

HTH_psq

TremA : ARLLAIKDYETKQISSIRVAAKTYELPYTTLYDRIRGGTTYTN
 TremB : ---LLAIRAYETKQISSIRAAKAYGVSAATLSNRLHGGIPRVK
 TremC : -RLILAIQAFKNGQISSVRAAKLYTVPRSTIGDRVHGRTARVN
 TremD : -RLIELAISAIKKQEITSIREAARHFNVSRITLGYRLSCLPARVN
 TremE : -RLIELAIKSIRNDEKLSIREAAKLFNVPRSTIQDHLKHRPSRVN
 Mariner1_AF : ----LAVSALKNKEILNIREAARVYNVPTTLQRRRLKCHTFR--
 Mariner2_AO : -RLILAISAIKKQEIRTIAEAARIYNIPRTTLRRRLNGHTFR--
 Pot2_MG : -QLISAINDVNNGN--PIAKTSRKWGTIPRSTIQSRLKGSQPYKK
 Tan1_AN : -RLILAIKAIKRGQITSIREAARVYDVARTTLQARLSCLRVFAKN

CENPB

TremA : RKLTSTEEESTVQWILSMDERGQPRIATVREMANILLAREST-TTTTVGGRWVEREIQRHSEL--
 TremB : QKLTPTEEEEALVQWIIISMDERGLPPRIASVRYMAIELLRARGSS-ISPSIGECWVRREIKXHSSEL--
 TremF : QKLTNSQEEELIRYINRLTDGRFPPTPRITQNLVEEILQEP-----TGEHWISREICQRHKDR--
 Mariner3_AO : -----QEKALIRWIRQLDNLYSPPTAGMIEQSANQILCRNITDGQSRTVDKNWVYREIKRLPEEFK
 Pot2_MG : QRLSTEQEKHLADWVLTQTALGLPPTHQELRFFAERILCAAGET-KG--LGKRWITRFLARYPIL--
 Pogo_DM : KGAHDLVEEATYIYIFGQQESKNVILDRHVILAKAKEFCQKFNDAFEP---DASWLWRWRKRHNI---

DDE

170 230

TremA : ITSEDIYNEDEIGFTMGVISTSWVVRRAERAGR---PSLLQPGNREWATVIEAVNATWALPEMILFKGK--LHQASNYK---QLPKDWTIGVSEKGWTTDAISLDWIRKVENGATKACT--KGRY
 TremB : ILPEDIYNEDEVGFTLMGVISTTLVVRERERAGK---ASLIQPGNREWVTVIESVNARCSLPPMILKKGK--LHQASNYT---NLPADWVIGVSENGWTTDQIGLIWLKEVENKHTQAYT--VGRY
 TremC : -----HGSERARN---PKLVQPGDQEWVTVIAGVNVSWALRTMILKKGK--MHQSCWYEAELGPRDWVIGVRENGWTTDQIGLYWLKEVENKETLP-----
 TremD : ILAEDIYNEDETGFMGLCATTKVITSAERYGR---AKLLQAGNREWVTTIESVNASQWALPPYILKKGQ--NLQEGNE--DGLPDGWRDLVSSNGWTTDEIGIRWLTRIFIPAVNPRR--VGTH
 TremE : IVPEDIYNEDETGFMGLCATTKVITSSSEHYGR---AKLLQAGNCEWVTVIESVNASQWALPPYILKKGQ--GLLEDNE--ELGPEGWRLDVSPNGWTTDEIGIRWLQRFVIPAADPRR--VGRS
 TremF : -----QDGSREHISILAAKSASCRSTPEGLIYQSDSGDLLQDTLEDFDSDKEHEVFFAASPNGWSSDQYGLHWIQRVENPHTKARN--G-AW
 TremG : IQDCDVYNEDETGFRIGIGRDQWIIARDPRRRT---YV-GSSNNRVTLITIEGIATDFTIPPLYILTAK--QLQERWTDIEK--DAMIATSDTGYNNDQISFQWIQ--HEHCSTKAHI--KGTH
 TremH : ---CDTYNEDEIGFQEGGCGEWWITAFKEANS---II-PSSFSRGLITVIECVSMDNHVIPLEILILASK--THLEDNYTQ-TDLPSNYRIAISDTGFTNDEIGFEWLK--HENTATEKRQ--KGS
 Mariner1_AF : ITLEDIYNEDETGFMGLVATAKVVRRAEMLSR---PFLIQPGNREWVTSIECINSTEWLPPCILFKGK--VHIEGWYQDT-ALPADWRIEVSNGWTTDQIGIRWLQKVFIPATTSRT--TGRY
 Mariner2_AO : IQPDDIYNEDETGFMGLISTTKVVTAEALAGR---PFLIQPGNREWVTSIKYISSRG-FLPECLIFKKGK--VHIEGWY-EM-GLPSDWRIETSANGWTTDEIGIRWLQKVFIPFPTAGRT--VGRY
 Mariner3_AO : IPPKNIYNEDETGFLRQKGTQKVVTMPPLRAA---RGNPSKEVGELISATECIAADGFTLPPYHIFKGT--YHLERWYD--ADIPPEYRISLSPKGYTTDKTSFDWIQ--HEHRTKHRISTKKEV
 Mariner5_AF : ---DLYNEDETGFIGIGKQDWIVTREFKKPS---FS-PSNTNQEYTTVVEAISADCHFIHPPHIFKGT--CILAGNHDV-CDEF-DYIIGLSDSGYINDILAFQWIQ--HEHHTRRRM--LGVK
 Mariner9_AN : -EPGNIYNMKKKFLIGMLSKGLRIFSKRKYKQGNFKQRLQDGNREWITATACIACDCTILSPVILTYQAASSDIQDTLQDFDPQHHTKFFASSPSGWNTDKLYAWILTVGEDRETAKDA--RRQW
 Pot2_MG : IKPENRWNMDETGIMEGKGSNGLVIGLINGIR-P--LQ-RKEPGTREGWTTIECISATEVALPELILFKGK--NVQQQNEPTDLSPFDDNWQFHATENGWTTNQTAEWLKQVFIPYTQPLT--P-EK
 Tan1_AN : ISSDDIYNEDETGFMGMIAITYKVVTSSQRAGR---PSLVQPGNREWVTAIECRSNCEVLESTLIFKKGK--THLKAWYEGQ-SIPPTWRFEVSDNGWTTDKIGIRWLQKHFIPLIRGKS--VGKY
 Pogo_DM : YNPEDIENADETALFYKAMPNATFFICGKQLNG-----QKSQVRVLTILFICNATEYKKTFFVIGRSK----SPRCQKN-ANVP--IPYANKKAWMTKDIWRKIMT-GEDEEMKQN----RK

