SUPPLEMENTARY MATERIAL

Table S1.

Gene-Specific	primers
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Degenerate primers			
Sirt2-F1 CCMGACTTCCGTAGTCC	Sirt2-F2 AACCACAGGCKATATT Sirt2-R1 TCCCCCCATCCSAGTCT		
Sirt2-R2 CCSGCCTTCTCACGGTT	Sirt2-F3 GAATTATTTCCAGGAAG		
PGAM-F1 TGTKATGATYCGTCATGG	PGAM-F2 GAATGGAAYCAGAARAA		
PGAM-F3 GCWGAAGGCTATCAGTT	PGAM-R2 AACATTGTTCCAGTAWGG		
PGAM-R1 GGCAGRTTCAAYTCCAT			
PK-F1 ATCTGTACYATYGGACC	PK-F2 GTGCTVGAGAAGATGAT		
PK-R1 GGGTASTCGCCCTTGGC	PK-R2 ATACCCAGATCATCCACG		
PK-R3 TTGATGTTCTTBCCTTC			
PEPCK-F1 GAAGGATGGCTSGCCGA	PEPCK-F2 GACGACATMGCCTGGATG		
PEPCK-R1 CGGAACCAGTTBACGTG	PEPCK-R2 GCCGAAGTTGTAGCCGAA		
PEPCK-R3GTGGCCTCGSWCCTCAT			
Overexpression primers			
Sirt2 F CCGGAATTCTATGTCTGCAAA	ITCACCGCCAGG		
Sirt2 R CCGCTCGAGCGTCATAGTTCG	GGCTCCTGTGG		
PK F CGGGATCCATGGTGTATACAAC	TATTTACGAT		
PK R CCGGAATTCCATTCCGCTTGGA	TGACACGCATGGT		
PGAM F CGGGATCCACATGGGACGTC	CAAAAGGAAAATT		
PGAM R CCCTCGAGCGCTTGGCCTTGGCAAGCAAC			
PEPCK F CCGGAATTCCATGTTGCACC	PEPCK F CCGGAATTCCATGTTGCACCTGCAGGCTGACC		
PEPCK R CCGCTCGAGGGTGACTGTT	GGACATTTTTCCTAAG		
Prokaryotic expression primers			
Sirt2 F CCGGAATTCGTGGAGGCTCAC	GGCACCTTC		
Sirt2 R CCGCTCGAGGCTCCTGTGGCG	TGACGTG		
RNA interference primers			
Sirt2-Ri-F1 GGATCCTAATACGACTCA	CTATAGGGTGTTCTTCGGCGAGAGTCTC		
Sirt2-Ri-F2 GTG TTCTTCGGCGAGAGTCTC			
Sirt2-Ri-R1 GGATCCTAATACGACTCACTATAGGTAGTTC GGG CTCCTGTGGCGT			
Sirt2-Ri-R2 TAGTTCGGGCTCCTGTGGCGT			
GFP-Ri-F1: GGATCCTAATACGACTCACTATAGGAAGGGCGAGGAGCTGTTCACCG			
GFP-Ri-F2: AAGGGCGAGGAGCTGTTCACCG			
GFP-Ri-R1: GGATCCTAATACGACTCACTATAGGCAGCAGGACCATGTGATCGCGC			
GFP-Ri-F2: CAGCAGGACCATGTGATCGCGC			
Primers used for PCR in this study. M=A/C;	R=A/G; W=A/T; S=G/C; Y=C/T; K=G/T; V=A/G/C; H=A/T/C; B=G/T/C; D=G/A/T.		

