

IV	hsHDAC11	1	:-	HTHTTQNYQHVPSTRWPIVYS	SPRYNTTFMGLS	-----	KHFPDAGKWKVINF	KBEKLLS	-----	DSMLVBARBASED	LLVVH	:	75																	
	aaHDLP	1	:-	-----	KKVKLIGTLY	-GKYRYP	-----	KNHPLKPRVSL	LLRFLDAMNLI	-----	SKELIKSRPAT	KEELLI	FFH	:	60															
I	hsHDAC1	1	:-	MAQTQGT	RRKCYYYD	GVGNYYYGQ	-----	GHPMKPHRIRMT	HNLLNLYGLYR	-----	KMFIYRPHKAN	AEBMT	TKYH	:	68															
	hsHDAC2	1	:-	MAYSQGGG	KKKVCYYYD	GTIGNYYYGQ	-----	GHPMKPHRIRMT	HNLLNLYGLYR	-----	KMFIYRPHKATA	AEBMT	TKYH	:	69															
	hsHDAC3	1	:-	MAKTVA	YFYD	PDVGNFYGA	-----	GHPMKPHRLAL	THSLVLYHYGLYK	-----	KMIVFKPYQAS	QHD	MCRFH	:	62															
	hsHDAC8	1	:-	NEEPEFP	ADSGQSLV	PYYTYS	PFYVSMCDS	-----	LAKTPKRAS	VMVHSLTEAYALHK	-----	QMRTV	KPKVASMEEM	ATFH	:	71														
II	hsHDAC6_D1	70	:	GIQGM	DNLEAEALACT	GLVLD	EQINFHCLWD	-----	DSFP	EGPRLHAJK	QLIQGLLD	-----	RCV	SQARE	AKKEEL	MLVH	:	145												
	hsHDAC6_D2	7	:	PEVLP	PLITW	PVLSRRT	GLVYDONMMNH	CNLWD	-----	SHH	PEVPORTLIR	ICRLEEL	GLAG	-----	RCL	TLTPRP	ATE	ABELL	TCH	:	82									
	hsHDAC10	1	:-	-----	NGTALVY	HEDMTA	TRLLWD	D	-----	EC	ERPRRL	TAAL	DRLR	ORGL	EQ	-----	RCL	RSARE	ASEEEL	GLVH	:	64								
	hsHDAC4	647	:-	PTKPR	FTTGLVY	DTLML	KHQC	TCGSS	-----	SSH	PEHAGRI	QST	WSRL	QBT	GLRG	-----	KCE	CLRGR	KAT	LEEL	QTVH	:	715							
	hsHDAC7	512	:-	PART	PF	TG	LIYDS	VMLKHQ	CSCGN	-----	SRH	PEHAGRI	QST	WSRL	QBT	GLRS	-----	QCE	CLRGR	KAT	LEEL	QTVH	:	581						
	hsHDAC9	628	:-	QPG	SAT	GIAYD	PMLKHQ	CVCNS	-----	TH	PEHAGRI	QST	WSRL	QBT	GLLN	-----	KCE	R	GRKAS	LEEL	QTVH	:	694							
	hsHDAC5	676	:-	PV	KHLETT	GVVYD	FMLKHQ	CMCGNT	-----	HV	PEHAGRI	QST	WSRL	QBT	GLLS	-----	KCE	R	GRKAT	LEEL	QTVH	:	744							
Ila	dmHDAC4	819	:-	KVT	TGLAYD	PMLKH	SCICGN	-----	AQ	PEHAGRI	QST	WSRL	QBT	GLV	-----	RC	DR	LARKAT	Q	LEEL	QTVH	:	883							
	dpHDAC4	741	:-	KITT	TGLAYD	PMLKH	SCICGN	-----	AQ	PEHAGRI	QST	WSRL	QBT	GLV	-----	RC	DR	LARKAT	Q	LEEL	QTVH	:	805							
