Table S1. List of sources and biochemical characteristics of purified microbial type I pullulanases.

Source	TE	MM (kDa)	T_{opt} (ºC)	pH_{opt}	Reaction product [a]						Ref.
					Pullulan	Starch	Amylopectin	Glycogen	β-limit dextrin	Amylose	
Type I pullulanase											
Anaerobranca gottschalkii DSM 13577^T	R	96	70	8.0	G3	ND	G1–G_o	ND	G5–G_o	-	[1]
Anoxybacillus sp. AR-29	R	85	55	6.0	RD	ND	ND	ND	ND	ND	[2]
Anoxybacillus sp. LM14-2 [b]	R	82	70	6.0	RD	RD	RD	RD	ND	-	[3]
Anoxybacillus sp. LM18-11 [c]	R	82	60	6.0	G3	ND	ND	ND	ND	-	[4]
Anoxybacillus sp. SK3-4	R	80	60	6.0	G3	-	-	-	G3, G4, G5	-	[5]
Aureobasidium pullulans	N	73	ND	ND	G3	G2, G3	ND	G2, G3	ND	-	[6]
Bacillus acidopullulyticus [c]	R	101	60	5.0	G3, G4	RD	RD	RD	ND	-	[7,8]
Bacillus acidopullulyticus	N	115	60–65	5.0	G3, G4	RD	RD	RD	RD	-	[9]
Bacillus acidopullulyticus	N	116	60–65	5.0	G3, G4	RD	RD	RD	RD	-	[9]
Bacillus amyloliquefaciens HxP-21	N	51	55	4.5	RD	RD	RD	RD	ND	-	[10]
Bacillus cereus Nws-bc5	R	80	40	6.0	G3	G2, G3	RD	ND	ND	-	[11]
Bacillus cereus	N	110	50	6.0–6.5	G3	ND	RD	ND	G2, G3, G4	ND	[12]
Bacillus deramificans	R	101	55	4.5	RD	ND	ND	ND	ND	ND	[13]
Bacillus flavocaldarius KP 1228	R	55	83–85	ND	RD	RD	RD	RD	ND	-	[14]
Bacillus flavocaldarius KP 1228	N	55	75–80	6.3	G3	RD	RD	ND	RD	-	[15]

G1: glucose; G2: maltose; G3: maltotriose; G4: maltotetraose; G5: maltopentaose; G6: maltohexaose; G7: maltoheptaose; G_o: oligosaccharides (≥ G8); TE: type of enzyme; MM: molecular mass; T_{opt}: optimum temperature; pH_{opt}: optimum pH; R: recombinant; N: native; ND: not determined; RD: substrate was reduced as inferred from enzymatic assay; -: no product detected; T: type strain; a: reaction products were determined using high-performance liquid chromatography or thin-layer chromatography in the respective reference; b: the enzyme was characterized from crude; c: the crystal structures were solved and the data were available in RCSB Protein Data Bank (PDB) database; d: consists of several subunits.

Table S1. *Continued*.

Source	TE	MM (kDa)	T_{opt} (°C)	pH_{opt}	Reaction product [a]						Ref.
					Pullulan	Starch	Amylopectin	Glycogen	β-limit dextrin	Amylose	
Type I pullulanase											
Bacillus megaterium WW1210	R	112	55	6.5	G3	ND	G3–G7	ND	ND	ND	[16]
Bacillus methanolicus PB1	R	66	50	5.5	G3	RD	RD	ND	ND	-	[17]
Bacillus naganoensis ATCC 53909^T	R	101	60	4.5	RD	ND	ND	ND	ND	ND	[18]
Bacillus subtilis 168 [c]	R	81	40	6.0	RD	ND	ND	ND	ND	ND	[19]
Bacillus subtilis BK07	R	90	40	8.0	RD	ND	ND	ND	ND	ND	[20]
Bacillus subtilis PY22	R	90	40	6.0	RD	ND	ND	ND	ND	ND	[20]
Bacillus subtilis WY-34	R	76.2	40	6.0	RD	RD	ND	ND	ND	-	[21]
Bacillus pseudofirmus 703	R	87	45	7.0–8.0	G3	RD	RD	ND	ND	ND	[22]
Bacillus sp. AN-7	N	106	90	6.0	G2, G3	G2	G2	ND	ND	-	[23]
Bacillus sp. CICIM 263	R	101	70	6.5	G3	G2, G3, G4	G2, G3	G2, G3	ND	-	[24]
Bacillus sp. KSM-1876	N	120	50	10.0–10.5	G3	RD	RD	RD	ND	-	[25]
Bacillus sp. S-1	N	180	60	9.0	G3	RD	RD	RD	RD	-	[26]
Bacillus sp. S-1	N	140	60	9.0	G3	RD	RD	RD	RD	-	[26]
Clostridium thermosulfurogenes SV2	N	80	75	6.0	G3	ND	ND	ND	ND	ND	[27]

