Biochemical and Structural Insights into the Cytochrome P450 reductase from *Candida tropicalis*

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Supplementary Information

Figure S1: Multiple sequence alignment of CPRs of different species.

Figure S2: Saturation curves of CtCPR for (A) ferricyanide and (B) cytochrome c.

Figure S3: GC-MS chromatograms and mass spectra of biotransformations of dodecanoic acid by CYP52A21.

Figure S4: Control of the consumption of NADPH with the different components of the reaction.

Figure S5: Control reactions of the quantification of H_2O_2 stability.

Figure S6: Control reactions of the total H₂O₂ detected with and without SOD.

Table S1. Data collection and refinement statistics. Values in parentheses are for highest resolution shell.

Figure S7: Interactions of the FMN group of CtCPR with the residues and water molecules.

Figure S8: Interactions of the FAD group of CtCPR with the residues and water molecules.

Figure S9: Alignment between the FMN and FAD groups of the different CPR structures.

Figure S10: Interaction of the hinge region with the FMN and FAD domains for CPRs from different species.

Table S2: Uncoupling percentage (%) relative to NADPH consumed at different ionic strength.

Table S3: Uncoupling percentage (%) relative to NADPH consumed at different pH.

Table S4: Uncoupling percentage (%) relative to NADPH consumed at different temperatures.

Figure S11: Full-length SDS-PAGE gel used in the preparation of the cropped insert for Figure 1 in the main text.

