

A

GH31-1 MKIRDFIKSFGIRKGRQISTTNLVSFEAF-----YDDRGNKFP
GH31-2 MA-----
GH31-3 MERSD-----
GH31-4 MA-----
GH31-5 MDRKKYRNATKYNKVPQEIPKIVLAAAPSTENLSLLDSEMDSKSRNDNNSPDKTDDVIQRDTPRPPMRKNSISMPNLDDLKVFIEQEGDGYDTSTEKIN
GH31-6 ME-----
GH31-7 M-----
GH31-8 MK-----
GH31-9 MS-----
GH31-10 MT-----TFIQQQ

GH31-1 DIKESCTKSNPSQNEEYIGGYVRFKETSEAKPVFRP-----SLPIILVIFILISVF
GH31-2 -----QN-----LLYISLILFIVLYAS
GH31-3 -----KM-----LRPLLLLALIASYVS
GH31-4 -----EM-----IRYAILLVVLTATA
GH31-5 TTIQEEPEPDEFQNISSYPRSVRRKSVLSPRMLKPPEDTELGGSPSNSITSVNSIASLLKEKIQNLPTFRKKKSPEYKTKVVFVGLLFTTIIIVLIVTAYF
GH31-6 -----LKICFNVLTLL
GH31-7 -----ILK-----Y-----LLAIAIAINFATAKY
GH31-8 -----CTTSSAVYSIIKGMNCWRAI-----LIAILLVGVNVQ--L
GH31-9 -----KGCHKLF-----TFLIFLTTLHSIRGI
GH31-10 NELREDEDETATASVKWTVWTTILCKTTIVGWFF-----TFAFALIVPVLTYYL

GH31-1 IILPIIYLVNCFRFTFDNQDFYHRNAPAIYSDTSTKEPKDQTKRPWKLHDLVPPAPDYNQCKLLTDLDFDCFPEDGANAEKCEARGCCWIIPRKNKSVL
GH31-2 AV-----DKNNFKTCEQSSFCRRLRS--VKP
GH31-3 CA-----NHTIYKDCSRIPFCKKLR--TIE
GH31-4 AI-----DKTVFKSCSERPFCNRLRNVVD
GH31-5 LY-----QQKVLA
GH31-6 VF-----
GH31-7 TY-----
GH31-8 VQ-----
GH31-9 VV-----
GH31-10 VV-----NLGTYKEVDTFTCFVNSTFRVPCGKVNISEHECVKLACCYDKPTDSCY

GH31-1 ---SQAPLDVPYCFYPPNYNTYKVVNVTTSETSFGLIAFWRRQYRTAYPDDVDELK--MIVKYETETRLR--VKFVDPSS-----FRFEPYPEV--
GH31-2 GE--SKYELDESLEITDNSVESKLLN-----TEAGILFKFSLTAISGNIFR--LQVDEASPLYARYRPQF--ALRGEPQVAKLKL
GH31-3 NH--SKFTAQLDKLSQTGNVISIPLTN-----SDSQELI--LQISLLVHETAR--IKIAEKGS--KRYQLAD--VLAEEPQTLEISA
GH31-4 DK--SKYSADVYSASIKDNILTVPLKN-----ENGNSLN--LLVSMFEGNKIR--VKVEDPDS--KRFEGLDIVIIIEELKELPLVS
GH31-5 KVYFGNMKLNKAK-----RTVKIFN-----DEGEDVVKLHLGLTTLNVDNVLNCLPADNR-----
GH31-6 ---SFGAEAKIDLKP---TTNGLSISVFN-----DDNEVTLQGTIGFIDFTVS--DCQNHYTQ-----
GH31-7 --KLGDEIDFTA---TSNGIEIYIRD-----AEIGSQLYGTIGVG---KNA--SCIDFPR-----
GH31-8 --CSTVNEIILKP---SSNGLAIEVNQ-----KE--EKKLKGITIGVIDFTNI--NCYGQES-----
GH31-9 --KNGNITLQLEP---KSNGISFAAYD-----GK--IKKLEGILGRGINFSNV--DCIGTQV-----
GH31-10 HYLPSRYSYDLAGSSYKASRSSPFTN-----TAVEEMQ--ISVNEISINKVS--IILHKPS-----

