

Table S1. Parameters for homology protein modeling and verification

Fungi	Enzyme name	Pfam	Subfamily		Template PDB	Similarity to template	ProQ ³		RMS Z-scores ⁴	
			CE1 ¹	FAE ²			LGscore	MAXsub	length	angle
<i>Aspergillus niger</i>	AxeA	Esterase_phd/ Peptidase_S9	CE1_SF1	-	5X6S	1.554	4.552	0.243	0.876	1.217
<i>Rasamsonia emersonii</i>	Axe1	Esterase_phd/ Peptidase_S9	CE1_SF1	-	5X6S	1.394	4.403	0.282	0.881	1.214
<i>Thermothelomyces thermophilus</i>	Fxe3	Esterase_phd/ Peptidase_S9	CE1_SF1	-	5X6S	1.181	4.361	0.259	0.881	1.214
<i>Chaetomium thermophilum</i>	AxeA	Esterase_phd/ Peptidase_S9+CBM	CE1_SF1	-	5X6S	1.175	4.478	0.280	0.911	1.294
<i>Corynascus sepedonium</i>	Axe1	Esterase_phd/ Peptidase_S9	CE1_SF1	-	5X6S	0.844	5.087	0.527	0.899	1.238
<i>Acremonium thermophilum</i>	Axe1	Esterase_phd/ Peptidase_S9	CE1_SF1	-	5X6S	0.972	4.788	0.452	0.931	1.373
<i>Corynascus sepedonium</i>	Fae1	Esterase_phd/ Peptidase_S9	CE1_SF2	SF6	5X6S	0.826	4.376	0.208	0.905	1.336
<i>Chaetomium thermophilum</i>	AxeB	Esterase_phd/ Peptidase_S9	CE1_SF2	SF6	5X6S	0.803	5.814	0.528	0.985	1.352
<i>Chaetomium globosum</i>	Fxe1	Esterase_phd/ Abhydrolase_2	CE1_SF5	SF5	5X6S	0.154	4.150	0.403	0.992	1.416
<i>Corynascus sepedonium</i>	Fae2	Esterase_phd/ Peptidase_S9	CE1_SF5	SF5	5X6S	0.288	4.104	0.406	0.992	1.365
<i>Corynascus sepedonium</i>	Fae3	Esterase_phd/ Peptidase_S9+CBM	CE1_SF5	SF5	5X6S	0.253	3.929	0.412	0.999	1.357
<i>Chaetomium thermophilum</i>	FaeA	Esterase_phd/ Peptidase_S9	CE1_SF5	SF5	5X6S	0.258	4.627	0.433	1.081	1.46

¹ Based on Fig. 1. ² Based on [10]. ³ LGscore >4 indicates extremely good model, >2.5 indicates very good model; MAXsub >0.5 indicate very good model, >0.1 indicate fairly good model [34]. ⁴ RMS Z-scores, should be close to 1.0 (Protein Model Check <https://swift.cmbi.umcn.nl/servers/html/index.html>).