Mch-GLP-1(44)----------------------------------------------------------------------------------  
Cjp-GLP-1 MHSFWV-ALLLGSLIAAAGAQLFGGSCSDGNNCR-HGTCVTG-PIENTFWCRC---------------QDGFGGDFCERRCT  
Cbr-GLP-1 MRGFWLLPSLLLLLSSGSLAQIIGGSCSDGDTCAPHGKCMDE-ESTSRLPCAPESFPMSFPSTMPGKQNKKMKQEVVAGECS  
Ce-GLP-1 -MRVLL---ILLAFFAPIASQLMGGECGREGACSVNGKCYNG-KLIETYWCRC---------------KKGFGGAFCERECD  
Cre-GLP-1 -MRIFIISAFILLYSKTATSQILSGLCSDGQMCAPHGKCMDG-YQKDTYWCRC---------------DNGYGGEFCEKECN  
Mj-GLP-1(05) ----------------------------------------------------------------------------------  
Mch-GLP-1(57)----------------------------------------------------------------------------------  
Gpl-GLP-1 ----------------------------------------------------------------------------------  
Mfl-GLP-1 ------------------------------MTATTSSWALDADKFNWHWECNC---------------PDGFEGERCERIVD  
Mi-GLP-1 -----------------------------------------------------------------------------------  
Mhp-GLP-1 -----------------------------------------------------------------------------------   
  
Mch-GLP-1(44)-----------------------------------------------------------------------------------  
Cjp-GLP-1 LECGD-REKCSFDANGKE-KCSCQGVEC-------------------------------------------------------  
Cbr-GLP-1 LQCDD-DEKCGFDAFGKNPRCICKDCDPN------GKKICPKGFGGERDRDRGDADSRDKNFGTFFAGNLIFVVFFSFRFLVL  
Ce-GLP-1 LDCKR-GEKCIYDVYGENPTCICQDCEDETPPTERTQKGCEEGYGGP------------------------------------  
Cre-GLP-1 LECEDDDEKCGFDESGQHPQCICKDCSTD------GRKVCPFGYEGD------------------------------------  
Mj-GLP-1(05) -----------------------------------------------------------------------------------  
Mch-GLP-1(57)-----------------------------------------------------------------------------------  
Gpl-GLP-1 -----------------------------------------------------------------------------------  
Mfl-GLP-1 N-CIT------------------------------GRTICVNGGQCV-------------------------H-----PWLEI  
Mi-GLP-1 -----------------------------------------------------------------------------------  
Mhp-GLP-1 -----------------------------------------------------------------------------------   
  
  
Mch-GLP-1(44)-----------------------------------------------------------------------------------  
Cjp-GLP-1 --------LRLRNVSTSNPCNGNPCNNGKCIPYNDGFMCICNDGFGGSYCDTGHDHCVDNMCQAGSKCVNQMNGYYCDCPTGR  
Cbr-GLP-1 CKN--RPNCANKLTSEENPCLNEPCGNGKCFPFSGGFQCICNDGFGGSYCEIGKDHCVNHNCKTGSQCVNNVNGYICACPPGR  
Ce\_GLP-1 -------DCKTPLFSGVNPCDSDPCNNGLCYPFYGGFQCICNNGYGGSYCEEGIDHCAQNECAEGSTCVNSVYNYYCDCPIGK  
Cre-GLP-1 -------NCEIQIEHLVNPCLNNPCHEGRCAPFSGGFQCICKNGFGGSYCEIGTDNCKNHLCRPGSTCVSTINDYYCACPPGR  
Mj-GLP-1(05) -----------------------------------------------------------------------------------  
Mch-GLP-1(57)-----------------------------------------------------------------------------------  
Gpl-GLP-1 -----------------------------------------------------------------------------------  
Mfl-GLP-1 FENIGNDNITKSVQQRWHPSEWLCQNGATCMNRHGTYLCLCVAGFEGRYCENNIDDCIDNLCYAGSTCLDGISRYTCLCAPDR  
Mi-GLP-1 -----------------------------------------------------------------------------------  
Mhp-GLP-1 ---------------------------------------------------------------------------------   
  