GH31-1 -----PIVDKASLALSIIQIN-----TFKSGFKVLRKSDN-----VTIFDSNNFLNLI-----YSNQ--
GH31-2 LE--RNKEYVSI---EYNNKVVIV-----HARP--FKIEVFDKDELISVNVNGRGLFKFEHFRKKPEQNNEGEQQVEAEDPGTWEENFKSHHDS
GH31-3 KT---SRE--VSIAPTNASYSYKVVVT-----TGTS--FKVEFYDD-----NTRKIALNGEQLV-----FDKEDN--
GH31-4 DTLDGTDGS--LLVTPKDESPLYKVVVID-----AGPP--LNITFY--G-----GLKQVVLDERLV-----YESTDES
GH31-5 -----DGGSLCLEWMHRARLYMNFDDLGSVDKCYNVQWIALS-----ESL-----
GH31-6 -----CAFNGSSLSIN-----EVDSGYQIVWNSVY-----TDG-----
GH31-7 -----CKVGDNDVAFRF-----LPGTSLSVISTTNN-----TQE-----
GH31-8 -----CQVGDADFSVK-----QSEDFHIKWETNN-----LTS-----
GH31-9 -----CVINDSNFSVE-----PISAGFRLKWKTFN-----TRR-----
GH31-10 -----TSAIENTVNVREYVVKK-----AAEK--LMVEIFRPN-----GDRIFSTAKGPLI-----ASEN--

GH31-1 -----MLQISSKL---PSKYIYGIGEHRSNL--LLSTE-----WSKFTLFNNDMVP-----TDNKNLYGSHPFYLMENSTKSHGVLLNS
GH31-2 KPKGPSAVGLDISF---PGALRVYGLPEHADRL--PLRTTGGPG---VDPYRLYNLDVFE-----YELDSTMAIYGAI PV--VYAHSPKRTIGAFWLNA
GH31-3 -----SFAFATEF---INAKRLYGLHHHPVKL--ELPSTRDVGKVLMDPYRNRNADNDH-----YEVGSPMAVYGSVPV--VYGHSENQTSGIFLHNA
GH31-4 K----AFTFKADF---PEANRLYGLLDHAWSL--ALGDTNNGTAES--GDPLRLRNSDSWG-----YEANSPMALYGARPV--VYGHSAKNTSGIFLHNA
GH31-5 -----APTDCFDM---SHSHWYGGQTAENAWPLEKGSHF---YQPFITGNIETHEWGNVLKRYFINS-----KGAAIIVVDNE
GH31-6 -----EFVDKQFL---NSGNSYWFGGPERYLQN--PLEKLVNNG---NDPYVIKKAADNFA---VAERYWLSN-----KGTFFIFDDK
GH31-7 -----VLKDCFFTAFPSASTQWYGGPERRVQTWPLQHMRI SQ---SSPYLSRKDDNHA---VAERYWLSN-----LGIIYIYLSEE
GH31-8 -----VFQDCDFD---EEGVHWHYGGPERKKQSWPIEKLEIES---YQAYVLHQLDNFA---VAERYWLSN-----KGLYIYLNK
GH31-9 -----AFQDCYDL---TEGWQWYGGPTIFSLIWIPIQTNEIDG---SSPYVLDNKGKMP---YAERYWLSN-----KGSYIFLDDD
GH31-10 -----YWEWTVHL---TDHSLFGLDKT---LLQRHKNST---ISKVFYKKNNDHS-----NFPV--IWAYHRGQFHGLTVKHD

