--------
CYP6A2     ETFDPERFSPE----------------------KVAARESVEWLPFGDGPRN-CIGMRFGQMQARIGLAQIISRFRVSVCDTTEIPLKYSPM-------
CYP6B4     EKFDPERFSPE----------------------NVRNRHPCAYIPFGAGQRK-CLGMRFGQWQVQVCIIKLLSKFRFEPSTKTMSEFNYDPK-------
CYP28A1    QAFKPERFMQPD---------------------AAKMYREQGVFMAFGDGPRV-CIGMRFALTQIKGALVELLTKFIIRVNPKTRSDNEYDPT-------
CYP28C1    DVFRPERFLDG----------------------GLKNCKQQGIFLGFGNGPRQ-CVGMRLGLAMAKAALAAIVQRFEVVVSPRTLNGTELDPL-------
CYP13A2    KEFKPERWSTDE---------------------PLEHKG---AYLPFGLGPRQ-CIGMRLAIMEQKILLTHLLKNYTFETGNKTRIPLKLVGS--------
CYP13B1    DDFVPERWLEPS---------------------SRHTM---SWIPFGAGPRQ-CVGMRLGLSEAKTALAHLLRRYDLVAGVETEKELNILGC--------
CYP72A8    HEFNPERFADG----------------------ISKATKNQVSFLPFGWGPRF-CPGQNFALMEAKMALVLILQRFSFE-LSPSYTHAPHTVL-------
CYP72B1    NEFNPARFADG----------------------VPRAAKHPVGFIPFGLGVRT-CIGQNLAILQAKLTLAVMIQRFTFH-LAPTYQHAPTVLM-------
CYP721A1   EEFNPRRFED-----------------------PKKQSALLVPFGLGPRT-CVGQNLAVNEAKTVLATILKYYSFR-LSPSYAHAPVLFV--------
CYP709A1   NQFNPERFGG-----------------------RPFASGRHFIPFAAGPRN-CIGQQFALMEAKIILATLISKFNFT-ISKNYRHAPIVVL-------
CYP709B1   DKFNPMRFANG----------------------VSRAANHPNALLAFSVGPRA-CIGQNFVMIEAKTVLTMILQRFRFISLCDEYKHTPVDNV-------
CYP715A1   NEFKPERFDGN----------------------LHGGCKNKMGYMPFGFGGRM-CIGRNLTTMEYKIVLSLVLSRFEIS-VSPGYRHSPTYML-------
CYP714A1   NEFNPERFSEG----------------------VSKACKHPQSFVPFGLGTRL-CLGKNFGMMELKVLVSLIVSRFSFT-LSPTYQHSPVFRM-------
CYP4C3     EQFNPDNFLPEN---------------------CAGRHPFAYIPFSAGPRN-CIGQKFAILEEKAVISTVLRKYKIEAVDR-REDLTLLGE--------
CYP31A2    DVFDPDRFLPEN---------------------SIGRKSFAFIPFSAGSRN-CIGQRFALMEEKVIMAHLLRNFNIKAVEL-MHEVRIGNT--------
CYP37A1    EVFDPERFNEDE---------------------ISKRHAYAYIPFSAGPRN-CIGQKFAMQEEKTVISWVLRRFHIHTDIG-LLENMPLPE--------
CYP37B1    NQYNPENFSEDK---------------------IGSRHAYSDIPFSAGPRN-CIGQKFAMMEEKAVISWFFRKYRVTASQP-FGMNKILPE--------
CYP32A1    DTYNPDNFDIDA---------------------IAGRDPYAYIPFSAGPRN-CIGQKFALLEQKTILSTFFRKYEVESLQT-EENLRPVPE--------
CYP29A2    TEFNPDRFLPDE---------------------VSKRHPYDFMPFLAGPRN-CIGQKFAQLNEKVMISHIVRNFKIEPTLK-YNDTKPCLE--------
CYP86A1    LEFRPERWLTADG--------------------ERFETPKDGYKFVAFNAGPRT-CLGKDLAYNQMKSVASAVLLRYRVFPVPG--HRVEQKMS------
CYP86B1    LEFRPERWLRDG---------------------RFMS-ESAYKFTAFNGGPRL-CLGKDFAYYQMKSTAAAIVYRYKVKVNG--HKVEPKLA------
CYP96A1    SEFKPERWISES---------------------GRLIHVPSFKFLSFNAGPRT-CLGKEVAMTQMKTVAVKIIQNYEIKVVEG--HKIEPVPS------
CYP96C1    LEFKPERWLSDK---------------------GKLIPVQTNKFLAFGTGPRI-CPGKELGLNRVKAVAAAIIPKYSFKIMRN--KPVMPAAC------
CYP94A1    AEFRPERWLEKDEVNG------------------KWVFVGRDSYSYPVFQAGPRV-CLGKEMAFMQMKRIVAGIVGKFKVVPEAHLAQEPGFISF------
CYP94B1    DEFKPNRWFEEEPSYGT-----------------KPVLKSVSSFKFPVFQAGPRV-CIGKEMAFTQMKYVVGSVLSRFKIIPVCNNR--PVFVPL------
CYP704A1   EEFKPERWLKDG---------------------VFQPESQFKFISFHAGPRI-CIGKDFAYRQMK-IVSMALLHFFRFKMADENSKVSYKKM-------
