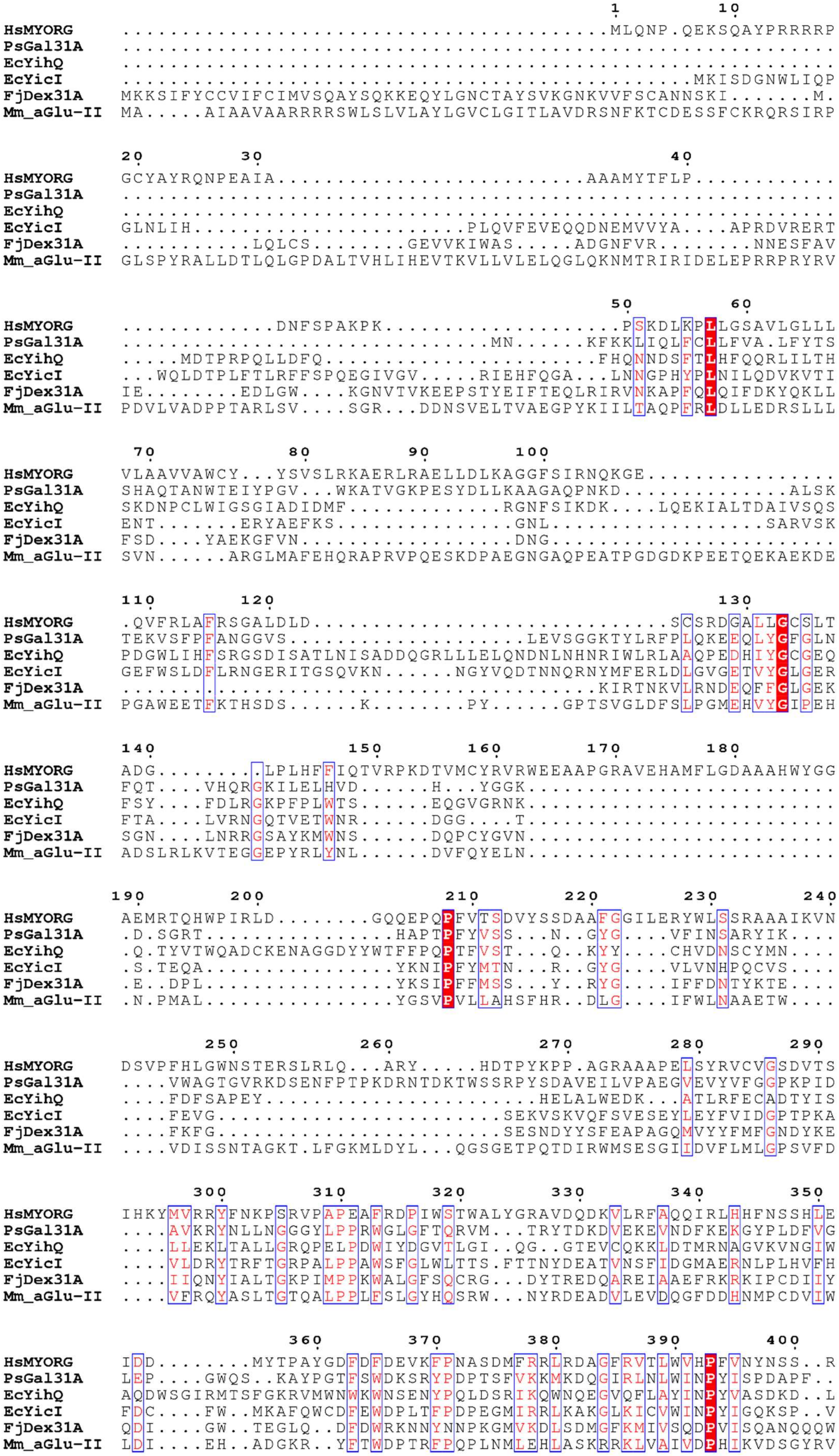

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                                                       1        10
HsMYORG       .........................................MLQNP.QEKSQAYPRRRRP
PsGal31A      ............................................................
EcYihQ        ............................................................
EcYicI        ................................................MKISDGNWLIQP
FjDex31A      MKKSIFYCCVIFCIMVSQAYSQKKEQYLGNCTAYSVKGNKVVFSCANNSKI.......M.
Mm_aGlu-II    MA.....AIAAVAARRRRSWLSLVLAYLGVCLGITLAVDRSNFKTCDESSFCKRQRSIRP