	10	20	30	40	50	60	70	80	90	100
CtCPR		· · · · · · · · · · ·	••••						· • • • • • • • 	· · · ·
CalCPR										
YCPR										
ATR2	MKNMMNYKLKLCS	SVSKNSKGVSLSPI	PHLTKPPTIE	TERDLLLPSSS	FFLLLSS	SSYNIYNAMSS	SSSSSTSMI	DLMAAIIKGEI	VIVSDPANA	SAYES
ApaCPR1							MDSRL			R
ApaCRP2 GhiCPB1						MD:	SNYEKLSPF	DLMFAIIEAVE	CLDRMH	G
GhiCPR2						MDSSSS	SSSSGPSPL	DLMSALVKAK-	MDPSNAS	SSD
CsuCPR MdoCPR						M	NSKMSESAQ	DVVQ		D M
hCPR							MINMGDSHV	D		T
rCPR							MGDSHE	D		T
	110	100	120	1.4.0	150	1.00	170	100	1.0.0	200
		.	.		150 •• ••••	.		180		
CtCPR		MALDKLDLYVI	ITLVVAVA-	AYFAKNQFLDQP	QDTG	FLNTDSG	SNSRDVLST	-LKKNNKNTLI	LFGSQTGTA	EDYAN
CalCPR		MALDKLDLYVI MVDTNLLASVAV	VTLVVAVA-A ALVVVFVA-Y	YKYFNGGLEVQS-	QDTG SNAGSS	TPFGNAKADED	GSSRNILET GDSRNFVAL	-LKKNNKNTLI -MEKNNKNVIV	JEFGSQTGTAI /FYGSQTGTAI	EDYAN EDLAS
YCPR		MPFG-IDNTDF	TVLAGLVLA	LLYVKRNSIKE	LLMSDD	GDITAVS	SGNRDIAQV	-VTENNKNYLV	/LYASQTGTA	EDYAK
ATR2 CanCPR	VAAELSSMLIE SIESAIGVSLG	NRQFAMIVTTSI SDAVLMLLTTSF	AVLIGCIV-N AVIVGLVV	LVWRRSGSGNS- FFLKRSSDRS-	KRVE KEVK	PLKPLV	IKPREEE VEPEEEIE-	-IDDGRKKVTI -VEPGKVKVT\	JFFGTQTGTAI	EGFAK EGFAK
ApaCPR1	SVEQALGVKLG	-DETVVLVLTTSV	AVILGLLV	FLWKRSGDNRS	KDAR	QVVVPKPVS	LKDDDEDEY	-VGPDKTKLTI	FFGTQTGTA	EGFAK
ApaCRP2 GhiCPR1	FPQAVVARLME FVESVLGVSLEGS	NKDLLMLITTSI SVTDSMIVIATTSI	AVLVGCVV-V	/LLYRSATGSAK- -FFWKKSGSERS-	KVAE	PPKIVVI	RKEPEETEQ	-VDDGKKKVTI VIAAGKTKVTI	IFFGTQTGTAI	EGFAK Egfak
GhiCPR2	SAAQVTTVLFE	NREFVMILTTSI	AVLIGCVV-1	LIWRRSASQKP-	KQIQ	LPLKPSI	IKEPELE	-VDDGKKKVT1	LFGTQTGTA	EGFAK
CsuCPR MdoCPR	AAAAVAG	TSLFSTFDIVMI	IVLLGAAV-W	WLYSSRKENKK-	DEIVLS	KYSIQTAGSIQ	VAENSFIKK TTENSFIKK	-LKSSGRSLV	/FYGSQTGTGI	EEFAG
hCPR	SSTVSEAVAEE	VSLFSMTDMILF	SLIVGLLTY	FLFRKKKEEVP-	EFTK	IQTLTSS	VRESSEVEK	-MKKTGRNIIV	FYGSQTGTA	EEFAN
rCPR	SATMPEAVAEE	VSLFSTTDMVLF Membrane ancho	SLIVGVLTY	WFIFRKKKEEIP-	EFSK	IQTTAPP	VKESSFVEK	-MKKTGRNIIV	FYGSQTGTAI FMN bin	EEFAN ding
										lang
	210	220	230	240	250	260	270	280	290	300
CtCPR	KLSRELHSRFGLE	KTM-VADFADYDWD	NFGDITE	DILVFFIVATY	GEGEPTDN	ADEFHTWLTE-	EADT	LSTLRYTVFGI	GNSTYEFFN	AIGRK
CalCPR	KLSRELHSRFGL	NTM-VADFADYDFD	NFGDITI	DILVFFIVATY	EGEPTON	ADEFHTWLTD-	EADT	LSTLRFTVFGI	GNSTYEFYN	AIGRK
YCPR	KFSKELVAKFNLM	VM-CADVENYDFE	SLNDVP-	VIVSIFISTY	GEGDFPDO	AVNFEDFICNA	EAGA	LSNLRYNMFGI	LGNSTYEFFN	GAAKK
ATR2	ALGEEAKARYEKT	TRFKIVDLDDYAAD	DDEYEEKLK	XEDVAFFFLATY	DGEPTDN	AARFYKWFTEG	NDRGEW	LKNLKYGVFGI	GNRQYEHFN	KVAKV
CanCPR ApaCPR1	ALSEEIKARYEKA	AVVKVVDMDDYAAD	DDDTYEEKLK	XETIAFFMVATY(XETLAFFMVATY(SDGEPTDN SDGEPTDN	IAARFYKWFTEG- IAARFYKWFTEG-	QERGVW.	LQHLTYGVFGI LQQLSYGIFGI	LGNRQYEHFNI	KIGKV
ApaCRP2	ALAEEAKARYQQ	AHFTVLDLDDFAAD	EEEFEKKMK	KETLAIFFLATY	DGEPTDN	IAARFYKWFTEG-	KERGNW	LKDLQYGVFGI	GNRQYEHFNI	KIAIV
GhiCPR1	ALAEEIKARYEK	AAVKVVDLDDYAME	DEEVEEKIK	KETLAFFMVATY(DGEPTDN	AARFYKWFTEG	NERLPW	LQQLTYGVFGI	GNROYEHEN	KIAKV
CsuCPR	RLAKEGV-RYKM	KGM-VADPEECDME	ELTKLQDIP	NSLAV-FCMATY	GEGDPTD	AMEFYEWLKS-	GEPD	LTGLNYAVFGI	GNKTYEHYN	AVAIY
MdoCPR	RLAKEGL-RYRM	KGM-VADPEECDME	ELLOMKDIP	NSLAV-FCLATY	EGDPTD	AMEFYEWITN-	GEVD	LTGLNYAVFGI	GNKTYEHYN	KVAIY
rCPR	RLSKDAH-RYGM	RGM-SADPEEIDLA	DLSSLPEIDI	KSLVV-FCMATY	GEGDPTD	AQDF IDWLQE-	TDVD	LIGVKFAVEGI	LGNKTYEHEN	AMGKI
							FMN bin	ding		
	310	320	330	340	350	360	370	380	390	400
		.							· · · · · · · ·	· · · · <u>· </u>
CtCPR CalCPR	FDRLLSEKGGDR	FAEYAEGDDGTGTI FAEYGEGDDGTGTI	DEDFLSWKD	SVFDALKNDLNFI SVFDSLKNNLNYI	SEK-ELKY	EPNVK	LTERDDLSA LTERDDLTV	ADSQVSLGEPN DDSNVSLGEPN	KKYI-NSE-	GI GV
CapCPR	MHKFLTDLGGHS:	I GPYG <mark>EGDDSKGM</mark> I	EEDYMAWKDI	ZFLAALV TK WGLJ	KER-EAVY	EPAIS	VKDIEE-DA	QSHDVYLGEPN	ILKHLQASK-	A R
yCPR ATR2	AEKHLSAAGAIRI VDDILVEOGAORI	LGKLGEADDGAGTI LVOVGLGDDD-OCI	DEDYMAWKDS	SILEVLKDELHLI ALWPELDTILREI	DEQ-EAKI	TSQFQ	YTVLNEIT- VSIHDSEDA	DSMSLGEPS	SAHYLPSHQLI NGY	NRNAD
CanCPR	IDEQLSEQGAKRI	LVPVGLGDDD-QC1	EDDFSAWRE	QLWPELDQILRDI	EDDASSAS	TPYTAAILEYR	LVIHDT-TM	SLEDKHASMAN	IGN	
ApaCPR1	IDEKLSEQGAKRI	LVQLGLGDDD-QCI	EDDFTAWKE	QLWPELDQILRGI	EESLDSVS	TPYTAAIPEYR	VVIHDAAIP	SYDDNHAFVAN		
GhiCPR1	LDEQLSEQGAKRI	LIEVGLGDDD-QCI	EDDFTAWRE	LLWPELDQLLRDI	EDDENATS	TPYTAAIPEYR	VVVHDPAVM	HVEENYSNKAN	NGN	
GhiCPR2	VDELLTEQGAKR	IVPLGLGDDD-QCI	EDDFTAWRE	LVWPELDQLLRDI	EDD-ATVS	TPYTAAVLEYR	VVFYDPADA	PLEDKNWSNAM	IGH	
CSUCPR MdoCPR	VDKRLEELGATR	FELGLGDDD-ANI	EDDFITWKD	REWPAVCEKENII REWPSVCDFFGII	ISTGEEEI IGSGEEVI	MROFR	LUSHOPEET	OPDRIYTGEI	ARLH-	TY SM
hCPR	VDKRLEQLGAQR	IFELGLGDDD-GNI	EEDFITWRE	QFWPAVCEHFGVI	EATGEESS	IRQYE	LVVHTDI	DAAKVYMGEMO	GRLK-	SY
rCPR	VDQRLEQLGAQR:	IFELGLGDDD-GNI	EEDFITWRE	QFWPAVCEFFGVI	SATGEESS Hing	IRQYE	LVVHEDM	DVAKVYTGEMO	SRLK-	SY
					Ting					
	410	420	430	440	450	460	470	480	490	500
CtCPR	DLTKGPFDHTHP	YLARITETRELFS-	SKERHCIHVI	EFDISESNLKYT'	TGDHLAIN	PSNSDENIKQF	AKCFGLEDK	LDTVIELKALL	STYT	IP
CalCPR	DLSKGPFDHTHP	YLAKITKTKELEN-	SKDRNCVHVI	FDISDSNLKYS	TGDHLAV	PSNSDENIKQF	LKCFGLEDK	ENTVIELKALL	STYS	IP
CapCPR vCPR	GIOLGPFDLSOP	MLAKVTAAQELFT- YIAPIVKSRELFS-	SNDRNCIHS	EFDTTGARYT EFDLSGSNIKYS	rgdhlafv rgdhlavv	CONNEEEVORF PSNPLEKVEOF	AKALGITN-	PQQPIAISVLE PETIFDLKPLE	DETVE	VP
ATR2	TVFDAQHP	YKANVAVKRELHT	ESDRSCIHLI	EFDIAGSGLTYE	TGDHVGVI	CDNLSETVDEA	LRLLDMS	PDTYFSLHAEP	KEDGTPI-SS	SLPPP
CanCPR	TTYDIHHPO	KVNVAVQRELHT	ESDRSCIHL	SFDISGTGIFYE	ICDHVGVI	AENSEETVEEA	ARLLGQS	LDLTFSIHADE	CEDGTAL-GG	SLPPP
ApaCPRI ApaCRP2	TVYDAQHPO	CKVNVAVQRELHTE	ASDRSCTHLI	EFDISGTGLVYE	IGDHVGVI	TENLLETVEEA	ERMLNLP	PQTYFSLHTD	KDDGSP1-GG	TLPPP
GhiCPR1	ATYDLHHPO	RVNVAVQRELHK	ESDRSCIHLI	EFDISGTGITYE:	TGDHVGVY	ADNCVETVEEA	ARLLGQP	LDLLFSIHTDN	EDGTSA-GS	SLPPP
GhiCPR2	OVOR PRVDAKND	CRSNVAVRKELHAP	CODRSCT HU	EFDIAGTGLSYE	CDHVGV	CENLDEVVDEA	CALTKAD	PDTYFSVHTDE	KEDGTPLGGS:	SLPSS
MdoCPR	QNQRPPFDAKNPI	FLASVIVNRELHK-	GGGRSCMHI	ELDIDGSKMRYD	AGDHIAM	PINDKILVEKL	GKLCDAN	LDTVFSLINT	TDSSKK	HP
hCPR	ENQKPPFDAKNPI	FLAAVTTNRKLNQ-	GTERHLMHLI	ELDISDSKIRYE:	GDHVAVY	PANDSALVNQL	GKILGAD	LDVVMSLNNLE	DEESNKK	HP
rCPR	ENQKPPFDAKNPI	FLAAVTANRKLNQ-	GTERHLMHLI	ELDISDSKIRYE!	SGDHVAVY	PANDSALVNQI	GEILGAD	LDVIMSLNNL	DEESNKK	HP

