

Sarah D. Bobardt

# Homework 1

1. a. P450[All Fields] AND hydroxylase[All Fields] AND "Homo sapiens"[Organism] AND swissprot[filter]

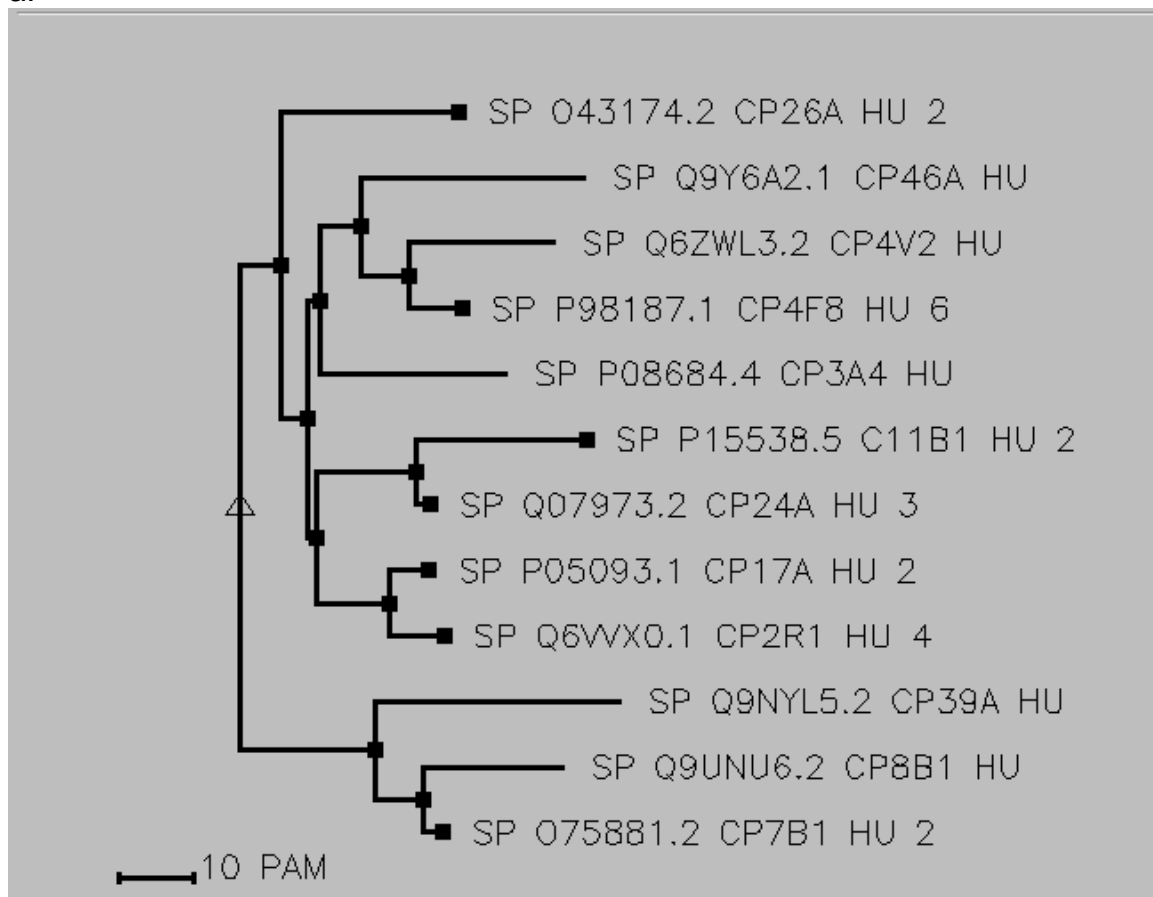
2. GI files

a. 26 GI files

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

4.

a.




