Supporting Information

Hatori et al. 10.1073/pnas.1015959108

SI Materials and Methods

Animals. Animal experiments were conducted in accordance with the guidelines of the University of Tokyo. Newly hatched male chicks were purchased from a local supplier (Ohata Shaver) and maintained under 12-h light/12-h dark (LD) cycles for 7 d with the light provided by white fluorescent lamps (\approx 300 lx at the level of the heads of chicks). They were transferred to constant darkness thereafter. On day 8, they were exposed to a 1-h pulse of the 300lx light from circadian time (CT) 2, CT6, CT10, CT14, CT18, or CT22. CT0 and CT12 correspond to the times of lights on and off, respectively, in the previous LD cycles. Control animals were kept in the dark during the irradiation period of 1 h. The pineal glands were isolated from the light-exposed and dark-kept (control) animals at CT3, CT7, CT11, CT15, CT19, or CT23 on day 8. All of the procedures during the dark period were performed under dim red light (>640 nm).

GeneChip and Quantitative RT-PCR Analyses. Total RNA was prepared from the isolated pineal glands by using TRIzol reagent (Invitrogen). Nine micrograms of total RNA from six pineal glands was used to synthesize biotinylated cRNA by using Affymetrix GeneChip one-cycle cDNA synthesis kit and IVT labeling kit (Affymetrix). Twenty micrograms of biotinylated cRNA was hybridized to GeneChip Chicken Genome Array (37,703 probe sets including >32,773 chicken genes) for 16 h at 45 °C. The arrays were washed and stained by using the Affymetrix Model 450 Fluidics Station and then scanned by the Affymetrix Model 3000 scanner according to the GeneChip Manual. The scanned array image was processed by GeneChip Operating Software Version 1.4 (Affymetrix) to calculate the signal intensity data for each probe set. Original data were deposited in Gene Expression Omnibus (GEO) (accession no. GSE21915). Quantitative RT-PCR analysis was performed as described (1) or by using QuantiTect SYBR Green PCR Kit (Qiagen) and GeneAmp 5700 (Applied Biosystems). The levels of spliced and total Xbp1 (Xbp1s and Xbp1t, respectively) were analyzed by real-time PCR by modifying the method of Back et al. (2). The primers and optimal cycle numbers were summarized in Table S1.

Preparation of Protein Samples and Immunoblot Analysis. Thirty pineal glands and 0.5 mg of liver of 8-d-old male chicks were homogenized in 600 µL and 4.5 mL, respectively, of buffer I (10 mM Hepes-KOH at pH 7.6, 10 mM KCl, 1 mM EDTA, 1.5 mM MgCl₂, 0.5 mM DTT, 5 µg/mL pepstatinA, 2 µg/mL aprotinin, 10 $\mu g/mL$ leupeptin, and 50 $\mu g/mL$ *N*-acetylleucylleucylnorleucinal) by using a Dounce homogenizer, and the homogenate was centrifuged for 10 min at $1,000 \times g$. The resulting nuclear pellet was resuspended in 80 μ L (for pineal gland) or 330 μ L (for liver) of buffer II (20 mM Hepes-NaOH at pH 7.6, 0.5 M NaCl, 1 mM EDTA, 1.5 mM MgCl₂, 25% glycerol, 5 µg/mL pepstatinA, 2 µg/ mL aprotinin, 10 µg/mL leupeptin, and 50 µg/mL N-acetylleucylleucylnorleucinal), and the mixture was rotated for 60 min at 4 °C, followed by a centrifugation for 30 min at $22,000 \times g$. The supernatant was used as a nuclear extract. Protein concentration of each sample was measured by the Bradford method.

Proteins were separated by SDS/PAGE and transferred to a polyvinylidene difluoride membrane. The blot was incubated with a blocking solution [1% skim milk in TBS (50 mM Tris·HCl at pH 7.4, 200 mM NaCl, and 1 mM MgCl₂)] for 1 h at 37 °C and then incubated at 4 °C overnight with anti-SREBP-1 2A4 antibody (4 μ g/mL; Santa Cruz Biotechnology), anti-cHSF1c, anti-

HSF2-4, or anti-HSF3 γ (3) (1:1,000 dilution). Immunoreactivities were visualized by enhanced chemiluminescence system (PerkinElmer Life Sciences) using a horseradish peroxidaseconjugated antibody against mouse or rabbit Ig (0.2 µg/mL; Kirkegaard & Perry Laboratories). The blot was reprobed with anti-TBP antibody (0.4 µg/mL; Santa Cruz Biotechnology).

Plasmid Construction. The coding regions corresponding to amino acids 1-461 of chicken SREBP-1 (GenBank accession no. NP_989457) and 1-454 of chicken SREBP-2 (CAC93938) were amplified by PCR from pineal cDNA and subcloned into pcDNA3.1-TOPO (Invitrogen) to yield expression plasmids nSREBP-1/pcDNA3.1 and nSREBP-2/pcDNA3.1, respectively. The nucleotide sequence corresponding to 5' upstream region of chicken E4bp4 gene was determined by direct sequencing of chicken liver genome. The determined sequence contained a region identical to the 5' region of an EST clone isolated from the chicken liver (GenBank accession no. BG71112, nucleotides 7-199) that is highly similar to the first exon region of human E4bp4 cDNA (NM 005384, nucleotides 1-223). The transcription initiation site (+1) was estimated from the sequence alignment between the EST clone and the genome sequence data. A DNA fragment corresponding to -2,033 to +101 of chicken E4bp4 (deposited in GenBank; accession no. EF221611) was amplified by PCR from chicken genomic DNA and cloned into pGL3 basic vector (Promega) to yield E4bp4us2.0 reporter vector. Similarly, DNA fragments corresponding to -975 to +101, -517 to +101, -258 to +101, -207 to +101, -154 to +101, and -104 to +101 of E4bp4 gene were cloned into pGL3 basic vector to create six kinds of reporter vectors termed E4bp4us1.0, E4bp4us0.5, E4bp4us0.25, E4bp4us0.2, E4bp4us0.15, and *E4bp4*us0.1, respectively. The reporter vectors containing human HMG-CoA synthase promoter and Squalene synthase promoter were described (4).

Transcriptional Assay. CHO-K1 cells were seeded on 24-well plates at a density of 1.6×10^5 cells per well in DMEM/Ham's F-12 supplemented with 10% FBS. After 24 h, the cells in each well were transfected by using Lipofectamine 2000 (Invitrogen) with various amounts of expression plasmid (total amount was adjusted to 200 ng by adding empty vector pcDNA3.1), 30 ng of firefly luciferase reporter plasmid, and 0.3 ng of *Renilla* luciferase reporter plasmid pRL-CMV (Promega) as an internal control. The cell lysates were prepared 48 h after the transfection and subjected to dual-luciferase assay by a luminometry (Promega). To investigate the effect of sterol application, the cells were seeded in the medium supplemented with 5% FBS. Four hours after transfection, the cells were washed with PBS, and the medium was changed to DMEM/Ham's F-12 supplemented with 5% lipoprotein-deficient serum, 1 µg/mL 25-hydroxycholesterol, and 10 µg/mL cholesterol.

Measurement of 7 α -Hydroxypregnenolone Production by HPLC. The pineal glands, diencephalons, and adrenal glands were dissected from 7- to 8-d-old male chicks exposed to 1-h light pulse from CT14. Their homogenates (each 10 mg of wet weight tissue) were incubated at 40 °C in PBS containing 70 nM [7-³H]pregnenolone [1 × 10⁶ cpm (2 × 10⁶ dpm)] and 0.24 mM NADPH. After incubation for indicated time periods, steroids were extracted by ethyl acetate and subjected to HPLC to analyze pregnenolone metabolites as described (5, 6).

Measurement of 7α -Hydroxypregnenolone Concentration by Gas Chromatography/Mass Spectrometry (GC-MS). The entrained male or female chicks were transferred to constant darkness on day 7, and they were exposed to a 20-min pulse of the 300-lx white fluorescent light from CT6, CT14, or CT22. Control animals were kept in the dark during the irradiation period of 20 min. The pineal glands were isolated from the light-exposed and dark-kept (control) animals and a pool (eight pineal glands in each well) were cultured in 450 µL of medium (Medium 199 supplemented with 10 mM Hepes-NaOH at pH 7.4, 100 U/mL penicillin, and 100 µg/mL streptomycin) in 6-well plates at 37 °C under 5% CO₂/80% O₂. After 3-h culture in the light or in the dark, steroids secreted into the medium were extracted by ethyl acetate and subjected to GC-MS analysis to measure 7α -hydroxypregnenolone concentrations as described (5, 6).

7α-Hydroxypregnenolone Administration and Behavioral Analysis. All surgery was performed under ketamine-xylazine anesthesia. Using a stereotaxic instrument, 5-d-old male chicks were chronically implanted with a 9-mm, 23 gauge steel guide cannula aimed at the lateral ventricle of the brain. Five days after the surgery, 7α -hydroxypregnenolone (0, 10, or 200 ng) dissolved in 10 µL PBS containing 0.2% DMSO was injected into the lateral

- 1. Hatori M, Okano T, Nakajima Y, Doi M, Fukada Y (2006) *Lcg* is a light-inducible and clockcontrolled gene expressed in the chicken pineal gland. *J Neurochem* 96:1790–1800.
- 2. Back SH, Schröder M, Lee K, Zhang K, Kaufman RJ (2005) ER stress signaling by regulated splicing: IRE1/HAC1/XBP1. *Methods* 35:395–416.
- Fujimoto M, Nakai A (2010) The heat shock factor family and adaptation to proteotoxic stress. FEBS J 277:4112–4125.
- Inoue J, Sato R, Maeda M (1998) Multiple DNA elements for sterol regulatory elementbinding protein and NF-Y are responsible for sterol-regulated transcription of the genes for human 3-hydroxy-3-methylglutaryl coenzyme A synthase and squalene synthase. J Biochem 123:1191–1198.

ventricle via a 12-mm, 30 gauge stainless steel injector over a period of 30 s at Zeitgeber time (ZT) 14–16 (ZT0 and ZT12 correspond to the times of lights on and off, respectively, in the LD cycles) under dim red light. After the injection, chicks were placed individually in an open field apparatus (O'Hara & Co.) for locomotor activity measurement for 20 min under infrared light. The obtained data were analyzed by using Image OF1 software (O'Hara & Co.).

Measurement of Light Response of the Behavior. The entrained 8- to 12-d-old male chicks were transferred to constant darkness. On the next day, they were placed individually in an open field apparatus for locomotor activity measurement for 10 min under infrared light at CT6–8, CT14–16, or CT22–24. Immediately after the measurement, they were exposed to \approx 300-lx white fluorescent light for 10 min and then placed individually in an open field apparatus for locomotor activity measurement for 10 min under white LED light (\approx 300 lx). Pinealectomy and sham operation were performed as described (7) with slight modification for 4-d-old male chicks under isoflurane anesthesia. After the surgery, they were further entrained for 15 d, and their locomotor activities were measured at CT14–16.

- Matsunaga M, Ukena K, Baulieu EE, Tsutsui K (2004) 7α-Hydroxypregnenolone acts as a neuronal activator to stimulate locomotor activity of breeding newts by means of the dopaminergic system. Proc Natl Acad Sci USA 101:17282–17287.
- Tsutsui K, et al. (2008) 7α-Hydroxypregnenolone mediates melatonin action underlying diurnal locomotor rhythms. J Neurosci 28:2158–2167.
- Ubuka T, Bentley GE, Ukena K, Wingfield JC, Tsutsui K (2005) Melatonin induces the expression of gonadotropin-inhibitory hormone in the avian brain. Proc Natl Acad Sci USA 102:3052–3057.



Fig. S1. Expression profiles of the clock genes in the pineal gland. Dark-kept animals were exposed to a 1-h light pulse (open bars) from CT6, CT14, or CT22, or kept in the dark as a control (solid bars). The GeneChip profiles of the clock genes are displayed (mean with variation, n = 2). The gene expression analysis program indicated that the signals for *Npas2* and *CK1* ε were "Absent", because their signals were too low and/or unreliable. No probe set was assigned to *Per1*, *Dbp*, *Ror* γ , and *Rev-erb* α .



Fig. 52. Time-of-day dependence and functional classification of light-induced genes in the pineal gland. (*A*) Venn diagram showing time-of-day dependence of the light induction. One hundred eleven probe sets (corresponding to 62 genes and 40 ESTs) exhibited >2.5-fold increase of their signal intensities by the light pulse in at least a single time point. Shown are the numbers of probe sets or corresponding genes (in parentheses) induced at each time point. Two probe sets against the gene for heat shock protein 105 kDa were included in the list, and each of them belonged to different category (CT22 group and all time group). (*B*) Functional classification of the 62 light-induced genes.