Н.	armigera	MYY <mark>TTIYDG KYEAGSND KPAMQMCAANAA</mark> SHLQAMCSLDIDSKSSEVRLSGIICTIGPASRDVAMLERMMETGMNVARMNFSHGSHEYHAETI	93
Р.	xuthus	MKAVETRNRKYQSGSAEKPGMQMAAADVGSHLEHMCSLDIDSKASYVRLSGIICTIGPASRDVAMLEKMMETGMNVARMNFSHGSHEYHAETI	93
В.	mori	MYYPTIHDGETEAGAVEKPTVANVGSQLQHMCGLDIDSKSSYTRLSGIICTIGPASRNVAVLEKMMETGMNVARMNFSHGSHEYHAETI	89
Н.	sapiens	MEGPAGYLRRASVAQLTQELGTAFFQQQQLPAAMADTFLEHLCLLDIDSEPVAARSTSIIATIGPASRSVERLKEMIKAGMNIARLNFSHGSHEYHAETI	100
Н.	armigera	KNCREAEKNYSAKLGSPFSLAIALDTKGPEIRTGLLEGGGSAEVELKKG <mark>D</mark> TIK <mark>E</mark> TTDPAY <mark>A</mark> ERGTAATIYVDYKNITSVVKPGNRIFIDDGLISVICQSA	193
Р.	xuthus	KNCREAEKNYSAKLGVPFSLAIALDTKGPEIRTGLLEGGGSAEVELKKGETIKLTTNPAYQEKGTAA <mark>NIE</mark> VDYKNITGVVKPGNRIFIDDGLISVICQSS	193
В.	mori	RNCREAEKSYSAKLGSPFSLAIALDTKGPEIRTGLLEGGGSAEVELKKGETIKLTTSSDYQEKGNADTIYVDYKNITNVVKPGNRIFIDDGLISVICQSV	189
Н.	sapiens	ANVREAVESFAGSPLSYRPVATALDTKGPEIRTGILGGGPESEVELVKGSQVLVTVDPAFRTRGNANTVWVDYPNTVRVVPVGRIFIDDGLISLVVQKT	200
Н.	armigera	S <mark>S</mark> DTLTCTIENGGMLGSRKGVNLPGLPVDLPAVSEKDKSDLLFGVEQGVDMIFASFIRNGAALTEIR <mark>N</mark> ILGEKG <mark>R</mark> NIKIISKIENHQGMVNLDEII <mark>T</mark> ASD	293
Р.	xuthus	TADTLVCTIENGGMLGSRKGVNLPGLPVDLPAVSEKDKSDLLFGVEQGVDMIFASFIRNGAALTEIRGILGEKGKNIKIISKIENHQGMVNLDEIIAASD	293
В.	mori	SADTLTCTIENGGMLGSRKGVNLPG <mark>I</mark> PVDLPAVSEKDKSDLLFGVEQGVDMIFASFIRNGAALHEIRGILGEKGKNIKIISKIENHQGMVNLDEIIAE	289
Н.	sapiens	SPEGLVTQVENGG <mark>V</mark> LGSRKGVNLPG <mark>AQ</mark> VDLPGLSE <mark>Q</mark> DVRDLRFGVEHGVDTVFASFVRKASDVAAVRAALGPEGHGIKIISKIENHEGVKRFDEILEVSD	300
Н. Р. В. Н.	armigera xuthus mori sapiens	GIMVARGDLGIE IPPEKVFLAQKTM IARCNRVGKPV I CATQMLESMVKKPRPTRAE I SDVANA I LDGADCVMLSGETAK GDYPLECVLTMAN I CKEAEAA GIMVARGDLGIE I PPEKVFLAQKTM IARCN <mark>R</mark> VGKPV I CATQMLESMVKKPRPTRAETSDVANA I LDGADCVMLSGETAK GDYPLECVLTMAN I CKEAEAA GIMVARGDLGIE I PPEKVFLAQKTM I ARCNRVGKPV I CATQMLESMVKKPRPTRAE I SDVANA I LDGADCVMLSGETAK GDYPVECV <mark>H</mark> TMAN I CKEAEAV GIMVARGDLGIE I PP <mark>A</mark> EKVFLAQKIMI I G <mark>RCNLA</mark> GKPV <mark>V</mark> CATQMLESMVKKPRPTRAE I SDVANA I LDGADCVMLSGETAK GDYPVECVH GIMVARGDLGIE I PP <mark>A</mark> EKVFLAQKIMI I G <mark>RCNLA</mark> GKPV <mark>V</mark> CATQMLESMITKPRPTRAETSDVANA VLDGADCIMLSGETAK GNFPVEAVKMQHRI I AREAEAV	393 393 389 400
Н.	armigera	IWHRQLFNDLVVEVRPPIEPAHSTA LAAVEASTKCLAAA IVVITTSGKSAHLLSKYRPRCPIIAVTRHAQTARQAHLYRGVLPIVYSEAAAAGDWLKDVDN	493
Р.	xuthus	IWHRQLFTDLVAQVKCPIEPAHSTA LAAVEASSKOMASA IVVITTSGRSAHLLSKYRPRCPVIAVTRHPQTARQAHLYRGVLPLVYKEAAASDWLKDVDL	493
В.	mori	IWHRQLFNDLVSEVKPPIDPAHSAAIAAVEAATKCLASA IVVITTSGKSAHLLSKYRPRCPIIAVTRHPQTARQAHLYRGVLPIVYGEPTASDWLKDVDN	489
Н.	sapiens	VYHRQLFEELRRAAPLSRDPTEVTAIGAVEAAFKCCAAAITVITTGRSACLLSRYRPRAAVIAVTRSAAARQVHLCRGVFPLUYREPPEATWADDVDR	500
H.	armigera	RVQSGLKFGR <mark>ARGFIKTGDSVVVVTGWKQGSGFTNTMRVIQA<mark>E</mark>— 536</mark>	
P.	xuthus	RVQFGLQFGRQRGFIKRGDQVIVVTGWRQGSGYTNTMR <mark>I</mark> IPVVD 537	
B.	mori	RVQSGL <mark>RFGRQRGFVHPGDNAVVVTGWRQGSGFTNTV</mark> RVIQL <mark>E</mark> — 532	
H.	sapiens	RVQFG <mark>IESGKLRGFIRVGDLVIVVTGWRP</mark> GSGYTN <mark>IMRVL</mark> SIS— 543	