              20        30                                  40
HsMYORG       GCYAYRQNPEAIA..........................AAAMYTFLP............
PsGal31A      ............................................................
EcYihQ        ............................................................
EcYicI        GLNLIH.......................PLQVFEVEQQDNEMVVYA....APRDVRERT
FjDex31A      ...........LQLCS........GEVVKIWAS.....ADGNFVR........NNESFAV
Mm_aGlu-II    GLSPYRALLDTLQLGPDALTVHLIHEVTKVLLVLELQGLQKNMTRIRIDELEPRRPRYRV

                                                       50        60
HsMYORG       .............DNFSPAKPK....................PSKDLKPLLGSAVLGLLL
PsGal31A      ...............................MN......KFKKLIQLFCLLFVA.LFYTS
EcYihQ        .....MDTPRPQLLDFQ.......................FHQNNDSFTLHFQQRLILTH
EcYicI        ...WQLDTPLFTLRFFSPQEGIVGV.....RIEHFQGA...LNNGPHYPLNILQDVKVTI
FjDex31A      IE........EDLGW....KGNVTVKEEPSTYEIFTEQLRIRVNKAPFQLQIFDKYQKLL
Mm_aGlu-II    PDVLVADPPTARLSV....SGR...DDNSVELTVAEGPYKIILTAQPFRLDLLEDRSLLL

               70           80        90       100
HsMYORG       VLAAVVAWCY...YSVSLRKAERLRAELLDLKAGGFSIRNQKGE................
PsGal31A      SHAQTANWTEIYPGV...WKATVGKPESYDLLKAAGAQPNKD..............ALSK
EcYihQ        SKDNPCLWIGSGIADIDMF.............RGNFSIKDK....LQEKIALTDAIVSQS
EcYicI        ENT.......ERYAEFKS...............GNL..................SARVSK
FjDex31A      FSD....YAEKGFVN..................DNG........................
Mm_aGlu-II    SVN......ARGLMAFEHQRAPRVPQESKDPAEGNGAQPEATPGDGDKPEETQEKAEKDE

              110       120                                     130
HsMYORG       .QVFRLAFRSGALDLD..............................SCSRDGALLGCSLT
PsGal31A      TEKVSFPFANGGVS....................LEVSGGKTYLRFPLQKEEQLYGFGLN
EcYihQ        PDGWLIHFSRGSDISATLNISADDQGRLLLELQNDNLNHNRIWLRLAAQPEDHIYGCGEQ
EcYicI        GEFWSLDFLRNGERITGSQVKN......NGYVQDTNNQRNYMFERLDLGVGETVYGLGER
FjDex31A      ........................................KIRTNKVLRNDEQFFGLGEK
Mm_aGlu-II    PGAWEETFKTHSDS......K........PY......GPTSVGLDFSLPGMEHVYGIPEH

              140                150       160       170       180
HsMYORG       ADG.........LPLHFFIQTVRPKDTVMCYRVRWEEAAPGRAVEHAMFLGDAAAHWYGG
PsGal31A      FQT....VHQRGKILELHVD......H...YGGK..........................
EcYihQ        FSY....FDLRGKPFPLWTS......EQGVGRNK..........................
EcYicI        FTA....LVRNGQTVETWNR......DGG....T..........................
FjDex31A      SGN....LNRRGSAYKMWNS......DQPCYGVN..........................
Mm_aGlu-II    ADSLRLKVTEGGEPYRLYNL......DVFQYELN..........................

             190       200               210       220       230       240
HsMYORG       AEMRTQHWPIRLD........GQQEPQPFVTSDVYSSDAAFGGILERYWLSSRAAAIKVN
PsGal31A      .D.SGRT................HAPTPFYVSS...N..GYG....VFINSARYIK....
EcYihQ        .Q.TYVTWQADCKENAGGDYYWTFFPQPTFVST...Q..KYY....CHVDNSCYMN....
EcYicI        .S.TEQA................YKNIPFYMTN...R..GYG....VLVNHPQCVS....
FjDex31A      .E..DPL................YKSIPFFMSS...Y..RYG....IFFDNTYKTE....
Mm_aGlu-II    .N.PMAL................YGSVPVLLAHSFHR..DLG....IFWLNAAETW....

