

HsaCALR : -----MRFFTSRCLALFLLLN : 17
HsaCGRPR : -----MEKKCTLYFL : 10
S000611 : ----- : -
S001267 : ----- : -
S002353 : ----- : -
CinS93 : ----- : -
DmeCG13758 : MTLLSNILDCGCISAQRFTRLLRQSGSSGSPSAPTAGTFESKSMLEPTSSHSLATGRVPLLDHFDASTTESPGTYVLDGVARVAQAL : 90
DmeCG32843 : -----MSDQIGNPNAT : 11
CelC13B9.4 : -----MADATSPFNVSILDN-ST : 17
CelC18B12.2 : ----- : -
CbrCAE6326 : ----- : -
CbrCAE7012 : -----MADATSPFNVSILDNSTA : 18

HsaCALR : HPTPILPAFSNQTYPIEPKPFYLVVGRKKMMDAQKYCYDRMQQLP--AYQGEOPYCNRTWDSWLCWDDTPAGVLSYQFCPPYFPDFDPS : 105
HsaCGRPR : VLLPFFMILVTAELLESPEDSIQLGVTRNKIMTAQYECYQKIMQDPIQQAEG--VYCNRTWDSWLCWNVAAAGTESMQLCPYFPDFDPS : 98
S000611 : -----LGITRNKIVTAQFECYQKIMKDNDRSRGRGEPMCRNPWDSWLCWDDTKAGVISEQHCPPYFPDFDPS : 67
S001267 : -----SYCSRNDWDSWLCWDDTQAGTVASQNCPPYFFNTDPT : 36
S002353 : -----ANHTNLNQNIQAKNQFSCLCQCNMTWDSWLCWDDTAAGTTTEQSCPPYHNFDPQ : 55
CinS93 : -----MYNFEFTRQQNCFVNDLNI SRNSKSNFVCSFSCGAIWDGYACWPTQSSKEAVQNCPPYLPRFNTE : 68
DmeCG13758 : EPTVMDALPDSDEQVLGNLNSAPWNLTASAAATNFENCALFVNYTLPTQGLYCNWTDLCLLWCPPTPAGV/LARMNCPGGFHGVDR : 180
DmeCG32843 : FSGSGSGSTNVASIAESVAESGPDFDALRAACETRLNASQGLAGSGGGPAGAEAGTHCAGTFDWSWLCWDDTAVGTSAYELCPDFTIGFDPA : 101
CelC13B9.4 : KLSEMVESGWNVLASTSVQAFNEAMDVLEESYPLCKKMLDHNLFPERDPNDTRWCNATYDVLWCPPTPANSSVTLQCPHMKGLDPNK : 107
CelC18B12.2 : -----MTSIIIRAEEYAAQELKLENSYNNPGGCSVDFDKSLCWAFAHIGDQMDTRDCCPTFCTAIPG : 61
CbrCAE6326 : -----MTSIIQTEYEACEKLAQ--NNSYTGSGCSVDFDRSLCWAFAHIGDQMDTRDCCPKFCTSIIPG : 60
CbrCAE7012 : KLSEMVDGWNVLASTSVQAFNGAMDVLEESYPLCKKMLDHNLFPERDPNDTRWCNATYDVLWCPPTPANSSVTLQCPHMKGLDPNK : 108

HsaCALR : ----- : -
HsaCGRPR : ----- : -
S000611 : G----- : 68
S001267 : ----- : -
S002353 : ----- : -
CinS93 : ----- : -
DmeCG13758 : ----- : -
DmeCG32843 : R----- : 102
CelC13B9.4 : ----- : -
CelC18B12.2 : ----- : -
CbrCAE6326 : ----- : -
CbrCAE7012 : NIVKRCDEMGRWAGKPKPGWNTNFVCFKIDYEDVKFSSCVRLIRCNVFCVTPHKVPYSNHTRHQTHFLIRAILDLYLSNQP : 198