Figure S1. Homology comparison to other known PK proteins. The *H. armigera* PK amino acid sequence has high identity with PKs of other species: *P. xuthus* (89%), *B. mori* (87%), and *H. sapiens* (57%). Black shading represents \geq 50% sequence identity. *H. armigera*, GenBankTM number KY412773; *P. xuthus*, XP_013164662.1; *B. mori*, XP_004931176.2; *H. sapiens*, AY352517.1. The red line below the amino acid sequence shows peptide synthesized as an immunogen.

Н.	armigera	MPAKYKIVMIRHGESEWNQKNLFCGWFDADLSDKGREEAVAAGKALK <mark>S</mark> EGYEFDVAHTSVLKRAQITLNTILNEIGKPDLPVEKTWRLNERHYGGLTGLN	10
Р.	machaon	Maakykivmirhgesewnqknlfcgwydadlsdkgreeavaagkalkaegyqfdvahtsvlkraqitlnsilteigqpdlpvnktwrlnerhyggltgln	10
В.	mori	Mpakykivmirhgesewnqknlfcgwfdadlsdkgrdeavaagkalkaegyqfdvahtsvlkraqitlnsilkeigqpdiptektwrlnerhyggltgln	10
Н.	sapiens	—Ma <mark>thrl</mark> vmyrhgestwnqenrfcgwfdaelsekgteeakrgakatkdakmefdicytsvlkratrtlwaildgtdqmwlpvvrtwrlnerhyggltgln	99
Н.	armigera	KAETAAKYGEAQVQIWRRSFDVPPPPMEKDHPYYDTIVKDPRYA <mark>S</mark> DPKPEEFPMFESLKLTIERTLPYWNNVIVPQIKAGKRIIIAAHGNSLRGIVKHLD	20
Р.	machaon	KAETAAKYGEAQVQIWRRSFDIPPPPMEK <mark>B</mark> HPYY <mark>B</mark> TIVKDPRYAGDPKPEEFPMFESLKLTIERTLPYWNNVIVPQIKEGKRIIIAAHGNSLRGIVKHLD	20
В.	mori	KAETAAKYG <mark>C</mark> AQVQIWRRSFDVPPP <mark>A</mark> MEKDHPYYDTIVNDPRYAADPKPEEFPMYESLKLTIERTLPYWNNVIVPQIKEGKKIIIAAHGNSLRGIVKHLD	20
Н.	sapiens	KAETAAKHGE <mark>EQVK</mark> IWRRSFDIPPPPM <mark>DEK</mark> HPYY <mark>NS</mark> IS <mark>KERRYAG-LKPGELPTCESLKDTIA</mark> RALPFWNEEIVPQIKAGKRVIIAAHGNSLRGIVKHLD	19
H.	armigera	GLSD <mark>SAIMELNLPTGIPFVYELDEDM</mark> KPVDSMVFLGDEETVKKAMEAVASQGKAK 255	
P.	machaon	NLSDAAIMELNLPTGIPFVYELDENLQPVDSMVFLGDEETVRKAMAAVAAQGKAK 255	
B.	mori	DLSDAAIMELNLPTGIPFVYELDENLKPVDSMVFLGDEETVRKAMAAVAAQGKAK 255	
H.	sapiens	GMSDQAIMELNLPTGIP <mark>I</mark> VYEL <mark>NKE</mark> LKPTKPMQFLGDEETVRKAMEAVAAQGKAK 253	