DNAC

CT6 CT14 CT22			
	gene name	function	Affymetrix ID
	bromodomain and PHD finger containing, 3	transcription	GgaAffx.22111.1.S1_s_at
	similar to G protein-coupled receptor 35	receptor	GgaAffx.3477.1.S1_at
l T	MHC class II antigen B-F minor neavy chain similar to solute carrier family 26 member 0 isoform at anion transporter/exchanger 0	Immune response	Gga.217.1.51_X_at
	similar to solute camer family 26, member 9 isoform a, anion transporter/exchanger-9 similar to Protein FAM13A1	unknown	Gga/ffy 23210 1 S1 e at
	Finished cDNA, clone ChEST945i16	NA	Gga.17626.1.A1_at
	ENSEMBL Prediction	NA	GgaAffx.5195.1.S1_at
	sodium channel, voltage-gated, type I, alpha	channel	Gga.563.1.S1_at
	phosphoenolpyruvate carboxykinase 1 (soluble)	enzyme	Gga.4447.1.S1_at
	similar to Ubiquitin carboxyl-terminal hydrolase 8	protein modification	Gga.9669.1.S1_at
	similar to hypothetical protein	unknown	Gga 10149 1 S1_at
	Finished cDNA, clone ChEST578i21	NA	Gga.7487.1.S1_at
	similar to ATP synthase mitochondrial F1 complex assembly factor 1	mitochondria	Gga.8001.3.S1_at
	deiodinase, iodothyronine, type II	enzyme	Gga.1819.2.S1_a_at
	bone morphogenetic protein 2	secreated protein	Gga.3950.1.S1_at
	Finished cDNA, clone ChEST31m24	NA	Gga.9046.1.S1_at
	Similar to ceramide kinase isoform a: linid kinase I K4	enzyme	Gga 16530 1 S1 at
	similar to TBX2 protein ; ADP-ribosylation factor-like 6 interacting protein	unknown	Gga.8062.2.S1_at
	Finished cDNA, clone ChEST48d15	NA	Gga.13750.1.S1_at
	similar to RIKEN cDNA 6030419C18 gene	unknown	Gga.19193.1.S1_at
	solute carrier family 4, sodium bicarbonate cotransporter, member 7	transporter	Gga.9352.1.S1_at
	similar to Stac protein (SHC homology 3 and cysteine-rich domain protein)	signal transduction	GgaAffx.7640.1.S1_at
	Finished cDNA, clone ChEST205k6 Finished cDNA, clone ChEST295b22	NA	Gga 18807 1 S1 x at
	zinc finger CCCH-type, antiviral 1	transcription	GgaAffx.20602.1.S1_at
	Finished cDNA, clone ChEST279o4	NA	Gga.1890.1.S1_at
	tRNA splicing endonuclease 54 homolog (SEN54, S. cerevisiae)	RNA splicing	GgaAffx.22444.1.S1_s_at
	glutamate receptor, ionotrophic, AMPA 3	receptor	Gga.3321.1.S1_s_at
	Finished cDNA, clone ChEST238m5	NA	Gga.15043.1.S1_at
	Finished cDNA, clone ChEST546d12	NA	Gga.118826.1 S1_at
	Finished cDNA, clone ChEST258016	NA	Gga.15700.1.S1_at
	EST	NA	Gga.6530.1.A1_at
	sal-like 1 (Drosophila)	transcription	Gga.1817.1.S2_at
	chemokine (C-X-C motif) receptor 4	receptor	Gga.2305.1.S1_at
	solute carrier tamily 4, sodium bicarbonate cotransporter, member 7	transporter	GgaAffx.23557.10.S1_s_at
	AHA1, activator of heat shock 90kDa protein ATPase homolog 1 (yeast) ENSEMPL Prodiction	cochaperone	GgaAffx.23236.1.S1_at
	Einished cDNA_clone_ChEST734i19	NA	Gga 16816 1 S1 at
	similar to ADMP	unknown	Gga.11984.2.S1 a at
4	melanotransferrin/EOS47	cell surface	Gga.3484.1.S1_at
r	similar to KIAA0433 (Histidine acid phosphatase domain containing 1)	unknown	GgaAffx.9722.1.S1_at
	Finished cDNA, clone ChEST769a21	NA	Gga.16489.1.S1_at
	Finished cDNA, clone ChEST127b12	NA	Gga.13119.1.S1_at
	similar to LUC126/31 period homolog 2 (Drosonbile)	circadian clock	GgaAffX./026.1.51_at Gga 3823 1 52 at
	similar to hypothetical protein EL 110324	unknown	Gga 15116 1 S1 at
	adenylate cyclase activating polypeptide 1 (pituitary)	secreated protein	Gga.616.1.S1_s_at
	ENSEMBL Prediction	NA	GgaAffx.10937.4.S1_s_at
	similar to brain adenylate cyclase 1	enzyme	Gga.10932.1.S1_at
	C-type lectin domain family 3, member A	unknown	Gga.3536.1.S1_at
	similar to TBC1 domain family member 1	unknown	Gga.10/25.1.51_at
	Einished aDNA, along ChEST122m4	NA	Gap 11572 1 S1 at
Гл	Finished cDNA, clone ChEST133m4 similar to protein kinase related to Baf protein kinases	NA signal transduction	Gga.11572.1.S1_at
	Finished cDNA, clone ChEST133m4 similar to protein kinase related to Raf protein kinases Finished cDNA, clone ChEST625e21	NA signal transduction NA	Gga.11572.1.S1_at GgaAffx.26564.1.S1_s_at GgaAffx.21402.1.S1_at
	Finished cDNA, clone ChEST133m4 similar to protein kinase related to Raf protein kinases Finished cDNA, clone ChEST625e21 LON peptidase N-terminal domain and ring finger 3	NA signal transduction NA proteolysis	Gga.11572.1.S1_at GgaAffx.26564.1.S1_s_at GgaAffx.21402.1.S1_at Gga.17046.1.S1_at
	Frinished cDNA, clone ChEST133m4 similar b protein kinase vellated to Raf protein kinases Finished cDNA, clone ChEST625621 LON petidiase N-terminal domain and ring finger 3 similar to hypothetical protein FL22344 (LON peptidase N-terminal domain and ring finger 1)	NA signal transduction NA proteolysis proteolysis	Gga.11572.1.S1_at GgaAffx.26564.1.S1_s_at GgaAffx.21402.1.S1_at Gga.17046.1.S1_at GgaAffx.8741.1.S1_at
	Frinshet dDNA, clone ChEST133m4 similar to protein kinase related to Raf protein kinases Finishet CDNA, clone ChEST825821 LON peptiase N-terminal domain and ring finger 3 similar to hypothetical protein FL23749 (LON peptiase N-terminal domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptiase N-terminal domain and ring finger 1)	NA signal transduction NA proteolysis proteolysis proteolysis	Gga.11572.1.S1_at GgaAffx.26564.1.S1_s_at GgaAffx.21402.1.S1_at Gga.17046.1.S1_at GgaAffx.8741.1.S1_at GgaAffx.8742.1.S1_at
	Frinished CDNA, clone ChEST133m4 animal to poteink timase related to Parl protein kinases Frinished CDNA, clone ChEST025621 LCDN peptidase Netminal comain and ring finger 3 similar to hypothetical protein FL/23744 (LCDN peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL/23744 (LCDN peptidase N-terminal domain and ring finger 1) similar to Pipetiatin b providegy domain containing family G member 1 extendination science and interfield 1. J failultania 1.	NA signal transduction NA proteolysis proteolysis proteolysis unknown cossected pathin	Gga.11572.1.S1_at GgaAffx.26564.1.S1_s_at GgaAffx.2102.1.S1_at Gga.17046.1.S1_at GgaAffx.8741.1.S1_at GgaAffx.8742.1.S1_at GgaAffx.20924.1.S1_at GgaAffx.20924.1.S1_at
	Frielshed 20NA, clone ChEST133m4 similar b proferits hinase related to Raf protein kinases Finished cDNA, clone ChEST625621 LON petidiase N-terminal domain and ring finger 3 similar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) adenylate cyclase activating polypeptide 1 (bitturary) protein photophatese 2 (trametri 24) are evaluators simue B° abba	NA signal transduction NA proteolysis proteolysis proteolysis unknown secreated protein signal transduction	Gga.11572.1.S1_at GgaAffx.26564.1.S1_s_at GgaAffx.21402.1.S1_at GgaAffx.8741.1.S1_at GgaAffx.8741.1.S1_at GgaAffx.8742.1.S1_at GgaAffx.20924.1.S1_at GgaAffx.20924.1.S1_at Gga.11409.1.S1_at
	Frinshet dDNA, clone ChEST133m4 aimlar to protein kinase related to Raf protein kinases Finishet dDNA, clone ChEST82621 LON petidase N-terminal domain and ring finger 3 aimlar to hypothetical protein FL233749 (LON pepidase N-terminal domain and ring finger 1) aimlar to hypothetical protein FL233749 (LON pepidase N-terminal domain and ring finger 1) aimlar to proteckstin homology domain containing family G member 1 adenylate to pleokstin homology domain containing family G member 1 adenylate to pleokstin homology domain containing family G member 1 EST	NA signal transduction NA proteolysis proteolysis proteolysis unknown secreated protein signal transduction NA	Gga.11572.1.S1_at GgaAfK.240564.1.S1_s_at GgaAfK.2402.1.S1_at GgaAfK.2402.1.S1_at GgaAfK.8741.1.S1_at GgaAfK.8742.1.S1_at Gga.11409.1.S1_at Gga.15070.1.S1_at Gga.15291.1.S1_at
	Frielded CDNA, clone ChESTS054 similar to protein kinase related to Braf protein kinases Frielded CDNA, clone ChESTS05621 LCD repatitase Netrminal comain and ring finger 3 aimilar to hypothetical protein FLI23749 (LCDN psptidase N-terminal domain and ring finger 1) aimilar to hypothetical protein FLI23749 (LCDN psptidase N-terminal domain and ring finger 1) aimilar to hypothetical protein FLI23749 (LCDN psptidase N-terminal domain and ring finger 1) aimilar to hypothetical protein FLI23749 (LCDN psptidase N-terminal domain and ring finger 1) aimilar to hypothetical protein fLi23749 (LCDN psptidase N-terminal domain and ring finger 1) protein phosphatea 2 (Iometri 24, X), regulatory subunit B ⁺ , alpha EST Finished CDNA, clone ChESTS05/21	NA signal transduction NA proteolysis proteolysis unknown secreated protein signal transduction NA	Gga.11572.151_at GgaAffx2.26564.1.51_s_at GgaAffx2.1402.1.51_at GgaAffx2.1402.1.51_at GgaAffx2.41.51_at GgaAffx2.41.1.51_at GgaA1fx2.0924.1.51_at Gga.11400.1.51_at Gga.18704.1.51_at Gga.15591.1.51_at
	Frinshed cDNA, clone ChEST136m4 similar b profet hinase related to Raf protein kinases Finished cDNA, clone ChEST625621 LON peptidase N-terminal domain and ring finger 3 similar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) protein phosphatase 2 (formethy 2A), regulatory subunit B*, alpha EST Frished CDNA, clone ChEST505(2) ENSEMBL Frediction	NA signal transduction NA proteolysis proteolysis proteolysis unknown secreated protein signal transduction NA NA	$\label{eq:gamma} \begin{array}{l} Gga_{11572}.1.S1_at\\ GgaAffz_21626.5.S1_at\\ GgaAffz_21402.1.S1_at\\ GgaAffz_21402.1.S1_at\\ GgaAffz_8741.1.S1_at\\ GgaAffz_8741.1.S1_at\\ GgaAffz_8741.1.S1_at\\ Gga_{11400}.1.S1_at\\ Gga_{1150}.1.S1_at\\ Gga_{1150}.1.S1_at\\ Gga_{11470}.1.S1_at\\ Gga_{11470}.1.S1_at\\$
	Finished CDNA, clone ChESTI36n4 aminar to protein kinase related to Parl protein kinase Finished CDNA, clone ChESTG25621 (LON peptidase Neterminal comain and ring finger 3 similar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) similar to Pleckstrin homology domain containing family G member 1 admylar b Pleckstrin homology domain containing family G member 1 admylar b cycles activiting objective 1 (publicat) protein phosphatase 2 (Iomerly 2A), regulatory subunit B*, alpha ESIZMBL Prediction Finished cDNA, clone ChESTG34c21	NA signal transduction NA proteolysis proteolysis unknown secreated protein signal transduction NA NA NA NA	G_{0A} :1157.2.1.5.1_at G_{0A} Affr.26564.1.51_s.at G_{0A} Affr.2402.1.51_at G_{0A} Affr.2402.1.51_at G_{0A} Affr.2674.1.51_at G_{0A} Affr.2674.1.51_at G_{0A} Affr.2674.1.51_at G_{0A} 1.15704.1.51_at G_{0A} 1.15704.1.51_at G_{0A} 1.1575.1.51_at G_{0A} 4.1675.1.51_s_at G_{0A} 4.1675.1.51_s_at G_{0A} 4.16466.1.51_s_at G_{0A} 4.16466.1.51_st G_{0A}
	Finished cDNA, clone ChEST30:44 similar to protein kinase related to Braf protein kinases Finished cDNA, clone ChEST40:542 LON peptidase N terminal comain and ring finger 3 similar to hypothetical protein FL/23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL/23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL/23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL/23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL/23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL/23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL/23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein fL/23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein fL/23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein fL/23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein fL/23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein fL/23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein fL/23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein fL/23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein fL/23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein fL/23749 (LON peptidase N-terminal domain and ring finger 2) similar to hypothetical protein fL/23749 (LON peptidase N-terminal domain and ring finger 2) similar to hypothetical protein fL/23749 (LON peptidase N-terminal domain and ring finger 2) similar to hypothetical protein fL/23749 (LON peptidase N-terminal domain and ring finger 2) similar to hypothetical protein fL/23749 (LON peptidase N-terminal domain and ring finger 2) similar to hy	NA signal transduction NA proteolysis proteolysis proteolysis unknown sacraated protein signal transduction NA NA NA Cell cycle drool machalism	Gga.1157.2.1.51_at GgaAfH.2565.1.51_a, at GgaAfH.2565.1.51_a, at GgaAfH.2656.1.51_at GgaAfH.2674.1.51_at GgaAfH.2074.1.51_at GgaAfH.2074.1.51_at GgaAfH.2074.1.51_at Gga.1150.1.51_at Gga.1570.1.51_at Gga.16551.1.51_at Gga.1625.1.51_at Gga.1625.1.51_at
	Finished 20NA, clone ChEST133n4 similar to protein kinase related to Raf protein kinase Finished 20NA, clone ChEST625621 LCO neptidase Netminal domain and ring finger 3 similar to hypothetical protein FL232749 (LCN peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL232749 (LCN peptidase N-terminal domain and ring finger 1) similar to Pieckstrin homology domain containing family G member 1 adenyteis cyclase activating polyepiedle 1 (publiary) protein phosphatase 2 (formerly 2A), regulatory subunt B°, alpha EST Finished dDNA, clone ChEST30621 Finished dDNA, clone ChEST30421 Noted dDNA, clone ChEST334c21 nucleophomin insulin nickeed gene 1 [Insig-1] cheater B	NA signal transduction NA proteolysis proteolysis unknown secreated protein signal transduction NA NA NA OA Cell cycle sterol metabolism	Gqa.1157.2.1.51_at GqaAftz.265.4.151_s_at GqaAftz.264.151_s_at GqaAftz.264.151_s_at GqaAftz.264.151_at GqaAfts.274.151_at GqaAfts.274.151_at GqaAfts.2024.151_at Gqa.1550.1.51_at Gqa.1550.1.51_at Gqa.14896.1.51_at Gqa.14896.1.51_at Gqa.1280.51.51_at Gqa.1280.51.51_at Gqa.1280.51.51_at Gqa.1280.51.51_at