Mch-GLP-1(44)-----------------------------------------------------------------------------------  
Cjp-GLP-1 AGQFCERFNCN----EMS-GICNHGTCVDSPLSDKHFDCSCEPGFEGELCNMDKNECIVEDIC-LNNGTCINLP---------  
Cbr-GLP-1 GGAFCEITNCT----LMGEGICNHGKCIDTFSADKSFECQCDEGYEGEFCTKDKNECLQGDMC-GAHGTCYNLA---------  
Ce-GLP-1 SGRYCERTECA----LMG-NICNHGRCIPNRDEDKNFRCVCDSGYEGEFCNKDKNECLIEETC-VNNSTCFNLH---------  
Cre-GLP-1 AGTFCELTNCT----LLGDEICNHGKCIDKFWNDKNFICECDAGYEGEFCTQDRNECLDEGIC-SHRGTCQNLA---------  
MJ-GLP-1(05) -----------------------------------------------------------------------------------  
Mch-GLP-1(57)-----------------------------------------------------------------------------------  
Gpl-GLP-1 -----------------------------------------------------------------------------------  
Mfl-GLP-1 VGNLCEFPNPCFNTSNNNNGPCLNGKCYPDFEF-GNHSCHCDEGWMGQNCDIDIDECAHPFTNKCSKGKCVNTVGGEKPDPCY  
Mi-GLP-1 -----------------------------------------------------------------------------------  
Mhp-GLP-1 -----------------------------------------------------------------------------------   
  
Mch-GLP-1(44)-----------------------------------------------------------------------------------  
Cjp-GLP-1 ------------GSFRCQCPRGFSGKFCESRVDMC------LFHKCENGGSCVHTERQEPVCQCKNGFVGKRCQEACPSGFGG  
Cbr-GLP-1 ------------GSFVCACKPGFTGTNCQHPVNMC------ESYGCKNGGSCDHLPDQTPVCSCPPGFMGQKCEKACPPGKGG  
Ce-GLP-1 ------------GDFTCTCKPGYAGKYCEEAIDMC------KDYVCQNDGYCAHDSNQMPICYCEQGFTGQRCEIECPSGFGG  
Cre-GLP-1 ------------GGFVCSCKNGFKGKHCQDTVDMC------QEYHCKNGGDCVHLPDRTPVCQCKQGFIGHKCEQACPPGFGG  
Mj-GLP-1(05) -----------------------------------------------------------------------------------  
Mch-GLP-1(57)-----------------------------------------------------------------------------------  
Gpl-GLP-1 -----------------------------------------------------------------------------------  
Mfl-GLP-1 QNHCATDSNEDIEHFTCECLNGWTGPLCDKQIDNEIEVCPLASNPCQNGGQCVGVDGNRG-------------NNKIQKIDGG  
Mi-GLP-1 -----------------------------------------------------------------------------------  
Mhp-GLP-1 -----------------------------------------------------------------------------------   
  
Mch-GLP-1(44)-----------------------------------------------------------------------------------  
Cjp-GLP-1 ERCDLPLHSPVCARNGGSCSNGGRCIRGFCVCPPDFVGNNCELRRNSLT--KE-----NSCASDPCMNHATCTD----VDAHI  
Cbr-GLP-1 YNCSLLLDRPHCSRTNGMCYNGGVCNGGFCKCPPSFTGDRCELNRTAVL-PME-----VSCDHNPCMNDGKCVD----YG--D  
Ce-GLP-1 IHCDLPLQRPHCSRSNGTCYNDGRCINGFCVCEPDYIGDRCEINRKDFKFPDI-----QSCKYNPCVNNATCID----LK-NS  
Cre-GLP-1 YDCKLPLNRPNCSRFNGTCFNDGRCINGFCKCPPGFVGDRCERNWTSVDPYLS-----TSCEFNPCMNNGRCVD----VG--D  
Mj-GLP-1(05) -----------------------------------------------------------------------------------  
Mch-GLP-1(57)-----------------------------------------------------------------------------------  
Gpl-GLP-1 -----------------------------------MNGNLEEGLFD--IPNYGNFREPET--NKL----------AHQLGKD-  
Mfl-GLP-1 EHLSSQFL--------------SSSTFFECICPRGFTGPLCEILPKSTKNNYENIDERQKCINKGCRNGGKCVKNLRNVGDGD  
Mi-GLP-1 -----------------------------------------------------------------------------------  
Mhp-GLP-1 -----------------------------------------------------------------------------------  
consensus 421 g e   
Mch-GLP-1(44)----------------------------------------------------------------------------------  
Cjp-GLP-1 GYVCTCQPGFEGDICERRTDFCAENPCANGGKCSQ-TRSTFSCSCPSG------FRGERCDEKE-KMSCGRNPCVNDGICVR  
Cbr-GLP-1 GYACICPPGFYGLNCDRRL-RCATTTCANGGFCRM-DNNTMTCACPLG------YSGDYCEIME-RLDCKQNPCKNGGVCN-  
Ce-GLP-1 GYSCHCPLGFYGLNCEQHL-LCTPTTCANGGTCEG-VNGVIRCNCPNG------FSGDYCEIKD-RQLCSRHPCKNGGVCK-  
Cre-GLP-1 GYACICPPGFYGPDCDGLL-QCAPTTCANGGICSV-GKRSLSCSCPLG------FSGEYCEVRD-GLDCSRKPCLNGGFCEA  
Mj-GLP-1(05) ----------------------------------------------------------------------------------  
Mch-GLP-1(57)----------------------------------------------------------------------------------  
Gpl-GLP-1 --------------NRAR--MKTVVQCQLGG---ELGGSIVNNPQLPLFFLDDRMMGEIMQRRGKFLIVFDRVCANGGKCQD  
Mfl-GLP-1 LWTCLCPPGFQGSQCESEINACLNVTCKHKGKCVNLGGVDFRCDCAPG------WSGHVCE--INIDDCENIVCLNGGVCVD  
Mi-GLP-1 ----------------------------------------------------------------------------------  
Mhp-GLP-1 ----------------------------------------------------------------------------------  
consensus c g g c n g c