G1: glucose; G2: maltose; G3: maltotriose; G4: maltotetraose; G5: maltopentaose; G6: maltohexaose; G7: maltoheptaose; G_o: oligosaccharides (≥ G8); TE: type of enzyme; MM: molecular mass; T_{opt}: optimum temperature; pH_{opt}: optimum pH; R: recombinant; N: native; ND: not determined; RD: substrate was reduced as inferred from enzymatic assay; -: no product detected; T: type strain; a: reaction products were determined using high-performance liquid chromatography or thin-layer chromatography in the respective reference; b: the enzyme was characterized from crude; c: the crystal structures were solved and the data were available in RCSB Protein Data Bank (PDB) database; d: consists of several subunits.

Table S1. *Continued.*

Source	TE	MM (kDa)	T_{opt} (°C)	pH_{opt}	Reaction product [a]						Ref.
					Pullulan	Starch	Amylopectin	Glycogen	β-limit dextrin	Amylose	
Type I pullulanase											
Exiguobacterium acetylicum YH5	R	100	50	6.0	G3	G2, G3, G_o	G2, G3, G_o	G2, G3, G_o	G2, G3, G_o	-	[28]
Exiguobacterium sp. SH3	R	108	45	8.5	G3	RD	RD	ND	ND	-	[29]
Fervidobacterium nodosum Rt17-B1	R	95	80	5.0	G3	G2–G6	G2–G6	ND	ND	ND	[30]
Fervidobacterium pennavorans Ven5	R	93	80	6.0	G3	G2, G3	G2, G3	G2, G3	ND	-	[31]
Fervidobacterium pennavorans Ven5	N	240 [d]	85	6.0	G3, G_o	ND	ND	ND	ND	-	[32]
Geobacillus kaustophilus DSM 7263^T	R	80	65	6.0	G3	RD	RD	RD	ND	-	[33]
Geobacillus thermopakistaniensis	R	80	ND	ND	ND	ND	ND	ND	ND	ND	[34]
Geobacillus stearothermophilus TRS128	N	83	65	6.0	G3	ND	ND	ND	ND	ND	[35]
Geobacillus thermoleovorans US105	R	160 [d]	70	6.0	G3	ND	ND	ND	ND	-	[36]
Klebsiella pneumoniae [c]	R	145	30–37	5.0	G3	RD	RD	RD	RD	-	[37-39]
Klebsiella variicola SHN-1	R	118	55	5.0	G3	ND	ND	ND	ND	ND	[40]
Laceyella sacchari No. 15	N	79	70	7.0	G3	G2, G3	G2, G3	ND	G2, G3	ND	[41]

G1: glucose; G2: maltose; G3: maltotriose; G4: maltotetraose; G5: maltopentaose; G6: maltohexaose; G7: maltoheptaose; G_o: oligosaccharides (≥ G8); TE: type of enzyme; MM: molecular mass; T_{opt}: optimum temperature; pH_{opt}: optimum pH; R: recombinant; N: native; ND: not determined; RD: substrate was reduced as inferred from enzymatic assay; -: no product detected; T: type strain; a: reaction products were determined using high-performance liquid chromatography or thin-layer chromatography in the respective reference; b: the enzyme was characterized from crude; c: the crystal structures were solved and the data were available in RCSB Protein Data Bank (PDB) database; d: consists of several subunits.

