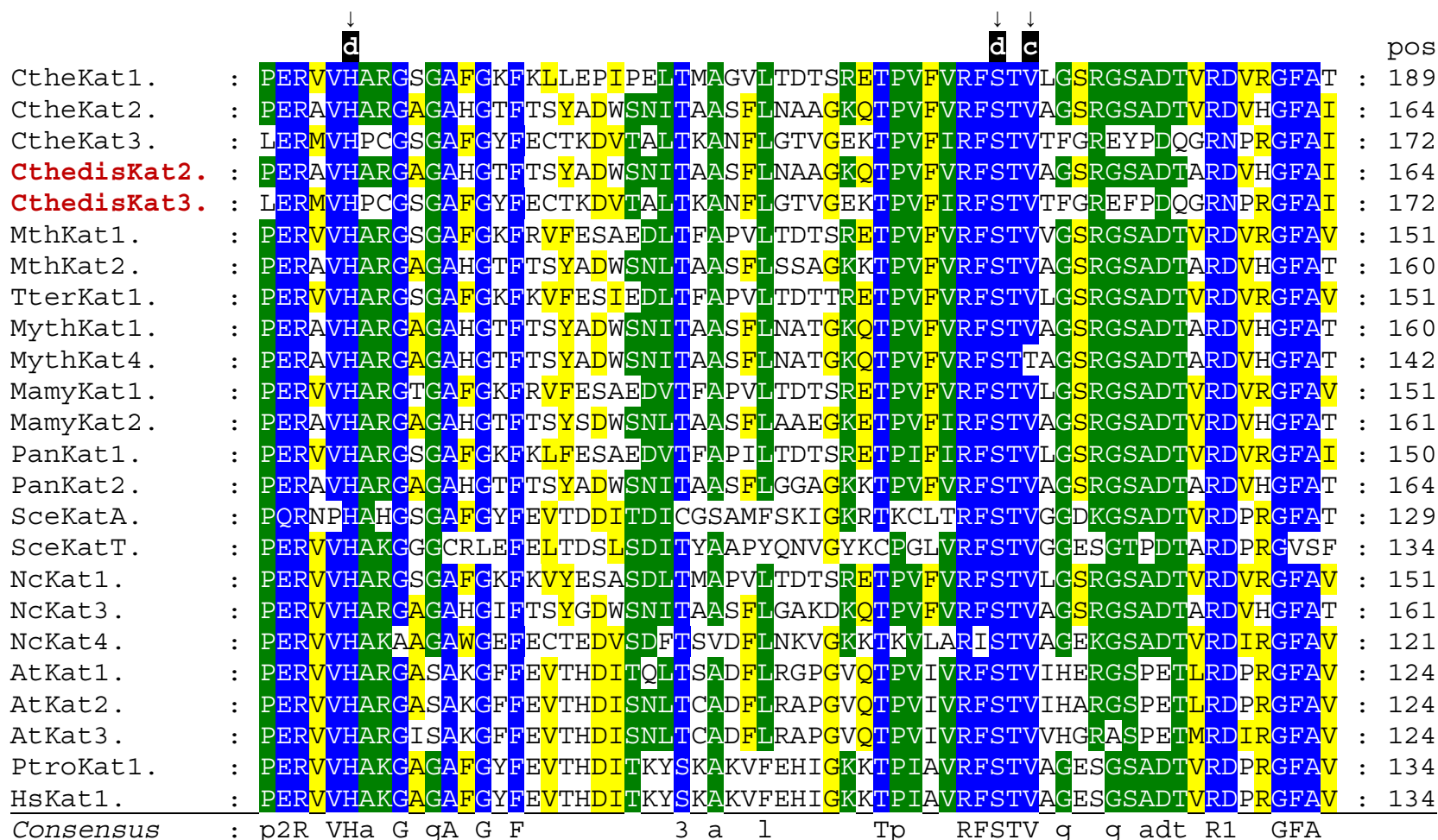


A)



Suppl. Figure 4. Multiple sequence alignment showing conserved essential regions of typical heme catalases obtained with Muscle implemented in MEGA X package [14]. Presented highly conserved regions are A) distal side of heme & B) proximal side of heme. Color scheme: blue - highly conserved positions (above 95% of all aligned sequences), green - moderately conserved (between 75-95%), yellow - weakly conserved positions (between 50-75%). Numbers on the right represent corresponding amino acid position of each sequence.