CYP704B1   ALFKPERWLKDG---------------------VFQNASPFKFTAFQAGPRI-CLGKDSAYLQMK-MAMAILCRFYKFHLVP-NHPVKYRMM-------
CYP97A3    EKFNPERWPLDGPN-------------------PNETNQNFSYLPFGGGPRK-CIGDMFASFE--VAIAMLIRRFNFQIAPG-APPVKMTTG-------
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CYP97B3    HDFEPERFLRTKESNGIEGWAGFDPSRSPGALYPNEIIADFAFLPFGGGPRK-CIGDQFALMESTVALAMLFQKFDVELRGT-PESVELVSG--------
CYP1A1     SEFLPERFLTPDGAI-------------------DKVLSEKVIIFGMGKRK-CIGETIARWEVFLF-------LAILLQRVEFSVPL-GVK--------
CYP1B1     EDFDPARFLDKDGFI-------------------NKALASSVMIFSVGKRR-CIGEELSKTLLFLF-------ISILAHQCNFKANQ-NEP--------
CYP17A1    DQFMPERFLDPTGSQ-------------------IIVPSSSYLPFGAGPRS-CVGEALARQEIFLI-------TAWLLQKFDLEVPEGGQL--------
CYP19A1    DLFMPERFLDPTGTQ-------------------LISPSLSYLPFGAGPRS-CVGEMLARQELFLF-------MSRLLQRFNLEIPDDGKL--------
CYP2A7     RDFNPQHFLGEKGQF-------------------KKRDA--FVPFSIRKRN-CFGEGLARMELFLF-------FTTVMQNFRLKSSQSPKD--------
CYP2M1     DEFDPENFLDENGVF-------------------KKNDG--FFAFGVGKRA-CPGEALARVELFLF-------FTSVLQRFTFTGTKPPEE--------
CYP33A1    ERFVPERYLDESGNL-------------------KKIEE--LVPFSIGKRV-CLGEGLARMELFLF-------TANSFNRYEFNC--GSNG--------
CYP33C1    YTFNPDRFIDENGKL-------------------KKVDE--LAPFSVGKRS-CPGEGLARMELFLF-------IANFLNRYKIHP--SKEG--------
CYP33B1    QRFDPNRFIDENGKL-------------------KKIEE--LCPFSMGKRQ-CIGEGLARMEIFLL-------AANLFNYFEFLP--ASDG--------
CYP23A1    EEFNPSRFLDEDNNV-------------------KKIDE--FLPFSIGRRQ-CLGESLARAELYLV-------FANLIQNFNFEV--ADD---------
CYP35A1    QEFDPERFIRDE----------------------ELLQK--VIPFGVGKRS-CIGESLARAELYLISLLCICGTSNKSFLHKYLPLWNSVA--------
CYP35B1    DKFYPERFIENE----------------------QLLSQ--IIPFGIGKRS-CVGENIAKSELYLM-------IGNLILRYDIKPHGSEPS--------
CYP34A1    TEFRPERFLEND----------------------DLDKK--LIPFGIGRRS-CLGESLAKAELYLV-------LGNLLLDYDLEPVGEIPK--------
CYP71A12   EEFKPERHLDS----------------------TLDYHGKDLNFIPFGSGRRI-CPGINLALGLVEVT-------VANLVGRFDWR--AEAGPN----GDQ
CYP71C1    EEFFPERFLEQGR----------------DAEVDMYGKDIRFVPFGAGRRI-CAGATFAIATVEIM-------LANLIYHFDWEMPAEMERT----GAK
CYP71D11   ERFCPERFID------------------SSIDYKGTNFEHLPFGAGRRI-CPGINYGMANVELV-------LALLLYHFDWTLPKGIKN------ED
CYP726A1   GKFNPERFKD------------------CAIDYKGTTFELVPFGAGKRI-CPGITSAITNLEYV-------IINLLYHFNWELADGITP------QT
CYP71K1    EEFAPERFEG-------------------VGAADFKGTDFEYIPFGAGRRM-CPGMAFGLANMELA-------LAALLYHFDWELPGGMLP------GE
CYP99A1    EEFRPERFADDDGSSA-------------AVAVDYRGSQFEYIPFGSGRRM-CPGNTFGLAALELM-------VARLLYYFDWSLPDGMRP------EE
CYP71E1    DEFNPDRFVG-------------------SDVDYYGSHFELIPFGAGRRI-CPGLTMGETNVTFT-------LANLLYCYDWALPGAMKP------ED
CYP71N1    HVFDPERFMH-------------------DSTEASGQDFKLIPFGEGRRI-CPGKNLGMLMVELV-------LANLLYSFDWHLPPGMVK------ED
CYP71B2    EEFNPERFAN-------------------SSVDFRGQHFDLLPFGSGRRI-CPGMPMAIASVELA-------LMNLLYYFDWSMPDGTKG------ED
CYP83A1    DEFRPERFL--------------------EKEVDFKGTDYEFIPFGSGRRM-CPGMRLGAAMLEVP-------YANLLLSFNFKLPNGMKP------DD
CYP83B1    NEFIPERFMNE------------------HKGVDFKGQDFELLPFGSGRRM-CPAMHLGIAMVEIP-------FANLLYKFDWSLPKGIKP------ED
