

## a. Report final query syntax from *Details* page.

Protein

Species: Animals (344)  Source databases: PDB (79) RefSeq (56) UniProtKB / Swiss-Prot (26)  Sequence length: Custom range... Molecular weight: Custom range... Release date: Custom range... Revision date: Custom range...

Summary  Sort by Default order

See the results of this search (4 items) in our new [Identical Protein Groups](#) database.

Find related data Database:

Items: 1 to 20 of 344 << First < Prev Page 1 of 18 Next > Last >>

☐ RecName: Full=25-hydroxyvitamin D-1 alpha **hydroxylase**, mitochondrial; AltName: Full=25-OHD-1 alpha-**hydroxylase**; AltName: Full=25-hydroxyvitamin D(3) 1-alpha-**hydroxylase**; Short=VD3 1A **hydroxylase**; AltName: Full=Calcidiol 1-monooxygenase; AltName: Full=Cytochrome **P450** subfamily XXVIIIB polypeptide 1; AltName: Full=Cytochrome P450C1 alpha; AltName: Full=Cytochrome P450VD1-alpha; AltName: Full=Cytochrome **p450** 27B1; Flags: Precursor  
508 aa protein  
Accession: O15528.1 GI: 3182968  
[PubMed](#) [Taxonomy](#) [Related Sequences](#)  
[GenPept](#) [Identical Proteins](#) [FASTA](#) [Graphics](#)

☐ RecName: Full=Cytochrome **P450** 11B1, mitochondrial; AltName: Full=CYPXIB1; AltName: Full=Cytochrome P-450c11; Short=Cytochrome P450C11; AltName: Full=Steroid 11-beta-**hydroxylase**; Flags: Precursor  
503 aa protein  
Accession: P15538.5 GI: 215274267  
[PubMed](#) [Taxonomy](#) [Related Sequences](#)  
[GenPept](#) [Identical Proteins](#) [FASTA](#) [Graphics](#)

☐ RecName: Full=Steroid 21-**hydroxylase**; AltName: Full=21-OHase; AltName: Full=Cytochrome P-450c21; AltName: Full=Cytochrome **P450** 21; AltName: Full=Cytochrome **P450** XXI; AltName: Full=Cytochrome **P450**-C21; AltName: Full=Cytochrome **P450**-C21B  
494 aa protein

Search details  
P450[All Fields] AND hydroxylase[All Fields] AND \"Homo sapiens\"[Organism]  
 

Recent activity    
Q P450[All Fields] AND hydroxylase[All Fields] AND \"Homo sapiens\"[O... (34) Protein  
Q P450 AND hydroxylase AND human[organism] AND , (344) Protein  
A A heme-binding domain controls regulation of ATP-dependent potassium channels  
RecName: Full=25-hydroxyvitamin D-1 alpha hydroxylase, mitochondrial; Alt Protein  
Q P450 AND hydroxylase AND human[organism] AND (swissprot[flite Protein

Retrieved GIs.

3182968  
215274267  
117275  
117283  
6686268  
117225  
116241312  
6166044  
20137526  
544084  
56757430  
399288  
84028191  
19862747  
218511987  
3041666  
12585217  
296439388  
10719963  
296434466  
62286619  
2493371  
20141320  
145559458  
308153428  
74746067

2. Save GIs from this final query to file (select GI List format under display)
- B. Report the number of retrieved GIs.

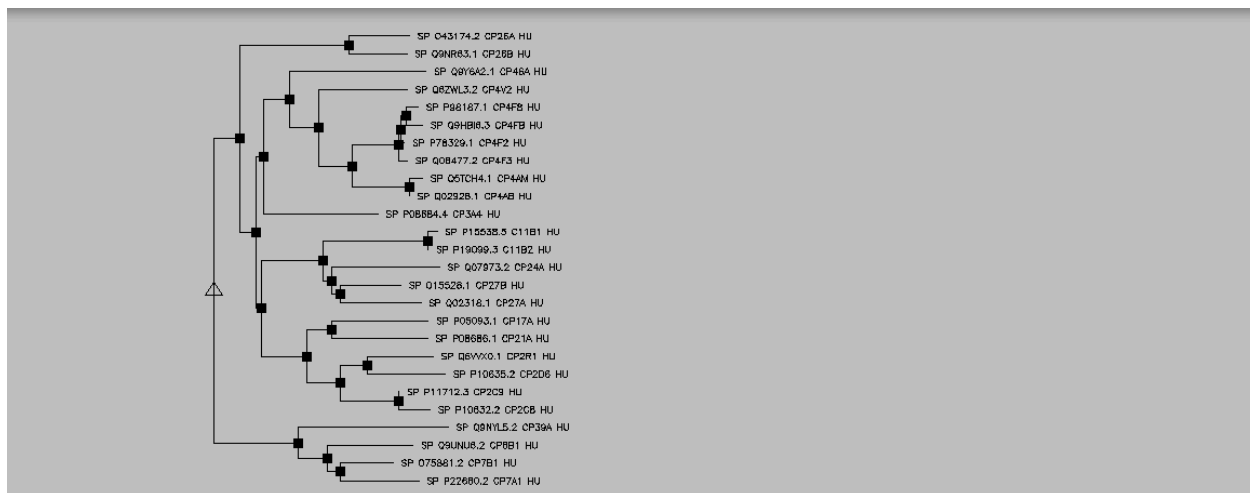
26 retrieved GIs

3. Retrieve the corresponding sequences through [Batch-Entrez](#) using GI list file as query input -> save sequences in FASTA format

4. Generate multiple alignment and tree of these sequences using [MultAalin](#)

1. Save multiple alignment and tree to file

## Tree



## Multiple Alignment

Multalin version 5.4.1

Copyright I.N.R.A. France 1989, 1991, 1994, 1996

Published research using this software should cite

Multiple sequence alignment with hierarchical clustering

F. CORPET, 1988, Nucl. Acids Res., 16 (22), 10881-10890

Symbol comparison table: blosum62

Gap weight: 12

Gap length weight: 2

Consensus levels: high=90% low=50%

Consensus symbols:

! is anyone of IV

\$ is anyone of LM

% is anyone of FY

# is anyone of NDQEBZ

MSF: 764 Check: 0 ..

Name: sp	P10632.2	CP Len:	764	Check:	1065	Weight:	0.81
Name: sp	P11712.3	CP Len:	764	Check:	1287	Weight:	0.81
Name: sp	P10635.2	CP Len:	764	Check:	1241	Weight:	1.13
Name: sp	Q6VVX0.1	CP Len:	764	Check:	3151	Weight:	1.17
Name: sp	P08686.1	CP Len:	764	Check:	8343	Weight:	1.26
Name: sp	P05093.1	CP Len:	764	Check:	7137	Weight:	1.26
Name: sp	Q02928.1	CP Len:	764	Check:	3805	Weight:	0.63
Name: sp	Q5TCH4.1	CP Len:	764	Check:	1710	Weight:	0.63
Name: sp	P78329.1	CP Len:	764	Check:	2146	Weight:	0.31
Name: sp	Q08477.2	CP Len:	764	Check:	500	Weight:	0.31
Name: sp	Q9HBI6.3	CP Len:	764	Check:	6604	Weight:	0.55
Name: sp	P98187.1	CP Len:	764	Check:	7499	Weight:	0.65
Name: sp	Q6ZWL3.2	CP Len:	764	Check:	7232	Weight:	1.20
Name: sp	P08684.4	CP Len:	764	Check:	7173	Weight:	1.28
Name: sp	Q9Y6A2.1	CP Len:	764	Check:	2802	Weight:	1.38
Name: sp	Q02318.1	CP Len:	764	Check:	75	Weight:	1.09
Name: sp	O15528.1	CP Len:	764	Check:	4905	Weight:	1.09
Name: sp	Q07973.2	CP Len:	764	Check:	145	Weight:	1.21
Name: sp	P19099.3	C1 Len:	764	Check:	3007	Weight:	0.78
Name: sp	P15538.5	C1 Len:	764	Check:	1299	Weight:	0.78
Name: sp	Q9NR63.1	CP Len:	764	Check:	1278	Weight:	1.23
Name: sp	O43174.2	CP Len:	764	Check:	2332	Weight:	1.23
Name: sp	P22680.2	CP Len:	764	Check:	7613	Weight:	1.23
Name: sp	O75881.2	CP Len:	764	Check:	9391	Weight:	1.23
Name: sp	Q9UNU6.2	CP Len:	764	Check:	4932	Weight:	1.26
Name: sp	Q9NYL5.2	CP Len:	764	Check:	1949	Weight:	1.49
Name: Consensus		Len:	764	Check:	8269	Weight:	0.00