Table S1. *Continued*.

Source	TE	MM (kDa)	T_{opt} (°C)	pH_{opt}	Reaction product [a]						Ref.
					Pullulan	Starch	Amylopectin	Glycogen	β-limit dextrin	Amylose	
Type I pullulanase											
Lactococcus lactis IBB 500	N	73	45	4.5	G2, G3	G2, G3	ND	ND	ND	-	[42]
Lactobacillus acidophilus NCFM	R	129	50	5.5	G3	G2, G3, G4	ND	ND	RD	ND	[43]
Micrococcus sp. 207	N	120	50	8.0	G3, G4	RD	RD	RD	ND	-	[44]
Metagenome sample (Pul_M)	R	80	40	6.0–7.0	RD	RD	ND	ND	ND	ND	[45]
Metagenome sample (PersiPul1)	R	71	60	7.0	RD	RD	RD	ND	ND	-	[46]
Mixed culture bacterium (AmyA1)	R	81.7	60	6.0	G3	RD	ND	RD	ND	ND	[47]
Paenibacillus barengoltzii CAU904	R	75	50	5.5	G3	RD	RD	ND	ND	-	[48]
Paenibacillus lautus DSM 3035^T	R	87.9	40	7.0	G3	RD	RD	RD	ND	-	[49]
Paenibacillus polymyxa Nws-pp2	R	99	35	6.0	G3	G2, G3	G2, G3	G2, G3	G2, G3	ND	[50]
Thermotoga maritima MSB8	N	89	90	5.9	G3	ND	ND	ND	ND	ND	[51]

G1: glucose; G2: maltose; G3: maltotriose; G4: maltotetraose; G5: maltopentaose; G6: maltohexaose; G7: maltoheptaose; G_o: oligosaccharides (≥ G8); TE: type of enzyme; MM: molecular mass; T_{opt}: optimum temperature; pH_{opt}: optimum pH; R: recombinant; N: native; ND: not determined; RD: substrate was reduced as inferred from enzymatic assay; -: no product detected; T: type strain; a: reaction products were determined using high-performance liquid chromatography or thin-layer chromatography in the respective reference; b: the enzyme was characterized from crude; c: the crystal structures were solved and the data were available in RCSB Protein Data Bank (PDB) database; d: consists of several subunits.

Table S1. *Continued*.

Source	TE	MM (kDa)	T_{opt} (°C)	pH_{opt}	Reaction product [a]						Ref.
					Pullulan	Starch	Amylopectin	Glycogen	β-limit dextrin	Amylose	
Type I pullulanase											
Thermotoga neapolitana KCCM 41025	R	93	80–85	6.5	G3	G2, G3, G_o	G2, G3, G_o	G2, G3, G_o	ND	-	[52]
Thermus aquaticus YT-1	N	83	85	6.5	G3	G1, G2, G3	G1, G2, G3	ND	ND	ND	[53]
Thermus caldophilus GK-24	N	65	75	5.5	G3	G1, G2, G3	G1, G2, G3	RD	RD	ND	[54]
Thermus thermophilus HB8	R	80	70	5.5–6.5	G3	ND	ND	ND	ND	ND	[55]
Shewanella arctica 40-3	R	155	35	6.0–7.0	G3	ND	ND	ND	ND	ND	[56]
Shewanella arctica 40-3	N	150	45	7.0	G3	RD	RD	ND	ND	-	[57]

G1: glucose; G2: maltose; G3: maltotriose; G4: maltotetraose; G5: maltopentaose; G6: maltohexaose; G7: maltoheptaose; G_o: oligosaccharides (≥ G8); TE: type of enzyme; MM: molecular mass; T_{opt}: optimum temperature; pH_{opt}: optimum pH; R: recombinant; N: native; ND: not determined; RD: substrate was reduced as inferred from enzymatic assay; -: no product detected; T: type strain; a: reaction products were determined using high-performance liquid chromatography or thin-layer chromatography in the respective reference; b: the enzyme was characterized from crude; c: the crystal structures were solved and the data were available in RCSB Protein Data Bank (PDB) database; d: consists of several subunits

Table S2: List of sources and biochemical characteristics of purified microbial type II pullulanases.

