```
CLUSTAL O(1.2.4) multiple sequence alignment


sp|Q9BY41|HDAC8_HUMAN    ------------------------------------------------------------ 0
sp|O15379|HDAC3_HUMAN    ------------------------------------------------------------ 0
sp|Q92769|HDAC2_HUMAN    ------------------------------------------------------------ 0
sp|Q13547|HDAC1_HUMAN    ------------------------------------------------------------ 0
sp|Q9UBN7|HDAC6_HUMAN    ------------------------------------------------------------ 0
sp|Q8WUI4|HDAC7_HUMAN    ---------------------------------------------------------MDLR 4
sp|Q9UKV0|HDAC9_HUMAN    ----------------------MHSMISSVDVKSEVPVGLEP---------ISPLDLR 27
sp|Q9UQL6|HDAC5_HUMAN    MNSPNESDGMSGREPSLEILPRTSLHSIPVTVEVKPVLPRAMPSSMGGGGGGSPSPVELR 60
sp|P56524|HDAC4_HUMAN    MSSQSHPDGLSGRDQPVELLNPARVNHMPSTVDVATALPLQVAPS--------AVPMDLR 52


sp|Q9BY41|HDAC8_HUMAN    ------------------------------------------------------------ 0
sp|O15379|HDAC3_HUMAN    ------------------------------------------------------------ 0
sp|Q92769|HDAC2_HUMAN    ------------------------------------------------------------ 0
sp|Q13547|HDAC1_HUMAN    ------------------------------------------------------------ 0
sp|Q9UBN7|HDAC6_HUMAN    ------------------------------------------------------------ 0
sp|Q8WUI4|HDAC7_HUMAN    VGQRP---PV-----EPPPEPTLLALQRPQRLHHHLFLAGLQQQRSVE------------ 44
sp|Q9UKV0|HDAC9_HUMAN    TDLRMMMPVVDPVVREKQLQQELLLIQQQQQIQKQLLIAEFQKQHENLTRQHQAQLQEHI 87
sp|Q9UQL6|HDAC5_HUMAN    ---GALVGSVDPTLREQQLQQELLALKQQQQLQKQLLFAEFQKQHDHLTRQHEVQLQKHL 117
sp|P56524|HDAC4_HUMAN    LDHQFSLPVAEPALREQQLQQELLALKQKQQIQRQILIAEFQRQHEQLSRQHEAQLHEHI 112


sp|Q9BY41|HDAC8_HUMAN    ------------------------------------------------------------ 0
sp|O15379|HDAC3_HUMAN    ------------------------------------------------------------ 0
sp|Q92769|HDAC2_HUMAN    ------------------------------------------------------------ 0
sp|Q13547|HDAC1_HUMAN    ------------------------------------------------------------ 0
sp|Q9UBN7|HDAC6_HUMAN    --------------MTSTGQ--------------DSTTTRQRRSR--------------- 17
sp|Q8WUI4|HDAC7_HUMAN    -----------------P--------MRLSMDTPMPELQVGPQEQELRQLLHKDKSRSA 79
sp|Q9UKV0|HDAC9_HUMAN    K---ELLAIKQQQELLEKEQKLEQQ-------RQEQEVERHRREQQLPPLRGKDRGRERA 137
sp|Q9UQL6|HDAC5_HUMAN    KQQQEMLAAKQQQEMLAAKRQQELEQQRQREQQRQEELEKQRLEQQLLILRNKEKSKESA 177
sp|P56524|HDAC4_HUMAN    KQQQEMLAMKHQQELLEHQRKLERH-------RQEQELEKQHREQKLQQLKNKEKGKESA 165


sp|Q9BY41|HDAC8_HUMAN    ------------------------------------------------------------ 0
sp|O15379|HDAC3_HUMAN    ------------------------------------------------------------ 0
sp|Q92769|HDAC2_HUMAN    ------------------------------------------------------------ 0
sp|Q13547|HDAC1_HUMAN    ------------------------------------------------------------ 0
sp|Q9UBN7|HDAC6_HUMAN    --------------------------------------------QNPQSPPQDSS-- 28