	ceHDA-4	344	:-	PT	CTTGL	GYDQ	AMVRHE	CCCGNN	-----	ASH	VENG	GRI	QST	WSRL	QBT	GLV	-----	KCE	KV	TAKKAS	LEEL	QTVH	:	409						
	cbHDA-4	478	:-	PT	FSTGL	GYD	P	MARH	CVCNN	-----	SNH	VENG	GRI	QST	WSRL	QBT	GLV	-----	KCE	R	TAKKAS	LEEL	QTVH	:	543					
	ciHDAC4	583	:-	RYT	TGLAYS	PV	M	LKHG	CACRDD	-----	HTE	HAGRI	QST	WSRL	QBT	GLV	-----	RC	DR	LARKAT	Q	LEEL	QTVH	:	656					
	csHDAC4	486	:-	RYT	TGLAYS	PV	M	LKHG	CACRDD	-----	HA	E	HAGRI	QST	WSRL	QBT	GLV	-----	RC	DR	LARKAT	Q	LEEL	QTVH	:	559				
	hrHDAC4	20	:-	RYT	TGLAYS	PV	M	LKHG	CACRDD	-----	HA	B	HAGRI	QST	WSRL	QBT	GLV	-----	K	CEN	DR	LARKAT	Q	LEEL	QTVH	:	82			
II	baFB188	1	:-	MAT	GYV	WNTLY	GWVDT	GTGSL	AAANL	TAR	QPT	SHHL	AHP	DT	KRR	PH	ELV	CA	SG	QTE	-----	H	LTP	AAVA	AT	D	DI	IRAH	:	76

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IV	hsHDAC11	76	:	T	RRYL	NEIK	W	SFAV	ATITE	---	P	PVIF	-----	P	NELV	Q	R	-	K	VLR	P	L	R	T	Q	T	G	T	I	M	A	G	K	L	A	V	E	R	---	G	W	A	I	N	G	-	G	F	H	C	S	S	D	R	G	:	149																																																		
	aaHDLP	61	:	T	E	D	Y	I	N	T	L	M	E	A	R	C	Q	C	P	K	-	G	A	R	E	K	Y	N	I	G	-----	G	Y	N	P	V	S	-	A	M	F	T	G	S	L	A	T	G	S	T	V	A	I	E	E	F	L	K	G	---	N	V	A	F	N	P	N	G	-	G	H	H	A	F	K	S	R	A	:	137																											
I	hsHDAC1	69	:	S	D	D	Y	I	K	F	L	R	S	I	R	P	D	N	M	S	E	Y	S	K	O	M	Q	R	F	N	---	G	E	D	C	P	V	F	-	G	L	F	E	C	Q	L	S	T	G	G	S	V	A	S	A	V	K	N	K	Q	O	T	---	D	I	A	V	N	W	A	G	-	G	L	H	H	A	K	K	S	E	A	:	147																							
	hsHDAC2	70	:	S	D	E	Y	I	K	F	L	R	S	I	R	P	D	N	M	S	E	Y	S	K	O	M	Q	R	F	N	---	G	E	D	C	P	V	F	-	G	L	F	E	C	Q	L	S	T	G	G	S	V	A	G	A	V	K	N	R	Q	O	T	---	D	M	A	V	N	W	A	G	-	G	L	H	H	A	K	K	F	E	A	:	148																							
	hsHDAC3	63	:	S	D	D	Y	I	K	F	L	R	S	I	R	P	D	N	M	S	E	Y	S	K	O	M	Q	R	F	N	---	G	E	D	C	P	V	F	-	G	L	F	E	C	S	R	Y	T	G	A	S	L	O	G	A	T	Q	L	N	N	K	I	C	---	D	I	A	I	N	W	A	G	-	G	L	H	H	A	K	K	F	E	A	:	141																						
