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      *          20          *          40          *          60          *
TxeA : MNQPPPPSAILEICLYTIDIKRARTFYETLEGYSVMAADRFCFEAGERQVLLIFLHGSDFHGSMMPFG : 70
ToxM : ---MLQLKRIIEITALYVNDLIDIAKEFYAKTEQLEVMVESVLVVLNIGGQNTLLLEKRGASLHTKYLSCG : 67
TflA : -----MTSIRKQLTLLTAELDRMLAFYTNMLGAQHVHEQADAFTIQLGVSQIQ--EAAAADG----- : 54

      80          *          100          *          120          *          140
TxeA : TIPPHDGGSPVHIGEGTSSSES---LPAWRIRLAEYGVAI-ESTITWP-RGGTSIYFRDPDGHIIIEIVTPG : 135
ToxM : EIPPHIASGRIVHVEAIDKQD---LEGWKERLARSGIPL-EGRTEWP-KGGSSIYFRDPDENIVELLTPG : 132
TflA : IRE-----FYHIAINIAANHFQEGKAWLSGFGELLTENDEQAYFEFFNAYSQYVEDESGNIIIEIVLSRQ : 118

      *          160          *          180          *          200          *
TxeA : IIRKLY----- : 140
ToxM : CRRPLY----- : 137
TflA : QAAPVLDKPFPSADQLLSIGEINITTSVDEQAATRLKQAELPVKLDQIEPAGLNFIGDQDLFLLLGPGRR : 188

      220          *          240
TxeA : ----- : -
ToxM : ----- : -
TflA : WLFSEKRVAVIYPLQMELDNGVSLAITETGELVI : 221

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S4 Fig. Amino acid sequence alignment of three toxoflavin-degrading enzymes. TxeA (GenBank accession no. KT210132) obtained from the metagenome in this study, ToxM (GenBank accession no. AAY90317) identified from the genome sequence of *Pseudomonas protegens* Pf-5 and TflA (GenBank accession no. ADK47414) cloned from *Paenibacillus polymyxa* JH2 are compared. The red squares indicate the conserved amino acids in metal-binding motif.