sp|Q8WUI4|HDAC7_HUMAN    VASSVVKQKLAEVILKKQQAALERT--V---HPNSPGIPYRTLEP--LETEG----ATRS 128
sp|Q9UKV0|HDAC9_HUMAN    VASTEVKQKLQEFLLSKSATKDTPTNGKNHSVSRHPKLWYTAAHHTSLDQSSPPLSG--- 194
sp|Q9UQL6|HDAC5_HUMAN    IASTEVKLRLQEFLLSKSK--EPTPGGLNHSLPQHPKCWGA--HHASLDQSSPPQSGPPG 233
sp|P56524|HDAC4_HUMAN    VASTEVKMKLQEFVLNKKK--ALAHRNLNHCISSDPRYWYGKTQHSSLDQSSPPQSG--- 220


sp|Q9BY41|HDAC8_HUMAN    ------------------------------------------------------------ 0
sp|O15379|HDAC3_HUMAN    ------------------------------------------------------------ 0
sp|Q92769|HDAC2_HUMAN    ------------------------------------------------------------ 0
sp|Q13547|HDAC1_HUMAN    ------------------------------------------------------------ 0
sp|Q9UBN7|HDAC6_HUMAN    --V--------------------TSKRNI------KKG-AVPRSIPNLAEVKKKGK-M 56
sp|Q8WUI4|HDAC7_HUMAN    MLSSFLPPVPSLPSDPPEHFPLRKTVSEPNLKLRYKPKKS-LERRKNPLLRK--ESAP-- 183
sp|Q9UKV0|HDAC9_HUMAN    TSPSYKYTLP-GAQDAKDDFPLRKTASEPNLKVRSRLKQKVAERRSSPLLRR--KDGNVV 251
sp|Q9UQL6|HDAC5_HUMAN    TPPSYKLPLP-GPYDSRDDFPLRKTASEPNLKVRSRLKQKVAERRSSPLLRR--KDGTVI 290
sp|P56524|HDAC4_HUMAN    VSTSYNHPVL-GMYDAKDDFPLRKTASEPNLKLRSRLKQKVAERRSSPLLRR--KDGPVV 277


sp|Q9BY41|HDAC8_HUMAN    ------------------------------------------------------------ 0
sp|O15379|HDAC3_HUMAN    ------------------------------------------------------------ 0
sp|Q92769|HDAC2_HUMAN    ------------------------------------------------------------ 0
sp|Q13547|HDAC1_HUMAN    ------------------------------------------------------------ 0
sp|Q9UBN7|HDAC6_HUMAN    KKLGQAMEEDLI-----------------------------VGLQGMDLN-LEAEALAG 85
sp|Q8WUI4|HDAC7_HUMAN    PSLRRRPAETLGDS---SPSSSSTPASGCSSPNDSEHGP----------NPILGSEALLG 230
sp|Q9UKV0|HDAC9_HUMAN    TSFKKRMFEVTE-----SSVSSSSPGSGPSSPNNGPTGSVTENETSVLPPTPHAEQMVSQ 306
sp|Q9UQL6|HDAC5_HUMAN    STFKKRAVEITGAGPGASSVCNSAPGSGPSSPNSSH-STIAENGFTGSVPNI-PTEMLPQ 348
sp|P56524|HDAC4_HUMAN    TALKKRPLDVT------DSACSSAPGSGPSSPNNSSGSVSAENGIAPAVPSI-PAETSLA 330
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sp|Q9BY41|HDAC8_HUMAN   ------------------------------------------------------------   0
sp|O15379|HDAC3_HUMAN   ------------------------------------------------------------   0
sp|Q92769|HDAC2_HUMAN   ------------------------------------------------------------   0
sp|Q13547|HDAC1_HUMAN   ------------------------------------------------------------   0
sp|Q9UBN7|HDAC6_HUMAN   TGLV-LDEQLNEFHCLWDDSFPEGPERLHAIKEQLIQEGLLDRCVSFQARFAEKEELMLV 144
sp|Q8WUI4|HDAC7_HUMAN   QRLRLQETSVAPFALPTVSLLPAITLGLPAPARADS----------------------- 266
sp|Q9UKV0|HDAC9_HUMAN   QRILIHEDSMNLLSLYTSPSLPNITLGLPAVPSQLNA----------SNSLKEKQ----- 351
sp|Q9UQL6|HDAC5_HUMAN   HRALPLDSSPNQFSLYTSPSLPNISLGLQATVTVTNS------HLTASPKLSTQQEA--- 399
sp|P56524|HDAC4_HUMAN   HRLVAREGSAAPLPLYTSPSLPNITLGLPATGPSAGT--------------AGQQDA--- 373