280 330

TremA : RLIVLDGHSHTATPDKFCLDHGIIISLYMPHSHSHLLQPLIDVSCFSPKRAYGKRV--QSVRLGISYIDREDFLASYTTARQEA MKDI-----TKNG-
 TremB : RLIVLDGHSHTATPDQFCRENATIALYMPHSHSHLLQPLIDVSCFAPLKAYCKQVE--SGMRLGINHVDRBGLLELYSAARKEALKDM-----TURNGE
 TremC : -----
 TremD : RLIVLDGHSHTATPDDHICKENRIIPLCMAHSHSHLLQPLIDVSVAVLKRAYGGLVE--QRMRLGFNTIRKGDGLDAYPAARAEAFKSQ-----NICSGE
 TremE : RLIVLDGHSHTATPDQICKDNATICLCMPHSHSHLLQPLIDVGVSFVLE-VYGLDVQ--QRMRLGFNAIQK-----
 TremF : RLIVLDGHSHTATPDDINADQNCIILAVLSPHSTHRLQPLIDVGIIFGLSKAYSQQVDFLRSAMGGVSIRKRNIFLLFHNNAWKQAVTKS-----NIESGF
 TremG : RLIVLDGHSHTATPDKHNTFFCDKHNIIPFYLIHPTSHLLQPLIDVGVEQAFKHHHSAAVE--EATRRGCEKFTFVBELHAITSIRKATFKVH-----TKQGW
 TremH : QLLIMDNHSHHTATPEIQYADLHKIILYGFESHATHLLQPLIDSLPFCQYKHYHSAVN--YAAHGLVKYERQCQLQDLSAMRKQTFKPD-----TAAAGW
 Mariner1_AF : RLIVLDGHSHTATPDQICTENDIIPICMAHSHSHLLQPLIDVGCFSPLKRAYGRLIE--DKMRLGFNHNIDFDBLEAYPQARTAFISAD-----NKSGE
 Mariner2_AO : RLIVLDGHSHTATPDIDICSNNIIPLCMAHSHSHLLQPLIDIGCGPLKRAYGGLVE--NKMRLDFNHNIRLDBLEAFQARAQIYTTT-----NICSGE
 Mariner3_AO : RLIVLDGHSHTATPELQFCGLHYIIPYCFPHPTTHLVQPLIDGQFQVYKHYFRKRN--ELACQGAEMDDSDFLKEIHSIRTMTFKQR-----TURDAP
 Mariner5_AF : RLIVLDGHSHTATPEIDFCEKNNIILYFLPHPTSHLLQPLIDVGVEHAYKHHSSEAE--DATCGRGKFTFVBELSALEFIRRTTFKQR-----TKHAF
 Mariner9_AN : RLIVLDGHSHTATMKFDYCDNKKILATYPHSHSTHSLQPLIDVGIFSPLSHAYSSELEAYLHISMGLSHITARD--FRLFFPAWVKALSSK-----NIISSW
 Pot2_MG : RLIVLDGHSHTATPEMLLCLQNNIQLLYLPHSHSHVLPQPLIDSVGFLKEAYRRQIG-FVSQFCCSTVIGARNELLCYRKABLKAFIAK-----TIQSGW
 Tan1_AN : RLIVLDGHSHTATPDQSCAENEVPIPCMAHSHSHLLQPLIDVGCFSVLKRTYGGMVQ--KQMCGYGRNHIDRLDBLEVYPKAHQCALSKS-----NIIISGF
 Pogo_DM : RLIVLDGHSHTATPEIDFENIKLCFMBPNATIALQPLIDQGIHSHFKLEYRRILVKQQLIAVNCGK-STVBLKSLSLDALYFVNQGWKNVKMLTQNCQ