Figure S2. Homology comparison to other known PGAM proteins. The *H. armigera* PGAM amino acid sequence has high identity with PGAMs of other species: *P. machaon* (92%), *B. mori* (92%), and *H. sapiens* (69%). Black shading represents \geq 50% sequence identity. *H. armigera*, GenBankTM number KY387804; *P. machaon*, XP_014361246.1; *B. mori*, NP_001037540.1; *H. sapiens*, NP_000281.2. The red line below the amino acid sequence shows peptide synthesized as an immunogen.

Н.	armigera	MLHLQADPEDYVRKTNQYAQVALAC <mark>G</mark> RAAHQTALRGASAPSPQLA <mark>A</mark> LTPKVRAFVERSAALCQPEHVHVCDGSEAEAAALLHIMQQQGMLKRLPKYDNCW	100
Л.	transitella	MLHENTVPEDYVKKTAQCAQVALGC-RSAHQTAARGVVKP-AQLATLTPKVRAFVERSVALCQPDHVHVCDGSEAEAAALLQLMQQQGTIRFLPKYDNCW	98
В.	mori	MLHEKATPEDYVRKTAKCAQVAIGCSRAAHQTALRGSTKPSPQLTTLTPKVRAFVERSAALCQPEHVHVCDGSETEARALLQLMQQQTTLKRLPKYDNCW	100
Н.	sapiens	MPPQLQNGLNLSAKVVQGS	76
Н.	armigera	LARTDPADVARVESRTFICSDKERDVVPIARAGQKSALGNYI <mark>A</mark> PSDY <mark>D</mark> KA <mark>IT</mark> ERFPGCMRGRTMYVIPFSMGPACSPLSKIGVEITDSPYVVYSMRVMTR	200
А.	transitella	LARTDPADVARVESRTFICS <mark>E</mark> KERDVVPIARAGQKSALGNYIT <mark>I</mark> SDYEKAVSERFPGCMKGRTMYVIPFSMGPVGSPLSKIGVEITDSPYVVYSMRVMTR	198
В.	mori	LARTDPADVARVESRTFICSD <mark>R</mark> DSDVPSARAGQKSALGNYISPFDYEKAVSDRFPGCMKGRTMYVIPFSMGPVGSPLSKIGVEITDSPYVVYSMRVMTR	200
Н.	sapiens	LARTDPRDVARTES <mark>KTVIVTQEQ</mark> RDTVPI <mark>PKTG-LSQLGRWNSEDDF</mark> EKAFNARFPGCMKGRTMYVIPFSMGPLGSPLSKIGTEITDSPYVVASMRVMTR	175
Н.	armigera	MGAKVLEALRQDEQFVRCLHAVGTGG ———IAGWPCDPPRTIILHKPADNEIVSYGSGYGGNSLLGKKCFALRLGSVIARREGWLAEHMLIVG <mark>V</mark> TDPK	294
Л.	transitella	IG <mark>S</mark> KVLEALRQDESFVKCLHA <mark>LGHA</mark> G ———APGWPCDPPRTLILHRPADSEIVSFGSGYGGNSLLGKKCFALRIGSVIARREGWLAEHMLIVGITDPQ	292
В.	mori	IGAKVLE <mark>ILRQDEQFVRCLHAVGSGG ———TPGWPCDPKN</mark> TIILHKPA <mark>E</mark> NEIVSYGSGYGGNSLLGKKCFALRLGSVIARREGWLAEHMLIVGITNPQ	294
Н.	sapiens	MGTPVLEAVG-DGEFVKCLHSVGCPLPLQKPLVNNWPCNPELTLIAHLPDRREIISFGSGYGGNSLLGKKCFALRMASRIAKBEGWLAEHMLILGITNPE	274