	510	520	530	540	550	560	570	580	590	600
CHODD										
CalCPR	FPTPITYGAVIRHHI	EISGPVSRQ-	EB	LSIAGEAPDE.	ETKKTETRLG-	GDKQEF	STITREEN	TADALLYSSNI	SKAWVDVPFE-	-FLIEN
CapCPR	IPSPTTYETIIRHFI	EINGPVSRO-	VI	SSIAPFAPSE	EVKKATOOLG-	SNKELF	SHVAAKKEN	IARLLLHLSG	GOPWKNVPFS-	FILET
YCPR	FPTPTTIGAAIKHYI	EITGPVSRQ-	LF	SSLIQFAPNA	DVKEKLTLLS-	KDKDQF	VEITSKYFN	TADALKYLSDO	GAKWDTVPMQ-	FLVES
ATR2	FP-PCNLRTALTRYA	CLLSSPKKS-	AI	VALAAHASDP	TEAERLKHLA-	-SPAGKDEYS	KWVVESQRS	LLEVMAEFPS	AKPPLG	/FFAGV
CanCPR	FPGPCTLRAALARYA	DLLNPPRKA-	TI	VALAAHATEP	SEAEKLKFLA-	-SPQGKDEYS	GOWVVASORS	LVEVMAEFPS	AKPPLG	/FFAAV
ApaCPR1	FPGPCTLRSALAHHA	DLLNPPRKA-	A FYL CECAL	TALAAHASET	NEAEKLKFLA-	-SPQGKDEY	QWVVGSQRS	LLEVMAEFPS	SKPPLG	FFAAL
GhiCPR1	FASPCTLEMALARY	DI.I.NPPRKA-	AT	TALAAHATEP	SEAEKLKELS-	-SPOCKDEY	SOWWASORS	LLEVMAEPSI	AKPPLG	TEFAGV
GhiCPR2	FP-PCTLRTALARYA	DLLSSPKKA-	AI	LALAAHASDP	TEADRLRHLA-	-SPAGKDEY	OWIVANORS	LLEVMAEFPS	AKPPLGV	FFAAV
CsuCPR	FPCPTSYRTALSHYI	EITAVPRTH-	II	RGLAEYCSDE	EDKKKLLLMAT	NSQEGKELY	SEVVDACRN	IVHILEDIKS	CKPPLD-	HLCEL
MdoCPR	FPCPTTYRTALTHYI	EITAIPRTH-	II	KELAEYCSDE	KDKEFLRNMAS	ITPEGKEKY	ONWIQNSSRN	IVHILEDIKS	CRPPID-	HICEL
hCPR	FPCPTSYRTALTYYI	DITNPPRTN-		YELAQYASEP	SEQELLRKMAS	SSGEGKELY	SWVVEARRH	ILAILQDCPSI	LRPPID-	HLCEL
FCPR	FPCPTTIRTALTIII	DITNPPRIN-		IELAQIASEP	SEQUENTINKWAS	SSGEGRELI	JSWVVEARRH	TLATLQDIPSI	LRPPID-	HICEL
	610	620	630	640	650	660	670	680	690	700
			••••	1				1		
CtCPR	IQHLTPRYYSISSS	LSEKQLINVT	AVVEAEEE-	ADGRPVT-	-GVVTNLLKNI	EIAQNKTGE-	KPL-VHYD	LSGPRGKENK	FKLPVHVRRSN	IFKLPK
CapCPR	TPHLOPRYYSISSS	VOSPNTISTT	AVVEROKL-	AGVDHEL	RGVATNOTLAL	SEALTGRESS	TYRLOOPHD	FTGSLNS-OD	TRVPVHTRHST	FKLPA
VCPR	VPOMTPRYYSISSSS	LSEKQTVHVT	SIVENEPNE	ELPDAPPVV-	-GVTTNLLRNI	QLAQNNVNI	ETNLPVHYD	LNGPRKLFAN	YKLPVHVRRSN	IFRLPS
ATR2	APRLQPRFYSISSS	KIAETRIHVT	CALVYEKM-	PTGRIHK-	-GVCSTWMKNA	VPYEKSENC	SSA		PIFVRQSN	FKLPS
CanCPR	APRLOPRYYSISSS	RFAPARVHVT	CALVYGPT-	PTGRIHK-	-GVCSTWMKNA	VPLEKSHNC-	SSA		PIFIRPSN	FKLPS
ApaCPR1	APRLQPRYYSISSSI	RFAPTRVHVT	CALVYGPS-	PTGRIHK-	-GVCSTWMKHA	VPLEKSSSC	SWA		PIFIRPSN	FKLPA
ApaCRP2	APRLOPREYSISSSE	KIASTRIHVT	CALVYERT-	PTGRIHK-	-GVCSTWMKNA	VDI FKSNDC-	SSA		PIFVRTSP	IFRIPA
GhiCPR2	APRLOPRYYSISSS	RLAPSRTHVT	CALVYEKT-	PTGRIHK-		VSSGKSDDC-	GWA		PIFVROSM	IFKLPS
CsuCPR	LPRLQPRYYSISSS	KLYPETVHIT	AVVVEYKT-	STGRVNK-	-GVATTWLAQH	KPEAGK	PLPRV		PVYIRKS	FRLPL
MdoCPR	LPRLQPRYYSISSSS	KLYPTNVHIT	AVLVQYET-	PTGRVNK-	-GVATSYMKEK	NPSVGE-	vk v		PVFIRKSQ	FRLPT
hCPR	LPRLQARYYSIASSS	KVHPNSVHIC	AVVVEYET-	KAGRINK-	-GVATNWLRAK	EPAGENGGR-	ALV		PMFVRKSÇ	FRLPF
rCPR	LPRLOARYYSIASSS	KVHPNSVHIC	AVAVEYEA-	KSGRVNK-	-GVATSWLRAK	EPAGENGGR-	ALV		PMFVRKS(2FRLPF
	FAD bir	naing								
	710	720	730	740	750	760	770	780	790	800
	710 	720 	730 	740	750	760 	770	780	790	800
CtCPR	710 NSTTPVILIGPGTGV	720 APLRGFVRER	730 VQQVK	740	750	760 DFLYKQEWAJ	770	780 EMFNAFSRQDI	790 P SKKVYVQDK I	800 LENSQ
CtCPR CalCPR CapCPR	710 NSTTPVILIGPGTGV NTTTPVILIGPGTGV KPTVPIIM/CPGTGV	720 VAPLRGFVRER VAPLRGFIRER	730 VQQVK VQQVK	740	750 LLFYGCRNSNE ILFYGCRNEHD	760 . DFLYKQEWAI DFLYKQEWSI DFLYRDEWK(770	780 EMFNAFSRQDI EMFNAFSRQDI DLETAFSRDSI	790 PSKKVYVQDKJ PSKKVYVQDKJ	800
CtCPR CalCPR CapCPR vCPR	710 NSTTPVILIGPGTGV NTTTPVILIGPGTGV KPTVPIIMVGPGTGV NPSTPVIMIGPGTGV	720 APLRGFVRER APLRGFIRER APFRGFVHER	730 VQQVK NQQVK AAQKA VAFLESOKK	740 NGVNVGKT NGVNVGKT AGKEVGKA GGNNVSLGKH	750 LLFYGCRNSNE ILFYGCRNEHD LLFTGSRHANE ILFYGSRNTD-	760 DELYKQEWAJ DELYKQEWSJ DELYRDEWKQ DELYRDEWKQ DELYODEWEJ	770 LYASVLGENF LYASVLGDKF DFSDFL LYAKKLDGSF	780 EMFNAFSRQDI EMFNAFSRQDI DLETAFSRDSI EMVVAHSRLPI	790 PSKKVYVQDKI PSKKVYVQDKI NT-KVYVQHKI NTKKVYVQDKI	800 LENSQ VENYK LKERAK LKDYED
CtCPR CalCPR CapCPR yCPR ATR2	710 NSTTPVILIGPGTGV NTTPVILIGPGTGV KPTVPIINVGPGTGV NPSTPVIMIGPGTGV DSKVPIIMIGPGTGI	720 APLRGFVRER APLRGFIRER APFRGFVHER APFRGFIRER APFRGFLQER	730 VQQVK AQQKA VAFLESQKK LALVE	740 NGVNVGKT NGVNVGKT AGKEVGKA GGNNVSLGKH SGVELGPS	750 LLFYGCRNSNE ILFYGCRNEHD LLFTGSRHANE ILFYGSRNTD- VLFFGCRNRRM	760 DFLYKQEWAJ DFLYKQEWSJ DFLYRDEWKG DFLYQDEWPJ DFLYEEELQJ	770 YASVLGENF YASVLGDKF PSDFL YAKKLDGSF RFVES-GALA	780 EMFNAFSRQDI EMFNAFSRQDI DLETAFSRDSI EMVVAHSRLPI ELSVAFSREGI	790 PSKKVYVQDKI PSKKVYVQDKI NT-KVYVQDKI NTKKVYVQDKI PT-KEYVQHKI	800
CtCPR CalCPR CapCPR yCPR ATR2 CanCPR	710 NSTTPVILICPGTGV NTTPVILICPGTGV KPTVPIINVCPGTGV NPSTPVINICPGTGU DSKVPIIMICPGTGI DPSIPIVMVGPGTGI	720 APLRGFVRER APLRGFIRER APFRGFVHER APFRGFIRER APFRGFIQER APFRGFIQER	730 VQQVK AAQKA VAFLESQKK LALVE AALKE	740 NGVNVGKT AGKEVGKA GGNNVSLGKH SGVELGPS DGAQLGPA	750 LLFYGCRNSNE ILFYGCRNEHD LLFTGSRHANE ILFYGSRNTD- VLFFGCRNRRM LLFFGCRNRRM	760 DFLYKQEWAJ DFLYKQEWSJ DFLYRDEWKG DFLYQDEWPJ DFIYEEELQJ DFIYEEELKS	770 SYASVLGENF SYASVLGDKF SFSDFL SYAKKLDGSF RFVES-GALA SFVDQ-GVIS	780 EMFNAFSRQDI EMFNAFSRQDI DLETAFSRQDI DLETAFSRCJI ELSVAFSREGI ELIIAFSREGI	790 II PSKKVYVQDKI PSKKVYVQDKI NT-KVYVQHKI NTKKVYVQDKI PT-KEYVQHKI PQ-KEYVQHKI	800 LENSQ VENYK LKERAK LKDYED MDKAS MEKAS
