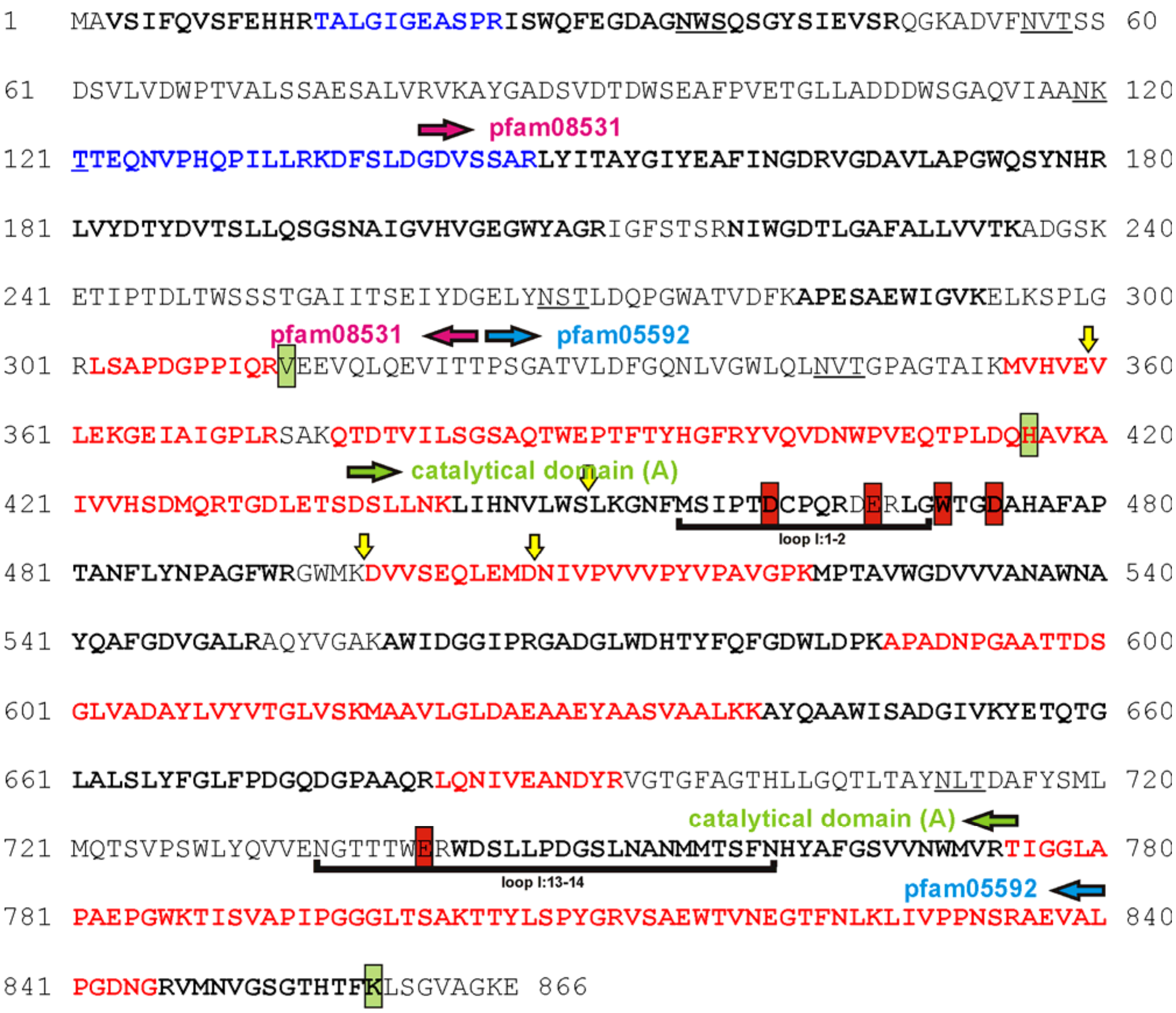

1 MA**VSIFQVSFEHHRTALGIGEASPRISWQFEGDAGNWSQSGYSIEVSR**QGKADVFNVTSS 60

61 DSVLVDWPTVALSSAESALVRVKAYGADSVDTDWSEAFPVETGLLADDDWSGAQVIAANK 120

121 **TTEQNVPHQPILLRKDFSLDGDVSSARLYITAYGIYEAFINGDRVGDAVLAPGWQSYNHR** 180

181 **LVYDTYDVTSLLQSGSNAIGVHVGEGWYAGR**IGFSTSR**NIWGDTLGAFALLVVTK**ADGSK 240

241 ETIPTDLTWSSSTGAIITSEIYDGELYNSTLDQPGWATVDFK**APESAEWIGVK**ELKSPLG 300

301 R**LSAPDGPPIQR**VEEVQLQEVITTPSGATVLDFGQNLVGWLQLNVTGPAGTAIK**MVHVEV** 360

361 **LEKGEIAIGPLR**SAK**QTDTVILSGSAQTWEPTFTYHGFRYVQVDNWPVEQTPLDQHAVKA** 420

421 **IVVHSDMQRTGDLETSDSLLNKLIHNVLWSLKGNFMSIPTDCPQR**DER**LGWTGDAHAFAP** 480

481 **TANFLYNPAGFWR**GWMK**DVVSEQLEMDNIVPVVVPYVPAVGPKMPTAVWGDVVVANAWNA** 540

541 **YQAFGDVGALR**AQYVGAK**AWIDGGIPRGADGLWDHTYFQFGDWLDPKAPADNPGAATTDS** 600

601 **GLVADAYLVYVTGLVSKMAAVLGLDAEAAEYAASVAALKKAYQAAWISADGIVKYETQTG** 660

661 **LALSLYFGLFPDGQDGPAAQRLQNIVEANDYR**VGTGFAGTHLLGQTLTAYNLTDAFYSML 720

721 MQTSVPSWLYQVVENGTTTWER**WDSLLPDGSLNANMMTSFNHYAFGSVVNWMVRTIGGLA** 780

781 **PAEPGWKTISVAPIPGGGLTSAKTTYLSPYGRVSAEWTVNEGTFNLKLIVPPNSRAEVAL** 840

841 **PGDNGRVMNVGSGTHTFK**LSGVAGKE 866

🟩 putative Calcium binding

🟥 catalytic residues or substrate recognition for rhamnosidase activity

⇩ intron position

bold = covered by peptide mapping (total = 68,82%)

peptides of the SDS protein fragments: blue = 39 kDa (PSM>7); red = 62 kDa (PSM>5)

underlined = putative N glycosylation sites

pfam08531 = alpha-L-rhamnosidase N-terminal domain

pfam05592 = bac_rhamnosid_N superfamily

catalytical domain (A) = according structure of 2OKX (Bacillus, Cui et al.)

Figure S 2: Amino acid sequence of *X. polymorpha* hydrolase (*Xpo*GH78), conserved amino acids and domains (pfam08531; pfam05592), potential *N*-glycosylation sites, putative calcium binding, and intron positions are marked. Bold letters represent the peptides identified by peptide mapping.