//

1

130

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sp|P10632.
sp|P11712.
TCHRMPEP-MP ALTNAMEFLL CYTCHRMPEM PALTNAMEFL LCYTCHRMPEP ---P-----
--
sp|P10635.
sp|Q6VVX0.
sp|P08686.
sp|P05093.
sp|Q02928.
ACIDMEGAHY DRXYL-----AS EALTNAMEFL LL-----
ARICACIDME GAHYDRXYLA
sp|Q5TCH4.
sp|P78329.
TCHRMPEPL-- --TBM-----EG AALTNAMEFL LL-----
EKTRIENEEM NXYGEN---A
sp|Q08477.
TBM-----EG AALTNAMEFL LL----- EKTRIENEEM NXYGEN---A
sp|Q9HBI6.
sp|P98187.
sp|Q6ZWL3.
sp|P08684.
TCHRMPEPLP ALTNAMEFLL CYTCHRMPEPN FALTNAMEFL LCYTCHRMPEP ---PCNALTN
AMEFLLNIFE DIPINEXIDA

```

```

sp|Q9Y6A2.
sp|Q02318.
R XYL-----AS EALTNAMEFL LVITAMINDH YDRXYLA--- -SEFLAGSPR
ECRSRMAALG
sp|O15528.          E NASEALTNAM EFLLCYTCHR MEP-----SB FAMIL-----Y
XXVIIIBPLYP EPT-----ID EALTNAMEFL LCYTCHRM EP CALPHAALTN
AMEFLLCYTC HRMEPVDALP
sp|Q07973.
MSSP
sp|P19099.
P CALTNAMEFL L--STERIDH YDRXYLA--- -SEFLAGSPR ECRSRMALRA
sp|P15538.
MALRA
sp|Q9NR63.
sp|O43174.
sp|P22680.
sp|O75881.
sp|Q9UNU6.
sp|Q9NYL5.
Consensus          ..... ..
.....
.....

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260
sp|P10632.
INH YDRXYLA SEMEPFVVLV LCLSFML--- --LFSLWRQS CRRRKLPPG(P) TPLPIIGNML
QIDVKDI--C
sp|P11712.  -BALTNAMEF LLSME-----
PHENYT INH YDRXYLA SEMDSLVLV LCLSCLL--- --LLSLWRQS SGRGKLPPG(P) TPLPVIGNIL
QIGIKDI--S
sp|P10635.
MG LEALVPLAVI VAIFLLL--- --VDLMHRRQ RWAARYPPG(P) LPLPGLGNLL HVDFQNT--P
sp|Q6VVX0.
MWKLWRAE EGAAALGGAL FLLLFAL--- --GVRQLLKQ RRPMGFPPG(P) PGLPFIGNIY
SLAASSELPH
sp|P08686.
CBMLL LGLLLL--- --LLAGARLL WNWWKLRS LH LPPLAPGFLH LLQPDLP I-Y
sp|P05093.    LTNAMEF LLSTE-----
RID--A LPHAMNXYGE NASEMWELVA LLLTLA--- --YLFWPKRR CPGAKYPKSL LSLPLVGS LP
FLPRHG H-H
sp|Q02928.  SEALTNAMEF LLLNGCHAIN FATTYACIDM EGAMNXYGEN ASEFLAGSPR
ECRSRMSVSV LSPSRLLGDV SGILQAASLL ILLLLLIKAV QLYLHRQWLL KALQQFPCP(P) S-
HWLFGHIQ ELQQD-QE-L
sp|Q5TCH4.
MSVSV LSPSRRLGGV SGILQVTSLL ILLLLLIKAA QLYLHRQWLL KALQQFPCP(P) S-HWLFGHIQ
EFQHD-QE-L
sp|P78329.  SEALTNAMEF LLEKTRIEN E-----BM EGAHYDRXYL ASEFLAGSPR
ECRSRMSQLS LSWLGLWPVA ASPWLLLLLV GASWLLAHVL AWTYAFYDNC RRLRCFPQP(P)
RRNFWGHQG MVNPT-EEGM
sp|Q08477.  SEALTNAMEF LLEKTRIEN E-----BM EGAHYDRXYL ASE-----
MPQLS LSSLGLWPMA ASPWLLLLLV GASWLLARIL AWTYTFYDNC CRLRCFPQP(P) KRNWFLGHLG
LIHSS-EEGL

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sp|Q9HBI6.  
 MPQLS LSWLGLGPVA ASPWLLLLLV GGSWLLARVL AWTYTFYDNC RRLQCFPQP(P) KQNWFWGHQG  
 LVTPT-EEGM  
 sp|P98187.  
 MSLLS LSWLGLRPVA ASPWLLLLLV GASWLLARIL AWTYAFYHNG RRLRCFPQPR KQNWFLGHLG  
 LVTPT-EEGL  
 sp|Q6ZWL3.  
 MAGLW LGLVWQKLLL WGAASALSIA GASLVLS-LL QRVASYARKW QQMRPIPTVA RAYPLVGHAL  
 LMKPDGREFF  
 sp|P08684. SEALTNAMEF LLQININEMN XYGENASEAL TNAMEFL--L TARCHENDEX  
 YCHLATEALP HAHYDRXYLA SEMALIPDLA METWLLLAWS LVLLLYLYGTH SHGLFKKLG  
 PGPTPLPFLG NILSYHKGFC  
 sp|Q9Y6A2.  
 MSPGLLL LGSAVLLAFG LCCTFVHRAR SRYEHIPGP(P) RPSFLLGHLP CFWKKDEVGG  
 sp|Q02318. CARLRWALRG AGRGLC-----  
 --- -PHGARAKAA IPAALPS--- DKATGAPGAG PGVRRRQ--- --RSLEEIPR LGQLRFFFQL  
 FVQGYALQLH  
 sp|O15528. HAALTNAMEF LLCYTCHRM PBFLAGS---  
 --- -PRECRSMT QTLKYASRVF HRVRWAPELG ASLGYREYHS ARSLADIPG PSTPSFLAEL  
 FCKGGLSRLH  
 sp|Q07973. ISKSRSLAAF LQQLRS-----  
 --- -PRQP-PRLV TSTAYTSPQP REVVVCPLTA GGETQNA--- --AALPGPTS WPLLGSLLQI  
 LWKGGLKKQH  
 sp|P19099. KAEVCVAAPW LSLQRA-----  
 --- -----RALG TRAARAPRTV LPFEAMPQHP GNRWLR--- -----LLQI  
 WREQGYEHLH  
 sp|P15538. KAEVCMAVPW LSLQRA-----  
 --- -----QALG TRAARVPRTV LPFEAMPRRP GNRWLR--- -----LLQI  
 WREQGYEDLH  
 sp|Q9NR63.  
 MLFEGDLVLS ALATLAACLV SVTLLLAWS QLWQLRWAAT RDKSCKLPI(P) KGSMGFPLIG  
 ETGHWLLQGS  
 sp|O43174.  
 MEMGLPA LLASALCTFV LPLLLFLAAI KLWDLYCVSG RDRSCALPL(P) PGTMGFPFFG  
 ETLQMVLR  
 sp|P22680.  
 MMTTSLIW GIAIAACCCL W---LIL-GI RR-RQTGEP(P) LENGILPYLG CALQFGANPL  
 sp|O75881.  
 MAGEVSAATG RFSLERLGLP GLALAAALL LA--LCL-LV RRTRRPGE(P) LIKGWLPYLG  
 VVLNLRKDPL  
 sp|Q9UNU6.  
 HYDR XYLASEMVLW GPVLGALLVV IAGYLCLPGM LRQRRPWEP(P) LDKGTVPWLG HAMAFRKNMF  
 sp|Q9NYL5.  
 MELISPTVII ILGCLALFLL LQKKNLRRP(P) CIKGWIPWIG VGFEFGKAPL  
 Consensus .....  
 .....(p) .....  
 .....