CtCPR CalCPR CapCPR yCPR ATR2 CanCPR ApaCPR1	710 NSTTPVILIGPGTGV NTTPVILIGPGTGV KPTVPIIMVGPGTGV DSKVPIMIGPGTGI DSSIPIVMVGPGTGI DSSIPIVMVGPGTGI	720 VAPLRGFVRER VAPLRGFIRER VAPFRGFVHER VAPFRGFLQER APFRGFLQER APFRGFLQER	730 VQQVK AAQKA VAFLESQKK LALVE AALKE MALKN	740 NGVNVGKT NGVNVGKT GGNNVSLGKH SGVELGPS DGAQLGPA DGAQLGPA	750 LLFYGCRNSNE ILFYGCRNEHD LLFTGSRHANE LLFTGCRNRRM LLFFGCRNRRM LLFFGCRNRRM	760 DFLYKQEWAI DFLYKQEWSI DFLYRDEWKG DFLYQDEWPI DFIYEEELQI DFIYEEELKS DFIYENELMI	770 YASVLGENF YASVLGDKF PSDFL YAKKLDGSF RFVES-GALA SFVDQ-GVIS DFVDQ-GVIS	780 EMFNAFSRQDI EMFNAFSRQDI DLETAFSRDSI EMVVAHSRLPI ELSVAFSREGI ELIIAFSREGI ELIVAFSREGI	790 PSKKVYVQDKJ PSKKVYVQDKJ MT-KVYVQDKJ MT-KVYVQDKJ PT-KEYVQHKJ QQ-KEYVQHKJ QQ-KEYVQHKJ	800 LENSQ VENYK LKERAK LKDYED MDKAS MEKAS (LEKAD
CtCPR CalCPR CapCPR yCPR ATR2 CanCPR ApaCPR1 ApaCRP2 CbiCDP1	710 NSTTPVILIGPGTGV NTTTPVILIGPGTGV KPTVPIIMVGPGTGV DSKVPIMIGPGTGI DSSIPIVMVGPGTGI DSSIPIVMVGPGTGI DPSVPIVMIGPGTGI	720 APLRGFVRER APLRGFVRER APFRGFIRER APFRGFLQER APFRGFLQER APFRGFLQER APFRGFLQER APFRGFLQER	730 VQQVK AAQKA VAFLESQKK LALVE AALKE LALKE LALKE	740 NGVNVGKT NGVNVGKT 	750 LLFYGCRNSNE ILFYGCRNEHD LLFTGSRHANE LLFFGCRNRRM LLFFGCRNRRQ LLFFGCRNRRQ LLFFGCRNRRM	760 DFLYKQEWAJ DFLYKQEWAJ DFLYRDEWKG DFLYRDEWKG DFLYRDEWEG DFIYEEELQI DFIYEEELK DFIYENELMI DFIYEDELWE	770 YASVLGENF YASVLGDKF 27SDFL YAKKLDGSF RFVES-GALA SFVDQ-GVIS DFVDQ-GVIS RFVEA-RVIS RFVEA-RVIS	780 EMFNAFSRQDI EMFNAFSRQDI DLETAFSRDSI EMVVAHSRLPI ELSVAFSREGI ELIVAFSREGI ELIVAFSREGI ELIVAFSREGI ELIVAFSREGI	790 PSKKVYVQDKJ PSKKVYVQDKJ MT-KVYVQDKJ MT-KVYVQDKJ PT-KEYVQHKN QQ-KEYVQHKN DT-KEYVQHKN PQ-KEYVQHKN	800 LENSQ LENSQ LVENYK LKEYED 4MDKAS 4MEKAS 4LEKAD 4AQKAS
CtCPR CalCPR CapCPR yCPR ATR2 CanCPR ApaCPR1 ApaCRP2 GhiCPR1 GhiCPR2	710 NSTTPVILIGPGGV NTTPVILIGPGGV NFSTPVIMIGPGGGV DSKVPIIMIGPGGGI DSSIPIVMVGPGGGI DSSIPIVMVGPGGGI DFKVPIVMIGPGGGI DFKVPIMIGPGGGI	720 APLRGFVRER APLRGFVRER APFRGFVRER APFRGFLOER APFRGFLOER APFRGFLOER APFRGFLOER APFRGFLOER	730 VQQVK AAQKA AAQKA AALKE MALKN LALKE LVLKE	740 NGVNVGKT AGKEVGKA GGNNVSLGKH SGVELGPA DGAQLGPA SGAELGPA AGAELGPS	750 ILFYGCRNEHD ILFTGSRHANE ILFFGCRNRRM LLFFGCRNRRM LLFFGCRNRRM LLFFGCRNRRM	760 DFLYKQEWAJ DFLYKQEWSJ DFLYQDEWSJ DFLYQDEWFJ DFIYEEELQI DFIYEEELKI DFIYENELNI DFIYEDELNI DFIYEDELNI	770 EYASVLGENF EYASVLGDKF EYAKKLDGSF EYVES-GALA SFVDQ-GVIS GFVEA-RVIS UFVEQ-GALS UFVEQ-GALS	780 II.S. EMFNAFSRQDI DLETAFSRQDI DLETAFSRQDI ELSVAFSREG ELIVAFSREG ELIVAFSREG ELVVAFSREG ELVVAFSREG	790 	800 LENSQ VENYK KERAK KDYED MDKAS MEKAS MLEKAD MDKAA MMEKAK
CtCPR CalCPR CapCPR ATR2 CanCPR ApaCPR1 ApaCRP2 GhiCPR1 GhiCPR2 CsuCPR	710 NSTTPVILIGPGTGV NTTPVILIGPGTGV NPSTPVIMIGPGTGV DSKVPIIMIGPGTGI DSSIPIVMVGPGTGI DSSVPIIMVGPGTGI DPSVPIIMVGPGTGI DTXVPIMIGPGTGI QTQTPIIMVGPGTG	720 APIRGFVHER APFRGFVHER APFRGFLQER APFRGFLQER APFRGFLQER APFRGFLQER APFRGFLQER APFRGFLQER	730 VQQVK AAQKA AAQKA AALKE MALKN LALKE LVLKE ALARA	740 NGVNVGKT ACKEVGKA GGNNVSLGKH SGVELCPS DGAQLGPA GAELGPS 	750 LLFYGCRNSNE ILFYGCRNEHD ILFYGSRNTD- VLFFGCRNRRM LLFFGCRNRRM LLFFGCRNRRM VLFFGCRNRRM VLFFGCRNRRM VLFFGCRNRRM	760 DFLYKQEWAJ DFLYKQEWSJ DFLYRDEWSJ DFLYRDEWSJ DFIYEEELSJ DFIYEEELSJ DFIYEDELTJ DFIYEDELTJ DFIYEDELNJ DFIYEDELNJ	770 YASVLCENF YFSVLGDKF YFSSFLG YFVDG-GVIS FFVDQ-GVIS FFVDQ-GVIS KFVEA-RVIS FFVEQ-GALS YEKD-GDV-	780 EMFNAFSRQDI DETAFSRDSI EMVVAHSRLPI ELSVAFSREGI ELIVAFSREGI ELVVAFSREGI ELVVAFSREGI QLNVAFSREGI QLNVAFSREGI	790 SKKVVVQDKJ SKKVVVQDKJ SKKVVVQDKJ NTKVVVQDKJ T-KEVVQHKM QC-KEVVQHKM CC-KEVVQHKM CC-KEVVQHKM CC-KEVVQHKM CC-KEVVQHKM CC-KEVVQHKM CC-KEVVQHKM CC-KEVVQHKM CC-KEVVQHKM	800 LENSQ VENYK KERAK KDYED MDKAS MEKAS MEKAS MDKAS MDKAA MDKAA
CtCPR CalCPR CapCPR yCPR ATR2 CanCPR ApaCPR1 ApaCPP2 GhiCPR1 GhiCPR2 CsuCPR MdoCPR	710 NSTTPVILICPGTGV NTTPVILICPGTGV KFTVPIIMUCPGTGV DSKVPIIMUCPGTGI DSSIPIVMVCPGTGI DSSVPIIMVCPGTGI DFKVPIVMICPGTGI DTKVPIMICPGTGI KSEIPIIMVCPGTGI	720 APIRGFVER APFRGFVER APFRGFUER APFRGFLQER APFRGFLQER APFRGFLQER APFRGFLQER APFRGFLQER APFRGFLQER APFRGFLQER	730 VQQVK AAQKA VAFLESQKK LALVE AALKE LALKE LALKE LALKE LALKE QFLRD	740 NGVNVGKT NGVNVGKT 	750 LLFYGCRNSNE ILFYGCRNEHD ILFYGGRNANE ILFFGCRNRRM LLFFGCRNRRM LLFFGCRNRRM LLFFGCRNRRM ILFFGCRNRRM ILFFGCRNRRM ILFFGCRNRRM ILFFGCRNRRM ILFFGCRNRRM	760 DFLYKQEWAJ DFLYKQEWSJ DFLYQDEWFJ DFIYEEELG DFIYEEELKI DFIYEDELNI DFIYEDELNI DFIYEDELNI DFIYEDELNI DFIYEELEG	770 YASVLCENF YASVLGDKF YASVLGDKF SYAKLDGSF RFVES-GALA SFVDQ-GVIS KFVEA-RVIS KFVEA-RVIS NFVNS-GALS YEKD-CDV- QVQN-GTIT	780 EMFNAFSRQDI DETAFSRDSI EMVVAHSRLPI ELSVAFSREGI ELIVAFSREGI ELVVAFSREGI ELVVAFSREGI QLNVAFSRDQI -LKTAFSRDQI	790 SKKVVQDKI SKKVVQDKI NT-KVVQHKI NTKVVVQDKI PT-KEVVQHKI QC-KEVVQHKI PT-KEVVQHKI PT-KEVVQHKI EL-KVVVHLI QE-KIVVTHLI QE-KIVVTHLI	800 LENSQ VENYK KERAK KDYED MDKAS MEKAS MEKAS MEKAS MEKAK QNNID EQDAD