TM1

HsaCALR : -----EKVKYCKDEKGVWFKHPENNR-----TWISNYTMCN-----AFTPEKLNAYVLYVLAIVGHSLSIPTLVIS : 166
HsaCGRPR : -----EKVTIKCDDQGNWFRHPASNR-----TWITNYTRCC-----VNTHEKVKALNLFVLTIIIGHGLSLIASLLIS : 159
S000611 : -----EMVTIKVCTDGGYWFQHPESNR-----TWITNYTRCC-----EHTHEGR-TAMNLFV/LALIGHGLSLTSLFIS : 128
S001267 : -----EKATKYCGEDGQWFRHPDTRN-----TWISNYTLCN-----ENTKAKLSAYILFYMAIVGHASIASLLIS : 97
S002353 : -----AVASKVCTENGEGWRHPESNR-----TWITNYENCI-----ANSTNHQTAAMHFVLYVIGHTLSLVSLIS : 116
CinS93 : -----EFAVRPCQANGWFRYPTTQY-----QWITNYSRQCLQ-----KGQEAUVAKYRLAISGYSVSMITLLVA : 127
DmeCG13758 : -----KFAIRKCELDGRWSSRPNATEVNP--QWTDYCPCKPEIIRLMQMGSKDFDAYIDIARRTRLEIVGLCLSLFALIVS : 258
DmeCG32843 : -----YAHKECGLDGEWFKHPLTNK-----TWISNYTTCVN-----LEDLNWRHTVNLISEVGYGTSLLAAILIS : 160
CelC13B9.4 : -----NITKDCHVSGVWSSGRNAGEMGPTLPQWTFNFTMCYTDDEVYIMQNLNNEESLITAEQVARNARKLEFVGLGLSLVSLILA : 185
CelC18B12.2 : -----CEEIKDRYMVSRNCNSMGVWQ--DSNYTMCIKVVEEYAAQCLG-----FCRVCPDVLRLDVI SVSLTSLFVSVILLVAA : 133
CbrCAE6326 : -----CEDIKKYMVSRNCNSMGVWQ--DTNYTMCIKVVEEYAAQCLG-----FCRVCPDVLRLDVI SVSLTSLFVSVILLVAA : 132
CbrCAE7012 : TSTKLYTSTENITKDCHVSGVWSSGRNAAEMGPTLPQWTFNFTMCYTDDEVYIMQNLNNEESLITAEQVARNARKLEFVGLGLSLVSLILA : 288

TM2 **TM3**

HsaCALR : LGIFVFFRKLTTIFPLNWKYRKALSLGCQRVTLHKNMFLTYILNSMII IHLVEVVPNGE-----LVRRDPVSCKELHFFHQYM : 245
HsaCGRPR : LGIFFFYFKS-----LSCQRITLHKNLFFSFCVNSVVTIIHLTAVANNQA-----LVATNPVSCKVSQFIHLYL : 222
S000611 : LGIFFFHN-----CQRITLHKNLFFSFCVNSVVTII IWLTAVANNQA-----MVQRNPTSCKVSQFIHLYL : 188
S001267 : LAISSTSGDKSDLG-----WIFLSCQRITLHKNLFFSFCVNSVVTII IYLVAVVANNPE-----VVSNR-VGCKLHFFHYM : 167
S002353 : LTIFFYFKS-----LSCQRITLHKNLFFSFCVNSVVTII IWLTVVANNQA-----HHTHYSAICK-LLMFHLYL : 178
CinS93 : LFIFFFHRS-----LQCRVITMHHKLFVSVYLNALASVWLVHSHTIPGVS-----QVYCKFLHAIHQYT : 186
DmeCG13758 : LLIFPCTFRS-----LRNNRTKIHKNLFFVAMVLOVIRLTLVLDQFRRGNKEAATN-TLSVSIENPTYLCEASYVLLLEYA : 331
DmeCG32843 : LAALGYFKS-----LKCARTLHMLNLFASFAANNSLWLVWVLLVMPNSE-----LLHQSMPRCAALHITLHFY : 223
CelC13B9.4 : ISIFSIFRR-----LRVFRNLHLHLMIAMLMVYIRLVLYIDLIFGTGENGPHNTSAEGKTIINTMPIVCEBMFFLEFY : 259
CelC18B12.2 : IVLFSIFDS-----IQCRRLSIHKNLATAFVFRFAVLAITWIVQSTNLFQDCTR--LTPLPLWDEWICKAILWFVVIYF : 205
CbrCAE6326 : IILFSVFDL-----IQCRRLSIHKNLATAFVFRFAVLAITWIVQSTNLFQDCTR--FHPLPIDWLEWICKAILWFVVIYF : 204
CbrCAE7012 : ISIFSIFRR-----LRVFRNLHLHLMIAMLMVYIRLVLYIDLIFGTGDI GPHNTSAEGKTIINTMPIVCEBMFFLEFY : 362