                     250          260            270        280       290
HsMYORG       DSVPFHLGWNSTERSLRLQ...ARY.....HDTPYKPP.AGRAAAPELSYRVCVGSDVTS
PsGal31A      ....VWAGTGVRKDSENFPTPKDRNTDKTWSSRPYSDAVEILVPAEGVEVYVFGGPKPID
EcYihQ        ....FDFSAPEY.......................HELALWEDK...ATLRFECADTYIS
EcYicI        ....FEVG........................SEKVSKVQFSVESEYLEYFVIDGPTPKA
FjDex31A      ....FKFG........................SESNDYYSFEAPAGQMVYYFMFGNDYKE
Mm_aGlu-II    ....VDISSNTAGKT.LFGKMLDYL...QGSGETPQTDIRWMSESGIIDVFLMLGPSVFD

                    300       310       320       330       340       350
HsMYORG       IHKYMVRRYFNKPSRVPAPEAFRDPIWSTWALYGRAVDQDKVLRFAQQIRLHHFNSSHLE
PsGal31A      ....AVKRYNLLNGGGYLPPRWGLGFTQRVM...TRYTDKDVEKEVNDFKEKGYPLDFVG
EcYihQ        ....LLEKLTALLGRQPELPDWIYDGVTLGI..QG..GTEVCQKKLDTMRNAGVKVNGIW
EcYicI        ....VLDRYTRFTGRPALPPAWSFGLWLTTS.FTTNYDEATVNSFIDGMAERNLPLHVFH
FjDex31A      ....IIQNYIALTGKPIMPPKWALGFSQCRG...DYTREDQAREIAAEFRKRKIPCDIIY
Mm_aGlu-II    ....VFRQYASLTGTQALPPLFSLGYHQSRW...NYRDEADVLEVDQGFDDHNMPCDVIW

                            360       370       380       390       400
HsMYORG       IDD........MYTPAYGDFDFDEVKFPNASDMFRRLRDAGFRVTLWVHPFVNYNSS..R
PsGal31A      LEP....GWQS..KAYPGTFSWDKSRYPDPTSFVKKMKDQGIRLNLWINPYISPDAPF..
EcYihQ        AQDWSGIRMTSFGKRVMWNWKWNSENYPQLDSRIKQWNQEGVQFLAYINPYVASDKD..L
EcYicI        FDC....FW..MKAFQWCDFEWDPLTFPDPEGMIRRLKAKGLKICVWINPYIGQKSP..V
FjDex31A      QDI....GW..TEGLQ..DFDWRKNNYNNPKGMVKDLSDMGFKMIVSQDPVISQANQQQW
Mm_aGlu-II    LDI....EH..ADGKR..YFTWDPTRFPQPLNMLEHLASKRRKLVAIVDPHIKVDSGYRV
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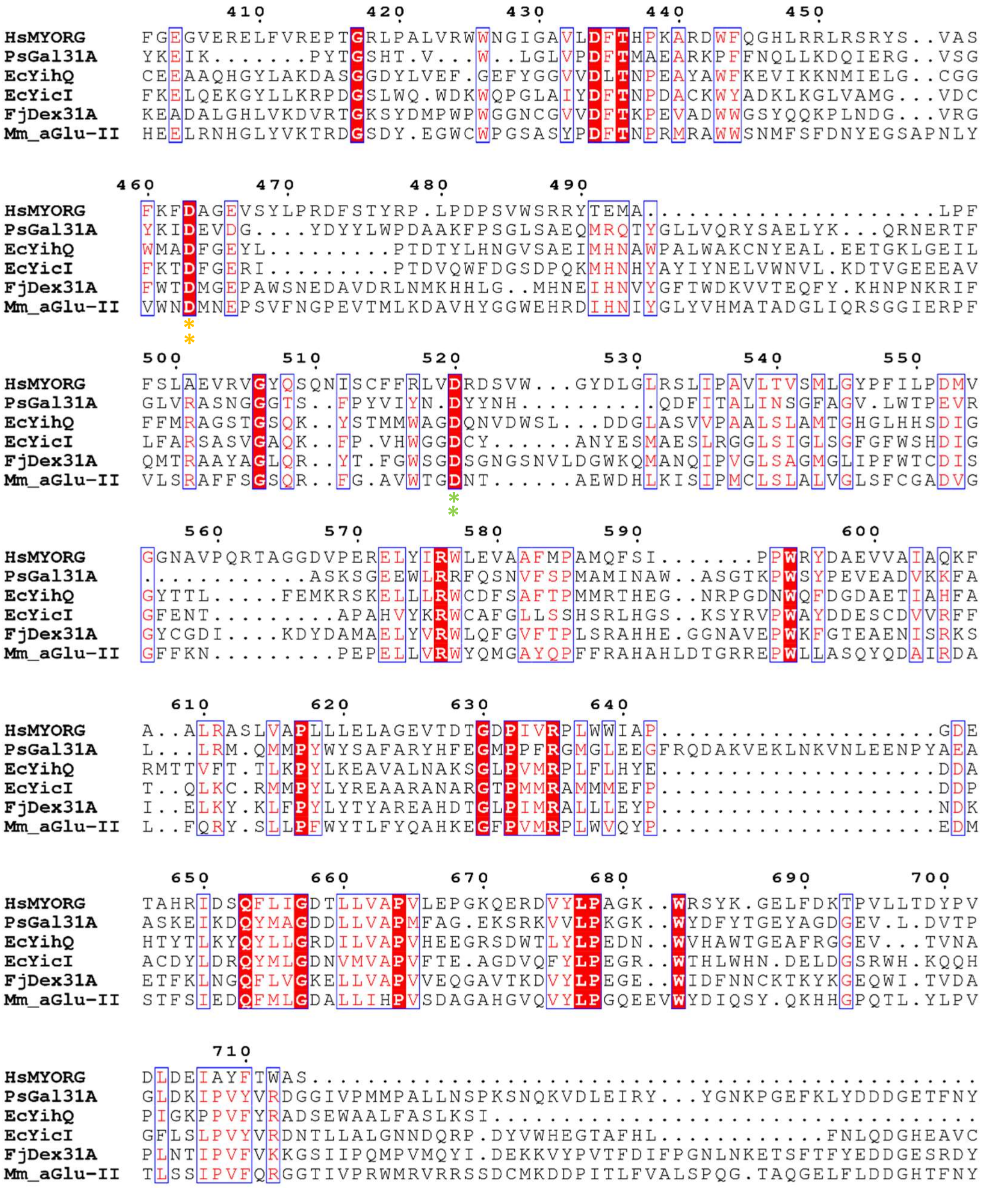

