

HTA13 -----MAGR--GKT-----LGS GVA-----KKSTSRSSKAGLQFPVGRiARfL
HTA10 -----MAGR--GKT-----LGS GSA-----KKATrRSSKAGLQFPVGRiARfL
HTA1 -----MAGR--GKT-----LGS GGA-----KKATSRSSKAGLQFPVGRiARfL
HTA2 -----MAGR--GKQ-----LGS GAA-----KKSTSRSSKAGLQFPVGRiARfL
HTA709 -----MAGR--GKA-----IGAGAA-----KKATSRSSKAGLQFPVGRiARfL
HTA703 -----MAGR--GKA-----IGAGAA-----KKATSRSSKAGLQFPVGRiARfL
HTA708 -----MAGR--GKA-----IGS GAA-----KKAMSRSSKAGLQFPVGRiARfL
HTA702 -----MAGR--GKA-----IGSSAA-----KKATSRSSKAGLQFPVGRiARfL
HTA711 -----MSSA--GGG----GGRGKSKG-----SKSVSRSSKAGLQFPVGRiARyL
HTA704 -----MSSS--QGG----GGRGKAkt-----TKAVSRSSKAGLQFPVGRiARyL
HTA5 -----MSTG--AGSGTTKGGRGKPKA-----TKSVSRSSKAGLQFPVGRiARfL
HTA3 -----MSSG--AGSGTTKGGRGKPKA-----TKSVSRSSKAGLQFPVGRiARfL
Hsh2A.X -----MSGR--GKT-----GGKAR-----AKAKSRSSRAGLQFPVGRVHRLL
HTA710 MDAAGAGAGGK--LKKGAAGRKAAG-PR-----KKA VSRSVKAGLQFPVGRiGRyL
HTA701 MDAAGAGAGGK--LKKGAAGRKAAG-PR-----KKA VSRSVKAGLQFPVGRiGRyL
HTA706 ---MEVGAKVP--KKAGAGRRGGGGPK-----KKPVSRSVKAGLQFPVGRiGRyL
HTA12 -----MDSGtK--VKKGAAGRRSGGGPK-----KKPVSRSVKAGLQFPVGRiGRyL
HTA707 ---MDVGVGGK--AAKKAVGRKLGG-PK-----KKPVSRSVKAGLQFPVGRiGRyL
HTA6 -----MESTGK--VKKAFGGRKPPGAPK-----TKSVSKSMKAGLQFPVGRiTRfL
HTA7 ---MESSQATTK--PTRGAGGRKGGD--R-----KKS VSKSVKAGLQFPVGRiARyL
HTA713 -----MAGK--GGKGLLAAKTtAAKS-AEKDKGKK-APVSRSSRAGLQFPVGRiHRQL
HTA712 -----MAGK--GGKGLLAAKTtAAKS-ADKDKDKK KAPVSRSSRAGLQFPVGRiHRQL
HTA705 -----MAGK--GGKGLLAAKTtAAKAAADKDKDRK KAPVSRSSRAGI QFPVGRiHRQL
HTA8 -----MAGK--GGKGLLAAKTtAAAA--NKDSVKK-KSISRSSRAGI QFPVGRiHRQL
HTA11 -----MAGK--GGKGLVAAKTMAANK--DKDKDKK-KPISR SARAGI QFPVGRiHRQL
HTA9 -----MSGK--GAKGLIMGKPSGS----DKDKDKK-KPITRSSRAGLQFPVGRVHRLL
Hsh2A.Z -----MAGGK--AGKDSGKAkt-----KAVSRsORAGLQFPVGRiHRHL
DmH2Av -----MFPVGRiHRHL
HTA4 -----MVCNT--NILKDVSTKISAFEN-----VRMIMVEGEMFQVARiHKQL
ScHt z1 -----MSGKAHGGK GKSGAKDSGSLR-----SQSS SARAGLQFPVGRiKRYL
consensus -----magr--g--g--k-gag-----kk-vsrsskaglgfpvgriarfL
1.....10.....20.....30.....40.....50.....

