

Figure Fsl			10	20	30	40	50	60	70		
Alias	PDB	ID%	1234567	8901234567	8901234567	89012345	678901234 567	890123456 7890-12345	6789012345		
1	hCyP18a	2CPL	MVNPTVF	FDIAVDGEPL	GRVSFELFAD	KVPKTAEN--	-FRALSTGEK	GFG-----	-YKGS CFHRI	IPGF-MCQGG	DFTRHNGTGG
2	hCyp18b	(85)	MVNSVVF	FDITVDGKPL	GRISIKLFAD	KILKTAEN--	-FRALSTGEK	GFR-----	-YKGS CFHRI	IPGF-MCQGG	DFTRHNGTGD
3	hCyPB	1CYN (63)	GPKVTVKVY	FDLRIGDEDV	GRVIFGLFGK	TVPKTVDN--	-FVALATGEK	GFG-----	-YKNSKFHRV	IKDF-MIQGG	DFTRGDGTGG
4	hCyP33	1ZCX (66)	SNPQVY	MDIKIGNKPA	GRIQMLLRSD	VVPMTAEN--	-FRCLCTHEK	GFG-----	-FKGSSFHRI	IPQF-MCQGG	DFTNHNGTGG
5	hCyP358	(65)	LSKETNPVVF	FDVCADGEPL	GRITMELFSN	IVPRTAEN--	-FRALCTGEK	GFG-----	-FKNSIFHRV	IPDF-VCQGG	DITKHDGTGG
6	hCyPD	2BIT (75)	SGNPLVY	LDVDANGKPL	GRVVLELKAD	VVPKTAEN--	-FRALCTGEK	GFG-----	-YKGSTFHRV	IPSF-MCQAG	DFTNHNGTGG
7	hCyPC	2RMC (54)	RGPSVTAKVF	FDVRIGDKDV	GRIVIGLFGK	VVPKTVEN--	-FVALATGEK	GYG-----	-YKGSKFHRV	IKDF-MIQGG	DITTDGDTGG
8	hCyP40	2Z6W (61)	PSNPSNPRVF	FDVDIGGERV	GRIVLELFAD	IVPRTAEN--	-FRALCTGEK	GIGHTTGKPL	HFKGC PFHRI	IKKF-MIQGG	DFSNQNGTGG
9	hCyP88	2GW2 (52)	RPRCF	FDIAINQPA	GRVVLELFSD	VCPKTCEN--	-FRCLCTGEK	GTGKSTQKPL	HYKSLFHRV	VKDF-MVQGG	DFSENGRGG
10	hCyP157	2HE9 (50)	PQCH	FDIEINREP	GRIMFQLFSD	ICPKTCEN--	-FLCLCSGEK	GLGKTTGKKL	CYKGS TFHRV	VKNF-MIQGG	DFSENGRGG
11	hCyP19	1QOI (53)	NSSPVNPVVF	FDVSIQGQEV	GRMKIELFAD	VVPKTAEN--	-FRQFCTGEF	RKD---GVPI	GYKGS TFHRV	IKDF-MIQGG	DFVNGDGTGV
12	hCyP18d	1XWN (38)	PPDSWQPP-N	VYLETS---M	GIIVLELYWK	HAPKTCEN--	-FAELARGY	-----	-YNGTKFHRI	IKDF-MIQGG	DPTG-TGRGG
13	hCyP18c	(30)	MS	VTLHTD---V	GDIKIEVFCE	RTPKTCMES	RCVPQAGVQW	-----	-RDLGSLQPP	PPGFKQVFCL	SLPR-TGRGG
14	hCyP18ci	(38)	MS	VTLHTD---V	GDIKIEVFCE	RTPKTCEN--	-FLALCASNY	-----	-YNGCIFHRN	IKGF-MVQTG	DPTG-TGRGG
15	hCyP58	1ZKC (37)	GY	VRLHTN---K	GDLNLELHCD	LTPKTCEN--	-FIRLCKKHY	-----	-YDGTIFHRS	IRNF-VIQGG	DPTG-TGTGG
16	hCyP73	2A2N (40)	AEGPKRVSDS	AIHHTS---M	GDIHTKLFVP	ECPKTVEN--	-FCVHSRNGY	-----	-YNGHTFHRI	IKGF-MIQTG	DPTG-TGMGG
17	hCyP57	(26)	MA	VLLETT---L	GDVVIDLYTE	ERPRACLN--	-FLKLCKIKY	-----	-YNYCLIHNV	QRDF-IIQTG	DPTG-TGRGG
18	hCyP54	(29)	IQEPPTNGK	VLLKTT---A	GDIDIELWSK	EAPKACRN--	-FIQLCLEAY	-----	-YDNTIFHRV	VPGF-IVQGG	DPTG-TGSGG
19	hCyP35	(43)	KHDFVFLD	ICIDSS--PI	GRLIFELYCD	VCPKTCEN--	-FQVLC TGA	GFSQ-RGIRL	HYKNSIFHRI	VQNG-WIQGG	DIVYGKGDNG
	80		90	100	110	120	130	140	150	160	
	6789012345	6-----7	8901234567	8901234567	8901234567	8-90123456	7890123456	7890123456	789-0-1234	5678901234	5
1	KSIYGEKFD	E-----N	FILKHTGPGI	LSMANAGPNT	NGSQFFICTA	K-TEWLDGKH	VVFGKVKEGM	NIVEAMERFG	SRN-G-KTSK	KITIADCGQL	E*