Mch-GLP-1(44)-----------------------------------------------------------------------------------  
Cjp-GLP-1 V----GDTAKCDCPYGFTGLKCEDRVVLTEPK--ESLIRNICEKRRCSLLSGNGHCDEECNQAACDFDGGDCSGGQ-NPFSKC  
Cbr-GLP-1 -----GTDGTCECMYGYTGTRCQEKVEIDKSK--EIMFRELCKKKNCKALAGNGICDEDCNYAECQFDGGDCSGGQ-QPFSRC  
Ce-GLP-1 ------NTGYCECQYGYTGPTCEEVLVIEKSK--ETVIRDLCEQRKCMDLASNGICNPECNLEECNFDGGDCSGGQ-RPFSKC  
Cre-GLP-1 FDRTKGNSGFCNCPFGYTGTMCQEKLVIEKKK--EVLVRDLCKQRNCDARASDGVCNPECNLEECKFDGGDCSGGQ-QPFSKC  
Mj-GLP-1(05) -----------------------------------------------------------------------------------  
Mch-GLP-1(57)-----------------------------------------------------------------------------------  
Gpl-GLP-1 K----VNNFWCECSRGFTGRHCEISVPVDKFNRTDLADRESCAKAGCEAKSGDRRCDPECNLFACQFDGGDCSTKQAQPFGRC  
Mfl-GLP-1 R----VNNYLCECARGFAGRHCEIFVPVDKFNRTDMVDMDNCRRQGCEQKATNGKCDPECNLYACQFDGGECSTRQINPFEKC  
Mi-GLP-1 -----------------------------------MVDMDNCRRQGCEQKATNGKCDPECNLYACQFDGGECSTRQINPFEKC  
Mhp-GLP-1 -----------------------------------------------------------------------------------  
consensus c c gf g c v l e l e c c g c ecn c fdggdcs q npf kc   
  
Mch-GLP-1(44)-----------------------------------------------------------------------------------  
Cjp-GLP-1 PYALKCADVFANGVCNQECNNEECLYDGMDCMSA-VVRCPAKIRKHCAARFGDGNCDPECNSIGCGFDGGDCAVNRTE-----  
Cbr-GLP-1 MYPAKCARSFADGICNPECNNEKCLYDGMDCQSE-LYHCPEYIRDYCIKKRGNGECDYACSFVGCGFDGGDCN-NGTG-----  
Ce-GLP-1 QYPARCADQFANGVCNQECNNEECLYDGLDCQSE-LFRCPAHIRKHCIERRGDGVCNLECSFIGCGFDGGDCN-NGTE-----  
Cre-GLP-1 RYPSRCADSFANGICNQECNNEGCLYDGLDCQSE-LYRCPKDIREYCMKKRGDGECDYACSFVGCGFDGGDCY-NETG-----  
Mj-GLP-1(05) -----------------------------------------------------------------------------------  
Mch-GLP-1(57)-----------------------------------------------------------------------------------  
Gpl-GLP-1 AQASYCAHLFADGKCDEICNNERCLFDGFDCLEGPQAKCPSM--DECAKVYADGHCDEQCNQANCGWDGGDCVNDAHEPDPAD  
Mfl-GLP-1 PQPSYCSHSFSNGKCDEVCNNERCLFDGFDCLPRPLAKCPRL--AECALRYANGQCDQQCNMAACGWDGGDCDHDVEP-----  
Mi-GLP-1 PQPSYCSHSFSNGKCDEVCNNERCLFDGFDCLPRPLAKCPRL--AECALRYANGQCDQQCNMAACGWDGGDCDHDVEP-----  
Mhp-GLP-1 -----------------VCNNERCLFDGFDCLPRPLAKCPRL--AECALRYANGQCDQQCNMAACGWDGGDCDHDVEP-----  
consensus c f g c cnne clydg dc l rcp c r g g cd c gcgfdggdc  
  