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                     410       420       430       440       450
HsMYORG        FGEGVERELFVREPTGRLPALVRWWNGIGAVLDFTHPKARDWFQGHLRRLRSRYS..VAS
PsGal31A       YKEIK.......PYTGSHT.V...W..LGLVPDFTMAEARKPFFNQLLKDQIERG..VSG
EcYihQ         CEEAAQHGYLAKDASGGDYLVEF.GEFYGGVVDLTNPEAYAWFKEVIKKNMIELG..CGG
EcYicI         FKELQEKGYLLKRPDGSLWQ.WDKWQPGLAIYDFTNPDACKWYADKLKGLVAMG...VDC
FjDex31A       KEADALGHLVKDVRTGKSYDMPWPWGGNCGVVDFTKPEVADWWGSYQQKPLNDG...VRG
Mm_aGlu-II     HEELRNHGLYVKTRDGSDY.EGWCWPGSASYPDFTNPRMRAWWSNMFSFDNYEGSAPNLY

             460       470        480       490
HsMYORG        FKFDAGEVSYLPRDFSTYRP.LPDPSVWSRRYTEMA.....................LPF
PsGal31A       YKIDEVDG....YDYYLWPDAAKFPSGLSAEQMRQTYGLLVQRYSAELYK...QRNERTF
EcYihQ         WMADFGEYL.........PTDTYLHNGVSAEIMHNAWPALWAKCNYEAL.EETGKLGEIL
EcYicI         FKTDFGERI.........PTDVQWFDGSDPQKMHNHYAYIYNELVWNVL.KDTVGEEEAV
FjDex31A       FWTDMGEPAWSNEDAVDRLNMKHHLG..MHNEIHNVYGFTWDKVVTEQFY.KHNPNKRIF
Mm_aGlu-II     VWNDMNEPSVFNGPEVTMLKDAVHYGGWEHRDIHNIYGLYVHMATADGLIQRSGGIERPF
                  *
                  *

               500       510       520          530       540       550
HsMYORG        FSLAEVRVGYQSQNISCFFRLVDRDSVW...GYDLGLRSLIPAVLTVSMLGYPFILPDMV
PsGal31A       GLVRASNGGGTS..FPYVIYN.DYYNH..........QDFITALINSGFAGV.LWTPEVR
EcYihQ         FFMRAGSTGSQK..YSTMMWAGDQNVDWSL...DDGLASVVPAALSLAMTGHGLHHSDIG
EcYicI         LFARSASVGAQK..FP.VHWGGDCY......ANYESMAESLRGGLSIGLSGFGFWSHDIG
FjDex31A       QMTRAAYAGLQR..YT.FGWSGDSGNGSNVLDGWKQMANQIPVGLSAGMGLIPFWTCDIS
Mm_aGlu-II     VLSRAFFSGSQR..FG.AVWTGDNT......AEWDHLKISIPMCLSLALVGLSFCGADVG
                                     *
                                     *