CtCPR CalCPR CapCPR yCPR ATR2 CanCPR ApaCPR1 ApaCPP2 GhiCPR1 GhiCPR2 CsuCPR MdoCPR hCPR	710 	720 APIRGFVER APFRGFVER APFRGFVER APFRGFLQER APFRGFLQER APFRGFLQER APFRGFLQER APFRGFLQER APFRGFLQER APFRGFLQER APFRGFLQER APFRGFLQER APFRGFLQER APFRGFLQER	730 VQQVK AAQKA VAFLESQKK LALVE AALKE LALKE LALKE LALKE LALKE AKIRQ AWIRQ	740 NGVNVCKT ACKEVCKA GGNNVSLGKH SCVELCPS DGAQLGPA DGAQLGPA DGAQLGPA DGAELCSS AGAELGPS 	750 LLFYGCRNSNE ILFYGCRNEHD ILFYGSRNTD- VLFFGCRNRRM LLFFGCRNRRM LLFFGCRNRRM LLFFGCRNRRM ILFFGCRNRKM ILFFGCRNRKM ILFFGCRNRKM ILYFGCRKKDE ILYYGCRRSDE LLYYGCRSDE	760 DFLYKQEWSJ DFLYRQEWSJ DFLYRDEWKJ DFLYRDEWKJ DFIYEEELQJ DFIYEEELKJ DFIYEDELNI DFIYEDELNI DFIYEDELNI DFIYEELEJ DFIYREELEJ DYLYREELAJ	770 EYASVLGDKF EYASVLGDKF EYASVLGDKF EYAKLDGSF RFVES-GALA SFVDQ-GVIS KFVEA-RVIS HFVEQ-GALS VFVNS-GALS VFVNS-GALS DFVRD-GALT DFHRD-GALT	780 EMFNAFSRQDI DETAFSRDSI EMFVAFSRDSI ELVVAFSREGI ELVVAFSREGI ELVVAFSREGI ELVVAFSREGI ELVVAFSREGI -LXTAFSRDQI -LXTAFSRDQI QLNVAFSRDQI -LXTAFSRDQI	790 SSKKVVQDK1 SSKVVVQDK1 NT-KVVVQHK1 NTKVVVQDK1 PT-KVVQHK0 QC-KEYVQHK0 PT-KEYVQHK0 PT-KEYVQHK0 PT-KEYVQHK1 QE-KIYVTHL1 SE-KIVVTHL1 SE-KIVVTHL1	800 ILLENSQ IVENYK KERAK KDYED MDKAS MEKAS MEKAS MDKAA MDKAA MEKAK LQNNID IEQDAD KQDRE
CtCPR CalCPR CapCPR ATR2 CanCPR ApaCPR1 ApaCRP2 GhiCPR1 GhiCPR2 CsuCPR MdoCPR hCPR rCPR	710 	720 	730 	740 	750 LLFYGCRNSNE ILFYGCRNEHD ILFYGSRNTD- VLFFGCRNRRM LLFFGCRNRRM LLFFGCRNRRM LLFFGCRNRRM LLFFGCRNRKM LLFFGCRNRKM LLFFGCRNRKM LLFFGCRNRKM LLFFGCRNRKM LLFFGCRNRKM LLYGCRRSDE LLYYGCRRSDE	760 DFLYKQEWAJ DFLYKQEWAJ DFLYKQEWAJ DFLYKQEWAJ DFLYEDELKI DFIYEDELKI DFIYEDELKI DFIYEDELKI DFIYEDELKI DFIYEDELKI DFIYEDELKI DYIYQEELEJ DYLYREELEAJ	770 EYASVLCENF EYASVLCENF EYASVLGDKF EYASVLGSF EYASVLGSF EYVDQ-GVIS FVVDQ-GVIS FVVDQ-GVIS FVVDQ-GALS FVVNS-GALS PFND-GALT EFHRD-GALT	780 II. EMFNAFSRQDI DLETAFSRQDI DLETAFSRQSI ELVVAHSRLF ELVVAFSREG ELVVAFSREG ULVAFSREG QLVVAFSREG QLVVAFSREQ QLVVAFSREQ QLVVAFSREQ	790 SKKVYVQDKJ SKKVYVQDKJ SKKVYVQDKJ TKKVVQDKJ PT-KEYVQHKJ QC-KEYVQHKJ C-KEYVQHKJ C-KEYVQHKJ E-KEYVQHKJ SH-KVYVQHLJ SH-KVYVQHLJ NADPH bJ	800 ILLENSQ IVENYK KERAK KDYED MDKAS MEKAS MEKAS MDKAA MDKAA MDKAA MDKAA MEKAK LQNNID IEQDAD KQDRE KRDRE
CtCPR CalCPR CapCPR ATR2 CanCPR ApaCPR1 ApaCRP2 GhiCPR1 GhiCPR2 CsuCPR MdoCPR hCPR rCPR	710 NSTTPVILIGPGTGV NTTTPVILIGPGTGV NFSTPVIMIGPGTGV DSKVFIMIGPGTGI DSSVFINMCPGTGI DFVFIMIGPGTGI DFVFIMIGPGTGI QTQTFIIMVCPGTGI KSEIFIIMVCPGTGI KSTTPVIMVCPGTGI KSTTPVIMVCPGTGI NADPH	720 	730 	740 	750 LLFYGCRNSNE ILFYGCRNEHD ILFYGSRHANE ILFYGCRNRRM LLFFGCRNRRM LLFFGCRNRRM LLFFGCRNRRM LLFFGCRNRKM ILFFGCRNRKM ILFFGCRNRKM LLFFGCRNRKM LLFGCRNRKM LLFGCRNRKM LLFGCRNRKM LLFGCRNRKM LLYGCRRSDE LLYYGCRRSDE	760 DFLYKQEWAJ DFLYKQEWAJ DFLYKQEWAJ DFLYKQEWAJ DFLYEDELKI DFIYEDELNI DFIYEDELNI DFIYEDELNI DFIYEDELNI DFIYEDELNI DFIYEDELNI DFIYEDELNI DFIYREELEX DYLYREELAJ	770 EYASVLGENF EYASVLGENF EYASVLGDKF EYASVLGSF RFVES-GALA SFVDQ-GVIS KFVEA-RVIS HFVEQ-GALS NFVNS-GALS PFND-GALT FHRD-GALT	780 II. EMFNAFSRQDI DLETAFSRQDI DLETAFSRQSI ELVVAFSREGI ELVVAFSREGI ELVVAFSREGI ELVVAFSREGI QLNVAFSRQQ QLNVAFSRQQ QLNVAFSREQI QLNVAFSREQI	790 SKKVYVQDKJ SKKVYVQDKJ SKKVYVQDKJ TKKVVQDKJ TKKVVQDKJ PT-KEYVQHKO 20-KEYVQHKO PT-KEYVQHKO PT-KEYVQHKO 20-KEYVQHKO 20-KEYVQHKI SH-KVYVQHLJ SH-KVYVQHLJ NADPH bi	800 LLENSQ EVENYK KERAK KDYED MDKAS MEKAS MEKAS MDKAA MEKAK CONNID LEQDAD LEQDAD LEQDAD LEQDAD
CtCPR CalCPR CapCPR ATR2 CanCPR ApaCPR1 ApaCRP2 GhiCPR1 GhiCPR2 CsuCPR MdoCPR hCPR rCPR	710 NSTTPVILIGPGTGV NTTTPVILIGPGTGV KPTVPIIMVGPGTGV DSKVPIVMIGPGTGI DSKVPIVMVGPGTGI DSKVPIVMVGPGTGI DFKVPIMVGPGTGI KSEIPIMVGPGTGI KSEIPIMVGPGTGI KSEIPIMVGPGTGI KSTTPVIMVGPGTGV KSTTPVIMVGPGTGV KSTPPIMVGPGTGI NADPH 810	720 APLRGFVRER APFRGFVRER APFRGFIQER APFRGFIQER APFRGFIQER APFRGFIQER APFRGFIQER APFRGFIQER APFRGFIQER APFRGFIQER APFRGFIQER APFRGFIQER APFRGFIQER APFNGFIQER BIDINGING 820	730 	740 IVVVGKT NGVNVGKT NGVNVGKT SGVELGPS SGVELGPS DGAQLGPA DGAQLGPA DGAQLGPA DGAELGSS AGAELGPS AGAELGPS GGKVVGDT GGKVVGDT QCKEVGET 840	750 LLFYGCRNSHE LLFTGSRHANE LLFTGSRHANE LLFFGCRNRRM LFFFGCRNRRM LLFFGCRNRRM VLFFGCRNRRM VLFFGCRNRRM VLFFGCRNRRM LLFYGCRRSDE LLYYGCRRSDE LLYYGCRRSDE 850	760 DFLYKQEWAJ DFLYKQEWAJ DFLYKQEWAJ DFLYKQEWAJ DFLYEDELMI DFIYEDELMI DFIYEDELMI DFIYEDELMI DFIYEDELMI DFIYEDELMI DFIYEELEKI DYLYREELAJ DYLYREELAJ 860	770 EXASVLCENF EXASVLCENF EXASVLCENF EVASVLCENF EVASVLCGSF EVVD2-GVIS EVVD2-GVIS EVVD2-GVIS EVVD2-GALS VFVNS-GALS EVNS-GALT EFHRD-GALT	780 II. EMFNAFSRQDI DLETAFSRQDI DLETAFSRQSI EMVVAHSRLFI ELIVAFSREGI ELVVAFSREGI QLNVAFSRQ QLNVAFSRQQ QLNVAFSREQI QLNVAFSREQI	790 SKKVYVQDK: SKKVYVQDK: SKKVYVQDK: SKKVYVQDK: TKKYVQDK: PT-KEYVQHK: Q-KEYVQHK: PT-KEYVQHK: SH-KVYVQHI: SH-KVYVQHI: AH-KVYVQHI: NADPH bi	800 LLENSQ EVENYK KERAK KDYED MDKAS MDKAS MDKAS MDKAS MDKAA MEKAK (QDRE LEQDAD LEQDAD LEQDAD LEQDAD
CtCPR CalCPR CapCPR YCPR ATR2 CanCPR ApaCPR1 ApaCRP2 GhICPR1 GhICPR2 CsuCPR MdoCPR hCPR rCPR	710 	720 APLRGFVER APFRGFVER APFRGFIRER APFRGFIQER APFRGFIQER APFRGFIQER APFRGFIQER APFRGFIQER APFRGFIQER APFRGFIQER APFRGFIQER Binging 820	730 	740 NGVNVGKT NGVNVGKT SGVELGPS DGAQLGPA DGAQLGPA DGAQLGPA DGALGPS AGAELGPS AGAELGPS AGAELGPS GGKVVGDT GGKEVGET 840 .	750 LLFYGCRNSHD LLFTGSRHANE LLFTGSRHANE LLFFGCRNRRM LLFFGCRNRRM LLFFGCRNRRM LLFFGCRNRRM LLFFGCRNRRM LLFFGCRNRRM LLFFGCRNRRM LLFFGCRNRRM LLFGCRNRRM LLFFGCRNRM LLFFGCRNRM LLFFGCRNRM LLFFGCRNRM LLFFGCRNRM LLFFGCRNRM LLFFGCRNRM LLFFGCRNRM LLFFGCRNRM LLFFGCRNRM LLFFGCRNRM LLFFGCRNRM LLFFGCRNRM LLFFGCRNRM LLFFGCRNRM LLFFGCRNRM LLFFGCRNRM LLFFGCRNRM LLYYGCRRSDE LLYYGCRRSDE AND AND AND AND AND AND AND AND AND AND	760 DFLYKQEWAJ DFLYKQEWAJ DFLYKQEWAJ DFLYKQEWAJ DFLYEELEK DFIYEELEK DFIYEELEK DFIYEDELMI DFIYEDELMI DFIYEELEAJ DYLYREELAJ DYLYREELAJ 860	770 YASVLCENF ZYASVLCENF ZYASVLCENF ZYASVLCENF SYASVLCOSF GYUQ-GVIS GYUQ-GVIS GYUQ-GVIS GYUQ-GVIS GYUQ-GALS GYUQN-GALT GHRD-GALT	780 	790 SKKVYVQDK: SKKVYVQDK: SKKVYVQDK: SKVYVQDK: T-KYVQHK: P-KYVQHK: Q-KYVQHK: 2Q-KYVQHK: P-KYVQHK: 2E-KIYVHL: 2E-KIYVHL: NADPH bi	800 I ILENSQ VENYK KERAK KERAK KIEKAD MDKAS MEKAK MDKAA MDKAA MDKAA MDKAA MDKAA MDKAA MDKAA MDKAA MDKAA MDKAA MDKAA MDKAA MDKAA MDKAA MDKAA MDKAA MDKAA MDKAA MDKAA
