



- 1 Type of the Paper (Article, Review, Communication, etc.)
- 2 Ion interaction and hydrogen bonds as main features
- 3 of protein thermostability in mutated T1 recombinant
- 4 lipase originated from Geobacillus zalihae
- Siti Nor Hasmah Ishak^{1,2}, Nor Hafizah Ahmad Kamarudin ^{1,3}, Mohd Shukuri Mohamad Ali^{1,4},
 Adam Thean Chor Leow^{1,5,6}, and Raja Noor Zaliha Raja Abd. Rahman^{1,2,6,7,*}
 - ¹ Enzyme and Microbial Technology Research Centre, Faculty of Biotechnology and Biomolecular Sciences, Universiti Putra Malaysia, 43400 UPM Serdang, Selangor, Malaysia; snhasmahishak@gmail.com; hafizah_kamar@upm.edu.my (N.H.A.K.); adamleow@upm.edu.my (T.C.L.); mshukuri@upm.edu.my (M.S.M.A.).
 - Department of Microbiology, Faculty of Biotechnology and Biomolecular Sciences, Universiti Putra Malaysia, 43400 UPM Serdang, Selangor, Malaysia.
 - ³ Centre of Foundation Studies for Agricultural Science, Universiti Putra Malaysia, 43400 UPM Serdang, Selangor, Malaysia
 - Department of Biochemistry, Faculty of Biotechnology and Biomolecular Sciences, Universiti Putra Malaysia, 43400 UPM Serdang, Selangor, Malaysia.
 - Department of Cell and Molecular Biology, Faculty of Biotechnology and Biomolecular Sciences, Universiti Putra Malaysia, 43400 UPM Serdang, Selangor, Malaysia.
 - ⁶ Institute of Bioscience, Universiti Putra Malaysia, 43400 UPM Serdang, Selangor, Malaysia.
 - Laboratory of Halal Science Research, Halal Products Research Institute, Universiti Putra Malaysia, 43400 UPM Serdang, Selangor, Malaysia
 - * Correspondence: rnzaliha@upm.edu.my
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D43E wt-HT1	GGCGTGCGCGGCGATATCGAACAATGGCTGAACGAGAACGGTTATCGAACGTATACGCTG GGCGTGCGCGGCGATATCGAACAATGGCTGAACGAACAACGGTTATCGAACGTATACGCTG
D43E	GCGGTCGGACCGCTCTCGAGCAACTGGGACCGGGCGTGTGAAGCGTATGCTCAGCTTGTC
wt-HT1	GCGGTCGGACCGCTCTCGAGCAACTGGGACCGGGCGTGTGAAGCGTATGCTCAGCTTGTC
	(a)
T118N	CAGCCAAGGGGGCAGAACGCCCGCATGCTTGTCTCGCTCCTAGAGAACGGAAGCCAAGA
wt-HT1	CAGCCAAGGGGGGCAGACGGCCCGCATGCTTGTCTCGCTCCTAGAGAACGGAAGCCAAGA
T118N	AGAGCGGGAGTACGCCAAGGCGCATAACGTGTCGTTGTCACCGTTGTTTGAAGGTGGACA
wt-HT1	AGAGCGGGAGTACGCCAAGGCGCATAACGTGTCGTTGTCACCGTTGTTTGAAGGTGGACA
	(b)
E226D Wt-HT1	CAATGGGGACTGCGCCGCCAGCCGGGTGAATCGTTCGACCATTATTTTGATCGGCTCAAG CAATGGGGACTGCGCCGCCAGCCGGGTGAATCGTTCGACCATTATTTTGAACGGCTCAAG
E226D	CGCTCCCCTGTTTGGACGTCCACAGATACCGCCCGCTACGATTTATCCGTTTCCGGAGCT
Wt-HT1	CGCTCCCCTGTTTGGACGTCCACAGATACCGCCCGCTACGATTTATCCGTTTCCGGAGCT

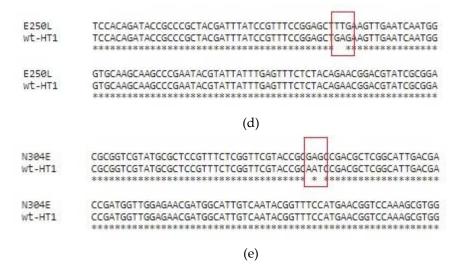


Figure S1. Partial sequence alignments of mutants D43E, T118N, E226D, E250L and N304E with wild-type HT1 sequence. (a) Asp (GAC) to Glu (GAG). (b) Thr (ACG) to Asn (AAC). (c) Glu (GAA) to Asp (GAT). (d) Glu (GAG) to Leu (TTG). (e) Asn (AAT) to Glu (GAG). The multiple sequences alignment was generated from https://www.ebi.ac.uk/Tools/msa/clustalo/. The mutated sequences are marked in red boxes.



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