sp|Q9BY41|HDAC8_HUMAN   ------------------------------------------------------------   0
sp|O15379|HDAC3_HUMAN   ------------------------------------------------------------   0
sp|Q92769|HDAC2_HUMAN   ------------------------------------------------------------   0
sp|Q13547|HDAC1_HUMAN   ------------------------------------------------------------   0
sp|Q9UBN7|HDAC6_HUMAN   HSLEYIDLMETTQYMNEGELRVLADTYDSVYLHPNSYSCACLASGSVLRLVDAVLGAEIR 204
sp|Q8WUI4|HDAC7_HUMAN   ---DRR----THPTLGPR--GPILGSP----H-----TPLFLP-HGLEPEA-GGTLPSRL 306
sp|Q9UKV0|HDAC9_HUMAN   ----KC----ETQTLRQG--VPLPGQYGGSIP-----ASSSHPHVTLEGKPPNSSHQALL 396
sp|Q9UQL6|HDAC5_HUMAN   ---ERQ----ALQSLRQG--GTLTGKFMSTSS-----IPGCLLGVALEGDGSPHGHASLL 445
sp|P56524|HDAC4_HUMAN   ---ERL----TLPALQQR--LSLF----PGTH-----LTPYLSTSPLERDG-GAAHSPLL 414


sp|Q9BY41|HDAC8_HUMAN   ------------------------------------------------------------   0
sp|O15379|HDAC3_HUMAN   ------------------------------------------------------------   0
sp|Q92769|HDAC2_HUMAN   ------------------------------------------------------------   0
sp|Q13547|HDAC1_HUMAN   ------------------------------------------------------------   0
sp|Q9UBN7|HDAC6_HUMAN   NGMAIIRPPGHHAQHSLMDGYCMFNHVAVAARYAQQKHRIRRVLIVDWDVHHGQGTQFTF 264
sp|Q8WUI4|HDAC7_HUMAN   QPILLLDPSGSHAPLLTVPGLGPL------------------------PFHFAQSLMTT 341
sp|Q9UKV0|HDAC9_HUMAN   QHLLLKEQMRQQKL--LVA--GGV------------------------PLHPQSPLATK 427
sp|Q9UQL6|HDAC5_HUMAN   QHVLLLEQARQQST--LI----AV------------------------PLHGQSPLVTG 474
sp|P56524|HDAC4_HUMAN   QHMVLLEQPPAQAP--LVTGLGAL------------------------PLHAQSL-VGA 446


sp|Q9BY41|HDAC8_HUMAN   ------------------------------------------------------------   0
sp|O15379|HDAC3_HUMAN   ------------------------------------------------------------   0
sp|Q92769|HDAC2_HUMAN   ------------------------------------------------------------   0
sp|Q13547|HDAC1_HUMAN   ------------------------------------------------------------   0
sp|Q9UBN7|HDAC6_HUMAN   DQDPSVLYFSIHRYEQGRFWPHLKASNWSTTGFGQG-QGYTINVPWNQVGMRDADYI-AA 322
sp|Q8WUI4|HDAC7_HUMAN   ER-LSG---------SGLHWPLSRTRSEPLPPSATAPPPPGPMQPRLEQLKTH------- 384
sp|Q9UKV0|HDAC9_HUMAN   ER-ISPGIRGTH--KLPRHRPLNRTQSAPLPQST--LAQLVIQQQHQQFLEKQKQY--QQ 480
sp|Q9UQL6|HDAC5_HUMAN   ER-VATSMRTVG--KLPRHRPLSRTQSSPLPQSPQALQQLVMQQQHQQFLEKQKQ----Q 527
sp|P56524|HDAC4_HUMAN   DR-VS---PSIH--KLRQHRPLGRTQSAPLPQNAQALQHLVIQQQHQQFLEKHKQQFQQQ 500


sp|Q9BY41|HDAC8_HUMAN   ------------------------------------------------------------   0
sp|O15379|HDAC3_HUMAN   ------------------------------------------------------------   0
sp|Q92769|HDAC2_HUMAN   ------------------------------------------------------------   0
sp|Q13547|HDAC1_HUMAN   ------------------------------------------------------------   0
sp|Q9UBN7|HDAC6_HUMAN   FLH--VLLP--------------VALEFQP-QLVLVAAGFDALQGDPKGEMAA----TP 360