GH31-1 NAMDVILQ-----PTPAITFRTIGGI--FDFYFFLGPTPS-----DVISQYTDLIGRPYMP-----PYWGL--GFHLRCRF
GH31-2 AETWVDINNSKDGVMSSIVNLVSGSKSENNVDVHFMSESGV--ADLFILLGPTPK-----AAVKQYASLTGVHPLP-----QYTTL--AYHQCRWN
GH31-3 AEQWIDIWYDEES-----TSGWSYFMVESGT--LDFILLGNQPK-----NVVRQFTKLTGVAHMP-----QLWTL--GYHQCRWS
GH31-4 AEQWIDASSGSEG-----KDPVYFIVERAA--FDLFI LLGPTPK-----EIVRQFTGLTGKAHL P-----QI WAL--GYHQCRFS
GH31-5 TPLYISIRDSP--KKEFCLRAQ-----YDNFAFVNKFTSTAQLNYSICTSANMSQLHVFLSEHTLWDGLKKEDSNIIDYFLTEPVWEM--PDMKEALTQ
GH31-6 VPLFIDQNNNE--NGALLLI AKCI-----NP---YVNRQRNI--LKYDLVTKKNAKEAHL---HAVNNYL GKPTGYPNENMIRKPIWTTWPKYKQPVDO
GH31-7 NPLFVSNQEDDSKDQVCFISKVQ-----SP---YINRDQNI--LEYVIYFSDDPKTAHL---NAVNTYL GKPNGYPNPKMIKEPIWTTWAKYKAPITD
GH31-8 VPLYVDQNISN--KNRVCFAKLE-----GP---YINRHKNF--LEYDIVIKDDPREAHV---HAVKTFLGKPSGYPDERMITPIWTTWAKYKTKISD
GH31-9 VPLYVDQNKLR--NNSVCFKSYIR-----DPFHAYFNRTNRV--LQYLYIFKDDVKQAHL---HAVNKFLGKPKDHPNEAMVAEPIWTTWAKYKTKIND
GH31-10 GPLEVSILT-----SNLIILKGLLGET---IELVLYTGPTPA-----DLHQHLEDSEQLDV-----PEWLL--KTHMCRKN

GH31-1 YKTLNNTNRHV---MQRNIDAGIPLDQWNLDDYMNDSNDFTYNQVNFKD-LPSFVRELHSGRMHYIPLIDPGVSASEKPGTYPPYDVGIEMDIFIKNSSG
GH31-2 YNEDDDVTV---VQTFDANDMPVDFMWLDIEYTNKKYFTWDPIKFPH-PEIMVNNLTATGRKLIVIDPHYKRESG---YFVHEDCLANDYYVKTND
GH31-3 YKTQEDTKFV---VAEMNANNFPMDAIWLDDIDYDQKRYFFWDPEYSD-PEELQRLNLSSTNKLVVILDPHIKVDE---YPVYGA-KGKYFVKKPNG
GH31-4 YKSQDDVKDV---VARLDENDFPWDAIWLGDHDTDDYKWFHWNHTTYTD-PVELQONI SATGRVCSV ISDPHIKVDDD---YDVYAGA-KGKYFTKWANG
GH31-5 DVIDNVTTKITNSVAVLKQGHILINEFW-----QEIQIGDFELDQSRFPD-FDKLIEKLRGRFRVFTIQPFIISTESF-----NFAEV-VRKLLVSRFS
GH31-6 NKVNEFVKSIVDH--NFLGGQIEIDENW-----EVCFGSHVFNKDKFPD-ENGLDISIKSQGFKTALWINPFVNNDCQ-----NYSNEGLDKGYFVKDVNG
GH31-7 DIVIEFAKSIREN--GFENGQLEIDDW-----EKCYGAQEFSEKFSK-PSDTVKQLKDMDFRVTLWVHPFVNECDK-----YRSDGIIQGGFFVKGVNG
GH31-8 EIVLDFAKDIRDN--GYEKGQIEIDDYW-----EKCYGAQEFPTPTTFPD-ITNTIKTLKWSYRVTLWIHPFVNSDCQ-----DNSKIGLEKGYFVLDQNG
GH31-9 SVVLFKFAKDIRNH--GYEKGQIEIDDNW-----ERCYGAQEF-SHNFTN-IKDTVKILKSNFRVTLWIHPFVNDNCN-----NNSQIGLEKGYFVIDKYG
GH31-10 EKFLNVSTLVSNFVLDSEADSFICIDENL-----LMGILAEARANDTSYQDAVQALITPLREKGGKFLLSVPPQVLTNSD-----FYNNASSLDLTYLTK

