```
HsaGCGR : ----------------------------------------MPPCQPQRPLLLLLLLLACQPQVPSAQVMDFLFEKWKLYGDQCHHNLS-- :  48
HsaGLP1R: -------------------------------------MAGAPGPLRLALLLLGMVGRAGPRPQGATVSLWETVQKWREYRRQCQRSLTE- :  52
HsaGLP2R: MKLGSSRAGPGRGSAGLLPGVHELPMGIPAPWGTSPLSFHRKCSLWAPGRPFLTLVLLVSIKQVTGSLLEETTRKWAQYKQACLRDLL-- :  88
HsaGIPR : -------------------------------------MTTSPILQLLLRLSLCGLLLQRAETGSKGQTAGELYQRWERYRRECQETLA-- :  51
S000537 : -------------------------------------MHYGDYVLKTVTVRLQFS---------SANSLELVKEQWSSYKNQCLDYLS-- :  42
S006614 : -----------------------------------------------------------------------------QYKDDCIQMIMNE :  13
S007267 : ------------------------------------------------------------------------------------------ :   -
CinS5B  : ------------------------------------------------------------------------MCKYMKYKEQCEKSLNET :  18
CinS5A  : ------------------------------------------------------------------------MCKYMQYRERCEKSLNET :  18
CinS70  : ------------------------------------------------------------------------------------------ :   -

HsaGCGR : LLPPPTELVCNRTFDKYSCWPDTPANTTANISCPWYLPWHHK---VQHRFVFKRCGPDGQWVRGP-RGQPWRDASQCQMDG--EEIEVQK : 132
HsaGLP1R: DPPPATDLFCNRTFDEYACWPDGEPGSFVNVSCPWYLPWASS---VPQGHVYRFCTAEGLWLQKDNSSLPWRDLSECEESK----RGERS : 135
HsaGLP2R: --KEPSGIFCNGTFDQYVCWPHSSPG-NVSVPCPSYLPWWSE---ESSGRAYRHCLAQGTWQTIENATDIWQDDSECSENH---SFKQNV : 169
HsaGIPR : AAEPPSGLACNGSFDMYVCWDYAAPNATARASCPWYLPWHHH---VAAGFVLRQCGSDGQWG-------LWRDHTQCENP---EKNEAFL : 128
S000537 : SAEPSTGLVCNRTFDLYACWPDGLPGTTVNVSCPWFLPWYRK-----------------------------------------------A :  85
S006614 : PLSPGGGLFCNRTFDRYACWPDAPAGSLVNISCPFYLPWYEK---VSQGVVRRRCGSDGLWERDD-SGHVWRDKSQCEEEEECHGLSLQL :  99
S007267 : ------GIYCKGTFDMFVCWPHSAPG-NVSVPCPSYLPWISE---DGSRRAHRECLENGTWRERENSSEPWRDDSECKEEH---YFKDKE :  77
CinS5B  : LKNFENQTFCPGFFDRQICWPHTPAGQLSTEPCPSYIEWR-----NESLVAYRFCEFDGSWMVRNDTGQSVQWVNRIQCDVATNGLQYEL : 103
CinS5A  : LKNFENQTFCPGIFDGYICWPHTPAGQLLTEPCPSYIEWKNVIHLQESLVAYRFCEFDGSWMVRNDTGQSVH-LDHLRGDHRTKMYVGNY : 107
CinS70  : ------------------------------------------------IPAMHCNATLGGWNERSSLHTCFNRSSDMDDDVASISN---D :  39

                               TM1                             TM2
HsaGCGR : EVAKMYSSFQVMYTVGYSLSLGALLLALAILGGLSKLHCTRNAIHANLFASFVLKASSVLVIDGLLRTRYSQKIGDDLSVSTWLSDGAVA : 222
HsaGLP1R: SPEEQLLFLYIIYTVGYALSFSALVIASAILLGFRHLHCTRNYIHLNLFASFILRALSVFIKDAALKWMY-STAAQQHQWDGLLSYQDSL : 224
HsaGLP2R: DRYALLSTLQLMYTVGYSFSLISLFLALTLLLFLRKLHCTRNYIHMNLFASFILRTLAVLVKDVVFYNSYSKRPDNENGWMSYLS-EMST : 258