sp|Q8WUI4|HDAC7_HUMAN   -VQVIKRSAKPSEKPRLRQ---IPSAEDLET--------------DGGG----PGQVVD 421
sp|Q9UKV0|HDAC9_HUMAN   QIHMNKLLSKSIEQLKQPGSHLEEAEEELQGDQAMQEDRA----PSSGNSTRSDSSACVD 536
sp|Q9UQL6|HDAC5_HUMAN   QLQLGKILTKTGELPRQPTTHPEETEEELTEQQEVLLGEGALTMPREGSTE--------- 578
sp|P56524|HDAC4_HUMAN   QLQMNKIIPKPSEPARQPESHPEETEEELREHQALLDEPYLDRLPGQKEAH--------- 551


sp|Q9BY41|HDAC8_HUMAN   ------------------------------------------------------------   0
sp|O15379|HDAC3_HUMAN   ------------------------------------------------------------   0
sp|Q92769|HDAC2_HUMAN   ------------------------------------------------------------   0
sp|Q13547|HDAC1_HUMAN   ------------------------------------------------------------   0
sp|Q9UBN7|HDAC6_HUMAN   AGFAQLTHLLMGLAGGKLILSLEGGYNLRALAEGVSASLHTLLGDPCPMLESPGAPCRSA 420
sp|Q8WUI4|HDAC7_HUMAN   DGL--------------------EH-----------RE-LGHGQPEARGPAP----- 441
sp|Q9UKV0|HDAC9_HUMAN   DTLGQVGAV--------K-VKEEP-VDSDEDAQ--------------------IQE--- 562
sp|Q9UQL6|HDAC5_HUMAN   ---SESTQE--------D-LEEED-EEDDGEEEEDCIQVKD-EEGESGAEEGPDLEE--- 621
sp|P56524|HDAC4_HUMAN   ---AQAGV--------Q-VKQEP-IES----------DE-EEAEPPREVEPGQRQ--- 582


sp|Q9BY41|HDAC8_HUMAN   ------------------------------------------------------------   0
sp|O15379|HDAC3_HUMAN   ------------------------------------------------------------   0
sp|Q92769|HDAC2_HUMAN   ------------------------------------------------------------   0
sp|Q13547|HDAC1_HUMAN   ------------------------------------------------------------   0
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sp|Q9UBN7|HDAC6_HUMAN       QASVSCALEALEPFWEVLVRSTETVERDNMEEDNVE---------ESEE----------- 460
sp|Q8WUI4|HDAC7_HUMAN       -----LQQHPQVLLWEQQRLAGRLPRGSTGDTVLLPLAQGGHRPLSRAQSSPAAPASLSA 496
sp|Q9UKV0|HDAC9_HUMAN       MESGEQAAFMQQPFLEPTHTRALSVRQAPLAAVGMD-GLEKHRLVSRTHSSPAASVLPHP 621
sp|Q9UQL6|HDAC5_HUMAN       P-----GAGYKKLFSDAQPLQPLQVYQAPLSLATVP-----HQALGRTQSSPAAPGGMKS 671
sp|P56524|HDAC4_HUMAN       PSEQELLFRQQALLLEQQRIHQLRNYQASMEAAGIPVSFGGHRPLSRAQSSPASATFPVS 642


sp|Q9BY41|HDAC8_HUMAN       ---------MEEPEEPADS------GQSLVPVYIYSPEYVSM------CDSLAKIPKRAS 39
sp|O15379|HDAC3_HUMAN       -------------------------MAKTVAYFYDPDVGNFH----YGAGHPMKPHRLA 30
sp|Q92769|HDAC2_HUMAN       ----------------MAYSQG------GGKKKVCYYYDGDIGNYY----YGQGHPMKPHRIR 37
sp|Q13547|HDAC1_HUMAN       --------------MAQTQ------GTRRKVCYYYDGDVGNYY----YGQGHPMKPHRIR 36
sp|Q9UBN7|HDAC6_HUMAN       ----------EGPWEPPVLPILTWPVLQSRTGLVYDQNMMNHCNLW--DSHHPEVPQRIL 508
sp|Q8WUI4|HDAC7_HUMAN       PEPASQARVLSSSETPAR-------TLPFTTGLIYDSVMLKHQCSCGDNSRHPEHAGRIQ 549
sp|Q9UKV0|HDAC9_HUMAN       A------------MDRPL-------QPGSATGIAYDPLMLKHQCVCGNSTTHPEHAGRIQ 662
sp|Q9UQL6|HDAC5_HUMAN       P------------PDQPV-------KHLFTTGVVYDTFMLKHQCMCGNTHVHPEHAGRIQ 712
sp|P56524|HDAC4_HUMAN       V------------QEPPT-------KPRFTTGLVYDTLMLKHQCTCGSSSSHPEHAGRIQ 683
