Figures

Figure 1 - Nucleotide and protein sequence of Aspergillus ochraceus *11 alpha hydroxylase*

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tggaagtttt tacacttatt atgccggagc cgaaagattc tgagtcgagg ggttggggaa      60
caacactata agacctacaa ccacttggat ttggtgaatt tacacgggca ttatcaaaac     120
agccacaagc tgacagctca ttatc atg ccc ttc ttc act ggg ctt ctg gcg        172
                            Met Pro Phe Phe Thr Gly Leu Leu Ala
                             1               5

att tac cat agt ctc ata ctc gac aac cca gtc caa acc ctg agc acc       220
Ile Tyr His Ser Leu Ile Leu Asp Asn Pro Val Gln Thr Leu Ser Thr
 10                  15                  20                  25

att gtc gta ttg gcg gca gcg tac tgg ctc gca acg ctc cag ccg agc       268
Ile Val Val Leu Ala Ala Ala Tyr Trp Leu Ala Thr Leu Gln Pro Ser
                 30                  35                  40

gac ctt cct gag ctg aat ccc gcc aaa cca ttc gag ttc acc aat cgt       316
Asp Leu Pro Glu Leu Asn Pro Ala Lys Pro Phe Glu Phe Thr Asn Arg
             45                  50                  55

cgt cgt gtt cat gag ttt gtt gaa aat agt aag agc ttg ctt gct cgg       364
Arg Arg Val His Glu Phe Val Glu Asn Ser Lys Ser Leu Leu Ala Arg
         60                  65                  70

ggg agg gaa ttg cac ggg cac gag ccg tac aga ctc atg tct gaa tgg       412
Gly Arg Glu Leu His Gly His Glu Pro Tyr Arg Leu Met Ser Glu Trp
     75                  80                  85

gga tcc ttg att gtc ctg ccc cca gag tgc gcc gac gag ctg cgc aac       460
Gly Ser Leu Ile Val Leu Pro Pro Glu Cys Ala Asp Glu Leu Arg Asn
 90                  95                 100                 105

gac cca aga atg gac ttt gag acg ccc acc acc gac gac tcc cac gga       508
Asp Pro Arg Met Asp Phe Glu Thr Pro Thr Thr Asp Asp Ser His Gly
                110                 115                 120

tat atc cct ggc ttc gac gct ctc aac gca gac ccg aac ctg act aaa       556
Tyr Ile Pro Gly Phe Asp Ala Leu Asn Ala Asp Pro Asn Leu Thr Lys
            125                 130                 135

gtg gtc acc aag tac ctc aca aaa gca ttg aac aag ctt act gct ccg       604
Val Val Thr Lys Tyr Leu Thr Lys Ala Leu Asn Lys Leu Thr Ala Pro
        140                 145                 150

atc tcg cat gaa gcg tcc atc gcc atg aaa gcg gtg ctg ggt gac gat       652
Ile Ser His Glu Ala Ser Ile Ala Met Lys Ala Val Leu Gly Asp Asp
    155                 160                 165

cca gat tgg cgt gag atc tac cca gcc aga gac ttg ctc cag ctc gtc       700
Pro Asp Trp Arg Glu Ile Tyr Pro Ala Arg Asp Leu Leu Gln Leu Val
170                 175                 180                 185

gcc cgg atg tcg aca aga gtg ttc ctt ggc gag gaa atg tgc aat aac       748
Ala Arg Met Ser Thr Arg Val Phe Leu Gly Glu Glu Met Cys Asn Asn
                190                 195                 200

cag gat tgg atc caa acc tca tca caa tac gcg gcc ctt gcc ttc ggt       796
Gln Asp Trp Ile Gln Thr Ser Ser Gln Tyr Ala Ala Leu Ala Phe Gly
            205                 210                 215

gtc ggt gac aag ctt aga ata tac ccg aga atg atc aga ccg ata gta       844
Val Gly Asp Lys Leu Arg Ile Tyr Pro Arg Met Ile Arg Pro Ile Val
        220                 225                 230

cat tgg ttc atg cca tcc tgt tgg gag ctg cgc cga tcg ctg cga cgc       892
His Trp Phe Met Pro Ser Cys Trp Glu Leu Arg Arg Ser Leu Arg Arg
    235                 240                 245

tgc cga cag att ctc acg ccg tac att cac aaa cgc aag tcc ctg aag       940
Cys Arg Gln Ile Leu Thr Pro Tyr Ile His Lys Arg Lys Ser Leu Lys
250                 255                 260                 265

ggg acc acg gac gag cag ggc aag ccc ctt atg ttt gat gat tcc atc       988
Gly Thr Thr Asp Glu Gln Gly Lys Pro Leu Met Phe Asp Asp Ser Ile
                270                 275                 280
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gag tgg ttc gag cga gag ctg ggt ccc aac cac gac gcg gtc ctg aag     1036
Glu Trp Phe Glu Arg Glu Leu Gly Pro Asn His Asp Ala Val Leu Lys
            285                 290                 295

cag gtc acg ctc tcc ata gtt gct atc cac acc acg agt gac cta ctc     1084
Gln Val Thr Leu Ser Ile Val Ala Ile His Thr Thr Ser Asp Leu Leu
        300                 305                 310

ttg cag gcc atg agc gat ctc gcg cag aac ccg aaa gtg cta caa gca     1132
Leu Gln Ala Met Ser Asp Leu Ala Gln Asn Pro Lys Val Leu Gln Ala
    315                 320                 325

gtg cgc gag gag gtg gtc cga gtg ctg agc acc gag ggg ctc agc aag     1180
Val Arg Glu Glu Val Val Arg Val Leu Ser Thr Glu Gly Leu Ser Lys
330                 335                 340                 345

gtc tcg ctt cac agt ctc aag ctc atg gac agc gcg ttg aag gaa agc     1228
Val Ser Leu His Ser Leu Lys Leu Met Asp Ser Ala Leu Lys Glu Ser
                350                 355                 360

cag cgt ctc agg cct acg ctt ctc ggc tcc ttt cgt cgg cag gca acg     1276
Gln Arg Leu Arg Pro Thr Leu Leu Gly Ser Phe Arg Arg Gln Ala Thr
            365                 370                 375

aat gac atc aag ctg aag agc ggg ttt gtc ata aag aaa ggg act aga     1324
Asn Asp Ile Lys Leu Lys Ser Gly Phe Val Ile Lys Lys Gly Thr Arg
        380                 385                 390

gtc gtg atc gac agc acc cat atg tgg aat ccc gag tat tac act gac     1372
Val Val Ile Asp Ser Thr His Met Trp Asn Pro Glu Tyr Tyr Thr Asp
    395                 400                 405

cct ctc cag tac gac ggg tac cgc tac ttc aac aag cgg cag aca ccc     1420
Pro Leu Gln Tyr Asp Gly Tyr Arg Tyr Phe Asn Lys Arg Gln Thr Pro
410                 415                 420                 425

ggc gag gac aag aac gcg ttg ctc gtc agc aca agc gcc aac cac atg     1468
Gly Glu Asp Lys Asn Ala Leu Leu Val Ser Thr Ser Ala Asn His Met
                430                 435                 440

gga ttc ggt cac ggc gtt cac gcc tgt cct ggc aga ttc ttc gcc tcc     1516
Gly Phe Gly His Gly Val His Ala Cys Pro Gly Arg Phe Phe Ala Ser
            445                 450                 455

aac gag atc aag att gcc ttg tgt cat atc atc tta aat tat gag tgg     1564
Asn Glu Ile Lys Ile Ala Leu Cys His Ile Ile Leu Asn Tyr Glu Trp
        460                 465                 470

cgt ctt cca gac ggc ttc aag ccc cag cct ctc aac atc ggg atg act     1612
Arg Leu Pro Asp Gly Phe Lys Pro Gln Pro Leu Asn Ile Gly Met Thr
    475                 480                 485

tat ctg gcg gat ccc aat acc agg atg ctg atc agg cca cgc aag gcg     1660
Tyr Leu Ala Asp Pro Asn Thr Arg Met Leu Ile Arg Pro Arg Lys Ala
490                 495                 500                 505

gag atc gat atg gcg agt tta act gtg tag gtcgaacacg aagtcctgat       1710
Glu Ile Asp Met Ala Ser Leu Thr Val  *
                510

gaagtgttat tggtcagtgg gtgaagcaag tcgcagaaat gtgtaacaat ttataagaat   1770
aaaaaa                                                              1776
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Figure 2 - Nucleotide and protein sequence of human oxidoreductase

