

Table S1.

Site-directed Mutagenesis Primers

Mutant	Forward or Reverse Primer	Primer Sequence
E47A	Forward	CTT TTT CTT CAA GGA TGC ACC GCT GAA CAC CTT CC
	Reverse	GGA AGG TGT TCA GCG GTG CAT CCT TGA AGA AAA AG
P48A	Forward	AGG TGT TCA GCG CTT CAT CCT TGA AGA AAA AGG TCT
	Reverse	AGA CCT TTT TCT TCA AGG ATG AAG CGC TGA ACA CCT
Y64A	Forward	GAA GCG GTT TCA GGG AGG CCT TCT CCA GCT CCT TGC
	Reverse	GCA AGG AGC TGG AGA AGG CCT CCC TGA AAC CGC TTC
D142A	Forward	ACA GGA TCT TGC CGG CCA GGA TGA GCT CC
	Reverse	GGA GCT CAT CCT GGC CGG CAA GAT CCT GT
R153A	Forward	GTG GAC ACC AAC TAC GCG GGC CTG GGC A
	Reverse	TGC CCA GGC CCG CGT AGT TGG TGT CCA C
H178A	Forward	GGC TGG AAC AGA GAA CGG CGT ACA CAT TGA TGC CGT
	Reverse	ACG GCA TCA ATG TGT ACG CCG TTC TCT GTT CCA GCC
C181A	Forward	ATG TGT ACC ACG TTC TCG CTT CCA GCC ACT ACT CCG
	Reverse	CGG AGT AGT GGC TGG AAG CGA GAA CGT GGT ACA
S186A	Forward	CCA GCC ACT ACG CCG CCC GGG TG
	Reverse	CAC CCG GGC GGC GTA GTG GCT GG
S182A/S186A	Forward	TCA ATG TGT ACC ACG TTC TCT GTG CCA GCC ACT ACG
	Reverse	CGT AGT GGC TGG CAC AGA GAA CGT GGT ACA
H220A	Forward	CCG GCG GCC CCG GCC GTA GGC ATC CA
	Reverse	TGG ATG CCT ACG GCC GGG GCC GCC GG

Table S2.

AANATA product characterization.

Sample	Retention Time	Mass/Charge
	(min)	[M + H] (<i>m/z</i>)
<i>N</i> -acetylserotonin Standard	0.78	219.1132
AANAT A Enzyme Assay ^a	0.78	219.1133

^a Reaction condition – 300 mM Tris-HCl pH 8.0, 500 μ M acetyl-CoA, 1 mM serotonin, 15 μ g AANATA.

Table S3.

Conserved *D. melanogaster* AANATA Arg153 Found in other GNAT Enzymes

Organism	Enzyme	PDB Data Base ID for Crystal Structure	Conserved Arginine
Drosophila	AANATA	3TE4	R153
Sheep	SNAT	1CJW	R131
Human	SSAT	2JEV	R101
Tuberculosis	AgNAT	1M4G	R91
Yeast	HAT (Hpa2)	1QSM	R100
Human	NMT	3JTK	R255

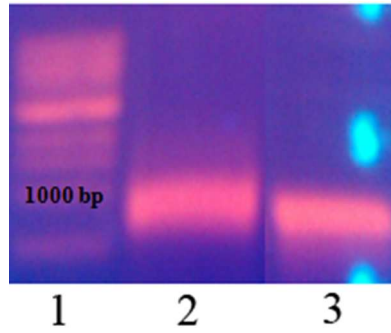


Figure S1. Cloning of *AANATA* and *AANATB* from *D. melanogaster*. (Lane 1) 1 kb DNA ladder (New England Biolabs), (Lane 2) *AANATB*; 828 bp band, (Lane 3) *AANATA*; 723 bp band.

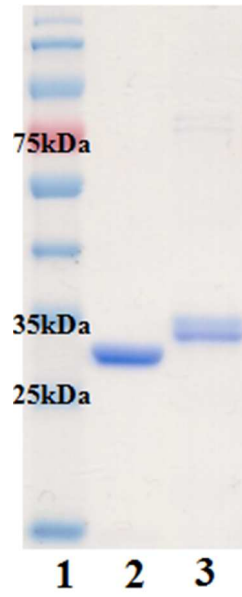


Figure S2. SDS-PAGE gel for purified AANATA and AANATB. (Lane 1) Precision Plus Protein™ Kaleidoscope™ Standards (Biorad), (Lane 2) AANATA; 27 kDa, (Lane 3) AANATB; 31 kDa.