                                                       *.   .                        *

sp|Q9BY41|HDAC8_HUMAN       MVHSLIEAYALHKQMRIVKPKVASMEEMATFHTDAYLQHLQKVSQEGDDDHPD------- 92
sp|O15379|HDAC3_HUMAN       LTHSLVLHYGLYKKMIVFKPYQASQHDMCRFHSEDYIDFLQRVSPTNMQGFTKS------ 84
sp|Q92769|HDAC2_HUMAN       MTHNLLLNYGLYRKMEIYRPHKATAEEMTKYHSDEYIKFLRSIRPDNMSEYSKQ------ 91
sp|Q13547|HDAC1_HUMAN       MTHNLLLNYGLYRKMEIYRPHKANAEEMTKYHSDDYIKFLRSIRPDNMSEYSKQ------ 90
sp|Q9UBN7|HDAC6_HUMAN       RIMCRLEELGLAGRCLTLTPRPATEAELLTCHSAEYVGHLRATE-----KMKTRELHRE- 562
sp|Q8WUI4|HDAC7_HUMAN       SIWSRLQERGLRSQCECLRGRKASLEELQSVHSERHV-LLYGTNPLSRLKLDNGKLAGLL 608
sp|Q9UKV0|HDAC9_HUMAN       SIWSRLQETGLLNKCERIQGRKASLEEIQLVHSEHHS-LLYGTNPLDGQKLDPRILLGDD 721
sp|Q9UQL6|HDAC5_HUMAN       SIWSRLQETGLLSKCERIRGRKATLDEIQTVHSEYHT-LLYGTSPLNRQKLDSKKLLGPI 771
sp|P56524|HDAC4_HUMAN       SIWSRLQETGLRGKCECIRGRKATLEELQTVHSEAHT-LLYGTNPLNRQKLDSKKLLGSL 742
                                   :    .*  :          *.  ::   *:  :   *

sp|Q9BY41|HDAC8_HUMAN       SIEYGLGYDCP----ATEGIFDYAA------AIGGATITAAQCLIDGM--CKVAINWSGG 140
sp|O15379|HDAC3_HUMAN       LNAFNVGDDCP----VFPGLFEFCS------RYTGASLQGATQLNNKI--CDIAINWAGG 132
sp|Q92769|HDAC2_HUMAN       MQRFNVGEDCP----VFDGLFEFCQ------LSTGGSVAGAVKLNRQQ--TDMAVNWAGG 139
sp|Q13547|HDAC1_HUMAN       MQRFNVGEDCP----VFDGLFEFCQ------LSTGGSVASAVKLNKQQ--TDIAVNWAGG 138
sp|Q9UBN7|HDAC6_HUMAN       -------------SSNFDSIYICPSTFACAQLATGAACRLVEAVLSGEVLNGAAVV-RPP 608
sp|Q8WUI4|HDAC7_HUMAN       AQRMFVMLPCGGVGVDTDTIWNELHSSNAARWAAGSVTDLAFKVASRELKNGFAVV-RPP 667
sp|Q9UKV0|HDAC9_HUMAN       SQKFFSSLPCGGLGVDSDTIWNELHSSGAARMAVGCVIELASKVASGELKNGFAVV-RPP 780
sp|Q9UQL6|HDAC5_HUMAN       SQKMYAVLPCGGIGVDSDTVWNEMHSSAVRMAVGCLLELAFKVAAGELKNGFAII-RPP 830
sp|P56524|HDAC4_HUMAN       AS-VFVRLPCGGVGVDSDTIWNEVHSAGAARLAVGCVVELVFKVATGELKNGFAVV-RPP 800
                                      ::                *     .  :             *:

sp|Q9BY41|HDAC8_HUMAN       WHHAKKDEASGFCYLNDAVLGILRLRR---KFERILYVDLDLHHGDGVEDAFSFTSKVMT 197
sp|O15379|HDAC3_HUMAN       LHHAKKFEASGFCYVNDIVIGILELLK---YHPRVLYIDIDIHHGDGVQEAFYLTDRVMT 189
sp|Q92769|HDAC2_HUMAN       LHHAKKSEASGFCYVNDIVLAILELLK---YHQRVLYIDIDIHHGDGVEEAFYTTDRVMT 196
sp|Q13547|HDAC1_HUMAN       LHHAKKSEASGFCYVNDIVLAILELLK---YHQRVLYIDIDIHHGDGVEEAFYTTDRVMT 195
sp|Q9UBN7|HDAC6_HUMAN       GHHAEQDAACGFCFFNSVAVAARHAQTISGHALRILIVDWDVHHGNGTQHMFEDDPSVLY 668
sp|Q8WUI4|HDAC7_HUMAN       GHHADHSTAMGFCFFNSVAIACRQLQQQS-KASKILIVDWDVHHGNGTQQTFYQDPSVLY 726
sp|Q9UKV0|HDAC9_HUMAN       GHHAEESTAMGFCFFNSVAITAKYLRDQL-NISKILIVDLDVHHGNGTQQAFYADPSILY 839
sp|Q9UQL6|HDAC5_HUMAN       GHHAEESTAMGFCFFNSVAITAKLLQQKL-NVGKVLIVDWDIHHGNGTQQAFYNDPSVLY 889
sp|P56524|HDAC4_HUMAN       GHHAEESTPMGFCYFNSVAVAAKLLQQRL-SVSKILIVDWDVHHGNGTQQAFYSDPSVLY 859
                             ***..    ***:.*. .:              ::* :* *:***:*.:. *     ::