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atg gga gac tcc cac gtg gac acc agc tcc acc gtg tcc gag gcg gtg      48
Met Gly Asp Ser His Val Asp Thr Ser Ser Thr Val Ser Glu Ala Val
 1               5                  10                  15

gcc gaa gaa gta tct ctt ttc agc atg acg gac atg att ctg ttt tcg      96
Ala Glu Glu Val Ser Leu Phe Ser Met Thr Asp Met Ile Leu Phe Ser
            20                  25                  30

ctc atc gtg ggt ctc cta acc tac tgg ttc ctc ttc aga aag aaa aaa     144
Leu Ile Val Gly Leu Leu Thr Tyr Trp Phe Leu Phe Arg Lys Lys Lys
        35                  40                  45

gaa gaa gtc ccc gag ttc acc aaa att cag aca ttg acc tcc tct gtc     192
Glu Glu Val Pro Glu Phe Thr Lys Ile Gln Thr Leu Thr Ser Ser Val
    50                  55                  60

aga gag agc agc ttt gtg gaa aag atg aag aaa acg ggg agg aac atc     240
Arg Glu Ser Ser Phe Val Glu Lys Met Lys Lys Thr Gly Arg Asn Ile
65                  70                  75                  80

atc gtg ttc tac ggc tcc cag acg ggg act gca gag gag ttt gcc aac     288
Ile Val Phe Tyr Gly Ser Gln Thr Gly Thr Ala Glu Glu Phe Ala Asn
                85                  90                  95

cgc ctg tcc aag gac gcc cac cgc tac ggg atg cga ggc atg tca gcg     336
Arg Leu Ser Lys Asp Ala His Arg Tyr Gly Met Arg Gly Met Ser Ala
            100                 105                 110

gac cct gag gag tat gac ctg gcc gac ctg agc agc ctg cca gag atc     384
Asp Pro Glu Glu Tyr Asp Leu Ala Asp Leu Ser Ser Leu Pro Glu Ile
        115                 120                 125

gac aac gcc ctg gtg gtt ttc tgc atg gcc acc tac ggt gag gga gac     432
Asp Asn Ala Leu Val Val Phe Cys Met Ala Thr Tyr Gly Glu Gly Asp
    130                 135                 140

ccc acc gac aat gcc cag gac ttc tac gac tgg ctg cag gag aca gac     480
Pro Thr Asp Asn Ala Gln Asp Phe Tyr Asp Trp Leu Gln Glu Thr Asp
145                 150                 155                 160

gtg gat ctc tct ggg gtc aag ttc gcg gtg ttt ggt ctt ggg aac aag     528
Val Asp Leu Ser Gly Val Lys Phe Ala Val Phe Gly Leu Gly Asn Lys
                165                 170                 175

acc tac gag cac ttc aat gcc atg ggc aag tac gtg gac aag cgg ctg     576
Thr Tyr Glu His Phe Asn Ala Met Gly Lys Tyr Val Asp Lys Arg Leu
            180                 185                 190

gag cag ctc ggc gcc cag cgc atc ttt gag ctg ggg ttg ggc gac gac     624
Glu Gln Leu Gly Ala Gln Arg Ile Phe Glu Leu Gly Leu Gly Asp Asp
        195                 200                 205

gat ggg aac ttg gag gag gac ttc atc acc tgg cga gag cag ttc tgg     672
Asp Gly Asn Leu Glu Glu Asp Phe Ile Thr Trp Arg Glu Gln Phe Trp
    210                 215                 220

ccg gcc gtg tgt gaa cac ttt ggg gtg gaa gcc act ggc gag gag tcc     720
Pro Ala Val Cys Glu His Phe Gly Val Glu Ala Thr Gly Glu Glu Ser
225                 230                 235                 240

agc att cgc cag tac gag ctt gtg gtc cac acc gac ata gat gcg gcc     768
Ser Ile Arg Gln Tyr Glu Leu Val Val His Thr Asp Ile Asp Ala Ala
                245                 250                 255

aag gtg tac atg ggg gag atg ggc cgg ctg aag agc tac gag aac cag     816
Lys Val Tyr Met Gly Glu Met Gly Arg Leu Lys Ser Tyr Glu Asn Gln
            260                 265                 270

aag ccc ccc ttt gat gcc aag aat ccg ttc ctg gct gca gtc acc acc     864
Lys Pro Pro Phe Asp Ala Lys Asn Pro Phe Leu Ala Ala Val Thr Thr
        275                 280                 285

aac cgg aag ctg aac cag gga acc gag cgc cac ctc atg cac ctg gaa     912
Asn Arg Lys Leu Asn Gln Gly Thr Glu Arg His Leu Met His Leu Glu
    290                 295                 300

ttg gac atc tcg gac tcc aaa atc agg tat gaa tct ggg gac cac gtg     960
Leu Asp Ile Ser Asp Ser Lys Ile Arg Tyr Glu Ser Gly Asp His Val
```

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305                 310                 315                 320

gct gtg tac cca gcc aac gac tct gct ctc gtc aac cag ctg ggc aaa     1008
Ala Val Tyr Pro Ala Asn Asp Ser Ala Leu Val Asn Gln Leu Gly Lys
                325                 330                 335

atc ctg ggt gcc gac ctg gac gtc gtc atg tcc ctg aac aac ctg gat     1056
Ile Leu Gly Ala Asp Leu Asp Val Val Met Ser Leu Asn Asn Leu Asp
            340                 345                 350

gag gag tcc aac aag aag cac cca ttc ccg tgc cct acg tcc tac cgc     1104
Glu Glu Ser Asn Lys Lys His Pro Phe Pro Cys Pro Thr Ser Tyr Arg
        355                 360                 365

acg gcc ctc acc tac tac ctg gac atc acc aac ccg ccg cgt acc aac     1152
Thr Ala Leu Thr Tyr Tyr Leu Asp Ile Thr Asn Pro Pro Arg Thr Asn
    370                 375                 380

gtg ctg tac gag ctg gcg cag tac gcc tcg gag ccc tcg gag cag gag     1200
Val Leu Tyr Glu Leu Ala Gln Tyr Ala Ser Glu Pro Ser Glu Gln Glu
385                 390                 395                 400

ctg ctg cgc aag atg gcc tcc tcc tcc ggc gag ggc aag gag ctg tac     1248
Leu Leu Arg Lys Met Ala Ser Ser Ser Gly Glu Gly Lys Glu Leu Tyr
                405                 410                 415

ctg agc tgg gtg gtg gag gcc cgg agg cac atc ctg gcc atc ctg cag     1296
Leu Ser Trp Val Val Glu Ala Arg Arg His Ile Leu Ala Ile Leu Gln
            420                 425                 430

gac tgc ccg tcc ctg cgg ccc ccc atc gac cac ctg tgt gag ctg ctg     1344
Asp Cys Pro Ser Leu Arg Pro Pro Ile Asp His Leu Cys Glu Leu Leu
        435                 440                 445

ccg cgc ctg cag gcc cgc tac tac tcc atc gcc tca tcc tcc aag gtc     1392
Pro Arg Leu Gln Ala Arg Tyr Tyr Ser Ile Ala Ser Ser Ser Lys Val
    450                 455                 460

cac ccc aac tct gtg cac atc tgt gcg gtg gtt gtg gag tac gag acc     1440
His Pro Asn Ser Val His Ile Cys Ala Val Val Val Glu Tyr Glu Thr
465                 470                 475                 480

aag gcc ggc cgc atc aac aag ggc gtg gcc acc aac tgg ctg cgg gcc     1488
Lys Ala Gly Arg Ile Asn Lys Gly Val Ala Thr Asn Trp Leu Arg Ala
                485                 490                 495

aag gag cct gcc ggg gag aac ggc ggc cgt gcg ctg gtg ccc atg ttc     1536
Lys Glu Pro Ala Gly Glu Asn Gly Gly Arg Ala Leu Val Pro Met Phe
            500                 505                 510

gtg cgc aag tcc cag ttc cgc ctg ccc ttc aag gcc acc acg cct gtc     1584
Val Arg Lys Ser Gln Phe Arg Leu Pro Phe Lys Ala Thr Thr Pro Val
        515                 520                 525

atc atg gtg ggc ccc ggc acc ggg gtg gca ccc ttc ata ggc ttc atc     1632
Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Ile Gly Phe Ile
    530                 535                 540

cag gag cgg gcc tgg ctg cga cag cag ggc aag gag gtg ggg gag acg     1680
Gln Glu Arg Ala Trp Leu Arg Gln Gln Gly Lys Glu Val Gly Glu Thr
545                 550                 555                 560

ctg ctg tac tac ggc tgc cgc cgc tcg gat gag gac tac ctg tac cgg     1728
Leu Leu Tyr Tyr Gly Cys Arg Arg Ser Asp Glu Asp Tyr Leu Tyr Arg
                565                 570                 575

gag gag ctg gcg cag ttc cac agg gac ggt gcg ctc acc cag ctc aac     1776
Glu Glu Leu Ala Gln Phe His Arg Asp Gly Ala Leu Thr Gln Leu Asn
            580                 585                 590

gtg gcc ttc tcc cgg gag cag tcc cac aag gtc tac gtc cag cac ctg     1824
Val Ala Phe Ser Arg Glu Gln Ser His Lys Val Tyr Val Gln His Leu
        595                 600                 605

cta aag caa gac cga gag cac ctg tgg aag ttg atc gaa ggc ggt gcc     1872
Leu Lys Gln Asp Arg Glu His Leu Trp Lys Leu Ile Glu Gly Gly Ala
    610                 615                 620

cac atc tac gtc tgt ggg gat gca cgg aac atg gcc agg gat gtg cag     1920
His Ile Tyr Val Cys Gly Asp Ala Arg Asn Met Ala Arg Asp Val Gln
625                 630                 635                 640

aac acc ttc tac gac atc gtg gct gag ctc ggg gcc atg gag cac gcg     1968
Asn Thr Phe Tyr Asp Ile Val Ala Glu Leu Gly Ala Met Glu His Ala
                645                 650                 655
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cag gcg gtg gac tac atc aag aaa ctg atg acc aag ggc cgc tac tcc      2016
Gln Ala Val Asp Tyr Ile Lys Lys Leu Met Thr Lys Gly Arg Tyr Ser
            660                 665                 670

ctg gac gtg tgg agc                                                2031
Leu Asp Val Trp Ser
        675
```

