```
GlyREM            1  MFA--------------LGIYLWE---TIVFFSLAASQQ-------------------------------AAA--------PSEFLDKLMGKVSGYDAR   43
DR_GlyR_alpha1    1  MFA--------------LGIYLWE---TIVFFSLAASQQ------------------------------AAARKAASPMPPSEFLDKLMGKVSGYDAR   51
HS_GlyR_alpha1    1  MYSFNT-----------LRLYLWE---TIVFFSLAASKE------------------------------AEAARSAPKPMSPSDFLDKLMGRTSGYDAR   55
CE_GluCl_alpha    1  MA-------------------TWI---VGKLIIASLILGIQAQQARTKSQDIFEDDNDNGTTTLESLARLTSPIHIPIEQPQTSDSKILAHLFTSGYDFR   78
HS_GABA_A_beta3   1  MWG----------LAGGRLFGIFS---APVLVAVVCCAQ-----------------------------------SVNDPGNMSFVKETVDKLLKGYDIR   51
HS_5HT3A          1  ML-------------------LWVQQALLALLLPTLLAQGEAR--------------------------------RSRNTTRPALLRLSDYLLTNYRKG   48
GLIC_GLOVI        1  MFPTGWRPKLSESIAASRMLWQPM---AAVAVVQIGLLW-----------------------------------------------FSPPVWGQDMV   47
ELIC_ERWINIA      1  ------------------------------------------------------------------------------------------------AP    2
nAChR_TM_alpha    1  MI-------------------LCSYWHVGLVLLLFSCCG-------------------------------------LVLGSEHETRLVANLLENYNKV   42

                                  β1                      β2                      β3                      β4      β5
GlyREM           44  IRPNF-KGPPVNVTCNIFINSFGSIAETTMDYRVNIFLRQQWNDPRLAYSEY--PDD-SLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRISKN  139
DR_GlyR_alpha1   52  IRPNF-KGPPVNVTCNIFINSFGSIAETTMDYRVNIFLRQQWNDPRLAYSEY--PDD-SLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRISKN  147
HS_GlyR_alpha1   56  IRPNF-KGPPVNVSCNIFINSFGSIAETTMDYRVNIFLRQQWNDPRLAYNEY--PDD-SLDLDPSMLDSIWKPDLFFANEKGAHFHEITTDNKLLRISRN  151
CE_GluCl_alpha   79  VRPPTDNGGPVVVSVNMLLRTISKIDVVNMEYSAQLTLRESWIDKRLSYGVKG-DGQ-PDFVILTVGHQIWMPDTFFPNEKQAYKHTIDKPNVLIRIHND  176
HS_GABA_A_beta3  52  LRPDF-GGPPVCVGMNIDIASIDMVSEVNMDYTLTMYFQQYWRDKRLAYSGI----PLNLTLDNRVADQLWVPDTYFLNDKKSFVHGVTVKNRMIRLHPD  146
HS_5HT3A         49  VRPVRDWRKPTTVSIDVIVYAILNVDEKNQVLTTYIWYRQYWTDEFLQWNPE---DFDNITKLSIPTDSIWVPDILINEFVDVGKS---PNIPYVYIRHQ  142
GLIC_GLOVI       48  SPPPPIADEPLTVNTGIYLIECYSLDDKAETFKVNAFLSLSWKDRRLAFDPV----RSGVRVKTYEPEAIWIPEIRFVNVENARD----ADVVDISVSPD  139
ELIC_ERWINIA      3  ADNA-ADARPVDVSVSIFINKIYGVNTLEQTYKVDGYIVAQWTGKPRKTPGDKPLIVENTQIERWINNGLWVPALEFINVVGSPD----TGNKRLMLFPD   97