GH31-1 Q---PFVGVWNRV-STVWPDFTNPNVVDYWTLM---LKNLHKE-----IQFDGAWIDMNEPSNFLSGAFNGCPNSTLETPPYFPDIDGGVINY
GH31-2 N---VYEGWCWPGS-SS-YIDFYKPEAAEYKYLRLNFKGTS-----HDVY-IWNMNEPSVF-----NGP-EITMPK-----
GH31-3 E---DFKGDWPGS-SS-YIDFLDPEARADYASWSYKFKKST-----PVLAGVWDMNEPSVF-----DDELEKTLPF-----
GH31-4 S---EYVADCWPGA-SS-WIDYLNPEAADYSTWFSFEKFNST-----PTLAGIWNMNEPAVF-----DDSTEKTMPW-----
GH31-5 DKRI PALTRYKSLQ-SAGVLDITNVQTI SWLLHK---LKKVMNT-----YKIDSYFLDYGVA-----YNNPH-----
GH31-6 D---T-RAIWESA-NAHQVDFTNPDAAKWFSDK---IKALADD-----PGLDGFKFDAGETDY-----AIPPH-----
GH31-7 L---N-NATWNGNGNGHQIDFTNPKAAEWYTD---LKKLQTN-----PGIDSFKFDAGEADY-----AEQPA-----
GH31-8 R---A-NGSWWNGN-DSYQIDFTNPEAAEWW SAR---LKKLQON-----PGIDSFKFDAGETDY-----SPQPS-----
GH31-9 R---H-TGWWNSN-DAYVIDFTNPQATEWWLQR---VKKLQKD-----FGFDSFKFDAGETDF-----CPQPA-----
GH31-10 T---IYQGGYLDQD-VS-YIDYSHENIQKYMVEVFGTFLEDFNHTIDGLVLTDNWPANEEFKMDNDSFPYF-----TKALQDAMSY-----

GH31-1 KTVCMASAKQYAGLHYNVHNLGLTEAIVTNFALAEIRG--KRPMVISRSSFGLGHYAGHWSGDVWSSW---DDLKFSVPTILSFLYGVPLMGADICGF
GH31-2 -DTI---HHGGWEHRDVHNEYALAHYATFQGLLQRTPN-KRPFILTRGHFPGSQRYTVVWTGDNAAEW---SHLAVSYPMCLSEALGGMSFCGADVGGF
GH31-3 -DVL---HHGNVPHRDHNIYGLFQTMATHQGLMQRDNGTKRPFILTRSHFAGSQRYTAMWTGDNTADW---PFLQVSYSECLISNIMGLVFCGADVGGF
GH31-4 -EVQ---HYGGVEHGDHNIYGLLHVKSTHKLMDARDQNAKRPVFLTRSNFAGSQRYAAMWTGDNSATW---EHFANSISECMNANMLGMVFCGADVGGF
GH31-5 -YYQ-----CEKALNLPDEYKTI FTNNLQG-----EVPLFGVNSAIERPRSPSFVVLPEFEFSW---DGLRKI IPTILTYGILGYPFLIPGAVGG
GH31-6 -QFD---HVE---DQEEVFNITFKKYVETCAQ-----FGDLIEVRSWRTQNLIPVFLRMI DKDSLWMTDDGLESVLTTLIQMNLNGYPLVLPDMVGG
GH31-7 -VFP---YVSRAEQNLLPNLITTEYIKTCAN-----FGDLIEVRSWRTQNLIPVFLRMI DKDSLWMTDDGLESVLTTLIQMNLNGYPLVLPDMVGG
GH31-8 -VYH---GV---NQEDVFNILSESYVRTCAK-----FGPLVEVRSWRTQNLIPVFLRMI DKDSLWMTDDGLESVLTTLIQMNLNGYPLVLPDMVGG
GH31-9 -VYK---TV---DQELIPNIFSGKYLRTCAT-----FGNLIEVRTGWRTQDLPI FTRMLDKTSNWAYRNLKSLVLTTLIQMNMVGYTMVLPDMVGG
GH31-10 -TIQWNTTANDILHIQKHSYGGYQYKSLDYFKS-----KEIFILSATKSIQVEP--MI IENVETSW---TNLRKYLDVLFDSII GNHLVSI PVCGD

