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Circulation Research 2011, 109:1105-1114: originally published online September 15, 2011 doi: 10.1161/CIRCRESAHA.111.251843 Circulation Research is published by the American Heart Association. 7272 Greenville Avenue, Dallas, TX 72514

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Data Supplement (unedited) at: http://circres.ahajournals.org/content/suppl/2011/09/15/CIRCRESAHA.111.251843.DC1.html

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# Terminal Differentiation, Advanced Organotypic Maturation, and Modeling of Hypertrophic Growth in Engineered Heart Tissue

Malte Tiburcy,\* Michael Didié,\* Oliver Boy, Peter Christalla, Stephan Döker, Hiroshi Naito, Bijoy Chandapillai Karikkineth, Ali El-Armouche, Michael Grimm, Monika Nose, Thomas Eschenhagen, Anke Zieseniss, Doerthe M. Katschinksi, Nazha Hamdani, Wolfgang A. Linke, Xiaoke Yin, Manuel Mayr, Wolfram-Hubertus Zimmermann

- <u>Rationale:</u> Cardiac tissue engineering should provide "realistic" in vitro heart muscle models and surrogate tissue for myocardial repair. For either application, engineered myocardium should display features of native myocardium, including terminal differentiation, organotypic maturation, and hypertrophic growth.
- <u>Objective</u>: To test the hypothesis that 3D-engineered heart tissue (EHT) culture supports (1) terminal differentiation as well as (2) organotypic assembly and maturation of immature cardiomyocytes, and (3) constitutes a methodological platform to investigate mechanisms underlying hypertrophic growth.
- <u>Methods and Results</u>: We generated EHTs from neonatal rat cardiomyocytes and compared morphological and molecular properties of EHT and native myocardium from fetal, neonatal, and adult rats. We made the following key observations: cardiomyocytes in EHT (1) gained a high level of binucleation in the absence of notable cytokinesis, (2) regained a rod-shape and anisotropic sarcomere organization, (3) demonstrated a fetal-to-adult gene expression pattern, and (4) responded to distinct hypertrophic stimuli with concentric or eccentric hypertrophy and reexpression of fetal genes. The process of terminal differentiation and maturation (culture days 7–12) was preceded by a tissue consolidation phase (culture days 0–7) with substantial cardiomyocyte apoptosis and dynamic extracellular matrix restructuring.
- <u>Conclusions</u>: This study documents the propensity of immature cardiomyocytes to terminally differentiate and mature in EHT in a remarkably organotypic manner. It moreover provides the rationale for the utility of the EHT technology as a methodological bridge between 2D cell culture and animal models. (*Circ Res.* 2011;109:1105-1114.)

Key Words: cardiac myocytes ■ caspase activation ■ extracellular matrix ■ maturation ■ hypertrophy ■ sarcomere ■ tissue engineering

Different myocardial tissue engineering formats have been developed throughout the past decade.<sup>1</sup> However, a low degree of cell maturation remains a key caveat in cardiac muscle engineering. A detailed understanding of "developmental" processes in tissue engineered myocardium probably is essential to guide tissue formation and maturation in vitro and to enhance the applicability of tissue engineered myocardium in substance screening, target validation, and tissue repair.

Normal heart muscle growth encompasses processes of terminal differentiation and maturation by hypertrophic growth, leading to the formation of binucleated and rodshaped myocytes.<sup>2</sup> Physiological maturation entails a characteristic shift in gene expression, including a reduction of transcripts encoding for fetal isoforms of myofibrillar proteins while the proportion of adult isoforms increases.<sup>3</sup> Terminal differentiation, for example, withdrawal from the cell cycle, is another hallmark of advanced maturation already reached very early during development.<sup>4</sup>

Cardiomyocyte monolayer cultures show neither the distinct morphological (rod-shaped) nor the molecular (adult gene expression program) make-up of mature myocytes,<sup>5–7</sup>

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Original received July 5, 2011; revision received August 22, 2011; accepted September 7, 2011. In August 2011, the average time from submission to first decision for all original research papers submitted to *Circulation Research* was 13.5 days.

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Non-standard Abbreviations and Acronyms									
ANP	atrial natriuretic peptide								
DAPI	4',6-diamidino-2-phenylindole								
ECM	extracellular matrix								
EHT	engineered heart tissue								
МНС	myosin heavy chain								
MLC2v	myosin light chain, ventricular isoform								
MMP	matrix metalloprotease								
PHD	prolyl-4-hydroxylase domain enzyme								
TIMP	tissue inhibitor of MMP								
VEGF	vascular endothelial growth factor								

probably as a consequence of the lack of a 3D growth environment and inappropriate biomechanical loading. Despite some evidence for advanced maturation in 3D tissue engineering models, it remains unclear whether cardiomyocytes in tissue engineered myocardium can, and if so to what extent, develop "physiologically" ex vivo.<sup>8,9</sup>

Three fundamentally different myocardial tissue engineering concepts are presently explored: (1) the classic approach involves cell seeding on preformed scaffold material<sup>10–14</sup>; (2) an alternative strategy is based on stacking cell sheets to generate multilayered muscle constructs<sup>15</sup>; (3) we have developed another method, taking advantage of the inherent capacity of immature cardiomyocytes to reassemble into spontaneously beating tissue if maintained at high density in a spatially defined culture environment under defined load.<sup>9,16,17</sup> This cell entrapment method was further refined yielding engineered heart tissues (EHTs) with functional properties of native myocardium.<sup>9</sup>

In the present study, we demonstrate that EHT cultures can support terminal differentiation and tissue-like cardiomyocyte maturation. This finding is underscored by the similarity of morphological and molecular features of EHT- and postnatal heart-derived cardiomyocytes. Interestingly, the process of cardiomyocyte maturation and EHT-development showed 2 distinct phases: (1) a consolidation phase during culture days 0-7 with high levels of apoptotic cell death as well as extracellular matrix (ECM) degradation and (2) a maturation phase during culture days 7-12 with myocyte binucleation, formation of anisotropically organized sarcomeres in preferentially rod-shaped cardiomyocytes, a shift from fetalskeletal to adult-cardiac actin transcript expression, and ECM build-up. Exposure to different hypertrophic stimuli during the maturation phase elicited distinct hypertrophic phenotypes, that is, concentric or eccentric hypertrophy.

#### Methods

#### **EHT Construction**

EHTs were prepared from collagen type I, Matrigel, as well as neonatal rat heart cells  $(2.5 \times 10^6)$  and cultured for 12 days.<sup>9</sup>

## <sup>3</sup>H-Thymidine Incorporation

EHTs were labeled with 1  $\mu$ Ci/mL <sup>3</sup>H-thymidine for 6 hours on the indicated culture days. DNA was prepared using standard procedures and subjected to liquid scintillation counting.

#### **Cell Isolation**

EHTs or hearts were digested with Liberase Blendzyme III in the presence of 30 mmol/L 2,3-butanedione monoxime at 37°C to prepare cardiomyocytes for morphological assessment by confocal laser scanning microscopy and flow cytometry.

#### One-Dimensional Electrophoresis and Immunoblotting

EHT protein was separated by SDS-PAGE. For detection of myosin heavy chain (MHC), isoforms gels were stained overnight with SYPRO Ruby. Blots were probed with monoclonal antibodies directed against indicated proteins and developed with ECL-plus.

#### Two-Dimensional Electrophoresis and Nanoflow Liquid Chromatography Tandem Mass Spectrometry

Protein extracts were separated by 2D electrophoresis. Protein spots were excised and enzymatically degraded. Peptides were separated by a nanoflow HPLC system on a reverse-phase column and applied to an LTQ ion-trap mass spectrometer.

#### <sup>3</sup>H-Phenylalanine and <sup>3</sup>H-Proline Incorporation

EHTs were labeled with 1  $\mu$ Ci/mL <sup>3</sup>H-phenylalanine or <sup>3</sup>H-proline as indicated. Protein was precipitated in 10% ice-cold trichloroacetic acid at 4°C overnight and subjected to liquid scintillation counting.

## <sup>35</sup>S-Cysteine/-Methionine Incorporation and Autoradiography

EHTs were labeled with 100  $\mu$ Ci/mL <sup>35</sup>S-cysteine/-methionine for 18 hours on the indicated culture days and proteins were separated by SDS-PAGE. Gels were stained with Coomassie blue, immersed in Amplify Fluorographic solution (Amersham Biosciences), vacuum dried, and subjected to autoradiography.

An expanded Methods section can be found online at http://circres.ahajournals.org.

#### **Results**

#### **Construction of Spontaneously Contracting EHT**

We generated spontaneously contracting EHTs from an initially liquid reconstitution mixture composed of enzymatically dispersed neonatal rat heart cells, collagen type I, and basement membrane proteins (Matrigel).<sup>9</sup> Cell clusters within condensing EHTs started to beat within 2–3 culture days (Online Video I). On culture day 7, all EHTs contracted spontaneously and in unison (Online Video II). After 12 culture days, EHTs demonstrated a solid composition and vigorous contractions (Online Video II).

#### Hypertrophic Growth of Cardiomyocytes in EHT

The changes in EHT morphology and function prompted us to assess indices of cell proliferation and hypertrophy. We observed a marked reduction in cell number to 30% of the input cells between EHT culture day 0 (day of EHT construction) and day 12 ( $2.5 \times 10^6$  versus  $0.8 \pm 0.03 \times 10^6$  cells/EHT; n=10; Figure 1A). Despite the cell loss, DNA content decreased only by 42% ( $45 \pm 3$  versus  $26 \pm 1 \mu$ g/EHT; n=17–20; Figure 1B), implying a relative increase of DNA content per cell ( $\approx 18$  versus  $\approx 32$  pg DNA/cell on culture days 0 and 12, respectively). Further analysis of cardiomyocyte ( $\alpha$ -actinin–positive; Online Figure I, A) and fibroblast (vimentin-positive; Online Figure I, B) quantity indicated that the initial cell loss was mainly the consequence of high cardiomyocyte loss while fibroblast content remained stable



Figure 1. Cell loss and DNA synthesis during EHT culture. A, Cell number at the time of EHT casting (culture day 0) and on subsequent culture days 3, 7, and 12 (n=10/time point). B, DNA content in EHTs on culture days 0 (n=18), 3 (n=20), 7 (n=17), and 12 (n=20). C, Number of cardiomyocytes (actinin-positive cells) and fibroblasts (vimentin-positive cells) at the time of EHT casting (culture day 0, n=8) and on subsequent culture days 3 (n=4), 7 (n=6), and 12 (n=4), assessed by flow cytometry after enzymatic dispersion of EHTs. D, DNA synthesis (S-phase) in cardiomyocytes and fibroblasts in EHT on culture days 0 (n=6), 3 (n=4), 7 (n=6), and 12 (n=4), assessed by flow cytometry in DAPI-stained actinin- and vimentin-positive cells. E, <sup>3</sup>H-thymidine incorporation in EHTs on culture days 0, 1, 3, 5, 7, 9, 11, and 12 (n=9/time point). F, Number of nuclei in neonatal rat heart-derived (postnatal days 1-3, n=60; white bar) and EHT-derived myocytes on culture day 12 (black bars; n=4 EHTs, 30-40 cells each); inset: example of a binucleated cardiomyocyte: bar: 10  $\mu$ m. \*P<0.05 versus day 0 (A through C); \*P<0.05 versus cardiomyocytes day 0 and §P<0.05 versus fibroblasts day 0 (D); ANOVA followed by Bonferroni multiple comparison test.

(Figure 1C). Cell cycle activity assessed by flow cytometry after 4',6-diamidino-2-phenylindole (DAPI) labeling identified highest levels of DNA-synthesis in fibroblasts ( $17\pm1\%$ ) and cardiomyocytes ( $9\pm0.2\%$ ) on culture day 0 with lower but constant DNA synthesis levels during culture days 3–12 (fibroblasts: 7% to 10%; cardiomyocytes: 3% to 5%; n=4-8; Figure 1D). Interestingly, <sup>3</sup>H-thymidine incorporation dropped markedly (P<0.05) during the first 24 hours of EHT culture to increase first slowly (until culture day 5) and then markedly (P<0.05) on culture days 7–12 (Figure 1E). The steep increase in DNA synthesis in the absence of increasing cell numbers appeared to be the consequence of (1) cardiomyocyte binucleation ( $37\pm2\%$ ; n=4 EHTs, 30-40 cells each; Figure 1F) and (2) enhanced nuclear DNA content (polyploidy) in a subset of cardiomyocytes (>2N:  $14\pm1\%$ ,

n=4) in advanced EHT cultures (Online Figure II). These properties, together with a high RNA/DNA ratio and <sup>3</sup>Hphenylalanine incorporation (Online Figure III) appear to be signs of terminal differentiation and hypertrophic growth, suggesting advanced organotypic maturation in particular during late EHT culture.

## Apoptotic Cell Death in Early EHT

The marked cell loss in EHT (Figure 1A) led us to investigate whether this was a consequence of apoptosis and represents a particular shortcoming of EHT versus conventional 2D cultures. Activated caspase-3, a surrogate for apoptosis, was especially high during early EHT culture (Figure 2A and Online Video IV). In agreement with this, high proapoptotic bax (Figure 2B) and low antiapoptotic Bcl-2 (Figure 2C) transcript abundances were observed, resulting in a markedly elevated bax/Bcl-2 ratio (Figure 2D). Notably, parallel cultures of EHT versus 2D showed similar levels of apoptosis (analyzed by flow cytometry), Trypan blue exclusion, and drop in cardiomyocyte number (Online Figure IV, A through C), collectively arguing against a unique apoptotic burden in EHT.

#### Lack of Evidence for Hypoxia in EHT

Hypoxia has been suggested as a limitation in tissue engineering and could have triggered apoptotic cell death. Surprisingly, we did not observe a regulation of highly sensitive hypoxia-response genes, for example, prolyl-4-hydroxylase domain isoforms 2 and 3 (prolyl-4-hydroxylase domain enzyme; PHD2/PHD3) mRNA and hypoxia-inducible factor-1 $\alpha$  (HIF-1 $\alpha$ ) protein (Figure 3A through 3C). This led us to conclude that cells sensed normoxic conditions comparable to physiological tissue conditions throughout EHT culture and that elevated VEGF-A transcripts observed in late EHT culture (Figure 3D) were unrelated to hypoxia.

#### **Sarcomere Maturation in EHT**

A hallmark of maturation in terminally differentiated cardiomyocytes is the shift from a fetal to an adult gene expression program. This encompasses an increase in  $\alpha$ -cardiac ( $\alpha$ -cd) actin and a decrease in  $\alpha$ -skeletal ( $\alpha$ -sk) actin transcript concentration<sup>10,18</sup> as well as a shift from  $\beta$ -(fetal/slow)-MHC to  $\alpha$ -(adult/fast)-MHC in rodents.<sup>3,18</sup> We could indeed observe an increase in  $\alpha$ -cd actin and a parallel decrease in  $\alpha$ -sk actin transcripts (Figure 4A and 4B), leading to an overall increase in total *a*-sarcomeric actin protein in late EHTcultures (Figure 4C). In contrast,  $\alpha$ -MHC transcript expression was unchanged, whereas  $\beta$ -MHC transcripts were elevated, resulting in a lower  $\alpha$ -/ $\beta$ -MHC transcript ratio in EHT as compared with adult myocardium (7±2 versus 88±19fold n=10/9; Figure 4D through 4F). Notably, also on protein level we identified a  $4\pm0.8$ -fold (n=8)  $\alpha$ -MHC excess in day 12 EHT (Figure 4F, inset). Direct comparison of atrial natriuretic peptide (ANP), a-sk actin, and a-cd actin transcript abundance in monolayer and EHT cultures documented that so called fetal genes (ANP,  $\alpha$ -sk actin) were more abundant in monolayer as compared with EHT cultures (Online Figure V).



**Figure 2.** Apoptosis as main cause of cell death in EHT. **A**, Active caspase-3 (red) in EHTs; **bottom right**: percentage of caspase-positive cells at individual time points (green: f-actin; blue: DAPI-labeled nuclei; bars: 50  $\mu$ m; refer also to Online Video IV). **B**, Bax (n=10/ time point), and **C**, Bcl-2 (n=10/time point) transcripts per GAPDH transcript. **D**, Bax/Bcl-2 transcript ratio(n=10/time point). \**P*<0.05 versus day 0; ANOVA followed by Bonferroni multiple comparison test.

#### **Dissection of the EHT Proteome**

Increasing fluorescence intensity after  $\alpha$ -actinin immunolabeling (in particular in day-12, EHT-derived cardiomyocytes; Online Figure I, A) provided additional evidence for tissue maturation. Subsequently, we performed proteome analyses to obtain a more comprehensive snapshot of the EHT proteome on culture days 0 and 12 (Figure 5A). The identity of a select set of proteins was confirmed by mass spectrometry (Online Table I). In agreement with the notion of advanced organotypic and in particular ventricular maturation in EHT, we observed a markedly enhanced level of the ventricular isoform of myosin light chain (MLC2v) protein per cardiomyocyte in day 12 versus day 0 EHTs (Figure 5B). Robust detection of tropomyosin isoforms, desmin, and M-type creatine kinase provided further evidence for the presence of cardiomyocytes with an advanced degree of maturation. Vimentin protein, characteristically expressed in fibroblasts, did not significantly change during EHT culture (Figure 5C), indicating phenotypic stability in this most abundant cellular constituent of EHT.

#### Structural Properties of EHT-Derived Cardiomyocytes

The shape and size of cardiomyocytes changed dramatically during EHT maturation from round and unstructured directly after isolation (mean diameter:  $10\pm0.2 \ \mu$ m; volume:  $570\pm32 \ \mu$ m<sup>3</sup>, n=60) to rod-shaped and clearly cross-striated with sarcomeres in registry in 12-day-old EHTs (mean diameter:  $5.8\pm0.1 \ \mu$ m, length:  $72\pm2 \ \mu$ m, volume:  $2,040\pm120 \ \mu$ m<sup>3</sup>, n=113; Figure 6). Compared with cardiomyocytes from 12-day-old rats, EHT-derived cardiomyocytes acquired a similar length but were thinner and consequently less voluminous (mean diameter:  $9.2\pm0.1 \ \mu$ m, length:  $67\pm1 \ \mu$ m, volume:  $4,724\pm154 \ \mu$ m<sup>3</sup>, n=3 hearts, 80–100 cells each; Figure 6). Myocytes from adult rats were clearly larger than EHT- and 12-day-old, rat heart-derived myocytes (mean



Figure 3. Lack of signs of intense hypoxia in EHT culture. A, PHD2, and B, PHD3 transcripts per GAPDH transcript during EHT culture (n=4/ time point). **C**, HIF-1 $\alpha$  protein in EHT at different time points in culture, in isolated cardiomyocytes (CM), and cell free EHT matrix (CFM, composed of collagen and Matrigel); note that CFM is high in HIF-1 $\alpha$  protein (extracellular), which is gradually washed out during EHT culture; calsequestrin 2 (CSQ2) is displayed as cardiomyocyte housekeeping protein; equal amounts of protein were loaded. D, VEGF-A transcripts per GAPDH transcript (n=10) during EHT culture. \*P<0.05 versus EHT day 0; ANOVA followed by Bonferroni multiple comparison test.





**Figure 4.** Molecular evidence for myocardial maturation in EHT. **A**,  $\alpha$ -Cardiac (cd) actin (n=8–10/time point), and **B**,  $\alpha$ -skeletal (sk) actin (n=7–10/time point) transcripts per calsequestrin 2 (CSQ2) transcript in EHT and rat myocardium. **C**,  $\alpha$ -Sarcomeric actin protein content in EHT (indexed to CSQ2; n=9–12/time point). **D**,  $\alpha$ -MHC (n=9–10/time point), and **E**,  $\beta$ -MHC (n=7–10/time point) transcripts per CSQ2 transcript in EHT and rat myocardium. **F**,  $\alpha$ -/ $\beta$ -MHC transcript ratio in EHT and rat myocardium (n=10/time point). **Inset**: representative SYPRO Ruby-stained PAGE indicating  $\alpha$ -/ $\beta$ -MHC protein composition in day 12 EHT. \**P*<0.05 versus EHT day 0 (**A**, **B**, **E**, and **F**) and EHT day 3 (**C**) or between indicated columns (in **B**, **D**, and **F**); ANOVA followed by Bonferroni multiple comparison test.

diameter:  $24.7\pm0.4 \ \mu\text{m}$ , length:  $114\pm1 \ \mu\text{m}$ , volume:  $57\ 102\pm1735 \ \mu\text{m}^3$ , n=3 hearts, 80–100 cells each; Figure 6). Mean diastolic sarcomere length was similar in all groups (EHT-derived:  $1.85\pm0.04 \ \mu\text{m}$  [n=31]; day-12 rat heart:  $1.83\pm0.02 \ \mu\text{m}$  [n=28]; adult rat heart:  $1.84\pm0.02 \ \mu\text{m}$ , [n=27]).

#### Organotypic Response of EHT to Hypertrophic Stimuli

We cultured EHTs during the maturation phase (culture days 7–12) in the presence of phenylephrine (20  $\mu$ mol/L; PE) and angiotensin II (100 nmol/L; Ang) to assess their responsive-



**Figure 5.** EHT proteome. **A**, Proteins were isolated from EHT (culture days 0 and 12) and separated by 2D electrophoresis using an immobilized pH gradient strip (3–10 nonlinear); overlay of day 0 EHT (Cy3-labeled; green) and day 12 EHT (Cy5-labeled; red); overlay: yellow. **B**, Abundance of ventricular MLC2 isoform (MLC2v) in day 0 and day 12 EHT (normalized to GAPDH and cardiomyocyte [CM] number; n=3/time-point). **C**, Abundance of vimentin in day 0 and day 12 EHT (normalized to GAPDH and nonmyocyte [NM] number; n=3/time point). \**P*<0.05; 2-tailed unpaired Student *t* test.

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**Figure 6.** Hypertrophic cardiomyocyte growth in EHT and native heart. **A**, Length, **B**, mean width, and **C**, volume of EHT-derived cells at culture day 0 (n=60 cells) and day 12: (1) untreated (n=113 cells), (2) simulated neurohumoral overstimulation with phenylephrine ( $20 \ \mu$ mol/L; PE) and angiotensin-2 (100 nmol/L; Ang; n=111 cells), and (3) in the presence of hypertrophy-inducing serum (HIS; 10%; n=153 cells) during EHT culture days 7–12. Cell dimensions from postpartum day 12 (n=3 hearts, 80–100 cells each) and adult (n=3 hearts, 80–100 cells each) rat hearts are displayed for comparison. **D**, Immunostaining of cardiomyocytes from EHT culture days 0, 3, and 12 (untreated, PE/Ang, and HIS) and rat myocardium. Red:  $\alpha$ -actinin, blue: DAPI-labeled nuclei; bar: 20  $\mu$ m. The image is an assembly of individual photographs of representative cells from each group. \**P*<0.05 versus day-12 native heart; §*P*<0.05 versus EHT day 0; ANOVA followed by Bonferroni multiple comparison test.

ness to simulated neurohumoral overstimulation. Compared with standard medium conditions (EHT, day 12), we observed a concentric hypertrophy at the cellular level with a marked increase in cell width without major changes in cell length (Figure 6). During the course of these experiments, we also identified dramatic differences in responses to serum (10% in the culture medium) with "hypertrophy-inducing serum" (HIS), leading to a remarkable elongation of cardiomyocytes without major changes in cell width (Figure 6).

These findings highlight the necessity for rigorous serum screens but also indicate the opportunity to use EHT for phenotypic screens to identify hypertrophy inducing secretomes and/or specific hypertrophic factors. Importantly, the phenotypic changes induced by PE/Ang and HIS were accompanied by distinct patterns of hypertrophic gene expression with particularly high ANP in HIS and low  $\alpha/\beta$ -MHC ratio as well as high  $\alpha$ -sk actin transcript abundance in PE/Ang treated EHTs (Figure 7).



**Figure 7.** Fetal gene transcription program in "hypertrophic" EHT. **A**, ANP transcripts per calsequestrin 2 (CSQ2) transcript. **B**,  $\alpha$ -/ $\beta$ -MHC transcript ratio. **C**,  $\alpha$ -skeletal (sk) actin transcripts per CSQ2 transcript. **D**,  $\alpha$ -cardiac (cd) actin transcripts per CSQ2 transcript. **White bars:** control EHTs; **black bars:** EHTs stimulated with 20  $\mu$ mol/L phenylephrine and 100 nmol/L angiotensin-2 during culture days 7–12; **gray bars:** EHTs stimulated with HIS (10%) during culture days 7–12. Group size: n=7–10. \**P*<0.05 versus control (Ctr); ANOVA followed by Bonferroni multiple comparison test.



Figure 8. Intense ECM restructuring during EHT culture. A, Protein content of EHT at different time points during culture. The day 0 column indicates the contribution of collagen, culture medium ECM, and cell suspension (contains 23% cell protein and 77% serum protein) fractions to total EHT protein content at the time of casting. **B**, <sup>3</sup>H-proline incorporation in EHTs during culture days 0 to 3, 3-7, and 7-12 (n=7-8). C, PAGE separation of proteins from neonatal rat heart cells (Cells), collagen (Coll.), ECM, horse serum (HS), chick embryo extract (CEE), and EHT from culture days 0, 3, 7, and 12. EHTs were labeled with <sup>35</sup>S-cysteine/methionine on culture days 3, 7, and 12 (upper left panel: Coomassie-stained PAGE; lower left panel: autoradiography; right panel: superimposition of Coomassie-stained PAGE and corresponding autoradiography; 25, 50, 75  $\mu$ g of pooled day 3, 7, and 12 EHT-protein were loaded as reference). D, Collagen type I (Coll-I) and collagen type III (Coll-III) transcripts per GAPDH transcript in EHT and rat myocardium (n=8-10/time-point). **E**, Sirius red staining of collagen fibers: thick collagen fibers (orange); thin, newly synthesized collagen fibers (green; highlighted in inset; bars: 10 μm). F, Ultrastructure of collagen fiber in day 12 EHT with characteristic cross-striations; bar: 100 nm. \*P<0.05 versus EHT day 3 (A), EHT days 0 to 3 (B), or EHT day 0 (D); ANOVA followed by Bonferroni multiple comparison test.

**Intense Matrix Restructuring During EHT Culture** At the time of casting, EHT contained  $0.5\pm0.05$  mg rat tail collagen, 1.1±0.02 mg extracellular basement membrane protein, 2.7±0.1 mg serum protein (in 210 µL DMEM with 20% horse serum and 4% chick embryo extract), and a cell suspension containing 2.2 $\pm$ 0.1 mg proteins (2.5 $\times$ 10<sup>6</sup> cells in 377 µL DMEM with 10% fetal calf serum: cells, 0.5 mg; serum, 1.7 mg; n=4 in each group; Figure 8A). The nominal EHT protein content decreased from  $6.4\pm0.1$  mg (n=4) to  $0.8\pm0.05$  mg during culture (n=4; Figure 8A) despite elevated incorporation of <sup>3</sup>H-phenylalanine (Online Figure III, B), <sup>3</sup>H-proline (Figure 8B), and <sup>35</sup>S-methionine/cysteine (Figure 8C). Experiments with the latter isotope mixture demonstrated pronounced incorporation especially in 40-kDa and >200-kDa proteins probably resembling actin (molecular weight: 43 kDa; see also Figure 4C) and myosin/collagen (molecular weight: 220/290 kDa). High <sup>3</sup>H-proline incorporation (Figure 8B) and high collagen type I/III transcript levels (Figure 8D) at later stages of EHT culture provided further evidence for endogenous ECM synthesis during the EHT maturation phase (culture days 7-12). Sirius red staining documented thick collagen fibers (orange in polarized light) aligned along the major force axis in 12-day-old EHTs and thin collagen fibers (green in polarized light), which represent freshly synthesized collagen (Figure 8E). Additional evidence for de novo collagen matrix production stems from transmission electron microcopy, which identified cross-striated mature collagen (Figure 8F), being absent in the original collagen hydrogel. Cell loss (Figure 1A) and matrix disaggregation were apparently key factors for EHT protein loss, especially during EHT consolidation (culture days 0-7). Upregulation of matrix metalloproteinases (MMP-2 and MMP-14; Online Figure VI, A and B) and their tissue inhibitors (TIMP-1 and TIMP-2; Online Figure VI, C and D) supported the hypothesis of intense matrix restructuring. MMP-3 and MMP-13 could not be reliably detected in

neonatal rat heart cells (Ct values: >40 [MMP-3] and >35 [MMP-13]; n=10/target), but were clearly present at EHTculture day 3 (Ct values: 28 [MMP-3] and 25 [MMP-13]; n=10/target), supporting the general concept of strong MMPbased matrix remodeling, especially at early time points of EHT culture.

#### Discussion

We investigated the hypothesis that immature rat cardiomyocytes undergo terminal differentiation and a process of advanced organotypic maturation in 3D EHT cultures and made the following key observations: (1) cardiomyocytes matured in EHT in a partially organotypic manner as indicated by the formation of a clearly anisotropic and cross striated rod-shaped cell morphology, abundant binucleation, and a fetal-to-adult actin isoform shift; (2) the ventricular MLC2 isoform was identified in EHT and strongly upregulated on protein level, providing further evidence for advanced ventricular maturation; (3) cardiomyocytes in EHTs responded to different hypertrophic stimuli with distinct morphological (concentric versus eccentric hypertrophy) and molecular (fetal gene expression) changes; (4) apoptosis in enzymatically isolated myocytes limited cell and especially cardiomyocyte survival in EHT; (5) EHT resembled normoxic tissue at all investigated time points; (6) matrix restructuring paralleled EHT-development and resulted in at least partial replacement of ECM constituents. Collectively, our data documents that the EHT culture format induces terminal differentiation and advanced maturation of initially immature cardiomyocytes to a "ventricle-like" phenotype in vitro. The process of EHT "development" can be classified as "EHT-consolidation" (culture days 0-7) followed by "EHTmaturation" (culture days 7-12). Demonstration of qualitatively different responses, for example, concentric versus eccentric hypertrophy, to distinct hypertrophic stimuli, for example, PE/Ang versus HIS, suggests that EHT can be exploited as a novel test-bed to dissect mechanisms of hypertrophic growth.

Using tissue-engineered myocardium as a model of myocardial development or in substance screening clearly depends on its close resemblance with bona fide heart muscle. Classical monolayer cultures display little structural, molecular, and also functional similarities with mature myocardium and do in general not respond reliably to hypertrophic stimuli, unless subject to inherently hostile serum starvation at low seeding density. Most notably, cardiomyocytes in monolayer cultures quickly lose their regular rod-shaped morphology and concomitantly reexpress fetal genes, indicating a molecular "resetting" to a prenatal state of development.<sup>5–7</sup> Growth on patterned substrates may partially improve this condition and support anisotropic growth<sup>19,20</sup>; yet, morphological and molecular data documenting advanced maturation and formation of 3D tissue on a macroscopic scale are limited.

Particular morphological hallmarks of advanced cardiomyocyte maturation are a rod-shaped geometry and binucleation. Cardiomyocytes enzymatically isolated from EHTs were rod-shaped and abundantly binucleated (37%), resembling to some degree a state of maturity observed in cardiomyocytes from 10- to 12-day-old rat hearts.<sup>2,21,22</sup> However, compared with heart-derived cardiomyocytes, EHT-derived cardiomyocytes were thinner (length/width ratio, 12:1 in EHT versus 7:1 in 12-day-old rat hearts and 5:1 in adult rat hearts). This difference in aspect ratio was at least in part "normalized" under PE and Ang stimulation (length/width ratio, 10:1; Figure 6) but also paralleled by a "mild" induction of ANP, all in the presence of "normal" serum. Interestingly, HIS caused marked cardiomyocyte elongation and ANP upregulation, responses which have been implicated in "pathological" hypertrophy. Although additional studies are warranted to establish phenotype "serome" relationships and identify distinct underlying mechanisms, we believe that our data provide compelling evidence for EHTs as a robust and nearly "physiological" in vitro system, which could be used, for example, to decipher the complex paracrine regulation of physiological versus pathological growth. In line with this notion, we could recently provide confirmatory evidence for the role of the MEK1-ERK1/2 pathway in concentric versus eccentric myocyte hypertrophy, conditions associated with pressure and volume overload, respectively, by making use of the EHT system.23

During physiological myocyte development, elongation of cardiomyocytes precedes parallel sarcomere assembly.<sup>22,24</sup> Subsequently, concentric hypertrophy, being the morphological correlate of parallel sarcomeric assembly, represents a compensatory mechanism to adapt to increasing load. Similarly, multinucleation and polyploidy have been reported to be enhanced under increasing load.<sup>25</sup> Accordingly, DNA synthesis (Figure 1D and 1E) was markedly elevated particularly after day 7 of EHT culture, that is, the time when EHTs were subjected to phasic stretch. Interestingly, enhanced DNA synthesis did not go along with an increase in myocyte or nonmyocyte cell number, suggesting load-induced karyo-kinesis, in the absence of palpable cytokinesis.

On the molecular level, the shift from skeletal to cardiac actin transcript expression (Figure 4A and 4B and Online Figure V) and the detection of elevated ventricular MLC2 in 12-day EHT (Figure 5B) provided further evidence for advanced organotypic maturation of cardiomyocytes in EHT. In apparent disagreement with this notion was the absence of the commonly reported massive  $\beta$ - to  $\alpha$ -MHC transcript isoform shift. This may, however, be a consequence of the low (subphysiologic) endogenous beating frequency of EHT ( $\approx 2$  Hz), making faster actin-myosin kinetics dispensable. Whether electric stimulation of EHT at near physiological frequencies (6 Hz) would facilitate a shift from the observed  $\approx$ 7-fold  $\alpha$ -MHC transcript excess in spontaneously beating EHTs to a  $\approx$ 88-fold excess as observed in adult heart muscle (Figure 4F), needs further investigation. Interestingly, PE/ Ang and HIS lowered the  $\alpha$ -/ $\beta$ -MHC transcript ratio, as anticipated under hypertrophy-inducing conditions.

Abundant caspase-3 activation and elevated bax expression suggested that apoptosis limited cell survival in EHT. It is important to note that caspase activation does not always lead to fully executed apoptosis with nuclear fragmentation but is also involved in reversible myofilament breakdown after cell isolation.<sup>26</sup> Induction of apoptosis during enzymatic cell isolation and cell loss during early culture are also commonly observed in monolayer cardiomyocyte cultures (Online Figure IV). This set of data collectively argues against the notion that the reported apoptosis represents a specific tissue engineering limitation. We could recently demonstrate that activation of prosurvival pathways such as the Akt pathway can protect cardiomyocytes in early EHT cultures from apoptosis.<sup>27</sup>

Hypoxia-induced apoptosis has been suggested as a main limitation for cell survival in tissue-engineered myocardium,28 and we initially interpreted VEGF-A transcript elevation as a sign of chronic hypoxia in particular in later stages of EHT culture. However, more comprehensive investigations of more sensitive biomarkers for acute (HIF-1 $\alpha$ ) and chronic (PHD2/3) hypoxia did not provide any evidence in support of EHT hypoxia during culture. We emphasize that cardiomyocytes are physiologically exposed to oxygen pressure below 40 mm Hg, which corresponds to <5% ambient oxygen,29 and that the provided oxygen supply (21% ambient oxygen) is apparently sufficient for normoxic EHT maintenance. Although the stimulus for enhanced VEGF-A expression has not been identified, one should consider that VEGF-A by itself may be cardioprotective<sup>30</sup> and in fact may be an important prerequisite for the observed rapid vascularization of EHT grafts in vivo.31,32

Of particular interest for in vivo applications in regenerative medicine is also the apparent replacement of the original hydrogel by endogenously produced ECM. This remodeling process is on the one hand crucial for the formation of mechanically stable EHTs. On the other hand, it provides a perspective for the generation of nonimmunogenic "therapeutic" EHTs from autologous cells.

