

Table S4: Q₁₀ values for enzyme-catalyzed reactions calculated from specific activity measurements

Thermophilic Enzyme	Organism	Q ₁₀ ^{meas}	Low temperature (T ₁)		High temperature (T ₂)		references
			[°C]	U Activity ^a [$\mu\text{mol min}^{-1} \text{mg}^{-1}$]	[°C]	U Activity ^a [$\mu\text{mol min}^{-1} \text{mg}^{-1}$]	
Adenylate kinase (TNAK)	<i>Thermotoga neapolitana</i>	1.66	30	675	80	8400	[61]
D-xyllose isomerase	<i>Clostridium thermosulfurogenes strain 4</i>	1.66	40	0.93	80	7.10	[62]
D-xyllose isomerase	<i>Thermoanaerobacter strain B6A</i>	1.94	40	0.62	80	8.80	''
Formyltransferase	<i>Methanopyrus kandleri</i>	1.64	22	86.2 ^c	88	2327.6 ^c	[63]
Thioredoxin reductase (ApTR)	<i>Aeropyrum pernix K1</i>	1.73	30	7.9	90	202.9	[64]
Aspartyl-tRNA synthetase (AspRS)	<i>Pyrococcus sp. KOD1</i>	1.18	35	65.9 ^d	65	110.00 ^d	[65]
Citrate synthases (TACS)	<i>Thermoplasma acidophilum</i>	1.58	40	46.5	70	183.6	[66]
Citrate synthases (PICS)	<i>Pyrococcus furiosus</i>	1.91	40	4.4	90	110.6	''
Glutamate dehydrogenase (Pho-GDH forward)	<i>Pyrococcus horikoshii</i>	1.76	35	0.2	90	4.4	[67]
Glutamate dehydrogenase (Pho-GDH reversed)	<i>Pyrococcus horikoshii</i>	1.48	35	2.0	89	17.4	''
Glutamate dehydrogenase (GDH)	<i>Symbiobacterium toebii</i>	1.69	40	35.0 ^e	60	100.0 ^e	[68]
3-phosphoglycerate kinase (PGK)	<i>Thermus thermophilus</i>	1.42	25	255 ^b	75	1450 ^b	[69]
Xylose isomerases [XIs (ITXI)]	<i>Thermosulfurigenes</i>	1.76	44	1.4	85	13.7	[70]
Xylose isomerases [XIs (TNXI)]	<i>Thermotoga neapolitana</i>	1.60	55	3.6	97	25.9	''
sn-glycerol-1-phosphate dehydrogenase Gro1P	<i>Aeropyrum pernix K1</i>	1.61	55	2.2	96	15.2	[71]
Pullulanase	<i>Pyrococcus woesei</i>	1.99	40	1.60 ^b	100	100 ^b	[72]
F ₄₂₀ H ₂ quinone oxidoreductase	<i>Archaeoglobus fulgidus</i>	1.27	20	35.2	60	92.4	[73]
Thermitase	<i>Thermoactinomyces vulgaris</i>	1.80	20	25.3	76	654.9	[74]
Amylopolulinanase	<i>Thermococcus litoralis</i>	2.37	60	1.33	98	35.5	[75]
		1.97	50	1.84	98	48.3	''
Amylopolulinanase	<i>Pyrococcus furiosus</i>	1.78	60	2.69	114	60.4	''
		2.47	50	1.10	98	80.2	''
Azoreductase (AzrG)	<i>Gaobacillus stearothermophilus</i>	1.32	10	11.7	84	93.8	[76]
Azoreductase (AzrB)	<i>Bacillus sp. B29</i>	1.21	10	31.9 [*]	69	100.0 [*]	[77]
Azoreductase (AzrC)	<i>Bacillus sp. B29</i>	1.30	10	30.9 ^b	55	100.0 ^b	''
Azoreductase (AZR-BSPo)	<i>Bacillus sp. OYI-2</i>	1.37	15	7.5	65	36.0	[78]
Aeropyrolysin	<i>Aeropyrum pernix K1 (JCM 9820)</i>	1.62	50	0.1 ^f	100	1.2 ^f	[79]
Archaeolysin	<i>Desulfurococcus-related organism</i>	1.69	22	13.3 ^g	99	756.1 ^g	[80]
Azoreductase (AzrA)	<i>Bacillus sp. B29</i>	1.39	10	16.7	65	100.0 ^h	[81]
3-Isopropylmalate dehydrogenase (IPMDH)	<i>Thermus thermophilus HB8</i>	1.63	40	18.0	75	98.0	[82]
Esterase (Est-AF)	<i>Archaeoglobus fulgidus DSM 4304</i>	1.34	50	195.3	80	469.5	[83]
Ornithine carbamoyltransferase	<i>Pyrococcus furiosus</i>	1.95	45	5 [*]	90	100 [*]	[13]