261

390

sp|P10632. KSFTNFSKV(Y) (G)P---V(F)TV YF(G)MNPI(V)VF HGYEAVKEA(L)  
 IDNGEEFSGR GNSPISQRIT ---K(G)L(G)IIS SN-GKR(W)KEI (R)RFSLTTLRN FG(M)GK-  
 RSIE DRVQEEAHCL VEELRKTAS P----CDPTF

sp|P11712. KSLTNLSKV(Y) (G)P----V(F)TL YF(G)LKPI(V)VL HGYEAVKEA(L)  
 IDLGEEFSGR GIFPLAERAN ---R(G)F(G)IVF SN-GKK(W)KEI (R)RFSMLTLRN FG(M)GK-  
 RSIE DRVQEEARCL VEELRKTAS P----CDPTF  
 sp|P10635. YCFDQLRRR(F) (G)D----V(F)SL Q(L)AWTPV(V)VL NGLAAVREA(L)  
 VTHGEDTADR PPVPITQILG FGPRSQ(G)VFL ARYGPA(W)REQ (R)RFSVSTLRN LG(L)GK-KSLE  
 QWVTEEAACL CAAFANHSGR P----FRPNG  
 sp|Q6VVX0. VYMRKQSQV(Y) (G)E----I(F)SL D(LG)GIST(V)VL NGYDVVKEC(L)  
 VHQSEIFADR PCLPLFMKMT ---KMG(G)LLN SRYGRG(W)VDH (R)RLAVNSFRY FGYGQ-KSFE  
 SKILEETKFF NDAIETYKGR P----FDFKQ  
 sp|P08686. --LLGLTQK(F) (G)P----I(Y)RL H(LG)LQDV(V)VL NSKRTIEEA(M)  
 VKKWADFAGR PEPLTYKLVS --KNYPDL SL GDYSL(W)KAH KKLTRS--AL LLGIR-DSME  
 PVVEQLTQEF CERMQPQT P----VAIEE  
 sp|P05093. NNFFKLQKK(Y) (G)P----I(Y)SV R(MG)TKTT(V)IV GHQLAKEV(L)  
 IKKGKDFSGR PQMATLDIAS --NNRK(G)IAF ADGAH(W)QLH (R)RLAMATFAL FKDG-DQLE  
 KIICQEISTL CDMLATHNGQ S----IDISF  
 sp|Q02928. QRIQKWVET(F) PSA--CPHWL WG(G)-KVR(V)QL YD(P)DYMKVI(L) GRSD---  
 PKS H---GSYRFL APWI(G)Y(G)LLL LNG-QT(W)FQH (R)RMLTPAFHY DI(L)KPYVGLM  
 ADSVRVMDK WEELGQDSP -----LEVFO  
 sp|Q5TCH4. QRIQERVKT(F) PSA--CP(Y)WI WG(G)-KVR(V)QL YD(P)DYMKVI(L) GRSD--  
 -PKS H---GSYKFL APRI(G)Y(G)LLL LNG-QT(W)FQH (R)RMLTPAFHN DI(L)KPYVGLM  
 ADSVRVMDK WEELGQDSP -----LEVFO  
 sp|P78329. RVLTQLVAT(Y) PQG--FKVWM GPI-SPLLSL CH(P)DIIRSVI NASAAIAPKD K--  
 -FFYSFL EPWL(G)D(G)LLL SAG-DK(W)SRH (R)RMLTPAFHF NI(L)KPYMKIF NESVNIMHAK  
 WQLLASEGSA C----LDMFE  
 sp|Q08477. LYTQSLACT(F) (G)DM--CCWV GPW-HAI(V)RI FH(P)TYIKPV(L)  
 FAPAAIVPKD K---VFYSFL KPWL(G)D(G)LLL SAG-EK(W)SRH (R)RMLTPAFHF  
 NI(L)KPYMKIF NESVNIMHAK WQLLASEGSA R----LDMFE  
 sp|Q9HBI6. KTLTQLVTT(Y) PQG--FKLWL GPT-FPLLIL CH(P)DIIRPIT SASAAVAPKD M--  
 -IFYGFL KPWL(G)D(G)LLL SGG-DK(W)SRH (R)RMLTPAFHF NI(L)KPYMKIF NKSVNIMHDK  
 WQLLASEGSA R----LDMFE  
 sp|P98187. RVLTQLVAT(Y) PQG--FVRWL GPI-TPI(I)NL CH(P)DIVRSVI NTSDAITDKD  
 I---VFYKTL KPWL(G)D(G)LLL SVG-DK(W)RHH (R)RLLTPAFHF NI(L)KPYIKIF  
 SKSANIMHAK WQLLAMEGST C----LDVFE  
 sp|Q6ZWL3. QQIIEYTEE(Y) RHMPLLKLWV GPV--PM(V)AL YNAENVEVI(L) TSSKQIDKSS  
 M-----YKFL EPWL(G)L(G)LLT STG-NK(W)RSR (R)KMLTPTFHF TI(L)EDFLDIM  
 NEQANILVKK LEKHINQEA- -----FNCFF  
 sp|P08684. MFDMECHKK(Y) (G)K---VWGFY DGQ-QPVLAI TD(P)DMIKT(V) VKECYSVFTN  
 R---RPFGPV G-FMKSAISI AED-EE(W)KRL (R)SLLSPTFTS GK(L)KEMVPII AQYGDVLVRN  
 LRREAETGKP -----VTLKD  
 sp|Q9Y6A2. RVLQDVFLDW AKKYGPVVRV NVFHKTS(V)IV TS(P)ESVKKF(L) MSTKYNKDSK  
 MYRALQTVFG ERLF(G)Q(G)LVS ECNYER(W)HKQ (R)RVIDLAFSR SS(L)VSLMETF  
 NEKAEQLVEI LEAKADGQTP -----VSMQD  
 sp|Q02318. QLQVLYKAK(Y) (G)P----MWMS Y(LG)PQMH(V)NL ASAPLLEQV(M)  
 RQEGKYPVRN DMELWKEHRD QHDLTY(G)PFT TEGHHWYQLR QALNQRLK AEAALYTDFA  
 NEVIDDFMTR LDQLRAESAS GNQ-VSDMAQ  
 sp|O15528. ELQVQGAH(F) (G)P----VWLA SF(G)TVRT(V)YV AA(P)ALVEEL(L)  
 RQEGPRPERC SFSPWTEHRR CRQAC(G)LLT AEGEEWQRLR SLLAPLLLRP QAAARYAGTL  
 NNVCCLVRR LRRQGRGTG PPALVRDVG  
 sp|Q07973. DTLVEYHKK(Y) (G)K----I(F)RM K(LG)SFES(V)HL GS(P)CLLEALY  
 RTESAYPQRL EIKPWKAYRD YRKE(G)Y(G)LLI LEGEDWQVR SAFQKKLMKP GEVMKLDNKI  
 NEVLADFMGR IDELCDERGH ----VEDLYS  
 sp|P19099. LEMHQTFOEL (G)P----I(F)RY N(LG)GPRM(V)CV ML(P)EDVEKLQ  
 QVDSLHPCRM ILEPWVAYRQ HRGHKC(G)VFL LNGPEWRFNR LRLNPDVLS KAVQRFPLMV  
 DAVARDFSQA LKKKVLQNR G-SLTLDVQP