	Finished CDNA, clone ChESTI30n4 amilar la poteink linear entiated to Parl protein kinases Finished CDNA, clone ChESTB026e21 (LON peptidase Netwinal domain and ring finger 3 similar to hypothetical protein FL/23744 (LON peptidase N-terminal domain and ring finger 1) similar to Pipothetical protein FL/23744 (LON peptidase N-terminal domain and ring finger 1) similar to Pipothetical protein FL/23744 (LON peptidase N-terminal domain and ring finger 1) similar to Pipothetical protein FL/23744 (LON peptidase N-terminal domain and ring finger 1) similar to Pipothetical protein FL/23744 (LON peptidase N-terminal domain and ring finger 1) protein priosphatase 2 (cometry 2A), 19 (updatory subunit B*, alpha EST Finished CDNA, clone ChEST30521 ENSEMBL Prediction Finished CDNA, clone ChEST304c21 nucleophosmin Finished CDNA, clone ChEST304c21 Shydroxy-S-methylgidatay(Coencyme A synthase 1 (soluble) [HMG-CoA synthase] Finished CDNA, clone ChEST304010	NA signal transduction NA proteolysis proteolysis proteolysis unknown secreated protein signal transduction NA NA NA cell cycle sterol metabolism NA	Gqa.1157.2.1.51_at GqaAft2.2664.1.51_a, at GqaAft2.2664.1.51_a, at Gqa.1704.61.51_at Gqa.1704.61.51_at GqaAft2.2674.1.51_at GqaAft2.2674.1.51_at Gqa.11040.1.51_at Gqa.1570.41.51_at Gqa.1670.41.51_at Gqa.1626.1.51_at Gqa.1626.1.51_at Gqa.1626.1.51_at Gqa.1633.71_51_at
	Finished cDNA, clone ChEST136n4 similar to protein kinase related to Braf protein kinases Finished cDNA, clone ChEST625621 LOD peptidase N terminal domain and ring finger 3 similar to hypothetical protein FL/23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL/23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL/23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL/23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL/23749 (LON peptidase N-terminal domain and ring finger 1) adenylate cyclase activating polypeptide 1 (plutary) protein phosphatez 2 (Iometry 42A), regulatory subunit B ⁺ , alpha EST Finished cDNA, clone ChEST505(2) Finished cDNA, clone ChEST505(2) Finished cDNA, clone ChEST505(2) Finished cDNA, clone ChEST506(1) makin induced gene 1 (Insig-1) cluster B Shydrory-S-methylgidatary-Coenzyme A synthase 1 (soluble) (HMG-CoA synthase) Finished cDNA, clone ChEST506(1) miclear factor, interketikin 3 regulated [Edipt]	NA signal transduction NA proteolysis proteolysis unknown secreated protein signal transduction NA NA NA cell cycle sterol metabolism sterol metabolism NA Cradian clock	Gqa.1157.2.1.51_at GqaAfr.2564.151_a,at GqaAfr.2664.151_at GqaAfr.2664.151_at GqaAfr.2640.151_at GqaAfr.2040.151_at GqaAfr.2042.151_at GqaAfr.2042.151_at Gqa.1570.41.51_at Gqa.1550.1.51_at Gqa.1457.51.51_at Gqa.1459.51.51_at Gqa.1459.51.51_at Gqa.1459.51.51_at Gqa.1459.51_31_at Gqa.1459.51.51_at Gqa.1459.51_31_at Gqa.1530.71.51_a_at Gqa.1530.71.51_a_at Gqa.1530.71.51_a_at
	Finished 20NA, clone CRESTIG3m4 similar to protein kinase related to Raf protein kinases Finished 20NA, clone CREST626521 LON peptidase Netwinial domain and ring finger 3 similar to hypothetical protein FL/23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL/23749 (LON peptidase N-terminal domain and ring finger 1) similar to Piecketin homology domain containing family G member 1 admylste optidase activating optioperide 1 (publiar) protein phosphatase 2 (Iomerly 2A), regulatory subunit B*, alpha EST Finished 20NA, clone CREST63621 ENSIMBL Prediction Finished 20NA, clone CREST63620 Shytomy-Smethylgilatar/Conrzyme A synthase 1 (soluble) [HMG-CoA synthase] Finished COA, clone CREST60610 madoar factor, interfacialis A spudated [Edp4] Chac, caitor Interfacialis A spudated [Edp4]	NA signal transduction NA proteolysis proteolysis proteolysis secreated protein signal transduction NA NA NA NA Call cycle call cycle call cycle call cycle ared metabolism sterol metabolism NA CALL CALL CALL CALL CALL CALL CALL CAL	$\label{eq:Gamma} \begin{array}{l} Ggan 11572.1.51_at\\ GgaAH7.2666.1.51_a,tt\\ GgaAH7.2666.1.51_at\\ Ggan 17046.1.51_at\\ Ggan 17046.1.51_at\\ GgaAH7.6742.1.51_at\\ GgaAH7.6742.1.51_at\\ GgaAH7.6704.1.51_at\\ Ggan 1409.1.51_at\\ Ggan 1409.1.51_at\\ GgaAH7.1.675.1.51_a,t\\ GgaAH7.1.675.51_51_a,t\\ GgaAH7.1.675.51_a,t\\ GgaAH7.1.675.51_a,t\\ GgaAH7.1.675.51_a,t\\ GgaAH7.1.675.51_a,t\\ GgaAH7.1.675.51_a,t\\ GgaAH7.1.675.51_a,t\\ GgaAH7.1.675.51_a,t\\ GgaAH7.1.51_a,t\\ GgaAH7.1.51_a,t\\ GgaAH7.51.51_a,t\\ GgaAH7.51_a$
	Finished cDNA, clone ChESTI30n4 amilar la poteink times related to Bral protein kinases Finished cDNA, clone ChEST626521 LCD repetitase Netminal comain and ring finger 3 amilar to hypothetical protein FL/23749 (LCD repetidase N-terminal domain and ring finger 1) aimlar to hypothetical protein FL/23749 (LCD repetidase N-terminal domain and ring finger 1) aimlar to hypothetical protein FL/23749 (LCD repetidase N-terminal domain and ring finger 1) aimlar to hypothetical protein FL/23749 (LCD repetidase N-terminal domain and ring finger 1) aimlar to hypothetical protein FL/23749 (LCD repetidase N-terminal domain and ring finger 1) adom/site 2 (Longer 2), regulatory suburit B*, alpha EST Finished cDNA, clone ChEST30521 ENSEMBL Prediction Finished cDNA, clone ChEST304221 nucleophoestrini finastin riduoced gene 1 [Insig-1] 3-hydroxy-s-methylgitasty-Coenzyme A synthase 1 (soluble) [HMG-CoA synthase] Finished cDNA, clone ChEST30421 CAC, clone therefore S1 [Insig-1] hat athock protein 25 [Insig5] cluster A	NA signal transduction NA proteolysis proteolysis proteolysis unknown secreated protein signal transduction NA NA NA Cell cycle sterol metabolism Sterol metabolism NA circadian clock unknown protein folditiog	Gqa.1157.2.1.51_at GqaAfr.2664.1.51_a.t GqaAfr.2664.1.51_a.t GqaAfr.21402.1.51_at GqaAfr.21402.1.51_at GqaAfr.2742.1.51_at GqaAfr.2742.1.51_at GqaAfr.2742.1.51_at Gqa.1570.4.1.51_at Gqa.1570.4.1.51_at Gqa.14570.5.1.51_a Gqa.1459.5.1.51_at Gqa.1459.5.1.51_at GqaAfr.130.51_at GqaAfr.2009.1.51_at GqaAfr.2009.1.51_at GqaAfr.2009.1.51_at GqaAfr.2009.1.51_at GqaAfr.2009.1.51_at GqaAfr.2009.1.51_at
	Finished cDNA, clone ChEST136n4 similar to protein kinase related to Braf protein kinases Finished cDNA, clone ChEST625621 LON peptidase N-terminal domain and ring finger 3 similar to hypothetical protein FL/23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL/23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL/23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL/23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL/23749 (LON peptidase N-terminal domain and ring finger 1) adenylate cyclase activating polypeptide 1 (futury) protein phosphates 2 (formetry 2A), regulatory subunit B [*] , alpha EST Finished cDNA, clone ChEST305(21 Finished cDNA, clone ChEST305(21 Finished cDNA, clone ChEST305(21 Finished cDNA, clone ChEST305(21 Finished cDNA, clone ChEST306(21) Cluster B Shydrory-S-methylgiduary-Coencyme A synthase 1 (soluble) [HMG-CoA synthase] Finished cDNA, clone ChEST306(21) ChaC, clant nanoport regulater-like 1 (E coli) heat shok protein 25 [Heg25] cluster A heat shok protein 25 [Heg25] cluster A Finished cDNA, clone ChEST306(20)	NA signal transduction NA proteolysis proteolysis unknown secreated protein signal transduction NA NA NA Cell cycle sterol metabolism sterol metabolism sterol metabolism NA NA NA NA NA NA NA NA NA NA NA NA	Gqa.1157.2.1.51_at GqaAft2.2654.151_a,at GqaAft2.2654.151_at GqaAft2.2654.151_at GqaAft2.654.151_at GqaAft2.674.151_at GqaAft2.674.151_at GqaAft2.674.151_at Gqa.1670.41.51_at Gqa.1670.41.51_at Gqa.16370.41.51_at Gqa.16351.151_at Gqa.16351.151_at Gqa.16351.151_at Gqa.16351.151_at Gqa.16351.151_at Gqa.16351.151_at Gqa.16351.151_at Gqa.15337.151_a_at Gqa.9561.51_at
	Finished cDNA, clone ChESTI36n4 aimlar to protein kinase related to Parl protein kinases Finished cDNA, clone ChEST625621 LON peptidase Netromial domain and ring finger 3 aimlar to hypothetical protein FL/327349 (LON peptidase N-terminal domain and ring finger 1) aimlar to hypothetical protein FL/327349 (LON peptidase N-terminal domain and ring finger 1) aimlar to hypothetical protein FL/327349 (LON peptidase N-terminal domain and ring finger 1) aimlar to hypothetical protein FL/327349 (LON peptidase N-terminal domain and ring finger 1) aimlar to hypothetical protein FL/327349 (LON peptidase N-terminal domain and ring finger 1) aimlar to hypothetical protein FL/327349 (LON peptidase N-terminal domain and ring finger 1) adarylatic orgitaes activiting polypophetic 1 (plutary) protein phosphatase 2 (formerly 2A), regulatory subunit B*, alpha EST Finished CDNA, clone ChEST506/21 ENSEMBL Prediction Finished CDNA, clone ChEST606/20 Finished CDNA, clone ChesT606/20 Fi	NA signal transduction NA proteolysis proteolysis proteolysis escreated protein signal transduction NA estimation NA cell cycle sterol metabolism sterol metabolism sterol metabolism vA circadian clock unknown protein folding protein folding NA	Gqa.1157.2.1.51_at GqaAH7.2664.1.51_a.t GqaAH7.2664.1.51_a.t GqaAF7.2664.1.51_at GqaA17.2645.1.51_at GqaA17.874.1.51_at GqaA17.874.1.51_at GqaA17.870.4.1.51_at Gqa.1450.1.51_at GqaA150.1.51_at GqaA150.1.51_at GqaA150.1.51_at GqaA150.1.51_at GqaA150.1.51_at GqaA150.1.51_at GqaA150.1.51_at GqaA150.1.51_at GqaA150.1.51_at GqaA90.1.51_at GqaA90.1.51_at GqaA90.1.51_at GqaA90.1.51_at GqaA90.1.51_at GqaA90.1.51_at GqaA90.1.51_at GqaA90.1.51_at GqaA90.1.51_at GqaA90.1.51_at
	Finished CDNA, chone ChESTIS3n4 similar to potien kinase related to Braf protein kinases Finished CDNA, chone ChEST625621 LCD repetitase Nethminal domain and ring finger 3 similar to hytochetical protein FLI23749 (LCDN peptidase N-terminal domain and ring finger 1) aimliar to hytochetical protein FLI23749 (LCDN peptidase N-terminal domain and ring finger 1) aimliar to hytochetical protein FLI23749 (LCDN peptidase N-terminal domain and ring finger 1) aimliar to Picksta b nonkolgy domain containing family G member 1 adenylate cyclase activating polypeptide 1 (plutary) protein priosphatea 2 (lomenty 2A), regulatory subunit B*, alpha EST Finished CDNA, chone ChEST505[21 ENSEMBL Prediction Finished CDNA, chone ChEST334c21 nucleophonemin insulin ritudicad gene 1 [Insig-1] cluster B 3-hydroxy-5-methylghtary-Concryme A synthase 1 (soluble) [HMG-CoA synthase] Finished CDNA, chone ChEST505010 nuclear factor, interfeckin 73 singulated [E40p4] ChaG, caton transport regulater-like 1 (e, coli) heat shock protein 25 [Hsp25] cluster A heat shock protein 25 [Hsp25] cluster A heat shock protein 25 [Hsp25] cluster A heat shock protein 05 (KDa (Heat shock 110 KDa protein) aimliar to Haat-shock protein 105 (KDa (Heat shock 110 KDa protein)	NA signal transduction NA proteolysis proteolysis proteolysis unknown secreated protein signal transduction NA NA NA NA Cell cycle sterol metabolism sterol metabolism NA circadian clock unknown protein folding protein folding NA protein folding	Gqa.1157.2.1.51_at GqaAH7.2664.1.51_a,at GqaAH7.2664.1.51_a,at GqaA174.2645.1.51_at GqaA174.671.51_at GqaA174.874.2.1.51_at GqaA174.2024.1.51_at GqaA174.2024.1.51_at GqaA175.2024.1.51_at GqaA175.151_at GqaA176.151_at GqaA176.151_at GqaA166.1.51_at
	Finished 2DNA, clone ChEST133m4 similar to protein kinase related to Bra protein kinases Finished 2DNA, clone ChEST625621 LCN peptidase Netrimial domain and ring finger 3 similar to hypothetical protein FL232749 (LCN peptidase N-4emnial domain and ring finger 1) similar to hypothetical protein FL232749 (LCN peptidase N-4emnial domain and ring finger 1) similar to hypothetical protein FL232749 (LCN peptidase N-4emnial domain and ring finger 1) similar to hypothetical protein FL232749 (LCN peptidase N-4emnial domain and ring finger 1) similar to hypothetical protein FL232749 (LCN peptidase N-4emnial domain and ring finger 1) similar to hypothetical protein FL23749 (LCN peptidase N-4emnial domain Protein phosphalase 2 (Iomerni f 2ah), regulatory subunit B°, alpha EST Finished tONA, clone ChEST305(21 Finished 2DNA, clone ChEST305(21 Finished 2DNA, clone ChEST306(21 Finished 2DNA, clone ChEST306(21 Finished 2DNA, clone ChEST306(21 Cluster B Shydroxy- matrix/glutash-Clonoryme A synthase 1 (soluble) [HMG-CoA synthase] Finished 2DNA, clone ChEST306(21 Cluster A hast shock protein 25 [Hg25] Cluster A hast shock protein 25 [Hg25] Finished 2DNA, chone ChEST806(20 similar to Hast-shock protein to Kba (Hast shock 110 KDa protein) similar to Hast-shock protein to Kba (Hg188) homocyclient-holdbace, protein relaudu metres-induckle, ublqulin-like domain nember, 1 monocyclient-holdbace, endoplater	NA signal transduction NA proteolysis proteolysis proteolysis unknown secreated protein signal transduction NA NA NA CAL Startor Inetabolism ateror Inetabolism ateror Inetabolism protein folding protein folding protein folding protein folding protein folding	$\label{eq:Gamma} \begin{array}{l} Gga 11572.1.51_at\\ Gga 4474.2664.1.51_a,tt\\ Gga 4474.2664.1.51_at\\ Gga 4746.24402.1.51_at\\ Gga 4746.2742.1.51_at\\ Gga 4746.2742.1.51_at\\ Gga 4746.2742.1.51_at\\ Gga 11409.1.51_at\\ Gga 12650.1.51_at\\ Gga 12650.1.51_at\\ Gga 12650.1.51_at\\ Gga 4000.1.51_at\\ Gga 4000.1.51_at$
	Finished CDNA, clone ChEST136n4 almalar bo protein kinase related to Pal protein kinases Finished CDNA, clone ChEST825621 LON peptidase Netminal domain and ring finger 3 almalar bo hypothetical protein FL/23744 (LON peptidase N-terminal domain and ring finger 1) almalar bo hypothetical protein FL/23744 (LON peptidase N-terminal domain and ring finger 1) almalar bo hypothetical protein FL/23744 (LON peptidase N-terminal domain and ring finger 1) almalar bo hypothetical protein FL/23744 (LON peptidase N-terminal domain and ring finger 1) almalar bo hypothetical protein FL/23744 (LON peptidase N-terminal domain and ring finger 1) adarylate cyclase activating polypeptide 1 (plutary) protein phosphateas 2 (lomenty 2A), regulatory subunit B*, alpha EST Finished CDNA, clone ChEST305(21 ENSEMBL Prodiction Finished CDNA, clone ChEST304221 nucleophonimi insulin induced gene 1 [Insig-1] Shydroxy-S-methylgidaryCoenzyme A synthase 1 (soluble) [HMG-CoA synthase] Finished CDNA, cone ChEST805(0) nuclear factor, interlexiki n Segulated [E4bp4] Chac, cation transport regulator-like (E, coli) heat shock protein 25 [Hap25] Finished CDNA, cone ChEST805(2) Finished CDN	NA signal transduction NA proteolysis proteolysis proteolysis secreated protein signal transduction NA Signal transduction NA cell cycle sterol metabolism sterol metabolism terol metabolism vahrown protein folding protein folding protein folding protein folding protein folding protein folding protein folding protein folding protein folding protein folding	Gqa.1157.2.1.51_at Gqa.M72.2664.151_a. Gqa.M72.2664.151_at Gqa.M72.6645.151_at Gqa.17046.151_at Gqa.17046.151_at Gqa.17046.151_at Gqa.1870.4.151_at Gqa.1870.4.151_at Gqa.1870.4.151_at Gqa.1870.4.151_at Gqa.1870.4.151_at Gqa.1865.1.51_at Gqa.1865.1.51_at Gqa.1870.51_51_at Gqa.1870.51_51_at Gqa.1870.51_51_at Gqa.1870.51_51_at Gqa.965.1.51_at Gqa.965.1.51_at Gqa.985.1.51_at Gqa.985.1.51_at Gqa.985.1.51_at Gqa.985.1.51_at Gqa.985.1.51_at Gqa.985.1.51_at Gqa.985.1.51_at Gqa.985.1.51_at Gqa.985.1.51_at Gqa.985.1.51_at Gqa.985.1.51_at Gqa.985.1.51_at Gqa.985.1.51_at Gqa.985.1.51_at Gqa.985.1.51_at