Н. Л. В. Н.	armigera transitella mori sapiens	GRKRY I AAAFPSACGKTNLAMMTPTLPGYKVECVGDD I AWMKFDKNGVLRA INPENGFFGVAPGTS <mark>E</mark> ATNP I AMSTVFQNTVFTNVGETSDGGVWWEGMG GRRY I AAAFPSACGKTNLAMMTPTLPGYKVECVGDD I AWMKFDKNGVLRA INPENGFFGVAPGTS <mark>S</mark> TNP I AMSTIF <mark>S</mark> NTVFTNVAETEDGGVWWEGMG G <mark>RKRY I AAAFPSACGKTNLAMMTPTLPGYKVECVGDD I AWMKFDKD</mark> GVLRA INPENGFFGVAPGTS <mark>A</mark> ATNP I AMATVFKNTVFTNVAETPE G <mark>BKRY I A</mark> AAFPSACGKTNLAMMTPSLPGWKVECVGDD I AWMKFDAQGHLRA INPENGFFGVAPGTS <mark>A</mark> ATNP I AMATVFKNTVFTNVAETPE GBKRY I AAAFPSACGKTNLAMMTPSLPGWKVECVGDD I AWMKFDAQGHLRA INPENGFFGVAPGTS <mark>A</mark> ATNP I AMATVFKNTVFTNVAETPE GBKRY I AAAFPSACGKTNLAMMTPSLPGWKVECVGDD I AWMKFDAQGHLRA INPENGFFGVAPGTSVKTNPIAMATVFKNTVFTNVAETSDGGVWWEGMG	394 392 394 374
Н.	armigera	NAPESLTDWKGQPWD <mark>A</mark> SKKTPAAHPNSRFCTPAEQCPIIDPEWESAEGVPISAILLGGRRPAGVPLVVESRDWQHGVFMGATMRSEATAAAEHAGKV	491
Л.	transitella	KAPAKLTDWKGQPWTPE <mark>S</mark> KTPAAHPNSRFCTPADQCPIIDSEWESAEGVPISAILLGGRRPAGVPLVVEARDWTHGVFMGASMRSESTAAAEHSGKV	489
В.	mori	PAPERLVDWKGQPWDPSKKTPAAHPNSRFCTPAEQCPTIDGEWESSEGVPISAILLGGRRPAGVPLVVESRDWQHGVFMGASMRSESTAAAEHSGKV	491
Н.	sapiens	EPLASPER	474
Н.	armigera	VMHDPFAMRPFFGYDFGEY <mark>I</mark> KHWLSMPG-OGROMPKTFHVNWFRK <mark>N</mark> DEGKFLWPG <mark>Y</mark> GENSRVLDWTLRRCDNEPCYTE <mark>S</mark> PLG <mark>NTPTEGDLNTDNLGP</mark> TDM	590
А.	transitella	VM <mark>N</mark> DPFAMRPFFGYNFGEYLKHWLSMPG-AGRKMPKTFHVNWFRKSDEGKFLWPGFGENSRVLDWTLRRCDNEPCYTETPLGYVPREGDLNTDNLGPTDM	588
В.	mori	VMHDPFAMRPFFGYNFG <mark>D</mark> YLKHWLSMPG-PGRKMPKTFHVNWFRKDEQGKFLWPGFGENSRVLDWTLRRCDGEPCHAETPLGYIPRAGALNT <u>B</u> NLSAVDM	590
П.	sapiens	IMIDPFAMRPFFGYNFG <mark>K</mark> YLAHWLSMAGIIPAAKLPKTFIVNWFRKD <mark>E</mark> GGKFLWPGFGENSRVLDWMFNR <mark>TIGGKASTKLTPT</mark> GYIPR <mark>BDALNTB</mark> NLSAVDM	574
H. A. D. H.	armigera transitella mori sapiens	NTLFSIPKDFWLQEADAIEKYFKEEVGEDLPPAMW <mark>E</mark> ELNKLRKNVQQS	