	hsHDAC8	72	:	T	D	A	Y	L	Q	H	L	Q	K	V	S	Q	E	G	D	D	H	-	P	O	S	I	E	Y	G	---	G	Y	D	C	P	A	T	E	-	G	I	F	Y	A	A	A	T	G	G	A	T	I	T	A	A	Q	C	L	I	G	M	C	-	K	V	A	I	N	W	S	G	-	G	W	H	A	K	K	D	E	A	:	149																								
II	hsHDAC6_D1	146	:	S	I	E	Y	I	D	L	M	E	T	T	O	Y	M	N	E	G	---	S	L	R	V	L	A	---	---	---	T	Y	D	S	V	L	H	P	N	S	Y	S	C	A	C	L	A	S	G	S	V	L	R	L	V	D	A	V	I	G	A	B	T	---	R	N	G	M	A	I	R	P	P	G	H	A	Q	H	S	L	H	:	222																								
	hsHDAC6_D2	83	:	S	A	E	Y	V	G	H	I	R	A	T	E	K	M	K	T	R	---	S	L	H	R	E	S	---	---	---	N	F	D	S	I	Y	I	C	P	S	T	F	A	C	A	Q	L	A	T	G	A	A	C	R	L	V	E	A	V	L	S	G	E	V	---	L	N	G	A	A	V	V	R	P	P	G	H	A	B	O	D	A	:	159																							
	hsHDAC10	65	:	S	P	H	Y	S	L	V	R	E	T	O	V	L	G	K	E	---	S	Q	A	L	S	G	---	---	---	Q	F	D	A	I	F	H	P	S	T	F	H	C	A	R	L	A	G	A	G	L	O	L	V	D	A	V	L	T	G	A	V	---	O	N	G	L	A	L	M	R	P	P	G	H	G	O	R	A	A	:	141																										
	hsHDAC4	716	:	S	E	A	H	T	L	L	Y	G	T	N	P	L	N	R	O	K	L	D	S	K	K	L	I	G	S	L	---	S	V	F	V	R	L	P	C	G	G	V	G	V	D	---	S	D	T	I	W	N	E	L	H	S	A	G	A	R	L	A	V	G	C	V	V	L	V	F	K	V	A	T	G	E	L	---	K	N	G	F	A	V	V	R	P	P	G	H	A	B	E	S	T	P	:	809									
	hsHDAC7	582	:	S	E	R	H	V	L	L	Y	G	T	N	P	L	N	R	O	K	L	D	S	K	K	L	I	G	S	L	---	Q	R	M	F	V	M	L	P	C	G	G	V	G	V	D	---	T	D	T	I	W	N	E	L	H	S	S	N	A	A	R	W	A	A	G	S	V	T	D	L	A	F	K	V	A	S	R	E	L	---	K	N	G	F	A	V	V	R	P	P	G	H	A	D	H	S	T	A	:	676						
	hsHDAC9	695	:	S	E	H	H	S	L	L	Y	G	T	N	P	L	N	R	O	K	L	D	S	K	K	L	I	G	S	L	---	P	R	I	L	L	G	D	S	Q	K	F	F	S	L	P	C	G	G	L	G	V	D	---	S	D	T	I	W	N	E	L	H	S	S	G	A	R	M	A	V	G	C	V	L	E	L	A	S	K	V	A	S	G	E	L	---	K	N	G	F	A	V	V	R	P	P	G	H	A	B	E	S	T	A	:	789
	hsHDAC5	745	:	S	E	Y	H	T	L	L	Y	G	T	N	P	L	N	R	O	K	L	D	S	K	K	L	I	G	S	L	---	Q	K	M	Y	A	V	L	P	C	G	G	L	G	V	D	---	S	D	T	V	W	N	E	L	H	S	S	A	V	R	M	A	V	G	C	V	L	E	L	A	F	K	V	A	A	G	E	L	---	K	N	G	F	A	I	R	P	P	G	H	A	B	E	S	T	A	:	839								
Ila	dmHDAC4	884	:	T	E	A	H	A	M	L	F	G	S	N	Q	C	L	S	R	P	K	---	L	E	N	T	L	S	A	---	S	F	V	R	L	S	C	G	G	L	G	V	D	---	L	D	T	W	N	E	L	H	T	A	T	A	A	R	M	A	A	G	C	V	I	D	L	A	K	T	A	K	G	D	L	---	R	N	G	F	A	V	V	R	P	P	G	H	A	B	E	A	N	L	A	:	974										