Taken together, cardiomyocyte maturation in EHT compares favorably to myocyte maturation in monolayer culture and does to some extent simulate physiological development in vivo. The observed differences in cardiomyocyte size and MHC isoform composition may be a consequence of "subphysiologic" loading and low intrinsic contraction frequency and thus may be interpreted as a "physiological" response to partially unphysiologic culture conditions. Interestingly, concentric and eccentric hypertrophic growth could be stimulated in EHT using simulated neurohumoral/serum activation. These data in particular suggest that EHT may constitute a unique model system to study mechanisms governing hypertrophic growth in cardiomyocytes. As a consequence of the observed differentiation and maturation inducing capacity, EHT cultures may also find a novel application as in vitro test-bed to define the fate of progenitor cells in a tissue-like context.

#### Acknowledgments

We thank M. Bauer and N. Feifel for designing qPCR primer-probe sets, B. Endress for excellent technical assistance, and C. Perske for helping with light microscopy of Sirius red stained samples.

#### Sources of Funding

This study was supported by the German Research Foundation (DFG; Zi708/7–1, 8–1, 10–1, FOR604, and KFO155 to D.K., W.A.L., and W.H.Z.), the Federal Ministry for Education and Research (01GN 0520, 01GN0827, and 01GN0957 to W.H.Z.), the Deutsche Stiftung für Herzforschung (F29/03 to W.H.Z.), and the European Union (EU FP7 CARE-MI to W.H.Z.).

#### None.

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## **Novelty and Significance**

#### What Is Known?

- Tissue-engineered myocardium may be used as in vitro tool for drug development and as a surrogate for heart muscle for in vivo applications in myocardial repair.
- Cardiac myocytes dedifferentiate in culture, leading to a loss in organotypic cell morphology and reexpression of fetal genes.
- The validity of classical monolayer cultures as in vitro platform for modeling of hypertrophic cardiomyocyte growth is limited.

#### What New Information Does This Article Contribute?

- Engineered heart tissue (EHT) formation is a staged process comprising an early tissue consolidation phase with selection of the "fittest" myocytes and fibroblasts as well as comprehensive extracellular matrix (ECM) remodeling; this is followed by a phase of organotypic maturation.
- Organotypic maturation of cardiomyocytes in EHT includes terminal differentiation, abundant binucleation, development of an essentially rod-shaped morphology, and a fetal-to-adult shift in gene expression pattern.
- EHT may be useful in modeling of concentric versus eccentric cardiomyocyte hypertrophy.

Tissue engineering could potentially provide realistic heart muscle models and surrogate myocardium. However, cellular maturity in tissue-engineered myocardium has been sparsely documented. We show that a unique collagen hydrogel-based, cardiac tissue-engineering format, EHT, supports organotypic maturation in originally immature cardiomyocytes from neonatal rats. Our studies provide novel insight into the developmental properties of EHT, for example, hypertrophic growth under normoxic conditions and comprehensive ECM remodeling leading to replacement of the original hydrogel scaffold with ECM. The latter finding highlights the predicted but thus far undemonstrated capacity of the cardiac fibroblast to function as a key "engineer" in myocardial tissue engineering. We have established appropriate experimental conditions that differentially affect cardiomyocyte growth (ie, concentric hypertrophy under simulated neurohumoral activation and eccentric hypertrophy in the presence of hypertrophy-inducing serum). Collectively, the results of this study enhance the utility of the EHT technology as methodological bridge between classic 2D cell culture and animal models. It may represent a useful tool for identifying specific environmental cues that facilitate organotypic maturation of cardiomyocytes from human (stem) cell sources as well.

## **Supplement Material:**

# Terminal Differentiation, Advanced Organotypic Maturation, and Modeling of Hypertrophic Growth in Engineered Heart Tissue

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## **EXPANDED MATERIALS AND METHODS**

Experimental animals were maintained in accordance with the guiding principles of the American Physiological Society. Animal experiments were approved by the local authorities (Regierung von Mittelfranken: 621.2531.31-2/00 and -17/01; BWG of the Freie und Hansestadt Hamburg; Niedersächsisches Landesamt für Verbraucherschutz und Lebensmittelsicherheit).

EHT construction and treatment. Heart cells were isolated from neonatal rats (postnatal days 1-3) using a fractionated DNase/Trypsin digestion protocol without preplating to maintain the original cardiomyocyte:non-myocyte composition<sup>1, 2</sup>. EHTs (reconstitution volume: 0.9 ml) were prepared by pipetting a mixture containing the isolated heart cells  $(2.5 \times 10^6 \text{ cells in DMEM with } 10\% \text{ fetal calf})$ serum, 1 mmol/l glutamine, 100 U/ml penicillin, and 100 µg/ml streptomycin), pH-neutralized collagen type I from rat tails (0.5 mg/EHT - measured by the Sircol Collagen Assay; Biocolor), basement membrane protein containing Engelbreth-Holm-Swarm tumor exudate (10% v/v; BD Biosciences), and concentrated serum-containing culture medium (2xDMEM, 20% horse serum, 4% chick embryo extract, 200 U/ml penicillin, and 200 µg/ml streptomycin) in circular molds (inner diameter, 8 mm; outer diameter, 16 mm; height, 5 mm<sup>3</sup>). Spontaneously beating EHTs were transferred to stretch devices on culture day 7 to continue culture under phasic load (from 100 to 110% of slack length at 2 Hz) for additional 5 days. EHTs were treated with 20 µmol/L phenylephrine and 100 nmol/L angiotensin-II from day 7-12 with daily medium change to induce hypertrophy. For 2D culture experiments neonatal heart cells were seeded in 6-well plates ( $5x10^{5}$ /well) coated with the EHT matrix (diluted 1:50 in PBS) and cultured in parallel to EHTs in standard primary cardiomyocyte culture medium (DMEM, 10% fetal calf serum, 100 µmol/L 5-bromo-2'-deoxyuridine, 100 U/ml penicillin, and 100 µg/ml streptomycin).

<sup>3</sup>H-thymidine incorporation. EHTs were maintained in standard culture medium with 1  $\mu$ Ci/ml <sup>3</sup>H-thymidine for 6 hours on the indicated culture days. After washing in ice cold PBS, EHTs were dissolved in ice cold lysis buffer (10 mmol/L trishydroxylaminomethane [Tris; pH 8], 1 mmol/L ethylene-diamine-tetraacetic acid [EDTA; pH 8], 0.1% sodium dodecyl sulfate [SDS]) followed by 6 h proteinase K (0.1  $\mu$ g/ $\mu$ l) digestion at 55 °C. DNA was precipitated in isopropanol after DNase-free RNase treatment (0.02  $\mu$ g/ $\mu$ l for 60 min at 37 °C) and protein extraction in potassium acetate solution (3 mol/L potassium/5 mol/L acetate). After washing in 70% ethanol, DNA was resuspended in Tris/EDTA-buffer (100 mmol/L Tris, 10 mmol/L EDTA; pH 7.6). DNA content was measured by spectrophotometry and <sup>3</sup>H-activity was assessed by liquid scintillation counting.

**Cell isolation from EHT.** EHTs were immersed in modified Bicarbonate-Free Hanks' Balanced Salt Solution with HEPES (BFHH; NaCl 136.9 mmol/L, KCl 5.36 mmol/L, MgSO<sub>4</sub> 0.81 mmol/L, glucose 5.55 mmol/L, CaCl<sub>2</sub> 0.0125 mmol/L, KH<sub>2</sub>PO<sub>4</sub> 0.44 mmol/L, Na<sub>2</sub>HPO<sub>4</sub> 0.34 mmol/L, HEPES 20 mmol/L) containing 0.035 mg/ml Liberase Blendzyme III (Roche) and 30 mmol/L BDM (2,3-

butanedione monoxime) at 37 °C for 60 min. Enzymatic activity was stopped by addition of 10% FBS, 5 mmol/L EDTA. Isolated cells were fixed for immunostaining or flow cytometry as described below.

Histology. EHTs or dispersed single cells were fixed in neutral buffered 4% formaldehyde/1% methanol, pH 7.4 with 30 mmol/L BDM and subjected either to light (LM) or confocal laser scanning (CLSM; Zeiss 510 Meta or 710/NLO LSM) microscopy, as described recently<sup>3</sup>. Crvo-sections (10 um; Leica CM3050 S) were stained with phalloidin-Alexa 488 (3.3 U/ml; Molecular Probes) to label f-actin, DAPI (4',6-diamidino-2-phenylindole; 1 µg/ml) to label nuclei, and antibodies directed against  $\alpha$ -actinin (1:1000; Sigma), and activated caspase-3 (1:250; Promega) with appropriate secondary antibodies. For Sirius red staining EHTs were embedded in paraffin, and sectioned at a thickness of 6  $\mu$ m. After de-waxing in Roti-Histol (Roth) for 2x 15 min, the sections were hydrated through a decreasing ethanol series and washed with distilled water for 2x 5 min. Sections were incubated for 60 min in a solution of 0.5 g Sirius red F3B (C.I. 35782) in 500 ml of saturated aqueous solution of picric acid, briefly washed in acidified water (5 ml glacial acetic acid per liter of distilled water), dehydrated and mounted in Histokitt. Sections were then subjected to polarized light microscopy (Olympus BX41). Green and red channels were separated by setting a threshold in the green-red distribution using the CIE lab function of ImageJ. Respective images of above and below threshold signals as well as merged image were computed applying identical settings. For transmission electron microscopy (TEM) EHTs were fixed in 2.5% glutaraldehyde (in PBS with 1 mmol/L CaCl<sub>2</sub> and 30 mmol/L BDM) overnight at 4°C. After extensive washing in PBS, EHTs were postfixed for 2 h in osmiumtetroxyd/PBS (1:1). After epon embedding, ultrathin sections (50 nm) were cut (Ultracut UCT, Leica), contrasted with uranyl acetate and lead citrate, and imaged with a Zeiss Leo 906 EM.

**Flow cytometry.** Dispersed cells from neonatal rat (P0-3) and EHTs at different time-points were fixed in ice-cold 70% ethanol. Staining for  $\alpha$ -actinin (Sigma) or vimentin (Abcam) was performed in the presence of 0.5% Triton-X at 4°C for 45 min. Appropriate secondary antibodies were applied for 30 min at room temperature. Negative controls were incubated with the secondary antibody alone. DNA was stained with DAPI (1 µg/ml). Samples were run on a LSRII cytometer and analysed with FacsDiva software (BD Biosciences). The gating strategy to exclude cell clumps and multinucleated cells was based on the width of the DAPI signal. DNA content/cell cycle was analyzed using ModFit LT 3.2 software (Verity).

**Cell isolation from native heart.** After an intra-peritoneal bolus injection of heparin (500 IU) 12 day and 12 week old Wistar rats were euthanized. Hearts were quickly excised and cells were isolated using a modified Langendorff method<sup>4</sup>. Briefly, hearts were digested with 0.1 mg/ml Liberase Blendzyme III (Roche) in oxygenized perfusion buffer (NaCl 113 mmol/L, KCl 4.7 mmol/L, KH<sub>2</sub>PO<sub>4</sub> 0.6 mmol/L, MgSO<sub>4</sub> 1.2 mmol/L, NaHCO<sub>3</sub> 12 mmol/L, KHCO<sub>3</sub> 10 mmol/L, HEPES 10 mmol/L, taurine 30 mmol/L, glucose 5.55 mmol/L, BDM 10 mmol/L, calcium 0.0125 mmol/L). Single cells were fixed for immunostaining as described above.

**RNA/DNA isolation and quantitative RT-PCR (qPCR).** RNA and DNA were isolated using the Trizol<sup>®</sup>-method (Invitrogen) and quantified by spectrophotometry. cDNA was prepared from 2  $\mu$ g total RNA by reverse transcription with MMLV-RT (Invitrogen) utilizing random hexamere primers (Roche) following standard protocols (Invitrogen). qPCR was performed in a 384 well format ABI prism HT 7900 system (Applied Biosystems) using gene-specific primers and fluorogenic probes (5' FAM and 3' TAMRA; **Online Table II**) as described earlier<sup>5</sup>, unless indicated otherwise (see below). The reaction mixture contained 20 ng input cDNA, 3 mmol/l MgCl<sub>2</sub>, 0.4 µmol/l forward and reverse primer, 0.5 µmol/l probe, 0.8 mmol/l NTP (Applied Biosystems), and 0.05 U TaqGold polymerase (Applied Biosystems) in a total volume of 10 µl supplemented with TaqPolymerase buffer II (Applied Biosystems). We used following temperature protocol: 30 sec at 50 °C and 10 min at 95 °C followed by 45 cycles of 30 sec at 95 °C and 1 min at 58 °C. GAPDH expression was similar in all study groups and was therefore employed to normalize for differences in RNA quantity and RT-efficiency. Cardiomyocyte-specific transcript quantity was indexed to the expression of muscle specific calsequestrin 2 (CSQ2). The linearity of each PCR was confirmed by analyzing serial cDNA

A

dilutions, prepared from total RNA isolated from neonatal rat hearts. Quantification of transcripts was performed using the Standard Curve algorithm<sup>6</sup>. PHD2 and PHD3 mRNA levels were quantified using 1  $\mu$ l of cDNA (Fermentas) and a SYBR Green qPCR reaction kit (Clontech) in combination with a MX3000P light cycler (Stratagene) as described before<sup>7</sup>. The initial template concentration of each sample was calculated by comparison with serial dilutions of a calibrated standard. Primer sequences: PHD2 forward TACAGGATAAACGGCCGACAC and PHD2 reverse

GGCTTGAGTTCAACCCTCAC; PHD3 forward GTTAACCCGAGACTGGACGA and PHD3 reverse CATACCGCTAGGCTTTGCTC.

Development of a cardiomyocyte specific qPCR assay. To better account for cardiomyocyte loss we developed a PCR-assay allowing the quantification of 17,500-1,750,000 cardiomyocytes in a mixed heart cell population, based on the detection of muscle specific calsequestrin 2 (CSQ2) transcripts (Online Figure VII). We designed intron-spanning fluorogenic TaqMan probes (5' FAM, 3' TAMRA) and adjacent primer pairs to amplify muscle specific CSQ2, GAPDH, and 18S-RNA. Rat heart cells were isolated as described and cardiomyocytes were enriched by preplating, resulting in a cell suspension containing 70% cardiomyocytes as identified by  $\alpha$ -sarcomeric actinin labeling<sup>2</sup>. Subsequently, heart cells were mixed with defined numbers of cardiac non-myocytes. Non-myocytes were prepared by propagating a quickly adhering cell fraction from the original neonatal rat heart cell isolate. This cell fraction was grown to subconfluency (70%), trypsinized, frozen in 7.5% DMSOcontaining cell culture medium, thawed, and re-grown. This procedure was repeated at least twice, vielding heart cell cultures free of beating or non-beating cardiomyocytes. Cell mixtures were subjected to RNA isolation (Trizol<sup>®</sup>, Invitrogen). Reverse transcription and qPCR were performed as described with different quantities of input cDNA (20 pg and 20 ng) to demonstrate that cardiomyocytes express constant levels of CSQ2 transcripts. This was further confirmed with two different CSQ2 primer-probe sets (see below). Similar cDNA loading was confirmed by GAPDH and 18S-RNA transcript analyses:

CSQ2: NCBI accession#: AF001334

Forward:	TTT CTG ACG GAG ACG TTC AGG
Probe:	TGG CTG CCT ACA GTA CGC TGG GAA C
Reverse:	TAG CAG GAC AGA GAG GGT GCA
CSQ2: Ens	emble accession#: ENSRNOG0000016243
Forward:	CCA AGA GGC TGG GCT TCA G
Probe:	CGA TCT CTA CTG GGT CCT CAA TGA GGT CCA
Reverse:	CCT CAT TCT TGA AAA AGC CAA GC

GAPDH: NCBI accession#: NC005103

Forward:	AAC TCC CTC AAG ATT GTC AGC AA
Probe:	ATG GAC TGT GGT CAT GAG CCC TTC CA
Reverse:	CAG TCT TCT GAG TGG CAG TGA TG

18S-RNA: NCBI accession#: V01270

Forward:ACG ACC CAT TCG AAC GTCProbe:CCT ATC AAC TTT CGA TGG TAG TCG CCG TReverse:CTT GGA TGT GGT AGC CGT TT

**Immunoblotting.** EHTs were washed thoroughly in ice cold PBS and rapidly homogenized in lysis buffer containing 30 mmol/L Tris (pH 8.8), 5 mmol/L EDTA (pH 8), 3% SDS, 10% glycerol, 30 mmol/L NaF, and 2  $\mu$ g/ml aprotinin or 4 mmol/L urea, 140 mmol/L Tris (pH 6.8), 1% SDS, 2% Nonidet P-40, and protease inhibitors (Roche Applied Science). After centrifugation at 13,000 g for 10 min, supernatants containing soluble proteins were subjected to protein concentration measurement using modified Lowry or Bradford methods, respectively. Equal amounts of protein (30-100  $\mu$ g) were resolved by SDS-PAGE and transferred onto polyvinylidene fluoride (sarcomeric actin) or nitrocellulose (HIF-1 $\alpha$ , calsequestrin) membranes by semidry blotting. Primary antibodies used were:

anti-sarcomeric actin (clone 5C5; Sigma), anti-HIF-1 $\alpha$  (Novus, NB100-479), anti-calsequestrin 2 (AffinitiBioReagents). Primary antibodies were detected with appropriate horseradish peroxidase coupled secondary antibodies. Sarcomeric actin immunocomplexes were enhanced with the ECL-plus kit (Amersham Biosciences) and recorded with a ChemiDoc system (Syngene). Signals were quantified with Gene-Tools software (Syngene). For detection of HIF-1 $\alpha$  membranes were incubated with 100 mmol/L Tris-HCl (pH 8.5), 2.65 mmol/L H<sub>2</sub>O<sub>2</sub>, 0.45 mmol/L luminol, and 0.625 mmol/L coumaric acid for 1 min. Chemiluminescence signals were detected with the LAS-3000 Image Reader (Fujifilm).

**Detection of myosin heavy chain isoforms.** To assess myosin heavy chain isoform composition EHTs were homogenized in sample buffer containing 50 mmol/L Tris-HCl (pH 6.8), 5 mmol/L EDTA, 10% glycerol, 8  $\mu$ g/ml leupeptin, 1% beta-mercaptoethanol, 20% SDS, 0.1% (w/v) dithiothreitol, 6  $\mu$ mol/L bromophenol blue, and washing buffer (5 mmol/L Tris-EDTA, pH 8.0). The separating gel contained 7.5% total acrylamide (acrylamide to bis-acrylamide ratio, 30:0.8), the stacking gel contained 4% total acrylamide. To check for linearity, different amounts of EHT (0.5–3.0  $\mu$ g) were loaded and the densities of the myosin heavy chain bands were analyzed; a load of 1.5  $\mu$ g per lane was selected as it was found to be within the linear range. After separation of proteins, gels were stained overnight with SYPRO Ruby (Molecular Probes). Fixation and washing were performed according to the manufacturer's guidelines. Gels were digitized using LAS-4000 Image Reader (Fujifilm; 460 nm/605 nm E<sub>x</sub>/E<sub>m</sub>) and signals were analyzed using Multi Gauge software (Fujifilm).

2D electrophoresis (2-DE). EHT samples were homogenized in 9 mol/L urea, 1% DTT, 4% CHAPS, protease and phosphatase inhibitors (Complete Mini, Roche), and 0.8% Pharmalytes 3-10. For difference in-gel electrophoresis (DIGE), proteins were precipitated (ReadyPrep 2D Clean-up kit, Biorad) and re-suspended using a lysis buffer (30 mmol/L TrisCl pH 8.5, 8 mol/L urea, 4% w/v CHAPS) compatible with DIGE labelling (GE healthcare). After centrifugation at 13,000 g for 10 min, the supernatant containing soluble proteins was harvested and the protein concentration was determined using a modification of the method described by Bradford. The fluorescence dye labelling reaction was carried out at a dye/protein ratio of 200 pmol/L / 50 µg. After incubation on ice for 30 min, the labelling reaction was stopped by scavenging non-bound dyes with 10 mmol/L lysine (L8662, Sigma) for 15 min. Protein extracts (50 µg/sample) were loaded on nonlinear immobilized pH gradient (IPG) 18-cm strips, pH 3-10 (GE Healthcare) using an in-gel rehydration method. Loaded IPG-strips were rehydrated in 8 mol/L urea, 0.5% w/v CHAPS, 0.2% w/v DTT, and 0.2 % w/v Pharmalyte pH 3-10 overnight in a reswelling tray. Strips were isoelectrically focused at 0.05 mA/IPG-strip and 35 kVh at 20 °C (IPGphor, GE healthcare) and subsequently equilibrated in 6 mol/L urea containing 30% v/v glycerol, 2% w/v SDS, and 0.01% w/v bromphenol blue, with addition of 1% w/v DTT for 15 min, followed by the same buffer without DTT, but with the addition of 4.8% w/v iodoacetamide for 15 min. Large-format gradient gels (5-10% stack, 10-16% linear, 16-20% stack) were cast using a 2-DE optimizer (NextGen Sciences, Huntingdon, UK). Gels were subsequently overlaid with water-saturated butanol (2:3) and left to polymerize overnight. SDS-PAGE was performed using the Ettan DaltSix system (GE healthcare). After electrophoresis, fluorescence images were acquired by using the Ettan DIGE Imager (GE Healthcare) with the following parameters: exposure time: Cy2, 0.8 sec, Cy3, 0.3 sec, Cy5, 0.5 sec, pixel size: 0.1 mm. Images were analyzed by DeCyder software (version 7.0, GE Healthcare). The 2-DE gels were fixed overnight in methanol:acetic acid:water solution (4:1:5 v/v/v) and visualized by silver staining using the Plus one silver staining kit (GE healthcare) without glutaraldehyde to ensure compatibility with subsequent mass spectrometry analysis. Silver-stained gels were scanned in transmission scan mode using a calibrated scanner (GS-800, Biorad).

**Nanoflow liquid chromatography tandem mass spectrometry (LC-MS/MS).** Gel pieces containing selected protein spots were treated overnight with modified trypsin (Promega) according to a published protocol modified for use with an Investigator ProGest (Genomic Solutions) robotic digestion system<sup>8</sup>. Following enzymatic degradation, peptides were separated by a nanoflow HPLC system on a reverse-phase column (Acclaim PepMap100, C18, 25cm, 5µm, 100Å, Dionex) and applied to a LTQ ion-trap mass spectrometer (Thermo Fisher Scientific) with electron transfer

dissociation (ETD). Spectra were collected from the ion-trap mass analyzer using full ion scan mode over the mass-to-charge (m/z) range 450-2000. MS-MS scans were performed on each ion using dynamic exclusion and alternating collision-induced dissociation (CID) and ETD. Database search was performed using the SEQUEST (Thermo Fisher Scientific) and X! Tandem software. Two missed cleavages per peptide were allowed and carbamidomethylation of cysteine as well as partial oxidation of methionine were assumed. Peptide identifications were accepted if they could be established at greater than 95% probability as specified by the Peptide Prophet algorithm. Protein identifications were accepted if they could be established at greater than 99% probability with at least two independent peptides.

<sup>3</sup>**H-phenylalanine and** <sup>3</sup>**H-proline incorporation.** EHTs were maintained in standard culture medium with 1  $\mu$ Ci/ml <sup>3</sup>H-phenylalanine or <sup>3</sup>H-proline as indicated. Protein was precipitated in 10% ice-cold trichloroacetic acid (TCA) at 4 °C over night. The supernatant was collected and subjected to liquid scintillation counting to assess the non-incorporated fraction of the isotopes. The protein precipitate was washed twice in ice-cold PBS, suspended in 1 mmol/L NaOH containing 0.01% SDS for 2 h at 37 °C, and subjected to liquid scintillation counting. Total protein content was analyzed by a modified Lowry-Assay (Bio-Rad DC Protein Assay).

<sup>35</sup>S-cysteine/-methionine incorporation, PAGE, and autoradiography. EHTs were cultured in cysteine- and methionine-free EHT culture medium with 4.5 g/l glucose for 6 h and subsequently incubated for 18 h in fresh cysteine- and methionine-free EHT culture medium supplemented with 100  $\mu$ Ci/ml <sup>35</sup>S-cysteine/-methionine on the indicated culture days. EHT protein was prepared and quantified as described above. Similar quantities of total proteins were loaded on 7% SDS-polyacrylamide gels and separated electrophoretically. Gels were stained with Coomassie blue, immersed in Amplify Fluorographic solution (Amersham Biosciences), vacuum dried, and subjected to autoradiography on intensifier screens (Expo Hyperfilm; Amersham Biosciences) for 6.5 h at -80 °C.

**Statistical analyses.** Data are presented as mean  $\pm$  standard error of the mean (SEM). Statistical differences were determined using two-sided, unpaired Student's *t*-tests or one-way analysis of variance (ANOVA) followed by Bonferroni's multiple comparison test. A *P* value < 0.05 was considered statistically significant.

## **Supplementary References**

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## **ONLINE FIGURE/TABLE/VIDEO LEGENDS**

**Online Table I. Protein identifications by tandem mass spectrometry (LC-MS/MS).** The amino acid sequences and scores of the identified peptides are provided. The blue color highlights the number of unique peptides, unique spectra, total spectra, and the sequence coverage as obtained by CID. The corresponding values for ETD (if applicable) are given below, but are not highlighted.

## Online Table II. qPCR primers and probes.

Online Figure I. Quantification of cardiomyocytes and fibroblasts during EHT culture by flow cytometry. Representative plots identify distinct  $\alpha$ -actinin- (A) and vimentin-positive cell populations (B) at the indicated days of EHT culture. Panels resemble overlays of individual dot plots: in red cell pools labeled for actinin (A) or vimentin (B); in grey cell pools exposed to secondary antibody only.

**Online Figure II. DNA content in mononucleated cardiomyocytes and non-myocytes during EHT culture assessed by flow cytometry. A**, Representative plots of DNA content in mononucleated cardiomyocytes (actinin-positive, red) and non-myocytes (actinin-negative, dark grey) at day 0 and day 12 of EHT culture. **B**, Fractions of mononucleated cardiomyocyte (top panel) and non-myocyte (lower panel) populations at day 0 (n=6) and day 12 (n=4) of EHT culture with 2N, 4N, and 8N DNA content.

**Online Figure III.** Surrogate parameters suggesting hypertrophic growth in EHTs. A, RNA/DNA ratio in EHTs on culture days 0 (n=18), 3 (n=19), 7 (n=10), and 12 (n=16). **B**, <sup>3</sup>Hphenylalanine incorporation during EHT culture days 0-3 (n=7), 3-7 (n=8), and 7-12 (n=5). \*P < 0.05vs. EHT day 0 (**A**) and EHT days 0-3 (**B**); ANOVA and Bonferroni's multiple comparison test.

**Online Figure IV**. **Cell death in EHT and monolayer (2D) culture. A**, Analysis of DNA content in EHT- and 2D culture-derived cells (n=3 each). Sub-G1 fraction (green) denotes dead/apoptotic cells with condensed nuclei. **B**, Trypan-blue exclusion in EHT- and 2D culture-derived cells at culture day 1 (n=5 [EHT], n=4 [2D]). **C**, Comparison of CSQ2 transcript abundance in EHT (black bars) vs. 2D culture (white bars), n=5-6/time-point. \**P*<0.05 vs. day 0 (grey bar); ANOVA and Bonferroni's multiple comparison test.

**Online Figure V. Molecular markers of maturation in monolayer (2D) vs. EHT culture. A**, ANP transcripts per GAPDH transcript; **B**, skeletal actin transcripts per GAPDH transcript; **C**, cardiac actin transcripts per GAPDH transcript in isolated neonatal heart cells at day 0 (black bars; n=5), 2D cultured cells at day 12 (blue bars; n=6), and EHT at day 12 (green bars; n=5). **D**, Correlation of cardiac and skeletal actin transcript abundance in freshly isolated neonatal heart cells (d0; black), in 2D culture (culture days 3,7, and 12 [left panel]) and EHT culture (culture days 3, 7, and 12 [middle panel]) - black arrows denote the trend in expression pattern change in 2D and EHT culture; right panel: direct comparison of 12 day 2D vs. EHT cultures and neonatal cardiomyocytes. \*P<0.05 2D vs. EHT; Student's t-test.

**Online Figue VI. ECM restructuring during EHT development. A**, matrix metalloprotease-2 (MMP-2; n=8-10); **B**, MMP-14 (n=7-10); tissue inhibitor of matrix metalloprotease-1 (**C**, TIMP-1; n=7-10), and TIMP-2 (**D**; n=7-10) transcripts per GAPDH transcript in EHT and native rat heart tissue. \*P<0.05 vs. EHT day 0; ANOVA followed by Bonferroni's multiple comparison test.

**Online Figure VII. Development of a cardiomyocyte-specific qPCR assay to allow approximation of cardiomyocyte content in mixed cell populations.** Detection of CSQ2 (NCBI accession#: AF001334; squares) and GAPDH (NCBI accession#: NC005103; circles) transcripts in 2.5x10<sup>6</sup> cells containing the indicated cardiomyocyte fraction by qPCR. High Ct-values indicate low transcript abundance. Symbols indicate individual Ct-values. Bars indicate the respective means. A Ct-value difference of 3.3 ideally represents a 10-fold difference in transcript abundance. Similar data could be obtained using alternative primer-probe pairs for muscle specific CSQ2 (Ensemble accession#: ENSRNOG00000016243) or 18S-RNA (NCBI accession#: V01270).

Online Video I: Spontaneous contractions in EHTs on culture day 3.
Online Video II: Spontaneous contractions of EHTs on culture day 7.
Online Video III: Spontaneous contractions of EHTs on culture day 12.
Online Video IV: Animated 3D reconstruction of adjacent optical sections from EHTs on culture days 0, 3, 7, and 12.

# Online Table I

Database Set: 2 Databases	Database Name: a sub Database Name: the u	zset of the uniprot_sprot databa Taxonomy: All Entries Number of Proteins: 193 Iniprot_sprot.fasta.hdr database Taxonomy: All Entries	se																	
Search Engine Set: 2 Search Engines	Search Engline: Sequer Search Engline: XI Tanr Peptide Thresholds: 95	Number of Proteins: 267334 Version: 27, rev. 12 Samples: All Samples Fragment Tolerance: 1:00 bit Prave Michaelone: 2:0 bit All Fragment Michaelone: 2:0 bit All Protein Michaelone: 2:0 bit All Digestion fingment: Prysini Max Mescel Cenarges: 2 don Pratein Michaelones: - 10 bit Pratein Michaelones: - 2:0 bit Pratein Michaelones: - 2:0 bit Michaelones:	(Monoisotopic) (Carbamidom n M (Oxidation asta.hdr datab (Monoisotopic) ; (Carbamidom prot_sprot dat	.) )) asse (267354 entri .) nethy() )) abase	es)															
	Protein Inresnoids: 99	.0% minimum and 2 peptides r	ninimum																	
rotern name  Nidogen-1 precursor (Entactin) - Mus musculus (Mouse)	NID1_MOUSE	pers Protein molecular v 136	603,6	100,00% 99,80%	4 2	2	2	0,21% 0,08%	4,10% ASLHGGEPTTIR OTITFOECAHDDAR TNSVIAMDLAISK VLFDTGLVNPR 2,17% ASLHGGEPTTIR OTITFOECAHDDAR	R Q R P K E R G R Q R P	ext amino actest Pepide i Bes 95,00% 95,00% 95,00% 95,00% 95,00%	2,61 3,01 2,82 2,73 4,08 2,97	0,356 0,233 0,274 0,0978 0,322 0,152	-0,146 0 -0,699 1,96 0		1 1 1 0 1 0 1 0 1 0 1 0 1 0 1 0	0 0 0 0 0 0 0 0	2 1351,7336 2 1691,745 2 1378,7252 2 1378,7252 2 1378,7252 2 13230,6848 2 1351,7336 2 1691,745	1003 609 1168 1055 1003 609	1015 622 1180 1065 1015 622
Collagen alpha-1(I) chain precursor (Alpha-1 type I collagen) - Mus musculus (N	Mouse CO1A1_MOUSE	138	8014,7	100,00%	2	2	2	0,09%	2,00% DRDLEVDTTLK GETGPAGPAGPIGPAGAR	R S R G	95,00% 95,00%	2,56 2,96	0,38 0,446	-1,04 0,553	0	1 O 1 O	0	2 1304,6702 2 1532,7826	1215 1056	1225 1073
Vinculin (Metavinculin) - Mus musculus (Mouse)	VINC_MOUSE	116	701,4	100,00%	9	9	9	0,36%	10,60% AGEVINOPMMMAAR	к о	95,00%	2,9	0,184	0,0506	0	1 0	0	2 1566,7079	890	903
				100,00%	3	3	3	0,12%	DHASSHEDAGGAIR LLAVAA JAPPDAPRR MAGOMTDOVADLR MSAEINEIIR MTGLVDEAIDTK OVATALONLOTK VMLWNSMITVK 3.57% AL350LODSLK LLAVAATAPPDDAPRR OVATALONLOTK	R D R E K E K A K S K T R E R E K E K T	95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00%	2,9 2,11 3,1 2,05 2,85 2,69 2,77 3,02 2,7 3,22	0,377 0,297 0,27 0,391 0,146 0,268 0,248 0,231 0,24 0,279 0,196	2,33 -0,301 -0,699 0 1,72 0 0,337 1,89 0 0 0 0		1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0	000000000000000000000000000000000000000	2 1173,6461 2 1477,6936 2 1476,8176 2 1509,7043 2 1191,6044 2 1308,636 2 1314,7383 2 1267,6388 2 1173,6481 2 1476,8176 2 1314,7383	286 608 327 237 709 465 189 571 608 465	300 622 339 246 720 476 581 622 476
Nidogen-1 procursor (Entactin) - Mus musculus (Mouse)	NID1_MOUSE	134	603,6	100,00%	12	6	6	0,78%	11 SOV, ACLIPADOR ASLIGUERTIIR CCIVECVHISOR CCIVECVHISOR CCIVECVHISOR MCVGGDGR CVAEGSGR CVAEG	R R G R G R C C R C C K R C C K R C C K R C C K R C C K R C C K R C C K R C C R C C K C C K C C K C C K C C R C C R C R	45,00% 95,00%	2,75 3 3,16 2,27 3,65 2,49 2,66 0 3,32 3,59 2,96 2,41 3,16 3,47 2,52 3,77 2,84	0,217 0,431 0,343 0,172 0,422 0,343 0,463 0,406 0,433 0,274 0,274 0,273 0,289 0,229 0,253 0,291	2,75 1,85 0,0269 -0,146 0 3,09 3,6 0,921 2,57 2,29 0 0 0 0 0 0 0 0 0 0 0 0 0		I         O           2         0           1         0           1         0           1         0           1         0           1         0           2         0           2         0           2         0           2         0           2         0           2         0           1         0           1         0           1         0           1         0		2 1212,5797 2 1351,7236 2 13558,6055 2 1716,77 2 2116,8188 2 0996,454 2 1283,675 2 1114,4951 2 1351,6753 2 1321,6753 2 1321,6753 2 1321,6753 2 1321,6753 2 13716,77 2 1392,6348 2 1176,6377	1131 1003 734 719 701 828 517 422 609 1032 1055 649 1003 719 828 609 649	1141           705           733           718           836           528           421           1042           1065           659           733           652           659           659           659
Nologan-1 precursor (Entaclin) - Mus musculus (Mouse)	NID1_MOUSE	134	÷603,6	100,00%	14	14	15	0,61%	13.50% ACLIARADOR ALLACATINE COMMUCINILIZATION COMMUCINILIZATION COMMUCINILIZATION COMMUCINILIZATION COMMUNICATION PARTICICATION PARTICICATION PARTICICATION PARTICICATION VILLANDOVON VIL	R C C C R P P R C C C R P P R C C C C R P P R C C C C	95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00%	2,13 2,52 3,2 3,17 3,23 2,33 2,34 1,68 2,49 3,35 3,13 2,63 2,63 2,62 2,47 3,75 2,53 2,99 2,94 2,59	0,037 0,104 0,327 0,335 0,147 0,147 0,147 0,146 0,146 0,421 0,422 0,421 0,422 0,422 0,422 0,424 0,251	1.38 6.37 0.181 0.181 0.0555 1.03 0 2.43 1.14 0.0555 1.03 0 2.43 1.14 0.495 3.35 1.51 0 0 0 0 0 0 0 0		1         0           0         1           1         0           1         0           1         0           1         0           1         0           1         0           1         0           1         0           1         0           1         0           1         0           1         0           1         0           1         0           1         0           1         0           1         0		2 1212.5797 2 1331,7336 2 1558,6055 2 1776,77 2 1336,6876 2 1326,6876 2 1326,6876 2 1324,6074 2 1285,6178 2 1328,6074 2 1328,6075 2 1334,0742 2 1328,06848 2 1176,5377 2 1325,6876 2 1325,6876 2 1325,6876 2 1325,6876	1131 1003 734 719 852 1074 505 1160 645 517 1032 977 1055 649 1003 719 852 517 649	1141           1015           745           743           665           166           1166           1700           1028           1042           988           10055           659           528           528           528           528
Nidogen-1 precursor (Entactin) - Mus musculus (Mouse)	NID1_MOUSE	136	603,6	100,00%	4	5	5	0,23%	3,94% AECLNPAOPGR CPDNTLGVDCIER EHILGAAGGADAOR	R R R - R P	95,00% 95,00% 95,00%	2,55 2,79 1,83	0,283 0,302 0,326	3,26 0 0	0	1 0 1 0 1 0	0	2 1212,5797 2 1548,679 2 1365,6876	1131 1232 852	1141 1244 865
(Nidogen-1 precursor (Entactin) - Mux musculus (Neuse)	NID1_MOUSE	136	603,6	100,00%	7	11	11	0,48%	TALSINSIGP/R 6.67% ACLEMPLOPEDR ASLHOGGPTTHIR CEVEWHFSDR CPDNTLCVDLER NGFSITGGEFTR VLEDTGLVMPR YLLSNSIGP/R	R R Q R G R G R - K Q R G R D	95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00%	2,76 2,24 2,71 2,79 2,56 2,49 2,8 0	0,325 0,217 0,401 0,286 0,278 0,313 0,376 0	3,05 1,39 -0,806 -0,82 0,0915 2,28 3,8		2 0 1 0 1 0 1 0 1 0 1 0 3 0	0 0 0 0 0 0 0	2 1176,6377 2 1212,5797 2 1351,7336 2 1558,6055 2 1548,679 2 1285,6178 2 1230,6448 2 1176,6377	649 1131 1003 734 1232 505 1055 649	659 1141 1015 745 1244 516 1065 659

Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1 metal-binding globulin) TRFE_HORSE	78076,6	100,00%	21	34	35	1,30%	31,30% AACVCQELHNQQASYGK	к	N 95,00%	4,79	0,471	2,21	0	2 0	0	2 1963,8756	621	637
							AVSNFFAGSCVPCADR	к	T 95,00%	3,47	0,422	0,602	0	1 0	0	2 1757,774	165	180
							CGLVPVLAENYETR	ĸ	S 95,00%	3,32	0,407	0,0269	0	2 0	0	2 1620,8058 2 1322,6417	423	436
							DCYLASIPSHAVVAR	ĸ	S 95,00%	3,56	0,433	0,721	0	2 0	0	2 1658,8324	261	275
							DDTQCLANLQPTTTYK	R	T 95,00%	3,29	0,0889	3,29	0	0 1	0	2 1868,8705	660	675
							DEVQLLCR	R	D 95,00%	2,09	0,163	2,55	0	2 0	0	2 1096,51	242	249
							EDIRPEVPKDECK	R	K 95.00%	3.01	0,181	2,33	0	2 0	0	2 12/1,61/3 2 1614.78	302	312
							FCLFQSATK	к	D 95,00%	2,53	0,199	3,37	0	2 0	0	2 1101,5404	646	654
							GDVAFVK	A	H 95,00%	1,83	0,124	1,52	1	0 0	0	2 735,4042	221	227
							KNSNFQLNQLQGK	ĸ	K 95,00%	3,91	0,191	0,796	0	1 1	0	2 1518,803	119	131
							NSNFOLNOLOGK	ĸ	K 95.00%	3.39	0.283	2,59	0	1 0	0	2 1245,6415	120	131
							SIVPAPPLVACVKR	к	T 95,00%	0	0	2,82	0	0 1	0	2 1506,8832	45	58
							SKDFHLFSSPHGK	к	D 95,00%	3,24	0,351	0,131	0	1 0	0	2 1486,7445	300	312
							SSSDPDLTWNSLK	ĸ	G 95,00%	3,02	0,433	4,55	0	1 0	0	2 1449,6863	457	469
							WCTVSNHEVSK	R	A 95,00%	2,12	0,176	0.796	0	1 0	0	2 1013,4979 2 1346,6162	25	35
							YLTAVANLR	ĸ	Q 95,00%	1,32	0,261	1,39	1	4 0	0	2 1020,5842	682	690
							YYGYTGAFR	R	C 95,00%	2,2	0,178	2,14	0	2 0	0	2 1097,5056	541	549
		100,00%	10	12	12	0,45%	19,10% AACVCQELHNQQASYGK	к	N 95,00%	4,2	0,348	0	0	2 0	0	2 1963,8756	621	637
							CACSNHEPYFGYSGAFK	ĸ	C 95,00%	2,62	0,294	0	0	1 0	0	2 1994,8165	198	214
							DCVI ASIPSHAVVAR	ĸ	S 95,00%	3,30	0,295	0	0	1 0	0	2 1522,0417	215	275
							DDTQCLANLQPTTTYK	R	T 95,00%	4,49	0,348	0	0	0 1	0	2 1868,8705	660	675
							HQTVEQNTDGRNPDDWAK	к	D 95,00%	4,32	0,304	0	0	J 1	0	2 2110,9544	562	579
							KNSNEQLNQLQGK	ĸ	K 95,00%	4,54	0,162	0	0	1 1	0	2 1518,803	119	131
							SKDFHLFSSPHGK	ĸ	D 95.00%	3.26	0.227	0	0	1 0	0	2 1486.7445	300	312
							SSSDPDLTWNSLK	к	G 95,00%	2,82	0,304	0	0	1 0	0	2 1449,6863	457	469
Aconitate hydratase, mitochondrial precursor (EC 4.2.1.3) (Citrate hydro-lyase) (AcoACON_RAT	85418,1	100,00%	9	12	12	0,48%	14,90% ADIANLAEEFK	R	D 95,00%	1,94	0,14	2,01	0	1 0	0	2 1220,6165	313	323
							IVYGHLDDPANQEIER	к	G 95,00%	2,55	0,301	-0,342	0	1 0	0	2 1868,9144	69	84
							LEAPDADELPR	ĸ	S 95,00%	2,33	0,159	0,62	0	1 0	0	2 1225,6067	524	534
							NAVTOFFGPVPDTAR	R	Y 95,00%	2.59	0,348	-0.146	0	2 0	0	2 1247,0036	634	648
							NINIVR	ĸ	K 95,00%	1,71	0,0453	1,43	1	0 0	ō	2 728,4418	51	56
							SQFTITPGSEQIR	к	A 95,00%	3	0,391	0,62	0	1 0	0	2 1463,7495	412	424
							VGLIGSCTNSSYEDMGR	R	S 95,00%	2,64	0,428	0	0	2 0	0	2 1845,8113	379	395
		100.00%	4	4		0.16%	7 54% LTGTLSGWTSPK	R	E 95,00%	3,25	0,366	0,367	0	2 0	0	2 1007,7000	65/ 224	246
		100,00%	4	*	-	0,10%	SDFDPGQDTYQHPPK	R	D 95.00%	3.26	0.386	ő	0	0 1	0	2 1247,0036	535	549
							VGLIGSCTNSSYEDMGR	R	S 95,00%	2,3	0,363	0	0	1 0	0	2 1845,8113	379	395
							WVVIGDENYGEGSSR	R	E 95,00%	2,39	0,213	0	0	1 0	0	2 1667,7666	657	671
Manufacture execution entropy of the sector	( 7002 0	100.000/	2			0.20%	A DEV. ALCIEDED	0	K OF OOK	1.50	0.0045	2.54	0	2	0	0.007 5110	272	370
moreni (neurenne-ordeniend externeur deze brocen) - round aduerta (rounen) - moren-roused	07003,0	100,0070	3	-	-	0,2070	AQMVQEDLEK	ĸ	T 95,00%	2,85	0,123	1,54	0	1 0	0	2 1206,5677	449	458
							AQQELEEQTR	к	R 95,00%	2,86	0,258	1,1	0	1 0	0	2 1231,592	361	370
Pyrivate kinase isozymes M1/M2 (EC 2.7.1.40) (Pyrivate kinase miscle isozyme) - IKPYM_RAT	57800.6	100.00%	6	8	9	0.38%	11 90% AATESEASDPILYR	R	P 95.00%	2.62	0 393	0	0	1 0	0	2 1540 7648	93	106
		,	-			-,	APIIAVTR	R	N 95,00%	1,67	0,279	1,92	1	0 0	0	2 840,5308	448	455
							GDYPLEAVR	к	M 95,00%	2,61	0,339	2,54	0	1 0	0	2 1019,5163	368	376
							GIFPVLCK	R	D 95,00%	1,87	0	2,96	0	1 0	0	2 933,5234	468	475
							NTGIICTIGPASR	R	S 95.00%	2,75	0,403	4,65	0	3 0	0	2 1359.7057	44	43 56
Pyruvate kinase isozymes M1/M2 (EC 2.7.1.40) (Pyruvate kinase muscle isozyme) - IKPYM_RAT	57800,6	100,00%	5	8	9	0,41%	9,61% APIIAVTR	R	N 95,00%	1,65	0,178	1,43	1	<u>a o</u>	0	2 840,5308	448	455
							LALAAVEHR ITI DNAVMER	R	C 95,00%	2,09	0,106	3,37	0	2 0	0	2 1029,5118	384	392
							LDIDSAPITAR	R	N 95.00%	2.97	0,348	1.5	0	1 0	0	2 1213,5776	33	43
							NTGIICTIGPASR	R	S 95,00%	3,73	0,384	2,09	0	3 0	0	2 1359,7057	44	56
T. complex protein 1 subunit damma (TCP, 1, damma) (CCT, damma) , Por taunus (PoTCPG, POMIN	40549.2	100.00%	2	2	2	0.09%	4 22% AVAGALEVIDE	P	T 95.00%	2.04	0.208	2 20	0	1 0	0	2 1166 6999	429	440
r-complex protein r subunit gamma (rce-r-gamma) (cor-gamma) - Bos tauros (Borrero_Bovin	00307,2	100,00%	4	-	-	0,04%	4,22% AVADALEVIPR TLIONCGASTIR	R	L 95.00%	3.53	0.371	-0.447	0	1 0	0	2 1333.6899	450	447
Fascin (Singed-like protein) - Mus musculus (Mouse) FSCN1_MOUSE	54490,2	100,00%	4	4	4	0,19%	9,13% FLVVAHDDGR	R	W 95,00%	2,13	0,11	1,21	0	1 0	0	2 1128,5802	91	100
							YEGGTEDR	R	L 95,00%	0	0,152	2,75	0	1 0	0	2 944,4114	111	118
							YLAADKDGNVTCER	R	E 95,00%	2,66	0,326	0	0	1 0	0	2 1611,7439	69	82
Septin-TT - Homo sapiens (Human) SEPTI_HUMAN	49381,1	100,00%	3	3	3	0,16%	FESDPATHNEPGVR	ĸ	K 95,00%	2.05	0,451	-0.0414	0	1 0	0	2 1957,0105	400	418
							SYELQESNVR	R	L 95,00%	2,5	0,267	2,08	ō	1 0	ō	2 1224,5859	84	93
								"										
Prospilogiyterate kitase ( (cc 2.7.2.3) - mus inusculus (mouse) PGK1_mOUSE	44033,1	100,00%	3	2	-	0,1995	VI NNMEIGTSLYDEEGAK	ĸ	95,00%	2.58	0.37	1,4	2	1 0	0	2 1998 9331	247	264
							VLPGVDALSNV	ĸ	- 95,00%	2,76	0,212	1,4	0	1 0	ō	2 1083,6051	407	417
Aspartate aminotransferase, cytoplasmic (EC 2.6.1.1) (Transaminase A) (Glutamate AATC_RAT	46411,5	100,00%	4	5	5	0,28%	13,10% ITWSNPPAQGAR	R	I 95,00%	3,01	0,308	1,17	0	0 1	0	2 1297,6654	294	305
							SCASQLVLGDNSPALR	R	E 95,00%	2,26	0,254	-1	0	2 0	0	2 1687,8439	82	97
							VGGVQSLGGTGALR	R	I 95,00%	3,4	0,378	4,64	0	1 0	0	2 1271,7074	101	114
		100,00%	2	2	3	0,17%	6,30% LIADFRDDPDPR	ĸ	K 95,00%	3,31	0,245	0	0	3 1	0	2 1429,708	21	32
							VGGVQ3EGGTGAER	ĸ	45,00%	2,41	0,293	0	0	2 0	0	2 12/1,/0/4	101	114
Creatine kinase M-type (EC 2.7.3.2) (Creatine kinase M chain) (M-CK) - Mus musculi KCRM_MOUSE,KCRM_RAT	43027,6	100,00%	1	2	3	0,16%	3,68% GGDDLDPNYVLSSR	к	V 95,00%	2,88	0,414	-0,505	0	3 0	0	2 1507,7031	117	130
l ong-chain specific acvi. Coà debydrogenase, mitochondrial pregator (EC 1 2 99 12) ACADI - DAT	47855.9	100.00%	6	0	0	0.24%	13 70% AODTAELEEEDVP	ĸ	1 05.009	3.94	0.422	948.0	0	1 0	6	2 1540 7397	255	267
	*****	100,0070				0,0470	IFSSEHDIFR	R	E 95,00%	2,42	0,342	2,36	0	1 0	0	2 1250,6169	52	61
							LPASALLGEENK	R	G 95,00%	3,73	0,323	3,54	0	4 0	0	2 1241,6743	268	279
							SGSDWILNGSK	R	V 95,00%	0	0	2,55	0	1 0	0	2 1163,5698	191	201
		100.00%	2		4	0.26%	VQPIYGGTNEIMK 5.13% IESSEUDIED	R	E 95,00%	2,51	0,432	0	0	1 0	0	2 1465,7363	407	419
			-	-	-	-,	LPASALLGEENK	R	G 95,00%	3,5	0,339	0	0	5 0	0	2 1241,6743	268	279
									-									
Serum albumin precursor (Allergen Equ c 3) - Equus caballus (Horse) ALBU_HORSE	68581,9	100,00%	6	6	7	0,35%	9,56% APOVSTPTLVEIGR	ĸ	T 95,00%	2,27	0,409	-1,42	0	2 0	0	2 1467,8174	438	451
							LPCSENHLALALNR	R	к 95,00% L 95,00%	2,10	0,308	3,15	0	1 0	0	2 1111,4514 2 1607,8329	499	482
							QIKKQSALAELVK	ĸ	H 95,00%	0	0	4,13	0	0 1	ő	2 1438,8636	545	557
							QSALAELVK	к	H 95,00%	1,91	0,166	2,26	0	1 0	0	2 958,5574	549	557
							TYEATLEK	к	L 95,00%	1,59	0,282	1,75	1	J 0	0	2 954,4784	375	382
Macrophage-capping protein (Actin-regulatory protein CAP-G) - Rattus norvegicus (RCAPG_RAT	38781,7	99,10%	2	3	3	0,16%	6,59% TTSGTTPAAIR	к	K 95,00%	1,95	0,0501	1,13	0	1 0	0	2 1075,5749	128	138
							VSDATGQMNLTK	к	V 95,00%	3,11	0,241	1,1	0	2 0	0	2 1280,6157	255	266
Aldose reductase (EC.1.1.1.21) (AP) (Aldebyde reductase) - Rattus popuenicus (Rat) ALDR .RAT	35779 7	100.00%	3	3	2	0.16%	7 91% EVGVALOEK	ĸ	I 95 00%	1.91	0.163	3 38	0	1 0	0	2 972 5267	54	62
www.reweiwe.teo.remail(RR) (Addingdo.reductaso) - Rattus Introgicus (Rat) ALDR_RAT	30/17,1	100,00%	3	3	3	0,10%	TTAQVLIR	ĸ	F 95,00%	2,8	0,235	4,05	0	1 0	0	2 901,5472	244	251
							VAIDMGYR	к	H 95,00%	2,02	0,194	3,48	0	1 0	0	2 940,4563	34	41
		100,00%	2	2	2	0,10%	5,38% EVGVALQEK	ĸ	L 95,00%	2,17	0,249	0	0	1 0	0	2 972,5367	54	62
							TINGVLIN	r.	· 45,00%	3,04	0,12	U	0	. 0	U	2 9U1,5472	244	201
Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH) - Columba livia G3P_COLLI	35748,9	100,00%	2	2	2	0,10%	8,11% GAAQNIIPASTGAAK	R	A 95,00%	3,09	0,154	0,569	0	1 0	0	2 1369,7441	199	213
							VVDLMVHMASKE	R	- 95,00%	2,56	0,232	0	0	. 0	0	2 1390,671	322	333
Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose-phosphate isomerase) - Rattu TPIS_RAT	26830.7	100,00%	3	4	4.	0,25%	16,50% CNVSEGVAQCTR	к	I 95.00%	1.94	0,264	0	0	1 0	0	2 1380.6001	195	206
							HIFGESDELIGQK	R	V 95,00%	2,51	0,296	-0,748	0	1 1	0	2 1472,7388	101	113
							VTNGAFTGEISPGMIK	ĸ	D 95.00%	2.23	0.263	0	0	1 0	0	2 1637.8212	70	85