sp|P15538. LEVHQTFQEL (G)P----I(F)RY D(LG)GAGM(V)CV ML(P)EDVEKLQ  
 QVDSLPHPHRM SLEPWVAYRQ HRGHKC(G)VFL LNGPEWRFNR LRLNPEVLSP NAVQRFLPMV  
 DAVARDFSQA LKKKVLQAR G-SLTLDVQP  
 sp|Q9NR63. GFQSSRREK(Y) (G)N----V(F)KT H(L)LGRPL(I)RV TGAENVRKI(L)  
 MGEHHLVSTE -----WPRST RMLL(G)PNTVS NSIGDIHRNK (R)KVFSKIFSH EA(L)ESYLPKI  
 QLVIQDTLRA WSSHPE-A-- -----INVYQ  
 sp|O43174. KFLQMKRRK(Y) (G)F----I(Y)KT H(L)FGRPT(V)RV MGADNVRRI(L)  
 LGEHRLVSVH -----WPASV RTIL(G)S(G)CLS NLHDSSHKQR KKVIMRAFSR EA(L)ECYVPVI  
 TEEVGSSLEQ WLSCGERG-- -----LLVYP  
 sp|P22680. EFLRANQRKH (G)H----V(F)TC K(L)MGKYVHFI TN(P)LSYHKV(L) CH-  
 GKYFDWK K---FHFATS AKAF(G)HRSID PMDGNTTENI NDTFIKTLOG HA(L)NSLTESM  
 MENLQIRMRP PVSSNSKTA- -----AWVTE  
 sp|O75881. RFMKTLOKQH (G)D----T(F)TV L(LG)GKYITFI LD(P)FOYQLVI KN-HKQLSFR  
 V---FSNKLK EKAFFISQLQ KNHDMNDEL- -HLCYQFLOG KS(L)DILLES MQLNKQVFEP QLL---  
 KTT- -----SWDTA  
 sp|Q9UNU6. EFLKRMRTKH (G)D----V(F)TV Q(LG)GOYFTFV MD(P)LSFGSI(L)  
 KDTQRKLDLFQ Q---YAKKLK LKVF(G)YRSVQ GDH----EMI HSASTKHLRG DG(L)KDLNETM  
 LDSLSFVMLT SKGWSLDAS- -----CWHEH  
 sp|Q9NYL5. EFIEKARIK(Y) (G)P----I(F)TV FAMGNRMFTV TEEGINVF(L) KS--KKVDFE  
 L---AVQNIY YRTASIPKNV FL-----AL HEKLYIMLKG KMGTVNLHQF TGQLTEELHE QLE---  
 NLG- -----THGTM  
 Consensus .....(Y) (g).. ..(f).. ..(lg)....(v).. ..(p).....(l)  
 ..... ..(g).(g)... .....(w)... (r).....  
 ..(l)..... .

391

520  
 sp|P10632. ILGCAPCNV(I) CSVV(F)QKRFD ----YKDQNF LTLMKRFNEN FRILNSPWIQ  
 VCNNFPLLID CFPGTH-NKV LKNVALTRSY IREKVKEHQA SLD-VNNPRD FIDCFLIKM- -----  
 EQEKD NQKSEFNEN  
 sp|P11712. ILGCAPCNV(I) CSII(F)HKRFD ----YKDQQF LNLMEKLNEN IKILSSPWIQ  
 ICNNFSPIID YFPGTH-NKL LKNVAFMKSY ILEKVKEHQE SMD-MNNPQD FIDCFLMKM- -----  
 EKEKH NQPSFTIES  
 sp|P10635. LLDKAVSNV(I) ASLTCGRFE ----YDDPRF LRLDLAQEG LKEESGFLRE  
 VLNAVAVLL- HIPALA-GKV LRFQKAFLTQ LDELLTEHRM TWDPAQPPRD LTEAFLAEM- -----  
 EKAKG NPESFNEN  
 sp|Q6VVX0. LITNAVSNT NLII(F)GERFT ----YEDTDF QHMIELFSEN VELAASASVF  
 LYNAFPWIGI LPFGKH-QQL FRNAAVVYDF LSRLIEKASV NRKP-QLPQH FVDAYLDEM- -----  
 DQGNK DPSSTF(S)KEN  
 sp|P08686. EFSLTCSI(I) CYLT(F)GDKIK ----D-DNLM PAYYKCIQEV LKTWSHWSIQ  
 IVDVIPFLRF FPNPGL-RRL KQAIEKRDHI VEMQLRQHE SLV-AGQWRD MMDYMLQGV- ----  
 AQPSME EGSGQ(L)LEGH  
 sp|P05093. PVFVAVTNV(I) SLIC(F)NTSYK ----NGDPEL NVIQNYNEGI IDNLSKDSL- -  
 VDLVPWLKI FPNKTL-EKL KSHVKIRNDL LNKILENYKE KFR-SDSITN MLDTLMAKM  
 NSDNGNAGPD QDSEL(LS)DNH  
 sp|Q02928. HVSLMTLDT(I) MKCA(F)SHQGS IOVDRNSQSY IQAISDLNNL VFSRVNRAFH  
 QNDTIYSLTS AGRWTH-RAC QLAHQHTDQV IQLRKAQLQK EGE---LEKI KRK---RHLD  
 FLDILLAKM ENGSI(LS)DKD  
 sp|Q5TCH4. HVSLMTLDT(I) MKSA(F)SHQGS IOVDRNSQSY IQAISDLNSL VFCCMRNAFH  
 ENDTIYSLTS AGRWTH-RAC QLAHQHTDQV IQLRKAQLQK EGE---LEKI KRK---RHLD  
 FLDILLAKM ENGSI(LS)DKD  
 sp|P78329. HISLMTLDSL QKCV(F)SFDSD CQ--EKPSEY IAAILELSAL VSKRHHEILL  
 HIDFLYYLTP DGQRFR-RAC RLVHDFTDV IQERRRTLPS QGV---DDFL QAKAKSKTLD  
 FIDVLLLSKD EDGKK(LS)DED