	Finished 2DNA, chone ChESTIS3n4 similar to potien kinase related to Bal protein kinases Finished 2DNA, chone ChEST625621 LCDN peptidase Netrminal domain and ring finger 3 similar to hypothetical protein FL/23749 (LCN peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL/23749 (LCN peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL/23749 (LCN peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL/23749 (LCN peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL/23749 (LCN peptidase N-terminal domain and ring finger 1) adenylate zyclase activating polypeptide 1 (plutary) protein proteptiates 2 (lometry 2A), regulatory suburin B°, abha EST Finished 2DNA, chone ChEST505/21 ENSEMBL Prediction Finished 2DNA, chone ChEST304c21 nucleophoemini naclar factor, interlexitin S regulated [E4bp4] ChaC, clant nampot regulator 4 (LC coli) heat shork protein 25 (Hag25) Chat athock protein 105 KDa (Heat shock 110 KDa protein) similar to Heat-shock protein 105 KDa (Heat shock 110 KDa protein) imilar to heat-shock protein 105 KDa (Heat shock 110 KDa protein) timilar to Heat-shock protein 105 KDa (Heat shock 110 KDa protein) timilar to Heat-shock protein 105 KDa (Heat shock 110 KDa protein) timilar to Heat-shock protein 105 KDa (Heat shock 110 KDa protein) timilar to Heat-shock protein 105 KDa (Heat shock 110 KDa protein) timilar to Heat-shock protein 105 KDa (Heat shock 110 KDa protein) timilar to Heat-shock protein 105 KDa (Heat shock 110 KDa protein) timilar to Heat-shock protein 105 KDa (Heat shock 110 KDa protein) timilar to Heat-shock protein 105 KDa (Heat shock 110 KDa protein) timilar to Heat-shock protein 105 KDa (Heat shock 110 KDa protein) timilar to Heat-shock protein 105 KDa (Heat shock 110 KDa protein) timilar to Heat-shock protein 105 KDa (Heat shock 110 KDa protein) timilar to Heat-shock protein 105 KDa (Heat shock 110 KDa protein) timilar to Heat-shock protein 105 KDa (Heat shock 110 KDa protein) timilar	NA signal transduction NA proteolysis proteolysis proteolysis unknown secreated protein signal transduction NA NA NA cell cycle sterol metabolism sterol metabolism sterol metabolism unknown protein folding protein folding	Gqa.1157.2.1.51_at GqaM74.2566.1.51_a,at GqaM74.2566.1.51_a,at GqaM74.2566.1.51_at GqaM74.266.1.51_at GqaM74.2140.2.151_at GqaM74.2024.1.51_at GqaM74.2024.1.51_at GqaM74.130_at GqaM74.2356.151_at GqaM74.2356.151_at GqaM74.2356.151_at GqaM74.2356.151_at GqaM74.2356.151_at
	Finished CDNA, clone ChEST133m4 alimal to potieth kinase related to Parl protein kinases Finished CDNA, clone ChEST625621 LCN peptidase Netrimial containing farger 3 alimal to hypothetical protein FL23749 (LCNA peptidase N-terminal domain and ring finger 1) alimal to hypothetical protein FL23749 (LCNA peptidase N-terminal domain and ring finger 1) alimal to hypothetical protein FL23749 (LCNA peptidase N-terminal domain and ring finger 1) alimal to hypothetical protein FL23749 (LCNA peptidase N-terminal domain and ring finger 1) alimal to hypothetical protein FL23749 (LCNA peptidase N-terminal domain and ring finger 1) alimal to hypothetical protein FL23749 (LCNA peptidase N-terminal domain and ring finger 1) adversary to the state of the terminal domain and ring finger 1 protein phosphatase 2 (Iomerly 2A), regulatory subunit B*, alpha EST Finished CDNA, clone ChEST63621 ENSEMBL Prediction Finished CDNA, clone ChEST636101 maclain inducer finger 1 (LE (coli) hast shok protein 25 (Hag25) Finished CDNA, cone ChEST636202 Finished CDNA, cone ChEST636202 Finis	NA signal transduction NA proteolysis proteolysis proteolysis screated protein signal transduction NA NA Call cycle sterol metabolism sterol metabolism sterol metabolism sterol metabolism sterol metabolism sterol metabolism nA na protein folding protein regonse NA unfolded protein response unfolded protein response	Gqa.1157.2.1.51_at Gqa.M47.2664.1.51_a_at Gqa.M47.2642.1.51_at Gqa.M74.2642.1.51_at Gqa.M74.874.1.51_at Gqa.M74.874.1.51_at Gqa.M74.874.1.51_at Gqa.M74.874.1.51_at Gqa.M74.875.1.51_at Gqa.M74.875.1.51_at Gqa.M74.1058.1.51_at Gqa.M74.1058.1.51_at Gqa.M74.1058.1.51_at Gqa.M74.1058.1.51_at Gqa.M74.1058.1.51_at Gqa.M74.1058.1.51_at Gqa.M74.1058.1.51_at Gqa.M74.1058.1.51_at Gqa.M74.151_at.151_at Gqa.M74.2059.1.51_at Gqa.M74.2059.1.51_at Gqa.M74.2057.1.51_at
	Finished cDNA, clone ChESTI36n4 similar to potein kinase related to Parl potein kinases Finished cDNA, clone ChEST626521 LCD repetitase Netminal comain and ring finger 3 similar to Physichetical potein FL/23749 (LCN peptidase N-terminal domain and ring finger 1) similar to Physichetical potein FL/23749 (LCN peptidase N-terminal domain and ring finger 1) similar to Physichetical potein FL/23749 (LCN peptidase N-terminal domain and ring finger 1) similar to Physichetical potein FL/23749 (LCN peptidase N-terminal domain and ring finger 1) similar to Phesical a potein FL/23749 (LCN peptidase N-terminal domain and ring finger 1) aderylate cyclase activating potpeptide 1 (phulary) potein phosphateal 2 (lormetry 2A), regulatory subunit B*, apha EST Finished cDNA, clone ChEST305/21 ENSEMBL Prediction Finished cDNA, clone ChEST305/201 nuclear degrees 1 [Insig-1] cluster B 3-hydroxy-S-methylghtaryt-Coenzyme A synthase 1 (soluble) [HMG-CoA synthase] Finished cDNA, clone ChEST305/201 nuclear factor, interfexikin 3 regulated [E4:bp4] CAGA, clone tance (TEST650620 anniar to Heat-shock protein 105 Kba (Heat shock 110 KDa protein) anniar to Heat-shock protein 105 Kba (Heat shock 110 KDa protein) anniar to Heat-shock protein 105 Kba (Heat shock 110 KDa protein) anniar to Heat-shock protein 105 Kba (Heat shock 110 KDa protein) timatro to Heat-shock protein total (httpBB) homocytelme-inducble, endoplasmic reticulum stress-inducble, ubiquiti-kike domain member 1 [Heipord1] procolagen-proline, 2-oxogultarate 4-dioxyganase (groline 4-hydroxylase), ahina potypeptide II homocytelme-inducble, endoplasmic reticulum stress-inducble, ubiquiti-kike domain member 1 BC22-associated athanogene 3	NA signal transduction NA proteolysis proteolysis proteolysis unknown secreated protein signal transduction NA NA cell cycle sterol metabolism sterol metabolism sterol metabolism sterol metabolism protein folding protein folding unfolded protein response NA	Gqa.1157.2.15.1_at GqaAH7.2664.15.1_a,at GqaAH7.2664.15.1_at GqaAF7.2664.15.1_at GqaAF7.2664.15.1_at GqaAF7.2024.15.1_at GqaAF7.2024.15.1_at GqaAF7.2024.15.1_at GqaAF7.2024.15.1_at GqaAF7.15.1_at
	Finished 20NA, clone ChEST133n4 similar to protein kinase related to Raf protein kinases Finished 20NA, clone ChEST625621 (LON peptidase Netrimial Contain and ring finger 3 similar to hypothetical protein FL237349 (LON peptidase N-4emnial domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase N-4emnial domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase N-4emnial domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase N-4emnial domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase N-4emnial domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase N-4emnial domain Protein to Discher 1) similar to Nuch clone ChEST505[21 Finished 20NA, clone ChEST505[21 Finished 20NA, clone ChEST5026110 nucleophomin Finished 20NA, clone ChEST5026110 nucleophomin Finished 20NA, clone ChEST5026110 nucleon clones 2 [Hg25] CuBC, calon tanaport regulates (Hsp68) Finished 20NA, clone ChEST602610 similar to Nata-shock protein to Sta (Hat shock 110 kDa protein) similar to Nata-shock protein to Sta (Hat shock 110 kDa protein) similar to Nata-shock protein to Sta (Hat shock 110 kDa protein) similar to Nata-shock protein to Sta (Hat shock 110 kDa protein) similar to Nata-shock protein to Sta (Hat shock 110 kDa protein) similar to Nata-shock protein to Sta (Hat shock 110 kDa protein) similar to Nata-shock protein to Sta (Hat shock 110 kDa protein) similar to Nata-shock protein to Sta (Hat shock 110 kDa protein) similar to Nata-shock protein to Sta (Hat shock 110 kDa protein) similar to Nata-shock protein to Sta (Hat shock 110 kDa protein) similar to Nata-shock protein to Sta (Hat shock 110 kDa protein) similar to Nata-shock protein to Sta (Hat shock 110 kDa protein) similar to Nata-shock protein to Sta (Hat shock 110 kDa protein) similar to Nata-shock protein to Sta (Hat shock 110 kDa protein) similar to Nata-shock protein to Sta (Hat shock 110 kDa protein) similar to Nata-shock protein to Sta (Hat shock 110 kDa p	NA signal transduction NA proteolysis proteolysis proteolysis accreated protein signal transduction NA NA NA Call cycle sterol metabolism NA cell cycle sterol metabolism NA cell cycle sterol metabolism NA cell cycle sterol metabolism protein folding protein response NA unfolded protein response cochaperone cochaperone	$\label{eq:Gamma} \begin{array}{l} Gga 11572.1.51_at \\ Gga 4474.2664.1.51_at \\ Gga 4747.2664.1.51_at \\ Gga 4747.674.1.51_at \\ Gga 4747.674.1.51_at \\ Gga 4747.674.1.51_at \\ Gga 4747.674.1.51_at \\ Gga 11409.1.51_at \\ Gga 12650.1.51_at \\ Gga 12650.1.51_at \\ Gga 12650.1.51_at \\ Gga 4000.1.51_at \\ Gga 4000.0.51_at \\ Gga 4000.0$
	Finished CDNA, clone ChEST136n4 almalar b protein kinase related to Pal protein kinases Finished CDNA, clone ChEST625621 LCD repetitase Netminal domain and ring finger 3 almalar to hypothetical protein FL237349 (LCDA peptidase N-terminal domain and ring finger 1) almalar to hypothetical protein FL237349 (LCDA peptidase N-terminal domain and ring finger 1) almalar to hypothetical protein FL237349 (LCDA peptidase N-terminal domain and ring finger 1) almalar to Peokstrin homology domain containing family G member 1 aderylate cyclase activating polypeptida I (plutary) polyan phosphatase 2 (lommity 2A), regulatory subunit B*, sipha EST Finished CDNA, clone ChEST305(21 ENSEMBL Prediction Finished CDNA, clone ChEST304221 nucleoptomini insulin riduced gene 1 [Insig-1] cluster B 3-hydroxy-S-methylgitaty-Coencyme A synthase 1 (soluble) [HMG-CoA synthase] Finished CDNA, clone ChEST306(20 CAC, cation transport regulator-life (E, coli) Neat shock protein 25 [Hap55] Finished CDNA, clone ChEST506(20 Heat shock protein 25 [Hap56] Finished CDNA, clone ChEST506(20 Heat shock protein 26 [Hap58] Henorosystem-inducble, endoplasmic reliculum stress-inducble, ubiquitin-kike domain member 1 EST [Herput1] proollagen-proline.2-conglutated 4-dioxygenase (protein 4-hydroxyles), [hap hypothetical Henorosystem-inducble, endoplasmic reliculum stress-inducble, ubiquitin-kike domain member 1 homosystem-inducble, endoplasmic reliculum stress-inducble, ubiquitin-kike d	NA signal transluction NA proteolysis proteolysis proteolysis secrested protein signal transduction NA NA cell ayduction sterol metabolism sterol metabolism sterol metabolism sterol metabolism NA circadian clock unknown protein folding protein folding	Gqa.1157.2.1.51_at Gqa.474.2666.1.51_a.t Gqa.474.2666.1.51_a.t Gqa.17046.1.51_at Gqa.17046.1.51_at Gqa.17046.1.51_at Gqa.17407.1.51_at Gqa.17407.1.51_at Gqa.17407.1.51_at Gqa.17407.1.51_at Gqa.17407.1.51_at Gqa.17407.1.51_at Gqa.17407.1.51_at Gqa.17407.1.51_at Gqa.17407.1.51_at Gqa.17407.1.51_at Gqa.17407.1.51_at Gqa.17407.1.51_at Gqa.17407.1.51_at Gqa.056.1.51_at Gqa.056.1.51_at Gqa.056.1.51_at Gqa.056.1.51_at Gqa.056.1.51_at Gqa.057.1.51_at Gqa.057.1.51_at Gqa.057.1.51_at Gqa.077.1.51_at
	Finished CDNA, cone ChEST905/201 miller to proteins herminal domain and ring finger 3 similar to proteins homology domain containing family G member 1 aimlar to Physichen homology domain containing family G member 1 aimlar to Physichen homology domain containing family G member 1 adenylate cyclase activating polyceptide 1 (plutary) protein phosphateal grotein FL23749 (LON peptidase N-terminal domain and ring finger 1) aimlar to Pheside activating to protein FL23749 (LON peptidase N-terminal domain and ring finger 1) adenylate cyclase activating polyceptide 1 (plutary) protein phosphateal 2 (lomerity 2A), regulatory subunit B*, apha EST Finished CDNA, cone ChEST905/21 ENSEMBL Prediction Finished CDNA, cone ChEST905/21 ENSEMBL Prediction muclear dator, interfexitin 3 regulated (E4op4) ChaQ, conten ChEST905/10 muclear factor, interfexitin 3 regulated (E4op4) ChaQ, conten ChEST9505/10 muclear factor, interfexitin 3 regulated (E4op4) ChaQ, conten ChEST965/10 finished CDNA, cone ChEST965/20 cluster A Finished CDNA, chone ChEST965/20 cluster A Finished CDNA, chone ChEST965/20 cluster A Finished CDNA, chone ChEST965/20 aimlar to Heat-shock protein 105 Kba (Heat shock 110 KDa protein) aimlar to Heat-shock protein 105 Kba (Heat shock 110 KDa protein) aimlar to Heat-shock protein 105 Kba (Heat shock 110 KDa protein) aimlar to Heat-shock protein 105 Kba (Heat shock 110 KDa protein) aimlar to Heat-shock protein test (HepB0) homocytelme-induckle, endoplasmic reticulum stress-induckle, ublquitin-ške domain member 1 BC2-associated athanogeres 3 aimlar to pLA1 chaperone aimlar to pLA1 chaperone aimlar to PLA1 chaperone aimlar to PLA1 chaperone	NA signal transduction NA proteolysis proteolysis proteolysis unknown secreated protein signal transduction NA NA cell cycle sterol metabolism sterol metabolism sterol metabolism sterol metabolism protein folding protein folding protein folding protein folding protein response NA protein response unfolded protein folding protein folding	Gqa.1157.2.15.1_at GqaAH7.2664.15.1_a,at GqaAH7.2664.15.1_at GqaAF7.2664.15.1_at GqaAF7.2664.15.1_at GqaAF7.2024.15.1_at GqaAF7.2024.15.1_at GqaAF7.2024.15.1_at GqaAF7.2024.15.1_at GqaAF7.15.1_at