ATP synthase D chain, mitochondrial (EC 3.6.3.14) - Rattus norvegicus (Rat) ATP5H RAT	18746	100.00%	3	4	5 0.25%	24.20% ANVDKPGLVDDFK	R	N 95.00%	2.78	0.329	-0.74	0	1	1	0	2 1417.7329	59	71
						NCAQFVTGSQAR	к	V 95,00%	3,05	0,262	-0,875	0	2	0	0	2 1338,6224	100	111
						YTALVDAEEKEDVK	к	N 95,00%	3,18	0,292	0	0	1	0	0	2 1609,7963	86	99
		99,80%	2	2	2 0,10%	16,80% ANVDKPGLVDDFK	R	N 95,00%	2,98	0,338	0	0	1	0	0	2 1417,7329	59	71
						YTALVDAEEKEDVK	к	N 95,00%	3,52	0,323	0	0	1	0	0	2 1609,7963	86	99
													-					50
Myosin regulatory light chain 2, ventricular/cardiac muscle isotorm (MLC-2) (MLC-2V,MLKV_BOVIN	18963,3	100,00%	5	6	6 U,32%	24, 10% DIFAALGR	R	V 95,00%	1,72	0,0754	1,19	1	0	0	0	2 850,4424	51	58
						ENTTOATD	K K	5 95,00%	2,78	0,133	0,215	0		0	0	2 1240,5632	101	100
						NIVHITHGEFK	ĸ	P 95,00%	2 73	0.215	-0.204	0	2	0	0	2 1389 7493	154	165
						NI VHII THGEEKD	ĸ	95.00%	2.87	0.384	0	0	1	0	0	2 1504 7762	154	166
T-complex protein 1 subunit zeta (TCP-1-zeta) (CCT-zeta-1) (TCp20) (HT TCPZ_HUMAN, TCPZ_PONPY	58007,3	100,00%	3	4	4 0,19%	5,46% ALQFLEEVK	к	V 95,00%	1,91	0	1,89	0	1	0	0	2 1076,5994	130	138
						MLVSGAGDIK	к	L 95,00%	2,65	0,207	3,02	0	1	0	0	2 1006,5244	46	55
						TEVNSGFFYK	к	S 95,00%	1,82	0,0381	2,11	0	2	0	0	2 1191,5686	242	251
														-				
Myosin regulatory light chain 2A, cardiac muscle isotorm (G2) (MLC-2A) - Gallus gallMLKA_CHICK	18688,1	44,80%	2	5	18 3,49%	9,09% GADPEETILNAFK	ĸ	V 95,00%	3,84	0,21	1,2	0	8	0	0	2 1404,7013	92	104
						EKGADPEETILIVAFK	~	93,00%	-	0,331	0,52	0	-	0	0	2 1040,0004	90	104
Tronomyosin alpha, 4 chain (Tronomyosin, 4) (TM, 4) - Rattus norvegicus (Rat) TPM4 RAT	28492.4	100.00%	4	7	8 1 39%	17.70% IOLVEELDRAGER	R	1 95.00%	1.88	0.0703	6.51	0	0	1	0	2 1727 8929	56	69
······································						LVILEGELER	К	A 95.00%	2.68	0.292	4.92	0	1	0	0	2 1170.6736	133	142
						LVILEGELERAEER	к	A 95,00%	3,77	0,313	5,3	0	1	3	0	2 1655,897	133	146
						SSDLEEELKNVTNNLK	к	S 95,00%	4,75	0,281	6,6	0	2	0	0	2 1832,9242	154	169
Actin-1 - Aedes aegypti (Yellowfever mosquito) ACT1_AEDAE	41773,6	100,00%	5	9	24 1,89%	26,60% DLTDYLMK	R	1 95,00%	2,64	0,131	2,54	3	3	0	0	2 998,4871	185	192
						DLYANTVLSGGTTMYPGIADR	ĸ	M 95,00%	5,28	0,312	7	0	1	1	0	2 2231,0659	293	313
						KDI VANTA SCOTTAVDGIADD	P	M 95,00%	4 96	0,0191	10.2	0	0	1	0	2 1313,7490	202	212
						LDLAGRDI TDYLMK	R	1 95.00%	2 31	0,217	7.46	0	0	2	0	2 1639 8369	179	192
						SYELPDGQVITIGNER	ĸ	F 95,00%	3,83	0,318	6,08	ō	15	4	ō	2 1790,8926	240	255
						VAPEEHPVLLTEAPLNPK	R	A 95,00%	4,52	0,285	1,68	0	6	13	0	2 1954,0653	97	114
						VAPEEHPVLLTEAPLNPKANR	R	E 95,00%	3,49	0,086	2,96	0	0	1	0	2 2295,2463	97	117
						YPNEHGIITNWDDMEK	к	1 95,00%	2,42	-0,0819	3,52	0	1	0	0	2 1961,8706	70	85
Actin, muscle 2/4/4A - Halocynthia roretzi (Sea squirt) ACT2_HALRO	41997	100,00%	9	17	45 3,54%	28,30% DLTDYLMK	R	1 95,00%	2,64	0,131	2,54	3	3	0	0	2 998,4871	187	194
						CVED/TAED	N	M 95,00%	4,67	0,248	3,66	0	-		0	2 2244,001	295	313
						IMULTEVNELD	r v	V 95.00%	2 22	0.0191	4,00	0	ô	2	0	2 1616 7494	200	09
						KDLYANNVLSGGTTMYPGIADR	R	M 95.00%	5.2	0.158	2.85	ő	ö	2	ő	2 2372.156	294	315
						LDLAGRDLTDYLMK	R	1 95.00%	2.31	0	7.46	0	0	2	0	2 1639.8369	181	194
						SYELPDGQVITIGNER	к	F 95,00%	3,83	0,318	6,08	0	15	4	0	2 1790,8926	242	257
						VAPEEHPTLLTEAPLNPK	R	A 95,00%	3,84	0,18	5,3	0	4	4	0	2 1956,0447	99	116
						YPIEHGIITNWDDMEK	к	I 95,00%	3,87	0,116	2,75	0	0	1	0	2 1976,9066	72	87
-																		
Tropomyosin-1 alpha chain (Alpha-tropomyosin) - Horno sapiens (Human) TPM1_HUMAN	32692	100,00%	9	16	42 5,10%	33,80% CAELEEELK	ĸ	T 95,00%	2.42	0 334	3,52	1	5	0	0	2 1103,4933	190	198
						GTEDEL DKYSEALKDAOEK	r v	1 95,00%	3,43	0,334	7.42	0	0	3	0	2 1070,7404	52	205
						IOI VEEEI DR	R	A 95.00%	2 79	0.155	4.16	0	5	0	0	2 1243 6536	92	101
						IQLVEEELDRAQER	R	L 95,00%	2,15	0,0281	4,15	ō	ō	1	ō	2 1727,8929	92	105
						LVIIESDLERAEER	к	A 95,00%	1,88	0,0172	3,59	0	0	1	0	2 1671,8918	169	182
						MEIQEIQLK	к	E 95,00%	2,72	0,0549	5	0	1	0	0	2 1131,6086	141	149
						QLEDELVSLQK	к	K 95,00%	0	0	4,11	1	11	0	0	2 1284,669	38	48
						SIDDLEDELYAQK	к	L 95,00%	4,67	0,428	8,26	0	6	4	0	2 1538,7228	252	264
VINE_BOVIN				2	4 0.439/	A 70K ULAFLEOLK	~	C 0E 00W	2.24	0.222	F F 2	0	2	0	0	2 11/0 71/0	120	120
	55710,0	100,00%	2	2	4 0,42%	4,72% ILLAELEQLK VESLOFFIAFI K	ĸ	G 95,00%	3,34	0,222	5,52	0	3	0	0	2 1169,7148	130	139
	33710,0	100,00%	2	2	4 0,42%	4,72% ILLAELEOLK VESLQEEIAFLK	ĸĸ	G 95,00% K 95,00%	3,34 3,19	0,222 0,192	5,52 6,85	0	3 1	0	0	2 1169,7148 2 1405,7581	130 224	139 235
Vimentin - Bos taurus (Bovine) VIME_BOVIN	53710,8	100,00%	2	2	4 0,42%	4,72% ILLAELEOLK VESLOEEIAFLK 4,51% ILLAELEOLK	к к	G 95,00% K 95,00%	3,34 3,19 3,51	0,222 0,192 0,209	5,52 6,85 6,19	0	3 1 1	0 0	0	2 1169,7148 2 1405,7581 2 1169,7148	130 224 130	139 235 139
Vimentin - Bos taurus (Bovine) VIME_BOVIN	53710,8	100,00%	2	2	4 0,42% 2 0,21%	4,72% ILLAELEOLK VESLOEEIAFLK 4,51% ILLAELEOLK MALDIEIATYR	K K K	G 95,00% K 95,00% G 95,00% K 95,00%	3,34 3,19 3,51 3,44	0,222 0,192 0,209 0,276	5,52 6,85 6,19 6,16	0 0 0	3 1 1 1	0 0 0	0 0 0 0 0 0	2 1169,7148 2 1405,7581 2 1169,7148 2 1311,662	130 224 130 391	139 235 139 401
Vimenin - Box Isarus (Bovino) VIME_BOVIN	53710,8	100,00%	2	2	4 0,42% 2 0,21%	4,72% ILLAELEOLK VESLOEEIAFLK 4,51% ILLAELEOLK MALDIEIATYR	K K K	G 95,00% K 95,00% G 95,00% K 95,00%	3,34 3,19 3,51 3,44	0,222 0,192 0,209 0,276	5,52 6,85 6,19 6,16	0	3 1 1 1	0	0	2 1169,7148 2 1405,7581 2 1169,7148 2 1311,662	130 224 130 391	139 235 139 401
Vimentin - Bos taurus (Bovine) VIME_BOVIN ATP synthwse subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (HATPB_HUMAN	53710,8	100,00%	2	2	4 0,42% 2 0,21% 27 4,86%	4,72% ILLAELECK VESIOEEIAALK 4,51% ILLAELECK MALDIEIATYR 22,90% AIAELEIYPANDPLDSTSR	K K K	G 95,00% K 95,00% G 95,00% K 95,00% I 95,00%	3,34 3,19 3,51 3,44 3,15	0,222 0,192 0,209 0,276 0,0584	5,52 6,85 6,19 6,16 2,47	0	3 1 1 1		0	2 1169,7148 2 1405,7581 2 1169,7148 2 1311,662 2 1988,0343	130 224 130 391 388	139 235 139 401 406
Vimentin - Bos taurus (Bovine) VIIME_BOVIN ATP synthase subunit beta, mitochendrial precursor (EC 3.6.3.14) - Hono sapiens (hATPB_HLMAN	53710,8	100,00%	2	2 2	4 0,42% 2 0,21% 27 4,86%	4,72% ILLAELOOK VESLOEEIAFLK 4,51% ILLAELOOK MALDIEIATVR 22,90% AIAELGIYPAVDPLDSTSR ECROLYHEMISSQVINLK	K K K R	G 95,00% K 95,00% G 95,00% K 95,00% I 95,00% I 95,00%	3,34 3,19 3,51 3,44 3,15 3,42 2,47	0,222 0,192 0,209 0,276 0,0584 0	5,52 6,85 6,19 6,16 2,47 6,3 8,32	0 0 0 0	3 1 1 1	0 0 0 0 2 2		2 1169,7148 2 1405,7581 2 1169,7148 2 1311,662 2 1988,0343 2 2076,9912 2 1475,7545	130 224 130 391 388 242 211	139 235 139 401 406 259
Vimentin - Box taurus (Bovino) VIME_BOVIN ATP symbase suburit beta, mitochondrial procursor (EC 3.4.3.14) - Homo sapiens (-ATPB_HEAMA	53710,8	100,00%	2	2	4 0,42% 2 0,21% 27 4,86%	4,72% ILLAELEGLK VESIGEIAPIK 4,51% ILLAELEGLK MALDEIATYR 22,90% ARELGIVPADVELOSTSR EGONOLYKAMISSONINK FFORASSIVSALIGR UV EVADHI GESTVP	K K K R R R R	G         95,00%           K         95,00%           G         95,00%           K         95,00%           I         95,00%           D         95,00%           I         95,00%           T         95,00%	3,34 3,19 3,51 3,44 3,15 3,42 3,67 4,79	0,222 0,192 0,209 0,276 0,0584 0 0,279 0,53	5,52 6,85 6,19 6,16 2,47 6,3 8,22 9,75	0 0 0 0	3 1 1 1 1 0 4 4	0 0 0 2 2 5		2 1169,7148 2 1405,7581 2 1169,7148 2 1311,662 2 1988,0343 2 2076,9912 2 1435,7545 2 1435,7545	130 224 130 391 388 242 311 95	139 235 139 401 406 259 324 109
Vimentin - Bos taurus (Bovinc) VIME_BOVIN ATP symthate subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (PATPB_HEMANA	53710,8 56542,5	100,00%	2 8	2	4 0,42% 2 0,21% 27 4,86%	4,72% ILLALECK K VFSLOELAFLK 4.51% ILLALECK MALDIEATYR 22,90% AIAELOPAUPPLSTSR EGRUTYMMESONIK FORDERSON VVENDERGER TVLMUNDERGER TVLMUNDERGER	K K K R R R R K	G         95,00%           K         95,00%           G         95,00%           K         95,00%           I         95,00%           D         95,00%           I         95,00%           T         95,00%           T         95,00%           A         95,00%	3,34 3,19 3,51 3,44 3,15 3,42 3,67 4,79 4,19	0,222 0,192 0,209 0,276 0,0584 0 0,279 0,53 0,335	5,52 6,85 6,19 6,16 2,47 6,3 8,22 9,75 8,96	0 0 0 0 0 0 0 0 0	3 1 1 1 0 4 4 3	0 0 0 2 2 5 0		2 1169,7148 2 1405,7581 2 1169,7148 2 1311,662 2 1988,0343 2 2076,9912 2 1435,7545 2 1650,918 2 1433,8351	130 224 130 391 388 242 311 95 213	139 235 139 401 259 324 109 225
Vimentin - Bos taurus (Bovino) VIME_BOVIN A19 synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapieris (P.4178_HB.4644	53710,8 56542,5	100,00%	2 8	2	4 0,42% 2 0,21% 27 4,86%	4.72% HLARECOLK VESIGERATIK 4.51% ILARECOLK MADDIELATYR 20,0% ARECHTWARDADDTSR EONXYHMINSOVINIL FTOACSOVALLOR UNDERGSTVR UNDERGSTVR VALTOLIVERYR	K K R R R R R R R R	G         95,00%           K         95,00%           G         95,00%           I         95,00%           D         95,00%           I         95,00%           T         95,00%           A         95,00%           D         95,00%	3,34 3,19 3,51 3,44 3,15 3,42 3,67 4,79 4,19 3,97	0,222 0,192 0,209 0,276 0,0584 0 0,279 0,53 0,335 0,077	5,52 6,85 6,19 6,16 2,47 6,3 8,22 9,75 8,96 8,13		3 1 1 1 0 4 4 3 1	0 0 0 2 2 5 0 0		2 1169,7148 2 1405,7581 2 1169,7148 2 1311,662 2 1988,0343 2 2076,9912 2 1435,7545 2 1650,918 2 1473,8351 2 1439,7899	130 224 130 391 388 242 311 95 213 282	139 235 139 401 406 259 324 109 225 294
Vimentin - Bos taurus (Bovine) VIII <u>E</u> BOVIN ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiene (PATPB_HUMAN	53710,8 56542,5	100,00%	2	2	4 0,42% 2 0,21% 27 4,86%	4.77% ILLARICAL VISIOLEMAIL 4.51% ILLARICAL 22.00% ADALEMAN CONTRACTOR CONTRACTOR VISIOLEMAN VISIONALIAN VISIONALIAN VISIONALIAN VISIONALIAN VISIONALIAN VISIONALIAN	K K K R R R R K K K	G         95,00%           K         95,00%           G         95,00%           D         95,00%           I         95,00%           I         95,00%           T         95,00%           A         95,00%           D         95,00%           D         95,00%           I         95,00%           J         95,00%           J         95,00%           J         95,00%           J         95,00%	3,34 3,19 3,51 3,44 3,15 3,42 3,67 4,79 4,19 3,97 4,67	0,222 0,192 0,209 0,276 0,0584 0,053 0,279 0,53 0,335 0,077 0,335	5,52 6,85 6,19 6,16 2,47 6,3 8,22 9,75 8,96 8,13 16	0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 1 1 1 0 4 4 4 3 1 0	0 0 0 2 2 5 0 0 2	0 0 0 0 0 0 0 0 0 0 0 0	2 1169,7148 2 1405,7581 2 1169,7148 2 1311,662 2 1988,0343 2 2076,9912 2 1435,7545 2 1650,918 2 1473,8351 2 1439,7899 2 1919,097	130 224 130 391 388 242 311 95 213 282 2125	139           235           139           401           259           324           109           225           294           143
Vimentin - Box taurus (Bovine) VIME_BOVIN ATP symthaes subunit beta, mitochondrial procursor (EC 3.6.3.14) - Homo sapiens (HATPB_HIAMAN	53710,8 56542,5	100,00%	2	2	4 0,42% 2 0,21% 27 4,86%	4.72% HLABECKK VESLGEHARK 4.51% HLABECK MALDIELATR 2.0% ALEURAVEN FOROSVSLLOR UNEVADIELOSTSR EONIX HEMISSOVALLOR UNEVADIELOSTVR TVI.IMELINWAK VLDSCARKEPVCPFTLOR VLDSCARKEPVCPFTLOR VLDSCARKEPVCPFTLOR	K K R R R R R K K K K	G         95,00%           K         95,00%           G         95,00%           I         95,00%           D         95,00%           I         95,00%           T         95,00%           A         95,00%           D         95,00%           G         95,00%           G         95,00%           G         95,00%	3,34 3,19 3,51 3,44 3,15 3,42 3,67 4,79 4,19 3,97 4,67 2,62	0,222 0,192 0,209 0,276 0,0584 0,053 0,335 0,077 0,375 0,0835	5,52 6,85 6,19 6,16 2,47 6,3 8,22 9,75 8,96 8,13 16 4,37		3 1 1 1 0 4 4 3 1 0 3	0 0 0 2 2 5 5 0 0 0 2 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 1169,7148 2 1405,7581 2 1149,7148 2 1311,662 2 1988,0343 2 2076,9912 2 1473,8351 2 1473,8351 2 1439,7899 2 1919,097 2 1088,6357	130 224 130 391 388 242 311 95 213 282 125 189	139           235           139           401           259           324           109           225           294           143           198
Vimentin - Box taurus (Bovine) VIME_BOVIN ATP synthase suburit beta, mitochondrial precursor (IC 3.6.3.14) - Homo sapiene (FATPB_HUMAN	53710,8 56542,5	100,00%	2 8	2	4 0,42% 2 0,21% 27 4,86%	4.72% ILLARICOLK VESLOCERATIK 4.51% ILLARICOLK MADIELATYR COREX VERMING ECOREX VERMING ECOREX VERMING ECOREX VERMING ECOREX VERMIN ECOREX VER	K K K R R R R R K K K K	G         95,00%           K         95,00%           G         95,00%           I         95,00%           D         95,00%           T         95,00%           T         95,00%           D         95,00%           J         95,00%           G         95,00%           G         95,00%           G         95,00%           G         95,00%	3,34 3,19 3,51 3,44 3,15 3,42 3,67 4,79 4,19 3,97 4,67 2,62	0,222 0,192 0,209 0,276 0,0584 0,0,53 0,035 0,077 0,335 0,077 0,375	5,52 6,85 6,19 6,16 2,47 6,3 8,22 9,75 8,96 8,13 16 4,37		3 1 1 1 0 4 4 3 1 0 3	0 0 0 2 2 5 0 0 2 2 0 0 2 0 0 2		2 1149,7148 2 1405,7581 2 1149,7148 2 1311,662 2 1988,0343 2 2076,9912 2 1435,7545 2 1650,918 2 1473,8351 2 1473,8351 2 1439,7899 2 1919,097 2 1088,6357	130 224 130 391 388 242 311 95 213 282 125 189	139           235           139           401           406           259           324           109           225           294           143           198
Vimentin - Box taurus (Bovine) VIME_BOVIN ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (PATPB_HIAMAN ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (PATPB_HIAMAN	56542,5	100,00%	2 8 10	2 14 16	4 0,42% 2 0,21% 27 4,86% 37 12,90%	4.72% ILLEECEK     VISUELEALK     VISUELEALK     4.51% ILLEECEK     MURIELEATR     VISUELEATR     EORAVTWENTSOVINK     FOAGSSVSALLOR     LIVLIVARISOVINK     FOAGSSVSALLOR     VISUELEATR     VISUEL	K K K R R R R K K K K	G         95,00%           K         95,00%           G         95,00%           D         95,00%           J         95,00%           J         95,00%           J         95,00%           J         95,00%           J         95,00%           G         95,00%           G         95,00%           J         95,00%           G         95,00%           J         95,00%	3,34 3,19 3,51 3,44 3,15 3,42 3,67 4,79 4,79 4,67 2,62 3,15	0,222 0,192 0,209 0,276 0,0584 0 0,0584 0,053 0,077 0,375 0,0835 0,0598	5,52 6,85 6,19 6,16 2,47 6,3 8,22 9,75 8,96 8,13 16 4,37 8,28		3 1 1 1 0 4 4 3 1 0 3 1 0 3	0 0 0 2 2 5 0 0 2 2 0 0 2 0		2 1169,7148 2 1405,7581 2 1169,7148 2 1311,662 2 1998,0343 2 2076,9912 2 1435,7545 2 1650,918 2 1439,7545 2 1650,918 2 1439,8599 2 1919,097 2 1088,6357 2 1998,0043	130 224 130 391 388 242 311 95 213 282 125 189 388 282 388	139 235 139 401 406 259 324 109 225 294 143 198 406
Vimentin - Bos taurus (Borino) VIME_BOVIN ATP synthase suburit beta, mitochondrial precursor (IC 3 & 3.16) - Homo sapiens (PATPB_HRAMA ATP synthase suburit beta, mitochondrial precursor (IC 3 & 3.14) - Homo sapiens (PATPB_HRAMA	53710,8 533710,8 56542,5 56542,5	100,00%	2 8 10	2 2 14 16	4 0,42% 2 0,21% 27 4,86% 37 12,90%	4.72% HLARLOOK VESLOEHALK 4.51% ILLARLOOK MADDIGATYR CORDUNEMICSONNAK CORDUNEMICSONNAK HUELONAKA VICTOREN VELINENNAK VILDSGAMINYOFELDR VILDSGAMINYOFELDR VILDSGAMINYOFELDR VILDSGAMINYOFELDR VIDSGAMINYOFELDR VIDSGAMINYOFELDR VIDSGAMINYOFELDR VIDSGAMINYOFELDR VIDSGAMINYOFELDR VIDSGAMINYOFELDR	K K K R R R R R K K K K R R K K	G         95,00%           K         95,00%           G         95,00%           L         95,00%           D         95,00%           T         95,00%           A         95,00%           L         95,00%           G         95,00%           G         95,00%           J         95,00%           G         95,00%           G         95,00%           I         95,00%           I         95,00%           J         95,00%           S         95,00%	3,34 3,19 3,51 3,44 3,15 3,42 3,67 4,79 4,79 4,79 4,79 3,97 4,67 2,62 3,15 0 4,26	0,222 0,192 0,209 0,276 0,0584 0 0,53 0,077 0,335 0,077 0,335 0,077 0,335 0,0835 0,0598 0 0,0598	5,52 6,85 6,19 6,16 2,47 6,3 8,22 9,75 8,96 8,13 16 4,37 8,28 5,19 9,7		3 1 1 1 0 4 4 3 1 0 3 3 1 0 3 4	0 0 0 2 2 2 5 0 0 0 2 0 0 0 1 1 2		2 1149,7148 2 1405,7581 2 1149,7148 2 1311,662 2 1988,0343 2 1076,9912 2 1425,7545 2 1650,918 2 1473,8251 2 1459,7545 2 1698,6357 2 1998,0343 2 1088,6357	130 224 130 391 388 242 311 95 213 282 125 189 388 242 311	139           235           139           401           406           259           324           109           225           294           143           198           406           259           324           09           225           294           143           198           406           259           324
Vimentin - Box taurus (Bovine) VIME_BOVIN ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (I-ATPB_HLAMAN ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (I-ATPB_HLAMAN	53710,8 53710,8 56542,5 56542,5	100,00%	2 8	2 14 16	4 0,42% 2 0,21% 27 4,86% 37 12,90%	4.72% ILLARICAL VESLEHARK     4.51% ILLARICAN     4.61% ILLARICAN     22.90% AIALIGINANDRIGHTS     22.90% AIALIGINANDRIGHTS     10005459ALIGR     10004000     1000400	K K K R R R R R K K K K K K R R R R R R	G 99,00% K 99,00% C 99,00% D 99,00% D 99,00% D 99,00% T 99,00% T 99,00% C 99,00% I 99,00% I 99,00% C 99,00% C 99,00%	3,34 3,19 3,51 3,44 3,15 3,42 3,67 4,79 4,19 3,97 4,67 2,62 3,15 0 4,36 3,07	0,222 0,192 0,276 0,279 0,279 0,058 0,058 0,058 0,058 0,058 0,0685 0,0685 0,0598 0,24 0,0891	5,52 6,85 6,19 6,16 2,47 6,3 8,22 9,75 8,96 8,13 16 4,37 8,28 5,19 9,7 5,54		3 1 1 1 4 4 3 1 0 3 1 0 4 4 2	0 0 0 2 2 5 5 0 0 2 2 0 0 2 0 0 1 2 0		2 1169,7148 2 1405,7581 2 1169,7148 2 1311,662 2 1988,0343 2 2076,9912 2 1435,7545 2 1455,7545 2 1455,7545 2 1453,7545 2 1473,8351 2 1473,8351 2 1473,8351 2 1998,0343 2 1998,0343 2 109,6912 2 105,7545 2 1355,7545	130 224 130 391 288 242 311 95 213 282 125 189 388 242 311 144	139           235           139           401           259           324           109           294           198           406           259           324           198           406           259           324           198           405           259           324           155
Vimentin - Bos taurus (Bovine) VIII6_BOVIN ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapieras (P.ATPB_HEBANA ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapieras (P.ATPB_HEBANA	53710,8 533710,8 56542,5 56542,5	100,00%	2 8 10	2 14 16	4 0,42% 2 0,21% 27 4,86% 37 12,90%	4.72% ILLAELCOK VESIGERAFIK     4.51% ILLAELCOK MADIELAIYR     MADIELAIYR     ECORUNYEMISOVINK     FICIOLSYNALLCO     CORUNYEMISOVINK     VIDSCAMIERVORTOR     VIDSCAMIERVORTOR     VIDSCAMIERVORTOR     VIDSCAMIERVORTOR     VIDSCAMIERVORTOR     POOKSEVALLCR     FICIOLSEVALLCR      FICIOLSEVALCR      FICIOLSEVALLCR      FICIOL	K K K R R R R R R K K K K K K K R R R R	G         95,00%           K         95,00%           G         95,00%           I         95,00%           D         95,00%           J         95,00%           G         95,00%           G         95,00%           G         95,00%           G         95,00%           G         95,00%	3,34 3,19 3,51 3,44 3,42 3,67 4,79 4,19 3,97 4,67 2,62 3,15 0 4,36 3,07 6,72	0,222 0,192 0,276 0,0584 0,058 0,053 0,335 0,077 0,335 0,0835 0,0835 0,0598 0 0,24 0,0891 0,368	5,52 6,85 6,19 6,16 2,47 6,3 8,22 9,75 8,96 8,13 16 4,37 8,28 5,19 9,7 5,54 11,7		3 1 1 1 0 4 4 3 1 0 3 1 0 4 2 0	0 0 0 2 2 5 5 0 0 2 0 0 0 1 1 2 0 1		2 1169,7148 2 1405,781 2 1169,7148 2 1311,662 2 1998,0043 2 4076,9912 1 4157,7445 2 1457,7445 2 1457,7445 2 1457,7445 2 1457,7445 2 1457,7445 2 1998,4357 2 1998,4377 2 1997,4377 2 1997,43777 2 1997,43777 2 1997,437777777777777777777777777777777777	130 224 130 391 388 242 311 95 213 282 125 189 388 242 311 144 325	139           235           139           401           406           224           109           224           109           224           198           406           259           324           198           406           259           324           155           345
Vimentin - Box taurus (Bovine) VIME_BOVIN ATP synthese subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiene, (FATPB_HEAMN ATP synthese subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiene, (FATPB_HEAMN)	53710,8 53710,8 56542,5 56542,5	100,00%	2 8	2	4 0,42% 2 0,21% 27 4,86% 37 12,90%	4.72% ILLARICAL VISUELEANIX     4.51% ILLARICAL     MADELEANIX     MADELEANIX     MADELEANIX     MADELEANIX     CONSCIPUENT     CONSCIPU	к к к к к к к к к к к к к к к к к к к	G         99,00%           K         99,00%           G         99,00%           I         99,00%           I         99,00%           I         99,00%           I         99,00%           I         99,00%           G         99,00%           G         99,00%           G         99,00%           I         99,00%	3,34 3,19 3,51 3,44 3,45 3,42 3,67 4,79 4,19 3,97 4,67 2,62 3,15 0 4,36 3,07 6,72 4,63	0,222 0,192 0,209 0,276 0,0584 0,053 0,077 0,335 0,0835 0,0835 0,0835 0,0835 0,0835 0,0835 0,0835 0,0835	5,52 6,85 6,19 6,16 2,47 6,3 8,22 9,75 8,96 8,13 16 4,37 8,28 5,19 9,7 5,54 11,7 10,5		3 1 1 0 4 4 3 1 0 3 3 1 0 3 3 1 0 5	0 0 0 2 2 5 5 0 0 2 0 0 2 0 0 1 2 0 0 1 7	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 1169,7148 2 1405,7581 2 1169,7148 2 1311,662 2 1988,0343 2 2076,9912 2 1435,7545 2 1450,918 2 1473,8331 2 1473,8331 2 1970,097 2 1088,0343 2 2076,9912 2 1088,0347 2 1988,0343 2 2076,911 2 1385,7101 2 1385,7101 2 1385,7101	130 224 130 391 288 242 311 95 213 282 125 189 388 242 311 144 325 95	139           235           139           401           406           259           324           139           400           229           224           133           198           406           259           324           259           324           355           345           109
Vimentin - Bos taurus (Bovine) VIME_BOVIN ATP synthase subunit bela, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (PATPB_HEMANI ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (PATPB_HEMANI	53710,8 532710,8 56542,5 56542,5	100,00%	2 8	2	4 0,42% 2 0,21% 27 4,86% 37 12,90%	4.72% ILLEFECK     VISUELEARK     VISUELEARK     4.51% ILLEFECK     MADUELARR     VISUELEARR     VISUELEAR	K K K R R R R R R K K K K K K K K	G         99,00%           K         99,00%           G         99,00%           I         99,00%           D         93,00%           D         93,00%           J         99,00%           J         99,00%           J         99,00%           J         99,00%           J         99,00%           I         99,00%	3,34 3,19 3,51 3,44 3,15 3,42 3,67 4,79 4,79 4,67 2,62 3,15 0 4,67 2,62 3,15 0 4,36 3,07 4,67 2,62 4,63 3,07 4,72 4,63 3,07 4,72	0,222 0,192 0,209 0,276 0,0584 0,053 0,335 0,037 0,0375 0,0835 0,0598 0,024 0,0691 0,368 0,466 0,281	5,52 6,85 6,19 6,16 2,47 6,3 8,22 9,75 8,96 8,13 16 4,37 8,28 5,19 9,7 5,54 11,7 10,5 8,96		3 1 1 1 0 4 4 3 1 0 3 1 0 4 4 2 0 5 5 3	0 0 0 2 2 5 5 0 0 2 2 0 0 1 2 0 1 7 7 0		2 1146,7148 2 1405,7581 2 1405,7581 2 1311,662 2 1998,0343 2 0276,9912 1 1450,918 1 473,3851 1 473,3851 2 1439,7899 1 1919,097 2 1088,6357 2 1998,0343 2 0276,9912 2 1988,0351 2 2076,9912 2 1988,0351 2 2076,9912 1 1957,7565 2 1385,7101 2 2288,0749 2 1455,7545 2 1455,7545 2 1455,7545 2 1455,754 2 1455,75402 2 1455,7402	130 224 391 388 242 311 95 213 282 125 189 288 242 311 144 325 95 213	139           225           139           401           259           324           109           225           244           143           198           266           259           244           155           324           155           345           109           225
Vimentin - Box taurus (Bovine) VIDE_BOVIN ATP synthase subunit beta, mitochondrial precursor (IC 3.6.3.14) - Homo sapiene (FATPB_HUMAN ATP synthase subunit beta, mitochondrial precursor (IC 3.6.3.14) - Homo sapiene (FATPB_HUMAN	50710,8 537710,8 56542,5 56542,5	100,00%	2 8	2	4 0,42% 2 0,21% 27 4,86% 37 12,90%	A.72% ILLARICOLK     VESIGERATIK     VESIGERATIK     A.51% ILLARICOLK     MALDIELATYR     MALDIELATYR     EORIX VERMISONIUL     EORIX VERMISONIUL     EORIX VERMISONIUL     LILLARIVAR     VESIGERATIK      VESIGERATIK      VESIGERATIK	K K K K R R R R R R R R R R R R R R R R	G         99,00%           K         99,00%           G         99,00%           I         99,00%           I         99,00%           I         99,00%           I         99,00%           G         99,00%           A         99,00%           A         99,00%           A         99,00%           A         99,00%	3,34 3,19 3,51 3,44 3,67 3,67 4,79 4,19 3,97 4,67 3,97 4,67 3,97 4,67 3,97 4,67 4,68 3,07 4,36 6,72 4,36 4,77 4,68 4,7 4,7 4,7	0,222 0,192 0,209 0,276 0,058 0,059 0,075 0,0000000000	5,52 6,19 6,10 2,47 6,3 8,22 9,75 8,96 8,13 16 4,37 8,28 5,19 9,7 5,54 11,7 110,5 8,96 6,54		3 1 1 1 0 4 4 4 3 1 0 3 1 0 4 2 0 5 3 0 1 0 5 3 0 5 3 0 5 3 0 5 3 0 5 3 0 5 5 5 5 5 5 5 5 5 5 5 5 5	0 0 2 2 5 0 0 2 2 0 0 0 0 0 0 0 0 0 0 0		2 1140,7148 2 1405,751 2 1405,751 2 1169,7148 2 1311,62 2 1988,0343 2 2076,9912 2 1423,7545 2 1423,7545 2 1423,3139 2 1473,3139 2 1010,097 2 1010,097 2 1010,097 2 1010,097 2 1010,097 2 1010,097 2 1020,571 2 1000,571 2 1000,571 2 10	130 224 391 388 242 311 95 213 282 125 189 388 242 311 114 325 95 213 282 213 282	139 235 1401 406 259 324 324 109 259 253 264 406 259 259 253 243 345 105 345 345 105 345 345 105 345 345 244
Vimentin - Bos taurus (Bovine) VIME_BOVIN ATP synthase subunit beta, mitochondrial presuraor (EC.3.6.3.14) - Homo sapiens (hATPB_HAMAN ATP synthase subunit beta, mitochondrial presuraor (EC.3.6.3.14) - Homo sapiens (hATPB_HAMAN	50710,8 53770,8 56542,5 56542,5	100,00% 100,00%	2 8	2	4 0,42% 2 0,21% 27 4,86% 37 12,90%	4.72% ILLASTOCK     VESTOCEARAK     VESTO	К К К К К R R R R R R R R R R R R R R R	G         99,00%           G         99,00%           G         99,00%           I         99,00%           I         99,00%           I         99,00%           I         99,00%           G         99,00%           J         99,00%           J         99,00%           J         99,00%           J         99,00%           J         99,00%           J         99,00%	3,34 3,19 3,51 3,42 3,67 4,79 4,19 3,97 4,67 2,62 3,15 0 4,67 4,67 4,67 4,67 4,67 4,67 4,67 4,63 4,7 3,86 4,7 3,86 4,7 3,86 4,7 3,86 4,7 3,86 4,7 3,86 4,7 3,86 4,7 3,86 4,7 4,7 4,7 4,7 4,7 4,7 4,7 4,7 4,7 4,7	0,222 0,192 0,209 0,276 0,276 0,276 0,279 0,53 0,375 0,0835 0,077 0,375 0,0835 0,077 0,385 0,0835 0,0835 0,0835 0,084 0,0835 0,084 0,0835 0,084 0,035 0,084 0,037 0,0835	5,52 6,85 6,19 6,16 2,47 6,3 8,22 9,75 8,96 8,13 16 4,37 8,28 5,19 9,7 5,54 11,7 8,28 9,7 5,54 11,7 10,5 8,96 4,55 5,54		3 1 1 1 0 4 4 3 1 0 4 4 3 1 0 4 2 0 5 3 0 1 4 4 2 0 5 3 0 1 4 4 4 4 5 6 6 6 6 6 7 6 7 7 7 8 8 8 7 8 7 8 7 8 8 8 7 8 8 8 7 8 8 8 7 8 8 8 8 8 8 8 8 8 8 8 8 8	0 0 0 2 2 5 0 0 0 2 0 0 0 0 1 2 0 0 0 1 3 0 0		2 1140,7148 2 1405,7531 2 1405,7531 2 1405,7531 2 1980,033 2 076,9912 1 453,7458 2 1433,7458 2 1433,7545 2 1433,7545 2 1433,7545 2 1433,7545 2 1930,097 2 1938,0343 2 2056,9912 1 433,7545 1 338,7109 2 2056,9912 1 435,7454 1 338,7109 2 2 1453,7454 1 338,7109 2 1 338,710 2 1 339,710 2 1 339,710 2 1 339,710 2 1 338,710 2 1 338,710 2 1 339,710 2 1 338,710 2 1 338,710 2 1 338,710 2 1 338,710 2 1 339,710 2 1 3 1 3 1 3	130 224 130 391 288 242 311 95 213 282 125 189 388 242 311 144 325 95 213 282 213 282 213 282 213 282 213 285 213 285 213 285 213 285 213 285 213 285 213 285 213 285 213 285 213 285 213 285 285 285 285 285 285 285 285 285 285	139           225           139           401           259           244           109           225           244           109           225           244           133           198           255           244           155           324           155           345           109           225           244           135           345           109           225           244           155           345           109           225           244           143
Vimentin - Box taurus (Bovine) VIME_BOVIN ATP symthase subunit beta, mitochondrial precursor (IC 3.6.3.14) - Homo sapieres (P.ATPB_HUMANI ATP symthase subunit beta, mitochondrial precursor (IC 3.6.3.14) - Homo sapieres (P.ATPB_HUMANI	53710,8 56542,5 56542,5	100,00% 100,00%	2 8	2	4 0,42% 2 0,21% 27 4,86% 37 12.90%	4.75% ILLARICOLK     VESIGERATIK     4.51% ILLARICOLK     MADIELATYR     MADIELATYR     CORD, VHEMISCONNEL	К К К К К R R R R R R R R R R R R R R R	G         99,00%           K         99,00%           G         99,00%           I         99,00%           J         99,00%           J         99,00%           J         99,00%           J         99,00%           J         99,00%           G         99,00%           J         99,00%           G         99,00%           G         99,00%           G         99,00%	3,34 3,19 3,51 3,42 3,67 4,79 4,19 3,97 4,67 2,62 3,15 0 4,36 6,72 4,36 6,72 4,36 4,36 4,36 4,36 4,36 4,36 4,36 4,37 4,38 6,30,72 4,63 2,25	0,222 0,192 0,279 0,276 0,276 0,279 0,53 0,335 0,0375 0,035 0,0375 0,035 0,0375 0,035 0,037 0,036 0,375 0,036 0,371 0,364 0,037 0,037	5,52 6,85 6,19 6,16 6,16 6,3 8,22 9,75 8,96 8,13 16 4,37 8,28 8,96 1,17 11,7 15,8 9,97 5,19 7,5 8,96 6,5 5 2,64		3 1 1 1 0 4 4 4 3 1 0 3 1 0 4 2 0 5 3 0 1 6	0 0 0 2 2 5 5 0 0 2 0 0 0 2 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 1140,7148 2 1405,7891 2 1405,7891 2 1199,7148 2 1998,0343 2 1998,044 2 1998,044 2 1998,044 1 2 105,745 1 453,745 1 453,745 1 453,745 2 1998,047 2 1998,047 2 1998,047 2 1998,047 2 1998,047 2 1998,047 2 1998,047 2 1998,047 2 1998,047 2 1993,745 2 1 1995,745 2 1 1995,745 2 1	120 224 130 391 242 242 213 125 125 189 242 242 242 242 395 243 311 144 44 242 242 242 242 242 125 189	139 235 1401 406 259 324 109 259 254 244 143 198 406 259 324 143 135 135 135 135 135 135 135 135 135 13
Vimentin - Box taurus (Bovine)     VIME_BOVIN       ATP synthese suburit beta, mitochondrial precursor (IC 3.6.3.14) - Homo sapiene (FATPB_HIAMN       ATP synthese suburit beta, mitochondrial precursor (IC 3.6.3.14) - Homo sapiene (FATPB_HIAMN)	53710.8 58542.5 58542.5	100,00% 100,00% 100,00%	2 8 10 13	2 14 16 19	4 0,42% 2 0,21% 27 4,86% 37 12,90%	A.72% ILLARICOLC VESTORIAN A.51% ILLARICOL ADMINISTRA COLORIAN ADMINISTRA COLORIAN	К К К К К R R R R R R R R R R R R R R R	G         99,00%           G         99,00%           G         99,00%           I         99,00%           J         99,00%           J         99,00%           J         99,00%           J         99,00%           J         99,00%           J         99,00%           D         99,00%           D         99,00%           G         99,00%           J         99,00%           J         99,00%           J         99,00%           J         99,00%           J         99,00%           G         99,00%           G         99,00%           G         99,00%           G         99,00%           G         99,00%           G         99,00%	3,34 3,19 3,51 3,44 3,67 4,79 4,19 3,97 4,67 2,62 3,15 0 4,36 3,07 4,67 2,62 3,15 0 4,36 3,07 4,63 3,07 4,63 3,07 4,63 3,07 4,63 3,07 4,64 3,07 4,64 3,07 4,64 3,07 4,64 3,07 4,64 3,07 4,64 3,07 4,64 3,07 4,64 3,07 4,64 3,07 4,64 3,07 4,64 3,07 4,67 4,07 4,67 4,07 4,07 4,07 4,07 4,07 4,07 4,07 4,0	0,222 0,192 0,279 0,279 0,53 0,077 0,53 0,077 0,53 0,077 0,53 0,077 0,53 0,077 0,53 0,077 0,0835 0,077 0,24 0,0891 0,2681 0,0281 0,0281 0,0281 0,0281 0,0281 0,0281 0,0281 0,0281 0,0281 0,0281 0,0281 0,00840000000000	5,52 6,85 6,16 6,16 6,16 6,16 6,16 6,16 6,16 6,1		3 1 1 1 0 4 4 3 1 0 3 1 0 4 2 0 5 3 0 1 6 1 	0 0 0 2 2 5 5 0 0 0 0 0 0 0 0 0 0 0 0 0		2 1140,7148 1455,7511 2 1145,7511 2 1147,7148 2 1311.462 2 1998,0343 2 205,0912 2 435,7455 1 435,7455 2 1459,7899 2 1998,0343 2 205,0912 2 1998,0343 2 205,0912 1 435,7451 2 1988,0343 2 2056,0912 1 435,7451 2 1457,450 2 1457,450	120 224 391 392 391 392 242 242 311 315 52 242 242 312 319 348 242 242 343 343 341 343 343 345 345 345 345 345 345 345 345	139 235 1406 259 259 259 209 209 209 209 209 209 229 209 229 22
Vimentin - Bos taurus (Bovine) VIHE_BOVIN ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (PATPB_HBAMA ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (PATPB_HBAMA Vimentin (Fragment) - Critotulus griseus (Chinese hamster) VIHE_CRIGR	53710.8 53542,5 56542,5 56542,5	100,00% 100,00%	2 2 8 10 10	2 2 14 16	4 0,42% 2 0,21% 27 4,86% 37 12,90% 51 7,46%	4.72% ILLAELECK     VSJELERAKK     VSJELERAKK     4.51% ILLAELECAK     MALEICAK     MALEICAK     MALEICAK     MALEICAKA     CONAVATALENA     CONAVATALENA     CONAVATALENA     CONAVATALENA     CONAVATALENA     CONAVATALENA     VALTALENAVE     VALTALE	K K K R R R R R R R R R R R R R R R R R	G         99,00%           G         99,00%           G         99,00%           I         99,00%           J         99,00%           G         99,00%           J         99,00%           G         99,00%      Image: G         99,00%	3,34 3,19 3,51 3,44 3,42 4,79 4,79 3,97 4,67 2,62 3,15 0 4,36 4,36 4,36 4,37 4,386 2,35 2,26 1,95 0 0	0,222 0,192 0,276 0,276 0,277 0,533 0,375 0,635 0,375 0,635 0,0375 0,635 0,0375 0,645 0,037 0,24 0,24 0,0491 0,24 0,24 0,24 0,0491 0,24 0,24 0,04 0,24 0,04 0,27 0,0370000000000	5.52 6.85 6.19 6.14 2.47 8.23 9.75 8.93 4.37 8.23 9.75 5.19 9.7 5.54 1.05 8.96 6.54 4.37 8.24 9.75 2.64	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 1 1 1 0 4 4 3 1 0 3 1 0 4 2 0 5 3 0 1 6 1 1 1 1 1 1 1 1 1 1 1 1 1	0 0 2 2 5 5 0 0 2 2 0 0 0 0 0 1 1 2 0 0 1 1 7 0 0 1 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 1140,7148 2 1405,7891 2 1405,7891 2 1405,7891 2 1311,662 2 1391,662 2 1998,0343 2 005,9791 2 1408,043 2 1433,891 1 459,1809 2 1438,51746 2 1385,7101 2 1998,0343 2 2088,0357 2 1998,034 2 1991,007 2 1994,642 2 1991,007 2 1991,007 2 1994,642 2 1991,007 2 1994,645 2 1994,647 2 1996,647 2 1996,6	130           224           130           391           382           242           311           25           125           189           384           242           311           311           322           25           135           131           312           25           311           312           313           314           325           315           3189           179           407	139 235 139 401 402 324 324 324 324 135 324 324 325 324 325 325 325 325 325 325 325 109 225 406 225 109 225 225 225 225 225 225 225 225 225 22
Vimentin - Box taurus (Bovine) VIME_BOVIN ATP synthase subunit beta, mitochondrial precursor (IC 3.6.3.14) - Homo sapiene (FATPB_HUMAN ATP synthase subunit beta, mitochondrial precursor (IC 3.6.3.14) - Homo sapiene (FATPB_HUMAN Vimentin (Fragment) - Cricotulus griseus (Chinese hamster) VIME_CRIGR	53710.8 16542.5 56542.5	100,00% 100,00% 100,00%	2 2 8 10 13	2 2 14 16	4 0.42% 2 0.21% 27 4.86% 37 12.90% 51 7.46%	4.72% ILLARECOLK     VESIGERATIK     VESIGERATIK     ASTIN     HLARECOLK     MALDIERATVR     MALDIERATVR     CALLENTRANDPLOSTSR     CALLENTRANDPLOSTSR     CALLENTRANDPLOSTSR     VESIGERATVR     VESIGER	KK KK R R R R R R R R R R R R R R R R R	G         99,00%           G         99,00%           G         99,00%           I         99,00%           I         99,00%           I         99,00%           I         99,00%           I         99,00%           I         99,00%           G         99,00%           G         99,00%           I         99,00%           I         99,00%           I         99,00%           I         99,00%           G         99,00%           F         99,00%           R         99,00%	3,34 3,15 3,44 3,42 3,42 3,42 3,47 4,79 4,79 4,79 4,67 2,62 3,15 0 0 4,30 4,30 4,30 4,30 4,30 4,30 4,30	0,222 0,192 0,279 0,279 0,279 0,53 0,077 0,375 0,077 0,375 0,0835 0,077 0,375 0,0835 0,0848 0,0948 0,094 0,094 0,094 0,094 0,095 0,005 0,095 0,00000000	5.52 6.85 6.19 6.14 6.14 6.2 9.75 9.75 9.75 9.76 8.96 8.96 8.96 8.96 8.96 8.96 8.97 9.7 5.54 9.7 5.17 10.5 8.96 6.52 2.49 2.45 8.96 8.96 8.96 8.96 8.96 8.96 8.96 8.96	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 1 1 1 4 4 3 1 0 3 1 0 4 2 0 5 3 0 1 6 1 0 1 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 1 1 0 1 1 1 1 1 1 1 1 1 1 1 1 1	0 0 0 2 2 2 5 5 0 0 0 2 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 1140,7148 1405,7811 2 1405,7811 2 1140,7148 2 1131,462 2 1988,0343 2 2076,9912 2 445,7845 1 453,7845 1 453,835 1 453,835 1 453,835 1 453,835 1 453,835 1 453,835 1 453,835 1 453,835 1 453,835 1 453,845 1 454,845 1 454,845 1 455,845 1 455,855 1 455,855 1 455,855 1 455,855 1 455,855	130           224           391           388           242           313           282           213           282           125           189           242           311           144           325           95           213           225           189           242           189           242           125           125           95           213           212           125           125           95           213           212           189           179           407	139           139           225           139           400           259           324           133           198           209           244           133           198           209           244           133           198           109           204           135           109           204           109           204           109           204           109           204           109           214           108           421