GH31-1 -----NGNSTAPLCNRWMLGAFYFPRSNHNTDDGIDQDPVAFGP---QVASSVKAL-TARYYLLPYLYTLFHKAHVTGETVARPLFFE
GH31-2 -----FNNPDTELLQRWYQAAVLWLPFRAHAHIDTRRREPFLFPD---DVKNRIRALT-RLRYAHLPLFYTLFWQHEISGEPVIRPLFYQ
GH31-3 -----FHNPETELVQRWYQAGVWLPFYRGAENNTDRREPIYIST---EVQDVIRNAL-RLRYKHIPVWYTLFYEHTRTGDPVVRPIFYD
GH31-4 -----IGDPSDELLQRWYQGAVWTFPFRGHSRESKRREPFLFSK---DVQDVIRNAL-RLRYQHPAIYTLFYEHTVTGDPPIISPLYQ
GH31-5 DYAVPTEMLVTNGTENVLADPELYIRWLQLATFLPVVRYRHL-----PNSYSQN--NIAGLAKELAKKRHESITPKLKKFARVSLNGLPLIIRPLWML
GH31-6 -----NSY-RQAPTAELIIRWTQANALMPALQFGFL-----PWFNSDEFNTELEIVKYYV-SLHEQYSDVIKAMERSVSDGSPVNPPIWWI
GH31-7 -----NGYGGNVPTAELIIRWTQANTFMPMQFSYL-----PWFNSDEFNTELEIVKYYV-SLHEQYSDVIKAMERSVSDGSPVNPPIWWI
GH31-8 -----NGYAGKLPDAELLVRWTQANTFMPAMQFSYL-----PWEITSTKFNVAKIVKKEV-DLHEKYADHII RAMKNSVEKGSFVNPPIWWI
GH31-9 -----NGY-GVQPDALFVRWTQANTFMPAMQFSYL-----PWFNETKFDVPAIAKSCV-KLHKEYSHI IIDAMKKSVLVYSGSPVNPPIWWI
GH31-10 -----TNVFDTSIQMKLCLRWYLI AATMPMFRISAPK-----PWRNPD---DLSAKYDQQAQALDTRNMLLAYNGLISSNEPVIIRPMFYD

GH31-1 FPQDKNTYGI DTHFLWGSDDLIVPVLKENDVNVTAYIPKGN-----WYNYFTLEG-FYSKGEN---F-TLDAPLDTIPLLVRGGAIVPLQ---
GH31-2 YPNDENVVDI DNEILVGSVLAAMI AEPGASVGVYLPGGANEY-----WYDIED--FRLYQGTGN---Y-NIPVSLDKSLAFYRGGSIIPRKD--
GH31-3 YPG---SVDQDYHILLGNSNILARPVMEKARSVTVNFPGSEDNQ-----WYRVDDGFSFKIYNGQSS---A-ILPVTILTSPYFYKAGSIIITRRD--
GH31-4 YPR---VNRDRTQMI GADIMSVAVTKPGVKSVEVYFPGGYSDTDPFKQKDFWYRADQKQFSQYRAGLV---E-QIEVDITSSPVYRAGSIVFVLE--
GH31-5 DSDDPACHLAVDEFSGID EII VAPVLHSGAREREIYLPAGV-----WKDGDID--GSLRKGSRW---IHDYRVEEDNVAYFERMP-----
GH31-6 DPTDSFSYTYIYDEFLLGEDVLVAPVLEGATSRNIYLPKGN-----WKDGNSS--GETFVGPLN---VTNYDAPIDVLPYFVKTD-----
GH31-7 DPTDPVALACNDEYLVGEDILVAPVLEEKSRNRYLPRGR-----WRDQGN--GTVYEGPLS---F-DYPADIDILPFIKED-----
GH31-8 APKDVQALGCDEYLVGEEKILVAPVLEKATSRDVLVYLPAGK-----WVDGNN--GDIYQGPVT---V-DYDAGIDILPFFILSQ-----
GH31-9 DPTDQKALKCDEYLVGEEKILVAPVLTQGATERDVLVYLPKGN-----WKDGNSS--GTYYQGPIT---L-DYADITTTIPFFILEQ-----
GH31-10 FYENTTTFSLYEQYMGKNMLVVHPLTADRTKMNVYLPPIADV-----WYEFWG--GDIYKPTKTNPWV-SISVTEADFVAFIPKGSVIPLIDGN