Figure S3. Homology comparison to other known PEPCK proteins. The *H. armigera* PEPCK amino acid sequence has high identity with PEPCKs of other species: *A. transitella* (85%), *B. mori* (86%), and *H. sapiens* (59%). Black shading represents ≥50% sequence identity. *H. armigera*, GenBank[™] number AFK28502.1; *A. transitella*, XP_013191765.1; *B. mori*, NP_001040542.1; *H. sapiens*, NP_002582.3. The red line below the amino acid sequence shows peptide synthesized as an immunogen.



Figure S4. Predicted acetylation site of the metabolic enzymes. (A) Potential acetylation sites of PK, PGAM, and PEPCK using a PSKAcePred software. (B) Predicted acetylation sites of PK, PGAM, and PEPCK compared with known acetylation sites. The red amino acids show the predicted acetylation sites and the green amino acids show the flanking residues. *H. sapiens, Homo sapiens.*



Figure S5. Effect of NAM treatment on *PK* **and** *PEPCK* **mRNA levels.** HzAm1 cells were treated with 0, 5, 10,15 mM NAM for 48 h. Total RNA was extracted and *PK* and *PEPCK* mRNA levels were detected by qPCR using *actin* as an internal standard. Each point represents the means±S.D. of three independent replicates. *, p<0.05; **, p<0.01 (determined by and independent t-test).