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AANATA      LIQPEDGEAVIAMLKTFFFKDEEPLNTFLDL----GECKELEKYSLKPLPDNCSYKAVNK 80
AANATB      LIQPEDGEAVIAMLKTFFFKDEEPLNTFLDL----GECKELEKYSLKPLPDNCSYKAVNK 115
AANATL2 (CG9486)  AMTIGDYEEVEAFLAVHFFKQEPLMLI PQEDPKQSEVSSAEAELHRS LI PQDLSLVAVD- 66
AANATL3 (CG10659) TMTKEDYPSVKAFLKDNFFQSEPLCQSTSE-NVQSQNEKENDEYHLSMIAQGTCLVAIDE 71
AANATL4 (CG18607) IMRPEDYAQVKA YMEAEYTSEPLCQSSGE-PVHQQNEEINDAFNQSI I AEGTSL LALDE 71
AANATL5 (CG10476) VMKEDDYPRVKT FMTDYFHYDEPMGMGLEE-P IHLQHEEEVDRQYLAVI RQGLSIVALDD 71
AANATL6 (CG18606) VMKEDDYPRVKT FMTDYFHYDEPMGMGLEE-P IHLQHEEEVDRQYLAVI RQGLSIVALDD 71
AANATL7 (CG13759) MIAPEHSEQVMEHLRRNFFADEPLNKAAGL-CQNGSSCPALEAHCAEAI QHRMSVMAVDA 63
AANATL8 (CG15766) QVDVGETEQLMT FLLAHYYPEEPLTAGTHP----PEPEAADKEFLLSNV PFGTCFVALH- 67
      : . : : : . * *: : . * :
AANATA      PDEELILDGKILSVDTNYRGLGIAGRLTERAYEYMRENGINVYHVLCSSHYSARVMEKLG 194
AANATB      PDEELILDGKILSVDTNYRGLGIAGRLTERAYEYMRENGINVYHVLCSSHYSARVMEKLG 229
AANATL2 (CG9486)  G-VERALYLYMLGVDVSIRRQRVGTRLVEATI ELGRQRFPPVVTSTCSNONSKRLMTALN 179
AANATL3 (CG10659)  G-ISKLLYSHIT SVESSMRGKGLGSR LAATIMDVGRAGFPAMTAYCTSFYSARQKEALG 185
AANATL4 (CG18607)  D-IPKALYSHVT SVASWKRGKGLGSR LAATIMELGRSNGFPLMMAFCTSFYSARQK GALG 187
AANATL5 (CG10476)  G-VSSYLSLLVI SVHPSMRQRGILVILSKCLF KLGRLRGLR LFTGSGTNHYSSRSAMKAG 185
AANATL6 (CG18606)  G-VSSYLSLLVI SVHPSMRQRGILVILSKCLF KLGRLRHTLFT TSGTNHYSSRSAMKAG 185
AANATL7 (CG13759)  D-VDCMFDVRI LSVDSCYRGQGIANELVKRSVAVAKKNGFRL LKADATGGIFSQKIFRSHG 179
AANATL8 (CG15766)  S-VPSCLHVHALGVD PQLRGRNLGGR LMETVAQRGRDLGHQLVSVDCTSVYSARLVQRLG 179
      : . * * : * : * : . * :
AANATA      FHEVFRMQFADYK-PQGEVVF KPAAPHVGIQVMAKEVGPAAQAQTKL-- 240
AANATB      FHEVFRMQFADYK-PQGEVVF KPAAPHVGIQVMAKEVGPAAQAQTKL-- 275
AANATL2 (CG9486)  MECILTKDYADYKDEHGEIVLRASEPHTSASVVA IRL----- 216
AANATL3 (CG10659)  MKCVHSLPYADYKDDQGRPI FT PAEPHTMARIMFIKL----- 222
AANATL4 (CG18607)  MECIYSIDYADYKDEGRVI FT PAAPHTKLRVMAIKL----- 224
AANATL5 (CG10476)  CECIHSVAYADYKDEQGRPI YNPPAPHTHIRVLASKL----- 222
AANATL6 (CG18606)  CECIHSVAYADYKDELGRPI YNPPAPHTHIRVLASKM----- 222
AANATL7 (CG13759)  FEVVFSEQPYSKYTDENGKVI LPVEAPHIKLOOLYKAI CADDQDEKKQSL 228
AANATL8 (CG15766)  YQLINTLRYVDHLDASGQVIRPPPPHESVQTFVLHL----- 216
      . . : : . * : ** . :

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Figure S3. Primary sequence alignment of AANATA with putative AANATL enzymes found in *D. melanogaster* using clustalW2.