GH31-1 -----KPKNTTDSRKSLELL-----IANDERKSASGDLYWDDGDSLNSYKEKQ---YSSLMELEENTLRSY---ATFI
GH31-2 -----RPRRASPLMKNDFPTLY-----IALDSNKKASGYLVDDNESFE-YKNQK-YLYLHFSF--EDNTF--N---SVLV
GH31-3 -----EERSSTAEMQDDPFVLY-----VNVDKENTASGNLYVDDYTSFE-YQNNQRYFYANLAY--QSNQI--D---ISIV
GH31-4 -----TPRKS AVEAKDDFYSIY-----VNVDRRNSAKGRLYKDDLYSFN-YQKDN-YFYSEAKWIPGSEKM--Y---MTTI
GH31-5 -----
GH31-6 -----
GH31-7 -----
GH31-8 -----
GH31-9 -----
GH31-10 TVNLI VALNFTSSKRTRSFIESSG SATGFMKT DGISITFTANIKSVDISSSSKKWSLHLGYVKVYQYLSNKPAYYDVRNSIDQDTQNMPYEPPTTTT

GH31-1 GSE----IPPNLDRVAVLGIEDSVKEVVVNGAS----HKNFDYNSKNKYLNIDKLDIPLQSP-----VISWK*
GH31-2 DKT-DYPTKEWVERLVLGPPKGIKAKLTSKSLGTVELDTSYSHEDRVLVVRKPGVSIKREK-----TIKL-Y*
GH31-3 DGN-FSGMTVTLGQVIVHQ--QSDKDEKRYTRTYVYTHLADGTPKLS-----INIVEKL-NGNNMVS LKL*
GH31-4 SGPDPQSRVYFVYKVVVHELLESETGELQIRKSMFTKTSGGIPLHK-----IDI AKALREGNGTLELSF*
GH31-5 -----DDTRF*
GH31-6 -----*
GH31-7 -----S*
GH31-8 -----*
GH31-9 -----*
GH31-10 ESTTSSTTTSTTTASTVTESTTEDTGTIISSTPTMESTGTSTGNTGSSSLISEITTADTGTSSSTPTRESTTEE