TM4 **TM5**

HsaCALR : MACNYFWMLCEGIYLT-LIVVAVFTEKQRLRWYVYLLGWGFPVLPVTTIHAITRAVYFNDCNWSVETHLL-----YIIHGPVMAALVVNL : 329
HsaCGRPR : MGCNYFWMLCEGIYLT-LIVVAVFAEKQHLWYVYLLGWGFPVLPVTTIHAITARSLYFNDCNWISSDTHLL-----YIIHGPVMAALVVNL : 306
S000611 : FGCNYFWMLCEGIYLT-LIVVAVFAEKQHLTWYVYLLGWGFPVLPVTTIHAITARSLYFNDCNWISSDTHLL-----YIIHGPVMAALVVNL : 269
S001267 : LGCNYFWMLCEGIYLT-LIVVAVFAEQHLLWYVYLLGWGFPVLPVTTIHAITARSLYFNDCNWISSDTHLL-----YAVHGPIVAALLVNL : 251
S002353 : LSCNYFWMLCEGIYLT-LIVVAVFAEKQHLWYVYLLGWGFPVLPVTTIHAITARSLYFNDCNWISSDTHLL-----YIIHGPVMAALVVNL : 262
CinS93 : ETSNYFWMLCEGIYLT-LVVVSVFREKQNLIIYVYLLGWGFPVLPVTTIHAITARSLYFNDCNWISSDTHLL-----YIIHGPVMAALVVNL : 270
DmeCG13758 : RTAMFMWMLIEGLYLT-LVVAVFQGSFPLKFFSRLGWCVPILMTTVYVARTVMYMDTSLGECLEWNYNLTP-YYNILEGPRLAVILLNL : 419
DmeCG32843 : LLSNYSWMLCEGIYLT-LVVAVFISEKRLKWLIAFGWGSFAIVFYVSMARGLGCTPEDNRHCWNNQNTNYQ--NILMVPCISMFNLN : 310
CelC13B9.4 : KTVTFWMLFLEGIYLT-LIVVAVFSEKRLKWLIAFGWGSFAIVFYVSMARGLGCTPEDNRHCWNNQNTNYQ-EPNILEGPRLAVILLNL : 347
CelC18B12.2 : NVASVMMMLIEGAFVLSRFTVFAAMRHSADPNLSYLACGWGFPVFPVVTAWALVHQYIISQQTNSFCWLPYAQGLHLNLAGTMSALIMNL : 295
CbrCAE6326 : QVASVMMMLIEGAFVLSRFTVFAAMRHSADPNLSYLACGWGFPVFPVVTAWALVHQYIISQQTNSFCWLPYAQGLHLNLAGTMSALIMNL : 294
CbrCAE7012 : KTVTFWMLFLEGIYLT-LIVVAVFSEKRLKWLIAFGWGSFAIVFYVSMARGLGCTPEDNRHCWNNQNTNYQ-EPNILEGPRLAVILLNL : 449