CtCPR CalCPR CapCPR ATR2 CanCPR ApaCPP1 ApaCRP2 GhiCPR1 GhiCPR2 CsuCPR MdoCPR hCPR rCPR	710 NSTTPVILIGPGTGV NTTTPVILIGPGTGV NTTTPVILIGPGTGV NPSTPVIMIGPGTGV DSSIPIVMVGPGTGI DSSIPIVMVGPGTGI DPSVPIMVGPGTGI DTXVPIMIGPGTGI QTQTPIIMVGPGTGV KSEIPIMVGPGTGV KSTTPVIMVGPGTGV NADPH 810 	720 	730 	740 NGVNVGKT NGVNVGKT SGVELGPS DGAQLGPA DGAQLGPA DGAQLGPA DGAELGPS AGAELGPS AGAELGPS AGAELGPS QGKEVGET QGKEVGET 840 AKSREISDR	750 	760 DFLYKQEWAI DFLYKQEWAI DFLYQDEWAI DFLYQDEWAI DFIYEELEKI DFIYEELEKI DFIYEDELNI DFIYEDELNI DFIYEDELNI DFIYEDELNI DFIYEELAI DFIYREELAI DYLYREELAI 0YLYREELAI 860 	770 YASVLENF YASVLGKF FFSDFL YAKKLDGSF SFVDQ-GVIS SFVDQ-GVIS SFVDQ-GVIS SFVDQ-GVIS SFVDQ-GVIS YFVS-GALS YEKD-CDV- QYVQN-GTLT SFHKD-GALT	780 	790 SKKVYVQDK: SKKVYVQDK: SKKVYVQDK: MT-KVYVQHKI MT-KVYVQHKI PT-KEYVQHKI QQ-KEYVQHKI PQ-KEYVQHKI PQ-KEYVQHKI PT-KEYVQHKI SH-KVYVYQHLI AH-KVYVQHLI NADPH bi	800 I.L.ENSQ IVENYK IKERAK IKDYED MIDKAS MIEKAD AQKAS MIDKAA MIEKAS ILEKAD IAQKAS MIDKAA MIEKAK QNNID EQDAD IKQDRE IKQDRE INGING
CtCPR CalCPR CapCPR ATR2 CanCPR ApaCPR1 ApaCRP2 GhiCPR1 GhiCPR2 CsuCPR MdOCPR hCPR rCPR CtCPR CalCPR CalCPR CapCPR	710	720 	730 	740 NGVNVGKT AGKEVGKA GGNNVSLGKH SGAVLGPS DGAQLGPA DGAQLGPA DGAQLGPA DGAELGPS AGAELGPS AGAELGPS AGAELGPS QGKEVGET 840 XKSREISEDK AKDRDISQES.	750 	760 DFLYKQEWAI DFLYKQEWSI DFLYRQEWSI DFLYRQEWSI DFIYEELQI DFIYEELKI DFIYEDELNI DFIYEDELNI DFIYEDELNI DFIYEDELNI DFIYEDELMI DYIYREELAJ DYLYREELAJ 860 	770 YASVLENF YASVLGDKF FFSDFL YAKKLDCSF FFVES-GALS SFVDQ-GVIS FFVDQ-GVIS (FVEA-RVIS VFVEQ-GALS XYEKD-CDV- YVQN-GTLT FHKD-GALT	780 	790 SKKVVVQKX SKKVVVQKX MT-KVVVQHXI MT-KVVVQHXI PT-KEVVQHKN 9Q-KEYVQHKN 9Q-KEYVQHKN 9Q-KEYVQHKN 9T-KEYVQHKN 9T-KEYVQHKN 8H-KVYVVHLI NADPH bi	800 I.L.ENSQ IVENYK KERAK KDYED MDKAS MEKAS MDKAA MDKAA MDKAA MEKAK QNNID EQDAD LKQDRE nging
CtCPR CalCPR CapCPR ATR2 CanCPR ApaCPR1 ApaCRP2 GhiCPR1 GhiCPR2 CsuCPR MdOCPR hCPR rCPR CtCPR CtCPR CalCPR CapCPR yCPR	710 NSTTPVILIGPGGV NTTTPVILIGPGGV NTTTPVILIGPGGV NSTPVIMIGPGGG DSSIPIVMVGPGGI DSSIPIVMVGPGGI DFSVPIMVGPGGI QTQTPIIMVGPGGG KSTPVIMVGPGGG KSTTPVIMVGPGGG NADPH 810 	720 	730 	740 NGVNVGKT AGKEVGKA GGNNVSLGKH SGVELGPS DGAQLGPA DGAQLGPA DGAQLGPA DGAQLGPA DGAELGPS AGAELGPS AGAELGPS AGAELGPS AGAELGPS AGAELGPS AGAELGPS AGAELGPS AGAELGPS AGAELGPS AGAELGPS AGAELSEDK %40 	750 	760 DFLYKQEWAJ DFLYKQEWSJ DFLYRDEWSJ DFLYRDEWSJ DFIYEELSJ DFIYEDELNI DFIYEDELNI DFIYEDELNI DFIYEDELNI DFIYEDELSJ DYLYREELAJ 860 NRYQEDVW- NRYQEDVW- GRYQEDVW-	770 YASVLENF YYASVLGDKF FFSDFL YAKKLDGSF FFVDQ-GVIS FFVDQ-GVIS FFVDQ-GVIS FFVDQ-GVIS KFVEA-RVIS KFVEA-RVIS KFVEA-COV- YVQN-GTLT YFVNS-GALS YFVD-GALT	780 II.SRQDI DETAFSRQDI DETAFSRQSI EMVVAHSRLPI ELSVAFSREGI ELIVAFSREGI ELVVAFSREGI QLVVAFSRQQI -LXTAFSRQQI QLVVAFSREQI QLNVAFSREQI QLNVAFSREQI	790 PSKKVVVQDKJ PSKKVVVQDKJ NT-KVVVQDKJ PT-KEVVQHKJ PQ-KEYVQHKJ PQ-KEYVQHKJ PQ-KEYVQHKJ PT-KEYVQHKJ BH-KVVVTHLJ SH-KVVVTHLJ SH-KVVVOHLJ NADPH bi	800 LLENSQ EVENYK KERAK KDYED MDKAS MEKAS MDKAS MDKAS MDKAA MDKAA MDKAA MEKAK QNNID EQDAD KQDRE KQDRE Nging
CtCPR CalCPR CapCPR ATR2 CanCPR ApaCPR1 ApaCRP2 GhiCPR1 GhiCPR2 CsuCPR MdoCPR hCPR rCPR CtCPR CalCPR CalCPR CalCPR CalCPR CalCPR CalCPR	710 	720 	730 	740 I	750 	760 DFLYKQEWAJ DFLYKQEWAJ DFLYKQEWAJ DFLYKQEWAJ DFLYKDELWI DFIYEDELNI DFIYEDELNI DFIYEDELNI DFIYEDELNI DFIYEDELNI DYIYQELENJ DYLYREELAJ MAGO NRYQEDVW- NRYQEDVW- NRYQEDVW- GRYLRDVW-	770 YASVLGENF YASVLGENF YASVLGENF YASVLGENF YASVLGENF YASVLGENF YASVLGENF YASVLGENF YVQS YVQS YVQN-GTLT YVQN-GTLT YFHKD-GALT	780 	790 SKKVYVQDKJ SKKVYVQDKJ SKKVYVQDKJ TKKVVQDKJ PT-KEYVQHKJ QC-KEYVQHKJ C-KEYVQHKJ C-KEYVQHKJ C-KEYVQHKJ SH-KVYVQHJJ SH-KVYVQHJJ NADPH bi	800 LLENSQ EVENYK KERAK KDYED MDKAS MEKAS MDKAS MDKAS MDKAA MEKAK MDEKAK MDEKAK MDEKAK MDEKAK MDEKAK
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Figure S1. Multiple sequence alignment of CPRs of different species generated by ClustalW. CtCPR, *Candida tropicalis* (AAV84084.1); CalCPR, *Candida albicans* (KGQ86567); CapCPR, *Candida apicola* (JQ015264); Ycpr, *Saccharomyces cerevisiae* (P16603); ATR2, *Arabidopsis thaliana* CPR2 (AEE85738.1); CanCPR, *Capsicum annuum* (AFV95075); ApaCRP1, *Andrographis paniculate* CPR1 (AQT38168); ApaCRP2, *A. paniculate* CPR2 (AQT38169); GhiCPR1, *Gossypium hirsutum* CPR1 (ACN54323); GhiCPR2, *G. hirsutum* CPR2 (ACN54324); CsuCPR, *Chilo suppressalis* (AGM20565); MdoCPR, *Musca domestica* (Q07994); hCPR, human (NP_000932); rCPR, rat (NP_113764).