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sp|Q08477.  HISLMTLDSL QKCV(F)SFDSH CQ--EKPSEY IAAILELSAL VTKRHQOILL
YIDFLYYLTP DGQRFR-RAC RLVHDFTDV IQERRRTLPS QGV---DDFL QAKAKSKTLD
FIDVLLLSKD EDGKK(LS)DED
sp|Q9HBI6.  HISLMTLDSL QKCV(F)SFESN CQ--EKPSEY IAAILELSAF VEKRNQOILL
HTDFLYYLTP DGQRFR-RAC HLVHDFTDV IQERRCTLPT QGI---DDFL KNKAKSKTLD
FIDVLLLSKD EDGKE(LS)DED
sp|P98187.  HISLMTLDSL QKCI(F)SFDSN CQ--EKPSEY ITAIMELSAL VVKRNNQOFFR
YKDFLYFLTP CGRRFH-RAC RLVHDFTDV IQERRRTLTS QGV---DDFL QAKAKSKTLD
FIDVLLLSKD KNGKE(LS)DED
sp|Q6ZWL3.  YITLCALDI(I) CETAMGKNIG AQ-SNDDSEY VRAVYRMSEM IFRRIKMPWL
WLDLWYLMFK EGWEHK-KSL QILHTFTNSV IAERANEMNA NEDCRGDGRG SAPSKNKRRA
FLDLLLSVTD DEGNR(LS)HED
sp|P08684.  VFGAYSMDV(I) TSTS(F)GVNID SL--NNPQDP F--VENTKKL LRFDFLDPFF
LSITVFPFLI PILEVL-NIC VFPREVTNFL RKSVMKES R-----LEDT QKHRVDFLQL
MIDSQNSKET ESHKA(LS)DLE
sp|Q9Y6A2.  MLTYTAMDIL AKAA(F)GMETS MLLGAQKPLS QAVKLMLEGI TASRNT----
LAKFLPGKRK QLREVR-ESI RFLRQVGRDW VQRRREALKR GEE-----V
PADILTQILK AEEGAQDDEG
sp|Q02318.  LFYYFALEA(I) CYIL(F)EKRIQ CLQRSIPEDT VTFVRSIGLM FQNSLYATFL
PKWT-RPVLP F-WKRYLDGW NAIFSFGKKL IDEKLEDMEA QLQAAGPDGI QVSGYLHFL- -----
-- LASGQ(LS)PRE
sp|O15528.  EFKYFGLEG(I) AAVLLGSRLG CLEAQVPPDT ETFIRAVGSV FVSTLLTMAM PHWL-
RHLVP GPWGRLCRDW DQMFAPAQRH VERREAFAAM RGGQPEKDL ESGAHLTHF- -----
LFREE(L)PAQS
sp|Q07973.  ELNKSWSFES(I) CLVL(Y)EKRFQ LLQKNAGDEA VNFIMAIAIKM MSTFGRMMVT
PVELHKSLNT KVVQDHTLAW DTIFKSVKAC IDNRLEKYSQ Q-----PSADFLCDI- -----
-- YHQNR(LS)KKE
sp|P19099.  SIFHYTIEAS NLAL(F)GERLG LVGHSPSSAS LNFLHALEVM FKSTVQLMFM
PRSLSRWISP KVKKEHFEAW DCIFQYGDNC IQKIYQELAF NRPQ-----HYTGIVAEL- -----
-- LLKAE(LS)LEA
sp|P15538.  SIFHYTIEAS NLAL(F)GERLG LVGHSPSSAS LNFLHALEVM FKSTVQLMFM
PRSLSRWTSP KVKKEHFEAW DCIFQYGDNC IQKIYQELAF SRPQ-----QYTSIVAEL- -----
-- LLNAE(LS)PDA
sp|Q9NR63.  EAQKLTFRMA IRVLLGFSIP -----EEDLG-- --HLFEVYQQ
FVDNVFSLPV DLPFSGYRRG IQARQILQKG LEKAIREKL- ---QCTQGKD YLDALDLII- -----
ESSK EHGKE(M)TMQE
sp|O43174.  EVKRLMFRIA MRILLGCEPQ -----LAGDGDS EQQLVEAFEE
MTRNLFSPLI DVPFSGLYRG MKARNLIHAR IEQNIRAKIC GLRASEAGQG CKDALQLLI- -----
EHSW ERGER(L)DMQA
sp|P22680.  GMYSFYCYVM FEAG(Y)LTIFG RDLTRRDTQK AHILNNLDNF KQFDKVFPAL
VAGLPI-HMF RTAHNAREKL AESLRHENLQ KRESISELIS LR-----
MFLN DTLSTFDDLE
sp|O75881.  ELYPFCSSI(I) FEIT(F)TTIYG KVIVCDNNKF ISELR--DDF LKFDDKFAYL
VSNIPi-ELL GNVKSIREKI IKCFSSSEKLA KMQGWSEVFQ SR-----
QDVL EKYYVHEDLE
sp|Q9UNU6.  SLFRFCYYIL FTAG(Y)LSLFG YT-KDKEQDL LQAGELFMEF RKFDLLFPRF
VYSLWPREW LEVGRQLRLF HKMLSVSHSQ EKEGISNWLQ NM-----
LQFL REQQVP(S)AMQ
sp|Q9NYL5.  DLNNLVRHLL YPVTVNMLFN KSLFSTNKKK IKEFHQYFQV YDEDFEYGSQ
LPECLLRNWS KSKWFLELF EKNIPDIKAC KSAKDNSMTL LQ-----
ATLD IVETET(S)KEN
Consensus .....(i) ....(f).....
.....
.....(ls)...

