

PVX_080100	MEGEKIKSNSISNFSVTYERESGANSNSDDKSVSSSENESENSFMNLTSDKNEKTENNSFILNNSFANMKDSLLESIDLVLDSNFDKDFLPS	95
KEAP1_Human	MQP-----DPRPSGA-----GACCRFLPLQSQCPPEGAGDA-----VMYASTECKAEVTPS	45
PVX_080100	NLS-----KNFNNL-----SKENLGNKYLNKLLNKSDSMFMSKGMNLMENNLSNNLPVKSSNKKEGFMDSST---PINAN	165
KEAP1_Human	QHGNRTFSYTTLEDHTKQAFGI MNELRLSQQLCDVTLQVKYQD----APAAQFMAHKVVL-----ASSSPVKAMFTNGLREQGMEVVSIEGI	128
PVX_080100	EDNAMNNLKKYSNANNINDTYEKKI IETELSDSSDFENMVGLRITFINWLKKTQMNFI REKDKLFDKKELEMERIRLYKEIENRKSIEEQKLH	260
KEAP1_Human	HPKVMERLIEFAYTASIS-----MGEKCVLHVMNGAVMYQ-IDSVVRACSDFLVQQL---DPSNAIG---IANFA-----EQIGCVLH	201
PVX_080100	DERKKLDIDISNGYKQIKKEKEEHRKRFDEERLRFLEIDKIKLVLYLEKEYF--QEYKNFENDKKKI-----VDANIATEMTIDINVGGA	345
KEAP1_Human	QRAREY---IYMHFGEVAKQ---EEFFNLSHCQLVTLISRDDLNVRCSEVFHACINWVKYDCQRRFYVQALLRAVRC HSLTPNFLQMQLKQC	289
PVX_080100	-IFETSRHTLTQQKDSFIEKLLS-----G---RYHVTRDKQGRIFLDRDSELFRILNFLRNPLTVPIPKD-LSESEALLKEAEFYGIKFLPFFL	430
KEAP1_Human	EILQSDS-----RCKDYLVKIFEELTLHKPTQVMPCRAPKVGRLIYT-AGGYFRQSLSYLEAYN--PSDGTWLRLADLQVPRSLAG--CVVGGL	374
PVX_080100	VFCMGGFD----GVEYLNSMELLDISQQCWRMCTPMSTKKAYFGSAVLNINFLYVFGNNYDYKALFETEYDRLRDTWVSSNLNIPRRNNGVT	521
KEAP1_Human	LYAVGGRNNSPDGNTDSSALDCYNPMTNQWSPCAPMSVPRNRIGVGVIDGHIYAVGGSHGCI-HHNSVERYEPERDEWHLVAPMLTRRIGVAV	468
PVX_080100	SNGRIYCIIGGYDGSSII PNVEAYDHRMKAWVEIAPLNTPRSSMCVAFDNKIYVIGGTNGE-RLNSIEVYDEKMNKWEQFPYALLEARSSGAAFN	616
KEAP1_Human	LNRLLYAVGGFDGTNRLNSAECYYPERNWRMITAMNTIRSGAGVCVLHNCIYAAGGYDGDQLNSVERYDVETETWTFVAPMK-HRRSALGITV	562
PVX_080100	YLNQIYVVGIDNEHNILDSVEQYQPFNKRWQFLNGVPEKKMNFGAATLSDSYIITGGENDVLNSCHFFSPDTNEWQIGPSLLVPRFGHSLVLIANI	712
KEAP1_Human	HQGRIYVLGGYD-GHTFLDSVECYDPDPTDWSEVTRMTSGRSGVGVAVTMEPCRKQI-----DQQNCTC-----	624