sp|Q9BY41|HDAC8_HUMAN       VSLHKFSPG-FFPG--TGDVSDVGLGKGRYYSVNVPIQDGIQ----DEKYYQICESVLKE 250
sp|O15379|HDAC3_HUMAN       VSFHKYGNY-FFPG--TGDMYEVGAESGRYYCLNVPLRDGID----DQSYKHLFQPVINQ 242
sp|Q92769|HDAC2_HUMAN       VSFHKYGEY--FPG--TGDLRDIGAGKGKYYAVNFPMRDGID----DESYGQIFKPIISK 248
sp|Q13547|HDAC1_HUMAN       VSFHKYGEY--FPG--TGDLRDIGAGKGKYYAVNYPLRDGID----DESYEAIFKPVMSK 247
sp|Q9UBN7|HDAC6_HUMAN       VSLHRYDHGTFFPMGDEGASSQIGRAAGTGFTVNVAWNG---PRMGDADYLAAWHRLVLP 725
sp|Q8WUI4|HDAC7_HUMAN       ISLHRHDDGNFFPG--SGAVDEVGAGSGEGFNVNNVAWAGGLDPPMGDPEYLAAFRIVVMP 784
sp|Q9UKV0|HDAC9_HUMAN       ISLHRYDEGNFFPG--SGAPNEVGTGLGEGYNINIAWTGGLDPPMGDVEYLEAFRTIVKP 897
sp|Q9UQL6|HDAC5_HUMAN       ISLHRYDNGNFFPG--SGAPEEVGGGPGVGYNVNVAWTGGVDPPIGDVEYLTAFRTVVMP 947
sp|P56524|HDAC4_HUMAN       MSLHRYDDGNFFPG--SGAPDEVGTGPGVGFNVNMAFTGGLDPPMGDAEYLAAFRTVVMP 917
                             :*:*:..    **     *    ::*   *  :.*     .       * .*    . ::

sp|Q9BY41|HDAC8_HUMAN       VYQAFNPKAVVLQLGADTIAGD--PMCSFNMTPVGIGKCLKYILQWQLATLI-LGGGGYN 307
sp|O15379|HDAC3_HUMAN       VVDFYQPTCIVLQCGADSLGCD--RLGCFNLSIRGHGECVEYVKSFNIPLLV-LGGGGYT 299
sp|Q92769|HDAC2_HUMAN       VMEMYQPSAVVLQCGADSLSGD--RLGCFNLTVKGHAKCVEVVKTFNLPLLM-LGGGGYT 305
sp|Q13547|HDAC1_HUMAN       VMEMFQPSAVVLQCGSDSLSGD--RLGCFNLTIKGHAKCVEFVKSFNLPMLM-LGGGGYT 304
sp|Q9UBN7|HDAC6_HUMAN       IAYEFNPELVLVSAGFDAARGD--PLGGCQVSPEGYAHLTHLLMGLASGRIILILEGGYN 783
sp|Q8WUI4|HDAC7_HUMAN       IAREFSPDLVLVSAGFDAAEGHPAPLGGYHVSAKCFGYMTQQLMNLAGGAVVLALEGGHD 844
sp|Q9UKV0|HDAC9_HUMAN       VAKEFDPDMVLVSAGFDALEGHTPPLGGYKVTAKCFGHLTKQLMTLADGRVVLALEGGHD 957
sp|Q9UQL6|HDAC5_HUMAN       IAHEFSPDVVLVSAGFDAVEGHLSPLGGYSVTARCFGHLTRQLMTLAGGRVVLALEGGHD 1007
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sp|P56524|HDAC4_HUMAN       IASEFAPDVVLVSSGFDAVEGHPTPLGGYNLSARCFGYLTKQLMGLAGGRIVLALEGGHD 977
                            :    : *  :::. * * *:   .   :      ::    .    . :        ::    **:

sp|Q9BY41|HDAC8_HUMAN       LANTARCWTYLTGVILGKTLSSEIPDHEFFTAYGPDYVLEITPSCRPD-RNEPHRIQQ-- 364
sp|O15379|HDAC3_HUMAN       VRNVARCWTYETSLLVEEAISEELPYSEYFEYFAPDFTLHPDVSTRIENQNSRQYLDQ-- 357
sp|Q92769|HDAC2_HUMAN       IRNVARCWTYETAVALDCEIPNELPYNDYFEYFGPDFKLHISPS-NMTNQNTPEYMEK-- 362
sp|Q13547|HDAC1_HUMAN       IRNVARCWTYETAVALDTEIPNELPYNDYFEYFGPDFKLHISPS-NMTNQNTNEYLEK-- 361
sp|Q9UBN7|HDAC6_HUMAN       LTSISESMAACTRSLLGDPP--------------PLLTLPRPPL-----SGALASITETI 824
sp|Q8WUI4|HDAC7_HUMAN       LTAICDASEACVAALLGNRVDP-L----------SEEGWKQKPN-----LNAIRSLEAVI 888
sp|Q9UKV0|HDAC9_HUMAN       LTAICDASEACVNALLGNELEP-L----------AEDILHQSPN-----MNAVISLQKII 1001
sp|Q9UQL6|HDAC5_HUMAN       LTAICDASEACVSALLSVELQP-L----------DEAVLQQKPN-----INAVATLEKVI 1051
sp|P56524|HDAC4_HUMAN       LTAICDASEACVSALLGNELDP-L----------PEKVLQQRPN-----ANAVRSMEKVM 1021
                            :    .  .   .     :                                  .    :