CYP83E1    EEFYPERFL--------------------ESSINFIGQDFELIPFGAGRRI-CPSIPMAVASLELI-------LANLLYSFDWKLPHGLVK------ED
CYP93B1    LEFRPERFLKLEGDSS-------------G--VVDVRGSHFQLLPFGSGRRM-CPGVSLAMQEVPAL-------LGAIIQCFDFHVVGPKGEILKGDDIV
CYP93C17   LEFRPERFLEEAD----------------IDLKGQHFELLPFGSGRRM-CPGVNLATAGMATL-------LSSVIQCFELQVVGPKGQILKGSDAK
CYP93A1    FEFRPERFIRDGQNQ--------------LDVRGQHYHFIPFGSGRRT-CPGASLAWQVVPVN-------LAIIIQCFQWKLVGGNG--------K
CYP705A1   DEFKPERFLASLS----------------REEDKKEKILNFLPFGSGRRM-CPGSNLGYIFVGTA-------IGMMVQCFDWE-INGDK---------
CYP712A1   DRFIPERFLESSEEKI-------------GEHQMQFKGQNFRYLPFGSGRRG-CPGASLAMNVMHIG-------VGSLVQRFDWKSVDGQK---------
CYP75A1    LEFYPERFLSG-RNS--------------KIDP-RGNDFELIPFGAGRRI-CAGTRMGIVMVEYI-------LGTLVHSFDWKLPS--EV------IE
CYP75B1    LAFKPERFLPGGEKS--------------GVDV-KGSDFELIPFGAGRRI-CAGLSLGLRTIQFL-------TATLVQGFDWELAGGVTP------EK
CYP92A2    EVFKPERFHEK---A--------------SIDV-KGHDYELLPFGVGRRM-CPGYSLGLKVIQAS-------LANLLHGFNWSLPDNMTP------ED
CYP84A1    DTFRPSRFLEP---G--------------VPDF-KGSNFEFIPFGSGRRS-CPGMQLGLYALDLA-------VAHILHCFTWKLPDGMKP------SE
CYP703A2   EDFRPERHWPVEGSG--------------RVEISHGPDFKILPFSAGKRK-CPGAPLGVTMVLMA-------LARLFHCFEWSSPG----------N
CYP98A3    FEFRPERFLEE------------------DVDMKGHDFRLLPFGAGRRV-CPGAQLGINLVTSM-------MSHLLHHFVWTPPQGTKP------EE
CYP706A1   NEFKPERFLEN------------------SLDFNGGDFKYLPFGSGRRI-CAAINMAERLVLFN-------IASLLHSFDWKAPQGQK---------
CYP81D1    DSFKPERFEKEE-----------------EAQKLLAFGLGRRA-CPGSGLAQRIVGLA-------LGSLIQCFEWERVGN---------VE
CYP81E6    TTFKPERFDKKG-----------------ELEKLIPFGLGRRA-CPGELLAIRAISMT-------LALLIQCFDWKRVSD---------EE
CYP81B1    ETFKPERFEGLEGT---------------RDGFKLLPFGSGRRS-CPGEGLAVRMLGMT-------LGSIIQCFDWERTSE---------EL
CYP82A2    LEFKPERFLTTDKD---------------IDMKGQHFLLPFGGGRRI-CPGINLGLQTVRLT-------LASFLHSFEILNPST---------EP
CYP82B1    SEFRPERFLDNQSNG--------------TLLDFRGQHFEYIPFGSGRRM-CPGVNFATLILHMT------LARLLQAFDLSTPSS---------SP
CYP76A2    MSFKPERFLG-------------------SKIDVKGQHYGLIPFGAGRRI-CVGLPLGHRMMHFA-------LGSLLREFEWELPDGVSP------KS
CYP76G1    IMFKPERFISDP-----------------DARDFKGQDYEFLPFGVGRRM-CPALPLASRVLPLA-------IGSMVRSFDWALENGLNA------EE
CYP76E1    NTFVPERFME-------------------CDINYKGNNFELIPFGAGKRI-CPGLPLAHRTMHLM-------VASLLHNFEWNLADGLIP------EH
CYP76F2    NSFVPERFLG-------------------LDMDVKGQNFELIPFGAGRRI-CPGLPLAIRMVHLM-------LASLIHSYDWKLEDGVTP------EN
CYP76C1    SQFEPERFLG-------------------KDMDVRGRDYELTPFGAGRRI-CPGMPLAMKTVSLM-------LASLLYSFDWKLPKGVLS------ED
CYP76B1    LEFKPQRFLE-------------------SRLDVRGHDFDLIPFGAGRRI-CPGIPLATRMVPIM-------LGSLLNNFDWKIDTKVPY------DV
CYP80A1    LKFQPERFLD-------------------SDIEYNGKQFQFIPFGSGRRI-CPGRPLAVRIIPLV-------LASLVHAFGWELPDGVPN------EK
CYP79A1    LRFYPDRHLAT------------------AASDVALTENDLRFISFSTGRRG-CIAASLGTAMSVML-------FGRLLQGFTWSKPAGVEA--------
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CYP79B2    LCFKPERHLN------------------ECSEVTLTENDLRFISFSTGKRG-CAAPALGTALTTMM-------LARLLQGFTWKLPENETR--------