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sp|P10632. LVGTVAD(L)FV (AG)TE(TT)STT(L) RYG(L)LL[L]LK(H)  
 [P](E)VTAKVQE[E] IDH----- VIG---RHRS PCMQ(D)RSH[M](P) YTDA(V)VH[E]IQ  
 [R]YSDLV(P)TGV PHAVTTDTKF R---N(Y)L(IPK) (GT)TIMALLTS -VLH(D)DKE(F)P  
 sp|P11712. LENTAVD(L)FG (AG)TE(TT)STT(L) RYA(L)LL[L]LK(H)  
 [P](E)VTAKVQE[E] IER----- VIG---RNRS PCMQ(D)RSH[M](P) YTDA(V)VH[E]VQ  
 [R]YIDLL(P)TSL PHAVTCDIKF R---N(Y)L(IPK) (GT)TILISLTS -VLH(D)NKE(F)P  
 sp|P10635. LRIVVAD(L)FS (AG)MV(TT)STT(L) A(W)G(L)LL[M]IL(H)  
 [P](D)V(Q)RRVQQ[E] IDD----- VIG---QVRR PEMG(D)QAH[M](P) YTTA(V)IH[E]VQ  
 [R]FGDIV(P)LGV THMTSRDIEV Q---G(F)R(IPK) (GT)TLITNLSS -VLK(D)EAVWE  
 sp|Q6VVX0. LIFSVGE(L)II (AG)TE(TT)TNV(L) R(W)AILF[M]ALY  
 [P](N)I(Q)GQVQK[E] IDL----- IMG---PNGK PSWD(D)KCK[M](P) YTEA(V)LH[E]V(L)  
 [R]FCNIV(P)LGI FHATSEDAVV R---G(Y)S(IPK) (GT)TVITNLYS -V(H)F(D)EKYWR  
 sp|P08686. VHMAAVD(L)LI G(G)TE(TT)ANT(L) S(W)AVVF[L]LH(H)  
 [P](E)I(Q)QRLQE[E] LDH----- ELGPGASSSR VPK(D)RAR[L](P) L(L)NATIA[E]V(L)  
 [R](L)R(P)VV(P)LAL PHRTTRPSSI S---G(Y)D(IPK) (GT)VIIPNLQG -A(H)L(D)ETVWE  
 sp|P05093. ILTTIGDIFG (AG)VE(TT)TSV K(W)T(L)AF[L]LHN [P](Q)VKKKLYE[E]  
 IDQ----- NVG---FSRT PTIS(D)RNR[L]L L(L)EATIR[E]V(L) [R](L)R(P)VA(P)MLI  
 PHKANVDSSI G---E(F)A(V)D(K) (GT)EVIINLWA -L(H)H(N)EKEWH  
 sp|Q02928. LRAEVDTFMF E(G)HD(TT)ASGI S(W)I(L)YA[L]AT(H) [P]KH(Q)ERCRE[E]  
 IHS----- LLG-DGA--S ITWNH(L)DQ[M](P) YTTMCI(K)[E]A(L) [R](L)Y(P)PV(P)GIG  
 (R)ELSTPVTFF D---GRSL(PK) (G)IMVLLSIYG -L(H)H(NP)KVWP  
 sp|Q5TCH4. LRAEVDTFMF E(G)HD(TT)ASGI S(W)I(L)YA[L]AT(H) [P]KH(Q)ERCRE[E]  
 IHG----- LLG-DGA--S ITWNH(L)DQ[M](P) YTTMCI(K)[E]A(L) [R](L)Y(P)PV(P)GIG  
 (R)ELSTPVTFF D---GRSL(PK) (G)IMVLLSIYG -L(H)H(NP)KVWP  
 sp|P78329. IRAEADTFMF E(G)HD(TT)ASG(L) S(W)V(L)YH[L]AK(H)  
 [P](E)Y(Q)ERCRO[E] VQE----- LLK-DREPKE IEWD(DL)AH[L](P)  
 F(L)TMCM(K)[E]S(L) [R](L)H(P)PV(P)VIS (R)HVTQDIVLP D---GRV(IPK)  
 (G)IICLISVFG -T(H)H(NP)AVWP  
 sp|Q08477. IRAEADTFMF E(G)HD(TT)ASG(L) S(W)V(L)YH[L]AK(H)  
 [P](E)Y(Q)ERCRO[E] VQE----- LLK-DREPKE IEWD(DL)AQ[L](P)  
 F(L)TMCI(K)[E]S(L) [R](L)H(P)PV(P)AVS (R)CCTQDIVLP D---GRV(IPK)  
 (G)IICLISVFG -T(H)H(NP)AVWP  
 sp|Q9HBI6. IRAEADTFMF E(G)HD(TT)ASG(L) S(W)V(L)YH[L]AK(H)  
 [P](E)Y(Q)EQCRQ[E] VQE----- LLK-DREPIE IEWD(DL)AQ[L](P)  
 F(L)TMCI(K)[E]S(L) [R](L)H(P)PV(P)VIS (R)CCTQDFVLP D---GRV(IPK)  
 (G)IVCLINIIG -I(H)Y(NP)TVWP  
 sp|P98187. IRAEADTFMF G(G)HD(TT)ASG(L) S(W)V(L)YN[L]AR(H)  
 [P](E)Y(Q)ERCRO[E] VQE----- LLK-DREPKE IEWD(DL)AQ[L](P)  
 F(L)TMCL(K)[E]S(L) [R](L)H(P)PI(P)TFA (R)GCTQDVVLP D---SRV(IPK)  
 (G)NVCNINIFA -I(H)H(NP)SVWP  
 sp|Q6ZWL3. IREEVDTFMF E(G)HD(TT)AAAI N(W)S(L)YL[L]GSN [P](E)V(Q)KKVDH[E]  
 LDD----- VFG-KSD-RP ATVE(DL)KK[L]R Y(L)EC(V)I(K)[E]T(L)  
 [R](L)F(P)SV(P)LFA (R)SVSEDCEVA G---YRVL-(K) (GT)EAVIIPYA -L(H)R(DP)RY(F)P  
 sp|P08684. LVAQSIIFIF (AG)YE(TT)SSV(L) SFI(M)YE[L]AT(H)  
 [P](D)V(Q)QKLQE[E] IDA----- VLP-NKA--P PTYDTVLQ[M]E Y(L)DM(V)VN[E]T(L)  
 [R](L)F(P)IAMRLE (R)VCKKDVEI- N---GMF(IPK) (G)VVMIPSYA -L(H)R(DP)KYWT  
 sp|Q9Y6A2. LLDNFVTFFI (AG)HE(T)SANH(L) AFTVME[L]SRQ [P](E)IVARLQA[E] VDE-  
 ----- VIG-SKR--Y LDVE(DL)GR[L]Q Y(L)SQ(V)L(K)[E]S(L) [R](L)Y(P)PAWGTF  
 (R)LLEETLI- D---GVR(VP)G N(T)PLLFSTYV -MGRMDTY(F)E  
 sp|Q02318. AMGSLPE(L)LM (AG)VD(TT)SNT(L) T(W)A(L)YH[L]SKD  
 [P](E)I(Q)EALHE[E] VVG----- VVP-AGQ--V PQHK(D)FAH[M](P)  
 L(L)KA(V)L(K)[E]T(L) [R](L)Y(P)VV(P)TNS (R)IIEKEIEV- D---G(F)LF(PK)  
 N(T)QFVFCHYV -VSR(DP)TA(F)S