Xylanase	<i>Clostridium thermocellum</i>	1.68	40	12 [*]	81	100 [*]	[12]
Cellulase	<i>Thermobifida fusca</i>	1.42	30	49 ^b	70	201 ^b	[84]
Cellulase	<i>Clostridium thermocellum</i>	1.56	30	31 ^b	80	278 ^b	[84]
Average (SD)		1.65 (0.30)					
Mesophilic Enzyme	Organism	Q ₁₀ ^{meas}	Low temperature (T ₁)		High temperature (T ₂)		references
			[°C]	U Activity ^a [$\mu\text{mol min}^{-1} \text{mg}^{-1}$]	[°C]	U Activity ^a [$\mu\text{mol min}^{-1} \text{mg}^{-1}$]	
Ornithine carbamoyltransferase	<i>Escherichia coli</i>	1.50	25	11	60	903	[13]
Rat kidney glutathione reductase	rat	1.49	20	0.085 ^g	65	0.51 ^g	[85]
Xylanase	<i>Streptomyces sp. S38</i>	1.60	20	15 [*]	60	100 [*]	[12]
Alpha-amylase	<i>Bacillus amyloliquefaciens</i>	2.02	10	3 [*]	60	100 [*]	[86]
Aspartate transcarbamylase	<i>Escherichia coli</i>	2.23	0	11 [*]	55	100 [*]	[87]
Purine nuclease	<i>Escherichia coli</i>	1.23	0	29 [*]	60	100 [*]	[88]
Protease	<i>Streptomyces sp. A6</i>	1.24	30	58 [*]	55	100 [*]	[89]
Chitinase	<i>Paenibacillus sp. D1</i>	1.46	25	39 [*]	50	100 [*]	[90]
Cellulase	<i>Clostridium cellulolyticum</i>	1.51	30	34 ^b	60	116 ^b	[84]
Average (SD)		1.59 (0.36)					
Psychrophilic Enzyme	Organism	Q ₁₀ ^{meas}	Low temperature (T ₁)		High temperature (T ₂)		references
			[°C]	U Activity ^a [$\mu\text{mol min}^{-1} \text{mg}^{-1}$]	[°C]	U Activity ^a [$\mu\text{mol min}^{-1} \text{mg}^{-1}$]	
Aspartate transcarbamylase	<i>TAD1</i>	1.49	0	0.03	35	0.12	[87]
isocitrate dehydrogenase	<i>colwellia psychrerythraea</i>	1.63	10	22	45	121	[91]
DHFR	<i>Moritella profunda</i>	1.7	0	35	34	215	[92]
alkaline phosphatase	<i>bacillus sp. P9</i>	1.4	5	0.33	40	1.08	[93]
protease	<i>Clostridium sp. LP3</i>	2.16	0	15	37	260	[94]
Ornithine Carbamoyltransferases	<i>Moritella abyssii</i>	2.1	0	21 [*]	22	100 [*]	[13]
Xylanase	<i>Pseudoalteromonas haloplanktis</i>	1.27	4	54 [*]	30	100 [*]	[95]
alpha-amylase	<i>TAC240B</i>	2.62	5	5 [*]	30	100 [*]	[86]
feruloyl esterase	<i>Pseudoalteromonas haloplanktis TAC125</i>	1.27	4	68 [*]	20	100 [*]	[96]
Purine nuclease	<i>Pseudoalteromonas sp. Bst590</i>	1.33	0	37 [*]	35	100 [*]	[88]
metalloprotease	<i>flavobacterium psychrophilum</i>	1.41	4	30 [*]	40	100 [*]	[97]
peptide synthesis (EF-G)	<i>Pseudoalteromonas haloplanktis</i>	2.26	10	13 [*]	35	100 [*]	[58]
lipase	<i>Aspergillus nidulans</i>	1.37	0	28 [*]	40	100 [*]	[98]
arginosuccinate lyase	<i>chloromonas ANT1</i>	1.53	4	24.5 [*]	37	100 [*]	[99]
aminopeptidase	<i>colwellia psychrerythraea</i>	2.27	3	4.8 [*]	40	100 [*]	[100]
Average (SD)		1.72 (0.44)					

^a - Data extracted from graphs

^b - Data published as numerical values

^c - Unspecified units

^d - Activity in units of 1nmol min⁻¹ mg⁻¹

^e - Relative activity

^f - Activity in units of 0.1 absorbance change per minute.

^g - Activity

^h - μM of released sugars

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