

PDGFA_HUMAN	1	MRTLACLLLLGCGYLAHVLAEEAEIPREVIERLARSQIHSIRDLQRLLLEI	50
		. . . :	
BAA00987.1	1	MRTWACLLLLGCGYLAHALAEEAEIPRELIERLARSQIHSIRDLQRLLLEI	50
PDGFA_HUMAN	51	DSVGSEDSLDTSLRAHGVHATKHVPEKRPLPIRRKRSIEEAVPAVCKTRT	100
		: : : : . . : :..:.. .:.:..	
BAA00987.1	51	DSVGAEDALETNLRAHGSHTVKHVPEKRVPPIRRREVLKPFQFARPGR	100
PDGFA_HUMAN	101	VIYEIPRSQVDPTSANFLIWPPCVEVKRCTGCCNTSSVKCQPSRVHHRVS	150
	:..	
BAA00987.1	101	SFTRYLGARWTPTSANFLIWPPCVEVKRCTGCCNTSSVKCQPSRVHHRVS	150
PDGFA_HUMAN	151	KVAKVEYVRKKPKLKEVQVRLEEHLACACATTSLNPDYREEDT	193
		: : : : :	
BAA00987.1	151	KVAKVEYVRKKPKLKEVQVRLEEHLACACATSNLNPDHREEET	193