sp|O15528. ILGNVTE(L)LL (AG)VD(T)VSNT(L) S(W)A(L)YE[L]SR(H)  
[P](E)V(Q)TALHS[E] ITA----- ALS-PGSSAY PSATV(L)SQ[L](P)  
L(L)KA(V)V(K)[E]V(L) [R](L)Y(P)VV(P)GNS (R)VPDKDIHV- G---D(Y)I(IPK)  
N(T)LVTLCHYA -TSR(DP)AQ(F)P  
sp|Q07973. LYAAVTE(L)QL (A)AVE(TT)ANS(L) M(W)I(L)YN[L]SRN  
[P](Q)V(Q)QKLLK[E] IQS----- VLP-ENQ--V PRAE(DL)RN[M](P)  
Y(L)KACL(K)[E]S(M) [R](L)T(P)SV(P)FTT (R)TLDKATVL- G---E(Y)AL(PK)  
(GT)VLMLNTQV -LGSSDN(F)E  
sp|P19099. IKANSME(L)TA GSVD(TT)AFP(L) LMT(L)FE[L]ARN [P](D)V(Q)QILRQ[E]  
SLA----- AAA-SIS--E HPQKATTE[L](P) L(L)RAAL(K)[E]T(L) [R](L)Y(P)VGLFLE  
(R)VVSSDLVL- Q---N(Y)H(IP)A (GT)LVQVFLYS -LGR(N)AAL(F)P  
sp|P15538. IKANSME(L)TA GSVD(TT)VFP(L) LMT(L)FE[L]ARN [P](N)V(Q)QALRQ[E]  
SLA----- AAA-SIS--E HPQKATTE[L](P) L(L)RAAL(K)[E]T(L) [R](L)Y(P)VGLFLE  
(R)VASSDLVL- Q---N(Y)H(IP)A (GT)LVRVFLYS -LGR(NP)AL(F)P  
sp|Q9NR63. LKDGTL(L)IF (A)AYA(TT)ASAS TSLIMQ[L]LK(H) [P]TVLEKLRD[E] LRA-  
--HGIL HSGGCPCEGT LRLDT(L)SG[L]R Y(L)DC(V)I(K)[E]V(M) [R](L)FTPISGGY  
(R)TVLQTFEL- D---G(F)Q(IPK) (G)WSVMYSIRD -T(H)DTAPV(F)K  
sp|O43174. LKQSSTE(L)LF G(G)HE(TT)ASAA TSLITY[L]GLY [P]HVLQKVRE[E] LKS---  
KGLL CKSNQ--DNK LDMEI(L)EQ[L]K YIGC(V)I(K)[E]T(L) [R](L)N(P)PV(P)GGF  
(R)VALKTFEL- N---G(Y)Q(IPK) (G)WNVISICD -T(H)DVAEI(F)T  
sp|P22680. KAKTHLVVLW (A)SQAN(T)IPAT F(W)S(L)FQ[M]IRN [P](E)AMKAATE[E]  
VKRTLENAGQ KVSLEGNPIC LSQA(EL)ND[L](P) V(L)DS(I)I(K)[E]S(L) [R](L)SSASLNIR  
TAKEDFTLHL EDG-S(Y)N(I)R(K) DDIIALYPQL -M(H)L(DP)EI(Y)P  
sp|O75881. IGAHHLGFLW (A)SVAN(T)IPT(M) F(W)A(M)YY[L]LR(H)  
[P](E)AMAAVRD[E] IDRLLOSTGQ KKG-SGFPIH LTRE(QL)DS[L]I C(L)ESSIF[E]A(L)  
[R](L)SSYSTTIR FVEEDLTLSS ETG-D(Y)C(V)R(K) (G)DLVAIFPPV -L(H)G(DP)EI(F)E  
sp|Q9UNU6. -DKFNF(M)LW (A)SQGN(T)GPTS F(W)A(L)LY[L]LK(H)  
[P](E)AIRAVRE[E] ATQVL---GE ARLETKQSFA FKLGA(L)QHT(P) V(L)DS(V)VE[E]T(L)  
[R](L)RAAPTLLR LVHEDYTLKM SSGQE(Y)LFRH (G)DILALFPYL SV(H)M(DP)DIHP  
sp|Q9NYL5. SPNYGLL(L)LW (A)SLSNAVPVA F(W)T(L)AYVLS(H) [P](D)IHKAIMEG  
ISSVFGKAGK DK-----IK VSED(DL)EN[L]L LIKWCVL[E]TI [R](L)KAPGVITR  
KVVKPVEIL- ----N(Y)I(IP)S (G)DLLMLSPFW -L(H)R(NP)KY(F)P  
Consensus .....(l).. (ag)..(tt)...(l) .(w).(l)..[\$]..(h)  
[P](e).(q).....[E] .....(dl)..[\$](p)  
.(l)..(v).(k)[E].(l) [R](l).(p)..(p)... (r)..... .(y).(ipk)  
(gt)..... .(h).(dp)..(f).

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764

sp|P10632. N(PN)I[F]D(P)GH(F) (L)DKNGNFKK- -----SDY- -FM(P)[F]SA[G]K(R)  
I[C]A[G]EGL[A]RM [E]LFLF(L)TTI(L) QN(F)NLKSVDD L-KNLNTTAV TKGI-VSL(P)P  
SYQICFIPV  
sp|P11712. N(PE)M[F]D(P)HH(F) (L)DEGGNFKK- -----SKY- -FM(P)[F]SA[G]K(R)  
I[C]V[G]EAL[A]GM [E]LFLF(L)TSI(L) QN(F)NLKSLVD P-KNLDTTPV VNGF-ASV(P)P  
FYQLCFIPV  
sp|P10635. K(P)FR[F]H(P)EH(F) (L)DAQGHFVK- -----PEA- -FL(P)[F]SA[G]R(R)  
A[C]L[G]EPL[A]RM [E]LFLFFTSL(L) QH(F)SFSVPTG Q-PRPSHHGV FAFL-VSPSP -  
YELCAVPR  
sp|Q6VVX0. D(PE)V[F]H(P)E(RF) (L)DSSGYFAK- -----KEA- -LV(P)[F]SL[G]R(R)  
H[C]L[G]EHL[A]RM [E]MFLFFTAL(L) QR(F)HLHFPHE L-V-PDLKPR LGMT-LQPQP -  
YLICAERR  
sp|P08686. R(P)HE[F]W(P)D(RF) (L)EPGKNSRA- ----- --LA[F](G)C[G]A(R)  
V[C]L[G]EPL[A]RL [E]LFVV(L)TRL(L) QA(F)TL-LPSG D-ALPSLQPL PHCS-VILKM  
QPFQVRLQPR GMGAHSPGQN Q