Mch-GLP-1(44)-----------------------------------------------------------------------------------  
Cjp-GLP-1 ---VTILTDIRLKIQIDPVE---FQSSGGQTLMEISTALRATVRIQRDE--EGPLVFEWDGNDELGRLS-----MDVKKLTNL  
Cbr-GLP-1 ---AMILNDIRIVIQIDPLV---FRETGGETLMEISTQLRAAVRIQKDE--SGPLVFKWDGESETERLK-----MDAEKLEQQ  
Ce-GLP-1 ---AIILSDIRIKVQIDPIE---FQATGGETLMQISANLRATVRIQRDE--LGPLVFRWDGEHEMERVE-----MNSSKLEDQ  
Cre-GLP-1 ---AMILNDIRLVIQIDPIV---FQETGGNTLMEISRHLRAAVRIQKDD--TGPLVFHWDGEHETERLQ-----MDTKKLSAQ  
MJ-GLP-1(05) -----------------------------------------------------------------------------------  
Mch-GLP-1(57)-----------------------------------------------------------------------------------  
Gpl-GLP-1 DHLQLLPGELFLVVAVHLSTLTNEPTLLRQFLVTLSAHLRASLALSMDQYDKKPKLFEWRSDKGIGQRIELPPELNATSLFNV  
Mfl-GLP-1 -ESHVLLGELVLVLAVQPEE--LFPNLLRQFLLSLSSHLRVSLSLSVDE-EGKPNLFRWSQDSGIGKRIDLPPGMNVTTMFSV  
Mi-GLP-1 -ESHVLLGELVLVLAVQPEE--LFPNLLRQFLLSLSSHLRVSLSLSVDE-EGKPNLFRWSQDSGIGKRIDLPPGMNVTTMFSV  
Mhp-GLP-1 -ESHVLLGELVLVLAVQPEE--LFPNLLRQFLLSLSSHLRVSLSLSIDE-EGKPNLFHWSRDSGIGKRIDLPPGMNVTTMFSV  
consensus mil di lvi i p f q lm is lr tv i de p vfkw e l r m l   
  
Mch-GLP-1(44)----------------------------------------------------------------------------------  
Cjp-GLP-1 ------------------SVLSTRIRRIRSIDLYSMRGIVLYLEVEEI-CQF--DCRFTTAQSVVDLISAG-----------  
Cbr-GLP-1 ------------------KVLSHHIRRYRNVG---IVGVVLYLEVEEI-CQPKSTCRFSTAQSVVNLIAAG-----------  
Ce-GLP-1 ------------------FVLSHHVRRYRQAV---VTGIVLYLEVEEI-CKPE-FCRFSTAQSVVDLIAAG-----------  
Cre-GLP-1 ------------------HVLSHHVRKYRRAE---ITGVVLYLEVEEI-CQPRSTCRFSTAQSVVNLIAAG-----------  
Mj-GLP-1(05) ----------------------------------------------------------------------------------  
Mch-GLP-1(57)----------------------------------------------------------------------------------  
Gpl-GLP-1 RYEQVNKRRSK--------------RLAGEEGEGVVEGIALYLRVDVTMCNMISPG--IRAAHPDRLVGVHTLCFSD---VE  
Mfl-GLP-1 HYYDSDIVVGEEEGKNKNEIVQDRRRKRNLNDISKKEGVALFLRVDVTMCNLLDSS--SPSTSMPRIIHQH--QIPEHPHRH  
Mi-GLP-1 HYYDSDIVVGEEEGKNKNEIVKDRRRKRNLSDI-SKKGVALFLRVDVTMCNLLDSS--SSSTSMPRIIHQH--QIPEHPHRH  
Mhp-GLP-1 HYYETENVGE--EKKNKNEIVQERRK-RDLNDISKKEGVALFLRVDVTMCNLLDSS--SSSTSLPRIIHHQIQEHAEHPHRH   
consensus vl r rr gi lyl ve cq st sv li   
  
Mch-GLP-1(44)-----------------------------------------------------------------------------------  
Cjp-GLP-1 -------LA-KTNGRTSLGLPITE--AMVASPRRT--DTSGWTRNQILLIVVISFLAFGTVVAGVIVKSNEPERSRKRKMVNA  
Cbr-GLP-1 -------LI-KSNGRQSLGFSITE--AMVAAPRRH-EGPVSWSRNQILLIALVAFLALGTVVAGVVVRAGEPERSRKRRIIHA  
Ce-GLP-1 -------LV-KSDGRMSLGLPITE--AMVAVPKRN-EIDEGWSRSQVILFACIAFLAFGTVVAGVIAKNG-PERSRKRKMVNA  
Cre-GLP-1 -------LV-KSDGRQSLGFPITE--AMVATPRRNTDVGEGMSRNQILLVVVIAFFALGTVVAGVMVKAGEPERSRKRKIIHA  
Mj-GLP-1(05) -----------------------------------------------------------------------------------  
Mch-GLP-1(57)-----------------------------------------------------------------------------------  
Gpl-GLP-1 NVAAYVGAANAKKSLNNIPAKILQSEGRIPTPSRL----HIWLAVLAF-----AMVATASAAVGAVFA---SGRIRKRQRRHA  
Mfl-GLP-1 HHHIYHSNNKLLGALQDIGVPILQSEARLSPHSSSKSFGFFWCVLVTL---------MFSLVIGSVII---IRRPKNNKMKSA  
Mi-GLP-1 HHHIYHSNNKLLGALQDIGVPILQSEARLSPHSSSKSFGFFWCVLLTL---------MFSLVIGSVII---IRRPKNNKMKSA  
Mhp-GLP-1 HHHIYHSNNKLLGALQDIGVPILQSEARLSPHSSSKSIGFFWYVLVTL---------MFSLVIGSVII---IRRPRNNKMKSA  
consensus g q lg pi a v w l tvv g iv r r km a