Vimentin - Bos taurus (Bovies)     VIME_BOVIN       ATP synthase suburit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiers (r-ATPB_HEANA       ATP synthase suburit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiers (r-ATPB_HEANA       ATP synthase suburit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiers (r-ATPB_HEANA	53710.8 53542,5 56542,5 51831,8	100,00% 100,00% 100,00%	2 2 8 10 10	2 14 16	4 0.42% 2 0.21% 27 4.86% 37 12.90% 51 7.46%	4.72% ILLAELCOK VESLEERAKK 4.51% ILLAELCOK 5.75% ILLAE	KK KK RRRRKKK RRRRKKK RRRRKK	G         99,00%           G         99,00%           G         99,00%           I         99,00%           D         95,00%           J         95,00%           J         95,00%           G         99,00%           J         95,00%           J         95,00%           G         95,00%           I         95,00%           G         95,00%           J         95,00%           G         95,00%	2,34 3,19 3,51 3,44 2,15 3,42 3,42 4,79 4,79 4,79 4,79 3,97 4,67 2,62 2,15 0 4,36 4,36 4,36 4,37 4,386 2,35 2,26 1,95 2,22	0,222 0,192 0,276 0,276 0,276 0,279 0,53 0,077 0,335 0,077 0,035 0,0898 0,0891 0,0893 0,0891 0,0891 0,0891 0,0891 0,0891 0,024 0,0171 0,0171	5.52 6.85 6.19 6.14 2.47 8.24 9.75 9.75 9.75 8.94 10.5 5.19 9.7 5.54 11.05 8.95 2.64 2.92 2.64	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 1 1 1 0 4 4 3 1 0 3 1 0 4 2 0 5 3 0 1 6 1 1 1 1 1 1 1 1 1 1 1 1 1	0 0 0 0 2 2 2 5 5 0 0 2 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 1140,7148 2 1465,7591 2 1476,7148 2 131,462 2 131,462 2 131,462 2 131,462 2 131,462 2 131,462 2 143,7546 1 143,7546 1 143,7546 2 1439,7899 1 191,667 2 1988,635 1 1439,7899 1 191,667 1 191,4602 1 191,470,4702 1 191,470,470	320           224           330           398           242           91           282           282           282           311           326           242           313           29           389           242           311           325           125           189           79           407           407           407           407           407	139           139           225           130           401           259           259           259           259           241           143           143           144           155           345           109           225           143           146           143           143           144           145           345           109           108           143           144           143           144           143           144           142           142           142           142           142           142           142
Vimentin - Box taurus (Bovine) VIME_BOVIN ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (FATPB_HUMAN ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (FATPB_HUMAN Mimentin (fragment) - Critetulus griseus (Chinese hamster) VIME_CRIGR	5442.5 56542.5 56542.5	100,00% 100,00% 100,00%	2 2 8 10 13	2 14 16	4 0,42% 2 0,21% 27 4,86% 37 12,40%	4.72% ILLAELECK VSLGERATK 4.51% 1.51% ILLAELECK 5.0% ARELECK EORAVIVATION EORAVIVATION EORAVIVATIONS EORAVIVAT	化化 化用程度化化化化化 的复数化化化化化化化化化	G         99,00%           G         99,00%           G         99,00%           I         99,00%           J         99,00%           G         99,00%           G         99,00%           G         99,00%           S         99,00%           S         99,00%	3,34 3,15 3,44 3,42 3,42 3,42 3,47 4,79 4,79 4,79 4,79 4,67 2,62 3,15 3,07 4,67 2,62 3,07 4,63 3,07 4,63 3,07 4,63 3,07 4,63 3,07 4,63 3,07 4,67 2,61 4,73 4,74 4,79 3,97 4,79 4,79 4,79 4,79 4,79 4,79 4,79 4	0,222 0,192 0,279 0,279 0,279 0,279 0,279 0,53 0,077 0,375 0,077 0,375 0,083 0,000 0,083 0,000 0,000 0,000 0,000 0,000 0,000 0,000 0,000 0,000 0,000 0,000 0,000 0,000 0,000 0,000 0,000000	5.52 6.85 6.19 6.14 6.14 6.247 6.2 9.75 8.76		3 1 1 1 0 4 4 3 1 0 4 4 2 0 5 3 0 1 6 1 1 0 4 4 2 0 5 3 0 1 4 4 2 0 1 1 1 1 1 1 1 1 1 1 1 1 1	0 0 0 0 0 2 2 2 2 5 0 0 0 0 0 0 0 0 0 0		2 1140,7148 2 1455,7511 2 1145,7511 2 1145,7511 2 113,62 2 205,6912 2 425,7481 1 45	130           224           391           388           242           213           223           225           189           242           213           223           3262           125           189           242           242           25           95           213           225           95           212           189           120           121           125           130           131           144           25           95           213           280           125           120           120           170           407           112	139 235 139 269 269 224 109 225 234 133 143 143 143 143 143 143 259 259 224 244 155 244 156 244 156 244 168 168 168 168 168 168 168 168 168 168
Vimentin - Box taurus (Borino) VIME_BOVIN ATP synthese suburit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiere, (HATPB_HEAMAN ATP synthese suburit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiere, (HATPB_HEAMAN Vimentin (Fragment) - Critetiulus griseus (Cheese hamster) VIME_CRICE	53710.8 56542,5 56542,5 56542,5	100,09% 100,09% 100,09%	2 2 8 10 10	2 14 16	4 0,42% 2 0,21% 27 4,86% 37 12,90% 51 7,66%	4.72% ILLAFLEGAC VESTOCEMARK     4.51% ILLAFLEGAC     5.45% ILLAFL	化化 化化化化化化化化 化化化化化化 化化化化化	G         99,00%           G         99,00%           G         99,00%           I         99,00%           J         99,00%           G         99,00%           G         99,00%           G         99,00%           G         99,00%           G         99,00%           S         90,00%           S         90,00%           S         90,00%           S         90,00%           S         90,00%	2.34 3.19 3.51 3.44 3.42 3.67 4.79 4.79 4.79 4.79 4.79 4.79 4.67 4.67 4.62 3.07 4.62 3.07 4.63 3.07 4.63 4.63 4.63 4.63 4.63 4.63 4.63 4.63	0,222 0,192 0,276 0,276 0,276 0,279 0,53 0,077 0,335 0,077 0,035 0,083 0,083 0,083 0,083 0,083 0,083 0,083 0,083 0,083 0,084 0,083 0,083 0,085 0,000000	5.52           6.85           6.19           6.16           2.47           8.22           9.75           8.96           8.13           14           3.17           5.19           5.19           5.51,19           5.54           6.54           5.2,64           2.92           3.62           2.92           3.64           9.92           3.62           3.64	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 1 1 1 1 0 4 4 3 1 0 4 4 3 1 0 4 2 0 0 1 0 4 4 3 1 0 3 1 0 4 4 3 1 0 4 4 3 1 0 4 4 3 1 0 4 4 3 1 0 4 4 3 3 1 0 1 0 4 4 3 3 1 0 1 1 0 1 1 0 1 1 1 1 1 1 1 0 1 1 1 1 1 1 1 1 1 1 1 1 1	0 0 0 0 2 2 2 5 5 0 0 2 0 0 0 0 0 0 0 0		2 1149,7148 2 1455,7511 2 1149,7148 2 131,452 2 1311,452 2 1311,452 2 1311,452 2 1311,452 2 1435,7545 1 1435,7545 1 1435,7545 1 1439,7899 2 139,0471 2 1988,033 2 0706,9912 2 1988,033 2 0706,9912 2 1988,035 1 165,918 1 165,918 2 1439,7899 1 1058,0457 2 1058,6457 2 1644,8496 1 169,7184 1 159,91714 2 159,91714 2 159,91714 2 159,9174 2 159,9917 1 159,9174 2 159,9917 1 159,9174 2 159,9917 1 150,9957 1 159,9917 1 159,9917 1 150,9957 1 159,9917 1 150,9957 1 150,957 1 1	130           224           391           242           311           95           213           213           213           213           288           242           311           95           213           288           242           311           95           213           255           213           288           242           311           348           242           312           313           314           315           315           316           317           318           319           319           319           310           311           312           313           314           315           316           317           318           318           318           319           310 <tr< th=""><th>139           139           225           139           4001           259           324           125           224           131           106           225           224           123           124           125           224           125           224           125           225           224           125           225           224           123           124           125           224           125           224           123           124           125           224           123           124           125           224           123           123           123           123           124           125           224           123           124           125           126           127</th></tr<>	139           139           225           139           4001           259           324           125           224           131           106           225           224           123           124           125           224           125           224           125           225           224           125           225           224           123           124           125           224           125           224           123           124           125           224           123           124           125           224           123           123           123           123           124           125           224           123           124           125           126           127
Vimentin - Box taurus (Bovine) VIME_BOVIN ATP synthase suburit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiers (HATPB_HAMMAATP Synthase suburit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiers (HATPB_HAMAAATP Synthase suburit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiers (HATPB_HAMAAAATP Synthase suburit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiers (HATPB_HAMAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	5700 53710.8 56542.5 56542.5 56542.5	100.00% 100.00%	2 2 8 10 13	2 14 16 19	4 0,42% 2 0,21% 27 4,86% 37 12,40%	4.72% ILLAELECK VESLEENAK     4.51% ILLAELECAK     5.5% ILLAELECAK     5% ILLEELECAK     5% ILLAELECAK	化化 化化化化化化化化化化化化化化化化化化化化化化化化化化化化化化化化化化化	G         99,00%           G         99,00%           G         99,00%           I         99,00%           J         99,00%           J         99,00%           J         99,00%           J         99,00%           J         99,00%           J         99,00%           G         99,00%           J         99,00%           J         99,00%           G         99,00%           S         90,00% <th>2.34 2.39 3.51 3.44 3.44 3.45 3.42 3.47 4.79 4.79 4.79 4.79 4.67 2.62 3.15 0 0 4.36 4.36 4.36 4.36 4.36 4.36 0 0 4.36 4.7 3.85 2.26 0 0 2.92 4.7 3.85 2.26 0 0 0 2.92 4.7 3.85 2.26 0 0 0 2.92 4.7 3.85 2.26 0 0 0 0 0 0 0 0 0 0 0 0 0</th> <th>0,222 0,192 0,276 0,276 0,276 0,276 0,275 0,025 0,0000000000</th> <th>5.52           6.85           6.19           6.16           2.47           6.3           8.22           9.75           8.74           4.37           9.75           5.19           9.7           9.73           8.74           4.37           10.5           5.19           5.74           11.7           2.92           6.54           9.92           4.92           9.92           4.92           9.92           9.81</th> <th></th> <th>3 1 1 0 4 4 3 1 0 4 4 3 0 4 2 0 5 3 0 1 6 1 1 5 3 0 1 6 1 1 1 0 4 4 3 0 1 1 1 1 1 1 1 1 1 1 1 1 1</th> <th>0 0 0 0 2 2 2 2 5 0 0 0 0 0 0 0 0 0 0 0</th> <th></th> <th>2 1140,7148 2 1465,7581 2 1465,7581 2 1145,7148 2 131,462 2 2026,6912 2 425,7541 1 435,7545 1 435,7545 1 435,7545 1 435,7545 1 435,7545 1 435,7545 1 435,7545 1 435,7545 1 435,7545 1 385,7101 2 2056,9912 2 435,7455 1 385,7101 2 2 1566,9912 2 455,7482 1 385,7101 2 2 1566,9912 2 455,7482 1 385,7101 2 2 1566,9912 2 1566,9912 2 1566,9912 2 1570,8957 1 1050,9914 1 1570,8957 1 1050,914 1 1570,8957 1 1500,914 1 1570,8957 1 1500,915 1 1500</th> <th>130           224           130           391           388           242           232           225           189           242           311           242           311           225           96           242           311           225           189           122           112           112           112           300           205</th> <th>138 225 1401 400 400 259 259 244 259 244 240 140 259 244 240 140 255 244 241 245 244 143 148 255 244 241 245 245 244 143 143 143 143 143 143 143 143 143 1</th>	2.34 2.39 3.51 3.44 3.44 3.45 3.42 3.47 4.79 4.79 4.79 4.79 4.67 2.62 3.15 0 0 4.36 4.36 4.36 4.36 4.36 4.36 0 0 4.36 4.7 3.85 2.26 0 0 2.92 4.7 3.85 2.26 0 0 0 2.92 4.7 3.85 2.26 0 0 0 2.92 4.7 3.85 2.26 0 0 0 0 0 0 0 0 0 0 0 0 0	0,222 0,192 0,276 0,276 0,276 0,276 0,275 0,025 0,0000000000	5.52           6.85           6.19           6.16           2.47           6.3           8.22           9.75           8.74           4.37           9.75           5.19           9.7           9.73           8.74           4.37           10.5           5.19           5.74           11.7           2.92           6.54           9.92           4.92           9.92           4.92           9.92           9.81		3 1 1 0 4 4 3 1 0 4 4 3 0 4 2 0 5 3 0 1 6 1 1 5 3 0 1 6 1 1 1 0 4 4 3 0 1 1 1 1 1 1 1 1 1 1 1 1 1	0 0 0 0 2 2 2 2 5 0 0 0 0 0 0 0 0 0 0 0		2 1140,7148 2 1465,7581 2 1465,7581 2 1145,7148 2 131,462 2 2026,6912 2 425,7541 1 435,7545 1 435,7545 1 435,7545 1 435,7545 1 435,7545 1 435,7545 1 435,7545 1 435,7545 1 435,7545 1 385,7101 2 2056,9912 2 435,7455 1 385,7101 2 2 1566,9912 2 455,7482 1 385,7101 2 2 1566,9912 2 455,7482 1 385,7101 2 2 1566,9912 2 1566,9912 2 1566,9912 2 1570,8957 1 1050,9914 1 1570,8957 1 1050,914 1 1570,8957 1 1500,914 1 1570,8957 1 1500,915 1 1500	130           224           130           391           388           242           232           225           189           242           311           242           311           225           96           242           311           225           189           122           112           112           112           300           205	138 225 1401 400 400 259 259 244 259 244 240 140 259 244 240 140 255 244 241 245 244 143 148 255 244 241 245 245 244 143 143 143 143 143 143 143 143 143 1
Vimentin - Bos taurus (Bovine) VIME_BOVIN ATP synthaue suburit bets, mitochondrial precursor (EC.3.6.3.14) - Homo sapiene (HATPB_HUMAN ATP-synthaue suburit bets, mitochondrial precursor (EC.3.6.3.14) - Homo sapiene (HATPB_HUMAN Vimentin (Fragment) - Criscilulus grisuus (Chinese hamster) VIME_CRIGR	5370.8 16542.5 56542.5	100.00% 100.00%	2 8 10	2 14 16 19	4 0,42% 2 0,21% 27 4,86% 37 12,90% 51 7,66%	4.72% ILLARICAL VISIOLETARIX     4.51% ILLARICAL     5.1% ILLARI	化化 化化 网络昆虫龙尾龙龙 网络昆虫昆虫龙昆龙龙 网络昆龙龙昆昆龙	C         99,00%           C         99,00%           G         99,00%           I         99,00%           J         99,00%           G         99,00%           J         99,00%           G         99,00%           G         99,00%           G         99,00%           G         99,00%           S         99,00%           S         90,00%           K         90,00%           K         90,00% <th>2.34 3.19 3.51 3.44 3.42 3.67 4.79 4.79 4.79 4.79 4.79 4.67 2.62 3.15 5.62 3.07 6.72 4.63 3.07 6.72 4.63 3.07 6.72 2.26 1.95 0.0 0 0.0 2.92 2.26 1.95 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.</th> <th>0,222 0,192 0,276 0,276 0,276 0,276 0,276 0,276 0,275 0,275 0,275 0,275 0,275 0,275 0,275 0,281 0,281 0,281 0,281 0,281 0,281 0,292 0,281 0,292 0,292 0,292 0,276 0,275 0,027 0,0000000000</th> <th>5.52           6.85           6.19           6.16           2.47           8.22           9.75           8.96           8.13           1.4           1.5           5.19           9.75           5.517           9.75           6.62           2.82           5.19           9.75           1.17           1.16           5.2,64           2.92           3.34           9.72           3.34           9.72</th> <th>0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0</th> <th>3 1 1 1 0 4 4 3 3 0 4 4 2 0 5 3 0 1 6 1 0 4 4 2 0 5 3 0 1 6 4 4 3 0 4 4 3 3 0 1 0 4 4 3 3 0 1 0 4 4 3 3 0 1 0 4 4 3 3 0 1 0 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 1 0 0 1 0 1 0 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 1 1 1 1 1 1 1 1 1 1 1 1</th> <th>0 0 0 2 2 5 5 0 0 0 0 0 0 0 0 0 0 0 0 0</th> <th></th> <th>2 1140,7148 2 1405,7831 2 1149,7148 2 131,742 2 131,742 2 131,742 2 131,742 2 205,9912 2 435,745 1 435,745 1 439,789 2 1088,457 2 1088,457 2 1988,034 2 2056,9912 2 1435,7451 2 2026,0749 2 1435,7451 2 2026,0749 2 1435,7451 2 1437,8409 1 437,8409 1 109,097 1 109,097 2 1088,457 1 109,097 1 101,097 1 101,097</th> <th>130           224           391           242           213           212           213           213           288           242           121           283           243           393           128           242           129           388           242           311           36           25           213           395           213           395           213           395           213           395           213           395           213           395           213           395           213           395           213           395           395           112           112           112           112           205           205           205           205           205           205      <t< th=""><th>138 225 139 4001 400 259 255 255 255 255 255 255 255 255 255</th></t<></th>	2.34 3.19 3.51 3.44 3.42 3.67 4.79 4.79 4.79 4.79 4.79 4.67 2.62 3.15 5.62 3.07 6.72 4.63 3.07 6.72 4.63 3.07 6.72 2.26 1.95 0.0 0 0.0 2.92 2.26 1.95 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	0,222 0,192 0,276 0,276 0,276 0,276 0,276 0,276 0,275 0,275 0,275 0,275 0,275 0,275 0,275 0,281 0,281 0,281 0,281 0,281 0,281 0,292 0,281 0,292 0,292 0,292 0,276 0,275 0,027 0,0000000000	5.52           6.85           6.19           6.16           2.47           8.22           9.75           8.96           8.13           1.4           1.5           5.19           9.75           5.517           9.75           6.62           2.82           5.19           9.75           1.17           1.16           5.2,64           2.92           3.34           9.72           3.34           9.72	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 1 1 1 0 4 4 3 3 0 4 4 2 0 5 3 0 1 6 1 0 4 4 2 0 5 3 0 1 6 4 4 3 0 4 4 3 3 0 1 0 4 4 3 3 0 1 0 4 4 3 3 0 1 0 4 4 3 3 0 1 0 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 1 0 0 1 0 1 0 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 1 1 1 1 1 1 1 1 1 1 1 1	0 0 0 2 2 5 5 0 0 0 0 0 0 0 0 0 0 0 0 0		2 1140,7148 2 1405,7831 2 1149,7148 2 131,742 2 131,742 2 131,742 2 131,742 2 205,9912 2 435,745 1 435,745 1 439,789 2 1088,457 2 1088,457 2 1988,034 2 2056,9912 2 1435,7451 2 2026,0749 2 1435,7451 2 2026,0749 2 1435,7451 2 1437,8409 1 437,8409 1 109,097 1 109,097 2 1088,457 1 109,097 1 101,097 1 101,097	130           224           391           242           213           212           213           213           288           242           121           283           243           393           128           242           129           388           242           311           36           25           213           395           213           395           213           395           213           395           213           395           213           395           213           395           213           395           213           395           395           112           112           112           112           205           205           205           205           205           205 <t< th=""><th>138 225 139 4001 400 259 255 255 255 255 255 255 255 255 255</th></t<>	138 225 139 4001 400 259 255 255 255 255 255 255 255 255 255
Vimentin - Box taurus (Bovine) VIME_BOVIN ATP synthase suburit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiers (FATPB_HRAMA ATP synthase suburit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiers (FATPB_HRAMA ATP synthase suburit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiers (FATPB_HRAMA ATP synthase suburit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiers (FATPB_HRAMA	53710.8 53542,5 56542,5 51831,8	100.00%	2 2 8 10 13	2 14 16 19	4 0,42% 2 0,21% 27 4,86% 37 12,90% 51 7,46%	A.72% ILLAELCOK VESLEERAKK     VESLEERAKK	化化 化尿管管管管管管管管管管管管管管管管管管管管管管管管管管管管管管管管管管	G         99,00%           G         99,00%           G         99,00%           I         99,00%           D         95,00%           J         95,00%           J         95,00%           G         99,00%           J         95,00%           J         95,00%           G         95,00%           G         95,00%           G         95,00%           J         95,00%           G         95,00%           G         95,00%           T         95,00%           G         95,00%           S         95,00%           S         95,00%           L         95,00%           G         95,00%           C         95,00%           C         95,00%           C         95,00%           C         95,00%           C         95,00% <th>2.34 2.34 3.51 3.44 3.45 3.42 3.47 3.47 4.79 4.79 4.79 4.79 4.67 2.62 3.15 0 4.36 6.72 4.63 0 4.36 6.72 4.63 0 4.36 6.72 4.63 0 0 4.38 6.235 0 0 2.92 4.73 4.73 4.73 4.75 1.95 0 0 0 2.92 4.73 2.85 0 0 0 0 2.92 2.75 0 0 0 0 0 0 0 0 0 0 0 0 0</th> <th>0,222 0,102 0,209 0,276 0,276 0,276 0,279 0,279 0,53 0,335 0,035 0,035 0,035 0,0635 0,0635 0,0635 0,0635 0,0699 0,0598 0,0598 0,0598 0,0598 0,0598 0,0598 0,0598 0,0598 0,0598 0,0598 0,0598 0,0598 0,0598 0,0598 0,059 0,050 0,00000000</th> <th>5.52           6.85           6.19           6.16           8.22           9.75           8.24           9.73           8.74           16           4.37           10.5           5.94           11.7           8.28           9.73           8.74           1.75           2.94           4.37           11.7           10.5           5.54           11.7           10.5           2.92           4.92           4.92           3.92           4.92           9.1           9.3           9.3           9.31           4.66</th> <th>0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0</th> <th>3 1 1 1 0 4 4 3 1 0 4 2 0 5 3 0 1 6 1 1 0 1 5 3 0 1 6 1 0 3 0 4 3 1 0 4 4 4 3 1 0 4 4 4 3 1 0 4 4 4 3 1 0 4 4 4 3 1 0 4 4 4 3 1 0 4 4 4 3 1 0 4 4 4 3 1 0 4 4 4 3 1 0 4 4 4 3 1 0 4 4 4 4 3 1 0 4 4 4 4 5 3 0 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5</th> <th>0 0 0 2 2 5 0 0 2 2 5 0 0 0 2 2 0 0 0 2 0 0 0 0</th> <th></th> <th>2 1140,7148 2 1465,7591 2 1405,7591 2 1140,7148 2 1311,662 2 1931,762 2 1935,7541 2 1235,7545 1 1235,7545 1 1235,7545 1 1235,7545 1 1235,7545 2 1249,7899 1 1910,6977 2 1098,6357 2 1298,674 2 1298,674 2 1355,7545 1 1355,7616 2 298,6746 1 1355,7616 2 1439,7899 1 1910,6977 1 1938,6357 1 1937,4662 2 1439,7899 1 1910,6977 1 1938,6575 1 1937,4662 2 1439,7899 1 1910,6977 1 1938,6575 1 1937,4662 2 1439,7899 1 1910,6977 1 1938,6575 1 1937,4662 2 1439,7899 1 1937,4662 2 1439,7899 1 1937,4662 2 1439,7899 1 1937,4662 1 1937,466</th> <th>130           224           130           391           242           213           223           213           213           225           189           242           213           214           225           280           242           241           311           144           225           255           255           189           179           407           407           407           407           407           407           407           407           407           407           407           407           407           205           205           205           205           205           205           205           205           205           205           205           205           205</th> <th>139           139           225           1401           406           259           225           244           139           225           244           239           225           244           259           243           259           244           255           244           225           244           225           244           225           244           225           244           225           244           225           244           226           245           246           225           244           221           212           213           214           217           218           217           218           217           218           217           218</th>	2.34 2.34 3.51 3.44 3.45 3.42 3.47 3.47 4.79 4.79 4.79 4.79 4.67 2.62 3.15 0 4.36 6.72 4.63 0 4.36 6.72 4.63 0 4.36 6.72 4.63 0 0 4.38 6.235 0 0 2.92 4.73 4.73 4.73 4.75 1.95 0 0 0 2.92 4.73 2.85 0 0 0 0 2.92 2.75 0 0 0 0 0 0 0 0 0 0 0 0 0	0,222 0,102 0,209 0,276 0,276 0,276 0,279 0,279 0,53 0,335 0,035 0,035 0,035 0,0635 0,0635 0,0635 0,0635 0,0699 0,0598 0,0598 0,0598 0,0598 0,0598 0,0598 0,0598 0,0598 0,0598 0,0598 0,0598 0,0598 0,0598 0,0598 0,059 0,050 0,00000000	5.52           6.85           6.19           6.16           8.22           9.75           8.24           9.73           8.74           16           4.37           10.5           5.94           11.7           8.28           9.73           8.74           1.75           2.94           4.37           11.7           10.5           5.54           11.7           10.5           2.92           4.92           4.92           3.92           4.92           9.1           9.3           9.3           9.31           4.66	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 1 1 1 0 4 4 3 1 0 4 2 0 5 3 0 1 6 1 1 0 1 5 3 0 1 6 1 0 3 0 4 3 1 0 4 4 4 3 1 0 4 4 4 3 1 0 4 4 4 3 1 0 4 4 4 3 1 0 4 4 4 3 1 0 4 4 4 3 1 0 4 4 4 3 1 0 4 4 4 3 1 0 4 4 4 3 1 0 4 4 4 4 3 1 0 4 4 4 4 5 3 0 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5	0 0 0 2 2 5 0 0 2 2 5 0 0 0 2 2 0 0 0 2 0 0 0 0		2 1140,7148 2 1465,7591 2 1405,7591 2 1140,7148 2 1311,662 2 1931,762 2 1935,7541 2 1235,7545 1 1235,7545 1 1235,7545 1 1235,7545 1 1235,7545 2 1249,7899 1 1910,6977 2 1098,6357 2 1298,674 2 1298,674 2 1355,7545 1 1355,7616 2 298,6746 1 1355,7616 2 1439,7899 1 1910,6977 1 1938,6357 1 1937,4662 2 1439,7899 1 1910,6977 1 1938,6575 1 1937,4662 2 1439,7899 1 1910,6977 1 1938,6575 1 1937,4662 2 1439,7899 1 1910,6977 1 1938,6575 1 1937,4662 2 1439,7899 1 1937,4662 2 1439,7899 1 1937,4662 2 1439,7899 1 1937,4662 1 1937,466	130           224           130           391           242           213           223           213           213           225           189           242           213           214           225           280           242           241           311           144           225           255           255           189           179           407           407           407           407           407           407           407           407           407           407           407           407           407           205           205           205           205           205           205           205           205           205           205           205           205           205	139           139           225           1401           406           259           225           244           139           225           244           239           225           244           259           243           259           244           255           244           225           244           225           244           225           244           225           244           225           244           225           244           226           245           246           225           244           221           212           213           214           217           218           217           218           217           218           217           218
Vimentin - Box taurus (Bovine)     VIME_BOVIN       ATP synthase suburit bets, mitochondrial precursor (IC 3.6.3.14) - Hemo sapiens (P-ATPB_HUMM)       ATP synthase suburit bets, mitochondrial precursor (IC 3.6.3.14) - Hemo sapiens (P-ATPB_HUMM)       ATP synthase suburit bets, mitochondrial precursor (IC 3.6.3.14) - Hemo sapiens (P-ATPB_HUMM)       Vimentin (Fragment) - Cricetulus griseus (Chinese hamster)     VIME_CRICR	5442.5 56542.5 56542.5	100.00% 100.00%	2 8 10	2 14 16 19	4 0.42% 2 0.21% 27 4.86% 37 12.40%	4.72% ILLAELECK VSLSLEARAK     4.51% ILLAELECK 5.5% ILLAELECK 5.5% ILLAELECK 5.5% ILLAELECK 5.5% ALALLEUNSKA 6.5% ALALLEUNSKA 7.5% ALALLEUNSKA 7.5% ALALLEUNSKA 7.5% ILLAELEN 7.5% ALALLEUNSKA 7.5% ALALLEUNSKA 7.5% ALALLEUNSKA 7.5% ALALLEUNSKA 7.5% ALALLEUNSKA 7.5% ALALLEUNSKA 7.5% ALALLEUNSKA 7.5% ILLAELEN 7.5% ILLAEL	化化 化化 的复数化化化化 化合物化合物化合物化合物化合物化合物化合物化合物化合物化合物化合物化合物化合物化	G         99,00%           G         99,00%           G         99,00%           I         99,00%           I         99,00%           J         99,00%           G         99,00%           G         99,00%           G         99,00%           G         99,00%           G         99,00%           G         99,00%           C         99,00%           E         99,00%           E         99,00%           C         99,00% <th>2.24 3.19 3.51 3.44 3.42 3.42 3.42 3.47 4.79 4.79 4.67 2.62 3.07 4.30 6.72 2.42 3.86 3.07 6.72 4.36 2.26 2.35 2.26 0 0 2.92 4.73 3.86 0 0 0 2.92 2.93 5.10 0 0 0 2.92 2.92 5.10 5.00 9 3.05 5.00 9 3.05 2.94</th> <th>0,222 0,192 0,276 0,276 0,276 0,276 0,276 0,275 0,275 0,275 0,275 0,275 0,275 0,275 0,285 0,244 0,2991 0,244 0,2991 0,245 0,245 0,245 0,275 0,075 0,00</th> <th>5.52           6.19           6.16           8.21           8.247           6.35           8.22           9.72           9.73           8.23           9.75           9.75           9.75           9.75           9.75           9.75           9.75           9.75           9.75           9.75           9.76           9.70           9.70           9.70           9.71           10.75           9.76           9.76           9.72           9.84           9.40           9.34           9.34           9.34           9.34           9.34           9.34           9.34           9.34           9.34           9.34           9.34           9.34           9.34           9.34           9.35</th> <th>0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0</th> <th>3 1 1 1 0 4 4 3 1 0 4 4 3 0 0 1 0 4 2 0 5 3 0 1 0 1 0 4 4 2 0 5 5 0 1 0 4 4 5 1 0 0 4 4 5 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0</th> <th>0 0 0 0 2 2 2 3 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0</th> <th></th> <th>2 1140,7148 2 1465,7581 2 1465,7581 2 1145,7148 2 131,462 2 2076,9912 1 423,7545 1 423,7545 1 423,7545 1 423,7545 1 423,7545 1 423,7545 1 423,7545 1 428,7545 1 429,7997 1 420,7977 1 420,7977 1</th> <th>320           224           330           391           388           242           310           282           213           282           128           282           213           282           213           282           213           282           213           282           213           282           213           282           213           282           213           282           213           283           212           128           129           112           112           112           112           205           205           205           205           205           205           205           205           205           205</th> <th>138 225 139 4001 400 259 259 259 244 109 225 244 109 225 244 109 225 244 109 229 244 109 229 244 108 108 108 109 224 241 108 108 108 108 108 108 108 108 108 10</th>	2.24 3.19 3.51 3.44 3.42 3.42 3.42 3.47 4.79 4.79 4.67 2.62 3.07 4.30 6.72 2.42 3.86 3.07 6.72 4.36 2.26 2.35 2.26 0 0 2.92 4.73 3.86 0 0 0 2.92 2.93 5.10 0 0 0 2.92 2.92 5.10 5.00 9 3.05 5.00 9 3.05 2.94	0,222 0,192 0,276 0,276 0,276 0,276 0,276 0,275 0,275 0,275 0,275 0,275 0,275 0,275 0,285 0,244 0,2991 0,244 0,2991 0,245 0,245 0,245 0,275 0,075 0,00	5.52           6.19           6.16           8.21           8.247           6.35           8.22           9.72           9.73           8.23           9.75           9.75           9.75           9.75           9.75           9.75           9.75           9.75           9.75           9.75           9.76           9.70           9.70           9.70           9.71           10.75           9.76           9.76           9.72           9.84           9.40           9.34           9.34           9.34           9.34           9.34           9.34           9.34           9.34           9.34           9.34           9.34           9.34           9.34           9.34           9.35	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 1 1 1 0 4 4 3 1 0 4 4 3 0 0 1 0 4 2 0 5 3 0 1 0 1 0 4 4 2 0 5 5 0 1 0 4 4 5 1 0 0 4 4 5 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 2 2 2 3 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		2 1140,7148 2 1465,7581 2 1465,7581 2 1145,7148 2 131,462 2 2076,9912 1 423,7545 1 423,7545 1 423,7545 1 423,7545 1 423,7545 1 423,7545 1 423,7545 1 428,7545 1 429,7997 1 420,7977 1	320           224           330           391           388           242           310           282           213           282           128           282           213           282           213           282           213           282           213           282           213           282           213           282           213           282           213           282           213           283           212           128           129           112           112           112           112           205           205           205           205           205           205           205           205           205           205	138 225 139 4001 400 259 259 259 244 109 225 244 109 225 244 109 225 244 109 229 244 109 229 244 108 108 108 109 224 241 108 108 108 108 108 108 108 108 108 10
Vimentin - Box taurus (Borino) VIME_BOVIN ATP synthese suburit beta, mitochondrial procursor (EC 3.6.3.14) - Homo sapiere, (HATPB_HEAMAN ATP synthese suburit beta, mitochondrial procursor (EC 3.6.3.14) - Homo sapiere, (HATPB_HEAMAN ATP synthese suburit beta, mitochondrial procursor (EC 3.6.3.14) - Homo sapiere, (HATPB_HEAMAN	53710.8 16542,5 16542,5	100.00%	2 8 10 13	2 14 16	4 0,42% 2 0,21% 27 4,86% 37 12,90% 51 7,46%	A729 ILLAFLOCK VESLEHARK VESLEHARK      A759 ILLAFLOCA      AMAL CHMANNELLAFR      20,000 AMAL CHMANNELLAFR      CONSTRUCTION     CONSTRU	化化 化化 使得觉我长得长长 使现得很长着长长 网络拉卡卡拉拉拉卡拉	G         99,00%           G         99,00%           G         99,00%           I         99,00%           J         99,00%           J         99,00%           J         99,00%           J         99,00%           J         99,00%           J         99,00%           G         99,00%           J         99,00%           G         99,00%           J         99,00%           J         99,00%           G         99,00%           S         90,00%           S         90,00%           G         90,00%           G         90,00%           G         90,00%           S         90,00%           G         90,00%           G         90,00%           G         90,00% <th>2.34 3.19 3.51 3.44 3.42 3.67 4.79 4.79 4.79 4.79 4.67 2.62 3.15 0.0 0.0 4.73 4.72 4.63 4.72 4.63 4.72 4.63 4.72 4.63 2.26 1.95 2.26 2.26 2.26 2.26 2.26 2.26 2.26 2.2</th> <th>0,222 0,192 0,209 0,276 0,276 0,2790</th> <th>5.52         6.85           6.16         6.16           6.16         6.16           6.16         6.16           8.247         6.32           8.76         8.76           8.78         8.73           8.78         8.73           8.79         8.74           9.75         8.76           9.77         8.74           9.78         8.96           8.13         1.17           10.5         5           9.79         5.44           2.92         2.44           2.94         4.92           4.92         4.92           4.92         4.92           4.92         4.92           4.92         4.92           5.78         9.42</th> <th>0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0</th> <th>3 1 1 1 0 4 4 3 1 0 4 2 0 5 3 0 1 6 1 1 0 1 4 1 0 2 0 5 3 0 1 6 2 0 4 2 0 5 3 0 1 0 4 2 0 5 3 0 1 0 4 2 0 5 3 0 1 0 5 3 0 1 0 5 3 0 1 0 5 3 0 1 0 5 3 0 1 0 5 3 0 1 0 5 3 0 1 0 5 3 0 5 3 0 5 3 0 5 3 0 5 3 0 5 5 5 5 5 5 5 5 5 5 5 5 5</th> <th>0 0 0 2 2 5 0 0 0 2 2 5 0 0 0 2 2 0 0 0 2 0 0 0 2 0 0 0 0</th> <th></th> <th>2 1140,7148 2 1465,7581 2 1145,7148 2 131,462 2 1311,462 2 1311,462 2 1311,462 2 1311,462 2 1435,7545 1 435,7545 1 435,7545 1 435,7545 1 435,7545 1 439,7899 2 159,6912 2 1439,7899 1 1088,635 2 0076,9912 2 1439,7899 1 1088,635 2 1439,7899 1 1088,635 2 1439,7899 1 1088,635 2 1439,7899 1 1088,635 2 1439,7899 1 1088,635 2 1439,7899 1 1088,635 2 1439,7899 2 159,9114 1 150,0959 2 159,9114 1 150,0957 2 137,780 2 137,780 2 137,780 2 137,780 2 137,780 2 137,780 2 140,7881 2 140,7881 2 140,7881 2 140,788 2 140</th> <th>330           224           330           391           388           244           313           313           321           321           321           322           232           232           3282           329           328           329           328           329           329           329           329           321           325           325           325           325           325           325           325           325           325           325           325           325           325           325           326           327           328           329           320           320           320           320</th> <th>139 235 1401 260 259 259 259 254 264 255 264 265 255 264 265 255 264 265 255 264 265 265 265 265 265 265 265 265 265 265</th>	2.34 3.19 3.51 3.44 3.42 3.67 4.79 4.79 4.79 4.79 4.67 2.62 3.15 0.0 0.0 4.73 4.72 4.63 4.72 4.63 4.72 4.63 4.72 4.63 2.26 1.95 2.26 2.26 2.26 2.26 2.26 2.26 2.26 2.2	0,222 0,192 0,209 0,276 0,276 0,2790	5.52         6.85           6.16         6.16           6.16         6.16           6.16         6.16           8.247         6.32           8.76         8.76           8.78         8.73           8.78         8.73           8.79         8.74           9.75         8.76           9.77         8.74           9.78         8.96           8.13         1.17           10.5         5           9.79         5.44           2.92         2.44           2.94         4.92           4.92         4.92           4.92         4.92           4.92         4.92           4.92         4.92           5.78         9.42	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 1 1 1 0 4 4 3 1 0 4 2 0 5 3 0 1 6 1 1 0 1 4 1 0 2 0 5 3 0 1 6 2 0 4 2 0 5 3 0 1 0 4 2 0 5 3 0 1 0 4 2 0 5 3 0 1 0 5 3 0 1 0 5 3 0 1 0 5 3 0 1 0 5 3 0 1 0 5 3 0 1 0 5 3 0 1 0 5 3 0 5 3 0 5 3 0 5 3 0 5 3 0 5 5 5 5 5 5 5 5 5 5 5 5 5	0 0 0 2 2 5 0 0 0 2 2 5 0 0 0 2 2 0 0 0 2 0 0 0 2 0 0 0 0		2 1140,7148 2 1465,7581 2 1145,7148 2 131,462 2 1311,462 2 1311,462 2 1311,462 2 1311,462 2 1435,7545 1 435,7545 1 435,7545 1 435,7545 1 435,7545 1 439,7899 2 159,6912 2 1439,7899 1 1088,635 2 0076,9912 2 1439,7899 1 1088,635 2 1439,7899 1 1088,635 2 1439,7899 1 1088,635 2 1439,7899 1 1088,635 2 1439,7899 1 1088,635 2 1439,7899 1 1088,635 2 1439,7899 2 159,9114 1 150,0959 2 159,9114 1 150,0957 2 137,780 2 137,780 2 137,780 2 137,780 2 137,780 2 137,780 2 140,7881 2 140,7881 2 140,7881 2 140,788 2 140	330           224           330           391           388           244           313           313           321           321           321           322           232           232           3282           329           328           329           328           329           329           329           329           321           325           325           325           325           325           325           325           325           325           325           325           325           325           325           326           327           328           329           320           320           320           320	139 235 1401 260 259 259 259 254 264 255 264 265 255 264 265 255 264 265 255 264 265 265 265 265 265 265 265 265 265 265