Figure 3 - Nucleotide and protein sequence of Aspergillus ochraceus *oxidoreductase*

```
                                                                        60
cttatttcgt ttaggaagag caccggcttc ggtgtccttc cttaccctct tattcttcct
                                                                       120
cttctgactc ccttttttgt attgatcgcc catctcggtg aacatttggg atatctttcc
                                                                       180
ctctcccccc cccgccccga ccctccttat cttctcctcc cgtccagcat ttagctcgcc
                                                                       238
atcgaattcg caattccttc ctcgtgactc ttcatcgctg agcgtcctca tc atg gcg
                                                          Met Ala
                                                           1

caa ctc gat act ctc gat ttg gtc gtc ctg gtg gcg ctc ttg gtg ggt      286
Gln Leu Asp Thr Leu Asp Leu Val Val Leu Val Ala Leu Leu Val Gly
        5                  10                  15

agc gtg gcc tac ttc acc aag ggc acc tac tgg gcc gtc gcc aaa gac      334
Ser Val Ala Tyr Phe Thr Lys Gly Thr Tyr Trp Ala Val Ala Lys Asp
    20                  25                  30

cct tat gcc tcg gct ggt ccg gcg atg aat gga ggc gcc aag gcc ggc      382
Pro Tyr Ala Ser Ala Gly Pro Ala Met Asn Gly Gly Ala Lys Ala Gly
35                  40                  45                  50

aag act cgc gac att gtt cag aaa atg gac gaa act ggc aaa aac tgt      430
Lys Thr Arg Asp Ile Val Gln Lys Met Asp Glu Thr Gly Lys Asn Cys
                55                  60                  65

gtg att ttc tac ggc tcg caa acc ggt acc gct gag gac tac gcg tcc      478
Val Ile Phe Tyr Gly Ser Gln Thr Gly Thr Ala Glu Asp Tyr Ala Ser
            70                  75                  80

aga ctg gcc aag gaa ggc tcc cag cga ttc ggt ctc aag acc atg gtg      526
Arg Leu Ala Lys Glu Gly Ser Gln Arg Phe Gly Leu Lys Thr Met Val
        85                  90                  95

gcc gat ctg gag gac tac gac tac gaa aac ctg gaa aag ttc ccc gag      574
Ala Asp Leu Glu Asp Tyr Asp Tyr Glu Asn Leu Glu Lys Phe Pro Glu
    100                 105                 110

gac aag gtt gtt ttc ttc gtt ctg gcc act tat ggc gag ggt gaa ccc      622
Asp Lys Val Val Phe Phe Val Leu Ala Thr Tyr Gly Glu Gly Glu Pro
115                 120                 125                 130

acg gat aat gcg gtt gaa ttc tac cag ttc gtc acg ggc gaa gat gct      670
Thr Asp Asn Ala Val Glu Phe Tyr Gln Phe Val Thr Gly Glu Asp Ala
                135                 140                 145

gct ttc gag agc ggc gct acc gcc gac gat aag cct ctg tct tct ctc      718
Ala Phe Glu Ser Gly Ala Thr Ala Asp Asp Lys Pro Leu Ser Ser Leu
            150                 155                 160

aag tat gtc acg ttt ggt ctg ggt aac aac acc tat gag cac tac aac      766
Lys Tyr Val Thr Phe Gly Leu Gly Asn Asn Thr Tyr Glu His Tyr Asn
        165                 170                 175

gct atg gtt cgc aat gtg gac gcc gct ctc aca aag ttc ggc gcc caa      814
Ala Met Val Arg Asn Val Asp Ala Ala Leu Thr Lys Phe Gly Ala Gln
    180                 185                 190

cgc att ggc tct gct ggt gag ggt gac gac ggc gct ggt aca atg gaa      862
Arg Ile Gly Ser Ala Gly Glu Gly Asp Asp Gly Ala Gly Thr Met Glu
195                 200                 205                 210

gag gat ttc ctg gcc tgg aag gaa ccc atg tgg gct gcc ctt tct gag      910
Glu Asp Phe Leu Ala Trp Lys Glu Pro Met Trp Ala Ala Leu Ser Glu
                215                 220                 225

gcg atg aac ctg caa gag cgc gat gcg gtc tac gag ccg gtc ttc aat      958
Ala Met Asn Leu Gln Glu Arg Asp Ala Val Tyr Glu Pro Val Phe Asn
            230                 235                 240

gtc acc gag gac gag tcc ctg agc ccc gaa gat gag aac gtt tac ctc     1006
Val Thr Glu Asp Glu Ser Leu Ser Pro Glu Asp Glu Asn Val Tyr Leu
        245                 250                 255

ggt gag ccc act caa ggt cat ctc caa ggc gag ccc aag ggc ccg tac     1054
Gly Glu Pro Thr Gln Gly His Leu Gln Gly Glu Pro Lys Gly Pro Tyr
    260                 265                 270

tct gcg cac aac ccg ttc atc gct ccc atc tcc gaa tct cgt gaa ctg     1102
Ser Ala His Asn Pro Phe Ile Ala Pro Ile Ser Glu Ser Arg Glu Leu
275                 280                 285                 290
```

```
ttc aac gtc aag gac cgc aac tgt ctg cac atg gaa atc agc atc gcc     1150
Phe Asn Val Lys Asp Arg Asn Cys Leu His Met Glu Ile Ser Ile Ala
                295                 300                 305

ggt agc aac ctc act tac cag act ggt gac cac atc gct gtt tgg ccc     1198
Gly Ser Asn Leu Thr Tyr Gln Thr Gly Asp His Ile Ala Val Trp Pro
            310                 315                 320