Source	TE	MM (kDa)	T_{opt} (°C)	pH_{opt}	Reaction product [a]						Ref.
					Pullulan	Starch	Amylopectin	Glycogen	β-limit dextrin	Amylose	
Type II pullulanase (amylopullulanase)											
Alkalilimnicola sp. NM-DCM-1	R	80	55	9.5	G3	G2, G3, G4	ND	ND	ND	G4, G5	[58]
Anoxybacillus sp. SK3-4	N	225	60	7.5	G1, G2, G3	G1, G2, G3	G1, G2, G3	G1, G2, G3	ND	G2, G3	[59]
Anoxybacillus sp. WB42	R	83	55–65	5.8	G3	G2–G5	G2–G5	ND	ND	G2–G5	[60]
Bacillus cereus H1.5	N	93	55	6.0	G3	RD	RD	ND	ND	RD	[61]
Bacillus circulans F-2	N	220	50	7.0	G3	G3–G_o	ND	ND	ND	ND	[62]
Bacillus megaterium Y103	R	110	45	6.5	G3	G1–G4	G1–G4	-	-	G1–G4	[63]
Bacillus sp. DSM 405	N	126	70	6.0	G3	G2, G3, G4	G2, G3, G4	G2, G3, G4	ND	G2, G3, G4	[64]
Bacillus sp. XAL601	R	224	70	9.0	G3	G2, G3, G4	ND	ND	ND	G2, G3, G4	[65]
Caldisericum exile	R	139	75	5.5, 8.5	G3	G1–G6	G1–G6	ND	ND	G1–G6	[66]
Cohnella sp. A01	R	127	70	8.0	G3	G2, G3, G4	ND	ND	ND	ND	[67]
Cohnella sp. A01	R	70	60	6.0	G3	G2, G3, G4	ND	ND	ND	ND	[67]

G1: glucose; G2: maltose; G3: maltotriose; G4: maltotetraose; G5: maltopentaose; G6: maltohexaose; G7: maltoheptaose; G_o: oligosaccharides (≥ G8); TE: type of enzyme; MM: molecular mass; T_{opt}: optimum temperature; pH_{opt}: optimum pH; R: recombinant; N: native; ND: not determined; RD: substrate was reduced as inferred from enzymatic assay; -: no product detected; T: type strain; a: reaction products were determined using high-performance liquid chromatography or thin-layer chromatography in the respective reference; b: the enzyme was characterized from crude; c: the crystal structures were solved and the data were available in RCSB Protein Data Bank (PDB) database; d: consists of several subunits.

Table S2. *Continued*.

Source	TE	MM (kDa)	T_{opt} (°C)	pH_{opt}	Reaction product [a]						Ref.
					Pullulan	Starch	Amylopectin	Glycogen	β-limit dextrin	Amylose	
Type II pullulanase (amylopullulanase)											
Caldivirga maquilingensis IC-167^T	R	62.7	100	5.0	RD	G6–G_o	G6–G_o	ND	ND	G6–G_o	[68]
Clostridium thermosulfurigenes EM1	N	100	60–65	5.5–6.0	G3	G2, G3	ND	G2, G3	ND	G2, G3, G4	[69]
Clostridium thermosulfurigenes SVM17	N	97	70	5.5–6.0	G3	G1, G2	ND	ND	ND	ND	[70]
Desulfurococcus mucosus DSM 2162^T	R	110 [d]	85	5.0	G3	G1, G2, G3	RD	-	ND	G1, G2, G3	[71]
Geobacillus stearothermophilus ATCC 12980^T	R	184	ND	ND	ND	ND	ND	ND	ND	ND	[72]
Geobacillus stearothermophilus G-82	N	56	60	7.0	G1, G2, G3	ND	G1, G2, G3	G1, G2, G3	ND	G1, G2, G3	[73]
Geobacillus stearothermophilus TS-23	R	220	ND	ND	ND	ND	ND	ND	ND	ND	[74]
Geobacillus thermoleovorans NP1	N	112	50	6.0	G1, G2, G3, G_O	G2, G3, G_O	ND	ND	ND	ND	[75]
Geobacillus thermoleovorans NP33	R	182	60	7.0	G3	G2, G3, G4	G2, G3, G4	G2, G3, G4	ND	G2, G3, G4	[76]