Vimentin - Box taurus (Bovine) VIME_BOVIN ATP synthase subunit beta, mitochondrial precursor (IC 3.6.3.14) - Homo sapiers, (PATPB_HUMAM ATP synthase subunit beta, mitochondrial precursor (IC 3.6.3.14) - Homo sapiers, (PATPB_HUMAM Vimentin (Iragment) - Cricetulus grisuus (Chinese hamster) VIME_CRICR	59703 53710,8 56542,5 56542,5 56542,5	100.00%	2 8 10	2	4 0,42% 2 0,21% 27 4,80% 37 12,90%	A.72% ILABLECK     VISUELEARX     VISUELEARX     VISUELEARX     AND     AND     AND     AND     CONTACT     C	长长 化化 用膏膏膏化化剂 化化合物化合物化合物化合物化合物	G         99,00%           G         99,00%           G         99,00%           I         99,00%           O         99,00%           I         99,00%           I         99,00%           I         99,00%           I         99,00%           G         99,00%           G         99,00%           G         99,00%           G         99,00%           G         99,00%           C         99,00%	2.24 3.19 3.51 3.44 3.42 3.42 3.42 4.79 4.79 4.79 4.67 2.62 0 4.36 6.72 2.42 3.05 2.26 1.95 2.26 0 0 2.92 4.73 3.86 2.35 2.26 0 0 0 2.92 2.42 3.51 3.61 3.61 3.67 4.67 9.79 4.79 4.79 4.79 4.70 4.70 4.70 4.70 4.70 4.70 4.70 4.70	0.222 0.102 0.276 0.276 0.276 0.277 0.533 0.279 0.233 0.275 0.233 0.235 0.240 0.24 0.24 0.24 0.24 0.24 0.24 0.2	5.52 6.85 6.85 6.85 6.40 6.16 6.7 6.7 8.96 8.75 8.96 8.11 6.75 8.96 8.11 8.11 8.11 8.19 9.7 5.54 9.75 8.96 8.11 8.11 8.10 9.7 5.54 9.752 9.75	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 1 1 1 0 4 4 3 1 0 4 4 3 0 3 0 1 0 4 2 0 5 3 0 1 6 1 1 0 3 0 1 0 4 4 4 3 1 0 5 5 1 0 1 0 4 4 3 1 0 0 3 0 1 1 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 1 1 1 1 1 1 1 1 1 1 1 1	0 0 0 2 2 2 5 5 0 0 2 2 0 0 0 2 2 0 0 0 0		2 1140,7148 2 1465,7581 2 1465,7581 2 1145,7148 2 131,462 2 2005,9912 2 425,7541 2 435,7545 1 385,7101 2 205,9912 1 435,7545 1 385,7101 2 2 455,7545 1 385,7101 2 2 455,7452 1 385,7101 2 2 155,9857 1 386,4594 2 455,7462 2 155,9857 2 153,8557 2 153,9577 2 153,95777 2 153,95777 2 153,95777 2 153,957777 2 153,95777777 2 153,9577777777777777777777777777777777777	130           224           391           388           242           313           242           313           242           325           189           242           325           326           327           328           329           348           329           329           329           329           129           120           330           301           302           303           304           205           303           304           205           206	138           139           225           130           406           259           330           225           241           140           406           259           243           244           149           259           244           143           153           245           243           143           153           143           143           143           143           143           143           143           143           143           143           1441           1451           1451           1451           1451           1451           1451           1451           1451           1451           1451           1451           1451           1451           1451           1451           1451           1451 </th
Vimentin - Box taurus (Bovine) VIME_BOVIN ATP synthase suburit bets, mitochondrial precursor (IC 3.6.3.14) - Homo sapiene (FATPB_HEAMN ATP synthase suburit bets, mitochondrial precursor (IC 3.6.3.14) - Homo sapiene (FATPB_HEAMN VIME_DELETER Status) VIME_CRICE	59703 53710,8 56542,5 56542,5 51831,8	100.00% 100.00% 100.00%	2 8 10 13	2 14 16 19	4 0.42% 2 0.21% 27 4.86% 37 12.90% 51 7.46%	A.72% ILLARICAL VISIOLEMAIX     A.51% ILLARICAL     ALAGUMANTIA     ALAGUMANTA     ALAGUMANTA     CONSTRUCTION	化化 化化 的复数化化化化化化化化化化化化化化化化化化化化化化化化化化化化化化化	C         99,00%           C         99,00%           G         99,00%           I         99,00%           J         99,00%           G         99,00%           L         99,00% <th>2.34 3.19 3.51 3.44 3.42 3.67 4.79 4.79 4.79 4.79 4.70 4.70 4.70 4.70 4.72 4.67 4.74 4.74 4.74 4.74 4.30 4.30 4.30 4.30 4.30 4.30 4.30 4.3</th> <th>0.222 0.192 0.279 0.274 0.279 0.53 0.279 0.279 0.273 0.279 0.273 0.275 0.279 0.273 0.275 0.279 0.24 0.0450000000000</th> <th>5.52           6.35           6.10           6.13           6.14           6.35           8.72           9.76           8.73           10           9.76           9.76           9.76           9.77           9.78           9.79           9.79           9.71           10.5           9.79           9.79           9.79           9.79           9.70     <!--</th--><th></th><th>3 1 1 0 4 4 3 1 0 4 4 2 0 5 3 0 1 6 1 1 0 4 4 2 0 5 3 0 1 6 1 1 0 0 4 4 4 4 4 4 4 4 4 4 4 4 4</th><th>0 0 0 2 2 2 5 5 0 2 2 0 2 0 0 0 0 0 0 0</th><th></th><th>2 1140,7148 2 1465,7591 2 1405,7591 2 1145,7591 2 1141,452 2 125,4591 2 153,459 1 143,7484 2 153,459 1 143,7484 2 153,459 1 153,459 1 153,459 2 153,459 2</th><th>130           224           130           391           388           242           130           213           213           2142           130           213           2142           123           212           2242           131           242           121           242           122           125           125           125           125           125           125           125           125           125           125           125           125           125           125           125           125           205           205           205           205           205           205           206           206           206           206           206           206           207           208  &lt;</th><th>138 225 139 4001 400 259 259 255 255 244 143 109 259 259 259 259 259 259 259 259 259 25</th></th>	2.34 3.19 3.51 3.44 3.42 3.67 4.79 4.79 4.79 4.79 4.70 4.70 4.70 4.70 4.72 4.67 4.74 4.74 4.74 4.74 4.30 4.30 4.30 4.30 4.30 4.30 4.30 4.3	0.222 0.192 0.279 0.274 0.279 0.53 0.279 0.279 0.273 0.279 0.273 0.275 0.279 0.273 0.275 0.279 0.24 0.0450000000000	5.52           6.35           6.10           6.13           6.14           6.35           8.72           9.76           8.73           10           9.76           9.76           9.76           9.77           9.78           9.79           9.79           9.71           10.5           9.79           9.79           9.79           9.79           9.70 </th <th></th> <th>3 1 1 0 4 4 3 1 0 4 4 2 0 5 3 0 1 6 1 1 0 4 4 2 0 5 3 0 1 6 1 1 0 0 4 4 4 4 4 4 4 4 4 4 4 4 4</th> <th>0 0 0 2 2 2 5 5 0 2 2 0 2 0 0 0 0 0 0 0</th> <th></th> <th>2 1140,7148 2 1465,7591 2 1405,7591 2 1145,7591 2 1141,452 2 125,4591 2 153,459 1 143,7484 2 153,459 1 143,7484 2 153,459 1 153,459 1 153,459 2 153,459 2</th> <th>130           224           130           391           388           242           130           213           213           2142           130           213           2142           123           212           2242           131           242           121           242           122           125           125           125           125           125           125           125           125           125           125           125           125           125           125           125           125           205           205           205           205           205           205           206           206           206           206           206           206           207           208  &lt;</th> <th>138 225 139 4001 400 259 259 255 255 244 143 109 259 259 259 259 259 259 259 259 259 25</th>		3 1 1 0 4 4 3 1 0 4 4 2 0 5 3 0 1 6 1 1 0 4 4 2 0 5 3 0 1 6 1 1 0 0 4 4 4 4 4 4 4 4 4 4 4 4 4	0 0 0 2 2 2 5 5 0 2 2 0 2 0 0 0 0 0 0 0		2 1140,7148 2 1465,7591 2 1405,7591 2 1145,7591 2 1141,452 2 125,4591 2 153,459 1 143,7484 2 153,459 1 143,7484 2 153,459 1 153,459 1 153,459 2	130           224           130           391           388           242           130           213           213           2142           130           213           2142           123           212           2242           131           242           121           242           122           125           125           125           125           125           125           125           125           125           125           125           125           125           125           125           125           205           205           205           205           205           205           206           206           206           206           206           206           207           208  <	138 225 139 4001 400 259 259 255 255 244 143 109 259 259 259 259 259 259 259 259 259 25
Vimentin - Box taurus (Bovine) VIME_BOVIN ATP synthase suburit beta, mitochondial precursor (IC 3.6.3.14) - Homo sapiers (FATPB_HRAMA ATP synthase suburit beta, mitochondial precursor (IC 3.6.3.14) - Homo sapiers (FATPB_HRAMA ATP synthase suburit beta, mitochondial precursor (IC 3.6.3.14) - Homo sapiers (FATPB_HRAMA Wimentin (Fragment) - Critectulus grisous (Chinese Ramster) VIME_CRICR Exterioudin precursor (CRP5)) (Categolin) (McDPJ (Ebplot) (CALBP) (Calcum-End CALR_RAT	53710.8 53542,5 56542,5 51831,8	100.00%	2 2 8 10 13	2 14 16 19	4 0.42% 2 0.21% 27 4.86% 37 12.90% 51 7.66%	A729 HARLOCK     VISUELEARX     VISUELEARX     VISUELEARX     AND     ALECON     VISUELEARX     CONSTRUCTION     CONSTRUCTION     CONSTRUCTION     CONSTRUCTION     CONSTRUCTION     VISUELEARX	化化 化化 使得觉得长度长长 网络带着肉带长带长长 网络带长长用骨板长用骨长 网络	G         99,00%           G         99,00%           G         99,00%           I         99,00%           J         99,00%           G         99,00%           I         99,00%           J         99,00%           G         99,00%           J         99,00%           J         99,00%           G         99,00%           G         99,00%           G         99,00%           K         99,00%           K         99,00%           K         99,00%           G         99,00%           K         99,00%           K         99,00%           G         99,00%           G         99,00%           K         99,00%           G         99,00%           G         99,00%           K         99,00%           G         99,00% <th>3.34 3.79 3.51 3.41 3.42 3.67 4.79 4.77 4.67 2.62 3.15 0 0.38 4.63 0.07 2.62 2.92 1.95 0.0 0 2.92 2.92 4.73 2.42 3.86 3.07 2.82 0.0 0 0.292 2.92 2.92 2.95 2.95 2.95 2.95 2.95</th> <th>0.222 0.102 0.276 0.276 0.276 0.279 0.53 0.279 0.233 0.279 0.233 0.233 0.235 0.240 0.24 0.24 0.24 0.24 0.24 0.24 0.2</th> <th>5.52 6.85 6.85 6.85 7.6 7.6 7.6 7.6 8.96 9.75 8.96 9.75 8.96 9.75 8.96 9.75 8.96 9.75 8.96 9.75 8.96 9.75 8.96 9.75 8.96 9.75 8.90 7.5 7.5 8.90 7.5 8.90 7.5 8.90 7.5 7.5 7.5 8.90 7.5 7.5 8.90 7.5 8.90 7.5 8.90 7.5 8.90 7.5 8.90 7.5 8.90 7.5 8.90 7.5 8.00 7.5 8.00 7.5 8.00 7.5 8.00 7.5 8.00 7.5 7.5 7.5 7.5 7.5 7.5 7.5 7.5 7.5 7.5</th> <th></th> <th>3 1 1 1 0 4 4 3 1 0 4 4 3 1 0 4 4 2 0 5 3 0 1 6 1 0 1 0 4 4 2 0 5 3 0 1 0 4 4 2 0 0 4 4 2 0 0 4 4 2 0 0 0 4 4 2 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0</th> <th></th> <th></th> <th>2 1140,7148 2 1465,7581 2 1145,7148 2 131,462 2 131,462 2 131,462 2 131,462 2 131,462 2 131,462 2 143,7448 1 133,7448 1 133,7448 2 1439,7899 1 131,402 2 1439,7899 1 131,402 2 1439,7899 1 131,402 2 1439,7899 1 131,462 2 1439,7899 1 1437,462 2 1439,7899 1 131,462 2 1439,7899 1 131,462 2 1439,7899 1 131,462 2 1439,7899 1 1437,462 2 1439,7899 1 1437,462 2 1439,789 1 1437,462 2 1439,7899 1 1437,462 2 1437,789 1 133,5579 1 1437,748 1 133,5579 1 1437,748 1 133,5579 1 1437,748 1 133,5579 1 1437,748 1 133,7574 1 133,5599 1 1437,748 1 133,7574 1 133,5599 1 1437,748 1 133,7585 1 133</th> <th>130           224           130           288           231           251           252           238           241           388           389           389           389           389           389           389           389           389           389           389           389           389           389           389           389           391           144           393           394           395           395           396           397           393           394           395           396           397           392</th> <th>139 225 1401 4001 259 259 259 264 265 264 265 264 265 264 265 264 265 264 265 264 265 265 264 265 265 264 265 265 265 265 265 265 265 265 265 265</th>	3.34 3.79 3.51 3.41 3.42 3.67 4.79 4.77 4.67 2.62 3.15 0 0.38 4.63 0.07 2.62 2.92 1.95 0.0 0 2.92 2.92 4.73 2.42 3.86 3.07 2.82 0.0 0 0.292 2.92 2.92 2.95 2.95 2.95 2.95 2.95	0.222 0.102 0.276 0.276 0.276 0.279 0.53 0.279 0.233 0.279 0.233 0.233 0.235 0.240 0.24 0.24 0.24 0.24 0.24 0.24 0.2	5.52 6.85 6.85 6.85 7.6 7.6 7.6 7.6 8.96 9.75 8.96 9.75 8.96 9.75 8.96 9.75 8.96 9.75 8.96 9.75 8.96 9.75 8.96 9.75 8.96 9.75 8.90 7.5 7.5 8.90 7.5 8.90 7.5 8.90 7.5 7.5 7.5 8.90 7.5 7.5 8.90 7.5 8.90 7.5 8.90 7.5 8.90 7.5 8.90 7.5 8.90 7.5 8.90 7.5 8.00 7.5 8.00 7.5 8.00 7.5 8.00 7.5 8.00 7.5 7.5 7.5 7.5 7.5 7.5 7.5 7.5 7.5 7.5		3 1 1 1 0 4 4 3 1 0 4 4 3 1 0 4 4 2 0 5 3 0 1 6 1 0 1 0 4 4 2 0 5 3 0 1 0 4 4 2 0 0 4 4 2 0 0 4 4 2 0 0 0 4 4 2 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0			2 1140,7148 2 1465,7581 2 1145,7148 2 131,462 2 131,462 2 131,462 2 131,462 2 131,462 2 131,462 2 143,7448 1 133,7448 1 133,7448 2 1439,7899 1 131,402 2 1439,7899 1 131,402 2 1439,7899 1 131,402 2 1439,7899 1 131,462 2 1439,7899 1 1437,462 2 1439,7899 1 131,462 2 1439,7899 1 131,462 2 1439,7899 1 131,462 2 1439,7899 1 1437,462 2 1439,7899 1 1437,462 2 1439,789 1 1437,462 2 1439,7899 1 1437,462 2 1437,789 1 133,5579 1 1437,748 1 133,5579 1 1437,748 1 133,5579 1 1437,748 1 133,5579 1 1437,748 1 133,7574 1 133,5599 1 1437,748 1 133,7574 1 133,5599 1 1437,748 1 133,7585 1 133	130           224           130           288           231           251           252           238           241           388           389           389           389           389           389           389           389           389           389           389           389           389           389           389           389           391           144           393           394           395           395           396           397           393           394           395           396           397           392	139 225 1401 4001 259 259 259 264 265 264 265 264 265 264 265 264 265 264 265 264 265 265 264 265 265 264 265 265 265 265 265 265 265 265 265 265
Vimentin - Box taurus (Bovine) VIME_BOVIN ATP synthase subunit beta, mitochondrial precursor (IC 3.6.3.14) - Homo sapiens (FATPB_HEMANI ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (FATPB_HEMANI ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (FATPB_HEMANI ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (FATPB_HEMANI ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (FATPB_HEMANI ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (FATPB_HEMANI ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (FATPB_HEMANI ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (FATPB_HEMANI ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (FATPB_HEMANI ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (FATPB_HEMANI ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (FATPB_HEMANI ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (FATPB_HEMANI ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (FATPB_HEMANI ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (FATPB_HEMANI ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (FATPB_HEMANI ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (FATPB_HEMANI ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (FATPB_HEMANI ATP synthase subunit beta, mitochondrial precursor (FATPB_HEMANI ATP synthase subunit beta, mitochondrial precursor (FATPB_HEMANI synthase subunit synthase subunit beta, mitochondrial precursor (FATPB_HEMANI synthase subuni	59900 59910.8 56542.5 56542.5 51831.8	100.00% 100.00% 100.00%	2 8 10 13	2 14 16	4 0.42% 2 0.21% 27 4.86% 37 12,90% 51 7.66%	A.72% ILABLECK VSLOEHARK      ASSA ASSA ASSA ASSA CONSTRUCTION CONSTRU	化化 化化 网络拉尔尼文化 化合物合合物合合物合合物合合物合合物合合物合合物合合物合合物合合物 化化化物合合物合合物合合物合合物合合物合合物合合物合合物合合物合合物合合物合合物	G         99,00%           G         99,00%           G         99,00%           I         99,00%           I         99,00%           J         99,00%           G         99,00%           G         99,00%           G         99,00%           G         99,00%           G         99,00%           C         99,00%           E         99,00%           E         99,00%           C         99,00%           K         99,00%           C         99,00%           K         99,00%           C         99,00%           C         99,00%           K         99,00%           V         99,00% <th>3.34 3.19 3.51 3.42 3.67 4.79 4.79 4.79 4.79 4.67 2.62 3.97 4.67 2.62 3.97 4.67 2.62 3.97 4.67 2.62 3.97 4.67 2.62 2.26 0 0 0 0 2.92 2.85 2.26 0 0 0 0 0 2.92 2.85 2.26 0 0 0 0 0 2.92 2.85 2.26 0 0 0 0 0 2.92 2.85 2.26 0 0 0 0 0 0 2.92 2.23 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0</th> <th>0.222 0.192 0.276 0.276 0.276 0.279 0.53 0.077 0.279 0.633 0.077 0.279 0.073 0.073 0.073 0.073 0.073 0.073 0.073 0.073 0.073 0.073 0.073 0.073 0.073 0.074 0.0693 0.0693 0.0693 0.0693 0.079 0.079 0.079 0.0693 0.0693 0.0693 0.079 0.0000000000</th> <th>5.52 6.85 6.85 6.85 7.47 6.247 6.247 7.52 8.90 9.75 8.90 9.75 8.90 9.75 8.90 9.75 8.90 7.75 8.90 7.75 8.90 7.75 8.90 7.75 8.90 7.75 8.90 7.75 8.90 7.75 8.90 7.55 7.97 7.24 7.92 7.55 7.97 7.24 7.92 7.55 7.97 7.24 7.92 7.92 7.92 7.92 7.92 7.92 7.92 7.92</th> <th>0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0</th> <th>3 1 1 1 0 4 4 3 1 0 4 4 3 1 0 4 4 2 0 5 3 0 1 0 4 4 2 0 5 3 0 1 0 0 4 4 2 0 0 0 0 0 0 0 0 0 0 0 0 0</th> <th>0 0 0 2 2 2 5 5 0 2 2 0 2 0 0 2 0 0 0 0</th> <th></th> <th>2 1140,7148 2 1465,751 2 1465,751 2 1467,744 2 131,462 2 131,462 2 2076,9912 1 435,7543 1 328,1709 2 1098,0371 2 1098,0372 1 435,7543 1 328,1709 2 1098,0372 1 328,1709 2 1098,0372 1 328,1709 2 1098,0372 1 328,1709 2 1098,0372 1 328,1709 2 1098,0372 1 338,039 2 1099,0314 1 339,014 1 359,014 1 353,014 1 354,014 1 354,014 1 354,014 1 354,014 1 354,014 1</th> <th>130           224           391           284           311           282           213           214           315           225           129           222           225           225           226           227           228           242           312           235           355           355           189           407           112           325           325           359           325           359           325           359           325           359           325           326           327           328           3204           3204           3205           326           3204           3205           329           320           3204           3205           320           320           3204     <!--</th--><th>138 225 1401 406 259 259 259 244 109 225 244 143 148 259 259 254 269 259 254 269 259 254 269 259 254 269 259 254 269 259 254 269 254 269 254 269 254 269 254 269 254 269 254 269 269 269 269 269 269 269 269 269 269</th></th>	3.34 3.19 3.51 3.42 3.67 4.79 4.79 4.79 4.79 4.67 2.62 3.97 4.67 2.62 3.97 4.67 2.62 3.97 4.67 2.62 3.97 4.67 2.62 2.26 0 0 0 0 2.92 2.85 2.26 0 0 0 0 0 2.92 2.85 2.26 0 0 0 0 0 2.92 2.85 2.26 0 0 0 0 0 2.92 2.85 2.26 0 0 0 0 0 0 2.92 2.23 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.222 0.192 0.276 0.276 0.276 0.279 0.53 0.077 0.279 0.633 0.077 0.279 0.073 0.073 0.073 0.073 0.073 0.073 0.073 0.073 0.073 0.073 0.073 0.073 0.073 0.074 0.0693 0.0693 0.0693 0.0693 0.079 0.079 0.079 0.0693 0.0693 0.0693 0.079 0.0000000000	5.52 6.85 6.85 6.85 7.47 6.247 6.247 7.52 8.90 9.75 8.90 9.75 8.90 9.75 8.90 9.75 8.90 7.75 8.90 7.75 8.90 7.75 8.90 7.75 8.90 7.75 8.90 7.75 8.90 7.75 8.90 7.55 7.97 7.24 7.92 7.55 7.97 7.24 7.92 7.55 7.97 7.24 7.92 7.92 7.92 7.92 7.92 7.92 7.92 7.92	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 1 1 1 0 4 4 3 1 0 4 4 3 1 0 4 4 2 0 5 3 0 1 0 4 4 2 0 5 3 0 1 0 0 4 4 2 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 2 2 2 5 5 0 2 2 0 2 0 0 2 0 0 0 0		2 1140,7148 2 1465,751 2 1465,751 2 1467,744 2 131,462 2 131,462 2 2076,9912 1 435,7543 1 328,1709 2 1098,0371 2 1098,0372 1 435,7543 1 328,1709 2 1098,0372 1 328,1709 2 1098,0372 1 328,1709 2 1098,0372 1 328,1709 2 1098,0372 1 328,1709 2 1098,0372 1 338,039 2 1099,0314 1 339,014 1 359,014 1 353,014 1 354,014 1 354,014 1 354,014 1 354,014 1 354,014 1	130           224           391           284           311           282           213           214           315           225           129           222           225           225           226           227           228           242           312           235           355           355           189           407           112           325           325           359           325           359           325           359           325           359           325           326           327           328           3204           3204           3205           326           3204           3205           329           320           3204           3205           320           320           3204 </th <th>138 225 1401 406 259 259 259 244 109 225 244 143 148 259 259 254 269 259 254 269 259 254 269 259 254 269 259 254 269 259 254 269 254 269 254 269 254 269 254 269 254 269 254 269 269 269 269 269 269 269 269 269 269</th>	138 225 1401 406 259 259 259 244 109 225 244 143 148 259 259 254 269 259 254 269 259 254 269 259 254 269 259 254 269 259 254 269 254 269 254 269 254 269 254 269 254 269 254 269 269 269 269 269 269 269 269 269 269
Vimentin - Box taurus (Bovine) VIME_BOVIN ATP synthese suburit bets, mitochondrial precursor (EC.3.6.3.14) - Horno sapiers, (HATPB_HEAMM ATP synthese suburit bets, mitochondrial precursor (EC.3.6.3.14) - Horno sapiers, (HATPB_HEAMM Vimentin (Fragment) - Cricetulus griseus (Chieses harmster) VIME_CBIGR Calenticulin precursor (CRPS3) (Calenguin) (HACBP) (ERpido) (CALBP) (Calcum-bindt CALR_BAT	13710.8 135142.5 15542.5 11831.8	100.00%	2 8 10 13	2 14 16 19 14	4 0.42% 2 0.21% 27 4.86% 37 12.90% 51 7.66%	A729 HUALICAK     VESUGEARAK	化化 化化 现得觉得长得长长 网络昆得昆昆长得长长 网络昆长长昆昆昆长昆昆长 网络龙龙属龙长昆龙长 网络昆普拉龙属龙长昆龙长属昆龙龙属昆长龙	G         99,00%           G         99,00%           G         99,00%           I         99,00%           J         99,00%           J         99,00%           J         99,00%           J         99,00%           J         99,00%           G         99,00%           G         99,00%           G         99,00%           G         99,00%           J         98,00%           G         99,00%           S         90,00%           L         90,00%           L         90,00%           L         90,00%           C         90,00%           C         90,00%           L         90,00% <th>3.34 3.79 3.51 3.44 3.42 3.42 3.42 3.42 4.07 4.07 4.07 4.07 4.07 4.07 4.07 4.07</th> <th>0.222 0.192 0.279 0.279 0.278 0.279 0.279 0.335 0.077 0.375 0.077 0.375 0.077 0.375 0.077 0.375 0.077 0.375 0.079 0.049 0.0491 0.0491 0.0491 0.0491 0.0491 0.0491 0.0491 0.0491 0.0491 0.0410000000000</th> <th>5.52           6.35           6.16           6.17           6.18           7.10           8.23           9.75           8.13           16           7.61           9.75           8.74           1.13           1.6           9.75           9.74           9.75           9.74           9.75           9.74           1.13           1.6           9.75           9.74           9.75           9.74           9.75           9.75           9.74           9.75           9.74           9.75           9.75           9.74           9.75           9.74           9.75           9.75           9.75           9.75           9.75           9.75           9.75           9.75           9.75           9.75           9.75           9.75           9.75     <th></th><th>3 1 1 1 0 4 4 4 3 1 0 4 4 2 0 5 3 0 1 6 1 0 1 6 1 0 1 0 4 4 2 0 5 3 0 1 0 4 4 4 2 0 5 5 0 0 4 4 4 2 0 0 4 4 4 2 0 0 1 0 0 4 4 4 2 0 0 1 0 0 1 0 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0</th><th>0 0 0 0 0 2 2 3 5 0 0 2 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0</th><th></th><th>2 1140,7148 2 1465,7531 2 1145,7148 2 131,462 2 131,462 2 131,462 2 131,462 2 131,462 2 131,462 2 143,7545 1 435,7545 1 435,7545 1 435,7545 1 435,7545 1 435,7545 1 439,7899 2 1010,0971 2 1088,033 2 2026,0749 1 1088,035 1 109,7168 1 109,7168 1 1038,057 1 1038,</th><th>130           224           130           381           392           242           311           282           125           189           244           311           282           125           189           244           311           321           321           321           321           323           324           325           189           241           255           180           321           323           324           325           326           327           328           329           320           206           206           206           206           206           207           329</th><th>139           139           225           4001           2009           324           259           243           139           200           259           244           198           259           244           198           255           244           198           255           244           198           421           121           125           244           198           421           122           123           124           125           244           126           217           218           217           218           217           218           217           218           217           218           217           218           217           218           217           218           217</th></th>	3.34 3.79 3.51 3.44 3.42 3.42 3.42 3.42 4.07 4.07 4.07 4.07 4.07 4.07 4.07 4.07	0.222 0.192 0.279 0.279 0.278 0.279 0.279 0.335 0.077 0.375 0.077 0.375 0.077 0.375 0.077 0.375 0.077 0.375 0.079 0.049 0.0491 0.0491 0.0491 0.0491 0.0491 0.0491 0.0491 0.0491 0.0491 0.0410000000000	5.52           6.35           6.16           6.17           6.18           7.10           8.23           9.75           8.13           16           7.61           9.75           8.74           1.13           1.6           9.75           9.74           9.75           9.74           9.75           9.74           1.13           1.6           9.75           9.74           9.75           9.74           9.75           9.75           9.74           9.75           9.74           9.75           9.75           9.74           9.75           9.74           9.75           9.75           9.75           9.75           9.75           9.75           9.75           9.75           9.75           9.75           9.75           9.75           9.75 <th></th> <th>3 1 1 1 0 4 4 4 3 1 0 4 4 2 0 5 3 0 1 6 1 0 1 6 1 0 1 0 4 4 2 0 5 3 0 1 0 4 4 4 2 0 5 5 0 0 4 4 4 2 0 0 4 4 4 2 0 0 1 0 0 4 4 4 2 0 0 1 0 0 1 0 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0</th> <th>0 0 0 0 0 2 2 3 5 0 0 2 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0</th> <th></th> <th>2 1140,7148 2 1465,7531 2 1145,7148 2 131,462 2 131,462 2 131,462 2 131,462 2 131,462 2 131,462 2 143,7545 1 435,7545 1 435,7545 1 435,7545 1 435,7545 1 435,7545 1 439,7899 2 1010,0971 2 1088,033 2 2026,0749 1 1088,035 1 109,7168 1 109,7168 1 1038,057 1 1038,</th> <th>130           224           130           381           392           242           311           282           125           189           244           311           282           125           189           244           311           321           321           321           321           323           324           325           189           241           255           180           321           323           324           325           326           327           328           329           320           206           206           206           206           206           207           329</th> <th>139           139           225           4001           2009           324           259           243           139           200           259           244           198           259           244           198           255           244           198           255           244           198           421           121           125           244           198           421           122           123           124           125           244           126           217           218           217           218           217           218           217           218           217           218           217           218           217           218           217           218           217</th>		3 1 1 1 0 4 4 4 3 1 0 4 4 2 0 5 3 0 1 6 1 0 1 6 1 0 1 0 4 4 2 0 5 3 0 1 0 4 4 4 2 0 5 5 0 0 4 4 4 2 0 0 4 4 4 2 0 0 1 0 0 4 4 4 2 0 0 1 0 0 1 0 0 1 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 2 2 3 5 0 0 2 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0		2 1140,7148 2 1465,7531 2 1145,7148 2 131,462 2 131,462 2 131,462 2 131,462 2 131,462 2 131,462 2 143,7545 1 435,7545 1 435,7545 1 435,7545 1 435,7545 1 435,7545 1 439,7899 2 1010,0971 2 1088,033 2 2026,0749 1 1088,035 1 109,7168 1 109,7168 1 1038,057 1 1038,	130           224           130           381           392           242           311           282           125           189           244           311           282           125           189           244           311           321           321           321           321           323           324           325           189           241           255           180           321           323           324           325           326           327           328           329           320           206           206           206           206           206           207           329	139           139           225           4001           2009           324           259           243           139           200           259           244           198           259           244           198           255           244           198           255           244           198           421           121           125           244           198           421           122           123           124           125           244           126           217           218           217           218           217           218           217           218           217           218           217           218           217           218           217           218           217
Vimentin - Box taurus (Bovine)     VIME_BOVIN       ATP synthase suburit beta, mitochondrial precursor (IC 3.6.3.14) - Henro sapiens (FATPB_HUMAN)       ATP synthase suburit beta, mitochondrial precursor (IC 3.6.3.14) - Henro sapiens (FATPB_HUMAN)       ATP synthase suburit beta, mitochondrial precursor (IC 3.6.3.14) - Henro sapiens (FATPB_HUMAN)       Vimentin (Fragment) - Critectulus grisous (Chinese hamster)     VIME_CRICR       Calvesticulin precursor (CRP55) (Calveguin) (HACBP) (ERB(K)) (CALBP) (Calcum-Eindi CALR_RAT)	5100 53710.8 56542.5 56542.5 51831.8	100.00% 100.00% 100.00%	2 8 10 13	2 2 14 16 19 14	4 0.42% 2 0.21% 27 4.86% 37 12.90% 51 7.46%	A729 ILABLECK     VISUELEARK     VISUELEARK     VISUELEARK     AND     AND     AND     AND     CONTRACT     CONTTACT     CONTTACT     CONTTACT	化化 化化 用骨肉瘤化胃化化 用用骨肉用用化用化化 的复数无足肉肉化化和化化 的复数化化化 的复数化化化化	G         99,00%           G         99,00%           G         99,00%           I         99,00%           G         99,00%           C         99,00%           C         99,00%           C         99,00%           C         99,00%           C         99,00%           D         99,00%           C         99,00%           D         99,00%           C         99,00% <th>3.34 3.19 3.51 3.42 3.67 4.79 4.79 4.79 4.79 4.67 2.62 3.07 4.67 2.62 3.07 4.67 2.62 3.07 4.67 2.62 3.07 4.67 2.62 3.07 4.67 2.35 3.07 4.63 4.7 3.86 4.7 3.86 2.35 3.07 4.63 4.7 3.85 2.25 3.07 4.63 4.7 3.85 2.25 3.07 4.63 4.7 3.85 2.25 3.07 4.63 4.7 3.85 0.07 2.62 2.62 3.07 4.67 2.52 2.53 3.07 4.7 3.85 0.07 2.62 2.53 3.07 4.7 3.85 0.07 2.62 2.53 3.07 2.62 3.07 2.62 3.07 2.62 3.07 2.62 2.53 3.07 2.62 2.53 3.07 2.62 2.53 3.07 2.62 2.53 3.07 2.62 2.54 3.07 2.62 2.54 3.07 2.62 2.54 3.07 2.62 2.54 3.07 2.54 3.07 2.62 2.54 3.07 2.62 2.54 3.07 2.62 2.54 3.07 2.54 2.53 3.07 2.62 2.54 3.07 2.62 2.54 3.07 2.54 3.07 2.54 2.54 3.07 2.54 3.07 3.07 3.07 3.07 3.07 3.07 3.07 3.07</th> <th>0.222 0.192 0.279 0.274 0.0084 0.0084 0.0084 0.0083 0.00835 0.00835 0.00835 0.00835 0.00835 0.00835 0.0081 0.00835 0.00810000000000</th> <th>5.52           6.195           6.16           2.47           8.23           9.76           8.13           1.3           4.37           9.1           8.9           9.1           9.1           9.1           9.2           9.3     &lt;</th> <th></th> <th>3 1 1 1 0 4 4 4 3 1 0 5 3 0 4 4 2 0 5 3 0 1 6 1 1 0 5 3 0 1 6 0 1 0 0 4 4 4 3 1 0 0 4 4 4 3 1 0 0 4 4 4 3 1 0 0 4 4 4 3 1 0 0 2 0 0 0 4 4 4 3 1 0 0 2 0 0 0 1 0 0 0 2 0 0 0 0 0 0 0 0</th> <th>0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0</th> <th>0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0</th> <th>2 1140,7148 2 1465,7811 2 1145,7148 2 131,462 2 131,462 2 131,462 2 131,462 2 205,6912 2 435,7648 1 435,7649 1 386,7019 2 205,6912 1 435,7649 1 386,7019 2 205,6912 1 435,7649 1 386,7019 2 206,6912 1 435,7649 1 386,7019 2 206,6912 1 435,7649 1 386,7019 2 206,6912 1 435,7649 1 386,7019 2 1088,6357 2 1086,637 2 1086,647 2 1086,647 2 1086,647 2 1086,647 2 1086,647 2 1086,647 2 1086</th> <th>130           224           130           391           288           313           242           130           282           131           282           132           283           284           331           341           343           213           283           213           284           336           213           283           213           284           3141           344           305           213           283           407           407           407           303           304           305           305           304           305           305           306           307           308           309           304           305           306           307           308           309</th> <th>138           139           225           139           400           209           324           139           205           201           139           202           203           204           131           198           205           204           198           191           212           316           316           316           317           218           219           310           212           313           314           315</th>	3.34 3.19 3.51 3.42 3.67 4.79 4.79 4.79 4.79 4.67 2.62 3.07 4.67 2.62 3.07 4.67 2.62 3.07 4.67 2.62 3.07 4.67 2.62 3.07 4.67 2.35 3.07 4.63 4.7 3.86 4.7 3.86 2.35 3.07 4.63 4.7 3.85 2.25 3.07 4.63 4.7 3.85 2.25 3.07 4.63 4.7 3.85 2.25 3.07 4.63 4.7 3.85 0.07 2.62 2.62 3.07 4.67 2.52 2.53 3.07 4.7 3.85 0.07 2.62 2.53 3.07 4.7 3.85 0.07 2.62 2.53 3.07 2.62 3.07 2.62 3.07 2.62 3.07 2.62 2.53 3.07 2.62 2.53 3.07 2.62 2.53 3.07 2.62 2.53 3.07 2.62 2.54 3.07 2.62 2.54 3.07 2.62 2.54 3.07 2.62 2.54 3.07 2.54 3.07 2.62 2.54 3.07 2.62 2.54 3.07 2.62 2.54 3.07 2.54 2.53 3.07 2.62 2.54 3.07 2.62 2.54 3.07 2.54 3.07 2.54 2.54 3.07 2.54 3.07 3.07 3.07 3.07 3.07 3.07 3.07 3.07	0.222 0.192 0.279 0.274 0.0084 0.0084 0.0084 0.0083 0.00835 0.00835 0.00835 0.00835 0.00835 0.00835 0.0081 0.00835 0.00810000000000	5.52           6.195           6.16           2.47           8.23           9.76           8.13           1.3           4.37           9.1           8.9           9.1           9.1           9.1           9.2           9.3     <		3 1 1 1 0 4 4 4 3 1 0 5 3 0 4 4 2 0 5 3 0 1 6 1 1 0 5 3 0 1 6 0 1 0 0 4 4 4 3 1 0 0 4 4 4 3 1 0 0 4 4 4 3 1 0 0 4 4 4 3 1 0 0 2 0 0 0 4 4 4 3 1 0 0 2 0 0 0 1 0 0 0 2 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 1140,7148 2 1465,7811 2 1145,7148 2 131,462 2 131,462 2 131,462 2 131,462 2 205,6912 2 435,7648 1 435,7649 1 386,7019 2 205,6912 1 435,7649 1 386,7019 2 205,6912 1 435,7649 1 386,7019 2 206,6912 1 435,7649 1 386,7019 2 206,6912 1 435,7649 1 386,7019 2 206,6912 1 435,7649 1 386,7019 2 1088,6357 2 1086,637 2 1086,647 2 1086,647 2 1086,647 2 1086,647 2 1086,647 2 1086,647 2 1086	130           224           130           391           288           313           242           130           282           131           282           132           283           284           331           341           343           213           283           213           284           336           213           283           213           284           3141           344           305           213           283           407           407           407           303           304           305           305           304           305           305           306           307           308           309           304           305           306           307           308           309	138           139           225           139           400           209           324           139           205           201           139           202           203           204           131           198           205           204           198           191           212           316           316           316           317           218           219           310           212           313           314           315