acc aac gcc ggt tcc gag gtc gat cgg ttc ctg cag gct ttt ggt ctc     1246
Thr Asn Ala Gly Ser Glu Val Asp Arg Phe Leu Gln Ala Phe Gly Leu
        325                 330                 335

gaa gga aag cgc cac tcc gtc atc aac att aag ggt atc gat gtg acc     1294
Glu Gly Lys Arg His Ser Val Ile Asn Ile Lys Gly Ile Asp Val Thr
    340                 345                 350

gct aag gtt ccg att ccc act cct acg acc tat gac gcc gca gtt cgc     1342
Ala Lys Val Pro Ile Pro Thr Pro Thr Thr Tyr Asp Ala Ala Val Arg
355                 360                 365                 370

tac tac ctg gaa gtc tgt gcc ccc gtt tcc cgt cag ttt gtc tcg act     1390
Tyr Tyr Leu Glu Val Cys Ala Pro Val Ser Arg Gln Phe Val Ser Thr
                375                 380                 385

ctc gct gcc ttt gcc cct gat gaa gcg acc aag gcg gag atc gtt cgt     1438
Leu Ala Ala Phe Ala Pro Asp Glu Ala Thr Lys Ala Glu Ile Val Arg
            390                 395                 400

ttg ggt ggc gac aag gac tat ttc cat gag aag att acc aac cga tgc     1486
Leu Gly Gly Asp Lys Asp Tyr Phe His Glu Lys Ile Thr Asn Arg Cys
        405                 410                 415

ttc aac atc gct cag gct ctc cag agc atc acg tcc aag cct ttc acc     1534
Phe Asn Ile Ala Gln Ala Leu Gln Ser Ile Thr Ser Lys Pro Phe Thr
    420                 425                 430

gcc gtc ccg ttc tcc ctg ctt atc gaa ggt atc acc aag ctt cag ccc     1582
Ala Val Pro Phe Ser Leu Leu Ile Glu Gly Ile Thr Lys Leu Gln Pro
435                 440                 445                 450

cgt tac tac tcg atc tcc tcg tct tcc ctg gtt cag aag gac aag att     1630
Arg Tyr Tyr Ser Ile Ser Ser Ser Ser Leu Val Gln Lys Asp Lys Ile
                455                 460                 465

agc att acc gcc gtt gtg gag tcg gtt cgc ttg cct ggt gag gaa cac     1678
Ser Ile Thr Ala Val Val Glu Ser Val Arg Leu Pro Gly Glu Glu His
            470                 475                 480

att gtc aag ggt gtg acc acg aac tat ctt ctc gcg ctc aag gaa aag     1726
Ile Val Lys Gly Val Thr Thr Asn Tyr Leu Leu Ala Leu Lys Glu Lys
        485                 490                 495

caa aac ggc gag cct tcc cct gac ccg cac ggc ttg act tac tct atc     1774
Gln Asn Gly Glu Pro Ser Pro Asp Pro His Gly Leu Thr Tyr Ser Ile
    500                 505                 510

act gga ccc cgt aac aag tac gat ggc atc cat gtc ccc gtt cac gtc     1822
Thr Gly Pro Arg Asn Lys Tyr Asp Gly Ile His Val Pro Val His Val
515                 520                 525                 530

cgc cac tcg aac ttc aaa ttg ccc tcg gat ccc tcg cga cct gtg atc     1870
Arg His Ser Asn Phe Lys Leu Pro Ser Asp Pro Ser Arg Pro Val Ile
                535                 540                 545

atg gtt gga ccc ggt act ggt gtt gct cct ttc cgt ggg ttt atc cag     1918
Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg Gly Phe Ile Gln
            550                 555                 560

gag cgt gct gcc ttg gcc gcg aag ggc gag aag gtc gga act acc ttg     1966
Glu Arg Ala Ala Leu Ala Ala Lys Gly Glu Lys Val Gly Thr Thr Leu
        565                 570                 575

ctt ttc ttc ggc tgc cgt aag tcc gac gaa gat ttc ttg tac aag gat     2014
Leu Phe Phe Gly Cys Arg Lys Ser Asp Glu Asp Phe Leu Tyr Lys Asp
    580                 585                 590

gaa tgg aag act ttt cag gag cag ctt ggc gac tcg ctc aag atc atc     2062
Glu Trp Lys Thr Phe Gln Glu Gln Leu Gly Asp Ser Leu Lys Ile Ile
595                 600                 605                 610

act gcc ttc tct cgt gaa tcg gct gag aaa gtc tac gtc cag cac agg     2110
Thr Ala Phe Ser Arg Glu Ser Ala Glu Lys Val Tyr Val Gln His Arg
                615                 620                 625

ctg cgt gag cat gcc gag ctg gtc agt gac ctg ctg aag cag aaa gcc     2158
```

```
Leu Arg Glu His Ala Glu Leu Val Ser Asp Leu Leu Lys Gln Lys Ala
                630                 635                 640

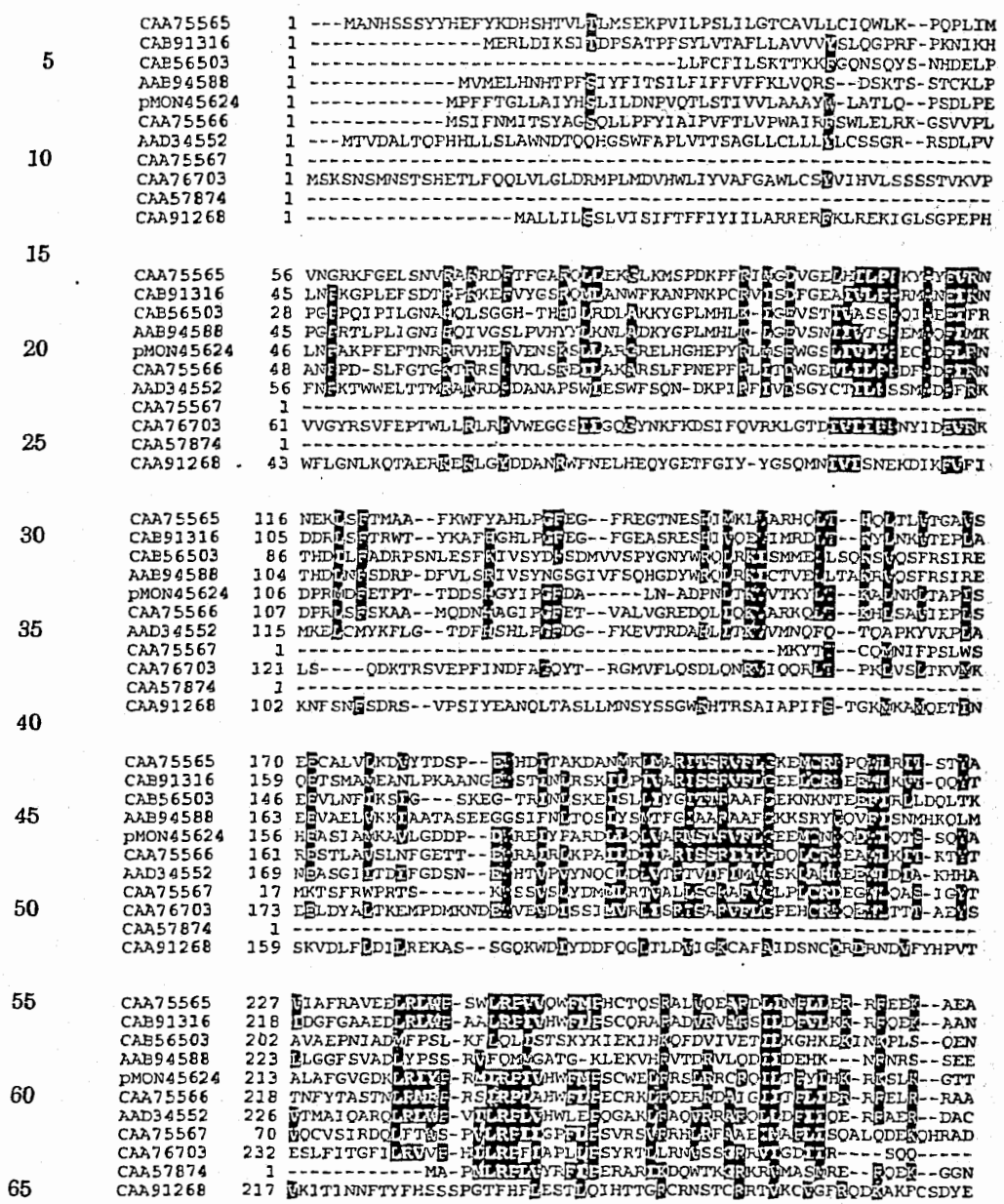
act ttc tat gtt tgc ggt gac gct gcc aac atg gcc cgt gaa gtc aac    2206
Thr Phe Tyr Val Cys Gly Asp Ala Ala Asn Met Ala Arg Glu Val Asn
        645                 650                 655

ctc gtg ctt ggg caa atc att gcc aag cag cgc ggt ctc cct gcc gag    2254
Leu Val Leu Gly Gln Ile Ile Ala Lys Gln Arg Gly Leu Pro Ala Glu
    660                 665                 670

aag ggc gag gag atg gtg aag cac atg cgc agc agc ggc agc tac cag    2302
Lys Gly Glu Glu Met Val Lys His Met Arg Ser Ser Gly Ser Tyr Gln
675                 680                 685                 690

gac gat gtc tgg tcc taa aa                                        2322
Asp Asp Val Trp Ser  *
                695
```