CYP79D1    LKYDPERHMNE-----------------GEFTVVLTEHELRFVTFSTGRRG-CVASLLGSCMTTML-------LARMLQCFTWTPPANVSK--------
CYP79E1    LRFDPDRHLHGGPT--------------AFTKVELAEPELRFVSFTTGRRG-CMGGPLGTAMTYML-------LARFVQGFTWGLRPAVEK--------
CYP79C1    LIYRPERHITGN---------------EVVLTEPDLRLVSFGTGRRG-CVGAKLGTSMIVTL-------LGRLLQGFDWTIPPGTTDR--------
CYP79F1    LVYKPERHLQGDG--------------ITKEVTLVETEMRFVSFSTGRRG-CIGVKVGTIMMVML-------LARFLQGFNWKLHQDFGP--------
CYP77A6    KKFNPDRFISGKE-------------EADITGVTGVKMMPFGIGRRI-CPGLAMATVHVHLM-------LAKMVQEFEWSAYPPESEID--------
CYP77B1    GKFRPERFLTGGDGV-----------DADWTGTRGVTMLPFGAGRRI-CPAWSLGILHINLM-------LARMIHSFKWIPVP-DSPPD------
CYP89A2    MAFKPERFMGEEE------------AVDLTGSRGIKMMPFGAGRRI-CPGIGLAMLHLEYY-------VANMVREFQWKEVQ-GHEVD------
CYP27A1    ESFQPHRWLRKREDDN----------SGIQHPFGSVPFGYGVRS-CLGRRIAELEMQLL-------LSRLIQKYEVVLSPGMGEVK------
CYP27B1    NSFRPARWLGE--------------GPTPHPFASLPFGFGKRS-CMGRRLAELELQMA-------LAQILTHFEVQPEPGAAPVR------
CYP11A1    DKFDPTRWLGKDKD------------LIHFRNLGFGWGVRQ-CVGRRIAELEMTLF-------LIHILENFRVEMQQ-IGDVN------
CYP11B1    EHYNPQRWLENKE-------------TYKHLAFGFGVRQ-CIGRRLAEVEMLLF-------LHHVLKSFCVETAF-QEDVK------
CYP12A1    KEYLPERWMRPTKEETEDSA-------TCPHALKASSPFIYLPFGFGPRS-CVGRRIVEMELELG-------IARLVRNFRIEFNY-PTENA------
CYP12C1    KEFIPERWLRRKDDDKSDVL-------MN----KDLNAFIYLPFGFGPRM-CVGKRIVDLEMELT-------VANLVRNFHIEYNY-STEKP------
CYP74A     DEFVPERFVGEEGEKLLR---------HVLWSNGPETETPTVGNKQ-CAGKDFVVLVARLF-------VIEIFRRYDSFDIEVGTSP-------
CYP74C1    EKFVGDRFVGEEGEKLLK---------YVYWSNERETVEPTAENKQ-CPGKNLVVMMGRII-------VVEFFLRYDTFTVDVADLA-------
CYP74D1    DEFVPDRFMND-GEKMLK---------HVLWSNGRETESPAPDNKQ-CPGKDLVHLLGRLI-------LVEFFIRYDTFTLEITPLF-------
CYP74B2    EEFKPDRYVGETGSELLN---------YLYWSNGPQTGTPSASNKQ-CAAKDIVTLTASLL-------VADLFLRYDTITGDSG----------
CYP24A1    HKFRPERWLQKEK---------------KINPFAHLPFGIGKRM-CIGRRLAELQLHLALCWIIQKYDIVATDNEPVEMLHLG----------
CYP10      EGILPERWLRMNGSQ-------------MDATIKSTSQLVWGHGARM-CIGRRIAEQEMHIT-------LSKIIQNFTLSYNHDDVEPILN----
CYP9A1     AKFDPERFSPENR-----------------HKILPFTYFSFCLGPRN-CIGSRFALCEIKVILYLLIREMEVYPFEKTIYPPQLSKDRFN-----
CYP9B1     QRFDPERFSERRK-----------------KDLIPYTYLPFGVGPRS-CIGNRYAVMQAKGMLYNLMLNYKIEASPRTTRDMWESARG-------
CYP14A2    SKFNPDRYLMADG---------------KTINKSVLERTIPFSVGKRN-CVGEGLARMELFLI-------FSALIQKYEFIPKTNIDVKP------
CYP21A1    SKFWPDRFLESG------------------KSPRIPTFGCGARV-CLGEPLARLEFFVVLARLLQTFTLLPPPDGTLPSLQPLPYTG-----
CYP36A1    EHFNPDRFLNSRG---------------EYIRDDRVNPFSMGKRS-CLGENLARMEVFLYFCTLMQNFEWHTDGPYAPPIDVITS-------
CYP45A1    ELFKPERFLPKAK---------------KDRHTMAYLGFGGGPRN-CLGLRFALMEMKLVLSSVIQRFYIKPCSHTKVPLTLVTRNVFTNPDE
CYP18A1    EEFRPSRFIDTEG---------------KVRKPEYFIPFGVGRRM-CLGDVLARMELFLFFASFMHCFDIALPEGQPLPSLKGNVG-------
CYP707A1   GKFDPSRFEVAP------------------KPNTFMPFGNGTHS-CPGNELAKLEMSIMIHHLTTKYRCVCVYYLLITFS------------