nAChR_TM_alpha   43  IRPVEHHTHFVDITVGLQLIQLINVDEVNQIVETNVRLRQQWIDVRLRWNPA---DYGGIKKIRLPSDDVWLPDLVLYNNADGDFAI--VHMTKLLLDYT  137

                                  β6                      β7      β8      β9                      β9                      β10
GlyREM          140  GNVLYSIRITLVLACPMDLKNFPMDVQTCIMQLESFGYTMNDLIFEWDEKGA---VQVADGLTLPQFILKEEKDLRYCTKHYN-------TGKFTCIEAR  229
DR_GlyR_alpha1  148  GNVLYSIRITLVLACPMDLKNFPMDVQTCIMQLESFGYTMNDLIFEWDEKGA---VQVADGLTLPQFILKEEKDLRYCTKHYN-------TGKFTCIEAR  237
HS_GlyR_alpha1  152  GNVLYSIRITLTLACPMDLKNFPMDVQTCIMQLESFGYTMNDLIFEWQEQGA---VQVADGLTLPQFILKEEKDLRYCTKHYN-------TGKFTCIEAR  241
CE_GluCl_alpha  177  GTVLYSVRISLVLSCPMYLQYYPMDVQQCSIDLASYAYTTKDIEYLWKEHSPL-QLKVGLSSSLPSFQLTNTSTTYCTS-VTN-------TGIYSCLRTT  267
HS_GABA_A_beta3 147  GTVLYGLRITTTAACMMDLRRYPLDEQNCTLEIESYGYTTDDIEFYWRGGDK--AVTGVERIELPQFSIVEHRLVSRNV-VFA-------TGAYPRLSLS  236
HS_5HT3A        143  GEVQNYKPLQVVTACSLDIYNFPFDVQNCSLTFTSWLHTIQDINISLWRLPEKVKSDRSVFMNQGEWELLGVLPYFREFSMES-------SNYYAEMKFY  235
GLIC_GLOVI      140  GTVQYLERFSARVLSPLDFRRYPFDSQTLHIYLIVRSVDTRNIVLAVDLEK----VGKNDDVFLTGWDIESFTAVVKPANFALE------DRLESKLDYQ  229
ELIC_ERWINIA     98  GRVIYNARFLGSFSNDMDFRLFPFDRQQFVLELEPFSYNNQQLRFSDIQVY----TENIDNEEIDEWWIRKASTHISDIRYDHLSSVQPNQNEFSRITVR  193
nAChR_TM_alpha  138  GKIMWTPPAIFKSYCEIIVTHFPFDQQNCTMKLGIWTYDGTKVSISPESDR----PDLSTFMESGEWVMKDYRGWKHWVYYTCCP-----DTPYLDITYH  228

                     β10      TM1                     TM2                     TM3
GlyREM          230  FHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSY-VKAIDIWMAVCLLFVFSALLEYAAVNFIARAGT  328
DR_GlyR_alpha1  238  FHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSY-VKAIDIWMAVCLLFVFSALLEYAAVNFIARQHK  336
HS_GlyR_alpha1  242  FHLERQMGYYLIQMYIPSLLIVILSWISFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSY-VKAIDIWMAVCLLFVFSALLEYAAVNFVSRQHK  340
CE_GluCl_alpha  268  IQLKREFSFYLLQLYIPSCMLVIVSWVSFWFDRTAIPARVTLGVTTLLTMTAQSAGINSQLPPVSY-IKAIDVWIGACMTFIFCALLEFALVNHIANKQG  366
HS_GABA_A_beta3 237  FRLKRNIGYFILQTYMPSILITILSWVSFWINYDASAARVALGITTVLTMTTINTHLRETLPKIPY-VKAIDMYLMGCFVFVFLALLEYAFVNYIFFGRG  335
HS_5HT3A        236  VVIRRRPLFYVVSLLLPSIFLMVMDIVGFYLPPN-SGERVSFKITLLLGYSVFLIIVSDTLPATAIGTPLIGVYFVVCMALLVISLAETIFIVRLVHKQD  334
GLIC_GLOVI      230  LRISRQYFSYIPNIILPMLFILFISWTAFWST--SYEANVTLVVSTLIAHIAFNILVETNLPKTPY-MTYTGAIIFMIYLFYFVAVIEVTVQHYLKVESQ  326