G1: glucose; G2: maltose; G3: maltotriose; G4: maltotetraose; G5: maltopentaose; G6: maltohexaose; G7: maltoheptaose; G_o: oligosaccharides (≥ G8); TE: type of enzyme; MM: molecular mass; T_{opt}: optimum temperature; pH_{opt}: optimum pH; R: recombinant; N: native; ND: not determined; RD: substrate was reduced as inferred from enzymatic assay; -: no product detected; T: type strain; a: reaction products were determined using high-performance liquid chromatography or thin-layer chromatography in the respective reference; b: the enzyme was characterized from crude; c: the crystal structures were solved and the data were available in RCSB Protein Data Bank (PDB) database; d: consists of several subunits.

Table S2. *Continued*.

Source	TE	MM (kDa)	T_{opt} (°C)	pH_{opt}	Reaction product [a]						Ref.
					Pullulan	Starch	Amylopectin	Glycogen	β-limit dextrin	Amylose	
Type II pullulanase (amylopullulanase)											
Geobacillus thermoleovorans NP33	N	48	80	ND	RD	RD	ND	ND	ND	ND	[77]
Geobacillus thermoleovorans NP33	N	105	80	7.0	G1, G2, G3	G1, G2, G3	ND	ND	ND	ND	[78]
Geobacillus sp. L14	N	100	65	5.5	G1, G2, G3	G1, G2	ND	ND	ND	ND	[79]
Halorubrum sp. Ha25	N	140	50	7.5	G1	G1	ND	ND	ND	ND	[80]
Lactobacillus amylophilus GV6	N	90	37	6.5	G3	G1, G2, G3	ND	ND	ND	ND	[81]
Metagenome sample (PulSS4)	R	164	40	9.0	G3	G1–G4	G1–G4	G1–G4	ND	G1–G4	[82]
Paenibacillus puldeungensis LK18	R	76	45	6.0	RD	ND	ND	ND	ND	ND	[83]
Pyrococcus furiosus DSM 3638^T	R	90	105	6.0	G3, G4	G1–G6	RD	RD	ND	RD	[84]
Pyrobaculum calidifontis VA1	R	111	90	5.6	RD	ND	ND	ND	ND	ND	[85]
Pyrococcus furiosus DSM 3638^T	N	119	100	5.5	G3	G1–G6	ND	G1–G6	ND	G1–G6	[86]
Pyrococcus woesei DSM 3773^T	R	90	100	6.0	G3	G1–G6	ND	G1–G5	ND	G1–G4	[87]
Pyrococcus yayanosii CH1	R	125	95	6.6	G3	ND	ND	ND	ND	$G5\text{-}G_o$	[88]

G1: glucose; G2: maltose; G3: maltotriose; G4: maltotetraose; G5: maltopentaose; G6: maltohexaose; G7: maltoheptaose; G_o: oligosaccharides (≥ G8); TE: type of enzyme; MM: molecular mass; T_{opt}: optimum temperature; pH_{opt}: optimum pH; R: recombinant; N: native; ND: not determined; RD: substrate was reduced as inferred from enzymatic assay; -: no product detected; T: type strain; a: reaction products were determined using high-performance liquid chromatography or thin-layer chromatography in the respective reference; b: the enzyme was characterized from crude; c: the crystal structures were solved and the data were available in RCSB Protein Data Bank (PDB) database; d: consists of several subunits.

Table S2. *Continued*.