CYP722A1   HKFNPLRFEEEAKAN-------------SFLAFGMGGRT-CLGLALAKAMMLVFLHRFITTYRWEVVDEDPSIEKWTLFAR------
CYP25A1    EEFHPERFENWEE----------------KSSSLKWIPFGVGPRY-CVGMRFAEMEFKTTIVKLLDTFELKQFKGEADLIPDCNG--------
CYP73A5    EEFRPERFFEEES--------------HVEANGNDFRYVPFGVGRRS-CPGIILALPILGITIGRMVQNFELLPPPGQSKVDTSEKGGQ------
CYP78A6    LEFKPERFVAKEGEVEFS-----------VLGSDLRLAPFGSGRRI-CPGKNLGFTTVMFWTAMMLHEFEWGPSDGNGVDLSEKLR--------
CYP4A4     EVFDPFRFAPDS----------------AYHSAFLPFSGGARN-CIGKQFAMRELKVAVALTLLRFELLPDPTRVPIPIARVVLK-----
CYP719     YKFMPERFLEGETGTAYN-----------KAMEQSFLPFSAGMRI-CAGMDLGKLQFAFALANLVNAFKWSCVEEGKLPDMGEELS-------
CYP44A1    REFKPQRWLEKSK----------------EVHPFAYLPFGFGPRM-CAGRRFAEQDLLTSLAKLCGNYDIRHRGDPITQIYETLLLP-----
CYP302A1   LRFQPDRWLQHRS----------------ALNPYLVLPFGHGMRA-CIARRLAEQNMHILLLRLLREYELIWSGSDDEMGVKTLLIN------
CYP22A1    KQFKPERFLDEEG----------------KYRVMEEFRPFGLGPRV-CLGERIARTELYLIFASLLQNFRFYLNRGDPIPVAERVIGG------
CYP52A1    YVFRPERWFEPETR----------------KLGWAYVPFNGGPRI-CLGQQFALTEASYVTVRLLQEFGNLKQDPNTEYPPKLQN-------
CYP701A3   EDWWPERFLDDGK---------------YETSDLHKTMAFGAGKRV-CAGALQASLMAGIAIGRLVQEFEWKLRDGEEENVDTYGLTS-------
CYP315A1   ERVLPERWCIGET----------------EQVHKSHGSLPFAIGQRS-CIGRRVALKQLHSLLGRCAAQFEMSCLNEMPVDSVLRMVT-------
CYP39A1    ELFKPERWKKAN----------------LEKHSFLDCFMAFGSGKFQ-CPARWFALLEVQMCIILILYKYDCSLLDPLPKQSYLHLVG-------
CYP711A1   EKFKPERFDPNGEEE-------------KHRHPYAFIPFGIGPRA-CVGQRFALQEIKLTLLHLYRNYIFRHSLEMEIPLQLDYG-------
CYP46A1    LTFNPDRFGPGAP---------------KPRFTYFPFSLGHRS-CIGQQFAQMEVKVVMAKLLQRLEFRLVPGQPRFGLQEQATLKP-----
CYP43A1    DCFRPSRFENLTE---------------QQRKAFMPFGVGPRQ-CVGMRFALLEMKTTAFRMLQKYSVFTNSPVHDRHGKTVRMTVR------
CYP59A1    ESFIPERWLVGSDHP-------------LYPAKGAWRAFEFGPRS-CIGQTLAMLELRVALAMTLREFDIAPAYDKWDHIYPNDAVKEFN-GH
CYP710A1   DRFDPDRFSETRQED-------------QVFKRNFLAFGWGPHQ-CVGQRYALNHLVLFIAMFSSLLDFKRLRSDGCDEIVYCP-------
CYP56A1    DDFKPERWGSDIETIRKN----------WRMAKNRCAVTGFHGGRRA-CLGEKLALTEIRISLAEMLKQFRWSLDPEWEEKLTPAGP-------
CYP57A1    SIFRPERWLEANEN--------------INIGGSFAFGAGSRS-CIGKNISILEMSKAIPQIVRNFDIEINHGDMTWKNECWWFVKP----
CYP53A1    EQFVPERWDPARLTP-------------RQKAAFIPFSTGPRA-CVGRNVAEMELLVICGTVFRLFEFEMQQEGPMETREGFLR-------
CYP58A1    DQFVPERWLGGDTR--------------VMQRSYVPFTKGSRS-CLGQNLSMAEISLVLAVLFRPDGPRMELFETDESDVKHVHD-------
CYP20A1    YKFDPERFDDES----------------VMKTFSLLGFS-GTRE-CPELRFAYMVTAVLLSVLLRRLHLLSVEGQVIETKYELVTS------
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CYP38A1    DSWDPDRFSPNGR------------------------RGNDFCPFGVHSRRKCPGYLFSYFEVGVFASILLSRFEIVPVEGQTVIQVHGLVTE------
CYP54A1    DVPDPLRFYNLRNEAREKGEAEQG-------ASGQFVSVNKEFLTFGYGRHA-CPGRFFAANEIKMILANLVMTYEMGLVEGETERYRDWDIAAG-----
CYP55A1    EFNMRKWPPQDP------------------------------LGFGFGDHR-CIAEHLAKAELTTVFSTLYQKFPDLKVAVPLGKINYTPLN-------
CYP727A1   CQFNPNRFLKKEINFEEILAAAHKGSNG-INLFTDECDKTESFLPFGSGSRA-CVGQKFAVLGIAMLIASLLRSYEVQPHPALSQEMESLVDSN------
consensus    . .....                           .... . .  *..  ..   . .    . ..