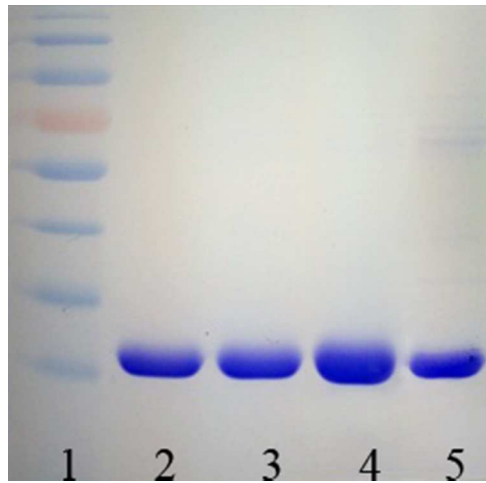


Figure S4. SDS-PAGE gel of purified AANATA mutants. (Lane 1) PageRuler™ Prestained protein ladder (Thermo Scientific), (Lane 2) E47A, (Lane 3) R153A, (Lane 4) S186A, (Lane 5) H220A.

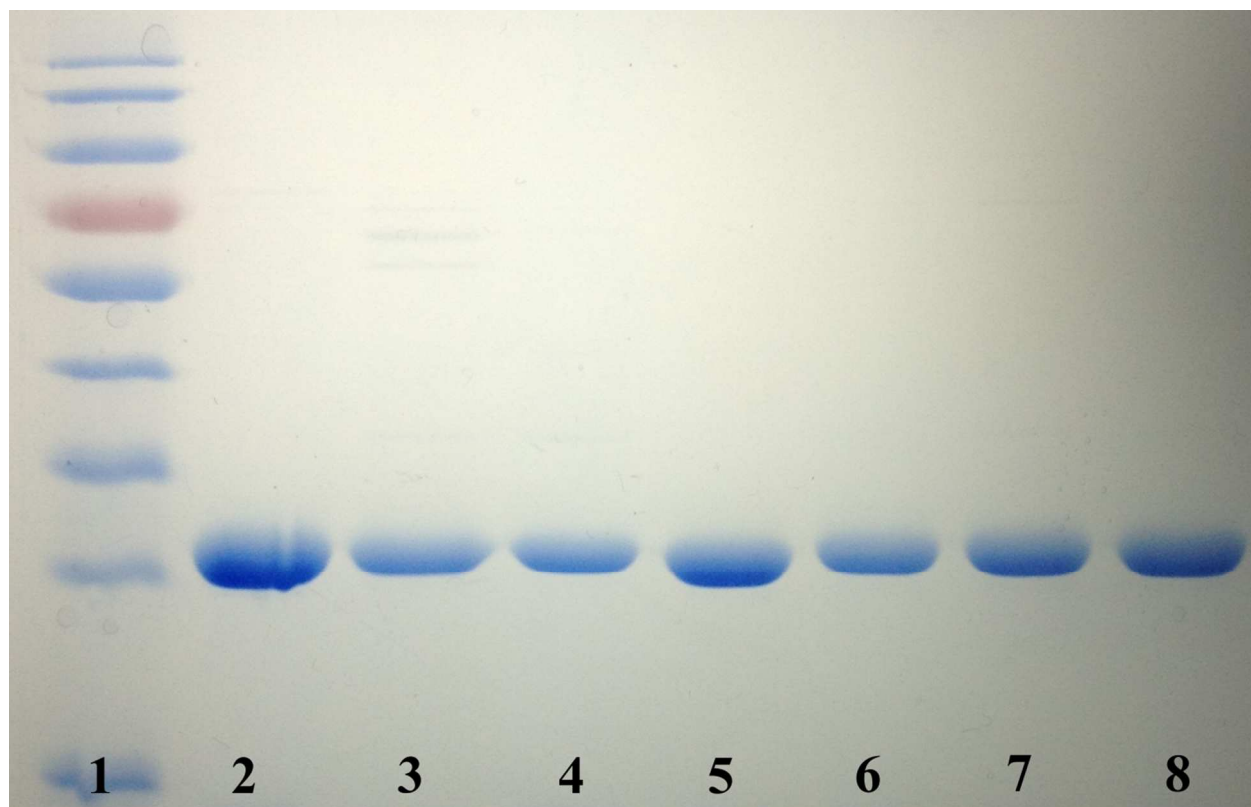


Figure S5. SDS-PAGE gel of purified AANATA mutants. (Lane 1) PageRuler™ Prestained protein ladder (Thermo Scientific), (Lane 2) P48A, (Lane 3) Y64A, (Lane 4) D142A, (Lane 5) H178A, (Lane 5) C181A, (Lane 5) S182A/S186A.

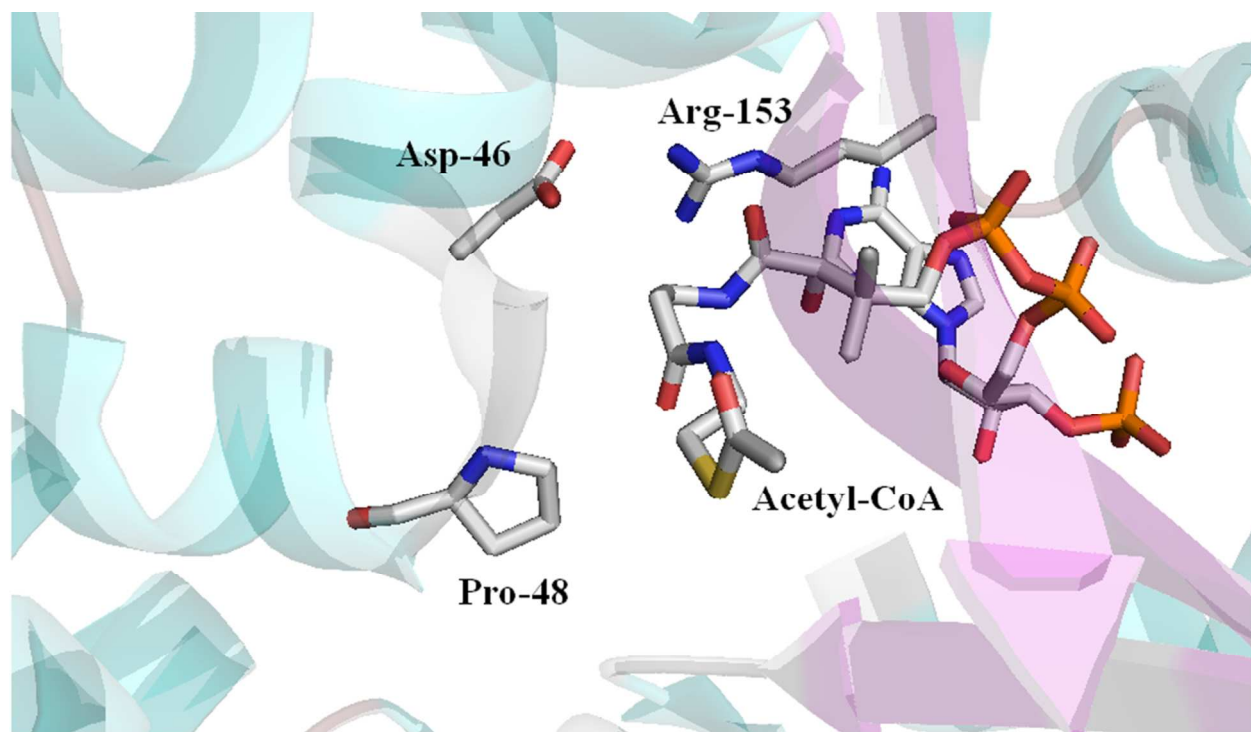


Figure S6. *D. melanogaster* AANATA Pro-48 (PDB: 3TE4) showing general location with respect to amine binding pocket and bound acetyl-CoA.