Figure S2. Saturation curves of *Ct*CPR for (**a**) ferricyanide and (**b**) cytochrome *c*. Values are the average of three independent measurements. Data was fit into the Michaelis-Menten equation.



Figure S3. GC-MS chromatograms and mass spectra of biotransformations of dodecanoic acid by CYP52A21. (a) Chromatograms of the biotransformations without (- *Ct*CPR) and with (+ *Ct*CPR) addition of *Ct*CPR. (b) Mass spectra of substrate dodecanoic acid (RT: 5.10), and products 12-hydroxydodecanoic acid (RT: 7.81), and 1,12-dodecanedioic acid (RT:8.32). Reaction conditions: buffer = 200 mM potassium phosphate pH 8.0, [CYP52A21] = 2 μ M, [*Ct*CPR] = 50 μ M, [dodecanoic acid] = 4 mM, [glucose] = 200 mM, [glycerol] = 100 mM, [1,2-diodecanoyl-*sn*-glycero-3-phosphocoline] = 45 μ M, [*Bm*GDH] = 0.2 U, [NADP⁺] = 0.5 mM. Reactions were incubated at 30°C for 24 hours with shaking (200 rpm).



Figure S4. Control of the consumption of NADPH with the different components of the reaction. The assays were carried in a final volume of 200 μL, containing 20 mM Tris-HCl pH 8.0, 0.2 μM *Ct*CPR and started with the addition of 12.5 mM NADPH (black circle). The different reactions contained: 2 U/mL superoxide dismutase (SOD, square), 0.2 U/mL horseradish peroxidase (HRP, diamond), 50 μM AmpifluTM Red (Ampi, triangle) and HRP, SOD and AmpifluTM Red (white circle).