A) (continued)

		<div>↓ d</div>	<div>↓ cc</div>		pos	
CtheKat1.	:	KFYTK	EGNWD	IVGNNI	PVFFFIQDAIKFPDVIHAGKPEPHNEVPQAQSAHNFW---DFQFNHTE-	: 250
CtheKat2.	:	RFYTDEGNFD	IVGNNI	PVFFFIQDAIRFPDLIHAVKPSPDSEIPQAATAHDSAW---DFFSSQPS-	: 225	
CtheKat3.	:	KFYTLEGNYDI	-----	PIFFCRDPLOGPDVIRSQYRNPRNFLLDW---DACF---	DLLANAPE-	: 224
CthedisKat2.	:	RFYTDEGNFD	IVGNNI	PVFFFIQDAIRFPDLVHAVKPSPDSEIPQAATAHDSAW---DFFSSQPS-	: 225	
CthedisKat3.	:	KFYTLEGNYDIVGL	NFPIFFCRDPLOGPDVIRSQYRNPRNFLLDW---DACF---	DLLANTPE-	: 229	
MthKat1.	:	KFYTDEGNWD	IVGNNI	PVFFFIQDAIKFPDVIHAVKPEPHNEVPQAQTAHNFW---DFEFNHTE-	: 212	
MthKat2.	:	RFYTDEGNFD	IVGNNI	PVFFFIQDAIQFPDLIHAVKPRPDNEIPQAATAHDSAW---DFFSSQPS-	: 221	
TterKat1.	:	KFYTQEGNWD	IIGNDI	PVFFFIQDAIKFPDVIHAGKPEPHNEVPQAQSAHNFW---DFQFNHTE-	: 212	
MythKat1.	:	RFYTDEGNFD	IVGNNI	PVFFFIQDAIQFPDLIHSV KPRPDNEIPQAATAHDSAW---DFFSQQPS-	: 221	
MythKat4.	:	RFYTDEGNFD	IVGNNI	PVFFFIQDAIQFPDLIHSV KPRPDNEIPQAATAHDSAW---DFFSQQPS-	: 203	
MamyKat1.	:	KFYTQEGNWD	IVGNNI	PVFFFIQDAIKFPDVIHAGKPEPHNEVPQAQSAHNFW---DFQYNHSE-	: 212	
MamyKat2.	:	RFYTDEGNFD	IVGNNI	PVFFFIQDAIHFPDLIHAVKPRPDNEIPQAASAHD SAW---DFFSSQPS-	: 222	
PanKat1.	:	KFYTQEGNWD	IVANNI	PVFFFIQDAIKFPDVIHAGKPEPHNEVPQAQTAHNFW---DFQYNHTE-	: 211	
PanKat2.	:	RFYTDEGNFD	IVGNNI	PVFFFIQDAIRFPDLIHSV KPSPDNEVPQAATAHDSAW---DFFSQQPS-	: 225	
SceKatA.	:	KFYTEEGNLDWVYNN	TPVFFFIRDPSKFPHFIHTQKRNPQTNLRDA---DMFW---	DFLT-TPEN	: 186	
SceKatT.	:	KFYTEWGNHDWFVNN	TPVFFFLRDAIKFPVFIHSQKRDPQSHLNQFQDT-TIYW---	DYLTLNPE-	: 194	
NcKat1.	:	KFYTEEGNWD	LVGNNI	PVFFFIQDAIKFPDVIHAGKPEPHNEVPQAQSAHNFW---DFQFNHTE-	: 212	
NcKat3.	:	RFYTDEGNFD	IVGNNI	PVFFFIQDAIRFPDLIHSV KPSPDNEVPQAATAHDSAW---DFFSSQPS-	: 222	
NcKat4.	:	KFFT EGNWDFVGNDL	PVFFFIRD	PVKFPSLNRSHKRHPQTNVPDS---TMFW---	DFHNNNQE-	: 178
AtKat1.	:	KFYTREGNFD	LVGNNF	PVFFFVRDGMKFDPDMVHALKPNPKSHIQE-----NWRILDFFSHHPE-	: 181	
AtKat2.	:	KFYTREGNFD	LVGNNF	PVFFFIRDGMKFDPDIVHALKPNPKSHIQE-----NWRILDFFSHHPE-	: 181	
AtKat3.	:	KFYTREGNFD	LVGNNTPVFFFIRDGIQFPDVVHALKPNRKTNIQE-----YWRILDYMSHLPE-	: 181		
PtroKat1.	:	KFYTEDGNWD	LVGNNTP	PIFFFIRDPILFPSFIHSQKRNPQTHLKDP---DMVW---	DFWSLRPE-	: 191
HsKat1.	:	KFYTEDGNWD	LVGNNTP	PIFFFIRDPILFPSFIHSQKRNPQTHLKDP---DMVW---	DFWSLRPE-	: 191
Consensus	:	4F5T	eGN D 6qn1	P6FF D 6 fPd 6h k P 6 5 D		

Suppl. Figure 4 continued.

B)

[illegible]

Suppl. Figure 4 continued.