	Finished 20NA, clone ChEST133n4 alimal to potieth kinase related to Parl protein kinases Finished 20NA, clone ChEST825621 LON peptidase Netrimial domain and ring finger 3 alimal to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) alimal to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) alimal to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) alimal to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) alimal to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) alimal to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) and ring the protein the protein the final domain and ring finger 1) protein phosphatase 2 (Immerly 2A), regulatory suburit B*, alpha EST Finished dONA, clone ChEST805(21 SNSMB, Prodeion Finished dONA, clone ChEST805(20) finished to ChA, clone ChEST805(20) Finished dONA, clone ChEST805(20) finished to ChA, clone ChEST	NA signal transduction NA proteolysis proteolysis proteolysis secreated protein signal transduction NA NA call system aterd metabolism sterd metabolism sterd metabolism sterd metabolism sterd metabolism transoun protein folding protein folding protein folding protein folding protein folding protein folding protein folding protein response NA unfolded protein response unfolded protein response unfolded protein response cochaperone cochaperone cochaperone cochaperone cochaperone cochaperone protein folding protein folding protein folding protein folding protein folding protein folding protein folding protein folding	Gqa.1157.2.1.51_at Gqa.M47.2664.1.51_a, at Gqa.M47.2642.1.51_at Gqa.M74.2642.1.51_at Gqa.M74.2642.1.51_at Gqa.M74.2742.1.51_at Gqa.M74.2742.1.51_at Gqa.M74.2742.1.51_at Gqa.M74.275.1.51_at Gqa.M74.275.1.51_at Gqa.M74.2054.1.51_at Gqa.M74.1056.1.51_a_at Gqa.M74.1056.1.51_at Gqa.M74.
	Finished CDNA, clone ChEST136n4 almalar b poteh kinase related to Parl protein kinases Finished CDNA, clone ChEST826521 LCD repetidase Netminal domain and ring finger 3 almalar b hypothetical protein FL/23744 (LCN peptidase N-terminal domain and ring finger 1) almalar b hypothetical protein FL/23744 (LCN peptidase N-terminal domain and ring finger 1) almalar b hypothetical protein FL/23744 (LCN peptidase N-terminal domain and ring finger 1) almalar b hypothetical protein FL/23744 (LCN peptidase N-terminal domain and ring finger 1) almalar b hypothetical protein FL/23744 (LCN peptidase N-terminal domain and ring finger 1) almalar b hypothetical protein FL/23744 (LCN peptidase N-terminal domain and ring finger 1) almalar b hypothetical protein FL/23744 (LCN peptidase N-terminal domain and ring finger 1) finished CDNA, clone ChEST305(2) ENSEMBL Prediction Finished CDNA, clone ChEST30421 nucleophonximi insulin induced gene 1 [Insig-1] cluster 8 3-hydroxy-3-methylgidaty-5 (Cencyme A synthase 1 (soluble) [MG-COA synthase] Finished CDNA, clone ChEST506020 nuclear factor, interlexin A singulated [E40p4] Chac, cation transport regulator-1 (E c. col) heat shok protein 25 [Hap25] Finished CDNA, clone ChEST506020 almalar to Hast-hock protein bat-8 (HspB8) Finished CDNA, clone ChEST506020 almalar to Hast-hock protein bat-8 (HspB8) EXCLassociated athanogene 3 [Herpot1] procobjean-inducble, endoplasmic reticulum stress-inducble, ubiquiti-like domain member 1 BCL2-associated athanogene 3 almalar to DJA1 chaperone almalar to DJA1 chaperone almalar to DJA1 chaperone almalar bothas for Plefy 70] cysteine and histifine-indu chaperone almalar to DJA1 chaperone almalar bothas for Plefy 70] cysteine and histifine-inducble, method CHORD)-containing 1 Dana (HspAD) honolog, subinally A, member 1	NA signal transluction NA proteolysis proteolysis proteolysis secreated protein signal transduction NA NA cell cycle sterol metabolism sterol metabolism sterol metabolism sterol metabolism torbin folding protein folding	Gqa.1157.2.1.51_at Gqa.M72.2664.1.51_a.at Gqa.M72.2664.1.51_a.at Gqa.M72.6645.1.51_at Gqa.17046.1.51_at Gqa.17046.1.51_at Gqa.11400.1.51_at Gqa.11470.1.51_at Gqa.16704.1.51_at Gqa.16704.1.51_at Gqa.16704.1.51_at Gqa.16351.1.51_at Gqa.16351.51_at Gqa.16351.51_at Gqa.161_51_at Gqa.161_51_at Gqa.16351.51_at Gqa.16351.51_at Gqa.961.51_at Gqa.961.51_at Gqa.961.51_at Gqa.961.51_at Gqa.961.51_at Gqa.961.51_at Gqa.971.01_51_at Gqa.971.01_51_at Gqa.971.151_at Gqa.972.151_at Gqa.974.1141.151
	Finished 20NA, clone ChEST133n4 similar to protein Name Pitatel to Raf protein kinases Finished 20NA, clone ChEST625621 LCN peptidase Netrimial Contain and ring finger 3 similar to hypothetical protein FL237349 (LCN peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL237349 (LCN peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL237349 (LCN peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL237349 (LCN peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL23749 (LCN peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL23749 (LCN peptidase N-terminal domain Protein hypothetical protein FL23749 (LCN peptidase N-terminal protein phosphatase 2) (mempi 2N), regulatory suburit B°, alpha EST Finished tONA, clone ChEST305(21 Finished 20NA, chore ChEST305(21 Finished 20NA, chore ChEST305(21 Finished 20NA, chore ChEST305(21) Chalca claim tampoot regulatoriskis 1 (soluble) [HMG-CoA synthase] Finished 20NA, chore ChEST305(21) Chalca claim tampoot regulatoriskis 1 (soluble) [HMG-CoA synthase] Finished 20NA, chore ChEST305(21) Chalca claim tampoot regulatoriskis 1 (soluble) [HMG-CoA synthase] Finished 20NA, chore ChEST305(21) Similar to Hata-shock protein 105 (Hzp82) Chalca claim tampoot regulatoriskis 1 (soluble) [HMG-CoA synthase] Finished 20NA, chore ChEST805(20) similar to Hata-shock protein 105 (Mzp82) Inter State-Stock protein 105 (Mzp82) Inter State-State-State-State-Stock Protein 105 (Mzp82) Inter State-St	NA signal transduction NA proteolysis proteolysis proteolysis secrested protein signal transduction NA NA CAL NA CAL SA NA CAL SA SA SA SA SA SA SA SA SA SA SA SA SA	$\label{eq:Gamma} \begin{array}{l} Gga 11572.1.51_at \\ Gga 4476.2664.1.51_at \\ Gga 4476.2664.1.51_at \\ Gga 476.21402.1.51_at \\ Gga 476.2742.1.51_at \\ Gga 476.2742.1.51_at \\ Gga 476.2742.1.51_at \\ Gga 11409.1.51_at \\ Gga 12636.1.51_at \\ Gga 12636.1.51_at \\ Gga 12636.1.51_at \\ Gga 12636.1.51_at \\ Gga 476.275.1.51_at \\ Gga 476.255.1.51_at \\ Gga 476.255.255.255.255.255.255.255.255.255.25$
	Finished CDNA, clone ChESTI33n4 almalar b protein kinase related to Parl protein kinases Finished CDNA, clone ChEST825621 LON peptidase Netminal domain and ring finger 3 almalar b hypothetical protein FL/23749 (LON peptidase N-terminal domain and ring finger 1) almalar b hypothetical protein FL/23749 (LON peptidase N-terminal domain and ring finger 1) almalar b hypothetical protein FL/23749 (LON peptidase N-terminal domain and ring finger 1) almalar b hypothetical protein FL/23749 (LON peptidase N-terminal domain and ring finger 1) almalar b hypothetical protein FL/23749 (LON peptidase N-terminal domain and ring finger 1) almalar b hypothetical protein FL/23749 (LON peptidase N-terminal domain adveylals optidase 2 (formerly 2A), regulatory subunit B*, alpha EST Finished CDNA, clone ChEST505(21 ENSEMBL Proteinton finished CDNA, clone ChEST505(21 ENSEMBL Proteinton finished CDNA, clone ChEST506(20 finished CDNA, clone ChEST506(20 almalar to Haashanck protein 105 Kba (Haat shock 110 kBa protein) almalar to Haashanck protein batas (HspBB) Homosysteme-induckle, endoplasmic relucum stress-induckle, ubiquitin-škk domain member 1 EST proteine-induckle, endoplasmic relucum stress-induckle, ubiquitin-škk domain member 1 BC2-associated athanogenes 3 [Herput1] BC2-associated athanogenes 3 [Herput1] BC2-asso	NA signal transduction NA proteolysis proteolysis proteolysis secreated protein signal transduction NA edi appatient secre atted protein call appatient secre atted protein call appatient secre atted protein secre atted protein protein folding protein folding	Gqa.1157.2.1.51_at Gqa.M47.2664.1.51_a.t Gqa.M47.2644.1.51_a.t Gqa.M47.2644.1.51_at Gqa.M7.2446.1.51_at Gqa.M7.2446.1.51_at Gqa.M7.2474.1.51_at Gqa.M7.274.1.51_at Gqa.M7.274.1.51_at Gqa.M7.274.1.51_at Gqa.M7.274.1.51_at Gqa.M7.2024.1.51_at Gqa.M4.2.1.51_at
	Finished CDNA, chone ChEST193m4 similar to potien kinase related to Parl protein kinases Finished CDNA, chone ChEST8026e21 LCD peptidase Netminal domain and ring finger 3 similar to hypothetical protein FL/23744 (LCD peptidase N-terminal domain and ring finger 1) similar to Parlextarin homology domain containing family G member 1 adenylate opticase activating polypeptide 1 (futurer) protein priorignatuse 2 (formet/2 AV (LCDA peptidase N-terminal domain and ring finger 1) similar to DiPotestarin homology domain containing family G member 1 adenylate z (formet/2 AV (LCDA peptidase N-terminal domain and ring finger 1) protein priorignatuse 2 (formet/2 AV (LCDA peptidase N-terminal EST insinde CDNA, chone ChEST305/21 ENSEMBL Prediction Finished CDNA, chone ChEST305/201 mulcer factor, interfexitin 3 regulated [E40p4] Charl, chone ChEST305/201 mulcer factor, interfexitin 3 regulated [E40p4] Charl, chone ChEST505/201 mulcer factor, interfexitin 3 regulated [E40p4] Finished CDNA, chone ChEST505/201 mulcer factor, interfexitin 3 regulated [E40p4] Charl, chone ChEST505/201 mulcer baset-shock protein 105 (future 1 (fe. col) Finished CDNA, chone ChEST505/202 animilar to Heats-shock protein 105 (future 1 (fe. col) Finished CDNA, chone ChEST505/202 animilar to Heats-shock protein 105 (future 1 (fe. col) Finished CDNA, chone ChEST505/202 animilar to Heats-shock protein 105 (future 1 (fe. col) Finished CDNA, chone ChEST505/202 animilar to Heats-shock protein 105 (future 1 (fe. col) finished CDNA, chone ChEST505/202 animilar to Heats-shock protein 105 (future 1 (fe. col) finished CDNA, chone ChEST505/202 animilar to Heats-shock protein 105 (future 1 (fe. col) finished CDNA, chone ChEST505/202 animilar to JDAI chaperone similar to JDAI chaperone similar to JDAI chaperone heat shock protein 2 (Heap01) coptiene-inducble, endoplasmic reticulum stress-inducble, ubiquitin-like domain member 1 BC/2-associated athanogene 3 aimilar to JDAI chaperone heat shock protein 2 (Heap01) coptiene-inducble, endoplasmic (reticulum stress-inducble,	NA signal transduction NA proteolysis proteolysis proteolysis proteolysis proteolysis proteolysis secrated protein na NA NA cell cycle sterol metabolism sterol metabolism sterol metabolism sterol metabolism sterol metabolism sterol metabolism protein folding protein folding	Gqa.1157.2.1.51_at Gqa.M72.2664.1.51_a.t Gqa.M72.2664.1.51_at Gqa.M72.2664.1.51_at Gqa.M72.616.1.51_at Gqa.M72.616.1.51_at Gqa.M72.674.1.51_at Gqa.M72.674.1.51_at Gqa.M72.674.1.51_at Gqa.M72.674.1.51_at Gqa.M72.674.1.51_at Gqa.M72.674.1.51_at Gqa.M74.0165.1.51_a_at Gqa.M74.0165.1.51_a_t Gqa.M74.0163.1.51_at Gqa.M74.0163.1.51_at Gqa.M74.0163.1.51_at Gqa.M74.0163.1.51_at Gqa.M74.0163.1.51_at Gqa.M74.0163.1.51_at Gqa.M74.0163.1.51_at Gqa.M74.0163.1.51_at Gqa.M74.0163.1.51_at Gqa.M74.0163.1.51_at Gqa.M74.0163.1.51_at Gqa.M74.0163.1.51_at Gqa.M74.0163.1.51_at Gqa.M74.0163.1.51_at Gqa.M74.0163.1.51_at Gqa.M74.0163.1.51_at Gqa.M74.0163.1.51_at Gqa.M74.015.015.1.51_at Gqa.M74.015.015.1.51_at Gqa.M74.015.015.1.51_at Gqa.M74.015.015.1.51_at Gqa.M74.015.015.1.51_at Gqa.M74.015.015.1.51_at Gqa.M74.015.015.1.51_at Gqa.M74.015.015.1.51_at Gqa.M74.015.015.1.51_at Gqa.M74.015.015.1.51_at Gqa.M74.015.015.1.51_at Gqa.M74.015.015.1.51_at Gqa.M74.015.015.1.51_at Gqa.M74.015.015.1.51_at Gqa.M
	Finished CDN, clone ChESTI33n4 alimal to potieth kinase related to Parl protein kinases Finished CDN, clone ChEST825621 LON peptidase Netwinal containing farger 3 alimal to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) alimal to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) alimal to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) alimal to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) alimal to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) alimal to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) adverse to the start of the terminal domain and ring finger 1) protein phosphatase 2 (Immerly 2A), regulatory suburit B*, alpha EST Finished CDNA, chore ChEST805(21 BNSMBL Production Finished CDNA, chore ChEST805(20 Finished CDNA, ch	NA signal transduction NA proteolysis proteolysis proteolysis secreated protein signal transduction NA NA NA Cell cycle aterd metabolism sterd metabolism sterd metabolism sterd metabolism NA circadian clock unknown protein folding protein folding signal transduction	Gqa.1157.2.1.51_at Gqa.M47.2664.1.51_a, at Gqa.M47.2664.1.51_a, at Gqa.M74.2642.1.51_at Gqa.M74.2642.1.51_at Gqa.M74.874.1.51_at Gqa.M74.874.1.51_at Gqa.M74.874.1.51_at Gqa.11409.1.51_at Gqa.11409.1.51_at Gqa.11409.1.51_at Gqa.11409.1.51_at Gqa.11409.1.51_at Gqa.11630.1.51_at Gqa.11630.1.51_at Gqa.1530.1.51_at Gqa.0153.71_51_at Gqa.0153.71_51_at Gqa.0153.71_51_at Gqa.0153.71_51_at Gqa.0153.71_51_at Gqa.026.1.51