尼 A R R 思	annigura tennoltolla Authus acri	MSANSPPCKSCDDPVDRFVPDVPPN-PIESLCARLRDLDVDSIRRYLACKLCPYEE-PETAAPIDQVLEEV MCVIYLSKSPWQVWTKIQSRNLRYLSKASANSPPCKSD-PAVDNIPPN-SPESLCSRLRDLDVDSIRRYLASKLCPYEE-SEPPIPTDQVLEEV MSANSPPCKSCGHETYDESPONVPTTISJESLCSRLRDLDVDSIRRYLASKLCPYEE-SEPPIPTDQVLEEV MSANSPPCKSCGHETYDESPONVPTTISJESLCSRLRDLDVDDVRMYLAUKLCLFSCDLBPAERREVLDEV
医人氏尿	anzigara transitella Authus auri	SLDG IVKWIQSERCKNI ITI LAGAGISTSAGIPDPRSPETCLYHNLQKY <mark>D</mark> LPEPQAIPE INHFRQNPKPFR <mark>I</mark> LAKELYPCSFKPTISHYP IRLLHEKGILL I NLDG IVKWIK <mark>C</mark> DRCKNI ITI AGAGISTSAGIPDFRSPETCLYHNLQKYNLPEPQAIPE INHFRQNPKPFFILAKELYPCSFKPT <mark>I</mark> SHYP IRLLHEKGILL I SLDG IVKWIKSE ^R CKNI ITI SGAGISTSAGIPDFRSPETCLYHNLQKYNLPEPQAIPE INHFRQNPKPFFILAKELYPCSFKPT ISHYP IRLLHEKGILL I SLMG IV <mark>R</mark> WIKSDRCK <mark>H</mark> I ITI SGAGISTSAGIPDFRSPETCLYHNLQKY <mark>E</mark> LF <mark>E</mark> PQAIPE INHFRQNPKPFFILAKELFPCSFKPT ISHYP IRLLHEKGILL I
E A R B	arnigara tenasi tel la Juthus auri	RHYTQNIDTLERGAGIPEEKLVEAHGIFYTSHCLDORKEYNLEYVKERIFADQIPICTEORGVVKPDIVFPGESLPDRPGRCLQEDRQQOMLIIMGSSL 210 RHYTQNIDTLERGA <mark>G</mark> IPEEKIVEAHGIFYTSHCLEORKEYGLEFVKERIFADQIPICTEORGVVKPDIVFPGEGLFORCLQEDRDRODLIIMGSSL 212 RHYTQNIDTLERGAGIPEEKIVEAHGIFYTSHCLDORKEYSLEYVKE <mark>I</mark> IFADQIPICTEORGINKPDIVFPGESLPDRPGRCLEEDRQODMLIIMGSSL 212 RHYTQNIDTLERGAGIPEEKLVEAHGIFYTSHCLDORKEY <mark>F</mark> LEFVKERIFADQIPICTEORGVVKPDIVFPGESLPDRPGRCLEEDRQODMLIIMGSSL 218
尼人贝贝	araigara transitalia Juthus aeri	EVQPLASLIDMVPDWCPRILINREKAG <mark>U</mark> RSPLIRIWG <mark>UNS</mark> GGLQLDEDAVRDVARIGDCDDGOQDLADRIGWGDELRALVASELARIDLAGAAVE—EAF 2009 EVQPFASTIDMVPDWCPRILINREKAGVRSETTIRIWGINGGGLQEDETADRIGDCDDGOQELADRIGWGDELRALVASELARIDLAGAAVE—EAF 2010 EVQPFASLIDMVPEWCPRILINREKAGERSPLIRIGG <mark>LA</mark> GGLQEDETAVRDVATIGDCDDGOQELADRIGWGDELRALVASELARIDLAGAAVE—EAF 2010 EVQPFASLIDMVPE <mark>WCPRILINREKAGERSPLIRIGGLAGGLQEGSTRDVATIGDCDEGOQDLADRIGWGDELRALVASELARIDAGELERE</mark> TAASE-EAF 2010 EVQPFASLIDMVPD <mark>SCPRILINREKAGERSPLIRIGGLAGGLQEGSTRDVARIGDCDEGOQDLADRIGWGDELRALVASELEREVGASEGRITASE-EAF</mark> 2010
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Figure S6. Homology comparison to other known Sirt2 proteins. The *H. armigera* Sirt2 amino acid sequence has high identity with Sirt2s of other species: *A. transitella* (83%), *P. xuthus* (84%), and *B. mori* (81%). Black shading represents ≥50% sequence identity. *H. armigera*, GenBank[™] number KY363351; *A. transitella*, XP_013184462.1; *P. xuthus*, XP_013171078.1; *B. mori*, NP_001036937.1.



Figure S7. Efficiency of Sirt2 knockdown. (A) HzAm1 cells were transfected with 1, 2, and 4 μ g Sirt2 dsRNA or 4 μ g GFP dsRNA for 48 h. (B) HzAm1 cells were transfected with 4 μ g Sirt2 dsRNA for 0, 24, 36, and 48 h. Protein (20 μ g for Sirt2) was extracted from the cells for immunoblotting with the anti-Sirt2 antibody. Protein bands were quantified and normalized to the levels of *H. armigera* actin (5 μ g). Each point represents the means±S.D. of three independent replicates. *, p<0.05; **, p<0.01 (determined by and independent t-test).



Figure S8. Effect of NAM injection on *PK* **and** *PEPCK* **mRNA levels**. Day-1 nondiapause-destined pupae were injected with NAM and pupal brains were dissected 48 hours after injection. *PK* and *PEPCK* mRNA levels were detected by qPCR using *actin* as an internal standard. Each point represents the mean±S.D. of three independent replicates. *, p<0.05; **, p<0.01 (determined by and independent t-test).