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*.