Mch-GLP-1(44)-----------------------------------------------------------------------------------  
Cjp-GLP-1 PVWMPPMDPAVEKSTRRNQS-----------------------------------NH--------SSQRSLIESNGYYGGGGT  
Cbr-GLP-1 PVWMPPPMESL------------------------------------------------------LCQSSLLEHSMHHVN-AA  
Ce-GLP-1 TVWMPPMESTNEKGR-RNQS-----------------------------------NH--------SSQCSLLDNSAYYHP-NT  
Cre-GLP-1 PVWTPPMETPIDKQTPHNSS-----------------------------------IY--------SSQVSLLNDSNMYLN-AP  
Mj-GLP-1(05) -----------------------------------------------------------------------------------  
Mch-GLP-1(57)-----------------------------------------------------------------------------------  
Gpl-GLP-1 KTWKPEIYDPKPIKNALA-------------------------------TMCGGGRHPPLIVGSASLF-------NPYTQHNH  
Mfl-GLP-1 KTWRPPIVEQPSSKYGSSSTLASHYPLHPPQQQTLRASSIWANYPAAPSSSCASSHM-PLMINHAVSMNSLSNQSNIYR----  
Mi-GLP-1 KTWRPPIVEQPSSKYGSSSTLASHFPLHPQQQQTLRASSIWPNYPAAPSSSCASSNM-PLMINHAVSMNSLSNQSNIYSQHSH  
Mhp-GLP-1 KTWRPPIVEQQNSKYGSSSTLASHQQLHQQ-QQALRAPTIWPHYPVASSSSCASSNM-PLMINHAVSMNSLSNQSNIYSQHTQ  
consensus w ppm s s sl s y   
  
Mch-GLP-1(44)-----------------------------------------------------------------------------------  
Cjp-GLP-1 KRH----------------------CGEYGKG---------------------------------------------------  
Cbr-GLP-1 KP----------------------RVDYSD-----------------------------------------------------  
Ce-GLP-1 KRH----------------------CSDYSTG---------------------------------------------------  
Cre-GLP-1 KRV----------------------RREFYLP---------------------------------------------------  
Mj-GLP-1(05) -----------------------------------------------------------------------------------  
Mch-GLP-1(57)-----------------------------------------------------------------------------------  
Gpl-GLP-1 QQHS---------------RAHQQQQTMYFAG-----------------NATESYASSTATSAMPLIKHADSLNSLA------  
Mfl-GLP-1 -----------------------------------------------------------------------------------  
Mi-GLP-1 PQQYQNNSMMQISNNNNNQHLHQQPNKHYCPHPYLPQHSSQQHSSTLPRNNGNCWTT--ATTTTALIGENKNLLTTSSTQNLN  
Mhp-GLP-1 H-QYQNSANSMIQLTNNHQHLQQQQNKLYRQHPYLQQHLLQQS-STLP-RNGNCWTT--ATTT--LIGENNKNI--------S  
consensus y

Mch-GLP-1(44)-----------------------------------------------------------------------------------  
Cjp-GLP-1 ---MEYGVGQYDQI----YPQTLANGFTGDFGAGAVV-----------NEAHDS--MK--------NIE--------------  
Cbr-GLP-1 -------GGLYQEI----YPRTLANGVIGDYAVPA-------------DIP---------------EEI--------------  
Ce-GLP-1 -----YNGEQYSQI----YPQTLANGYPGDYNELN------------FDFQSET--FA--------PAD--------------  
Cre-GLP-1 -----GPEEQYQEI----YPRTLANGVVGEYAAGGAAH-------RVINMPQEP--VM--------PEA--------------  
Mj-GLP-1(05) -----------------------------------------------------------------------------------  
Mch-GLP-1(57)-----------------------------------------------------------------------------------  
Gpl-GLP-1 -SSVHM-NNQQQQQQGQHFHHHLSHHYAQTQHGQ--KTPMPTTNSNN---H-------------------QTDQANLLHQTAL  
Mfl-GLP-1 -----------------------------------------------------------------------------------  
Mi-GLP-1 SSSIHY-GQQQPQL----L-----IGATGNVNGIAAALPLPNNNANIYNNQQQQQQ----------NIATTSTIVNNNNNSST  
Mhp-GLP-1 QQYLIS-SSQQQQL----L-----IGATGNINGIA-TLPIPNNTTNIYNNHNQHISLGNGEINHFPSVQTTTTTSIANNNSST  
consensus q i g g   
  