Vimentin - Box taurus (Bovine) VIME_BOVIN ATP synthase suburit bets, mitochondrial precursor (EC.3.6.3.14) - Homo sapiene (FATPB_HEMAN ATP synthase suburit bets, mitochondrial precursor (EC.3.6.3.14) - Homo sapiene (FATPB_HEMAN ATP synthase suburit bets, mitochondrial precursor (EC.3.6.3.14) - Homo sapiene (FATPB_HEMAN ATP synthase suburit bets, mitochondrial precursor (EC.3.6.3.14) - Homo sapiene (FATPB_HEMAN ATP synthase suburit bets, mitochondrial precursor (EC.3.6.3.14) - Homo sapiene (FATPB_HEMAN ATP synthase suburit bets, mitochondrial precursor (EC.3.6.3.14) - Homo sapiene (FATPB_HEMAN ATP synthase suburit bets, mitochondrial precursor (EC.3.6.3.14) - Homo sapiene (FATPB_HEMAN ATP synthase suburit bets, mitochondrial precursor (EC.3.6.3.14) - Homo sapiene (FATPB_HEMAN ATP synthase suburit bets, mitochondrial precursor (EC.3.6.3.14) - Homo sapiene (FATPB_HEMAN ATP synthase suburit bets, mitochondrial precursor (EC.3.6.3.14) - Homo sapiene (FATPB_HEMAN ATP_Synthase suburit bets, mitochondrial precursor (EC.3.6.3.14) - Homo sapiene (FATPB_HEMAN ATP_Synthase suburit bets, mitochondrial precursor (EC.3.6.3.14) - Homo sapiene (FATPB_HEMAN ATP_Synthase suburit bets, mitochondrial precursor (EC.3.6.3.14) - Homo sapiene (FATPB_HEMAN ATP_Synthase suburit bets, mitochondrial precursor (EC.3.6.3.14) - Homo sapiene (FATPB_HEMAN ATP_Synthase suburit bets, mitochondrial precursor (EC.3.6.3.14) - Homo sapiene (FATPB_HEMAN ATP_Synthase suburit bets, mitochondrial precursor (EC.3.6.3.14) - Homo sapiene (FATPB_HEMAN ATP_Synthase suburit bets, mitochondrial precursor (EC.3.6.3.14) - Homo sapiene (FATPB_HEMAN ATP_Synthase suburit bets, mitochondrial precursor (EC.3.6.3.14) - Homo sapiene (FATPB_HEMAN ATP_Synthase suburit bets, mitochondrial precursor (EC.3.6.3.14) - Homo sapiene (FATPB_HEMAN ATP_Synthase suburit bets, mitochondrial precursor (EC.3.6.3.14) - Homo sapiene (FATPB_HEMAN ATP_Synthase suburit bets, mitochondrial precursor (EC.3.6.3.14) - Homo sapiene (FATPB_HEMAN ATP_Synthase suburit bets, mitochondrial precursor	59703 59710,8 56542,5 56542,5 51831,8 51831,8	100.00%	2 8 10 13	2 2 14 16 19 14	4 0.42% 2 0.21% 27 4.86% 37 12.40% 51 7.46%	A.72% ILLAFICAL VESIGERARX     ALAGE CARA ALAGE CAR	化化 化化 预定合用化剂化化 配合管理合用性化用化化 网络哈龙龙合同首龙西首龙龙 网络龙龙龙龙	G         99,00%           G         99,00%           G         99,00%           I         99,00%           J         99,00%           G         99,00%           G         99,00%           G         99,00%           G         99,00%           G         99,00%           L         99,00%           L         99,00%           A         99,00%           A         99,00%           G         99,00%           G         99,00%           A         99,00%           A         99,00%           G         99,00% <th>3.34 3.19 3.41 3.42 3.42 4.79 4.79 4.79 4.62 3.97 4.62 3.97 4.62 4.30 4.30 4.30 4.30 4.30 4.30 4.30 4.30</th> <th>0.222 0.192 0.209 0.259 0.259 0.259 0.259 0.259 0.259 0.259 0.259 0.259 0.259 0.259 0.259 0.259 0.259 0.249 0.299 0.24 0.299 0.24 0.299 0.24 0.299 0.24 0.299 0.24 0.299 0.24 0.299 0.259 0.299 0.24 0.299 0</th> <th>5.52           6.85           6.19           6.14           6.27           6.28           6.29           6.75           6.76           6.73           6.75           6.76           7.75           8.9%           9.75           9.76           9.72           9.74           9.75           9.76           9.72           9.72           9.72           9.72           9.72           9.72           9.72</th> <th></th> <th>3 1 1 1 0 4 4 4 3 1 0 3 1 0 4 4 3 1 0 3 1 0 4 4 2 0 5 3 0 1 6 1 1 0 5 3 0 0 4 4 2 0 0 5 3 0 1 0 0 4 4 4 3 1 0 0 4 4 3 1 0 0 0 0 0 1 0 0 0 0 0 1 0 0 0 0 0 0</th> <th>0 0 0 0 2 2 5 5 0 2 2 5 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0</th> <th></th> <th>2 1146,7148 2 1465,7591 2 1465,7591 2 1145,7591 2 131,462 2 131,462 2 131,462 2 2056,9912 1 455,7549 1 455,7549 2 2056,9912 2 2056,9912 2 1058,6357 2 1058,655</th> <th>130           224           130           391           382           242           311           262           125           120           388           242           311           231           242           125           126           242           311           322           388           242           311           325           325           325           326           3275           326           3273           3264           3264           3265           3264           3264           3264           3264           3264           3264           3264           3264           3264           3264           3264           3264           3264           3264           3264           3264           3264           3</th> <th>138 225 139 4001 400 259 259 255 255 244 143 109 259 259 259 264 143 145 145 145 145 145 145 145 145 145 145</th>	3.34 3.19 3.41 3.42 3.42 4.79 4.79 4.79 4.62 3.97 4.62 3.97 4.62 4.30 4.30 4.30 4.30 4.30 4.30 4.30 4.30	0.222 0.192 0.209 0.259 0.259 0.259 0.259 0.259 0.259 0.259 0.259 0.259 0.259 0.259 0.259 0.259 0.259 0.249 0.299 0.24 0.299 0.24 0.299 0.24 0.299 0.24 0.299 0.24 0.299 0.24 0.299 0.259 0.299 0.24 0.299 0	5.52           6.85           6.19           6.14           6.27           6.28           6.29           6.75           6.76           6.73           6.75           6.76           7.75           8.9%           9.75           9.76           9.72           9.74           9.75           9.76           9.72           9.72           9.72           9.72           9.72           9.72           9.72		3 1 1 1 0 4 4 4 3 1 0 3 1 0 4 4 3 1 0 3 1 0 4 4 2 0 5 3 0 1 6 1 1 0 5 3 0 0 4 4 2 0 0 5 3 0 1 0 0 4 4 4 3 1 0 0 4 4 3 1 0 0 0 0 0 1 0 0 0 0 0 1 0 0 0 0 0 0	0 0 0 0 2 2 5 5 0 2 2 5 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0		2 1146,7148 2 1465,7591 2 1465,7591 2 1145,7591 2 131,462 2 131,462 2 131,462 2 2056,9912 1 455,7549 1 455,7549 2 2056,9912 2 2056,9912 2 1058,6357 2 1058,655	130           224           130           391           382           242           311           262           125           120           388           242           311           231           242           125           126           242           311           322           388           242           311           325           325           325           326           3275           326           3273           3264           3264           3265           3264           3264           3264           3264           3264           3264           3264           3264           3264           3264           3264           3264           3264           3264           3264           3264           3264           3	138 225 139 4001 400 259 259 255 255 244 143 109 259 259 259 264 143 145 145 145 145 145 145 145 145 145 145
Vimentin - Box taurus (Bovine)     VIME_BOVIN       ATP synthase suburit beta, mitochondisil precursor (IC 3.6.3.14) - Horno sapiers, (r.ATPB_HRAMA       ATP synthase suburit beta, mitochondisil precursor (IC 3.6.3.14) - Horno sapiers, (r.ATPB_HRAMA       ATP synthase suburit beta, mitochondisil precursor (IC 3.6.3.14) - Horno sapiers, (r.ATPB_HRAMA       Vimentin (fragment) - Critectulus grisuus (Chinese Ramster)     VIME_CRICR       Calveticulin precursor (CRPS) (Calregulin) (HACBP) (ERplot) (CALBP) (Calcium-bindi CALR_RAT	5100 53710,8 56542,5 56542,5 51831,8	100.00%	2 8 10 13	2 2 14 16 19 14	4 0.42% 2 0.21% 27 4.86% 37 12.90% 51 7.66%	A.72% ILLASTERACK     VESIGERATIK     VES	化化 化化 使得觉得长度长长 网络常常常常长常长长 的复数长长发的复数形式长长 网络龙龙龙龙龙	G         99,00%           G         99,00%           G         99,00%           I         99,00%           J         99,00%           G         99,00%           J         99,00%           J         99,00%           J         99,00%           J         99,00%           J         99,00%           G         99,00%           J         99,00%           G         99,00%           G         99,00%           K         99,00%           K         99,00%           K         99,00%           L         99,00%           J         99,00%           G         99,00%           G         99,00%           K         99,00%           G         99,00%           J         99,00%           J         99,00%           J         99,00% <th>3.14 3.19 3.51 3.41 3.45 3.45 4.79 4.79 4.79 4.79 4.79 4.79 4.70 4.72 4.72 4.72 4.72 4.36 6.77 2.62 3.67 4.36 5.22 0 0 4.36 4.36 2.25 0 0 2.92 4.73 2.85 0 2.25 0 0 2.92 4.73 2.85 0 0 2.92 4.73 2.85 0 0 2.92 4.73 2.85 0 0 2.92 4.73 2.85 0 0 0 2.92 4.73 2.85 0 0 0 0 2.92 4.73 2.85 0 0 0 0 2.92 4.73 2.85 0 0 0 0 2.92 4.79 2.85 0 0 0 0 0 0 2.92 4.73 0 0 0 0 0 0 0 2.92 4.73 0 0 0 0 0 0 0 2.92 4.73 0 0 0 0 0 0 0 0 0 2.92 4.73 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0</th> <th>0.122 0.192 0.274 0.274 0.274 0.274 0.274 0.275 0.275 0.275 0.275 0.245 0.255</th> <th>5.52 6.85 6.10 2.47 3.47 0.78 8.30 4.3 0.78 8.30 1.6 4.3 5.10 1.6 5.10</th> <th>0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0</th> <th>3 1 1 1 1 4 4 4 3 1 0 3 0 4 4 2 0 5 3 0 1 6 1 1 0 5 3 0 4 2 0 5 3 0 1 1 5 4 0 2 2 0 2 1 3 0 2 1 3 0 2 1 1 0 2 4 4 2 2 0 1 0 2 2 1 0 2 2 1 1 0 2 2 1 1 1 1</th> <th>0 0 0 2 2 2 5 5 0 0 2 0 0 2 0 0 0 0 0 0</th> <th></th> <th>2 1140,7148 2 1465,7581 2 1145,7148 2 131,462 2 131,462 2 131,462 2 131,462 2 131,462 2 131,462 2 1435,7464 1 1435,7464 2 1439,7899 1 1439,7899 1 1439,7899 2 1499,7899 2 1493,7899 2 1494,7899 2 1494,7899 2 14</th> <th>130           224           130           284           391           282           211           282           121           283           284           311           282           121           283           284           121           283           284           284           285           286           295           205           205           205           205           205           205           206           394           304</th> <th>139         139           139         225           1401         200           259         234           1205         244           1403         245           244         259           245         244           245         244           259         244           242         242           254         244           255         244           242         225           244         148           149         149           149         149           120         245           247         217           218         217           218         216           224         2217           218         316           324         325           325         225           217         218           218         219           219         212           212         22           213         120</th>	3.14 3.19 3.51 3.41 3.45 3.45 4.79 4.79 4.79 4.79 4.79 4.79 4.70 4.72 4.72 4.72 4.72 4.36 6.77 2.62 3.67 4.36 5.22 0 0 4.36 4.36 2.25 0 0 2.92 4.73 2.85 0 2.25 0 0 2.92 4.73 2.85 0 0 2.92 4.73 2.85 0 0 2.92 4.73 2.85 0 0 2.92 4.73 2.85 0 0 0 2.92 4.73 2.85 0 0 0 0 2.92 4.73 2.85 0 0 0 0 2.92 4.73 2.85 0 0 0 0 2.92 4.79 2.85 0 0 0 0 0 0 2.92 4.73 0 0 0 0 0 0 0 2.92 4.73 0 0 0 0 0 0 0 2.92 4.73 0 0 0 0 0 0 0 0 0 2.92 4.73 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.122 0.192 0.274 0.274 0.274 0.274 0.274 0.275 0.275 0.275 0.275 0.245 0.255	5.52 6.85 6.10 2.47 3.47 0.78 8.30 4.3 0.78 8.30 1.6 4.3 5.10 1.6 5.10	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 1 1 1 1 4 4 4 3 1 0 3 0 4 4 2 0 5 3 0 1 6 1 1 0 5 3 0 4 2 0 5 3 0 1 1 5 4 0 2 2 0 2 1 3 0 2 1 3 0 2 1 1 0 2 4 4 2 2 0 1 0 2 2 1 0 2 2 1 1 0 2 2 1 1 1 1	0 0 0 2 2 2 5 5 0 0 2 0 0 2 0 0 0 0 0 0		2 1140,7148 2 1465,7581 2 1145,7148 2 131,462 2 131,462 2 131,462 2 131,462 2 131,462 2 131,462 2 1435,7464 1 1435,7464 2 1439,7899 1 1439,7899 1 1439,7899 2 1499,7899 2 1493,7899 2 1494,7899 2 1494,7899 2 14	130           224           130           284           391           282           211           282           121           283           284           311           282           121           283           284           121           283           284           284           285           286           295           205           205           205           205           205           205           206           394           304	139         139           139         225           1401         200           259         234           1205         244           1403         245           244         259           245         244           245         244           259         244           242         242           254         244           255         244           242         225           244         148           149         149           149         149           120         245           247         217           218         217           218         216           224         2217           218         316           324         325           325         225           217         218           218         219           219         212           212         22           213         120
Vimentin - Box taurus (Bovine) VIME_BOVIN ATP synthase suburit bets, mitochondrial precursor (IC 3.6.3.14) - Horno sapiens (FATPB_HEMANI ATP synthase suburit bets, mitochondrial precursor (IC 3.6.3.14) - Horno sapiens (FATPB_HEMANI ATP synthase suburit bets, mitochondrial precursor (IC 3.6.3.14) - Horno sapiens (FATPB_HEMANI ATP synthase suburit bets, mitochondrial precursor (IC 3.6.3.14) - Horno sapiens (FATPB_HEMANI ATP synthase suburit bets, mitochondrial precursor (IC 3.6.3.14) - Horno sapiens (FATPB_HEMANI ATP synthase suburit bets, mitochondrial precursor (IC 3.6.3.14) - Horno sapiens (FATPB_HEMANI ATP synthase suburit bets, mitochondrial precursor (IC 3.6.3.14) - Horno sapiens (FATPB_HEMANI ATP synthase suburit bets, mitochondrial precursor (IC 3.6.3.14) - Horno sapiens (FATPB_HEMANI ATP synthase suburit bets, mitochondrial precursor (IC 3.6.3.14) - Horno sapiens (FATPB_HEMANI ATP synthase suburit bets, mitochondrial precursor (IC 3.6.3.14) - Horno sapiens (FATPB_HEMANI ATP synthase suburit bets, mitochondrial precursor (IC 3.6.3.14) - Horno sapiens (FATPB_HEMANI ATP synthase suburit bets, mitochondrial precursor (IC 3.6.3.14) - Horno sapiens (FATPB_HEMANI ATP synthase suburit bets, mitochondrial precursor (IC 3.6.3.14) - Horno sapiens (FATPB_HEMANI ATP synthase suburit bets, mitochondrial precursor (IC 3.6.3.14) - Horno sapiens (FATPB_HEMANI ATP synthase suburit bets, mitochondrial precursor (IC 3.6.3.14) - Horno sapiens (FATPB_HEMANI ATP synthase suburit bets, mitochondrial precursor (IC 3.6.3.14) - Horno sapiens (FATPB_HEMANI ATP synthase suburit bets, mitochondrial precursor (IC 3.6.3.14) - Horno sapiens (FATPB_HEMANI ATP synthase suburit bets, mitochondrial precursor (IC 3.6.3.14) - Horno sapiens (FATPB_HEMANI ATP synthase suburit bets, mitochondrial precursor (IC 3.6.3.14) - Horno sapiens (FATPB_HEMANI ATP synthase suburit bets, mitochondrial precursor (IC 3.6.3.14) - Horno sapiens (FATPB_HEMANI ATP synthase suburit bets, mitochondrial precursor (IC 3.6.3.14) - Horno sapiens (FATPB_HEMANI ATP synth	593710.8 56542,5 56542,5 51831,8	100.00% 100.00% 100.00%	2 8 10 13	2 2 14 16 19 14	4 0.42% 2 0.21% 27 4.86% 37 12.90% 51 7.46%	A.72% ILABLECK VSLGENARK      A.51% ILABLECK MADELEATR      CONSTRUCTION	化化 化化 的复数用化的 化化 的复数用的复数用的化的 化化 的复数化化化化化化化化化化化化化化化化化化化化化化化化化化化化化化	G         99,00%           G         99,00%           G         99,00%           I         99,00%           I         99,00%           J         99,00%           G         99,00%           G         99,00%           G         99,00%           G         99,00%           C         99,00%           E         99,00%           E         99,00%           K         99,00%           C         99,00%           K         99,00%           F         99,00%           F         99,00%           C         99,00%           G         99,00% <th>3.34 3.19 3.41 3.42 3.42 3.42 3.42 4.79 4.79 4.77 2.62 3.15 3.47 4.77 2.62 3.15 3.47 4.77 2.62 3.15 3.25 3.25 3.25 3.25 3.25 3.25 3.25 3.2</th> <th>0.222 0.192 0.209 0.279 0.0084 0.0084 0.009 0.0084 0.00900 0.00900000000</th> <th>5.52           6.85           6.16           6.13           6.14           6.3           8.23           975           976           8.13           4.14           9.5           9.5           9.5           9.5           9.6           9.7           9.8           9.8           9.9           9.5           9.5           9.5           9.5           9.5           9.5           9.6           9.7           9.8           9.9     <!--</th--><th></th><th>3 1 1 1 1 1 1 1 1 1 1 1 1 1</th><th>0 0 0 0 0 2 2 5 0 0 2 2 5 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 2 5 0 0 2 2 5 0 0 2 2 5 0 0 0 2 2 5 5 0 0 0 0</th><th></th><th>2 1140,7148 2 1465,751 2 1467,748 2 147,748 2 147,748 2 141,462 2 141,462 2 141,462 2 141,462 2 200,6912 1 423,546 1 423,748 1 423,7488 1 423,7488 1 423,7488 1 423,7488 1</th><th>130           224           130           391           288           313           281           132           283           153           284           153           283           284           313           285           284           311           285           312           281           282           311           344           351           369           172           373           364           206           304           206           304           206           304           206           304           206           304           206           302           304           206           304           206           302           304           205           304           205           304</th><th>138           139           225           139           406           259           310           269           275           241           178           269           244           185           109           224           185           109           224           143           109           224           135           109           224           231           125           126           227           138           129           128           129           121           123           124           125           128           324           218           121           122           123           124           125           121           122           123           124           125           125  </th></th>	3.34 3.19 3.41 3.42 3.42 3.42 3.42 4.79 4.79 4.77 2.62 3.15 3.47 4.77 2.62 3.15 3.47 4.77 2.62 3.15 3.25 3.25 3.25 3.25 3.25 3.25 3.25 3.2	0.222 0.192 0.209 0.279 0.0084 0.0084 0.009 0.0084 0.00900 0.00900000000	5.52           6.85           6.16           6.13           6.14           6.3           8.23           975           976           8.13           4.14           9.5           9.5           9.5           9.5           9.6           9.7           9.8           9.8           9.9           9.5           9.5           9.5           9.5           9.5           9.5           9.6           9.7           9.8           9.9 </th <th></th> <th>3 1 1 1 1 1 1 1 1 1 1 1 1 1</th> <th>0 0 0 0 0 2 2 5 0 0 2 2 5 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 2 5 0 0 2 2 5 0 0 2 2 5 0 0 0 2 2 5 5 0 0 0 0</th> <th></th> <th>2 1140,7148 2 1465,751 2 1467,748 2 147,748 2 147,748 2 141,462 2 141,462 2 141,462 2 141,462 2 200,6912 1 423,546 1 423,748 1 423,7488 1 423,7488 1 423,7488 1 423,7488 1</th> <th>130           224           130           391           288           313           281           132           283           153           284           153           283           284           313           285           284           311           285           312           281           282           311           344           351           369           172           373           364           206           304           206           304           206           304           206           304           206           304           206           302           304           206           304           206           302           304           205           304           205           304</th> <th>138           139           225           139           406           259           310           269           275           241           178           269           244           185           109           224           185           109           224           143           109           224           135           109           224           231           125           126           227           138           129           128           129           121           123           124           125           128           324           218           121           122           123           124           125           121           122           123           124           125           125  </th>		3 1 1 1 1 1 1 1 1 1 1 1 1 1	0 0 0 0 0 2 2 5 0 0 2 2 5 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 0 0 2 2 5 0 0 2 2 5 0 0 2 2 5 0 0 0 2 2 5 5 0 0 0 0		2 1140,7148 2 1465,751 2 1467,748 2 147,748 2 147,748 2 141,462 2 141,462 2 141,462 2 141,462 2 200,6912 1 423,546 1 423,748 1 423,7488 1 423,7488 1 423,7488 1 423,7488 1	130           224           130           391           288           313           281           132           283           153           284           153           283           284           313           285           284           311           285           312           281           282           311           344           351           369           172           373           364           206           304           206           304           206           304           206           304           206           304           206           302           304           206           304           206           302           304           205           304           205           304	138           139           225           139           406           259           310           269           275           241           178           269           244           185           109           224           185           109           224           143           109           224           135           109           224           231           125           126           227           138           129           128           129           121           123           124           125           128           324           218           121           122           123           124           125           121           122           123           124           125           125
Vimentin - Box taurus (Bovine) VIME_BOVIN ATP synthese suburit bets, mitochondrial precursor (IC 3.6.3.14) - Horno sapiers, (FATPB_HLMAM ATP synthese suburit bets, mitochondrial precursor (IC 3.6.3.14) - Horno sapiers, (FATPB_HLMAM ATP synthese suburit bets, mitochondrial precursor (IC 3.6.3.14) - Horno sapiers, (FATPB_HLMAM Vimentin (Iragment) - Critetulus griseus (Chieses harmter) VIME_CRIGR Calreticulin precursor (CRP5) (Calreguin) (HACBP) (ERgido) (CALBP) (Calcium-EindICALR_EAT	13710.8 13512.5 15542.5 11831.8 47979	100.00%	2 8 10 13	2 2 14 16 19 14	4 0.42% 2 0.21% 27 4.86% 37 12.90% 51 7.66% 19 1.76%	A729 HLARLOCK     VESUGEARX      VESUGEARX      VESUGEARX      VESUGEARX      VES	化化 化化 相同指用化物化化 用作用化化化化剂用作用化化剂用化化化化化化化化化化化	C         99,00%           C         99,00%           C         99,00%           I         99,00%           J         99,00%           G         99,00%           G         99,00%           G         99,00%           G         99,00%           G         99,00%           L         99,00%           L         99,00%           L         99,00%           C         99,00%           G         99,00%           G         99,00%           L         99,00%           C         99,00%           G         99,00% <th>3.34 3.19 3.41 3.43 3.43 3.42 4.9 4.9 4.9 4.9 4.9 4.9 4.9 4.9 4.9 4.9</th> <th>0.222 0.209 0.279 0.268 0.53 0.53 0.379 0.53 0.375 0.348 0.348 0.348 0.327 0.375 0.375 0.375 0.348 0.348 0.327 0.311 0.35 0.325 0.335 0.325 0.335 0.325 0.335 0.35</th> <th>5.52 6.35 6.16 6.16 6.16 6.16 7.47 8.24 9.70 9.70 8.70 8.70 9.70 8.70 9.70</th> <th></th> <th>3 1 1 1 1 1 1 1 1 1 1 1 1 1</th> <th>0 0 0 0 0 0 2 2 5 5 0 0 2 0 0 2 0 0 0 2 0 0 0 2 0 0 0 2 0 0 2 0 0 0 2 0 0 0 2 0</th> <th></th> <th>2 1140,7148 2 1465,7581 2 1145,7148 2 1145,7148 2 1311,462 2 1311,462 2 1311,462 2 1311,462 2 1435,7545 1 455,7545 1 455,7545 1 455,7545 1 455,7545 1 455,7545 1 455,7545 1 455,7545 2 0076,9912 2 1439,7899 1 1098,6353 2 0076,9912 1 1088,6353 2 0076,9912 1 1088,6353 2 0076,9912 1 1088,6353 1 1088,6353 1 1086,4595 1 1086,4595 1 1097,168 2 1559,9114 1 1086,459 1 1097,168 2 1559,9114 1 1086,459 1 1097,168 2 1559,9114 1 1086,459 1 1097,1788 2 1651,9712 1 1036,555 1 133,8559 2 1531,6657 2 1533,6557 1 1333,8559 1 1333,855</th> <th>130           224           130           381           242           311           282           125           128           125           189           244           311           242           311           243           125           189           244           251           189           241           144           252           189           241           242           311           321           322           125           189           241           125           180           321           323           324           325           326           326           326           326           326           326           326           326           326           326           326           326</th> <th>138           139           225           139           4001           406           259           139           251           139           406           252           131           132           259           259           131           132           259           259           259           259           259           259           259           259           259           259           259           259           259           259           254           254           255           254           255           256           257           258           259           251           251           252           251           252           253           254           255           256           257</th>	3.34 3.19 3.41 3.43 3.43 3.42 4.9 4.9 4.9 4.9 4.9 4.9 4.9 4.9 4.9 4.9	0.222 0.209 0.279 0.268 0.53 0.53 0.379 0.53 0.375 0.348 0.348 0.348 0.327 0.375 0.375 0.375 0.348 0.348 0.327 0.311 0.35 0.325 0.335 0.325 0.335 0.325 0.335 0.35	5.52 6.35 6.16 6.16 6.16 6.16 7.47 8.24 9.70 9.70 8.70 8.70 9.70 8.70 9.70		3 1 1 1 1 1 1 1 1 1 1 1 1 1	0 0 0 0 0 0 2 2 5 5 0 0 2 0 0 2 0 0 0 2 0 0 0 2 0 0 0 2 0 0 2 0 0 0 2 0 0 0 2 0		2 1140,7148 2 1465,7581 2 1145,7148 2 1145,7148 2 1311,462 2 1311,462 2 1311,462 2 1311,462 2 1435,7545 1 455,7545 1 455,7545 1 455,7545 1 455,7545 1 455,7545 1 455,7545 1 455,7545 2 0076,9912 2 1439,7899 1 1098,6353 2 0076,9912 1 1088,6353 2 0076,9912 1 1088,6353 2 0076,9912 1 1088,6353 1 1088,6353 1 1086,4595 1 1086,4595 1 1097,168 2 1559,9114 1 1086,459 1 1097,168 2 1559,9114 1 1086,459 1 1097,168 2 1559,9114 1 1086,459 1 1097,1788 2 1651,9712 1 1036,555 1 133,8559 2 1531,6657 2 1533,6557 1 1333,8559 1 1333,855	130           224           130           381           242           311           282           125           128           125           189           244           311           242           311           243           125           189           244           251           189           241           144           252           189           241           242           311           321           322           125           189           241           125           180           321           323           324           325           326           326           326           326           326           326           326           326           326           326           326           326	138           139           225           139           4001           406           259           139           251           139           406           252           131           132           259           259           131           132           259           259           259           259           259           259           259           259           259           259           259           259           259           259           254           254           255           254           255           256           257           258           259           251           251           252           251           252           253           254           255           256           257
Vimentin - Box taurus (Bovine)     VIME_BOVIN       ATP synthase suburit beta, mitochondial precursor (EC 3.6.3.14) - Homo sapiers (FATPB_HEAMA       ATP synthase suburit beta, mitochondial precursor (EC 3.6.3.14) - Homo sapiers (FATPB_HEAMA       ATP synthase suburit beta, mitochondial precursor (EC 3.6.3.14) - Homo sapiers (FATPB_HEAMA       Vimentin (fragment) - Criteriulus griseus (Chinese Namster)     VIME_CRIGR       Calenticulin precursor (CHP55) (Calenguin) (HACBP) (EBplot) (CALBP) (Calcum-Lindi CALR_PAIT       Aptra-1-antiproteinase 2 precursor (Aptra-1-antityppin 2) (Aptra-1-proteinase InbitATAT2_HORSE	51103 53710,8 56542,5 56542,5 51831,8 47979	100.00% 100.00% 100.00%	2 8 10 13 8 6	2 2 3 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	4 0.42% 2 0.21% 27 4.86% 37 12.90% 51 7,46% 19 1,76% 11 0,72%	A729 ILLAELOOK VISUELEANK VISUELEANK CONSTRUCTION	化化 化化 用膏膏膏化化剂化剂 用用膏膏膏用化用剂化剂 的复数化化剂用剂化剂剂化化剂 化化化化化化化 化	G         99,00%           G         99,00%           G         99,00%           I         99,00%           J         99,00%           G         99,00%           C         99,00%           K         99,00%           D         99,00%           G         99,00%           D         99,00%           D         99,00%           G         99,00%           G         99,00%           G         99,00% <th>3.34 3.49 3.41 3.43 3.43 3.43 3.43 3.44 4.79 4.79 4.79 4.79 7.47 7.47 7.47 7</th> <th>0.922 0.979 0.279 0.279 0.53 0.53 0.53 0.375 0.63 0.375 0.63 0.375 0.64 0.377 0.64 0.377 0.64 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.</th> <th>5.52 6.85 6.19 6.19 6.10 2.47 2.47 0.3 8.22 9.7 9.7 9.7 9.7 9.7 9.7 9.7 9.7</th> <th></th> <th>3 1 1 1 1 1 1 1 1 1 1 1 1 1</th> <th>0 0 0 0 0 0 2 2 2 2 5 5 0 0 2 0 0 0 0 0</th> <th></th> <th>2 1140,7148 2 1465,7581 2 1145,7148 2 131,462 2 131,462 2 131,462 2 131,462 2 143,7548 1 131,462 2 2006,6912 2 435,7548 1 132,455 1 132,455 1 132,455 2 435,7548 2 1437,7890 1 131,455 2 435,7548 1 145,7548 1 145,7548 2 145,7548 1 145,7548 1 145,7548 1 145,7548 1 145,7548 1 145,7548</th> <th>130           224           130           391           284           313           242           313           253           262           121           282           131           282           213           289           282           213           283           213           283           213           283           213           283           213           283           213           284           213           285           213           285           213           285           293           204           205           205           206           304           205           206           302           304           305           306           307           308           309           304  <th>138           139           225           139           4001           406           289           324           119           406           289           244           149           299           244           199           225           243           190           225           2441           421           422           316           316           316           317           218           411           225           316           317           218           316           317           318           321           322           323           324           325           325           326           327           321           321           322           323           324           325           325</th></th>	3.34 3.49 3.41 3.43 3.43 3.43 3.43 3.44 4.79 4.79 4.79 4.79 7.47 7.47 7.47 7	0.922 0.979 0.279 0.279 0.53 0.53 0.53 0.375 0.63 0.375 0.63 0.375 0.64 0.377 0.64 0.377 0.64 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.	5.52 6.85 6.19 6.19 6.10 2.47 2.47 0.3 8.22 9.7 9.7 9.7 9.7 9.7 9.7 9.7 9.7		3 1 1 1 1 1 1 1 1 1 1 1 1 1	0 0 0 0 0 0 2 2 2 2 5 5 0 0 2 0 0 0 0 0		2 1140,7148 2 1465,7581 2 1145,7148 2 131,462 2 131,462 2 131,462 2 131,462 2 143,7548 1 131,462 2 2006,6912 2 435,7548 1 132,455 1 132,455 1 132,455 2 435,7548 2 1437,7890 1 131,455 2 435,7548 1 145,7548 1 145,7548 2 145,7548 1 145,7548 1 145,7548 1 145,7548 1 145,7548 1 145,7548	130           224           130           391           284           313           242           313           253           262           121           282           131           282           213           289           282           213           283           213           283           213           283           213           283           213           283           213           284           213           285           213           285           213           285           293           204           205           205           206           304           205           206           302           304           305           306           307           308           309           304 <th>138           139           225           139           4001           406           289           324           119           406           289           244           149           299           244           199           225           243           190           225           2441           421           422           316           316           316           317           218           411           225           316           317           218           316           317           318           321           322           323           324           325           325           326           327           321           321           322           323           324           325           325</th>	138           139           225           139           4001           406           289           324           119           406           289           244           149           299           244           199           225           243           190           225           2441           421           422           316           316           316           317           218           411           225           316           317           218           316           317           318           321           322           323           324           325           325           326           327           321           321           322           323           324           325           325