Source	TE	MM (kDa)	T_{opt} (°C)	pH_{opt}	Reaction product [a]						Ref.
					Pullulan	Starch	Amylopectin	Glycogen	β-limit dextrin	Amylose	
Type II pullulanase (amylopullulanase)											
Staphylothermus marinus DSM 3639[T]	R	75.3	105	5.0	G3	ND	ND	ND	ND	ND	[89]
Streptomyces erumpens MTCC 7317	N	45	ND	ND	RD	G1, G2	ND	ND	ND	ND	[90]
Sulfolobus acidocaldarius DSM 639[T]	R	100 [d]	100	3.0	G1, G2, G3	G1, G2, G3	G1, G2, G3	G1, G2, G3	ND	G1, G2, G3	[91]
Thermoanaerobacter pseudethanolicus ATCC 33233[T]	R	140	90	5.5	G3	RD	RD	RD	RD	ND	[92-94]
Thermoanaerobacter thermohydrosulfuricus E101	R	165	80	ND	G3	ND	ND	ND	ND	ND	[95]
Thermoanaerobacter sp. B6A	N	450 [d]	75	5.0	G3	RD	RD	RD	RD	G2, G3, G4	[96]
Thermoanaerobium brockii	R	105	70	5.0	G3	$G3–G_o$	ND	ND	RD	ND	[97]
Thermoanaerobacterium saccharolyticum B6A-RI[T]	R	140	70–75	5.5–6.0	G3	RD	RD	RD	ND	RD	[98]

G1: glucose; G2: maltose; G3: maltotriose; G4: maltotetraose; G5: maltopentaose; G6: maltohexaose; G7: maltoheptaose; G_o: oligosaccharides (≥ G8); TE: type of enzyme; MM: molecular mass; T_{opt}: optimum temperature; pH_{opt}: optimum pH; R: recombinant; N: native; ND: not determined; RD: substrate was reduced as inferred from enzymatic assay; -: no product detected; T: type strain; a: reaction products were determined using high-performance liquid chromatography or thin-layer chromatography in the respective reference; b: the enzyme was characterized from crude; c: the crystal structures were solved and the data were available in RCSB Protein Data Bank (PDB) database; d: consists of several subunits.

Table S2. *Continued*.

Source	TE	MM (kDa)	T_{opt} (°C)	pH_{opt}	Reaction product [a]						Ref.
					Pullulan	Starch	Amylopectin	Glycogen	β-limit dextrin	Amylose	
Type II pullulanase (amylopullulanase)											
Thermoanaerobacterium saccharolyticum NTOU1	R	100	70	5.0	G2, G3	G2, G3	G2, G3	G2, G3	ND	G2, G3	[99]
Thermoanaerobacterium thermosaccharolyticum DSM 571^T	N	150	65	5.0–5.5	G3, G_o	RD	RD	RD	ND	RD	[100]
Thermoanaerobacterium thermosulfurigenes EM1	R	205	60	5.5	G3	G2, G3	ND	G2, G3	ND	G2, G3	[101-103]
Thermoanaerobium sp. Tok6-B1	N	120	80	5.5	G3	G2, G3, G4	G2, G3	ND	ND	G2, G3, G4	[104]
Thermococcus hydrothermalis	R	105	105	5.75	G3	G1–G7	ND	ND	ND	G1–G7	[105]
Thermococcus hydrothermalis AL662	N	128	95	5.5	G3	G4–G7	ND	G4–G7	ND	ND	[106]
Thermococcus kodakarensis KOD1^T	R	86	100	5.5	G3	G2, G3	ND	ND	ND	ND	[107]
Thermococcus kodakarensis KOD1^T	R	120	105	5.5	RD	RD	ND	ND	ND	ND	[108]
Thermococcus litoralis DSM 5473^T	N	110	100	5.5	G3	G1–G6	ND	G1–G6	ND	G1–G6	[86]
Thermococcus siculi HJ21	R	148.6	95	6.0	RD	ND	ND	ND	ND	ND	[109]