	dpHDAC4	806	:	T	E	A	H	A	M	L	F	G	S	N	Q	C	L	T	R	P	K	---	L	E	T	T	L	A	A	---	S	F	V	R	L	S	C	G	G	L	G	V	D	---	L	D	T	W	N	E	L	H	T	A	T	A	A	R	M	A	A	G	C	V	I	D	L	A	F	K	T	A	K	G	D	L	---	R	N	G	F	A	V	V	R	P	P	G	H	A	B	E	A	N	L	A	:	896									
	ceHDA-4																																																																																																										

		S	CZZ	S		
IV	hsHDAC11	150	:GGFCYADITLAIKFLFER--VEGTSRATITDIDAHQGNHGRDFMDDKRVYIMDVYNRH---YYPG--DRFAKQAIR-----RKVELEWG-----TEDDE	: 233		
	aaHDLP	138	:NGFCYINDPAVGIETYLK--KGFKRLLYIDIDAHHCQGVQAFYTDQVFLSLHQSFE-YAFPFK-KGFLEETGGKKGKYNINIPFK---GLNDNE	: 229		
I	hsHDAC1	148	:SGFCYVNDIVLAIIEELLK---YHORVLYIDIDIHGGDGVBAFYTTDRVMTVSFHKYGE--YFPG--TGDLRDIIAGKGYKYYAVNYPDRD---GIDDES	: 236		
	hsHDAC2	149	:SGFCYVNDIVLAIIEELLK---YHORVLYIDIDIHGGDGVBAFYTTDRVMTVSFHKYGE--YFPG--TGDLRDIIAGKGYKYYAVNYPDRD---GIDDES	: 237		
	hsHDAC3	142	:SGFCYVNDIVLAIIEELLK---YHORVLYIDIDIHGGDGVQAFYTTDRVMTVSFHKYGN-YFPG--TGDMYEVGAEISGRYYCINVPDRD---GIDDES	: 231		
	hsHDAC8	150	:SGFCYINDAVLIGTLRLRR---KFRRLYIDIDIHGGDVEDAFSETSKVMTVSLHKESP-GFFPG--TGDVSDVGLKGRYYSINVPDRD---GIDDES	: 239		
II	hsHDAC6_D1	223	:DGYCFNHVAVAAARYAQQK--HRIIRVLIQVWDVHHGGQTQTFDQDPSVLYFSIHRYSQGRFPHKASNWSSTGFGQGGYTNVVPWNO---VMGRDAD	: 318		
	hsHDAC6_D2	160	:CGFCFFNSVAVAAARHAQTI--SHALRLLIWDVWDVHHGNGTQHMFEDDPSVLYVSLHRYDHGTFFPMGDBGASSQTGRAAGTGFTVNVAVNG---PRMGDAD	: 255		
IIa	hsHDAC10	142	:NGFCFENNVAIAAAHAKOK--HGLHRIILVWDVWDVHHGGQTOYLEDDPSVLYFSWHRYEHRGFWPFRSDADAVGRGQGLGFTVNLVWNO---VMGNAD	: 237		
	hsHDAC4	810	:MGFCYFNSVAVAAKLLQQR--LSVSKLLIWDVWDVHHGNGTQQAIFYSDPSVLYMSLHRYDDGNFFPG--SGAPDEVTGTPGVGFNNMAFTGGGLDPPMGDAE	: 906		
	hsHDAC7	677	:MGFCFFNSVAVACRQLQQQ--SKASKLIIWDVWDVHHGNGTQOTFYQDPSVLYLSLHRHDDGNFFPG--SGAVDEVTGAGSGEGFNVAWAGGLDPPMGDPE	: 773		
	hsHDAC9	790	:MGFCFFNSVAVTAKYLKDC--LNIISKLLIWDVWDVHHGNGTQAIFYSDPSVLYLSLHRYDEGNFFPG--SGAPNEVTGTLGEGYNNIAWTGGGLDPPMGDVE	: 886		