	Finished CDNA, clone ChEST133n4 almalar b protein kinase related to Pal protein kinases Finished CDNA, clone ChEST825621 LCD reptidase Netminal domain and ring finger 3 almalar to hypothetical protein FL237349 (LCDA peptidase N-terminal domain and ring finger 1) almalar to hypothetical protein FL237349 (LCDA peptidase N-terminal domain and ring finger 1) almalar to hypothetical protein FL237349 (LCDA peptidase N-terminal domain and ring finger 1) almalar to hypothetical protein FL237349 (LCDA peptidase N-terminal domain and ring finger 1) almalar to hypothetical protein FL237349 (LCDA peptidase N-terminal domain and ring finger 1) almalar to hypothetical protein FL237349 (LCDA peptidase N-terminal domain and ring finger 1) almalar to hypothetical protein FL237349 (LCDA peptidase N-terminal domain EST Finished CDNA, clone ChEST30521 ENSEMBL Production Finished CDNA, clone ChEST304221 nucleoptomini imular in theat-shoch context finger 1 (soluble) (HMG-CoA synthase) Finished CDNA, clone ChEST30421 CAC, caciton transport regulator-like (E. coli) Neat shock protein 25 (Hap25) Finished CDNA, clone ChEST506020 almalar to Haat-shock protein to Kbaa (Heat shock 110 kBa protein) almalar to Haat-shock protein to Kbaa (Heat shock 110 kBa protein) almalar to Haat-shock protein to Kbaa (Heat shock 110 kBa protein) almalar to Haat-shock protein to Kbaa (Heat shock 110 kBa protein) almalar to Haat-shock protein to Kbaa (Heat shock 110 kBa protein) almalar to Haat-shock protein to Kbaa (Heat shock 110 kBa protein) almalar to DAAI chaperone similar to DAAI chaperone sim	NA signal transduction NA proteolysis proteolysis proteolysis proteolysis secrested protein signal transduction NA NA cell cycle sterol metabolism sterol metabolism sterol metabolism sterol metabolism valending protein folding protein fol	Gqa.1157.2.1.51_at Gqa.474.2666.1.51_a.at Gqa.474.2666.1.51_a.at Gqa.1704.61.51_at Gqa.1704.61.51_at Gqa.1704.61.51_at Gqa.1740.71.51_at Gqa.1740.71.51_at Gqa.1740.71.51_at Gqa.1740.71.51_at Gqa.1740.71.51_at Gqa.1740.71.51_at Gqa.1740.71.51_at Gqa.1740.71.51_at Gqa.1740.71.51_at Gqa.1740.71.51_at Gqa.1740.71.51_at Gqa.1740.71.51_at Gqa.1740.71.51_at Gqa.1740.71.51_at Gqa.926.1.51_at Gqa.926.1.51_at Gqa.926.1.51_at Gqa.927.1.51_at Gqa.927.1.51_at Gqa.926.1.51_at Gqa.927.1.5
	Finished 20NA, clone ChEST133n4 similar to protein Share related to Raf protein kinases Finished 20NA, clone ChEST3625621 (LON peptidase Netwinial Contain and ring finger 3 similar to hypothetical protein FL237349 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL237349 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL237349 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL237349 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase N-terminal domain Protein to the Starbing Dypothetical F (Johtan) Protein phosphatase 2 (Immerity 2A), regulatory suburit B*, alpha EST Finished LONA, clone ChEST305(21 Finished CDNA, chone ChEST305(21 ChaC calm hamport mejulase kin 1 (E coli) Inat athock protein 25 [Hg25] ChaC calm hamport mejulase kin 1 (E coli) Inat athock protein 25 [Hg25] Finished CDNA, chone ChEST305(20 similar to Hata-shock protein bota 3 (Hg26) Finished CDNA, chone ChEST305(20 similar to Hata-shock protein bota 3 (Hg26) Similar to Hata-shock protein 105 KDa (Hata shock 110 KDa protein) similar to pDA1 chapterone similar to pDA1 chapter	NA signal transduction NA proteolysis proteolysis proteolysis secrested protein signal transduction NA NA CAL SA SA SA SA SA SA SA SA SA SA SA SA SA	$\label{eq:gamma} \begin{array}{l} Gga 11572.1.51_at \\ Gga 4474.2664.1.51_at \\ Gga 4474.2664.1.51_at \\ Gga 4474.674.1.51_at \\ Gga 4476.6742.1.51_at \\ Gga 4476.6742.1.51_at \\ Gga 4476.6742.1.51_at \\ Gga 11409.1.51_at \\ Gga 12636.1.51_at \\ Gga 12636.1.51_at \\ Gga 12636.1.51_at \\ Gga 4474.10807.1.51_at \\ Gga 4474.10807.1.51_at \\ Gga 4472.1.51_at \\ Gga 4472.51_at \\ Gga 44$
	Finished CDNA, clone ChEST136n4 almalar b protein kinase related to Parl protein kinases Finished CDNA, clone ChEST625621 LCN peptidase Netrminal domain and ring finger 3 almalar b hypothetical protein FL237349 (LCN peptidase N-terminal domain and ring finger 1) almalar b hypothetical protein FL237349 (LCN peptidase N-terminal domain and ring finger 1) almalar b hypothetical protein FL237349 (LCN peptidase N-terminal domain and ring finger 1) almalar b hypothetical protein FL237349 (LCN peptidase N-terminal domain and ring finger 1) almalar b hypothetical protein FL237349 (LCN peptidase N-terminal domain and ring finger 1) almalar b hypothetical protein FL237349 (LCN peptidase N-terminal domain and ring finger 1) almalar b hypothetical protein FL237349 (LCN peptidase N-terminal domain EST Finished CDNA, clone ChEST505(2) ENSEMBL Production Finished CDNA, clone ChEST506(2) Finished CDNA, clone ChEST506(2) almalar to Hast-hock protein for SLNa (Haat shock 110 kDa protein) almalar to Hast-shock protein bat-8 (HspBB) Homosystem-induckle, endoplasmic reticulum stress-induckle, ubiquitin-ške domain member 1 EST proteine-induckle, endoplasmic reticulum stress-induckle, ubiquitin-ške domain member 1 BC2-associated athanogenes 3 [Herput1] BC2-associated athanogenes 3 EVERPUT1 BC2-associated athanogenes 4 atmitar to DLA1 chaperones tamitar to DLA1 chaperones t	NA signal transduction NA proteolysis proteolysis proteolysis escreated protein algonal transduction NA esti and transduction NA cell acycle sterol metabolism sterol metabolism sterol metabolism sterol metabolism sterol metabolism unfolden protein response na protein folding protein folding protein rolding protein folding protein fo	Gqa.1157.2.1.51_at Gqa.M47.2664.1.51_a.t Gqa.M47.2644.1.51_a.t Gqa.M47.2644.1.51_at Gqa.M7.2046.1.51_at Gqa.M7.2046.1.51_at Gqa.M7.2047.1.51_at Gq
	Finished 20NA, clone ChEST133n4 similar to protein Share related to Raf protein kinases Finished 20NA, clone ChEST3625621 (LON peptidase Netwinal domain and ring finger 3 similar to hypothetical protein FL232749 (LON peptidase Netwinal domain and ring finger 1) similar to hypothetical protein FL232749 (LON peptidase Netwinal domain and ring finger 1) similar to hypothetical protein FL232749 (LON peptidase Netwinal domain and ring finger 1) similar to hypothetical protein FL232749 (LON peptidase Netwinal domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase Netwinal domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase Netwinal domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase Netwinal domain and ring finger 1) similar to hypothetical protein FL33749 (LON peptidase Netwinal domain and ring finger 1) situation finadese advantag objecphical 4 (Johutan S Netwinal CONA, clone ChEST360511 Chall Chall Chall Chall (Long ChEST360510 Chall chall hypothetical S (Hadal (Edpd) Chall chall hypothetical hypothetical hypothetical hypothetical hypothetical millinar to Hada shock protein 105 400 (Hada shock 110 kDa protein) similar to Hada shock protein 105 400 (Hada shock 110 kDa protein) similar to Hada shock protein 105 400 (Hada shock 110 kDa protein) similar to Hada shock protein 105 400 (Hada shock 110 kDa protein) similar to Hada shock protein 105 400 (Hada shock 110 kDa protein) similar to Hada shock protein 105 400 (Hada shock 110 kDa protein) similar to Hada shock protein 105 400 (Hada shock 110 kDa protein) similar to pothal chapterso 3 (Herpot1) BC2-associated athanogenes 3 similar to pothal hypothetical hybrid shock 110 kDa protein) Finished CONA, cone CheST3110 Finished CONA, cone CheST3110 Finished CONA, cone CheST3110 Finished CONA, cone CheST3110 Finished CONA, cone C	NA signal transduction NA proteolysis proteolysis proteolysis sercested protein signal transduction NA NA CAL Secretaria NA CAL Secretaria NA CAL Secretaria NA CAL Secretaria NA protein folding protein fold	$\label{eq:constraints} \begin{array}{l} \mbox{Gapa.11572.1.51_at} \\ \mbox{GapaKF2.2664.1.51_at} \\ \mbox{GapaKF2.1402.1.51_at} \\ \mbox{GapaKF2.1402.1.51_at} \\ \mbox{GapaKF2.141.51_at} \\ \mbox{GapaKF2.141.51_at} \\ \mbox{GapaKF2.151_at} \\ GapAKF2.151_at$
	Finished CDN, cone ChESTI36n4 similar to protein kinase related to Bra protein kinases Finished CDN, cone ChESTB25621 LON peptidase Netwinal domain and ring finger 3 similar to hypothetical protein FL28749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL28749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL28749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL28749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL28749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL28749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL28749 (LON peptidase N-terminal domain Finished CDN, cone ChESTB3621 NENSMB, Prediction Finished CDN, cone ChESTB3621 Shydtoxy-Smethytigidar/Conrxyme A synthase 1 (soluble) [HMG-CoA synthase] Finished CDN, cone ChESTB3620 Cac, cainot mator (FLSB500) finished CDN, cone ChESTB3620 Finished CDN, cone ChESTB3720 Finished CDN, cone ChESTB37180 Finished CDN, cone ChESTB37180 Finished CDN, cone ChESTB37180 Finished CDN, cone ChESTB37180 Finished CDN, cone ChESTB37180	NA signal transduction NA proteolysis proteolysis proteolysis screated protein signal transduction NA NA Call cycle aterd metabolism sterd metabolism sterd metabolism sterd metabolism NA call cycle aterd metabolism sterd metabolism protein folding protein folding signal transduction Protein folding signal transduction protein folding protein folding signal transduction protein folding protein folding signal transduction protein folding signal transduction signal tra	Gqa.1157.2.1.51_at Gqa.M47.2664.1.51_a, at Gqa.M47.2664.1.51_a, at Gqa.M7.2664.1.51_at Gqa.M7.2646.1.51_at Gqa.M7.6274.2.15_at Gqa.M7.6274.2.15_at Gqa.M7.6274.2.15_at Gqa.11409.1.51_at Gqa.11409.1.51_at Gqa.11409.1.51_at Gqa.11409.1.51_at Gqa.11409.1.51_at Gqa.11630.1.51_at Gqa.11630.1.51_at Gqa.11630.1.51_at Gqa.11630.1.51_at Gqa.0153.71_51_at Gqa.0153.71_51_at Gqa.0153.71_51_at Gqa.0153.71_51_at Gqa.0153.71_51_at Gqa.026.1.51_at Gqa.026.1.51_at Gqa.026.1.51_at Gqa.026.1.51_at Gqa.026.1.51_at Gqa.026.1.51_at Gqa.026.1.51_at Gqa.027_1.51_at
	Finished CDNA, clone ChEST136n4 alimalar bo potieh kinase related to Pall potieh kinases Finished CDNA, clone ChEST625621 LON peptidase Netminal domain and ring finger 3 alimalar boychetical potieh FL23734 (LON peptidase N-terminal domain and ring finger 1) alimalar boychetical potieh FL23744 (LON peptidase N-terminal domain and ring finger 1) alimalar boychetical potieh FL23744 (LON peptidase N-terminal domain and ring finger 1) alimalar boychetical potieh FL23744 (LON peptidase N-terminal domain and ring finger 1) alimalar boychetical potieh FL23744 (LON peptidase N-terminal domain and ring finger 1) alimalar boychetical potieh FL23744 (LON peptidase N-terminal domain and ring finger 1) alimalar boychetical potieh FL23744 (LON peptidase N-terminal domain EST Finished CDNA, chore ChEST365(21 ENSEMBL Prediction Finished CDNA, chore ChEST36421 nucleophornin insulin ribudare gene 1 [Insig-1] Shydroxy-S-methytightary-Coencyme A synthase 1 (soluble) [HMG-CoA synthase] Finished CDNA, clone ChEST560600 nuclear factor, interfiexin A regulated [E4pJ4] CAC, cation transport regulator-left (E coli) Heat shock protein 25 [Hap25] Finished CDNA, clone ChEST560602 alimilar to Heat-shock protein botas (HspB8) Homocystein-induckle, endoplasmic reticulum stress-induckle, ubiquitin-kke domain member 1 EST protolager poline, 2-coeglutamic reticulum stress-induckle, ubiquitin-kke domain member 1 EGZ-associated almocigene 3 alimilar to JAL chaperone similar to JAL chaperone (Heat Hock 10 kB potish) Finished CDNA, clone ChEST50424 similar to JAL chaperone (Heat Hock 10 kB potish) Finished CDNA, clone ChEST50424 similar to JAL chaperone (Heat Hock 10 kB potish) Finished CDNA, clone ChEST50424 similar to JAL chaperone (Heat Hock 10 kB potish) Finished CDNA, clone ChEST50424 similar to JAL chaperone (Heat Hock 10 kB poti	NA signal transduction NA proteolysis proteolysis proteolysis proteolysis secreated protein signal transduction NA NA call cycle sterol metabolism sterol metabolism sterol metabolism sterol metabolism sterol metabolism sterol metabolism toreban folding protein folding tansacptica NA NA	Gqa.1157.2.1.51_at Gqa.M72.2664.1.51_a.t Gqa.M72.2664.1.51_at Gqa.M72.2664.2.51_at Gqa.M72.664.51_at Gqa.17046.1.51_at Gqa.11400.1.51_at Gqa.11400.1.51_at Gqa.11400.1.51_at Gqa.1675.1.51_at Gqa.1675.1.51_at Gqa.1630.1.51_at Gqa.1630.1.51_at Gqa.1630.1.51_at Gqa.1630.1.51_at Gqa.1630.1.51_at Gqa.17100.1.51_at Gqa.926.1.51_at Gqa.927.1.51_at Gqa.91147.2.2.51_at Gqa.91147.2.2.51_at Gqa.91147.2.2.51_at Gqa.91147.2.2.51_at Gqa.91147.2.2.51_at Gqa.91147.2.2.51_at Gqa.91147.2.2.51_at Gqa.91147.2.2.51_at Gqa.91147.2.2.51_at Gqa.9127.1.51_at Gqa.9127
	Finished 20NA, clone ChEST133n4 aminar to protein kinase related to Brap toroten kinases Finished 20NA, clone ChEST625621 LCN peptidase Netwinal domain and ring finger 3 almilar to hypothetical protein FL283749 (LCN peptidase N-terminal domain and ring finger 1) almilar to hypothetical protein FL283749 (LCN peptidase N-terminal domain and ring finger 1) almilar to hypothetical protein FL283749 (LCN peptidase N-terminal domain and ring finger 1) almilar to hypothetical protein FL283749 (LCN peptidase N-terminal domain and ring finger 1) almilar to hypothetical protein FL283749 (LCN peptidase N-terminal domain and ring finger 1) almilar to hypothetical protein FL283749 (LCN peptidase N-terminal domain and ring finger 1) almilar to hypothetical protein FL283749 (LCN peptidase N-terminal Protein hypothetical Protein ST35628210 maker factor, interaction 3 peptidase (Fl4pdel) Cucac, calon transport regulator kiel 1 (E. col) heat shock protein 25 [H4252] Cucac, calon transport regulator kiel 1 (E. col) heat shock protein 25 [H4252] Frinshed CDNA, chone ChEST856202 almilar to Hast-shock protein 105 KDa (Heat shock 110 KDa protein) almilar to Hast-shock protein 105 KDa (Heat shock 110 KDa protein) almilar to Hast-shock protein 105 KDa (Heat shock 110 KDa protein) almilar to JDA1 chaperone Homosystem-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1 BC2-associated athanogene 3 BC2-associated athanogene 3 BC2-associated athanogene 3 almilar to JDA1 chaperone haat shock protein 105 KDa (Heat shock 110 KDa protein) Finished CDNA, cone ChEST83241 almilar to JDA1 chaperone haat shock protein 105 KDa (Heat shock 110 KDa protein) Finished CDNA, cone ChEST83274 almilar to JDA1 chaperone haat shock protein 105 KDa (Heat shock 110 KDa protein) Finished CDNA, cone ChEST83749	NA signal transluction NA proteolysis proteolysis proteolysis proteolysis screated protein aignal transduction NA NA Call cycle sterol metabolism sterol metabolism sterol metabolism sterol metabolism sterol metabolism protein folding protein folding prot	Gqa.1157.2.1.51_at Gqa.M7.2666.1.51_a.t Gqa.M7.2666.1.51_at Gqa.M7.2666.1.51_at Gqa.M7.2064.1.51_at Gqa.M7.2064.1.51_at Gqa.M7.674.1.51_at Gqa.M7.674.1.51_at Gqa.11409.1.51_at Gqa.11409.1.51_at Gqa.1265.1.51_at
