

PpHac1 1 -----M
ScHac1 1 -----M
YlHac1 1 -----MSIKREESFTPTPEDLGSPITAD-----
AnHacA 1 MKSADRFSPVKMEDAFANSLPTTESLEVPIITVSPADTSLQTKNVVAQT-----
TrHac1 1 MAFQQSSPLVKFEASPAESFLSAPGDNFTSLFADSTPSTLNPRDMMTPDSVADIDSRLSVIPESQDAEDDESHSTSATAP

PpHac1 1 ----MFPVDSS-----HKTASPLPPRKRKRAKEEKEQRRVERILNRNRAAHASREKKRRHVEFLENVVDLESALQES
ScHac1 2 EMTDFELTSNSQSINLAIPTNFKSTLPPRKRRAKTEEKEQRRIERILNRNRAAHOSREKKRRLHIOYLERKCS-----
YlHac1 24 -SPGSPESGDKRKKDLTLPLPAGALPPRKRRAKTEEKEQRRIERILNRNRAAHASREKKRRHLEDLEKKCS-----EI
AnHacA 50 KPEEKKPAKKRKSWSGQELPVPKINLPPRKRRAKTEDEKEQRRIERILNRNRAAAQTSRERKRRLMEKLESEK-----IDM
TrHac1 81 STSEKKPVKKRKSWSGQVLPKPINLPPRKRRAKTEDEKEQRRVERILNRNRAAQSSRERKRRLVEALEKRNKELETLLIN

PpHac1 69 AKATNKLKEIQDITVSRLEALGG---TVSDLDLTVPEVDFPKSSDLEPMSD-----LSTSSKSEKAS
ScHac1 73 LLENLLNSVNLEKLADHEDALIT-----CSHDAFVASLDEYRDFQSTRG-----ASLDTRAS
YlHac1 96 SSENNDLHHQVITESKKTNMHLM-----EQHYSLVAKLQQLSSLVNMMAK-----SSGALAGVDV
AnHacA 123 EQNQFLLQRLAQMEAENNRLS-----QQVAQLSAEVRGSRHSTPTSS-----SPASVSPILT
TrHac1 161 QKTNLIIVEELNRFRRSSGVVTRSSSPLDSLQDSITLSQQLFGSRDQGTMSNPEQSLMDQIMRSAANPTVNFASLSPSLP

PpHac1 128 TSTRRSLTEDLDEDDVAEYDEEDEELPRKMKVLNDKNKSTSKQEKLNELPSPLSSDFS-----DVDE
ScHac1 124 -----SHSSSDTFTPSPLNCTMEPATLSPKSMR-----DS
YlHac1 149 P-----DMSIVSMAPKLEMPAAPSQPMGLASAPTLFNEDNETVVPDSP-----IVKT
AnHacA 176 PTLFK-----QEGDEVPLDRIPFPTPSVTDYSPTLKPSLSAESPLDTQHPAVSVG-----GLEG
TrHac1 241 PISDKFEFQTKEEDEEQADEEMEQTWHETKEAAAAKEKNSKQSRVSTDSTORPAVSI GGDAAPVVSDDAGANCLGLD

PpHac1 193 EKSTLTHLKLQQQQQQPVDNYVSTPLSLPEDSVDFIN-----PGNLKIESDENFLLSSNTLQIKHEN
ScHac1 154 ASDQETSABLQMFKTENVPESTLPAVDNNNLFDAVA-----SPLADPLCDDIAG-----NSLPFDN
YlHac1 197 BEVDSTNELLHTESSPPELAESTGSGSPSSTLSCDE-----TDVLVDRARHPAASAODFEIK
AnHacA 230 ESALTLLEDLGASIKHEPHTDLTAPLSDDDFRRLFNG-----DSSLES-----SSLEDGLAFDVLDD--SGDLSAFFFDS
TrHac1 321 VHQDDGPTSTIGHSGFLSAAALDADRYLLESQQLASPNASTVDDDYLAGDSAACFTNPLPSDVFDFINDFLTDDANHAAYDI

PpHac1 255 DTDYITTAPSGSINDFFNYSYDISESNRLHHPAAPFTANAFDINDFVFFQE--
ScHac1 211 SIDLDNWRNP-----EAQSGNLNFEINDFFITS--
YlHac1 256 DEPVDDDELGLHGLSDFTLFDNKQPAQHDFIADLAHYESSVSNLFGGLE--
AnHacA 299 MVDFTDEPTVLTLEDLQTNGLSDSASCKAASLQPSHGASTSRCDGQGTAAAGSA
TrHac1 401 VAASNYYAAADRELDEIHDPENQIPSRHSIQQPQSGASSHGCDGGTAVGV-