HsaGIPR : DQRLILERLQVMYTVGYSLSLATLLLALLILSLFRRLHCTRNYIHINLFTSFMLRAAAILSRDRLLP-RPGPYLG-DQALALWN--QALA : 214
S000537 : HYGLILGQLRIMYTVGYSLSLGALLLALGILLAFRKLHCMRNNIHMNLFASFILRAVSILVKDAFLTLTLDSRSSNNTQAQAPVNTTGIT : 175
S006614 : WFKQMMVNFRMVYTVGYSISLLTLSTALVILLSFRKLRCSRNYIHANLFLSLILRAVSVIIKDTMLERHWGREIV--------KQTDAAI : 181
S007267 : DEMHLQTALRLISIIGYSLSLFSLTVATLVMAMLRKLHCTRNYIHMNLFVSFILRAMAVILKEIIFYIKHFNLPKDDPQWKSYADSAIVL : 167
CinS5B  : GPLEGGPKHNDIYTAGYIFSLVCMVIALFILMFFKKLHCTRNYIHMNLMLSFIVRYVAVMVKDKVLEDHYAVGQTNLTQMEMSQYCDDVS : 193
CinS5A  : LLLSIIDIVTKIYTAGYIFSLVCMVIALFILMFFKKLHCTRNYIHMNLMLSFIVRYVAVMVKDKVIEDHYAVGRPNLTQMEMSQYCDDVA : 197
CinS70  : DYNARYEILTRYVTVGHALSLATLLVALALLACLKNIHCTRIYIHMNLMAAFMFRGLIWILHSAAFRGEQDLMVEILNNLVTLQN----- : 124

                             TM3                                     TM4
HsaGCGR : G-------CRVAAVFMQYGIVANYCWLLVEGLYLHNLLGLATLPERSFFSLYLGIGWGAPMLFVVPWAVVKCLF--ENVQCWTSNDNMGF : 303
HsaGLP1R: S-------CRLVFLLMQYCVAANYYWLLVEGVYLYTLLAFSVFSEQWIFRLYVSIGWGVPLLFVVPWGIVKYLY--EDEGCWTRNSNMNY : 305
HsaGLP2R: S-------CRSVQVLLHYFVGANYLWLLVEGLYLHTLLEPTVLPERRLWPRYLLLGWAFPVLFVVPWGFARAHL--ENTGCWTTNGNKKI : 339
HsaGIPR : A-------CRTAQIVTQYCVGANYTWLLVEGVYLHSLLVLVGGSEEGHFRYYLLLGWGAPALFVIPWVIVRYLY--ENTQCWERNEVKAI : 295
S000537 : W-------CRGAMVMMQYSVMANNYWLLVEGIYLHSLLVITVFSEKKYFYIYMAIGWGAPLMFVVPWTTVKYLY--ENEECWERNINMGF : 256
S006614 : G-------CRMAQAVMQYCVLANHCWFFGEAVYLYSVLIASVFIDNNKHLPYICLGWGTPLLFVIPWVVMKLLK--ENKECWAFNENMNY : 262
S007267 : S-------CRVSAVCMQYFVACNYFWLLVEAVFLHTLLFSAVLTKRRLLKRYMLLGWGTPVLFVTPWTVVKILH--ENTGCWSIMN-KWI : 247
CinS5B  : --------CRLVITLMHYAIIANYFWLLVEGVYLQ-LLLVFVMTEYKYFPIFMAFGWGAPWIPIGIWVAFRITF--ENVGCWEIYNALRT : 272
CinS5A  : GTDGLMVSCRLVITLMHYATIANYFWLLAEGVYLQ-LLLVFVMTEYKYFPIFMAFGWGATWIPIGIWIAFRITF--ENVGCWEVNNMIPI : 284
CinS70  : -------WCRLYNVFQIYFVTANYFWLLVEGLYLRLLLRAVLFSHTKYMKAFLVLGWGLPWLPVVAYFVPKSLDPEENRDCWYEDRNSAY : 207

                    TM5                                            TM6
HsaGCGR : WWILRFPVFLAILINFFIFVRIVQLLVAKLRA-----RQMHHTDYKFRLAKSTLTLIPLLGVHEVVFAFVTDEHAQ--GTLRSAKLFFDL : 386
HsaGLP1R: WLIIRLPILFAIGVNFLIFVRVICIVVSKLKA-----NLMCKTDIKCRLAKSTLTLIPLLGTHEVIFAFVMDEHAR--GTLRFIKLFTEL : 388
HsaGLP2R: WWIIRGPMMLCVTVNFFIFLKILKLLISKLKA-----HQMCFRDYKYRLAKSTLVLIPLLGVHEILFSFITDDQVE--GFAKLIRLFIQL : 422
HsaGIPR : WWIIRTPILMTILINFLIFIRILGILLSKLRT-----RQMRCRDYRLRLARSTLTLVPLLGVHEVVFAPVTEEQAR--GALRFAKLGFEI : 378
S000537 : WWIIRSPILFAYLINFFIFIRIIKILMSKLRA-----HQMRYTDYKFRLAKSTLTLIPLLGIHAILFTFVIDESVQKGSLLRLIRLFYDL : 341
S006614 : WWIIRLPILFASLINFLIFMKILKVILSKLRAN----KQSGYPDYKLRLAKATLTLIPLFGIHEIIFIFATDEQTT--GILRYIKVFFTL : 346