Figure S5. Control reactions of the quantification of H_2O_2 stability. AmpifluTM Red/HRP reaction was incubated with 8 mM H_2O_2 , one sample was heated at 80 °C (black) for 1 min and, after cooling down, the absorbance was measured and compared to reaction without the heating step (white).



Figure S6. Control reactions of the total H_2O_2 detected during the reactions with (black) and without (white) addition of SOD. Plot shows increase on absorbance at 560 nm over time.

	<i>Ct</i> CPR	CtCPR with NADPH
Data collection		
Space group	P 1 21 1	P 1 21 1
Cell dimensions		
a, b, c (Å)	74.29, 67.18, 143.47	74.66, 67.50, 143.99
α, β, γ (°)	90.00, 91.50, 90.00	90.00, 91.55, 90.0
Resolution (Å)	52.27 - 1.50 (1.55 -	74.63 - 2.08 (2.16 -
	1.50)*	2.08)
R _{merge}	0.081 (0.687)	0.191 (2.247)
<1/0l>	7.7 (1.5)	4.0 (0.5)
Completeness (%)	97.5 (96.8)	95.4 (86.9)
Redundancy	3.4 (3.5)	3.0 (2.9)
CC _{1/2}	0.99 (0.72)	0.99 (0.36)
Refinement		
Resolution (Å)	52.27 - 1.50	74.63 - 2.08
No. reflections used	220 256	82 237
Rwork / Rfree	0.176/0.202	0.219/0.264
Molecules in ASU	2	2
No. atoms		
Protein	10 253	10 184
Ligand/ion	62 (FMN), 106 (FAD)	62 (FMN), 106 (FAD),
		62 (NADPH)
Water	964	371
B-factors		
Protein	23.0	41.7
Ligand/ion	16.2 (FMN), 14.7	41.5 (FMN), 28.7
	(FAD)	(FAD), 36.4 (NADPH)
Water	30.1	38.9
R.m.s. deviations		
Bond lengths (Å)	0.014	0.007
Bond angles (°)	1.683	1.474
Ramachandran distribution	98.0/1.9/0.2	95.7/3.9/0.4
(%)		
Favoured/Allowed/Outliers		

Table S1. Data collection and refinement statistics. Values in parentheses are for highest resolution shell.



Figure S7. Interactions of the FMN group of *Ct*CPR with the residues and water molecules.



Figure S8. Interactions of the FAD group of *Ct*CPR with the residues and water molecules.



Figure S9. Alignment between the FMN and FAD groups of the different CPR structures. *Ct*CPR (green) CPR from *C. tropicalis.* yCRP (blue) *S. cerevisiae* CPR. hCPR (pink) human CPR. rCPR (salmon) rat CPR.



Figure S10. Interaction of the hinge region with the FMN and FAD domains for CPRs from different species. *C. tropicalis* (Ct), yeast *S. cerevisiae* (y), rat (r) and human (h) CPR structures are aligned. Residues from the hinge are displayed Ct (blue), y (green), r (grey), h (magenta) and their interactions with amino acids from the FMN domain (light blue for Ct and light green for y) and the FAD domain (salmon for r and pink for h).

NaCl (M)								
	0	0.1	0.15	0.2	0.5	1		
NADPH	100	100	100	100	100	100		
H ₂ O ₂	27	33	33	31	36	51		
Cytochrome c	73	67	67	69	64	49		

Table S2. Uncoupling percentage (%) relative to NADPH consumed at different ionic strengths.

рН								
	5.5	6.0	6.5	7.0	7.5	8.0		
NADPH	100	100	100	100	100	100		
H ₂ O ₂	34	30	27	28	29	28		
Cytochrome c	66	70	73	72	71	72		

Table S3. Uncoupling percentage (%) relative to NADPH consumed at different pH.

T (°C)							
	20	25	37	42			
NADPH	100	100	100	100			
H ₂ O ₂	28	31	24	29			
Cytochrome c	72	69	76	71			

Table S4. Uncoupling percentage (%) relative to NADPH consumed at different temperatures.



Figure S11: Full-length SDS-PAGE gel used in the preparation of the cropped insert for Figure 1 in the main text. Lane 1 represent the molecular weight marker, with subsequent lanes the eluted fractions from gel filtration chromatography.