           701......710.......720.......730.......740.......750.......760.......770.......780.......790........
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CYP7A1      ---------GLGILPPLNDIEFKYKLKHL------------------------------------
CYP7B1      ---------LFGIQYPDSDVLFRYKVKS------------------------------------
CYP8A1      ---------GFGLMQPEHDVPVRYRIRP------------------------------------
CYP8B1      ---------GFGTMQPTHDVRIRYRLKPLE----------------------------------
CYP51A1     ---------NALVVGAKGNVMVRYKRRPFS----------------------------------
CYP51A2     ---------NAMVVGVKGNVMVRYKRRQLS----------------------------------
CYP26A1     ---------YPVDNLPARFTYFQGDI--------------------------------------
CYP26C1     ---------HPVDGLRLFFHPLTPSVAGNGLCL-------------------------------
CYP716A1    ---------IPDKGLPIRIFPQS-----------------------------------------
CYP725A1    ---------LPANGFSIKLFPRS-----------------------------------------
CYP718      ---------FPSLGMPIKISPKVS----------------------------------------
CYP90A1     ----------QKRYPIFVKRRDFAT---------------------------------------
CYP90B1     ----------PNGLPIRVSRIL------------------------------------------
CYP724A1    ----------KRGMLLEIEPTKFLED--------------------------------------
CYP720A1    ----------------------------------------------------------------
CYP85A1     ----------PKGFHLRISPY-------------------------------------------
CYP87A2     ----------PNGYHVKLHKKRD-----------------------------------------
CYP708A1    ----------SKPIRITISENPLSSSHQNANLF-------------------------------
CYP702A1    ----------PNGCEVQFLKDTEVDNSSGSNPDCCNG---------------------------
CYP88A3     ----------PTDNCLARISYQ------------------------------------------
CYP88B1     ----------VKFKKLSISSNGN-----------------------------------------
CYP3A1      ---------GLLQPTK-PIILKVVPRDEIITGS-------------------------------
CYP5A1      ---------SALSPKN-GVYIRIVPR--------------------------------------
CYP6A2      ---------SIVLGTVGGIYLRVERI--------------------------------------
CYP6B4      ---------RLLVYPKSGIFLNIIPRNY------------------------------------
CYP28A1     ---------TFIGTCKGGIWLDFELRQ-------------------------------------
CYP28C1     ---------IFVGVHKGGIWLQFVPRKNVTTK--------------------------------
CYP13A2     ---------ATTSPEDVFVHLRPRIW--------------------------------------
CYP13B1     ---------TTTSPEAVTLYLKPRI---------------------------------------
CYP72A8     ---------TLHPQFGAPLIFHML----------------------------------------
CYP72B1     ---------LLYPQHGAPITFRRLTNHED-----------------------------------
CYP721A1    ---------TLQPQNGAHLLFTRISS--------------------------------------
CYP709A1    ---------TIKPKYGVQVILKPLVS--------------------------------------
CYP709B1    ---------TIQPQYGLPVMLQPLED--------------------------------------
CYP715A1    ---------SLRPGYGLPLIIRPL----------------------------------------
CYP714A1    ---------LVEPQHGVVIRVLRQ----------------------------------------
CYP4C3      ---------LILRPKDGLRVKITPRD--------------------------------------
CYP31A2     ---------AD-----------------------------------------------------
CYP37A1     --------TITRPSLGFPLKFTVRQQ--------------------------------------
CYP37B1     --------LILKSSLGFPLTVHHRTDNK------------------------------------
CYP32A1     --------LILRPYNGMKIKIKRREAADYVVFTTFFRMKLDECEKKSFFVFILSLMIDSPRRFLSNFSN
CYP29A2     --------VVTKPSNGIPVRLIRRN----------------------------------------
CYP86A1     --------LTLFMKNGLRVYLQPRGEVLA-----------------------------------
CYP86B1     --------LTMYMKHGLMVNLINRSVSEIDQYYAKSFDEGYIN---------------------
CYP96A1     --------IILHMKHGLKVTVTKRSNLL------------------------------------
CYP96C1     --------ATLYLKDGLIVRVNKII---------------------------------------
CYP94A1     --------LSSQMEGGFPVTIQKRDS--------------------------------------
CYP94B1     --------LTAHMAGGLKVKIKRREQCDSMYI--------------------------------
CYP704A1    --------LTLHVDGGLHLCAIPRTST-------------------------------------
CYP704B1    --------TILSMAHGLKVTVSRRS---------------------------------------
CYP97A3     --------ATIHTTEGLKLTVTKRTKPLDIPSVPILPMDTSRDEVSSALS--------------
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CYP97B3      ---------ATIHAKNGMWCKLKRRSK------------------------------------
CYP1A1       VDMTPIYGLTMKHACCEHFQMQLRS-------------------------------------
