

logo

CYP39A1	...EILNYIIPSGDLLMLSPFW.LHRNPKYFPEPELKKPERWKKANLEKHS.....FLDCFMAFGSGKFQCPARWFALLEVQMCIIILIYKYDCSLLD	441
CYP8B1	KMSSGQEYLFHRGDLALFPYLSVHMDPDHPEPTVFVKYDRFLNPNNGSRKVDFFKTGKKIHHTMPWGSQVSI	467
CYP7B1	SSETG.DYCVRKGDVAIFPPV.LHGDPEIFEAPEEFRYDRFIE.DGKKKTTFFKRGKKLKCYLMPFGTGT	476
CYP7A1	HLEDG.SYNIRKDDIIALYPQL.MHLDPEIYPDPLTFKYDRYLDENGKTCTTFYCNGLKLKYYMPFGSGG	471
CYP11B1LQNYHIPAGTLVRVFLYS.LGRNPALFPRPERYNPQRWLDIRG.....SGRN..FYHVPFGFGMRQCL	476
CYP11B2LQNYHIPAGTLVQVFLYS.LGRNAALFPRPERYNPQRWLDIRG.....SGRN..FHHVPFGFGMRQCL	476
CYP24A1LGEYALPKGTVLMNTQV.LGSSEDNFEDSSQFRPERWLQEKE.....KINP..FAHLPFVGVRKRMCI	488
CYP27B1VGDIIPKNTLVTLCHYA.TSRDPAQFPEPNSFRPARWLGEGP.....TPHP..FASLPFGFGKRS	482
CYP27A1VDGFLFPKNTQFVFCYV.VSRDPTAFSEPESEFQPHRWLRNSQPATPR...IQHP..FGSVPF	503
CYP26B1LDGFQIPKGWSVMYSIRD.THDTAPVFKDENVFDPDRFSQARS....E...DKDG.RFHYPFGGGV	468
CYP26A1LNGYQIPKGWNVISICD.THDAEIFTNKEEFNPDRFMLPHP....E...D.AS.RFSFIPFGGGL	469
CYP21A2	...SISGYDIPEGTVIIPNLQG.AHLDETVERPHEFWPDRFLEPGK....N.....SRALAFGCGARV	456
CYP17A1	...SIGEFAVDKGEVIINLWA.LHHNEKEWHQPDQFMPPERFLNPAG...T...QLISPSVSYPFGAG	469
CYP1B1	...SVLGYHIPKDTVVVFVNQWS.VNHDPLKWPNPENFDPARFLDKDG....L...INKDLTSRVMIF	495
CYP2U1	...VLQGYTIPKGTILILPNLWS.VHRDPAIWEKPEDFYPNRFLDDQG....Q...LIKK..ETFIPFG	517
CYP2R1	...VVRGYSIPKGTITVITNLYS.VHFDEKYWRDPEVFHPERFLDSSG....Y...FAKK..EALVPF	475
CYP2D6	...EVQGFRIPKGTTLITNLSS.VLKDEAVWEKPFERFHEHFLDAQG....H...FVKP..EAFLPF	470
CYP2E1	...IFRGYLIPKGTVVVPTLDS.VLYDNQEFDPDEKFKPEHFLNENG....K...FKYS..DYFKPF	464
CYP2C9	...KFRNYLIPKGTITILISLTS.VLHDNKEFPNPEMFDPHHFLDEGG....N...FKKS..KYFMP	462
CYP2C8	...KFRNYLIPKGTITIMALLTS.VLHDDKEFPNPNIFDPGHFLDKNG....N...FKKS..DYFMP	462
CYP46A1IDGVRVPGNTPLLFSTYV.MGRMDTYFEDPLTFNPDRFGPGAP....K....PR..FTYFPF	464
CYP3A4	...IN.GMFIPKGVVVMIPSYA.LHRDPKYWTEPEKFLPERFSKKNK....D...NIDP..YIYTPF	469
CYP4V2	...VAGYR.VLKGTEAVIIPYA.LHRDPRYFPNPEEFQPERFFPENAAAA..Q...GRHP..YAYVPF	494
CYP4F22	...LPDGRIPKGTICLVSIYG.THHNPTVWPDSKVYNPYRFDPDNP....Q...QRSP..LAYVPF	502
CYP4F8	...LPDSRVIPKGNVCNINIFA.IHHNPSVWPDPEVYDPFRFDPENAAAA..Q...KRSP..MAFIPF	495
CYP4F12	...LPDGRVIPKGTITCLIDIIG.VHHNPTVWPDPEVYDPFRFDPENAAAA..K...GRSP..LAFIPF	495
CYP4F2	...LPDGRVIPKGTICLVSVFG.THHNPAVWPDPEVYDPFRFDPENI....K...ERSP..LAFIPF	495
CYP4F3	...LPDGRVIPKGTICLVSVFG.THHNPAVWPDPEVYDPFRFDPKNI....K...ERSP..LAFIPF	495
CYP4X1	...FPDGGCTLPAGITVVLSIWG.LHHNPAVWKNPKVFDPLRFSQENS....D...QRHP..YAYLPF	481
CYP4A11	...FPDGRSLPKGIMVLLSIYG.LHHNPKVWPNLEVFDPFRFAPGSA.....QHS..HAFLPF	484
CYP4A22	...FPDGRSLPKGIMVLLSIYG.LHHNPKVWPNLEVFDPFRFAPGSA.....QHS..HAFLPF	484
consensus	** ***** * * * * * ! ! ** !!* ! ! ! ! * ! * * * * * *	

- non-conserved
- ≥ 50% conserved
- ≥ 90% conserved