sp|Q9BY41|HDAC8_HUMAN       -ILNYIKGNLKHVV-------------------------------------------- 377
sp|O15379|HDAC3_HUMAN       -IRQTIFENLKMLNHAPSVQIH-------DVPADLLTYDRTDEADAEERGPEENYS---- 405
sp|Q92769|HDAC2_HUMAN       -IKQRLFENLRMLPHAPGVQMQ-------AIPEDAVHEDSGDEDGED---PDKRISI--- 408
sp|Q13547|HDAC1_HUMAN       -IKQRLFENLRMLPHAPGVQMQ-------AIPEDAIPEESGDEDEDD---PDKRISI--- 407
sp|Q9UBN7|HDAC6_HUMAN       QVHRRYWRSLRVMKVEDREGPSSSKLVTKKAPQPAKPR----LAERMTTREKKVLEAGMG 880
sp|Q8WUI4|HDAC7_HUMAN       RVHSKYWGCMQRLASCPDSWV--PR-----VP-GADKE----EVEAVT--ALASLSVGIL 934
sp|Q9UKV0|HDAC9_HUMAN       EIQSMSLKFS------------------------------------------------- 1011
sp|Q9UQL6|HDAC5_HUMAN       EIQSKHWSCVQKFAAGLGRSL--RE-----AQ-AGETE----EAETVS--AMALLSVGAE 1097
sp|P56524|HDAC4_HUMAN       EIHSKYWRCLQRTTSTAGRSL--IE-----AQ-TCENE----EAETVT--AMASLSVGVK 1067
                             :

sp|Q9BY41|HDAC8_HUMAN       ---------------------------------------------------------- 377
sp|O15379|HDAC3_HUMAN       -----------RPEAPNE--------FYDGDHDNDK---------------------- 422
sp|Q92769|HDAC2_HUMAN       -------RASDKRIACDEE--------FSDSEDEGEGGRRNVADHK---KGAKK-AR--I 447
sp|Q13547|HDAC1_HUMAN       -------CSSDKRIACEEE--------FSDSEEEGEGGRKNSSNFK---KAKRV-KT--E 446
sp|Q9UBN7|HDAC6_HUMAN       KVTSASFGE-ESTPGQTNSETAVVALTQDQPSEAATGGATLAQTISEAAIGGAMLGQTTS 939
sp|Q8WUI4|HDAC7_HUMAN       AE---------DRPSEQ-------LVEEEEPMNL------------------------- 952
sp|Q9UKV0|HDAC9_HUMAN       --------------------------------------------------------- 1011
sp|Q9UQL6|HDAC5_HUMAN       QAQAAAAREHSPRPAEE-------PMEQEPAL-------------------------- 1122
sp|P56524|HDAC4_HUMAN       PA--------EKRPDEE-------PMEEEPPL-------------------------- 1084

sp|Q9BY41|HDAC8_HUMAN       ---------------------------------------------------------- 377
sp|O15379|HDAC3_HUMAN       ------------ESD------VEI---------------------------------- 428
sp|Q92769|HDAC2_HUMAN       EE--DKKETEDKKTD------VKEEDKSKDNSGEKTDTKGTKSE--------------- 483
sp|Q13547|HDAC1_HUMAN       DE--KEKDPE-EKKE------VTEEEKTKEE---KPEAKGVKEE--------------- 478
sp|Q9UBN7|HDAC6_HUMAN       EEAVGGATPDQTTSEETVGGAILDQTTSEDAVGGATLGQTTSEEAVGGATLAQTTSEAAM 999
sp|Q8WUI4|HDAC7_HUMAN       --------------------------------------------------------- 952
sp|Q9UKV0|HDAC9_HUMAN       --------------------------------------------------------- 1011
sp|Q9UQL6|HDAC5_HUMAN       --------------------------------------------------------- 1122
sp|P56524|HDAC4_HUMAN       --------------------------------------------------------- 1084

sp|Q9BY41|HDAC8_HUMAN       --------------------------------------------------------- 377
sp|O15379|HDAC3_HUMAN       --------------------------------------------------------- 428
sp|Q92769|HDAC2_HUMAN       -----------------QLSNP----------------------------------- 488