G1: glucose; G2: maltose; G3: maltotriose; G4: maltotetraose; G5: maltopentaose; G6: maltohexaose; G7: maltoheptaose; G_o: oligosaccharides (≥ G8); TE: type of enzyme; MM: molecular mass; T_{opt}: optimum temperature; pH_{opt}: optimum pH; R: recombinant; N: native; ND: not determined; RD: substrate was reduced as inferred from enzymatic assay; -: no product detected; T: type strain; a: reaction products were determined using high-performance liquid chromatography or thin-layer chromatography in the respective reference; b: the enzyme was characterized from crude; c: the crystal structures were solved and the data were available in RCSB Protein Data Bank (PDB) database; d: consists of several subunits.

Table S2. *Continued*.

Source	TE	MM (kDa)	T_{opt} (°C)	pH_{opt}	Reaction product [a]						Ref.
					Pullulan	Starch	Amylopectin	Glycogen	β-limit dextrin	Amylose	
Type II pullulanase (amylopullulanase)											
Thermofilum pendens Hrk 5	R	65.5	95–100	3.5	RD	ND	G6–G_o	ND	ND	ND	[110]
Thermus thermophilus HB27	R	52	70	6.5	G1, G2, G3	G1, G2, G3	G1–G4	ND	ND	G1, G2, G3	[111]
Uncultured bacterium (Env Npu193A)	R	66	75	7.0	G3	G2–G_o	ND	ND	ND	ND	[112]
Type II pullulanase (α-amylase-pullulanase)											
Alkalibacterium sp. SL3	R	226	50	9.0	G3	G1–G4	G1–G4	ND	ND	ND	[113]
Bacillus sp. KSM-1378	N	210	50	9.5	G3, G_o	G1–G6	G1–G6	G1–G6	ND	G1–G6	[114]
Bifidobacterium breve UCC2003	R	182.3	ND	ND	G3	G2, G3	G2, G3	G2, G3	ND	ND	[115]
Bifidobacterium adolescentis P2P3	R	180	55	5.0	G3	G3	RD	RD	ND	RD	[116]
Lactobacillus plantarum L137	R	211	40	4.0	G3	G1–G4	ND	ND	ND	G4–G_o	[117]
Streptococcus suis P1/7	R	230	ND	ND	ND	ND	ND	ND	ND	ND	[118]

G1: glucose; G2: maltose; G3: maltotriose; G4: maltotetraose; G5: maltopentaose; G6: maltohexaose; G7: maltoheptaose; G_o: oligosaccharides (≥ G8); TE: type of enzyme; MM: molecular mass; T_{opt}: optimum temperature; pH_{opt}: optimum pH; R: recombinant; N: native; ND: not determined; RD: substrate was reduced as inferred from enzymatic assay; -: no product detected; T: type strain; a: reaction products were determined using high-performance liquid chromatography or thin-layer chromatography in the respective reference; b: the enzyme was characterized from crude; c: the crystal structures were solved and the data were available in RCSB Protein Data Bank (PDB) database; d: consists of several subunits.

Table S3. List of sources and biochemical characteristics of purified microbial pullulan hydrolases.

Source	TE	MM (kDa)	T_{opt} (°C)	pH_{opt}	Reaction product [a]						Ref.
					Pullulan	Starch	Amylopectin	Glycogen	β-limit dextrin	Amylose	
Pullulan hydrolase type I (neopullulanase)											
Anoxybacillus flavithermus	R	72.8	60	5.5–6.5	P	G1, G2, G3	ND	ND	ND	ND	[119]
Alicyclobacillus acidocaldarius ATCC 27009^T	R	66	55	5.5	P	ND	ND	ND	ND	ND	[120]
Bacillus polymyxa CECT 155 [b]	R	58	50	6.0	P	RD	RD	ND	ND	RD	[121,122]
Bacillus sp. KSM-1876	R	68	40	7.5	P	ND	ND	ND	ND	ND	[123]
Bacteroides thetaiotaomicron 95-1	R	70	ND	ND	P	ND	ND	ND	ND	RD	[124]
Geobacillus stearothermophilus TRS40	R	62	60–65	6.0	G1, G2, P	G1, G2	G2	ND	ND	G1, G2	[125,126]
Geobacillus stearothermophilus IMA6503	R	140 [d]	55	6.0	P	G1, G2	ND	ND	ND	ND	[127]
Laceyella sacchari	R	69.1	ND	5.5–6.5	P	G1, G2, G3	ND	ND	ND	ND	[119]
Lactobacillus mucosae LM1	R	67	37	6.0	P	ND	ND	ND	ND	ND	[128]
Micrococcus halobius OR-1	N	53	50	8.0	P	G2, G3	G3, P	ND	ND	G2	[129]
Paenibacillus sp. KCTC 8848P	R	58	ND	ND	P	RD	ND	ND	ND	ND	[130]