Mch-GLP-1(44)-----------------------------------------------------------------------------------  
Cjp-GLP-1 ------------------FPPEEITLHQQASGP----ENI------------------------------------------T  
Cbr-GLP-1 ------------------LRPEHITLHVQAASS----API------------------------------------------T  
Ce-GLP-1 ------------------LPADEIPLHVQAAGP----DAI------------------------------------------T  
Cre-GLP-1 ------------------LPAEKILLHVQAAGS----YSL------------------------------------------T  
Mj-GLP-1(05) ------------------------------------------------------------MRPRFNFKFEAEMKVV-------  
Mch-GLP-1(57)-----------------------------------------------------------------------------------  
Gpl-GLP-1 YYSRSFSSGIGGSSTEHSPIGDNS--HCSAVVK-----------------SVENRKILAELRDSALFSRYGLLGQE----ERL  
Mfl-GLP-1 -----------------------------------------------------------------------------------  
Mi-GLP-1 SYSRCSSSGIGGSSTEHSPLGQLLPLHCSSANIVVDPSFVIVGNNNENEEQRQIGKLIKELQDFLMFKRRALLDCNSEIISKL  
Mhp-GLP-19.1 SYSRCSSSGIGGSSTEHSPLGQLLPLHCST---IVEPSLIC---NNENEEQKQRRRHIKELRDFVMFKRRGLLDVNSEIISKL  
consensus i lh i

Mch-GLP-1(44)--MTSSFVNEEERLFQLYPLHYMVFN------NDV---DALKSKLSSSDKLKENINSLDIHGRTPIMLSTVLGHIECAE-ILL  
Cjp-GLP-1 VPLTHESVNQMDCKYKRRVLHWLAAN------ARGKPEDVITAEAVQCISAGADVNARDIDENTPLMLAVKARRVRLAV-VLM  
Cbr-GLP-1 EPITAESVKITDTIYRRQVLHWIAGN------SNGKPEDQITSECLKCLDAGADVNARDFNEDTPLMFAVRARRVRLVS-LMM  
Ce-GLP-1 APITNESVNQVDSKYRRRVLHWLAAN------VRGKPEDVITTEAIRCLKAGADVNARDCDENTALMLAVRAHRVRLSV-VLL  
Cre-GLP-1 EAITRESVKQVDTKYGRQVLHWLAGN------TNGKAEDLVTSESVSCLEAGADVNALDNEENTPLMLAVRARRVRLAV-ILM  
Mj-GLP-1(05) --------PE-----SYKYLFRLVKQMLMIVSRTARLLECLEFNPDEFYQL------------------LRDAE-VAVREQL-  
Mch-GLP-1(57)-----------------------------------------------------------------------------------  
Gpl-GLP-1 GPCVVNASNER----GRTLLHLLFQNPNF---EE--DEQCLLKNIQLLFTKGAKMNALDSDDTSALLLAVRSQKVLAVRKLVA  
Mfl-GLP-1 -----------------------------------------------------------------------------------  
Mi-GLP-1 RTCIVNSTNER----GRTFLHLLFQNMFLMTAND--NEADLLANIDLLFKSGVSIDAQDADGTTALSLAVRNRKFRAVK-LMV  
Mhp-GLP-1 EPCIVNSTNER----GRTFLHLLFQNMLLMTSND--NETDLLANIDLLFKFGVSIDAKDDDGTTSLSLAVRNRKLRAVRKLII  
consensus s n r lh l n ed l g ina d d t lmlavr rhir ill   
  