2	KSIYGEKFD	E-----N	LIRKHTGSGI	LSMANAGPNT	NGSQFFICAA	K-TEWLDGKH	VAFGKVKERV	NIVEAMEHFG	YRN-S-KTSK	KITIADCGQF	*
3	KSIYGERFPD	E-----N	FKLKHYGPGW	VSMANAGKDT	NGSQFFITTV	K-TAWLDGKH	VVFGKVLEGM	EVVRKVESTK	TDSRD-KPLK	DVIIADCGKI	EVEKPFAlA
4	QSIYGKKFD	E-----N	FILKHTGPGL	LSMANS GPNT	NGSQFFLTCD	K-TDWLDGKH	VVFGEVTEGL	DVLRQIEAOG	SKD-G-KPKQ	KVIIADCGEY	V
5	KSIYGDKFED	E-----N	FDVKHTGPGL	LSMANQGQNT	NNSQFFVITLK	K-AEHLDFKH	VVFGFVKDGM	DTVKKIESFG	SPK-G-SVCR	RITITECGQI	*
6	VSIYGS RFPD	E-----N	F TLKHVGPV	LSMANAGPNT	NGSQFFICTI	K-TDWLDGKH	VVFGHVKEGM	DVVKKIESFG	SKS-G-RTSK	KIVITDCGQL	S
7	ESIYGETFPD	E-----N	FKLKHYGIGW	VSMANAGPDT	NGSQFFITLT	K-PTWLDGKH	VVFGKVIDGM	TVVHSIELQA	TDGHD-RPLT	NCSIINSGKI	DVKTPFVVE
8	ESIYGEKFD	E-----N	FHYKHDREGL	LSMANAGRNT	NGSQFFITTV	P-TPHLDGKH	VVFGQVIKGI	GVARILENVE	VKG-E-KPAK	LCVIAECGEL	KEGDDGGI
9	ESIYGGFFED	E-----S	FAVKHNKEFL	LSMANRGKDT	NGSQFFITTK	P-TPHLDGHH	VVFGQVISGQ	EVVREIENQK	TDAAS-KPFA	EVRILSCGEL	IPKSKVK
10	ASIYGGYFKD	E-----N	FILKHDRAFL	LSMANRGKHT	NGSQFFITTK	P-APHLDG VH	VVFGLVISGF	EVIEQIENLK	TDAAS-RPYA	DVRVIDCGVL	ATKSIKDV
11	ASIYRGP FAD	E-----N	FKLRHSAPGL	LSMANS GPST	NGCQFFITCS	K-CDWLDGKH	VVFGKIIDGL	LVMRKIENVP	TGPNN-KPKL	PVVISQC GEM	
12	NSIYGKQFED	EL-----H	PDLKFTGAGI	LAMANAGPDT	NGSQFFVTLA	P-TQWLDGKH	TIFGRVCQGI	GMVNRVGMVE	TN-SQDRPVD	DVKI IKAYPS	G
13	NSIWGKKFED	EY-----S	EYLKHNVRGV	VSMANN GPNT	NGSQFFITYG	K-QPHLDMKY	TVFGKVIDGL	ETLDELEKLP	VNEKTYRPLN	DVHIKDITIH	ANPFAQ
14	ESIWGKKFED	EY-----S	EYLKHNVRGV	VSMANN GPNT	NGSQFFITYG	K-QPHLDMKY	TVFGKVIDGL	ETLDELEKLP	VNEKTYRPLN	DVHIKDITIH	ANPFAQ
15	ESYWGKPFKD	EF-----R	PNLSHTGRG-	ISMANS GPNS	NRSQFFITFR	S-CAYLDK KH	TIFGRVVGGF	DVLTAMENVE	SDPKTDRPKE	EIRIDATTVF	VDPYEEADA
16	ESIWGGEFED	EF-----H	STLRHDRPYT	LSMANAGSNT	NGSQFFITVV	P-TPWLDNKH	TVFGRVTKGM	EVVQRISNVK	VNPKTDPYE	DVSIINITVK	
17	-SIFGQLYGD	QASFFEA EKV	PRIKHKKGT	VSMVNGSDQ	HGSQFLITTG	ENLDYLDGVH	TVFGEVTEGM	DI IKKINETF	VDK-DFVPYQ	DIRINHTVIL	DDP
18	ESIYGAPFKD	EF-----H	SRLRFNRRGL	VAMANAGSHD	NGSQFFFITLG	R-ADELNNKH	TIFGKVTGDT	VYNMLRLSEV	DID-DDERPH	NPHKIKSCEV	LFN
19	ESIYGPTFED	EN-----F	SVPHNKRGV-	LGMANKGRHS	NGSQFYITLQ	A-TPYLDRKF	VAFGQLIEGT	EVLKQLELVP	TQN-ERPIHM	CRITDSGDPY	A*

Multiple sequence alignment of the human CLDs (MSA19). The MSA was structured into twenty blocks consisting of 10-AA residues. The PDB code is shown in the third column. In parentheses are shown the sequence similarity scores (IDs) (expressed in percentage) between the archetypal hCyPA and the functional AAs were indicated in bold face. PPIL6 (culin) was omitted since it has a very weak sequence similarity with the CLD of hCyPA (ID=13%).