HTA13 KNGKYAT-RVGAGAPVYLAAVLEYLAAEVLELAGNAARDNKKTRIVPRHIQLAVRNDEEL
HTA10 KKGKYAE-RVGAGAPVYLAAVLEYLAAEVLELAGNAARDNKKTRIVPRHIQLAVRNDEEL
HTA1 KAGKYAE-RVGAGAPVYLAAVLEYLAAEVLELAGNAARDNKKTRIVPRHIQLAVRNDEEL
HTA2 KAGKYAE-RVGAGAPVYLAAVLEYLAAEVLELAGNAARDNKKTRIVPRHIQLAVRNDEEL
HTA709 KAGKYAE-RVGAGAPVYLAAVLEYLAAEVLELAGNAARDNKKTRIVPRHIQLAVRNDEEL
HTA703 KAGKYAE-RVGAGAPVYLAAVLEYLAAEVLELAGNAARDNKKTRIVPRHIQLAVRNDEEL
HTA708 KAGKYAE-RVGAGAPVYLAAVLEYLAAEVLELAGNAARDNKKTRIVPRHIQLAVRNDEEL
HTA702 KAGKYAE-RVGAGAPVYLAAVLEYLAAEVLELAGNAARDNKKTRIVPRHIQLAVRNDEEL
HTA711 KAGKYAE-RVGAGAPVYLSAVLEYLAAEVLELAGNAARDNKKNRIVPRHIQLAVRNDEEL
HTA704 KAGKYAE-RVGAGAPVYLSAVLEYLAAEVLELAGNAARDNKKNRIVPRHIQLAVRNDEEL
HTA5 KSGKYAE-RVGAGAPVYLSAVLEYLAAEVLELAGNAARDNKKTRIVPRHIQLAVRNDEEL
HTA3 KAGKYAE-RVGAGAPVYLSAVLEYLAAEVLELAGNAARDNKKTRIVPRHIQLAVRNDEEL
Hsh2A.X RKGHYAE-RVGAGAPVYLAAVLEYLtAEIleLAGNAARDNKKTRIIPRHQLAIRNDEEL
HTA710 KKGRYAQ-RIGTGAPVYLAAVLEYLAAEVLELAGNAARDNKKNRIIIPRHVLLAIRNDEEL
HTA701 KKGRYAQ-RIGTGAPVYLAAVLEYLAAEVLELAGNAARDNKKNRIIIPRHVLLAIRNDEEL
HTA706 KQGRYSQ-RIGTGAPVYLAAVLEYLAAEVLELAGNAARDNKKNRIIIPRHVLLAIRNDEEL
HTA12 KKGRYASK-RVGTGAPVYLAAVLEYLAAEVLELAGNAARDNKKNRIIIPRHVLLAIRNDEEL
HTA707 KKGRYAQ-RVGTGAPVYLAAVLEYLAAEVLELAGNAARDNKKNRIIIPRHVLLAIRNDEEL
HTA6 KKGRYAQ-RLGGGAPVYMAAVLEYLAAEVLELAGNAARDNKKSRIIIPRHLLAIRNDEEL
HTA7 KKGRYAL-RYGS GAPVYLAAVLEYLAAEVLELAGNAARDNKKNRINPRHLCLAIRNDEEL
HTA713 KQRTQANGRVGATAAVYSAAIleYLTAEVLELAGNASKDLKVKRITPRHLQLAIRGDEEL
HTA712 KSRSAHGRVgATAAVYSAAIleYLTAEVLELAGNASKDLKVKRITPRHLQLAIRGDEEL
HTA705 KGRVSAHGRVgATAAVYtAAIleYLTAEVLELAGNASKDLKVKRITPRHLQLAIRGDEEL
HTA8 KQRVSAHGRVgATAAVYtASAIleYLTAEVLELAGNASKDLKVKRITPRHLQLAIRGDEEL
HTA11 KTRVSAHGRVgATAAVYtASAIleYLTAEVLELAGNASKDLKVKRITPRHLQLAIRGDEEL
HTA9 KTRStAHGRVgATAAVYtAAIleYLTAEVLELAGNASKDLKVKRISPRHLQLAIRGDEEL
Hsh2A.Z KSRTTSHGRVgATAAVYSAAIleYLTAEVLELAGNASKDLKVKRITPRHLQLAIRGDEEL
DmH2Av KSRTTSHGRVgATAAVYSAAIleYLTAEVLELAGNASKDLKVKRITPRHLQLAIRGDEEL
HTA4 KNRVtSAHSSVgAtDVVYmTASAIleYLTAEVLELAGNASKDLKVKRITPRHLQLAIRGDEEL
ScHt z1 KRHATGRTRVGSKAIIYLTAVLEYLtAEVLELAGNAAKDLKVKRITPRHLQLAIRGDEEL
consensus k-gkya--rvGagapVYlaavLEYLaaEvLeLagNaarDnKk-RivPRHIqLAIrNDeEL
61.....70.....80.....90.....100.....110.....