CYP1B1       SNMSFSYGLSIKPKSFKIHVSLRESMKLLDSAVEKLQAEEACQ-------------------
CYP17A1      PSLEGIPKIVFLIDPFKVKITVRPAWKEAQAEGSA---------------------------
CYP19A1      PSLEGHASLVLQIKPFKVKIEVRQAWKEAQAEGSTP--------------------------
CYP2A7       IDVSPKHVVFATIPRNYTMSFLPR--------------------------------------
CYP2M1       INIEPACSSFGRLPRSYDCYIKLRTEK-----------------------------------
CYP33A1      VPSLERTFAFIAKAQDYTCQVKPRYSS-----------------------------------
CYP33C1      LPSMAKGSGPVVAPRLFTAILTRRF-------------------------------------
CYP33B1      LPSLYKDFSLVSHVIPYKCRQYIP--------------------------------------
CYP23A1      -VTTERVLGLTVSPVEYSCKITRRGLDHNQNSVK----------------------------
CYP35A1      LLLPVKLSRPAFAALISSLPLDKLLPHI----------------------------------
CYP35B1      TEDKLPYSAGKTPDKSVKLEFVKL--------------------------------------
CYP34A1      LKTLAPFGLLKQSPE-FRIRFVEVEKH-----------------------------------
CYP71A12     PDLTEAFG-LDVCRKFPLIAFPSSVI------------------------------------
CYP71C1      VDMSDQFG-MTLRRTQKLYLVPRIPKCVSSS-------------------------------
CYP71D11     LDLTEEFG-VTVSKKEDLCLIPSISHPLPST-------------------------------
CYP726A1     LDMTEAIG-GALRKKIDLKLIPIPYQVSLGSNIS----------------------------
CYP71K1      LDMTEALG-LTTRRCSDLLLVPALRVPLRDHER-----------------------------
CYP99A1      LDMDTVVG-STMRRRNHLHLVPSPYKETELTVGI----------------------------
CYP71E1      VSMEETGA-LTFHRKTPLVVVPTKYKNRRAA-------------------------------
CYP71N1      ISMEEAPG-VTVHREYALCLMATKYDATTA--------------------------------
CYP71B2      IDMEEAGN-ISIVKKIPLQLVPVQRY------------------------------------
CYP83A1      INMDVMTG-LAMHKSQHLKLVPEKVNKY----------------------------------
CYP83B1      IKMDVMTG-LAMHKKEHLVLAPTKHI------------------------------------
CYP83E1      IDTSMLPG-ITQHKKNPLCLIAKVPK------------------------------------
CYP93B1      INVDERPG-LTAPRAHNLVCVPVDRTSGGGPLKIIEC-------------------------
CYP93C17     ANMEERAG-LTVPRANSLMCVPLARSKVAAELLSS---------------------------
CYP93A1      VDMEEKSG-ITLPRANPIICVPVPRINPFPTI------------------------------
CYP705A1     INMEEATGGFLITMAHPLTCTPIPLPRTQNSLISHL--------------------------
CYP712A1     VDLSQGSG-FSAEMARPLVCNPVDHFNTF---------------------------------
CYP75A1      LNMEEAFG-LALQKAVPLEAMVTPRLPIDVYAPLA---------------------------
CYP75B1      LNMEESYG-LTLQRAVPLVHPKPRLAPNVYGLGSG---------------------------
CYP92A2      LNMDEIFG-LSTPKKFPLATVIEPRLSPKLYSV-----------------------------
CYP84A1      LDMNDVFG-LTAPKATRLFAVPTTRLICAL--------------------------------
CYP703A2     IDTVEVYG-MTMPKAKPLRAIAKPRLAAHLYT------------------------------
CYP98A3      IDMSENPG-LVTYMRTPVQAVATPRLPSDLYKRVPYDM------------------------
CYP706A1     FEVEEKFG-LVLKLKSPLVAIPVPRLSDPKLYTA----------------------------
CYP81D1      VDMKEGVG-NTVPKAIPLKAICKARPFLHKIIS-----------------------------
CYP81E6      IDMGERDG-FVLMKSIPVKAMCKSRPVINNVFK-----------------------------
CYP81B1      VDMTEGPG-LTMPKAIPLVAKCKPRVEMTNLLSEL---------------------------
CYP82A2      LDMTEVFR-ATNTKATPLEILIKPRLSPSCYESI----------------------------
CYP82B1      VDMTEGSG-LTMPKVTPLKVLLTPRLPLPLYDY-----------------------------
CYP76A2      INMDGSMG-VTARKRDSLKVIPKKA-------------------------------------
CYP76G1      MDMGERIG-ITLKKAVPLEAIPIPYRGT----------------------------------
CYP76E1      LNMDEQFG-LTLKRVQPLRVEAISSA------------------------------------
CYP76F2      MNMEERYG-ISLQKAQPLQALPVRV-------------------------------------
CYP76C1      LDMDETFG-LTLHKTNPLHAVPVKKRANIN--------------------------------
CYP76B1      LDMTEKNG-TTISKAKPLCVVPIPLN------------------------------------
CYP80A1      LDMEELFT-LSLCMAKPLRVIPKVRI------------------------------------
CYP79A1      VDLSESK--SDTFMATPLVLHAEPRLPAHLYPSISI--------------------------
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CYP79B2    VELMESS--HDMFLAKPLVMVGDLRLPEHLYPTVK------------------------------------
CYP79D1    IDLAETLDFTELTPATPISAFAKPRLAPHLYPTSP------------------------------------
CYP79E1    VELEEEKFTCSMFLGKPLRALAKPRQ--ELLQSF-------------------------------------
CYP79C1    VELVESK--ENLFMANPLMACVKPRLDPNMYPKLWTGPA--------------------------------
CYP79F1    LSLEEDD--ASLLMAKPLHLSVEPRLAPNLYPKFRP-----------------------------------
CYP77A6    ---FAGKLEFTVVMKKPLRAMVKPRV---------------------------------------------