	hsHDAC5	840	:MGFCFFNSVAVTAKLLQQR--LNVGKVLIIWDVWDVHHGNGTQAIFYSDPSVLYLSLHRYDNGNFFPG--SGAPDEVTGGGPGVGYNNVAWAGGLDPPMGDVE	: 936		
	dmHDAC4	975	:MGFCFFNSVAVAAKLLRQR--NPEVRRLLIWDVWDVHHGNGTQAIFYSDPSVLYLSLHRYDDGNFFPG--TGGPTECGSGAGLGFNNISWSGALNPPGLGDAE	: 1072		
	dpHDAC4	897	:MGFCFFNSVAVAAKLLRQR--NPEVRRLLIWDVWDVHHGNGTQAIFYSDPSVLYLSLHRYDDGNFFPG--TGGPTECGSGAGLGFNNISWSGALNPPGLGDAE	: 994		
	ceHDA-4	501	:MGFCFFNSVAVAVKYLQTKYPAQCAKLAIDWDVWDVHHGNGTQAIFYSDPSVLYLSLHRYDDGNFFPG--TGSVTEVTGKNDKGLTNNVPSGD---VMRDEE	: 596		
	cbHDA-4	635	:LGFCFFNSVAVTAKVLAQKYPQCAKLAIDWDVWDVHHGNGTQLSFDDDPNVLYMSLHRYDDGNFFPG--TGSVTEVTGKNDKGLTNNVPSGD---VMRDEE	: 730		
	ciHDAC4	747	:MAFCYFNSVAVAAKLLQRCQDPTVRRVLIWDVWDVHHGNGTQNIFFDDPSVLYLSIHRYSQGRFPHKASNWSSTGFGQGGYTNVVPWNO---VMGRDAD	: 845		
	csHDAC4	652	:MAFCFFNSVAVAAKLLQRCQDPTVRRVLIWDVWDVHHGNGTQNIFFDDPSVLYLSIHRYSQGRFPHKASNWSSTGFGQGGYTNVVPWNO---VMGRDAD	: 750		
	hrHDAC4	174	:MAFCYFNSVAVAAKLLQRCQDPTVRRVLIWDVWDVHHGNGTQNIFFDDPSVLYLSIHRYSQGRFPHKASNWSSTGFGQGGYTNVVPWNO---VMGRDAD	: 273		
	II	baFB188	150	:MGFCFENNTSVAAGYARAY--LGMERVAILIWDVWDVHHGNGTQDLMWNPVSVLTLISLHQLH---CFPP--DSGYSTERGAGNGHGYNNVLP---PGSGNAE	: 240	

		Z	C	Mot b		
IV	hsHDAC11	234	:YLKVERNKKSLOEHLPPVVVYNGTDILRGDR--GGLSISPAGLVQRDEIVFRVYRGR-RVPIILMVTSGGYCKRTARITADSTINFGIGLIGPE---	: 328		
	aaHDLP	230	:FLFALBKSTLIVKVFPEPEYLLQGTDPLEEDY--SKFNLSNVAFLKAFNIVREVFQ---EGVYIGGGGYHPYALARAWTLIWCBSGRVPEKLN	: 323		
I	hsHDAC1	237	:YBAIFKPVMSKVMENFQPSAVVLQCGSDLSGDR--GCFNLTIKGHAKCIVEVKSFN--PMLMIGGGYTIIRNVARCWTYETAVALDTEIPNELPY	: 330		
	hsHDAC2	238	:YQIFKPLISKVMEYQPSAVVLQCGADSLGDR--GCFNLTIVKGHAKCIVEVKTEN--PMLMIGGGYTIIRNVARCWTYETAVALDTEIPNELPY	: 331		
	hsHDAC3	232	:YKHIFQPVNQVDFYQPTCIVLQCGADSLGDR--GCFNLTISIRGHGCEVYKSFN--PMLMIGGGYTIIRNVARCWTYETAVALDTEIPNELPY	: 325		
	hsHDAC8	240	:YYQICBSVLKBYOAFENPKAVVLOGADTLGDEP--CSFNMTPEGLCKLKYLLQWOL---ATLILGGGYNLANTARCWTYLTGVILGKTSSEIPE	: 333		