B

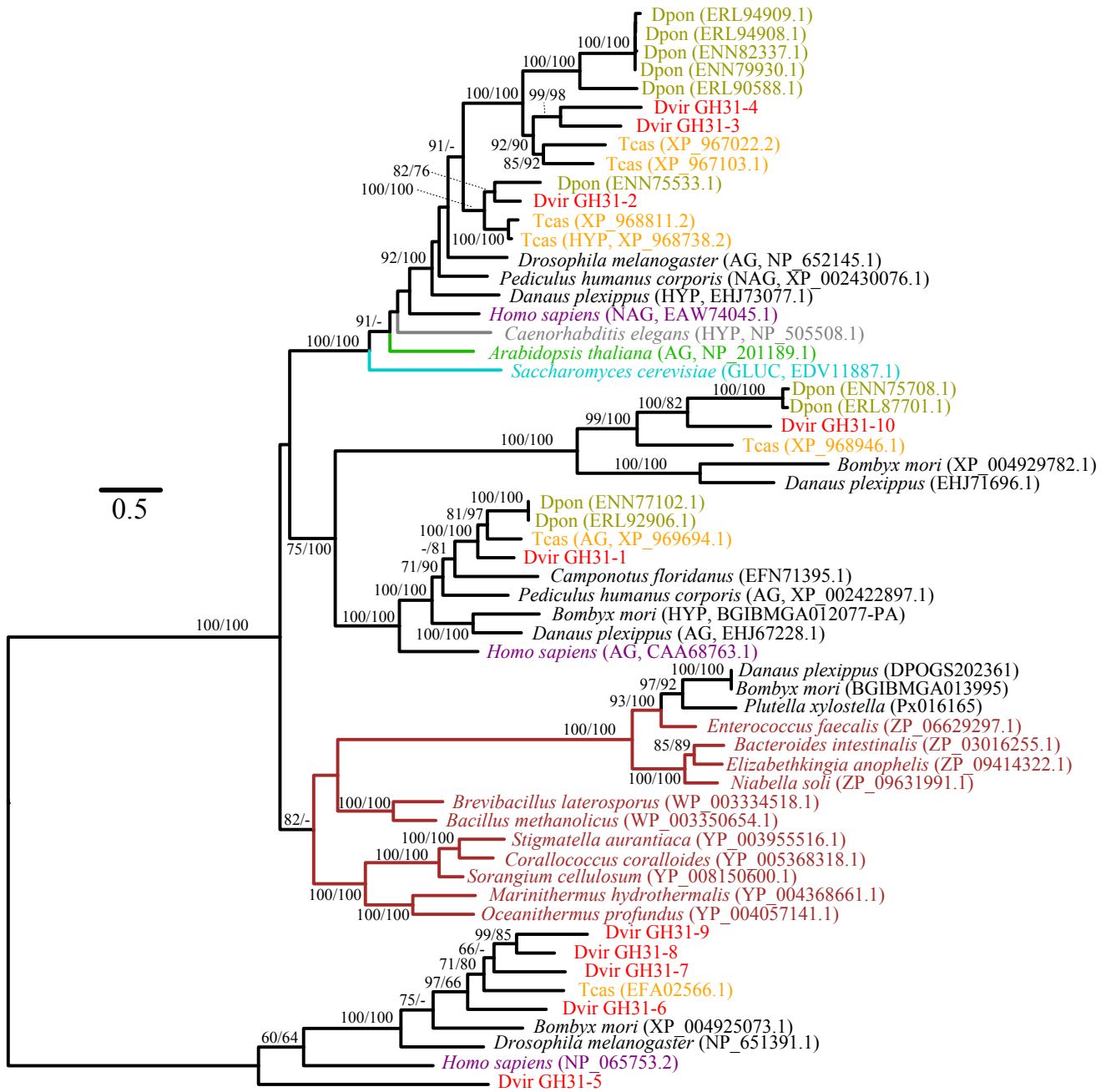


Figure S5. GH31 family gene sequences identified from the *D. v. virgifera* transcriptome (A) and the maximum-likelihood phylogeny of GH31 family proteins (B). In the alignment, the labels for partial sequences are shown in italics. In the phylogeny, labels for the coleopteran species belonging to the superfamily Curculionioidea, *D. v. virgifera*, and other beetle sequences are shown in olive, red, and orange, respectively. Their species abbreviations are found in Table S5. Arthropod, other metazoan, nematode, fungal, plant, and bacterial sequences are indicated by black, purple, grey, cyan, green, and brown, respectively. The numbers at internal branches show the bootstrap support values (%) for the maximum-likelihood and neighbor-joining phylogenies in this order. Supporting values are shown only when higher than 60%. The scale bar represents the number of amino acid substitutions per site.