sp|Q13547|HDAC1_HUMAN       -----------------VKLA------------------------------------- 482
sp|Q9UBN7|HDAC6_HUMAN       EGATLDQTTSEEAPGGTELIQTPLASSTDHQTPPTSPVQGTTPQISPSTLIGSLRTLELG 1059
sp|Q8WUI4|HDAC7_HUMAN       --------------------------------------------------------- 952
sp|Q9UKV0|HDAC9_HUMAN       --------------------------------------------------------- 1011
sp|Q9UQL6|HDAC5_HUMAN       --------------------------------------------------------- 1122
sp|P56524|HDAC4_HUMAN       --------------------------------------------------------- 1084

sp|Q9BY41|HDAC8_HUMAN       --------------------------------------------------------- 377
sp|O15379|HDAC3_HUMAN       --------------------------------------------------------- 428
sp|Q92769|HDAC2_HUMAN       --------------------------------------------------------- 488
sp|Q13547|HDAC1_HUMAN       --------------------------------------------------------- 482
sp|Q9UBN7|HDAC6_HUMAN       SESQGASESQAPGEENLLGEAAGGQDMADSMLMQGSRGLTDQAIFYAVTPLPWCPHLVAV 1119
sp|Q8WUI4|HDAC7_HUMAN       --------------------------------------------------------- 952
sp|Q9UKV0|HDAC9_HUMAN       --------------------------------------------------------- 1011
sp|Q9UQL6|HDAC5_HUMAN       --------------------------------------------------------- 1122
sp|P56524|HDAC4_HUMAN       --------------------------------------------------------- 1084

sp|Q9BY41|HDAC8_HUMAN       --------------------------------------------------------- 377
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sp|O15379|HDAC3_HUMAN    ------------------------------------------------------------ 428
sp|Q92769|HDAC2_HUMAN    ------------------------------------------------------------ 488
sp|Q13547|HDAC1_HUMAN    ------------------------------------------------------------ 482
sp|Q9UBN7|HDAC6_HUMAN    CPIPAAGLDVTQPCGDCGTIQENWVCLSCYQVYCGRYINGHMLQHHGNSGHPLVLSYIDL 1179
sp|Q8WUI4|HDAC7_HUMAN    ------------------------------------------------------------ 952
sp|Q9UKV0|HDAC9_HUMAN    ------------------------------------------------------------ 1011
sp|Q9UQL6|HDAC5_HUMAN    ------------------------------------------------------------ 1122
sp|P56524|HDAC4_HUMAN    ------------------------------------------------------------ 1084


sp|Q9BY41|HDAC8_HUMAN    ----------------------------------- 377
sp|O15379|HDAC3_HUMAN    ----------------------------------- 428
sp|Q92769|HDAC2_HUMAN    ----------------------------------- 488
sp|Q13547|HDAC1_HUMAN    ----------------------------------- 482
sp|Q9UBN7|HDAC6_HUMAN    SAWCYYCQAYVHHQALLDVKNIAHQNKFGEDMPHPH 1215
sp|Q8WUI4|HDAC7_HUMAN    ----------------------------------- 952
sp|Q9UKV0|HDAC9_HUMAN    ----------------------------------- 1011
sp|Q9UQL6|HDAC5_HUMAN    ----------------------------------- 1122
sp|P56524|HDAC4_HUMAN    ----------------------------------- 1084
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