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DrMEC-17 (34) PLQVTTVIDELGKASSKAQQ---*LPAPITSAAKLQA----N (68)
TtGcn5 (59) -THRNMKLLIDLKNIQSRQLP--KMPKEYIV-KLVFD----R (92)
ScGcn5 (110) -TKENMMVLTGLKNIFQQLP--KMPKEYIA-RLVYD----R (143)
HsPCAF (507) PNKKILMWLVGLQNVFSQLP--RMPKEYIT-RLVFD----P (541)
ScHAT1 (143) -DDFARRMHRRVQIFSLLFIE---A-ANYI---DETD----P (172)
OaAANAT (44) -----DAAGVFEIEREAFISVSGNCPNL-DEVQHFLTLC (77)
HsMOF (256) ----HKIYCQNLCLLAKLFLD---H--KTLY-FDVE----- (281)
HsMYST3 (586) ----STIYCQNLCLLAKLFLD---H--KTLY-YDVE----- (611)
HsTip60 (257) ----NKSYSQNLCLLAKCFLD---H--KTLY-YDTD----- (282)
ScEsa1 (244) ----QRTWCRNLCLLSKLFLD---H--KTLY-YDVD----- (269)

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**Supplementary information, Figure S5** Structure-based sequence alignment of the  $\alpha 2$ - $\alpha 3$  segment of DrMEC-17 with the equivalent regions of the representative acetyltransferases of the GNAT and MYST families.

The alignment was performed with the Dali server [16] and modified according to superposition of the structures onto the DrMEC-17/acetyl-CoA structure based on the core region. The PDB codes of the structures used in the alignment are as follows: TtGcn5 (1QSR), ScGcn5 (1YGH), HsPCAF (1CM0), ScHAT1 (1BOB), OaAANAT (1CJW), HsMOF (3QAH), HsMYST3 (2OZU), HsTip60 (2OU2), and ScEsa1 (1FY7). The abbreviations for the species are as follows: Dr, *Danio rerio*; Tt, *Tetrahymena thermophila*; Hs, *Homo sapiens*; Sc, *Saccharomyces cerevisiae*; Oa, *Ovis aries*. The secondary structure elements of DrMEC-17 are marked above the alignment. The positions of the conserved Gln, Leu, and Ile on the  $\alpha 2$ - $\alpha 3$  loop of DrMEC-17 are marked with red stars.