                  560       570       580       590              600
HsMYORG        GGNAVPQRTAGGDVPERELYIRWLEVAAFMPAMQFSI.......PPWRYDAEVVAIAQKF
PsGal31A       ............ASKSGEEWLRRFQSNVFSPMAMINAW..ASGTKPWSYPEVEADVKKFA
EcYihQ         GYTTL.....FEMKRSKELLLRWCDFSAFTPMMRTHEG..NRPGDNWQFDGDAETIAHFA
EcYicI         GFENT.........APAHVYKRWCAFGLLSSHSRLHGS..KSYRVPWAYDDESCDVVRFF
FjDex31A       GYCGDI....KDYDAMAELYVRWLQFGVFTPLSRAHHE.GGNAVEPWKFGTEAENISRKS
Mm_aGlu-II     GFFKN.........PEPELLVRWYQMGAYQPFFRAHAHLDTGRREPWLLASQYQDAIRDA

                 610       620       630       640
HsMYORG        A..ALRASLVAPLLLELAGEVTDTGDPIVRPLWWIAP....................GDE
PsGal31A       L...LRM.QMMPYWYSAFARYHFEGMPPFRGMGLEEGFRQDAKVEKLNKVNLEENPYAEA
EcYihQ         RMTTVFT.TLKPYLKEAVALNAKSGLPVMRPLFLHYE....................DDA
EcYicI         T..QLKC.RMMPYLYREAARANARGTPMMRAMMMEFP....................DDP
FjDex31A       I..ELKY.KLFPYLYTYAREAHDTGLPIMRALLLEYP....................NDK
Mm_aGlu-II     L..FQRY.SLLPFWYTLFYQAHKEGFPVMRPLWVQYP....................EDM

                 650       660       670       680          690       700
HsMYORG        TAHRIDSQFLIGDTLLVAPVLEPGKQERDVYLPAGK..WRSYK.GELFDKTPVLLTDYPV
PsGal31A       ASKEIKDQYMAGDDLLVAPMFAG.EKSRKVVLPKGK..WYDFYTGEYAGDGEV.L.DVTP
EcYihQ         HTYTLKYQYLLGRDILVAPVHEEGRSDWTLYLPEDN..WVHAWTGEAFRGGEV...TVNA
EcYicI         ACDYLDRQYMLGDNVMVAPVFTE.AGDVQFYLPEGR..WTHLWHN.DELDGSRWH.KQQH
FjDex31A       ETFKLNGQFLVGKELLVAPVVEQGAVTKDVYLPEGE..WIDFNNCKTKYKGEQWI.TVDA
Mm_aGlu-II     STFSIEDQFMLGDALLIHPVSDAGAHGVQVYLPGQEEVWYDIQSY.QKHHGPQTL.YLPV

                    710
HsMYORG        DLDEIAYFTWAS................................................
PsGal31A       GLDKIPVYVRDGGIVPMMPALLNSPKSNQKVDLEIRY...YGNKPGEFKLYDDDGETFNY
EcYihQ         PIGKPPVFYRADSEWAALFASLKSI...................................
EcYicI         GFLSLPVYVRDNTLLALGNNDQRP.DYVWHEGTAFHL............FNLQDGHEAVC
FjDex31A       PLNTIPVFVKKGSIIPQMPVMQYI.DEKKVYPVTFDIFPGNLNKETSFTFYEDDGESRDY
Mm_aGlu-II     TLSSIPVFQRGGTIVPRWMRVRRSSDCMKDDPITLFVALSPQG.TAQGELFLDDGHTFNY
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Figure S4. Sequence alignment of MYORG against other CAZy GH31 family enzymes. Sequence numbered relative to MYORG. Orange double asterisk indicates nucleophile residue. Green double asterisk indicates acid/base residue. UniProt identifiers: Q6NSJ0 (*Hs*MYORG), A0A0F7R6D6 (*Ps*Gal31A), P32138 (*Ec*YihQ), P31434 (*Ec*YicI), A5FBI1 (*Fj*Dex31A) and Q8BHN3 (*Mm*α-Glu II).