II	hsHDAC6_D1	319	:YIAAFLHVLIPVALEFPQQLVVAAGFDAIQGDPK--GEMAAIPAGFAQLTHLLMGLAGG---KLTLISLEGGYNLRALAEVSAISLHTLLG-DPCPML--	: 410		
	hsHDAC6_D2	256	:YLAAWHRLVLIPIAYEFNPBLVLSAGFDAARGDP--GGCQVSPFEGYAHLLHLLMGLASG---RIILLILEGGYNLTSISESMAACTRSLIG-DPPPLI--	: 347		
IIa	hsHDAC10	238	:YVAAFLHLLIPLAFEFDPDLVLSAGFDSALGDP--GOMQATPECF AHLTQHLQVLAGG---RVCVILEGGYHLESIAESVCHTIVQTLIG-DPPPEP--	: 329		
	hsHDAC4	907	:YLAAFRTVMPIASEFAPDVLVLSAGFDAVEGHPTPEGGYNSARCFGYLTQQLMGLAGG---RIVLALLEGGHLLTAICDASEACVSAALLGNELDELIP--	: 1001		
	hsHDAC7	774	:YLAAFRTVMPIAREFSPDLVLSAGFDAARGHPPIGGYHVSARCFGYMTQQLMNLAGG---AVVLALLEGGHLLTAICDASEACVAALLGNRVDFLS--	: 868		
	hsHDAC9	887	:YLAAFRTIVKPVAKFDPDMVLSAGFDAIRGHTPPGGYKVTAKCFGHLLTQQLMNLAGG---RVVLALLEGGHLLTAICDASEACVNALLGNELDELIP--	: 981		
	hsHDAC5	937	:YLAAFRTVMPIAREFSPDVLVLSAGFDAVEGHLSPIGGYHVSARCFGHLLTQQLMNLAGG---RVVLALLEGGHLLTAICDASEACVSAALLGNRVDFLS--	: 1031		
	dmHDAC4	1073	:YIAAFRTVMPIAREFNPDLVLSAGFDAATGHPIGGYHVSARCFGFMTRQLMNLANG---KVVLALEGGYDLAAICDASAQECVRAALLGDPAAPIA--	: 1167		
	dpHDAC4	995	:YIAAFRTVMPIAKGFNPDLVLSAGFDAATGHPIGGYHVSARCFGFMTRQLMNLANG---KVVLALEGGYDLAAICDASAQECVRAALLGDPAAPIA--	: 1089		
	ceHDA-4	597	:YLAAWRTVTEPVMASFCDPELIVLSAGFDACHGHNPALGGYEVTPPEFGYMTKSLINYSAG---KVVLALEGGYDLKSTSEAAQOCVQALIGESDDAGR--	: 691		
	cbHDA-4	731	:YLAAWRTVTEPVLASFCDPELIVLSAGFDACHGHNPALGGYEVTPPEFGYMTKCLLSYANG---KVVLALEGGYDLKSTSEAAQOCVQALIGESDDAGR--	: 825		
	ciHDAC4	846	:YLAAFRTIVPIARQFDPHEVLVLSAGFSAANGHPSTLGGYKTPNFCYGLLTLRSLSEVAGG---KIVLLEGGFELEPNCDCTEACVRLTLGNHSESNL--	: 940		
	csHDAC4	751	:YLAAFRSIVLPIARKFNPHFVLVSCGFSAAAGHPSTLGGYNTPNCFGYLTRSLSEVLAGG---KIVLLEGGFELEPNCNCAEACVQTLGKSEYSSL--	: 845		
	hrHDAC4	274	:YLAAFRTVMPIAREFDPDLVLSAGFSAANGHPSTLGGYKTPNFCYGLLTLRSLSEVAGG---RIVMILEGGFELEPNCDCSVEICVRLTLSEDNAAVY--	: 368		
	II	baFB188	241	:YLHAMDQVLPALRAYRPQLLIVGSGFDASMLDPE--ARMNVTAAGFRQMARRTIDCAADICGRIMEVQEGGYSPHYIPFCGLAVIEELTGVRSILPDPYH	: 339	