Figure 4 - Amino acid homology alignment of A. ochraceus *11 alpha hydroxylase with the top 10 BLAST hits from GenBank*



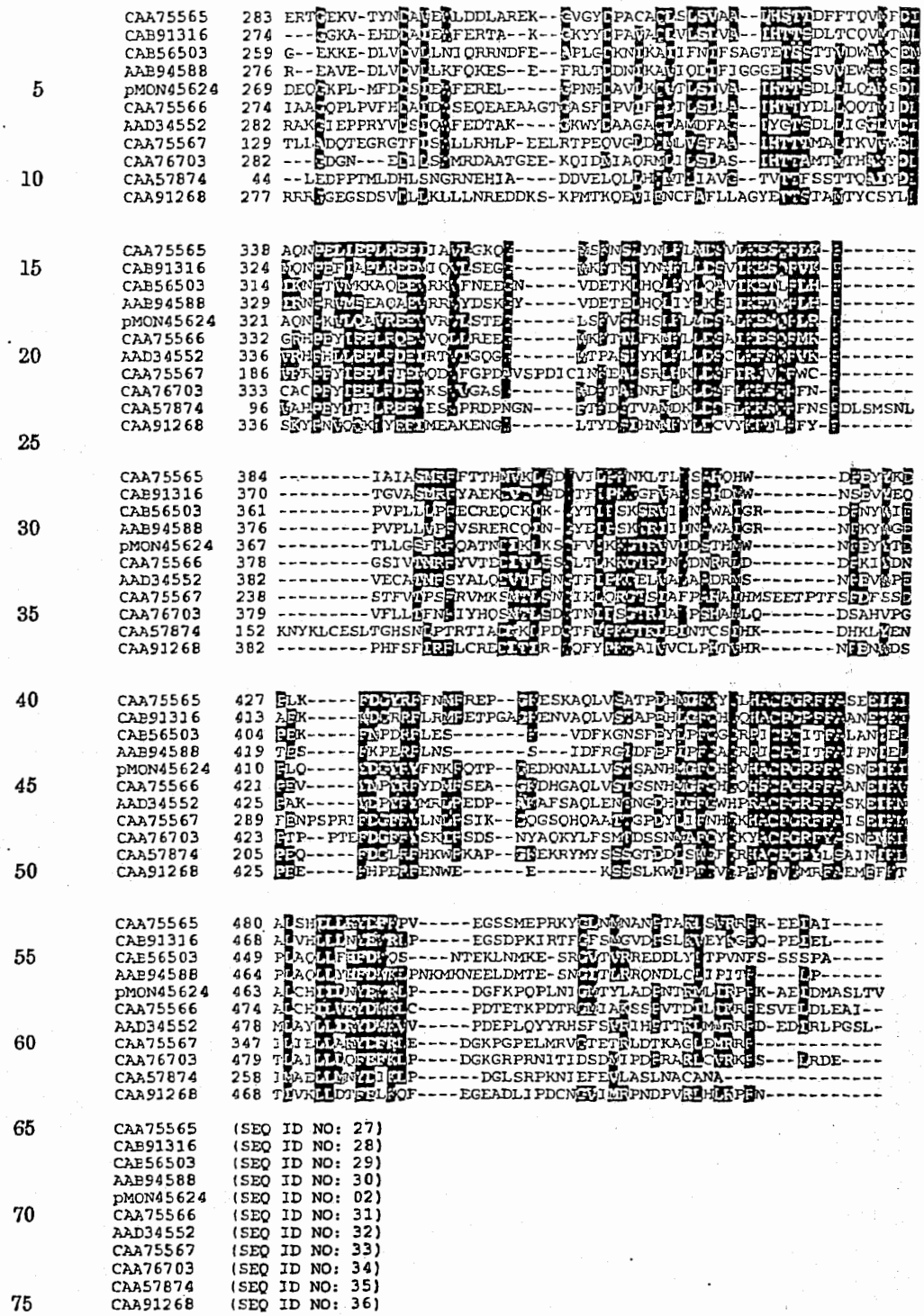

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CAB91316 274
CAB56503 259
AAB94588 276
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CAA75566 274
AAD34552 282
CAA75567 129
CAA76703 282
CAA57874 44
CAA91268 277
CAA75565 338
CAB91316 324
CAB56503 314
AAB94588 329
pMON45624 321
CAA75566 332
AAD34552 336
CAA75567 186
CAA76703 333
CAA57874 96
CAA91268 336
CAA75565 384
CAB91316 370
CAB56503 361
AAB94588 376
pMON45624 367
CAA75566 378
AAD34552 382
CAA75567 238
CAA76703 379
CAA57874 152
CAA91268 382
CAA75565 427
CAB91316 413
CAB56503 404
AAB94588 419
pMON45624 410
CAA75566 421
AAD34552 425
CAA75567 289
CAA76703 423
CAA57874 205
CAA91268 425
CAA75565 480
CAB91316 468
CAB56503 449
AAB94588 464
pMON45624 463
CAA75566 474
AAD34552 478
CAA75567 347
CAA76703 479
CAA57874 258
CAA91268 468
CAA75565 (SEQ ID NO: 27)
CAB91316 (SEQ ID NO: 28)
CAB56503 (SEQ ID NO: 29)
AAB94588 (SEQ ID NO: 30)
pMON45624 (SEQ ID NO: 02)
CAA75566 (SEQ ID NO: 31)
AAD34552 (SEQ ID NO: 32)
CAA75567 (SEQ ID NO: 33)
CAA76703 (SEQ ID NO: 34)
CAA57874 (SEQ ID NO: 35)
CAA91268 (SEQ ID NO: 36)

Figure 5 - Phylogenetic tree showing the relatedness of Aspergillus ochraceus *11 alpha hydroxylase to the top 10 BLAST hits from GenBank*

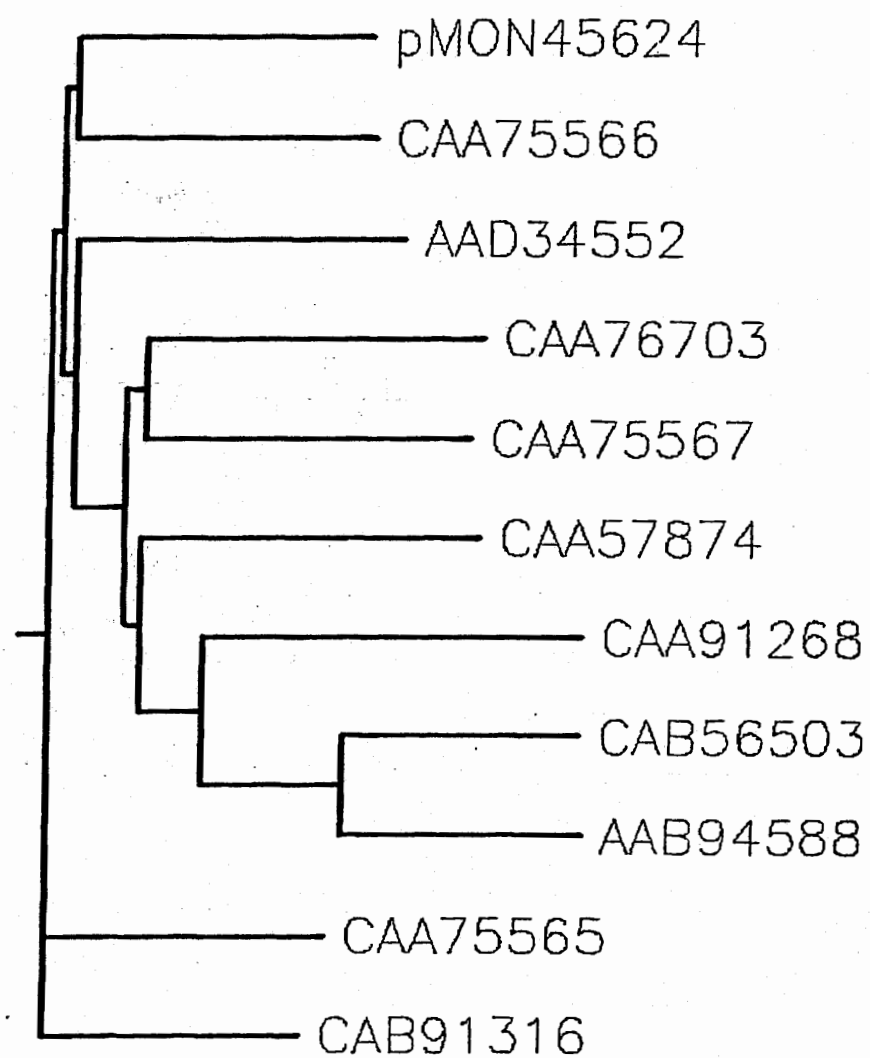
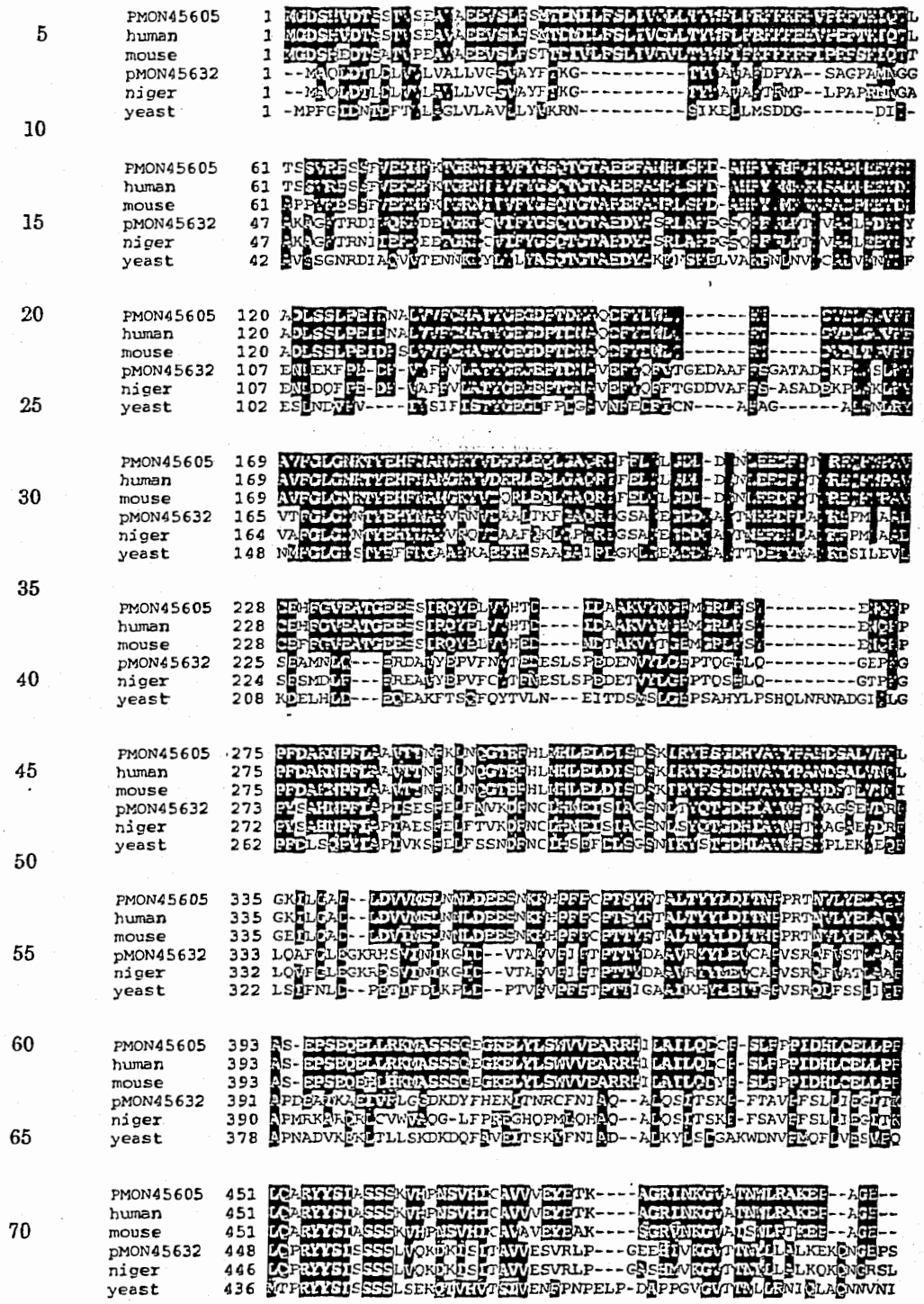