680 690 700 710 720 730

HYIPFGGGLRTCVGKHFAKIFLKIFTVELARHCDWQLLNGPFPTMKTSPTVHPV-DNLP  
 -YFPFSLGHRSCIGQQFAQMEVKVVMMAKLLQRLEFRLVPGQ-R----FGLQEQA-TLKP  
 -YVPFSAGPRNCIGQKFAVMEKTI LSCILRHFWIES-NQK-REE--LGLEGQL-ILRP  
 -FIPFSAGPRNCIGQQFAMAEMKVVLALTLLRFRILP-DHT-EIP--RRKP-EL-VLRA  
 -YTPFGSGPRNCIGMRFALNMKLLALIRVLQNF SFKPKET-QIP--LKLSLGG-LLQP  
 HHVPFGFGMRQCLGRRLAEAEMLLLHHV LKH FQVETLTQ--ED---IKMVYSF-ILRP  
 AHL PFGY GKRMC LGRR LAELHLALCWIIRKYDVQPAPDN-GP---VKMLHRG-VLVP  
 SYLPFGCGPRSCIGEPLARQELFLIMTWLLQRFDLEV PDDG-QLPSLEPIPHCV-FLID  
 -FMPFSAGRRHCLGEPLARMEFLFFTSLLQHFNLHFP HDL-PNPDHHPVFGFL-VSP  
 -FMAFGSGKFQCPARWFALLEVQMCIIILILYKYDCSLLDPLPKQSYLH----LVGVPQ  
 YTMPWGS GVSICPGRFFALSEVKLFILLMVTHFDLELVDPDTPLPHVDPQRWGF GTMQ  
 YYMPFGTGATICPGRFFAIHEIKQFLILMLTYFDLELIDGQAKCPPLDYSRAGFGILPP  
 YYMPFGAGKRSCIGRRFARMELKLF LALLQHFDLELVDDT-KQPSLMPMMHSIGVLQP

See above for the putative heme-binding cysteine.

5.

a. Cytochrome P450 2C8

Sites					
Feature key	Position(s)	Description	Actions	Graphical view	Length
Binding site <sup>1</sup>	100	Substrate			1
Binding site <sup>1</sup>	204	Substrate			1
Binding site <sup>1</sup>	241	Substrate			1
Metal binding <sup>1</sup>	435	Iron (heme axial ligand)			

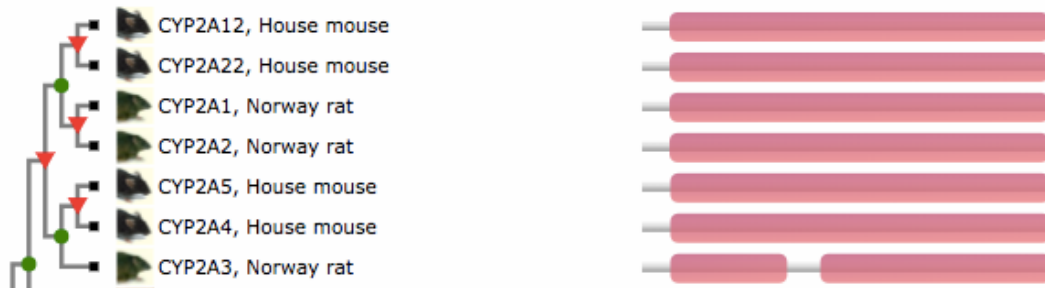
440

GKRICAGEGL AI

Different location than in the sequence alignment, but the P450 cytochrome sequence does appear to have a similar sequence leading up to the heme-binding cysteine (KRSC and KRIC). A strong motif is suggestive of functional importance in the organism, though is by no means sufficient to claim that this is certainly the heme-binding cysteine.