	Finished 20NA, clone ChESTI30n4 aimlar to protein kinase related to Parl protein kinases Finished 20NA, clone ChEST825621 (LON peptidase Netwinal domain and ring finger 3 aimlar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) aimlar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) aimlar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) aimlar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) aimlar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) aimlar to hypothetical protein FL23749 (LON peptidase N-terminal domain advylsie optidase adviking optigeptide 1 (publiary) protein phosphatase 2 (formerly 2A), regulatory subunit B*, alpha EST Finished CONA, clone ChEST80621 NetBML Prediction Finished CONA, clone ChEST80620 Clone ChEST80600 (EST80600) rundeer factor, interfixekin R regulated [E40p4] Chac, cation transport regulator-left [E colit) hast shock protein 25 [Hag25] Finished CONA, cone ChEST806020 aimlar to Mast shock protein 105 KDa (Hat shock 110 KDa protein) aimlar to Mast shock protein 105 KDa (Hat shock 110 KDa protein) aimlar to Hast-shock protein 105 KDa (Hat shock 110 KDa protein) aimlar to Hast-shock protein 105 KDa (Hat shock 110 KDa protein) aimlar to Hast-shock protein 105 KDa (Hat shock 110 KDa protein) aimlar to DAI shock protein 105 KDa (Hat shock 110 KDa protein) aimlar to pDAI shock protein 105 KDa (Hat shock 110 KDa protein) BC2-associated athanogenes 3 aimlar to pDAI shock protein 105 KDa (Hat shock 110 KDa protein) Alex (Hap40) honnidg, aud/amink A- disorgenase inducible, ubiquitin-kike domain member 1 BC2-associated athanogenes 3 aimlar to pDAI shock protein 105 KDa (Hat shock 110 KDa protein) Finated CONA, cone ChEST8224 aimlar to pDAI shock protein 105 KDa (Hat shock 110 KDa protein) Finated CONA, cone ChEST8224 KDA aimlar to bDAI shock protein 105 KDa (Hat shock 110 KDa protein) Finated CONA, cone ChEST8224 KDAI	NA signal transduction NA proteolysis proteolysis proteolysis secreated protein secreated protein secreated protein secreated protein secreated protein secreated protein sateral metabolism sterol metabolism sterol metabolism sterol metabolism sterol metabolism protein folding protein f	Gap.1157.2.1.51_at GapAH7.2564.1.51_a.t GapAH7.2664.1.51_a.t GapAH7.2664.1.51_at GapAH7.2664.2.151_at GapAH7.2674.1.51_at GapAH7.2474.1.51_at GapAH7.2474.1.51_at GapAH7.2474.1.51_at GapAH7.1475.1.51_at GapAH7.1478.1.51_at GapAH7.1390.1.51_at GapAH7.1391.51_at GapAH7.1351.51_at GapAH7.1351.51_at GapAH7.1351.51_at GapAH7.1351.51_at GapAH7.1351_a_1_at GapAH7.1351_a_1_at Ga
	Finished 20NA, clone ChEST133n4 similar to protein Share related to Fall protein kinases Finished 20NA, clone ChEST625621 (LON peptidase Netwrnial domain and ring finger 3 similar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL337429 Finished CNA, clone ChEST360511 Finished CNA, clone ChEST360510 Chalt clant hamoport fingular-like 1 (solubie) [HMG-CoA synthase] Finished CNA, clone ChEST360510 Chalt clant hamoport fingular-like 1 (E. col) Finished CNA, clone ChEST36020 and the theat shock protein 105 KDB (Heat shock 110 kDB protein) similar to Heat shock protein 105 KDB (Heat shock 110 kDB protein) similar to Heat shock protein 105 KDB (Heat shock 110 kDB protein) similar to Heat shock protein 105 KDB (Heat shock 110 kDB protein) similar to Heat shock protein 105 KDB (Heat shock 110 kDB protein) similar to Heat shock protein 105 KDB (Heat shock 110 kDB protein) similar to Heat shock protein 105 KDB (Heat shock 110 kDB protein) similar to Heat shock protein 105 KDB (Heat shock 110 kDB protein) similar to Heat shock protein 105 KDB (Heat shock 110 kDB protein) Finished CDNA, clangerone 3 BO22 associated athrongene 3 BO32 shock protein 105 KDB (Heat shock 110 KDB protein) Finished CDNA, clone CHEST30579 ENSMBL (Prodection Finished CDNA, clone CHEST30579 ENSMBL (Prodection) Finished CDNA, cl	NA signal transduction NA proteolysis proteolysis proteolysis sercested protein signal transduction NA NA NA Coll cycle sterol metabolism sterol metabolism sterol metabolism sterol metabolism sterol metabolism protein folding protein fold	$\label{eq:constraint} \begin{array}{l} \mbox{Gapa11722.1.S1_at} \\ \mbox{Gapa47A22656.1.S1_a,at} \\ \mbox{Gapa47A22656.1.S1_at} \\ \mbox{Gapa47A22674.1.S1_at} \\ \mbox{Gapa47A22574.1.S1_at} \\ Ga$
	Finished CDN, cone ChESTI36n4 similar to protein kinase related ba Rip protein kinases Finished CDN, cone ChESTI36562 LCN peptidase Netwinal domain and ring finger 3 similar to hypothetical protein FL28749 (LCN peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL28749 (LCN peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL28749 (LCN peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL28749 (LCN peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL28749 (LCN peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL28749 (LCN peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL28749 (LCN peptidase N-terminal domain Finished CDN, cone ChESTI3621 NENSMB, Prediction Finished CDN, cone ChESTI36201 finished CDN, cone ChESTI36020 finished	NA signal transduction NA proteolysis proteolysis proteolysis proteolysis proteolysis secreated protein signal transduction NA NA Call cycle aterd metabolism sterd metabolism sterd metabolism sterd metabolism sterd metabolism valender de transprotein notalin dolding protein folding protein folding pro	Gap.1157.2.1.51_at GapAH7.2564.1.51_a.t GapAH7.2664.1.51_at GapAH7.2664.2.51_at GapAH7.2664.2.51_at GapAH7.2664.2.51_at GapAH7.2674.1.51_at GapAH7.2074.1.51_at GapAH7
	Finished CDNA, clone ChEST133n4 aimlar to potieh kinase related to Palf potieh kinases Finished CDNA, clone ChEST625621 LON peptidase Netwinal domain and ring finger 3 aimlar to hypothetical potieh FL23734 (LON peptidase N-terminal domain and ring finger 1) aimlar to hypothetical potieh FL23744 (LON peptidase N-terminal domain and ring finger 1) aimlar to hypothetical potieh FL23744 (LON peptidase N-terminal domain and ring finger 1) aimlar to hypothetical potieh FL23744 (LON peptidase N-terminal domain and ring finger 1) aimlar to hypothetical potieh FL23744 (LON peptidase N-terminal domain and ring finger 1) aimlar to hypothetical potieh FL23744 (LON peptidase N-terminal domain and ring finger 1) aimlar to hypothetical potieh FL23744 (LON peptidase N-terminal domain and ring finger 1) aimlar to hypothetical potieh FL23744 (LON peptidase N-terminal domain and ring finger 1) aimlar to hypothetical potieh FL23744 (LON peptidase N-terminal domain and ring finger 1) finished CDNA, clone ChEST506/20 finished CDNA, clone ChEST506/20 f	NA signal transluction signal transluction proteolysis proteolysis proteolysis proteolysis acceated protein ascented protein signal transduction NA A add steri metabolism aterol metabolism aterol metabolism aterol metabolism aterol metabolism aterol metabolism aterol metabolism aterol metabolism aterol metabolism protein folding protein folding signal transduction DNA repleaton NA transcription NA NA NA NA NA NA	Gqa.1157.2.1.51_at Gqa.M7.2564.1.51_a.t Gqa.M7.2664.1.51_a.t Gqa.M7.2646.1.51_at Gqa.17046.1.51_at Gqa.17046.1.51_at Gqa.11409.1.51_at Gqa.11409.1.51_at Gqa.11409.1.51_at Gqa.1670.1.51_at Gqa.1670.1.51_at Gqa.1670.1.51_at Gqa.1670.1.51_at Gqa.1670.1.51_at Gqa.1670.1.51_at Gqa.1670.1.51_at Gqa.17109.1.51_at Gqa.921.51_at Gqa.921.51_at Gqa.921.51_at Gqa.921.51_at Gqa.922.1.51_at Gqa.911472.2.51_s_at Gqa.911472.2.51_s_at Gqa.911472.2.51_s_at Gqa.911472.2.51_s_at Gqa.911472.2.51_s_at Gqa.911472.2.51_s_at Gqa.9127.1.51_at Gqa.925.1.51_at Gqa.925.1.51_at Gqa.925.1.51_at Gqa.925.1.51_at Gqa.925.1.51_at Gqa.935.1.51_at Gqa.935.1.51_at Gqa.935.1.51_at Gqa.935.1.51_at Gqa.9445.1.51_at Gqa.945.1.51_at Gqa.945.1.51_at Gqa.945.1.51_at Gqa.945.1.51_at Gqa.945.1.51_at Gqa.945.1.51_at Gqa.945.1.51_at Gqa.945.1.51_at Gqa.945.1.51_at Gqa.945.1.51_at Gqa.945.1.51_at Gqa.945.1.51_at Gqa.945.1.51_at Gqa.945.1.51_at Gqa.945.1.51_at Gqa.945.1.51_at Gqa.945.1.51_at Gqa.
	Finished 20NA, clone ChEST133n4 similar to protein Name Protein Knames Finished 20NA, clone ChEST025621 LON peptidase Netwinal domain and ring finger 3 similar to hypothetical protein FL23749 (LON peptidase Networnial domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase Networnial domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase Networnial domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase Networnial domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase Networnial domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase Networnial domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase Networnial domain and ring finger 1) similar to Acone ChEST305(2) Finished LONA, clone ChEST305(2) StreSMBL Protein Finished LONA, clone ChEST304211 mader induced gene 1 [min;1] Calca clone transport regulate (Hapdi) Calca, calcin transport regulate Net 1 (E col) Finished CONA, clone ChEST30620 similar to Neta-Noto protein 105 Kia (Heat shock 110 KDa protein) similar to Neta-Noto protein 105 Kia (Heat shock 110 KDa protein) similar to Neta-Noto protein 105 Kia (Heat shock 110 KDa protein) similar to Heat-Noto protein 105 Kia (Heat shock 110 KDa protein) similar to JAlat-Noto protein 105 Kia (Heat shock 110 KDa protein) similar to JAlat-Noto protein 105 Kia (Heat shock 110 KDa protein) similar to JAlat-Noto protein 105 Kia (Heat shock 110 KDa protein) similar to JAlat-Noto protein 105 Kia (Heat shock 110 KDa protein) similar to JAlat-Noto protein 105 Kia (Heat shock 110 KDa protein) Similar to JAlat-Noto protein 105 Kia (Heat shock 110 KDa protein) Similar to JAlat-Noto protein 105 Kia (Heat shock 110 KDa protein) Finished CONA, clone ChEST3241 similar to JAlat Chaperone Net Meat-Noto protein 105 Kia (Heat shock 110 KDa protein) Finished CONA, clone ChEST3379 Net Similar to JAlat-Noto protein 105 Kia (Heat shock 110 KDa protein) Fini	NA signal transduction NA proteolysis proteolysis proteolysis proteolysis screated protein aignal transduction NA NA Call cycle aterol metabolism aterol metabolism aterol metabolism aterol metabolism aterol metabolism aterol metabolism aterol metabolism protein folding protein folding	Gqa.1157.2.1.51_at Gqa.M7.2666.1.51_at Gqa.M7.2666.1.51_at Gqa.M7.2666.1.51_at Gqa.M7.2066.1.51_at Gqa.M7.2067.1.51_at Gqa.M7.677.1.51_at Gqa.M7.677.1.51_at Gqa.M7.677.1.51_at Gqa.M7.677.1.51_at Gqa.M7.677.1.51_at Gqa.M7.2067.1.51_at Gqa.M7.2067.1.51_at Gqa.M7.2067.1.51_at Gqa.M7.2067.1.51_at Gqa.M7.1.606.1.51_at Gqa.M7.2067.1.51_at Gqa.M7.1.606.1.51_at Gqa.M7.1.606.1.51_at Gqa.M7.1.606.1.51_at Gqa.M7.1.606.1.51_at Gqa.M7.1.606.1.51_at Gqa.M7.1.606.1.51_at Gqa.M7.1.606.1.51_at Gqa.M7.1.606.1.51_at Gqa.M7.1.51_a
	Finished 20NA, clone ChESTI30n4 similar to protein kinase related to Parl protein kinases Finished 20NA, clone ChEST825621 LON peptidase Netwinal domain and ring finger 3 similar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) similar to hypothetical protein FL23749 (LON peptidase N-terminal domain and ring finger 1) similar to Machine achiving polypeptide 1 (publiary) protein phosphatase 2 (formerly 2A), regulatory subunit B*, sipha EST Finished CONA, clone ChEST80621 Nace Machine ChEST80600 (D) macher factor, interfacikin 7 segulated [E4p4] Chac, cation transport regulator-146 (E coli) hast shock protein 25 (Hag25) Finished CONA, cone ChEST80602 Similar to Machine Kop tretein 105 Kba (Haat shock 110 kBa protein) similar to Machine Kop tretein 105 Kba (Haat shock 110 kBa protein) similar to Machine Kop tretein 105 Kba (Haat shock 110 kBa protein) similar to Machine Kop tretein 105 Kba (Haat shock 110 kBa protein) similar to Machine Kop tretein 105 Kba (Haat shock 110 kBa protein) similar to Machine Kop tretein 105 Kba (Haat shock 110 kBa protein) similar to Machine Kop tretein 105 Kba (Haat shock 110 kBa protein) similar to Machine Kop tretein 105 Kba (Haat shock 110 kBa protein) similar to Machine Kop tretein 105 Kba (Haat shock 110 kBa protein) BC2-associated athanogenes 3 Berputti BC2-associated athanogenes 3 Berputti BC2-associated athanogenes 3 Berputti BC2-associated athanogenes 3 Berputti BC2-associated athanogenes 3 Berputti BC2-associated athanogenes 3 Berputti BC3-Berputti BC3-Berputti BC3-Berputti BC4 Berputti BC3-Berputti BC3-Berputti BC4 Berputti BC4 Berputti BC4 Berp	NA signal transduction NA proteolysis proteolysis proteolysis proteolysis secreated protein secreated protein secreated protein secreated protein secreated protein sateral metabolism ateral metabolism sterol metabolism sterol metabolism sterol metabolism protein folding protein folding NA franscripton protein folding NA franscripton protein folding NA franscripton protein folding NA franscripton NA franscripton NA NA NA NA NA NA NA NA NA NA NA NA NA	Gqa.1157.2.15.1_at Gqa.M47.2664.15.1_a. Gqa.M47.2644.15.1_a. Gqa.M47.2644.15.1_at Gqa.M47.2644.15.1_at Gqa.M47.2042.15.1_at Gqa.M47.2042.15.1_at Gqa.M47.2042.15.1_at Gqa.M47.2042.15.1_at Gqa.M47.1045.15.1_at Gqa.M47.114.15.1_at Gqa.M47.114.15.1_at Gqa.M47.114.15.1_at Gqa.M47.114.15.1_at Gqa.M47.114.15.1_at Gqa.M47.114.15.1_at Gqa.M47.114.15.1_at Gqa.M47.114.15.1_at Gqa.M47.114.15.1_at Gqa.M47.114.15.1_at Gqa.M47.114.15.1_at Gqa.M47.114.15.1_at Gqa.M47.114.15.1_at Gqa.M47.114.15.1_at Gqa.M47.114.15.1_at Gqa.M44.057.15.1_at Gqa.M44.057.15.1_at Gqa.M47.14.14.14 Gqa.M47.15.1.1.1 Gqa.M47.15.1.1.1 Gqa.M44.057.15.1_at Gqa.