G1: glucose; G2: maltose; G3: maltotriose; G4: maltotetraose; G5: maltopentaose; G6: maltohexaose; G7: maltoheptaose; G_o: oligosaccharides (≥ G8); P: panose; I: isopanose; TE: type of enzyme; MM: molecular mass; T_{opt}: optimum temperature; pH_{opt}: optimum pH; R: recombinant; N: native; ND: not determined; RD: substrate was reduced as inferred from enzymatic assay; -: no product detected; T: type strain; a: reaction products were determined using high-performance liquid chromatography or thin-layer chromatography in the respective reference; b: the enzyme was characterized from crude; c: the crystal structures were solved and the data were available in RCSB Protein Data Bank (PDB) database; d: consists of several subunits.

Table S3. *Continued*.

Source	TE	MM (kDa)	T_{opt} (°C)	pH_{opt}	Reaction product [a]						Ref.
					Pullulan	Starch	Amylopectin	Glycogen	β-limit dextrin	Amylose	
Pullulan hydrolase type I (neopullulanase)											
Thermoactinomyces vulgaris R-47 [c]	R	74	70	5.0	P	G1, G2	ND	ND	ND	RD	[131,132]
Thermoactinomyces vulgaris R-47 [c]	R	67	40	5.5	P	G1, G2	ND	ND	ND	ND	[133]
Uncultured bacterium (Amy 132)	R	69	55	5.5–6.5	P	G1, G2, G3	ND	ND	ND	ND	[119]
Pullulan hydrolase type II (isopullulanase)											
Aspergillus brasiliensis ATCC 9642^{T} [c]	R	90	40–45	3.5	I	ND	ND	ND	ND	ND	[134,135]
Aspergillus brasiliensis ATCC 9642^{T}	N	71	45	3.5	I	ND	ND	ND	ND	ND	[136]
Aspergillus brasiliensis ATCC 9642^{T}	N	69	40	3.5	I	ND	ND	ND	ND	ND	[136]
Bacillus sp. US149	N	200 [d]	60	5.0	I	-	-	-	ND	ND	[137]
Pullulan hydrolase type III											
Thermococcus aggregans DSM 10597	R	80	95	6.5	G1, G2, G3, P	G1, G2, G3	G1, G2, G3	ND	ND	G1, G2, G3	[138]
Thermococcus kodakarensis KOD1^{T}	R	80	95–100	3.5	G1, G2, G3, P	G1, G2, G3	G1, G2, G3	G1, G2, G3	ND	G2	[139]

G1: glucose; G2: maltose; G3: maltotriose; G4: maltotetraose; G5: maltopentaose; G6: maltohexaose; G7: maltoheptaose; G_o: oligosaccharides (≥ G8); P: panose; I: isopanose; TE: type of enzyme; MM: molecular mass; T_{opt}: optimum temperature; pH_{opt}: optimum pH; R: recombinant; N: native; ND: not determined; RD: substrate was reduced as inferred from enzymatic assay; -: no product detected; T: type strain; a: reaction products were determined using high-performance liquid chromatography or thin-layer chromatography in the respective reference; b: the enzyme was characterized from crude; c: the crystal structures were solved and the data were available in RCSB Protein Data Bank (PDB) database; d: consists of several subunits.

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