b. PFAM ID: PF00067

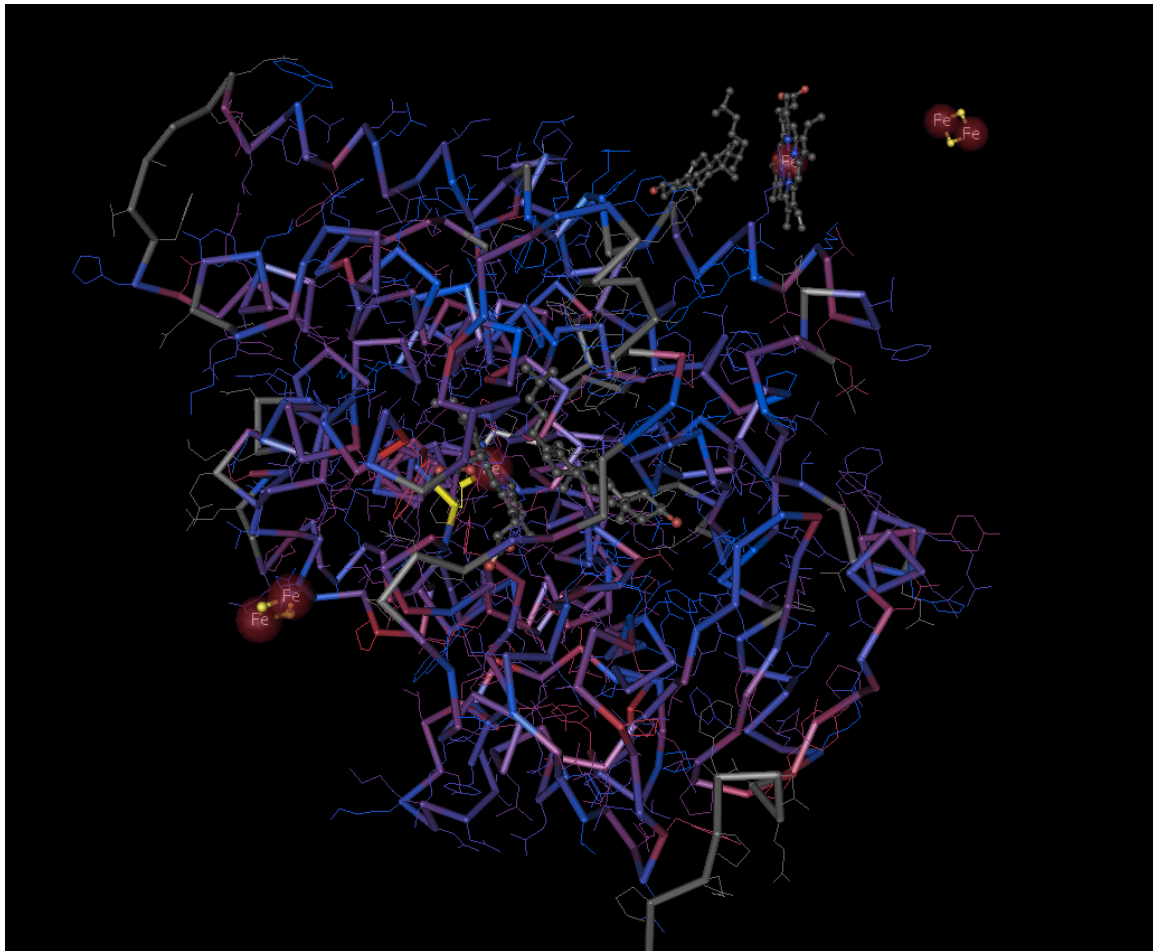
c. 48 Mouse sequences in this family tree (according to Treefam).



6.

a. There is a conserved C across all of the queries and includes similar preceding amino acids to the Cysteine (such as H and R). They do seem to be close in numerical location to the heme-binding site in PFAM as well. The overlap in the results of these three locations is potentially indicative that this is the correct heme-binding site.