Mch-GLP-1(44)DYGAEANTQNKQMWSLSHEAIL----LKNVDFLRRVLAARDFERYLETNKILKEIRNSFKD--SSDF--YVEMTWEFASWLPF  
Cjp-GLP-1 RAGGNPTIYNSSERSALHEAVV----NKDVRMLTILLTDKRL---------CKEIDELDRN--GMTA--LMLVARSDGDYQVE  
Cbr-GLP-1 KRGANPTIFNKSERSALHEATA----NRDVRMMTNLLRDPRM---------VDEIDELDRN--GRTA--LMMTAGGFGG--TE  
Ce-GLP-1 REGANPTIFNNSERSALHEAVV----NKDLRILRHLLTDKRL---------LKEIDELDRN--GMTA--LMLVARELGKHQVE  
Cre-GLP-1 RHGANPTIFNKSERSCLHEACV----NRDFRMVTILLTDARM---------LKEIDELDRN--GMTA--LMLIAGSYGPQQVE  
Mj-GLP-1(05) -GSGSARVPDL----PQYILTK-LGLDKNLSSLEKNIGEQTGD------EEEEENEEEFRQNKGQKDAQLTAQGLPFNPPNLN  
Mch-GLP-1(57)-----------------------------------------------------------------------------------  
Gpl-GLP-1 DFEADQRLADADGCTPLYAACECG----HVALAEFLIGEATCN------SGNPNINN--GSEEEQDGLVLCALYRRKETPLMR  
Mfl-GLP-1 -----------------------------------------------------------------------------------  
Mi-GLP-1 DRGADANLPDLDNKSPLYHICANLSTEEDLEIAEFLINGV-------------------------ADLKLDTLARETETPLIR  
Mhp-GLP-1 ECNADANLPDIDNKSPLYHICANLSTEEDLKIAEFLINEV-------------------------VDLKLDTLARETETPLIR  
consensus ga i rs l a kdv ml ll d ei k l ma v   
  
Mch-GLP-1(44)VKNMCPSDTYKIY-KHGN----SIRID--------------------------------------------------------  
Cjp-GLP-1 MAKL-------LL-SKGA----KIDAD---GASRKDSEIYKGRTALHYAALVGNMSVLEFLVSRNSNKDKQDEAGKTPLMLAA  
Cbr-GLP-1 MAEL-------LL-KKGA----KIDCD---GSERRDTDKYHGRTALHYAALSDNTQMVDFLVTMNSNKDKQDEKGMTPMMLAA  
Ce-GLP-1 MAEL-------LL-SKGA----KLDYD---GAARKDSNKYKGRTALHYAAMHDNEEMVIMLVRRSSNKDKQDEDGRTPIMLAA  
Cre-GLP-1 MAKL-------LL-VKGA----KIDAD---GVTRKDSDKYHGRTALHYAALCDNIEMVEFLVMKNSNKDKQDEAGQTPLMLAA  
Mj-GLP-1(05) NYKM----DIFMASSIGNYA--LVEEYILNNNELVNYKNKKGWTPIMYSAQSGNMDVCKLLLDNGANPELTNDVGKNANDLAV  
Mch-GLP-1(57)---MGDDTALHLAAAHGHR---QVVMKLLSKKAEVNVYNEHGMTPLHYACFWGYEQICEDLIRAGALAIISNKRGLTPIDVCQ  
Gpl-GLP-1 CAIMPCDQWLRIAELLIEAVAPEQRADFVNQTGDAEFLGYSGKTALHWAAECNNGPMVELLVRHGANREAIDQKGRTPLFVAV  
Mfl-GLP-1 -----------------------------------------------------------------------------------  
Mi-GLP-1 CAALCNPFSLRIAELIISRVEASQRIEFVNYSGK------TLTTALHRAASVGNEPMVRLLIRHGANKESTDKEGKSPLFVAV  
Mhp-GLP-1 CAALCNPFSLRIAELLISRVEVSQRIEFINFSGK------TLCTALHRAASVGNEPMVRLLIKHGANKEVPDKEGKTPLFVAV  
consensus a l i hg i d r kg talhya a n mv lv r nkd d gktpl la  
  