Figure 6 – Percent homology of Aspergillus ochraceus *11 alpha hydroxylase to the top 10 BLAST hits from GenBank*

Accession Number	Species	% ID to 11a OH
CAB91316	*Neurospora crassa*	40
CAA76565	*Gibberella fujikuroi*	37
CAA75566	*Gibberella fujikuroi*	37
AAD34552	*Aspergillus terreus]*	29
CAA75567	*Gibberella fujikuroi*	24
CAA57874	*Fusarium oxysporum*	24
CAA76703	*Gibberella fujikuroi*	23
CAB56503	*Catharanthus roseus*	14
AAB94588	*Glycine max*	14
CAA91268	*Caenorhabditis elegans*	12

Figure 7 – Amino acid homology alignment of A. ochraceus *and human oxidoreductase to NADPH cytochrome P450 reductases from* A. niger, *mouse, and* S. cerevisiae



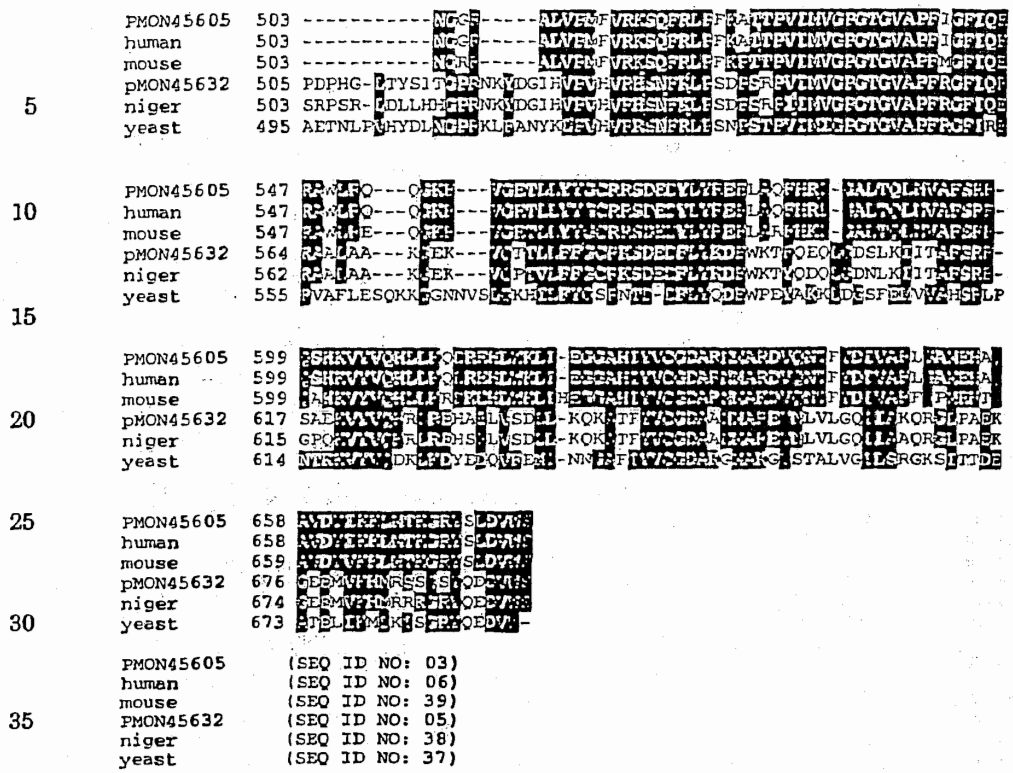
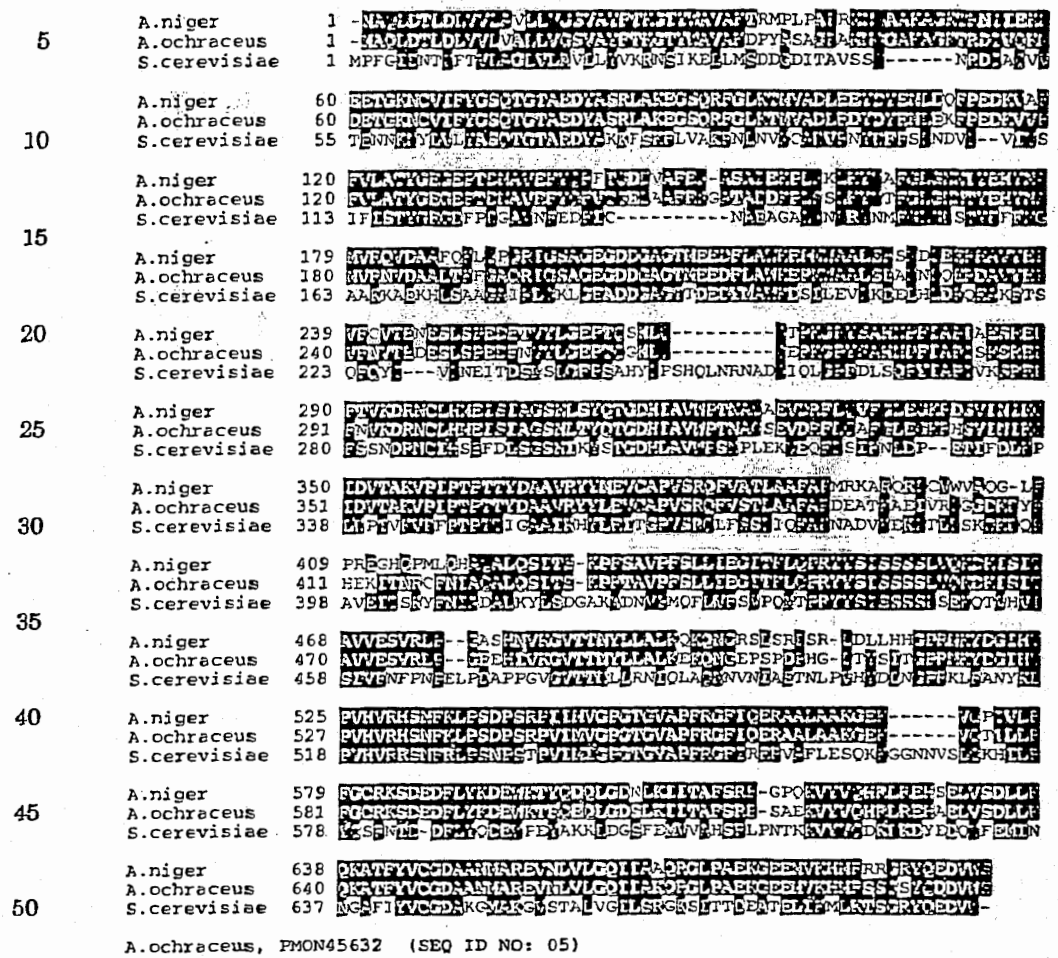

PMON45605 503
human 503
mouse 503
pMON45632 505
niger 503
yeast 495
PMON45605 547
human 547
mouse 547
pMON45632 564
niger 562
yeast 555
PMON45605 599
human 599
mouse 599
pMON45632 617
niger 615
yeast 614
PMON45605 658
human 658
mouse 659
pMON45632 676
niger 674
yeast 673
PMON45605 (SEQ ID NO: 03)
human (SEQ ID NO: 06)
mouse (SEQ ID NO: 39)
PMON45632 (SEQ ID NO: 05)
niger (SEQ ID NO: 38)
yeast (SEQ ID NO: 37)

Figure 8 – Amino acid homology alignment of A. ochraceus *oxidoreductase to NADPH cytochrome P450 reductases from* A. niger *and* S. cerevisiae



A.ochraceus, PMON45632 (SEQ ID NO: 05)

A.niger (SEQ ID NO: 38)

S.cerevisiae, yeast (SEQ ID NO: 37)

Figure 9 – Phylogenetic tree showing the relatedness of Aspergillus ochraceus and *human oxidoreductase to reductases from* A. niger, *yeast, and mouse.*