sp|P05093. Q(PD)Q[F]M(P)E(RF) (L)NPAGTQLI- -----SPSV  
SYL(P)[F](G)A[G]P(R) S[C]I[G]EIL[A]RQ [E]LFLI(M)AWL(L) QR(F)DLEVPDD G-  
QLPSLEGI PKVV-F(L)IDS FKVKIKVRQA WREAQAEGST  
sp|Q02928. N(PE)V[F]D(P)F(RF) APGSAQSH- -----A- -FL(P)[F]SG[G]S(R)  
N[C]I[G]KQ(F)[A]MN [E]L(K)VATALT(L) LR(F)ELLP-DP T-RIP--IPI A-RL-V(L)KSK  
NGIHLRLRRL PNPCEKDKQL  
sp|Q5TCH4. NL(E)V[F]D(P)S(RF) APGSAQSH- -----A- -FL(P)[F]SG[G]S(R)  
N[C]I[G]KQ(F)[A]MN [Q]L(K)VARALT(L) LR(F)ELLP-DP T-RIP--IPM A-RL-V(L)KSK  
NGIHLRLRRL PNPCEKDKQL  
sp|P78329. D(PE)V[Y]D(P)F(RF) DPENIKERS- -----PLA- -FI(P)[F]SA[G]P(R)  
N[C]I[G]QT(F)[A]MA [E]M(K)VV(L)ALT(L) LR(F)RVLP-DH T-E-P--RRK P-EL-V(L)RAE  
GGLWLRVEPL S  
sp|Q08477. D(PE)V[Y]D(P)F(RF) DPKNIKERS- -----PLA- -FI(P)[F]SA[G]P(R)  
N[C]I[G]QA(F)[A]MA [E]M(K)VV(L)GLT(L) LR(F)RVLP-DH T-E-P--RRK P-EL-V(L)RAE  
GGLWLRVEPL S  
sp|Q9HBI6. D(PE)V[Y]D(P)F(RF) DQENIKERS- -----PLA- -FI(P)[F]SA[G]P(R)  
N[C]I[G]QA(F)[A]MA [E]M(K)VV(L)ALT(L) LH(F)RILP-TH T-E-P--RRK P-EL-I(L)RAE  
GGLWLRVEPL GANSQ  
sp|P98187. D(PE)V[Y]D(P)F(RF) DPENAQKRS- -----PMA- -FI(P)[F]SA[G]P(R)  
N[C]I[G]QK(F)[A]MA [E]M(K)VV(L)ALT(L) LR(F)RILP-DH R-E-P--RRT P-EI-V(L)RAE  
DGLWLRVEPL G  
sp|Q6ZWL3. N(PE)E[F]Q(P)E(RF) FPENAQGRH- -----PYA- -YV(P)[F]SA[G]P(R)  
N[C]I[G]QK(F)[A]VM [E]E(K)TI(L)SCI(L) RH(F)WIES-NQ K-REE--LGL EGQL-  
I(L)R(P)S NGIWIKLKRR NADER  
sp|P08684. E(PE)K[F]L(P)E(RF) SKKNKDNID- -----PYI- -YT(P)[F](G)S[G]P(R)  
N[C]I[G]MR(F)[A]LM [N]M(K)LA(L)IRV(L) QN(F)SFKPCKE T-QIP--LKL SLGG-  
L(L)Q(P)E KPVLKVESR DGTVSGA  
sp|Q9Y6A2. D(P)LT[F]N(P)D(RF) GPGAPKPR-- -----FT- -YF(P)[F]SL[G]H(R)  
S[C]I[G]QQ(F)[A]QM [E]V(K)VV(M)AKL(L) QRLEFRLVPG Q-R----FGL QEQA-T(L)K(P)L  
DPVLCTLRPR GWQPAPPPPP C  
sp|Q02318. E(PE)S[F]Q(P)H(R)W (L)RNSQPATP- ----RIQHPF  
GSV(P)[F](G)Y[G]V(R) A[C]L[G]RRL[A]EL [E]MQLL(L)ARLI QK(Y)KVVLAPE T-GE---  
LKS VARI-V(L)V(P)N KKVGLQFLQR QC  
sp|O15528. E(PN)S[F]R(P)A(R)W (L)--GEGPTP- -----HPF  
ASL(P)[F](G)F[G]K(R) S[C]M[G]RRL[A]EL [E]LQMA(L)AQI(L) TH(F)EVQPEPG A-AP--  
-VRP KTRT-V(L)V(P)E RSINLQFLDR  
sp|Q07973. DSSQ[F]R(P)E(R)W (L)QEKEKI--- -----NPF AHL(P)[F](G)V[G]K(R)  
M[C]I[G]RRL[A]EL [Q]LHLA(L)CWIV RK(Y)DIQ-ATD N-EP---VEM LHSG-T(L)V(P)S  
RELPIAFCQR  
sp|P19099. R(PE)R[Y]N(P)Q(R)W (L)DIRGSG--- -----RNF  
HHV(P)[F](G)F[G]M(R) Q[C]L[G]RRL[A]EA [E]MLLL(L)HHV(L) KH(F)LVETLTQ --ED--  
-IKM VYSF-I(L)R(P)G TSPLLTFRAI N  
sp|P15538. R(PE)R[Y]N(P)Q(R)W (L)DIRGSG--- -----RNF  
YHV(P)[F](G)F[G]M(R) Q[C]L[G]RRL[A]EA [E]MLLL(L)HHV(L) KHLQVETLTQ --ED---  
IKM VYSF-I(L)R(P)S MFPLLTFRAI N  
sp|Q9NR63. DV(N)V[F]D(P)D(RF) SQARSEDKD- -----GRF HYL(P)[F](G)G[G]V(R)  
T[C]L[G]KHL[A]KL FL(K)VLAVELA STSRFELATR TFPRITLVPV LHPV-DGLSV KFFGLDSNQ  
EILPETEAML SATV  
sp|O43174. NK(E)E[F]N(P)D(RF) (M)LPHPEDAS- -----RF  
SFI(P)[F](G)G[G]L(R) S[C]V[G]KE(F)[A]KI LL(K)IFTVELA RHCDWQLLNG P-PTMKTSPT  
VYPV-DNL(P)A RFTHFHGEI  
sp|P22680. D(P)LT[F]KYD(RY) (L)DENGKTKTT FYCNGCLKLY YYM(P)[F](G)S[G]AT  
I[C]P[G]RL(F)[A]IH [E]I(K)QF(L)ILM(L) SY(F)ELELIEG QAKCPPLDQS  
RAGLGI(L)P(P)L NDIEFKYKFK HL

2. Identify putative heme binding cysteine in multiple alignment

**1. Open corresponding [UniProt page](#) and search for first P450 sequence in your list.**

**1. Compare putative heme binding cysteine with consensus pattern from Prosit database ([Syntax](#))**

Prosite pattern is consistent with previous analysis.

Hits for all PROSITE (release 2018\_03) motifs on sequence P10632 [UniProtKB/Swiss-Prot (release 2018\_03 of 28-Mar-18: 557012 entries)]:

found: 1 hit in 1 sequence

P10632 CP2C8\_HUMAN (490 aa)

RecName: Full=Cytochrome P450 2C8; EC=1.14.14.1 (ECO:0000269|PubMed:7574697); AltName: Full=CYP11C8; AltName: Full=Cytochrome P450 IIC2; AltName: Full=Cytochrome P450 MP-12; AltName: Full=Cytochrome P450 MP-20; AltName: Full=Cytochrome P450 form 1; AltName: Full=S-mephenytoin 4-hydroxylase.; Homo sapiens (Human)

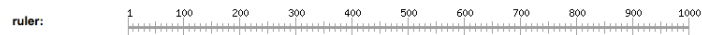
MEPFVVLVLCISFMLFSLNRQSCRRRLPPGFTPLPIGNLQIDVKDICKSFTNFSVYGPVFT  
VYFGMNPVVFHGYEAVKEALIDNGEEFSGRGNSPISQRTKGLGISSNGRWKEIRRFSLTLR  
NFGMGKBSIEDRVQEEAHLVEELRKTASPCDPTFLLCAPCNVICSVVTFQRFRDYKQNFLLM  
KRFNENRLLNSFMVQVCNFFLLIDCFPGHNVKLVKVALTRSYIREKESQASLDVNNRDFI  
DCFLFKWQEKQNKSEFNENLVGVADLVYACETTSCTLRVGLLLKHPVETAKVQEEIDHV  
IGRHRSQMDRSMPYTDVVHEIQRYSDLVFTGVPHAVTDTKFRNYLIPKGTIMALLTSVLH  
DDKEFPNPIFDGCHFLDKNGNFKSDYFMPFSAGKRICAGEGLARHLEFLTLTILQNFNLKSDV  
DLKRLNTAVTKGIVSLFFSYQICFIPV

Legend:

disulfide bridge    active site    other 'ranges'    other sites

Please note that the graphical representations of domains displayed hereafter are for illustrative purposes only, and that their colors and shapes are not intended to indicate homology or shared function. For more information about how these graphical representations are constructed, go to <https://prosite.expasy.org/mydomains/>.

hits by patterns: [1 hit (by 1 pattern) on 1 sequence]



P10632 (CP2C8\_HUMAN) (490 aa)

RecName: Full=Cytochrome P450 2C8; EC=1.14.14.1 (ECO:0000269|PubMed:7574697); AltName: Full=CYP11C8; AltName: Full=Cytochrome P450 IIC2; AltName: Full=Cytochrome P450 MP-12; AltName: Full=Cytochrome P450 MP-20; AltName: Full=Cytochrome P450 form 1; AltName: Full=S-mephenytoin 4-hydroxylase.; Homo sapiens (Human)

PS00086 CYTOCHROME\_P450 Cytochrome P450 cysteine heme-iron ligand signature: Hits of PS00086 on PDB 3D structures x-referenced by P10632: 1PQ2-A, 1PQ2-B, 2NNH-A, 2NNH-B, 2NNI-A, 2NNJ-A, 2VNO-A

428 - 437: [confidence level: (0)] FSAGKRICAG

## 2. Report corresponding Pfam ID

Pfam<sup>i</sup> View protein in Pfam  
PF00067. p450. 1 hit.

## 3. How many mouse (Mus musculus) sequences are in this family (use species tree from Pfam db)

48 Mouse

2. [BLASTP](#) against nr database (use again first P450 in your list); on next two pages click on P450 and CypX domains, respectively (this runs RPS-BLAST).

### 1. Compare resulting alignment with result from MultAlin

The alignment from BLASTP correlates with the Multalin

2. View 3D structure in Cn3D, save structure (screen shot) and highlight heme binding cysteine

- Organisms
- Statistics
- Protein
- Protein
- Structure
- ures

[illegible]