TM6 **TM7**

HsaCALR : FFLNINVRVLTCKMRETHEAE----SHMYLKAVKATMILVPLLLGIQFVVPFWR----PSNKMLGKIYDYVMHSLIHFGQFFVATIYCF : 410
HsaCGRPR : FFLNINVRVLTCKLVTHQAE----SNLYMKAVRATLILVPLLLGIQFVVPFWR----PEGKIAEEVYDIIMHILMHFGQLLVSTIFCF : 387
S000611 : FFLNINVRVLTCKLVTHKAE----SSLYMKAVRATLILVPLLLGIQFVVPFWR----PDGQVSEIYDIIMHIFMHFGQLLVSTIFCF : 350
S001267 : FFLNINVRVLTCKLRDTHRAE----SNMYMKAVRATLILVPLLLGIQFVVPFWR----PENRIAGEVYDIIMHILMHFGQLLVSTIFCF : 332
S002353 : FFLNINVRVLTCKLRVTHQAE----SSLYMKAVRATLILVPLLLGIQFVVPFWR----PDDPRVFESYDIIMEILMHYQGLLVSTIFCF : 343
CinS93 : IILMNLRLVLSKLR-ANRNN-----IQRYLGAIKATLVLIPLLGSQHLLIITLALY-IPN-ASVLRVLSYITNLVLSFGQFAVAIIFCF : 352
DmeCG13758 : CFLVNIIRVLLKLRQSQASD-----IEQTRKAVRAATLILVPLLLGIQFVVPFWR----KATATNFAVWYSGHTFLTSPQGFIALYLCF : 501
DmeCG32843 : LFLCNIRVLLKLNAPASIQSGCSPRTVLQAFRATLILVPLLLGIQFVVPFWR----PKHPWENTYDIISAFATASFGQGLVAVLFCF : 397
CelC13B9.4 : FFLCNIRVLLSKVRESNNTS----EAGLKKSVKAAMMLLPLLLGVPNMQITPFAPTRDNIMVFAVWYFASFTYMSQGLMVASLYCF : 432
CelC18B12.2 : IFLMIVVILVQKLRTEASAE----SKKIWRITIKATLILVPLLLGVSNIPLFYE----PEHP--SSVYMLGSAILOHSGQIFIAVLYCF : 374
CbrCAE6326 : IFLMIVVILVQKLRTEASAE----SKKIWRITIKATLILVPLLLGVSNIPLFYE----PEHP--SSVYMLGSAILOHSGQIFIAVLYCF : 373
CbrCAE7012 : LFLCNIRVLLSKVRESNNTS----EAGLKKSVKAAMMLLPLLLGVPNMQITPFAPTRDNIMVFAVWYFASFTYMSQGLMVASLYCF : 534

HsaCALR : NNEVQTTVKRQWAQFKIQWN-----QRWGRRPSNRSARAAAAAAEAGDIPIYICHQEPNNEPANNQGEESAEIIPLNIEQESSA- : 490
 HsaCGRPR : NGEVQAILRRNWNQYKIQFG-----NSFS-NSEALRSASYTVSTISDGP-GYSHDCPSEHLNGKSIHDIENVLLKPENLYN----- : 461
 S000611 : N--GEAVLRRHWNQHNIQFG-----SSVGNHSDAMRSASYPASSITEVQGCYSIDGHSEHMNGKGFHDTDTSMMLKSDSFFA----- : 424
 S001267 : NGEV----- : 336
 S002353 : NGEVQSVLRRHWNQORMQFT-----GTFA-SADFFRSASYVASSLTVHRCYSTESHAEHLNG---GKSYSDIFRSESFFV----- : 415
 CinS93 : HEEVLIPLLG-----SQHILLTIALYIPNASVLRVLSYITNVLSSFQGFVAIIFCFCHEEVGRIT----- : 413
 DmeCG13758 : NGEVRHQVTQLSICLKPSLFPKTIYIFAVLLKSLATQLSVRGHPEWAPKRASMYSGAYNTAPDPTDAVQPAQDP SATGKRISPPN----- : 585
 DmeCG32843 : NGEVIAQMKRKRMMCFNSR-----PRTNSYTATQVSVFVRCGPPLPGEEKV----- : 443
 CelC13B9.4 : NKEVNHVLKTFYARYRLLHKSQNELRRGSRVASHYAAKNGTANASAPQTNNAEFGKLSPFPSRSKKGSDDDSTTKLMKDAVMEEKKNAN : 522
 CelC18B12.2 : NSEIQGALKRQLSKVPFEFFFKTRNRFETERTYVPEARNATKNGVPMEE MNKTKNIESGENTESQDQVSTGKQIYSVSTKS----- : 454
 CbrCAE6326 : NSEIQGALKRQLSKVPFEFFFKSRNRFETERTYVPEARNATKNGVPMEE LNGTKKIESENIESQEANS SDKQIYSVPTKS----- : 453
 CbrCAE7012 : NKEVNHVLKAFYARYRLLHKSQNELRRGSRVASHYAAKNGTNTNAQQANNADENGLSPFPSRSKKGSDDDSTTKLMKDTVMEEKKNAN : 624

HsaCALR : ----- : -
 HsaCGRPR : ----- : -
 S000611 : ----- : -
 S001267 : ----- : -
 S002353 : ----- : -
 CinS93 : ----- : -
 DmeCG13758 : ----- : -
 DmeCG32843 : ----- : -
 CelC13B9.4 : NNGYGSAGEMTPLREGSNRSTKSP- : 546
 CelC18B12.2 : ----- : -
 CbrCAE6326 : ----- : -
 CbrCAE7012 : NNGYGSAGEMTPLREGYEE----- : 643