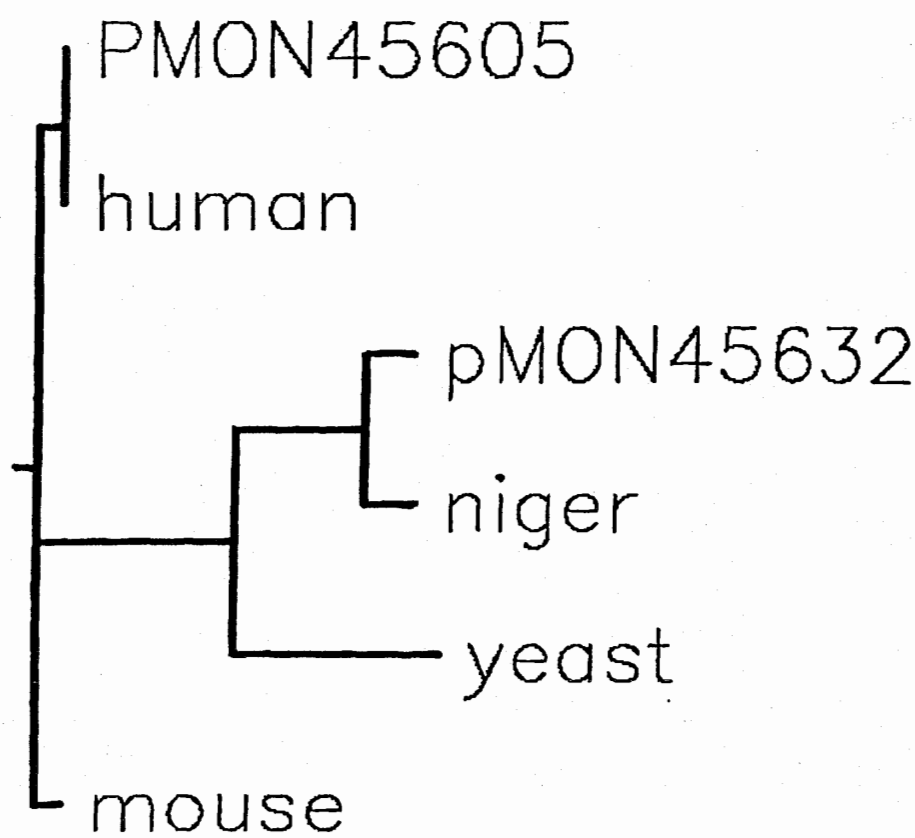
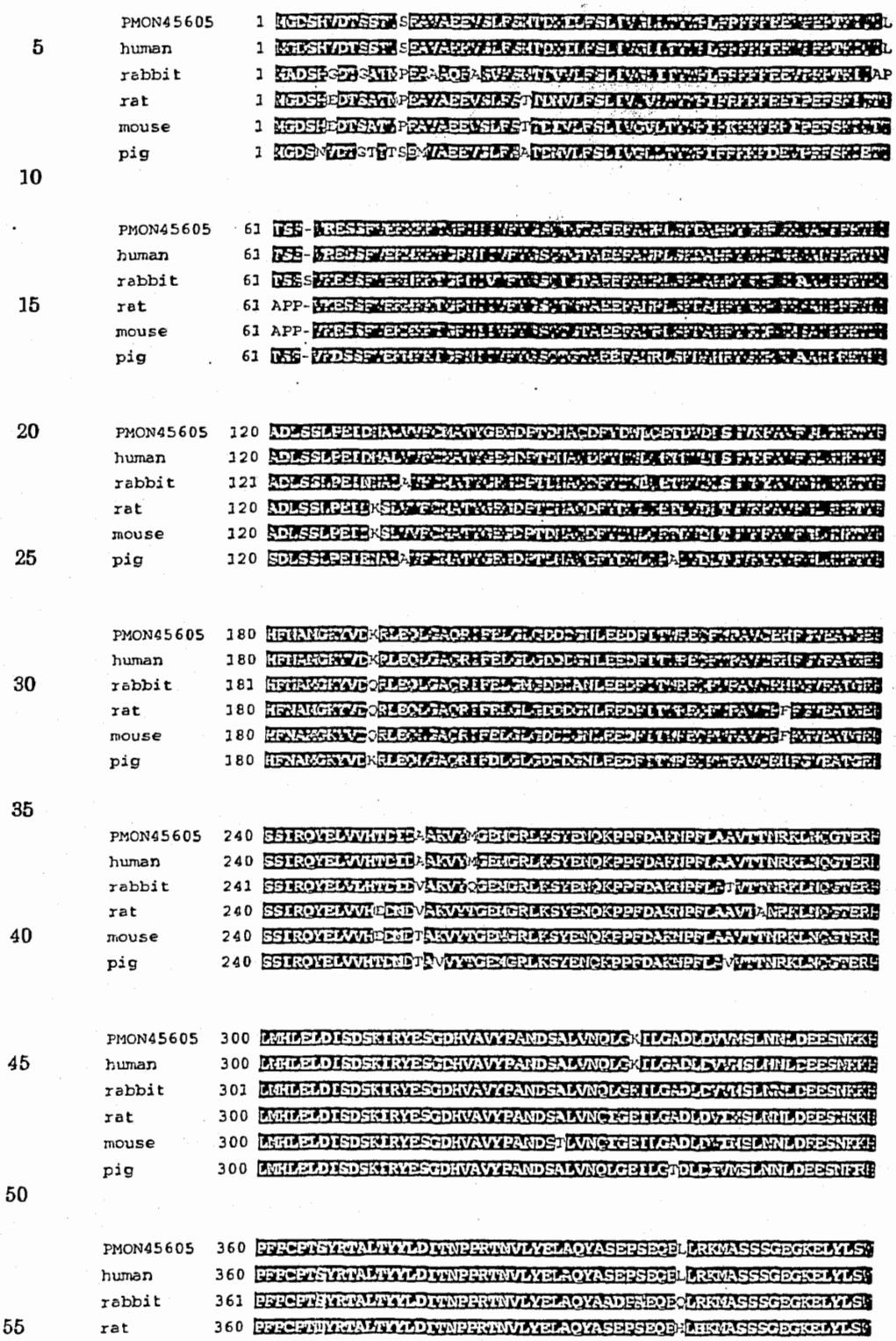
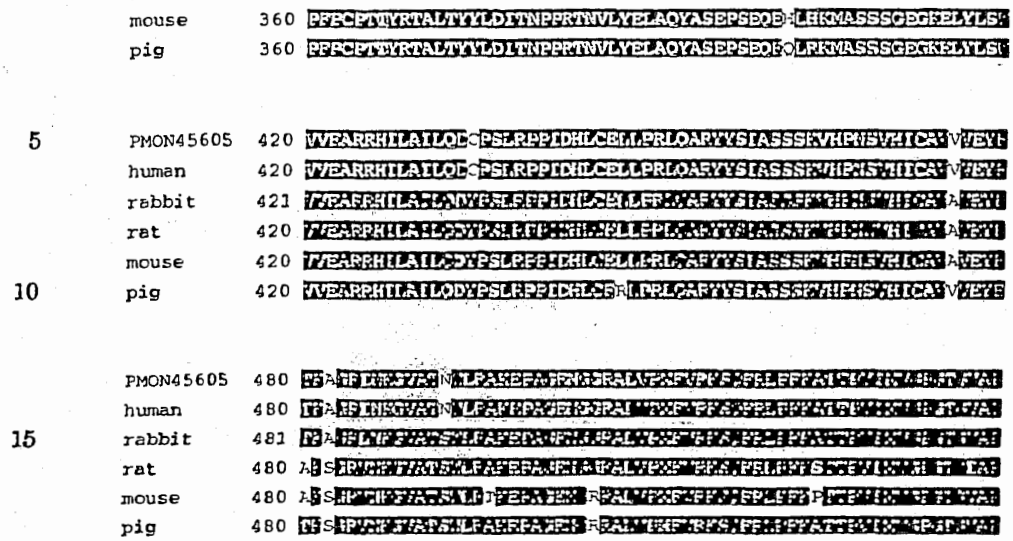


Figure 10 – Percent homology between Aspergillus ochraceus *oxidoreductase to reductases from* A. niger, *yeast, and mouse and human.*

Accession number	organism	% id to A.och oxred
CAA81550	*A. niger*	84
BAA02936	*S. cerevisiae*	37
BAA04496	mouse	34
AAB21814	human	33

Figure 11 – Amino acid homology alignment of human oxidoreductase with the top 4 hits from SwissProt




mouse 360
pig 360
PMON45605 420
human 420
rabbit 421
rat 420
mouse 420
pig 420
PMON45605 480
human 480
rabbit 481
rat 480
mouse 480
pig 480