PNAS PNAS



Fig. S4. (Continued)

SANG VAS



Fig. S4. Expression profiles of ATF4-, ATF6-, XBP1-, and SREBP-target genes in the pineal gland. (A) ATF4-, ATF6-, and XBP1-target genes. (B) SREBP-target genes. Dark-kept animals were exposed to the 1-h light pulse (open bars) from CT6, CT14, or CT22, or kept in the dark as a control (solid bars). The GeneChip profiles of the genes listed in Figs. 2C and 3B are displayed (mean with variation, n = 2).

DNA C



Fig. S5. Daily expression profile and feeding response of spliced Xbp1 mRNA levels. (A) Daily expression profile. Mice were housed in 12-h light/12-h dark cycles with foods and water freely available, and the liver was isolated at the indicated time point. (B) Feeding response. Mice were housed in 12-h light/12-h dark cycles with water freely available and foods available only at nighttime (ZT12–24) for a week. On day 7, foods were provided (open bars) or not (solid bars) from ZT12, and the liver was isolated at the indicated time point. Relative mRNA levels of Xbp1s and Xbp1t were determined by RT-PCR analysis. The lowest value (A) or the value at ZT12 (B) was set to 1. Data are the mean \pm SEM (n = 3).



Fig. S6. Light-response of *Srebp-1* and *Srebp-2* genes in the pineal gland. (*A*) Expression of *Srebp-1* and *Srebp-2* in the pineal gland and liver. Total RNA extracted from the tissues were subjected to reverse transcription with (+) or without (-) reverse transcriptase (RTase), followed by PCR amplification of *Srebp-1*, *Srebp-2*, *Pinopsin*, *NAT*, and *Tbp*. *Pinopsin* and *NAT* were expressed in the pineal gland. (*B*) Effect of light on the mRNA levels of *Srebp-1* and *Srebp-2*. Darkkept animals were exposed to a 1-h light pulse (open bars) or kept in the dark for 1 h (solid bars) at each time point, and the pineal glands were isolated for RT-PCR analysis as in Fig. 2A.



Fig. S7. A model for the role of SREBP in the light-input pathway of the pineal circadian clock. See text for details.



Fig. S8. Steroid production in the adrenal gland and 7α -hydroxypregnenolone release from the female pineal gland. (A) Production of steroids from pregnenolone in adrenal gland and pineal gland lysates. The homogenate from the adrenal gland or the pineal gland were incubated with [³H]pregnenolone for indicated time periods, and each extract was subjected to the reversed-phase HPLC. The elution positions of metabolites are indicated by vertical broken lines. (*B*) Comparison of 7α -hydroxypregnenolone release from the pineal glands between male and female chicks. The chicks were exposed to 20-min light pulse (\approx 300 lx with white fluorescent lamps) from CT14, and then the pineal glands were isolated and cultured in 450 µL of medium as a pool (8 pineal glands per well) for 3 h under the light condition. For dark control group, all procedures were performed in the dark. The amounts of 7α -hydroxypregnenolone released into the medium were measured by gas chromatography/mass spectrometric (GC-MS) analysis. Data are the mean \pm SEM (n = 4-5). **P < 0.01 and ***P < 0.005 by Student's t test. Data for the male sample are reproduced from Fig. 5E.

Table S1. Primers and cycle numbers for PCR analyses

Gene	Forward primer sequence (5'->3')	Reverse primer sequence (5'->3')	PCR cycle numbers
Per2	GGAAGTCCTTGCAGTGCATAC	ACAGGAAGCGGATATGCAG	24
E4bp4	CCTTTCTCAGTTCAGGTGAC	TGAAATGACATCATGAGTCCAG	21
StarD4	TACCACAGCATCGCCGACAG	TCCTTAAGAGGGACGCAGAACC	24
Insig-1	TGCCCAAAGGAAGTAGATCG	AAAGCCCTGACTCAAACAGG	20
Srebp-1	GTACCTTCAGCTGCTCAACG	TCCTGCTTGCTCAACATGG	26
Srebp-2	CTAAGCAGTCTGGTTGACAACG	AGAGGCACAGGAATGTCAGG	24
Pinopsin	CTGAAGGGTTGAGGACATCG	CTGCAGTGACATCTGCATGG	24
NAT	ATGAGATCCGCCACTTCCTAAC	AATCCTCGCACATGAGCACG	21
StAR	AATCACTCAGCATCCTCGG	GGACCTGGTTGATGATGGTC	27
P450scc	TGCAGGTTGGTCTCTACGC	CTCCAGGATGTGCATGAGG	24
Ρ4507α	ATGAACATTCGCATCAGCC	TCATCTCATTCATTGCGAGG	26
Tbp	GTCGAATATAATCCCAAGCG	TCTGCTCGAACTTTAGCACC	24
Hsp25	CCAAGGATGGAGCTGTCAGC	CGATGCAGACCGTTGTTCC	*
Hsp70	ACCGAAACCAGATGGCAGAG	TTGTGACAATCGGGTTGCAG	*
Herpud1	ACGTCGGTGAGCTTGAGTCC	CAGTGAAGGCCAGAGAAATGC	*
Hspa5	ATCAGAATCGGCTAACACCAGAG	TCCTCAGCAAACTTCTCAGCATC	*
Xbp1s	GAGTCCGCAGCAGGTG	ACTGCCATCAGAATCCATG	*
Xbp1t	AGTGCGAGTCTACGGATGTGAAG	CCGGTCACCAACCTGATGTC	*
Tbp	AGCAAGGAAGTACGCAAGAGTTG	AGCTGCCCACCATGTTCTG	*
Mouse Xbp1s	GAGTCCGCAGCAGGTG	GTGTCAGAGTCCATGGGA	*
Mouse Xbp1t	AAGAACACGCTTGGGAATGG	ACTCCCCTTGGCCTCCAC	*
Mouse Gapdh	TGCACCACCAACTGCTTAGC	ACAGTCTTCTGGGTGGCAGTG	*

*Real-time PCR.

PNAS PNAS