1E9X_A	372	- [12].WIPFG	AG. [1].HRCVGAFAIMQI	KAIFSVLLREYEFEMAQP. [6].D. [2].KVVVQLAQA	441
query	414	- [11].FMPFS	AG. [1].RICAGEGLARMEL	FLFLTTLQNFNLSVDD. [3].L	NTTAVTKGIV 477
gi 16119968	328	- [2].HQSPG	SG. [1].HHCAGAQISRQTV. [1]	.AIMLPTLFRFPNMTLTN. [2].A. [2].WRGFGFRGPI	384
gi 9296939	341	- [5].LFDMI. [8].KG	HRCPEGGITIEVM	KASLDLVLHQIEYDVPEQ. [5].L. [2].MPSLPESGFV	409
gi 6226478	337	- [2].HIAFG	HG. [1].HFCLGAPLARLEA	NIALTSLISAFPHMECVS	I. [2].IENSVIYGLK 390
gi 19551789	363	- [3].HLSFG	FG. [1].HYCLGNMLAKLQA	KICLEEVTRLVPSLHLVA. [3].I. [2].RENLSRVPT	420
gi 15842692	333	- [3].HIAFG	YG. [1].HACPASAYSRLCL	TTFFTSLTQRFQQLAR. [5].E. [2].GKGLHSVGIK	392
gi 17231238	376	- [8].YLPFG	GG. [1].RRCLGLAFAQWEM	KLALAKILTSYELELVNN. [6].K. [2].GLVTGPHRPI	441
gi 17232178	381	- [8].FMPFG	GG. [1].RGCICQALAMFEM	KIVLATVLSRYQLALADR. [5].Q. [2].GFTLTPTNGV	445
gi 17232258	378	- [8].YLPFG	GG. [1].RRCIGLAFAQYEM	KIVLATILSQFQVSRLSK. [5].V. [2].GLTLAAPGGM	442



p450 - Sequence/Alignment Viewer

<p>IN9Y_A</p> <p>query</p> <p>ii 259016202</p> <p>ii 146345403</p> <p>ii 117257</p> <p>IGPH_A</p> <p>ii 6166042</p> <p>ii 6166039</p> <p>ii 60391933</p> <p>ii 117224</p>	<p>LRDYMI PAKTLVQVAIYALGREPTFFDPENFDPTRWLSKDK~N~ITYFRNLGFGWGVRRQLGRRIAELEM TIFLINML</p> <p>FRNYLIPKGTTIMALLTSVLHDDKEFPNPNI FDPGHFLDKNGnF~KKSDYFMPFSAGKRICAGEGLARME LFLFTTIL</p> <p>FRGFLIPKGTDVITLLNTVHYDPSQFLTPQEFNPEHFLDANQ~SfKKSPA FMPFSAGRR LCLGESLARME LFLYLTAI L</p> <p>FRGFFLPKGTDVFPILGSLMTDPKFFPSPKDFDPQNFLDDKGqL~KKNA AFLPFSTGKR FCLGDGLAKME LFLLLTTI L</p> <p>LRDYFIPKDTMI FPLLSPILQDCKEFPNPEKFDPGHFLNANGtF~RRSDYFMPFSAGKRICAGEGLARME LFLFTSIL</p> <p>FRGYLIPKGTVVVPTLDSVLYDNQEFDPDEKFKPEHFLNENGkF~KYSDFKPFSTGKRVCAGEGLARME LFLLLCAI L</p> <p>FRDYVIPKGTTVLPMLSSVMLDQKEFANPEKFDPGHFLDKNGcF~KKTDFVPPSLGKRACVGESLARME LFLFFTLL</p> <p>FNGY LIPKGTDIIPSLTSVLYDDKEFPNPEKFDPGHFLDESGnF~KKSDYFMPFSAGKRACVGEGLARME LFLLLTTI L</p> <p>FRSYLIPKGTAVITSLTSMLYNDKEFPNPDRFDPGHFLDASGkF~RKSDYFMPFSTGKRVCVGEVLARME LFLFLTAI L</p> <p>FRNYLIPKGTKVLTSLTSVLHDSKEFPNPEMFDPGHFLDENGnF~KKSDYFLPF SAGKRACVGEGLARMQ LFLFLTTI L</p>
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