ELIC_ERWINIA    194  IDAVRNPSYYLWSFILPLGLIIAASWSVFWLE--SFSERLQTSFTLMLTVVAYAFYTSNILPRLPY-TTVIDQMIIAGYGSIFAAILLIIFAHHRQANGV  290
nAChR_TM_alpha  229  FIMQRIPLYFVVNVIIPCLLFSFLTVLVFYLPTD-SGEKMTLSISVLLSLTVFLLVIVELIPSTSSAVPLIGKYMLFTMIFVISSIIVTVVVINTHHRSP  327

GlyREM                ----------------------------------------------------------------------------------------------
DR_GlyR_alpha1  337  ELLRFQRRRRHLKEDEAGDGRFSFAAYGMGPA-----------------------------------------------------------CLQAKDGM  376
HS_GlyR_alpha1  341  ELLRFRRKRRHHKEDEAGEGRFNFSAYGMGPA-----------------------------------------------------------CLQAKDGI  380
CE_GluCl_alpha  367  VERKARTEREKAEIPLLQNLHNDVPTKVFNQE-----------------------------------------------------------EKVRTVPL  406
HS_GABA_A_beta3 336  PQRQKKLAEKTAKAKNDRSKSESNRVDAHGNILLTSLEVHNEMNEVSGGIGDTRNSAISFDNSGIQYRKQSM------------PREGHGRFLGDRSLPH  423
HS_5HT3A        335  LQQPVPAWLRHLVLERIAWLLCLREQSTSQRPP-ATSQATKTDDCSAMG---------NHCSHMGGPQDFEKSPRDRCSPPPPPREASLAVCGLLQELSS  424
GLIC_GLOVI      327  PAR-----------------------------------------------------------------------------------------  329
ELIC_ERWINIA    291  E-------------------------------------------------------------------------------------------  291
nAChR_TM_alpha  328  STHTMPQWVRKIFINTIPNLMFFSTMKRASKEK-QENKIFADDIDISDI---------SGKQVTGEVIFQTP------------LIKNPDVKSAIEGVKY  405

                                                  TM4                     Thrombin  His Tag
GlyREM          329  -------------------------KLFISRAKRIDTVSRVAFPLVFLIFNIFYWITYKLVPRGSHHHHHHH  376
DR_GlyR_alpha1  377  AIKGNNNNAPT-STNPPEKTVEEMRKLFISRAKRIDTVSRVAFPLVFLIFNIFYWITYKIIRSEDIHKQ----  444
HS_GlyR_alpha1  381  SVKGANNSNTTNPPPAPSKSPEEMRKLFIQRAKKIDKISRIGFPMAFLIFNMFYWIIYKIVRREDVHNQ----  449
CE_GluCl_alpha  407  NRRQMN----------SFLNLLETKTEWNDISKRVDLISRALFPVLFFVFNILYWSRFGQQNVLF--------  461
HS_GABA_A_beta3 424  KKTHLR----------RRSSQLKIKIPDLTDVNAIDRWSRIVFPFTFSLFNLVYWLYYVN-------------  473
HS_5HT3A        425  IRQFLEK----------RDEIREVARDWLRVGSVLDKLLFHIYLLAVLAYSITLVMLWSI----WQYA-----  478
GLIC_GLOVI      330  ------------------------------AASITRASRIAFPVVFLLANIILAFLFFGF------------  359
ELIC_ERWINIA    292  ------------------------------DDLLIQRCRLAFPLGFLAIGCVLVIRGITL------------  321
nAChR_TM_alpha  406  IAEHMKS----------DEESSNAAEEWKYVAMVIDHILLCVFMLICIIGTVCVFAGRLI----ELSQEG---  461
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