CYP77B1    ---PTETYAFTVVMKNSLKAQIRSRT---------------------------------------------
CYP89A2    ---LTEKLEFTVVMKHPLKALAVPRRCH-------------------------------------------
CYP27A1    -----SVSRIVLVPSKKVSLRFLQRQ---------------------------------------------
CYP27B1    -----PKTRTVLVPERSINLQFLDR----------------------------------------------
CYP11A1    -----TIFNLILTPDKPIFLVFRPFNQGPPQA---------------------------------------
CYP11B1    -----FAYRFVMMPTSAPLLTFRPVS---------------------------------------------
CYP12A1    -----FKFKLINVPNIPLKFKFTDVEN--------------------------------------------
CYP12C1    -----YKCRFLYKPNIPLKFKFTDLKY--------------------------------------------
CYP74A     ----------LGSSVNFSSLRKASF----------------------------------------------
CYP74C1    ----------LGPAVKFKSLTRATASV--------------------------------------------
CYP74D1    ----------RAPNVAFNTLTKASK----------------------------------------------
CYP74B2    ---------------SIKAVVKAK----------------------------------------------
CYP24A1    ----------ILVPSRELPIAFRPR---------------------------------------------
CYP10      ---------TMLTPDRPVRIEFKPRQ---------------------------------------------
CYP9A1     ---------MHLEGGAWVRLRVRPEKS--------------------------------------------
CYP9B1     ---------FNIIPTTGFWMQLVSRK---------------------------------------------
CYP14A2    -------VCGAVLTTKPYICELVPQAA--------------------------------------------
CYP21A1    --------INLLIPPFQVRLQPRNLAPQDQGQKSSTG----------------------------------
CYP36A1    ---------SLRAPKPFTVRASRR-----------------------------------------------
CYP45A1    GVWLTLHRRTTDLPHHYEPPTQVLYNRLCQVPLTK------------------------------------
CYP18A1    -ATITPESFKVCLKRRPLGPTAADPHHMRNVGAN-------------------------------------
CYP707A1   --------------FTHFVLFFQIYV---------------------------------------------
CYP722A1   ----------LKSGYPIRVSRRL-----------------------------------------------
CYP25A1    ---------VIMRPKDPVRLLLKPRN---------------------------------------------
CYP73A5    ---------FSLHILNHSIIVMKPRNC--------------------------------------------
CYP78A6    ---------LSCEMANPLPAKLRRRRS--------------------------------------------
CYP4A4     -------------SKNGIHLRLRKLH---------------------------------------------
CYP719     ---------FVLLMKTPLEARIAGRNV--------------------------------------------
CYP44A1    -----------RGDCTFEFKKL-------------------------------------------------
CYP302A1   -----------KPDAPVLIDLRLRRE---------------------------------------------
CYP22A1    ----------ITAPPKPYATRVEYLGNRLIN----------------------------------------
CYP52A1    --------TLTLSLFEGAEVQMYLIL---------------------------------------------
CYP701A3   -----------QKLYPLMAIINPRRS---------------------------------------------
CYP315A1   -----------VPDRTLRLALRPRTE---------------------------------------------
CYP39A1    ---------VPQPEGQCRIEYKQRI----------------------------------------------
CYP711A1   ---------IILSFKNGVKLRTIKRF---------------------------------------------
CYP46A1    -------LDPVLCTLRPRGWQPAPPPPPC------------------------------------------
CYP43A1    -------DTGTIWPTDKLGLVLKQR----------------------------------------------
CYP59A1    RAYQAEKGGGGAHPADGMPCLVTFRV--------------------------------------------
CYP710A1   ----------TISPKDGCTVFLSRRVAKYPNFS--------------------------------------
CYP56A1    ----------LCPLNLKLKFNENIME---------------------------------------------
CYP57A1    --------EYKAMIKPRRCCLSRDESLV-------------------------------------------
CYP53A1    ------------KPLGLQVGMKRRQPGSA------------------------------------------
CYP58A1    -------FVVPLPKLDSLGVRVMVR----------------------------------------------
CYP20A1    -----------SKEEAWITVSKRY----------------------------------------------
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CYP38A1     -------------PKDDIKIYIRSRKED-------------------------------------
CYP54A1     ------------TIPDPTKDVMFRKL---------------------------------------
CYP55A1     -------------RDVGIVDLPVIF----------------------------------------
CYP727A1    ---------SLHHIPNPKIILKKRSI--------------------------------------
consensus             .        .  .
            801......810.......820.......830.......840.......850.......860........
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