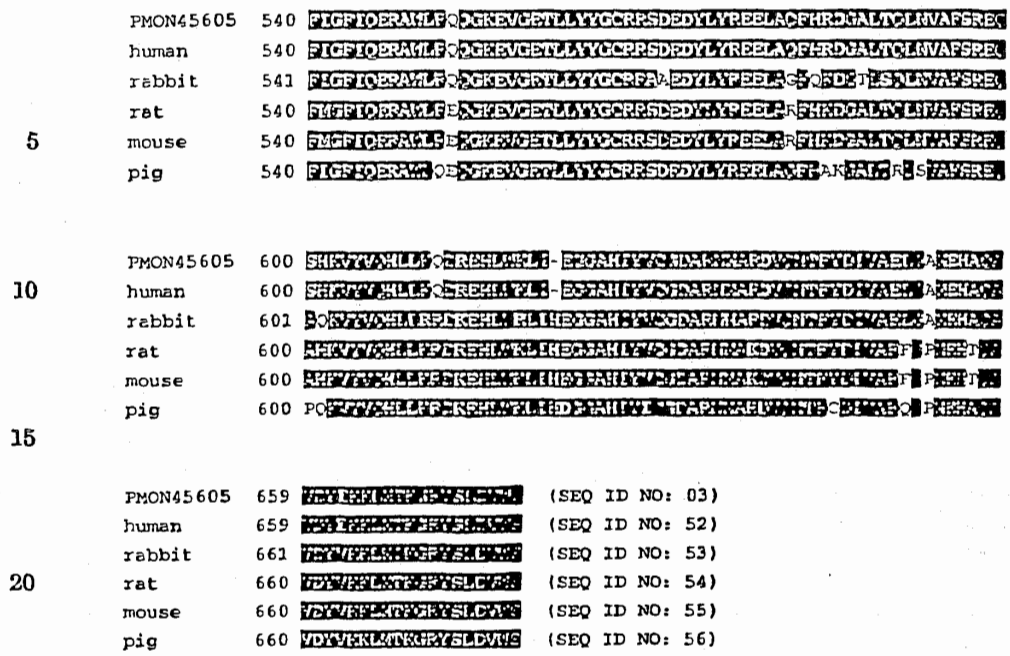
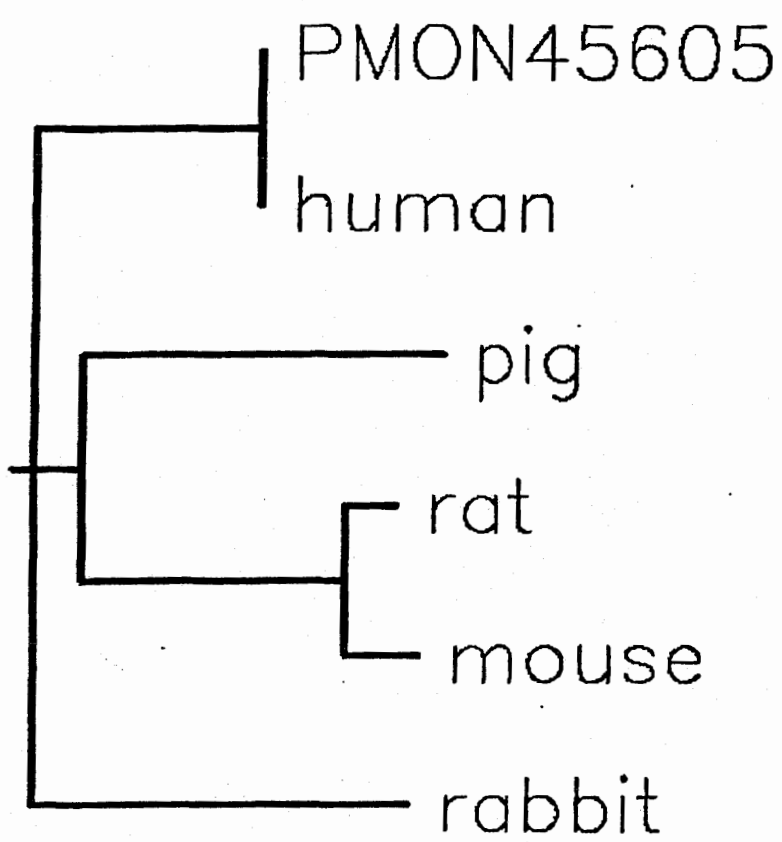

PMON45605 540
human 540
rabbit 541
rat 540
mouse 540
pig 540
PMON45605 600
human 600
rabbit 601
rat 600
mouse 600
pig 600
PMON45605 659 (SEQ ID NO: 03)
human 659 (SEQ ID NO: 52)
rabbit 661 (SEQ ID NO: 53)
rat 660 (SEQ ID NO: 54)
mouse 660 (SEQ ID NO: 55)
pig 660 (SEQ ID NO: 56)

Figure 12 – Phylogenetic tree showing the relatedness of human oxidoreductase (P16435) with top 4 hits from SwissProt



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Figure 13 – Percent homology between human oxidoreductase and top 4 hits from SwissProt

Accession number	Species	% id to human oxred
P00388	rat	92
P00389	rabbit	92
P37040	mouse	92
P04175	pig	91

Figure 14 - Expression of Aspergillus ochraceus *11 alpha hydroxylase in transfected Sf9 insect cells*

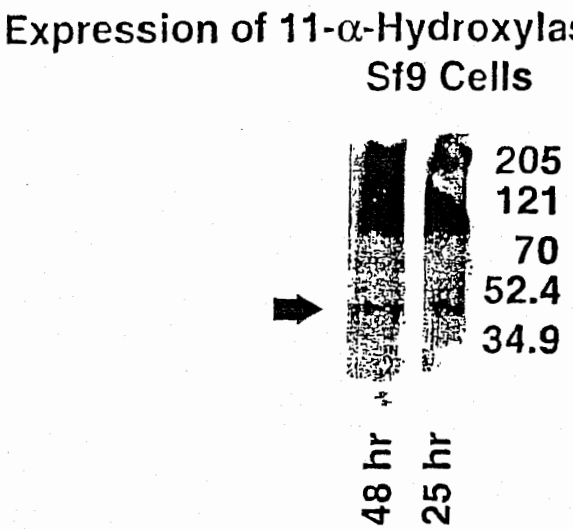


Figure 15 - Expression of Aspergillus ochraceus *P450 oxidoreductase in transfected Sf9 insect cells*

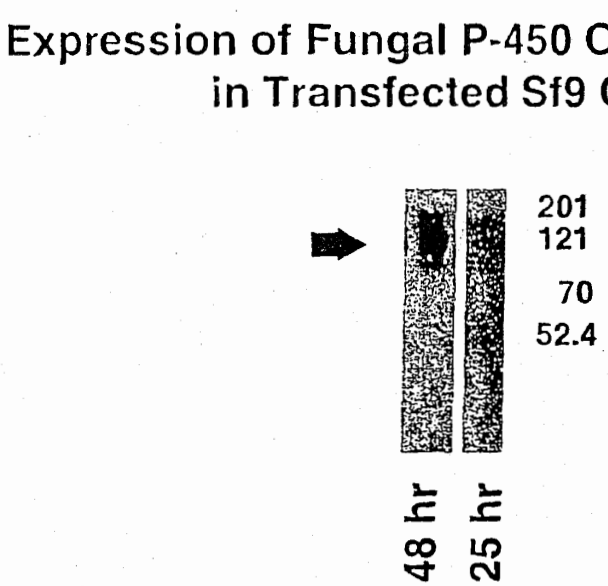
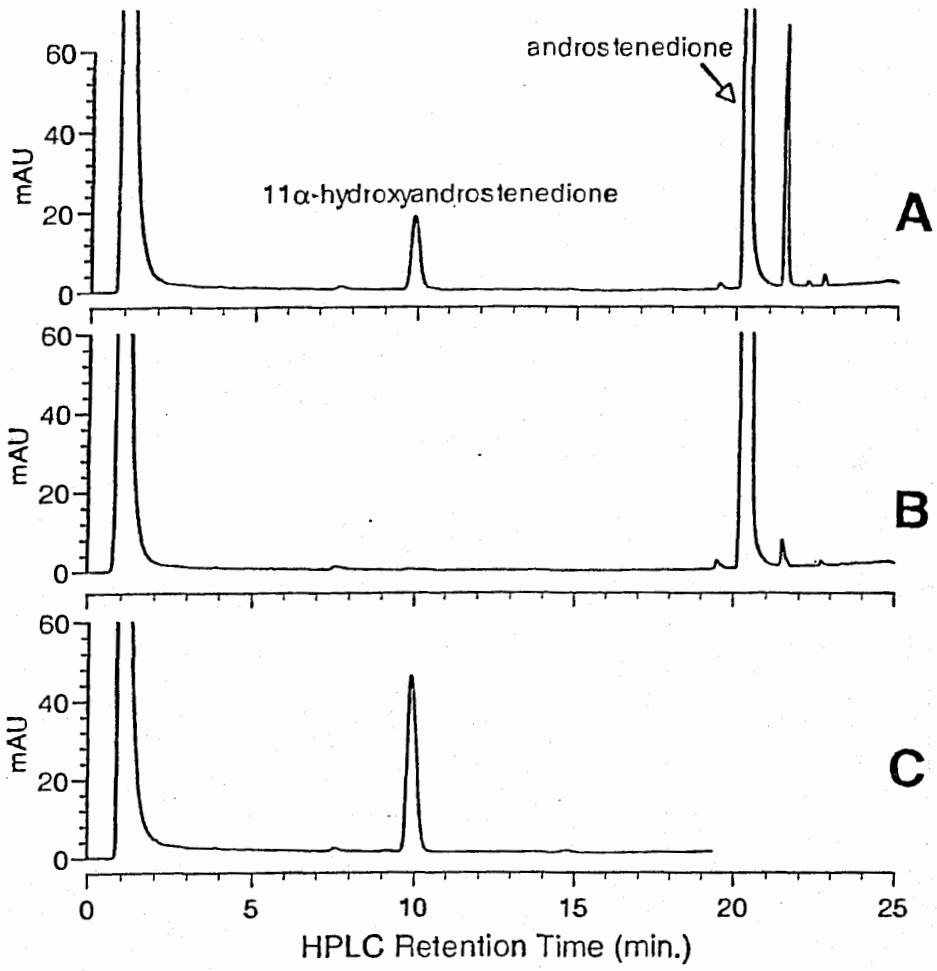


Figure 16 - Conversion of androstenedione to 11 alpha hydroxy androstenedione monitored by HPLC



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