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HTA13 SKLLGDVTIANGGVMPNIHSLLLPKKA-----GASKP-----SADED-----
HTA10 SKLLGDVTIANGGVMPNIHNLLLPKKT-----GASKP-----SAEDD-----
HTA1 SKLLGDVTIANGGVMPNIHNLLLPKKA-----GASKP-----QED-----
HTA2 SKLLGDVTIANGGVMPNIHNLLLPKKA-----GSSKP-----TEED-----
HTA709 TKLLGGATIASGGVMPNIHQHLLPKKA-----GSSKA-----STVDDDDN-----
HTA703 TKLLGGATIASGGVMPNIHQHLLPKKA-----GSSKA-----SHADDDDN-----
HTA708 SRLLGTVTIASGGVMPNIHNLLLPKKA-----GSSAK-----AAAGDDDN-----
HTA702 SRLLGAVTIANGGVMPNIHNLLLPKKA-----GSSAK-----AAAADDE-----
HTA711 SRLLGAVTIAAGGVLPHIHQTLLPKKG-----GDKA-----DIGSASQEF-----
HTA704 SRLLGTVTIAAGGVLPHIQVLLPKKG-----G-GKG-----DIGSASQEF-----
HTA5 SKLLGSVTIANGGVLPNIHQTLPSKV-----GKNKG-----DIGSASQEF-----
HTA3 SKLLGSVTIANGGVLPNIHQTLPSKV-----GKNKG-----DIGSASQEF-----
Hsh2A.X NKLLGGVTIAQGGVLPNIQAVLLPKKT-----SATVGPKAPSGGKKATQASQEY-----
HTA710 GKLLAGVTIAHGGVLPNINPVLPPKKT---AEKAAAAGKEAKSPKKAAGKSPKKA-----
HTA701 GKLLAGVTIAHGGVLPNINPVLPPKKT---AEKAAAAGKEAKSPKKAAGKSPKKA-----
HTA706 GKLLAGVTIAHGGVLPNINPVLPPKKTGSAAAKEAKEGKTPKSPKKATTKSPKKA AAAA--
HTA12 GTLLKGV TIAHGGVLPNINPILLPKKS----EKA AASTTKTPKSPSKAT-KSPKKS----
HTA707 GKLLAGVTIAHGGVLPNINPVLPPKKT-----AEKADKPAKASKDKAAKSPKKQARS--
HTA6 GKLLSGVTIAHGGVLPNINSVLLPKKS----ATKPAEEKATKSP----VKSPKKA-----
HTA7 GRLLHGV TIASGGVLPNINPVLPPKKS-----TASSSQAEKAS---ATKSPKKA-----
HTA713 DTLLIKG-TIAGGVIPHIHKSLINKSS-----KERKKAVTRSVKAGLQLPVSRIGRYLK
HTA712 DTLLIKG-TIAGGVIPHIHKSLINKTS-----KE-----
HTA705 DTLLIKG-TIAGGVIPHIHKSLINKTA-----KE-----
HTA8 DTLLIKG-TIAGGVIPHIHKSLVNKVT-----KD-----
HTA11 DTLLIKG-TIAGGVIPHIHKSLINKTT-----KE-----
HTA9 DTLLIKG-TIAGGVIPHIHKSLINKSA-----KE-----
Hsh2A.Z DSLIKA-TIAGGVIPHIHKSLIGKKG-----QQK-TV-----
DmH2Av DSLIKA-TIAGGVIPHIHKSLIGKKE-----ETVQDPQRKGNVILSQAY-----
HTA4 DTLLIKG-TIIGGSVIPHIH-----
ScHtz1 DSLIRA-TIASGGVLPHINKALLKVE-----KKGSKK-----
consensus -kLlggvTia-GgVmPnIh-l1lpkk-----g-----

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