S007267 : WWIIRGPITLTFVINFCIFIKILMLLLSKLKA-----DQLKFTDYRYRLAKAKLVLIPLLGIHEVVFMVLTDECME--GRSLYAKNFVNL : 330
CinS5B  : WWILSAPILISIAINFIIFINIIRMIVSKLRA-----NNMTRSDYKYRLARSTLALIPLLGIHYIIFMGVSDSVTN--STITKTKFAFEL : 355
CinS5A  : WWILRAPILISIAINFIIFINIIRMIVSKLSA-----NNMTRSDYKYRLARSTLALIPLLGIHYIVFMGVSDSVTDN-SAFINTKFAFEI : 368
CinS70  : WWIVKVPILISLLINFIIFVNVVCVVGAKLRVNQRQQADDRREDYKWRLTKSTLSLIPLLGTQYLITAFVHFDSEEN-PTAEFVKKAFEV : 296

                TM7
HsaGCGR : FLSSFQGLLVAVLYCFLNKEVQSELRRRWHRWRLGKVLWEERNTSN-------------------------------------------- : 432
HsaGLP1R: SFTSFQGLMVAILYCFVNNEVQLEFRKSWERWRLEHLHIQRDSSMK-------------------------------------------- : 434
HsaGLP2R: TLSSFHGFLVALQYGFANGEVKAELRKYWVRFLLARHSGCRACVLGKDFRFLGKCP--KKLSEGDGAEKLRKLQPSLNSGRLLHLAMRG- : 509
HsaGIPR : FLSSFQGFLVSVLYCFINKEVQSEIRRGWHHCRLRRSLGEEQRQLP-------------------------------------------- : 424
S000537 : LFSSFQ------------------------------------------------------------------------------------ : 347
S006614 : TLNSFQGLLVSVLYCYANKEVRTELRRKWHIWRTEAEFV--------------------------------------------------- : 385
S007267 : TLNSFQGFLVAVLYCFANGEVQAELKKRWQLFLFTNHFQVRGCFQGKPLKQLWKCTQGRRPQCSRQSDSCDEGEASTTHPQLLQVAVHRG : 420
CinS5B  : ILTSLQGSIIAILYCFLNGEVQTEIRKCWRNWRWSHRLPAASGKFSTYRSDVQMTSITYAHSIDKGD----------------------- : 422
CinS5A  : ILTSLQGSIIAILYCFLNGEVQTEIRKCWRNWRWSHRLPAASGKFSTYRSDVQMTSITYAHSMDKGD----------------------- : 435
CinS70  : SFVSIQGLLVAFIYCFFNGEVQEECGKTWRRWKTRWELERRERKHHR------------------------------------------- : 343

HsaGCGR : ------HRASSSPGHGPPSKELQFGRGGGSQDSSAETPLAGG-LPRLAESPF----------------------------- : 477
HsaGLP1R: ------PLKCPTSSLSSGATAGSSMYTATCQASCS---------------------------------------------- : 463
HsaGLP2R: ------LGELGAQPQQ--DHARWPRGSSLSECS-EGDVTMANTMEEILEESEI---------------------------- : 553
HsaGIPR : ------ERAFRALPSGSGPGEVPTSRG----LSSGTLPGPGNEASRELESYC----------------------------- : 466
S000537 : --------------------------------------------------------------------------------- :   -
S006614 : --------------------------------------------------------------------------------- :   -
S007267 : GRAVGVRGEVKGQGSGGCDSAGLDLLTRKSLSSSDGELTLGETMGEILEESEF---------------------------- : 473
CinS5B  : ------AHETSLLSPNNKHDHVDNKRSSTASCVSDQQTKIGDSSRLMCNGNGSPSKQLVV--------------------- : 476
CinS5A  : ------AHETSLLSPNNKHDHVDNKRSSTASCVSDQQTKIGDSSRLMCNGNGSPSKQLVV--------------------- : 489
CinS70  : ------MQRRRSMNHSSITNLFTSVVTRKSSLYTGES-------------------------------------------- : 374
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