Mch-GLP-1(44)-----------------------------------------------------------------------------------  
Cjp-GLP-1 KEGHEKAVKFLVDKDASLTTADAMDKTAAQ--LAQGNYHYE---------------IAEYLRN-MVVVR----NRERQNALRQ  
Cbr-GLP-1 KEGNLKSVKILACRGASVTIVDGFEKTASQ--YAQDAFHHD---------------VVAFLSN-KNNYL----PEVPQPDPR-  
Ce-GLP-1 KEGCEKTVQYLALNDASLGIVDSMDMTAAQ--VAEASYHHE---------------LAAFLRQ-VANE-----RHRND--IM-  
Cre-GLP-1 KEGHELTVRFLVGHGASVTMADVLDKTALQ--YAREGYHHE---------------VEEFLLT-WIRTE----RERKE--AP-  
Mj-GLP(05) YWGHPPF----------------------------------------------------------------------------  
Mch-GLP(57) PQVRQSIYEIALSSGQ------------------------------------NPQQKIQYNGDSWRNTK----TKRSQEATWS  
Gpl-GLP-1 EQGQYQSTEALLQLHADRTKANSADTKIIPELTSRPGFEHIAELFKMYPEQQHHLQIGRPCSTQQRHSSGEDGTKRPRNSGAK  
Mfl-GLP-1 -----------------------------------------------------------------------------------  
Mi-GLP-1 EQAQYETVSVLLELGADRNKSDMNDTKI-MELASQPGFEPISQLFRKFPENQNNHQHLQFFNSSTRSSSTPKDQQKNQNNGKR  
Mhp-GLP-1 EQAQYETVSVLLEMGADRNKSDMNDTKI-MELSSQ------------------------------------------------  
consensus g sv lv a d d y y   
Mch-GLP-1(44)-----------------------------------------------------------------------------------  
Cjp-GLP-1 QVKVIT-TNGGLAKAGRV-TFKTVKRAASQKPPA-----------------------------YSTSSSSRESNHLT------  
Cbr-GLP-1 SRVCKN-RESANTKGGRQ-TMKKVKRNGSKKTPM-----------------------------------IQETNHLT------  
Ce-GLP-1 R-QQIV-KSGHGAKSGRQ-TVKNIKRAGSRKTPT-----------------------------SA--ASSRETNHLT------  
Cre-GLP-1 QKPTNP-EKCVNQKTGRQ-TMKAVKRAGSRKSPT-----------------------------AST-PPSRDPNHLT------  
Mj-GLP-1(05) -----------------------------------------------------------------------------------  
Mch-GLP-1(57)RFTGVDLQSLALTKQISQSHSGTLYRGKWQGNEVIARVLNIPEVTQR---------ISRDFANEFPLLRIFASAHINPVLAAV  
Gpl-GLP-1 RSAGIDECS------------------KSQKTEIVGAEVAKKAALSTKREQFVQPQQNQ--TAGTSVLPSVCSAVVS------  
Mfl-GLP-1 -----------------------------------------------------------------------------------  
Mi-GLP-1 QRVGTKRRNTATTT-----------TNNSSSNSILQQSLNN--------SNILQNQQQQQISSSPPLLPSIHQNQFN------  
Mhp-glp-1 -----------------------------------------------------------------------------------  
consensus s l   
Mch-GLP-1(44)-----------------------------------------------------------------------------------  
Cjp-GLP-1 -PPPSDGSFSSPSPHYLHTTSSTPTA-----LESSPEYGYHSDITP-TTFMWNSTP---------------------------  
Cbr-GLP-1 -PPHSDGSFSSPSPHYFPMNMSN---------ASTPEFVYNPDM---VQPIWYPTP---------------------------  
Ce-GLP-1 -PPPSDGSFSSPSPHYYPTTTSTPNR-----METSPEYMFNHEMAPPVNAMWYTTP---------------------------  
Cre-GLP-1 -PPPSDGSFSSPSPHYFHTTASTPTA-----MESSPEYVYTQDV---TNSNWYPTP---------------------------  
Mj-GLP-1(05) -----------------------------------------------------------------------------------  
Mch-GLP-1(57)XXPPQL-----------------------------------------------------------------------------  
Gpl-GLP-1 -PPPPQNQQNAMQQHYQEMFCQSMAVQQQKHLQEHRQYVQDHQQ---TKWNWANGGGMATTATMATKQKQQQQNVVCGQQLQ-  
Mfl-GLP-1 -----------------------------------------------------------------------------------  
Mi-GLP-1 -EEDRI-VESSSSSIYSNIRTSSF--------PTATNTINN--T---ILNNYNNNEGISTTTFNVPLV-------SHKEPLKK  
Mhp-GLP-1 -----------------------------------------------------------------------------------  
consensus p y w   
  
Mch-GLP-1(44)-------------------------------------------------------------------  
Cjp-GLP-1 --SPYPDTT--YIHPMV----PTHPYSQTE------LMNNSFYC-----------------------  
Cbr-GLP-1 --QPTTYYGPPSNSSGS----STSPGHYEP------PHDGSFYC-----------------------  
Ce-GLP-1 --PPYQDPN---YRHVP----PNTAFQNAE------QMNGSFYC-----------------------  
Cre-GLP-1 --SSYHDLS----QNMP----PSSSSSGGD------PLNGSFYC-----------------------  
Mj-GLP-1(05) -------------------------------------------------------------------  
Mch-GLP-1(57)-------------------------------------------------------------------  
Gpl-GLP-1 MFSPTLAYP-SLVRNLPHLTPPSSGGNTTTNHLNVLPLGSVAGCYRQLPYKQGHVITREPAPLHQCQ  
Mfl-GLP-1 -------------------------------------------------------------------  
Mi-GLP-1 FMDVYLGYT-PI-------------------------------------------------------  
Mhp-GLP-19.1 -------------------------------------------------------------------

**Fig. S1.** Multiple sequence alignment of *glp-1* in different species of nematodes. Black shading indicates conserved amino acids. Different motifs conserved in these species in *glp-1* (LNR motif, transmembrane domain, RAM domain, ANK domain and PEST domain). Ce- *C. elegans*, Cbr- *C. briggsae,* Cjp*- C. japonica*, Cre- *C. remanei,* Mi*- M. incognita*, Mch- *M. chitwoodi*, Mj- *M. javanica*, Mfl- *M. floridensis*, Mhp- *M. hapla* and Gp- *G. pallida*.