Vimentin - Box taurus (Bovine)     VIME_BOVIN       ATP synthase suburit bets, mitochondrial precursor (EC 3.6.3.14) - Homo sapiene (FATPB_HEMAN)       ATP synthase suburit bets, mitochondrial precursor (EC 3.6.3.14) - Homo sapiene (FATPB_HEMAN)       Vimentin (Fragment) - Cricotulus griseus (Chinese hamster)     VIME_CRICR       Calreticulin precursor (CRP55) (Calregulin) (HACRP) (ERpido) (CALRP) (Calcum_Lindi CALR_RAT       Alpha-1-antiproteinase 2 precursor (Apha-1-antitypsin 2) (Apha-1-proteinase Inhib ATAT2_HORSE	19702 197108 56542,5 56542,5 51831,8 47979	100.00% 100.00% 100.00%	2 B 10 13 6	2 2 14 16 19 14 14	4 0.42% 2 0.21% 27 4.86% 37 12,99% 51 7.46% 19 1.76% 11 0.72%	A.72% ILABLECK VSISLEMARK      ASSOCIATION     AND A CONTRACT AND A CONTRAC	化化 化化 预理论的文化化化 脱位理论的现在分词 化化化化化化化化化化化化化化化化化化化化化化化化化化化化化化化化化化化化	G         99,00%           G         99,00%           G         99,00%           I         99,00%           J         95,00%           G         95,00% <th>3.34 3.19 3.51 3.44 3.44 3.40 4.97 4.97 7.24 4.97 7.24 4.97 7.24 4.97 7.24 4.97 7.24 7.25 2.26 0 0 0 2.47 7.25 2.26 0 0 0 0 2.47 1.25 2.26 0 0 0 0 2.47 1.25 2.26 0 0 0 0 0 2.47 1.25 2.26 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0</th> <th>0.222 0.192 0.209 0.268 0.0084 0.0084 0.009 0.253 0.0375 0.0375 0.0375 0.0375 0.0375 0.0375 0.0375 0.0375 0.04940000000000</th> <th>5.52 6.19 6.19 6.10 6.35 6.10 6.3 8.23 8.24 8.26 8.10 8.24 9.75 5.54 1.45 2.44 2.24 2.24 2.24 2.24 2.24 2.24 2.25 2.24 1.45 2.24 2.25 2.26 2.25 2.26 2.25 2.26 2.25 2.26 2.25 2.26 2.25 2.26 2.25 2.26 2.25 2.26 2.25 2.26 2.25 2.26 2.25 2.55 2</th> <th>0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0</th> <th>3 1 1 1 1 1 1 1 1 1 1 1 1 1</th> <th></th> <th></th> <th>2 1146,7148 2 1465,7581 2 1465,7581 2 1145,7148 2 131,462 2 131,462 2 131,462 2 205,6912 1 455,7481 1 455,7484 1 457,7484 1 457,7474 1 153,8559 1 144,7474 1 154,7474 1 154</th> <th>130           224           130           391           388           242           313           283           136           284           313           285           242           311           282           313           282           314           144           305           306           307           409           407           407           407           407           408           205           304           206           304           206           304           208           304           205           304           205           408           304           205           304           205           403           304           205           305           306           307           308</th> <th>138 225 139 400 400 259 259 255 264 264 275 275 275 275 275 275 275 275 275 275</th>	3.34 3.19 3.51 3.44 3.44 3.40 4.97 4.97 7.24 4.97 7.24 4.97 7.24 4.97 7.24 4.97 7.24 7.25 2.26 0 0 0 2.47 7.25 2.26 0 0 0 0 2.47 1.25 2.26 0 0 0 0 2.47 1.25 2.26 0 0 0 0 0 2.47 1.25 2.26 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.222 0.192 0.209 0.268 0.0084 0.0084 0.009 0.253 0.0375 0.0375 0.0375 0.0375 0.0375 0.0375 0.0375 0.0375 0.04940000000000	5.52 6.19 6.19 6.10 6.35 6.10 6.3 8.23 8.24 8.26 8.10 8.24 9.75 5.54 1.45 2.44 2.24 2.24 2.24 2.24 2.24 2.24 2.25 2.24 1.45 2.24 2.25 2.26 2.25 2.26 2.25 2.26 2.25 2.26 2.25 2.26 2.25 2.26 2.25 2.26 2.25 2.26 2.25 2.26 2.25 2.26 2.25 2.55 2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 1 1 1 1 1 1 1 1 1 1 1 1 1			2 1146,7148 2 1465,7581 2 1465,7581 2 1145,7148 2 131,462 2 131,462 2 131,462 2 205,6912 1 455,7481 1 455,7484 1 457,7484 1 457,7474 1 153,8559 1 144,7474 1 154,7474 1 154	130           224           130           391           388           242           313           283           136           284           313           285           242           311           282           313           282           314           144           305           306           307           409           407           407           407           407           408           205           304           206           304           206           304           208           304           205           304           205           408           304           205           304           205           403           304           205           305           306           307           308	138 225 139 400 400 259 259 255 264 264 275 275 275 275 275 275 275 275 275 275
Vimentin - Box taurus (Bovine)     VIME_BOVIN       ATP synthese suburit bets, mitochondisil precursor (EC 3.6.3.14) - Horno sapiers (FATPB_HRAMN       ATP synthase suburit bets, mitochondisil precursor (EC 3.6.3.14) - Horno sapiers (FATPB_HRAMN       ATP synthase suburit bets, mitochondisil precursor (EC 3.6.3.14) - Horno sapiers (FATPB_HRAMN       Vimentin (fragment) - Cricetulus grissus (Chinese Ramster)     VIME_CRICE       Exheticulin precursor (CRPSs) (Catrogulin) (HACIBP) (ERp60) (CALIBP) (Calcium-Bindi CALR_RAT       Alges-1-antiproteinase 2 precursor (Alges-1-antityppin 2) (Algeba-1-proteinase Inhib ATAT2_HORSE	19702 19710,8 19542,5 19542,5 19831,8 47979 46975,8	100.00% 100.00% 100.00% 100.00%	2 B 10 13 8 6	2 2 14 16 19 14 18	4 0.42% 2 0.21% 27 4.86% 37 12.90% 51 7.66% 19 1.76% 11 0.72%	A.729 ILABLECK     VISUELEARX     VISUELEARX     VISUELEARX     AND     ADDUCTOR     CONTRACTOR     CONTRA	化化 化化 用用用用化用化化 间接用用用化用化化 网络用化化用用化化用化化化化化化化化化化化化化化化	G         99,00%           G         99,00%           G         99,00%           I         99,00%           J         99,00%           G         99,00%           G         99,00%           J         99,00%           J         99,00%           J         99,00%           J         99,00%           J         99,00%           J         99,00%           G         99,00%           G         99,00%           G         99,00%           K         99,00%           K         99,00%           G         99,00% <th>3.34 3.49 3.44 3.44 3.44 3.44 3.45 3.44 3.45 4.97 4.97 4.97 4.97 4.97 4.97 4.97 4.97</th> <th>0.922 0.979 0.279 0.289 0.53 0.53 0.53 0.375 0.325 0.355 0.3</th> <th>5.52 6.85 6.10 2.47 0.70 8.70 8.70 8.70 9.70 8.70 1.6 1.6 1.6 1.6 1.6 1.6 1.6 1.6</th> <th>0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0</th> <th>3 1 1 1 1 1 1 1 1 1 1 1 1 1</th> <th></th> <th></th> <th>2 1140,7148 2 1465,7581 2 1145,7148 2 132,7581 2 131,462 2 131,462 2 131,462 2 131,462 2 131,462 2 143,7464 1 143,7464 2 144,7464 2 144,74</th> <th>130           224           130           281           391           282           311           282           121           283           284           311           282           121           283           284           212           189           241           341           344           323           212           189           212           189           212           180           212           181           213           215           216           217           117           112           112           113           206           206           206           206           206           206           206           206           206           207           208           208           204</th> <th>138           139           225           139           4001           205           239           239           229           241           143           143           269           234           235           244           255           244           255           244           101           125           249           241           421           422           247           218           217           218           217           218           217           218           219           211           212           213           325           325           325           326           327           328           329           321           121           121           121           121           121</th>	3.34 3.49 3.44 3.44 3.44 3.44 3.45 3.44 3.45 4.97 4.97 4.97 4.97 4.97 4.97 4.97 4.97	0.922 0.979 0.279 0.289 0.53 0.53 0.53 0.375 0.325 0.355 0.3	5.52 6.85 6.10 2.47 0.70 8.70 8.70 8.70 9.70 8.70 1.6 1.6 1.6 1.6 1.6 1.6 1.6 1.6	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 1 1 1 1 1 1 1 1 1 1 1 1 1			2 1140,7148 2 1465,7581 2 1145,7148 2 132,7581 2 131,462 2 131,462 2 131,462 2 131,462 2 131,462 2 143,7464 1 143,7464 2 144,7464 2 144,74	130           224           130           281           391           282           311           282           121           283           284           311           282           121           283           284           212           189           241           341           344           323           212           189           212           189           212           180           212           181           213           215           216           217           117           112           112           113           206           206           206           206           206           206           206           206           206           207           208           208           204	138           139           225           139           4001           205           239           239           229           241           143           143           269           234           235           244           255           244           255           244           101           125           249           241           421           422           247           218           217           218           217           218           217           218           219           211           212           213           325           325           325           326           327           328           329           321           121           121           121           121           121
Vimentin - Box taurus (Bovine)     VIME_BOVIN       ATP synthase suburit beta, mitochondisii precursor (IC 3.6.3.14) - Hono sapiens (FATPE_HEAMN       ATP synthase suburit beta, mitochondisii precursor (IC 3.6.3.14) - Hono sapiens (FATPE_HEAMN       ATP synthase suburit beta, mitochondisii precursor (IC 3.6.3.14) - Hono sapiens (FATPE_HEAMN       Mmentin (Fragment) - Criotulus grissus (Chinese hamster)     VIME_CRIGR       Calvesticulin precursor (CRP55) (Calregulin) (HACBP) (EBp60) (CALBP) (Calcium-Eindi CALR_RAT       Alpha-1-antiproteinase 2 precursor (Apita-1-antitrypsin 2) (Apita-1-proteinase inhib ATAT2_HORSE	5100 53710.8 56542.5 56542.5 51831.8 47979	100.00% 100.00% 100.00% 100.00%	2 8 10 13 8	2 2 14 16 19 14 8	4 0.42% 2 0.21% 27 4.86% 37 12.90% 51 7.46% 19 1.76% 11 0.72%	A.72% ILABLECK VSLOEHANK     VSLOEHANK     SANDELAYR     SANDELAYR     ZOY, AMALERYNNIK     ECNALWYNNEK ECNALWYNENESCYNIK FOACSSLUG ECNALWYNENESCYNIK FOACSSLUG ECNALWYNENESCYNIK FOACSSLUG ECNALWYNENESCYNIK FOACSSLUG WALCULYARWY YSLOEGANUN FOACSSLUG FOACSS	化化 化化 用理论用化化 的现在分词使用分析化化 的复数形式化量化化化化化化 化化化化化化化化化化化化化化化化化化化化化	G         99,00%           G         99,00%           G         99,00%           I         99,00%           I         99,00%           J         99,00%           G         99,00%           G         99,00%           G         99,00%           S         99,00%           E         90,00%           K         90,00%           K         90,00%           F         90,00%           G         90,00%           G         90,00%           G         90,00%           G         90,00%           G         90,00%           G         90,00% <th>3.34 3.49 3.51 3.44 3.42 3.44 3.44 3.44 3.44 3.44 3.44</th> <th>0,222 0,192 0,276 0,276 0,276 0,279 0,279 0,279 0,279 0,279 0,279 0,279 0,279 0,279 0,279 0,279 0,279 0,270 0,270 0,270 0,270 0,271 0,271 0,271 0,271 0,271 0,271 0,271 0,271 0,2750</th> <th>5.52           6.85           6.16           6.13           6.14           6.3           8.23           973           974           9.5     <th>0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0</th><th>3 1 1 1 1 1 1 1 1 1 1 1 1 1</th><th></th><th></th><th>2 1140,7148 2 1465,751 2 1467,748 2 147,748 2 147,748 2 147,7446 2 147,7446 2 147,7446 2 147,7446 2 207,6912 1 435,748 1 435,748 1</th><th>130           224           130           288           391           288           131           282           112           283           113           2842           113           2842           114           285           213           286           213           287           213           288           213           213           213           213           213           213           213           213           215           216           217           218           407           407           407           407           407           205           304           206           304           206           302           208           112           112           304           205           206</th><th>138 225 139 406 406 259 259 244 259 244 259 244 259 244 259 244 259 244 259 244 259 244 259 244 259 244 259 244 259 244 259 244 259 244 245 245 245 245 245 245 245</th></th>	3.34 3.49 3.51 3.44 3.42 3.44 3.44 3.44 3.44 3.44 3.44	0,222 0,192 0,276 0,276 0,276 0,279 0,279 0,279 0,279 0,279 0,279 0,279 0,279 0,279 0,279 0,279 0,279 0,270 0,270 0,270 0,270 0,271 0,271 0,271 0,271 0,271 0,271 0,271 0,271 0,2750	5.52           6.85           6.16           6.13           6.14           6.3           8.23           973           974           9.5 <th>0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0</th> <th>3 1 1 1 1 1 1 1 1 1 1 1 1 1</th> <th></th> <th></th> <th>2 1140,7148 2 1465,751 2 1467,748 2 147,748 2 147,748 2 147,7446 2 147,7446 2 147,7446 2 147,7446 2 207,6912 1 435,748 1 435,748 1</th> <th>130           224           130           288           391           288           131           282           112           283           113           2842           113           2842           114           285           213           286           213           287           213           288           213           213           213           213           213           213           213           213           215           216           217           218           407           407           407           407           407           205           304           206           304           206           302           208           112           112           304           205           206</th> <th>138 225 139 406 406 259 259 244 259 244 259 244 259 244 259 244 259 244 259 244 259 244 259 244 259 244 259 244 259 244 259 244 259 244 245 245 245 245 245 245 245</th>	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 1 1 1 1 1 1 1 1 1 1 1 1 1			2 1140,7148 2 1465,751 2 1467,748 2 147,748 2 147,748 2 147,7446 2 147,7446 2 147,7446 2 147,7446 2 207,6912 1 435,748 1	130           224           130           288           391           288           131           282           112           283           113           2842           113           2842           114           285           213           286           213           287           213           288           213           213           213           213           213           213           213           213           215           216           217           218           407           407           407           407           407           205           304           206           304           206           302           208           112           112           304           205           206	138 225 139 406 406 259 259 244 259 244 259 244 259 244 259 244 259 244 259 244 259 244 259 244 259 244 259 244 259 244 259 244 259 244 245 245 245 245 245 245 245
Vimentin - Box taurus (Bovine)     VIME_BOVIN       ATP synthese suburit beta, mitochondrial precursor (IC 3.6.3.14) - Horno sapiere, (r-ATPB_HUMAN       ATP synthese suburit beta, mitochondrial precursor (IC 3.6.3.14) - Horno sapiere, (r-ATPB_HUMAN       ATP synthese suburit beta, mitochondrial precursor (IC 3.6.3.14) - Horno sapiere, (r-ATPB_HUMAN       Vimentin (fragment) - Orientulus griseus (Chieses harmiter)     VIME_CBIGR       Calveticulin precursor (CRPSs) (Calvegalin) (HACBP) (ERGAD) (CALBP) (Calcum-Eindi CALR_HAT       Applea-1-antiprotenase 2 precursor (Applea-1-antitypian 2) (Applea-1-proteinase inhib ATAT2_HORSE	13710.8 13512.5 55512.5 51831.8 47979	100.00% 100.00% 100.00% 100.00%	2 B 10 13 8 6	2 2 3 1 4 1 6 1 9 1 4	4 0.42% 2 0.21% 27 4.86% 37 12.90% 51 7.66% 19 1.76% 11 0.72%	A.725 ILLAFLOCK VESIGLEARIK      VESIGLEARIK      A.751 ILLAFLOCK      AND ALLEARIK      CONSTRUCTION      CONSTRUC	化化 化化 和母母的女母女女 的复数母母女母女女 的复数马女女母母女女 的女女女女女女女女女女女女女女女女女女女女女女女女女女女女女女女	C         99,00%           C         99,00%           C         99,00%           I         99,00%           J         99,00%           G         99,00% <th>3.34 3.41 3.41 3.44 3.44 3.45 3.44 3.45 3.44 3.45 4.47 4.47 4.47 4.47 2.467 3.86 4.67 3.86 4.67 3.86 4.67 3.86 4.67 3.86 0 0 2.44 4.67 3.85 0 0 0 2.44 4.67 3.85 0 0 0 2.44 4.67 4.67 3.85 0 0 0 2.44 4.67 4.67 3.85 0 0 0 2.44 4.67 4.67 4.67 4.67 3.85 0 0 0 0 0 0 2.44 4.67 4.67 4.67 3.85 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0</th> <th>0.222 0.292 0.297 0.287 0.0088 0.53 0.53 0.375 0.035 0.375 0.035 0.375 0.035 0.375 0.035 0.375 0.035 0.375 0.035 0.375 0.035 0.466 0.466 0.385 0.385 0.325 0.316</th> <th>5.52           6.85           6.16           6.17           6.16           7.47           8.28           9.703           8.13           1.14           1.15           1.14           1.15           1.16           1.17           1.18           1.19           1.10           1.11           1.12           1.13           1.14           1.15           1.16           1.17           1.18           1.19           1.10           1.10           1.10           1.10           1.10           1.10           1.10           1.10           1.10           1.10           1.10           1.10           1.10           1.10           1.10           1.10           1.10           1.10           1.11           1.11           1.11           1.11           1.11</th> <th>0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0</th> <th>3 1 1 1 1 1 1 1 1 1 1 1 1 1</th> <th></th> <th></th> <th>2 1140,7148 2 1465,7581 2 1145,7146 2 1985,0741 2 123,7545 1 2 123,7545 1 2 123,7545 1 2 1243,7545 1 2 207,69712 2 4245,7545 1 2 207,69712 2 4245,7545 1 2 207,09712 1 2 1088,0377 2 1088,0357 2 2 208,0749 1 2 109,077 1 1088,0357 1 2 1088,0357 1 2 2 2 2 0,0749 1 2 109,077 1 1086,0357 1 2 1086,037 1 2 109,077 1 1058,037 1 1058,037</th> <th>130           224           130           381           391           284           311           282           125           189           244           311           282           125           189           241           212           189           241           212           189           241           242           311           141           255           265           265           265           265           265           266           266           266           266           266           266           266           266           266           266           267           371           372           372           373           374           375           376           377           378</th> <th>138           139           225           139           4061           259           259           130           259           130           259           130           259           131           259           132           133           143           108           109           1345           1345           1345           1345           1345           1345           1345           1345           1345           1345           1345           1345           1345           1345           1345           1341           1343           3140           2141           2151           2151           1351           2151           1351           2151           2151           2151           2151           2151           2151</th>	3.34 3.41 3.41 3.44 3.44 3.45 3.44 3.45 3.44 3.45 4.47 4.47 4.47 4.47 2.467 3.86 4.67 3.86 4.67 3.86 4.67 3.86 4.67 3.86 0 0 2.44 4.67 3.85 0 0 0 2.44 4.67 3.85 0 0 0 2.44 4.67 4.67 3.85 0 0 0 2.44 4.67 4.67 3.85 0 0 0 2.44 4.67 4.67 4.67 4.67 3.85 0 0 0 0 0 0 2.44 4.67 4.67 4.67 3.85 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.222 0.292 0.297 0.287 0.0088 0.53 0.53 0.375 0.035 0.375 0.035 0.375 0.035 0.375 0.035 0.375 0.035 0.375 0.035 0.375 0.035 0.466 0.466 0.385 0.385 0.325 0.316	5.52           6.85           6.16           6.17           6.16           7.47           8.28           9.703           8.13           1.14           1.15           1.14           1.15           1.16           1.17           1.18           1.19           1.10           1.11           1.12           1.13           1.14           1.15           1.16           1.17           1.18           1.19           1.10           1.10           1.10           1.10           1.10           1.10           1.10           1.10           1.10           1.10           1.10           1.10           1.10           1.10           1.10           1.10           1.10           1.10           1.11           1.11           1.11           1.11           1.11	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 1 1 1 1 1 1 1 1 1 1 1 1 1			2 1140,7148 2 1465,7581 2 1145,7146 2 1985,0741 2 123,7545 1 2 123,7545 1 2 123,7545 1 2 1243,7545 1 2 207,69712 2 4245,7545 1 2 207,69712 2 4245,7545 1 2 207,09712 1 2 1088,0377 2 1088,0357 2 2 208,0749 1 2 109,077 1 1088,0357 1 2 1088,0357 1 2 2 2 2 0,0749 1 2 109,077 1 1086,0357 1 2 1086,037 1 2 109,077 1 1058,037 1 1058,037	130           224           130           381           391           284           311           282           125           189           244           311           282           125           189           241           212           189           241           212           189           241           242           311           141           255           265           265           265           265           265           266           266           266           266           266           266           266           266           266           266           267           371           372           372           373           374           375           376           377           378	138           139           225           139           4061           259           259           130           259           130           259           130           259           131           259           132           133           143           108           109           1345           1345           1345           1345           1345           1345           1345           1345           1345           1345           1345           1345           1345           1345           1345           1341           1343           3140           2141           2151           2151           1351           2151           1351           2151           2151           2151           2151           2151           2151
Vimentin - Box taurus (Bovies)     VIME_BOVIN       ATP synthase suburit beta, mitochondial precursor (EC 3.6.3.14) - Homo sapiers (FATPB_HEAMA       ATP synthase suburit beta, mitochondial precursor (EC 3.6.3.14) - Homo sapiers (FATPB_HEAMA       ATP synthase suburit beta, mitochondial precursor (EC 3.6.3.14) - Homo sapiers (FATPB_HEAMA       Vimentin (fragment) - Critectulus griseus (Chrose Nameter)     VIME_CRIGR       Extensionin precursor (CRPS) (Caleguin) (HACBP) (Elipid) (CALBP) (Calcum-kind CALR_PAT       Apha-1-antiproteinase 2 precursor (Adpha-1-antityppin 2) (Alpha-1-proteinase Inhib ATAT2_HOBSE	5100 53710.8 56542.5 51831.8 47977 46925.8	100.00% 100.00% 100.00% 100.00%	2 8 10 13 8 6	2 7 14 19 14	4 0.42% 2 0.21% 27 4.86% 37 12.90% 51 7,46% 19 1,76% 11 0,72%	A.72% ILLASTOCK     VYSSICELAYAK     VYSSICELAYAK     VYSSICELAYAK     AMACOMMUNIK     COLUMNA	化化 化化 用骨肉瘤化用化化 用用用用用用化用用化 网络加尔斯 网络龙头龙头龙头 化化化化化化 化化化化化化	G         99,00%           G         99,00%           G         99,00%           I         99,00%           J         99,00%           G         99,00%           J         99,00%           J         99,00%           G         99,00%           C         99,00%           C         99,00%           C         99,00%           C         99,00%           C         99,00%           D         99,00%           D         99,00%           C         99,00%           D         99,00%           C         99,00% <th>3.34 3.49 3.51 3.44 3.42 3.44 3.44 3.44 4.97 4.49 4.97 2.62 2.49 4.94 4.97 4.97 4.97 4.97 4.97 4.97 4</th> <th>0.922 0.979 0.279 0.268 0.53 0.0088 0.53 0.375 0.037 0.375 0.037 0.375 0.037 0.375 0.04 0.368 0.377 0.375 0.375 0.375 0.375 0.375 0.375 0.375 0.375 0.375 0.375 0.375 0.375 0.375 0.375 0.375 0.375 0.375 0.375 0.375 0.325 0.</th> <th>5.52         6.85           6.19         6.16           2.47         6.3           8.22         8.7           9.7         1.1           4.37         1.1           4.37         1.1           9.7         1.1           9.7         1.1           1.1         1.1           1.1         1.1           1.1         1.1           1.1         1.1           1.1         1.1           1.1         1.1           1.1         1.1           1.1         1.1           1.1         1.1           1.1         1.1           1.1         1.1           1.1         1.1           1.1         1.1           1.1         1.1           1.1         1.1           1.1         1.1           1.1         1.1           1.2         1.1           1.3         1.2           1.4         1.2           1.2         1.2           1.3         1.2           1.3         1.2           1.4         1.3           1.</th> <th></th> <th>3 1 1 1 1 1 1 1 1 1 1 1 1 1</th> <th></th> <th></th> <th>2 1140,7148 2 1465,7581 2 1466,7581 2 1467,748 2 131,462 2 131,462 2 131,462 2 2006,6912 2 435,7541 2 435,7541 2 435,7541 2 435,7545 1 437,2851 1 437,2851 1 435,7545 2 437,8789 1 314,5785 1 388,71019 2 205,912 1 435,7545 1 388,71019 2 205,912 1 314,5755 2 1388,4575 2 1388,4575 2 1384,4594 2 1437,262 2 1437,362 2 1437,365 2 1447,465 2 1437,465 2 1437,465 2</th> <th>130           224           130           284           391           282           212           213           282           131           282           132           282           133           283           213           284           311           312           283           213           283           213           283           213           283           213           283           213           284           213           283           213           283           293           204           205           205           206           304           205           206           304           205           206           301           302           303           304           305           305</th> <th>138           139           225           139           4001           406           259           330           225           241           136           259           2441           149           259           2441           255           2441           252           143           149           149           140           151           143           143           143           143           143           143           143           143           143           143           143           143           143           143           143           1441           1451           1451           141           141           142           151           151           151           152           151           152     </th>	3.34 3.49 3.51 3.44 3.42 3.44 3.44 3.44 4.97 4.49 4.97 2.62 2.49 4.94 4.97 4.97 4.97 4.97 4.97 4.97 4	0.922 0.979 0.279 0.268 0.53 0.0088 0.53 0.375 0.037 0.375 0.037 0.375 0.037 0.375 0.04 0.368 0.377 0.375 0.375 0.375 0.375 0.375 0.375 0.375 0.375 0.375 0.375 0.375 0.375 0.375 0.375 0.375 0.375 0.375 0.375 0.375 0.325 0.	5.52         6.85           6.19         6.16           2.47         6.3           8.22         8.7           9.7         1.1           4.37         1.1           4.37         1.1           9.7         1.1           9.7         1.1           1.1         1.1           1.1         1.1           1.1         1.1           1.1         1.1           1.1         1.1           1.1         1.1           1.1         1.1           1.1         1.1           1.1         1.1           1.1         1.1           1.1         1.1           1.1         1.1           1.1         1.1           1.1         1.1           1.1         1.1           1.1         1.1           1.1         1.1           1.2         1.1           1.3         1.2           1.4         1.2           1.2         1.2           1.3         1.2           1.3         1.2           1.4         1.3           1.		3 1 1 1 1 1 1 1 1 1 1 1 1 1			2 1140,7148 2 1465,7581 2 1466,7581 2 1467,748 2 131,462 2 131,462 2 131,462 2 2006,6912 2 435,7541 2 435,7541 2 435,7541 2 435,7545 1 437,2851 1 437,2851 1 435,7545 2 437,8789 1 314,5785 1 388,71019 2 205,912 1 435,7545 1 388,71019 2 205,912 1 314,5755 2 1388,4575 2 1388,4575 2 1384,4594 2 1437,262 2 1437,362 2 1437,365 2 1447,465 2 1437,465 2	130           224           130           284           391           282           212           213           282           131           282           132           282           133           283           213           284           311           312           283           213           283           213           283           213           283           213           283           213           284           213           283           213           283           293           204           205           205           206           304           205           206           304           205           206           301           302           303           304           305           305	138           139           225           139           4001           406           259           330           225           241           136           259           2441           149           259           2441           255           2441           252           143           149           149           140           151           143           143           143           143           143           143           143           143           143           143           143           143           143           143           143           1441           1451           1451           141           141           142           151           151           151           152           151           152
Vimentin - Box taurus (Bovine)     VIME_BOVIN       ATP synthase suburit bets, mitochondisil precursor (EC.3.6.3.14) - Homo sapiene (FATPB_HEMAN)       ATP synthase suburit bets, mitochondisil precursor (EC.3.6.3.14) - Homo sapiene (FATPB_HEMAN)       Vimentin (fragment) - Orientulus grissus (Chinese hamster)     VIME_CRIGR       Calvesiculin precursor (CRPSS) (Calregulin) (HACRP) (ERB(d) (CALRP) (Calcum-lined CALR_DAT       Aptra-1-antiproteinase 2 precursor (Aptra-1-antitypsin 2) (Aptra-1-proteinase Inhib ATAT2_HOBSE	4975, 8 44975, 8	100.00% 100.00% 100.00% 100.00%	2 B 10 13 6 6	2 2 14 16 79 14 8 6	4 0.42% 2 0.21% 27 4.86% 37 12,99% 51 7.46% 19 1.76% 11 0.72% 6 0.58%	A.72% ILABLECK VSISLEMARK      A.51% ILABLECK MALELEARK      A.51% ILABLECK MALELEARK      CONSTRUCTION	化化 化化 网络拉拉尼瓦瓦 网络拉拉拉拉拉拉 网络拉尔龙拉拉拉龙龙拉拉龙龙龙龙龙龙龙龙龙龙龙龙龙龙龙龙龙龙龙 网络拉拉拉拉拉拉拉拉拉拉	G         99,00%           G         99,00%           G         99,00%           I         99,00%           G         99,00%           G         99,00%           C         99,00% <th>3.34 3.19 3.19 3.10 3.10 3.10 3.10 3.10 3.10 3.10 3.10</th> <th>0.222 0.192 0.209 0.268 0.0000 0.0000 0.00000 0.00000 0.000000</th> <th>5.52 6.19 6.19 6.35 6.48 6.36 6.3 8.23 8.24 6.3 8.24 6.3 8.24 6.3 8.24 6.3 8.24 6.3 8.24 6.3 8.24 6.3 8.24 6.3 8.24 6.3 8.24 6.3 8.24 6.3 8.24 6.3 8.24 6.3 8.24 6.3 8.24 6.3 8.24 6.3 8.24 8.34 8.24 8.24 8.34 8.24 8.34 8.24 8.34 8.24 8.34 8.24 8.34 8.34 8.24 8.344 8.344 8.344 8.345 8.344 8.345 8.345 8.344 8.345 8.34</th> <th>0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0</th> <th>3 1 1 1 1 1 1 1 1 1 1 1 1 1</th> <th></th> <th></th> <th>2 1146,7148 2 1465,7581 2 1465,7581 2 1455,7581 2 131,462 2 131,462 2 131,462 2 2056,6912 1 455,7484 1 457,7485 1 453,7484 1 457,7485 1 454,6586 2 777,4797 1 154,6586 2 777,4797 2 1 155,4586 2 777,4797 2 1 154,6586 2 777,4797 2 1 754,6586 2 777,4797 2 777,4797 2 777,4797 2 777,4797 2 777,4797 2 777,</th> <th>130           224           130           391           388           242           313           283           135           284           136           284           313           283           284           313           284           313           284           313           384           395           407           407           407           407           407           407           408           205           304           205           304           205           304           205           304           205           304           205           303           304           205           303           304           303           303           303           304           303           303</th> <th>138           139           225           130           406           259           310           259           244           198           406           259           244           259           244           259           244           259           244           109           244           108           109           125           244           242           125           126           127           128           3146           324           324           324           225           226           218           324           219           220           324           324           324           324           325           325           325           326           35           3212           226</th>	3.34 3.19 3.19 3.10 3.10 3.10 3.10 3.10 3.10 3.10 3.10	0.222 0.192 0.209 0.268 0.0000 0.0000 0.00000 0.00000 0.000000	5.52 6.19 6.19 6.35 6.48 6.36 6.3 8.23 8.24 6.3 8.24 6.3 8.24 6.3 8.24 6.3 8.24 6.3 8.24 6.3 8.24 6.3 8.24 6.3 8.24 6.3 8.24 6.3 8.24 6.3 8.24 6.3 8.24 6.3 8.24 6.3 8.24 6.3 8.24 6.3 8.24 8.34 8.24 8.24 8.34 8.24 8.34 8.24 8.34 8.24 8.34 8.24 8.34 8.34 8.24 8.344 8.344 8.344 8.345 8.344 8.345 8.345 8.344 8.345 8.34	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 1 1 1 1 1 1 1 1 1 1 1 1 1			2 1146,7148 2 1465,7581 2 1465,7581 2 1455,7581 2 131,462 2 131,462 2 131,462 2 2056,6912 1 455,7484 1 457,7485 1 453,7484 1 457,7485 1 454,6586 2 777,4797 1 154,6586 2 777,4797 2 1 155,4586 2 777,4797 2 1 154,6586 2 777,4797 2 1 754,6586 2 777,4797 2 777,4797 2 777,4797 2 777,4797 2 777,4797 2 777,	130           224           130           391           388           242           313           283           135           284           136           284           313           283           284           313           284           313           284           313           384           395           407           407           407           407           407           407           408           205           304           205           304           205           304           205           304           205           304           205           303           304           205           303           304           303           303           303           304           303           303	138           139           225           130           406           259           310           259           244           198           406           259           244           259           244           259           244           259           244           109           244           108           109           125           244           242           125           126           127           128           3146           324           324           324           225           226           218           324           219           220           324           324           324           324           325           325           325           326           35           3212           226
Vimentin - Box taurus (Bovin)     VIME_BOVIN       ATP synthese suburit bets, mitochondisil precursor (EC 3.6.3.14) - Horno sapiers (FATPB_HRAMN       ATP synthase suburit bets, mitochondisil precursor (EC 3.6.3.14) - Horno sapiers (FATPB_HRAMN       Vimentin (fragment) - Cricetulus grissus (Chinese harmster)     VIME_CRICE       Calenticulin precursor (CRPSs) (Calengulin) (HACIIP) (ERpto) (CALIP) (Calcum_Bindt CALR_PAT       Alges-1-antiproteinase 2 precursor (Alges-1-antitrypsin 2) (Algeba-1-proteinase Inhib ATAT2_HORSE	19702 19710.8 16542.5 19542.5 1831.8 47929 46925.8	100.00% 100.00% 100.00% 100.00%	2 B 10 13 8 6 5	2 7 14 16 19 14 8 6	4 0.42% 2 0.21% 27 4.86% 37 12.90% 51 7.66% 19 1.76% 11 0.72% 6 0.58%	A.729 ILABLECK VESUBLEATR     VESUBLEATR     VESUBLEATR     2.709 ALABLECK     VESUBLEATR     2.709 ALABLECK     VESUBLEATR     VESUBLE	化化 化化 使得觉得长度化长 的现在分词现在分词长长 的现在分词长长的复数形 网络长长长长长长 化长长长长长 网络马尔马马马马马马马马马马马马马马马马马马马马马马马马马马马马马马马马马马马	G         99,00%           G         99,00%           G         99,00%           I         99,00%           J         99,00%           G         99,00% <th>3.34 3.41 3.41 3.44 3.44 3.44 3.44 3.44</th> <th>0.922 0.979 0.279 0.289 0.539 0.539 0.539 0.537 0.375</th> <th>5.52 6.85 6.19 6.19 6.10 2.47 0.75 8.10 1.6 4.3 5.10 5.</th> <th>0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0</th> <th>3 1 1 1 1 1 1 1 1 1 1 1 1 1</th> <th></th> <th></th> <th>2 1140,7148 2 1465,7581 2 1405,7581 2 1145,7148 2 131,462 2 131,462 2 131,462 2 131,462 2 131,462 2 131,462 2 143,7464 1 143,7546 1 143,7546 2 143,7546 2 1439,7890 1 191,007 2 1086,637 2 1986,637 2 1986,64746 1 1937,7462 2 1431,256 2 1431,456 2 1431,456 2 1431,456 2 1441,455 2 144</th> <th>130           224           130           281           391           282           311           282           121           283           284           311           282           121           283           284           212           189           213           283           213           284           213           285           215           216           217           218           219           219           219           219           219           219           219           219           205           205           205           205           205           205           205           205           205           205           205           205           205           205           205</th> <th>138           139           225           139           4001           4005           259           324           139           269           224           234           335           345           324           325           244           421           421           422           217           218           316           3217           218           316           321           421           225           221           336           3270           422           320           221           320           221           320           422           431           432           433           434           432           433           434           432           433           434           434           431</th>	3.34 3.41 3.41 3.44 3.44 3.44 3.44 3.44	0.922 0.979 0.279 0.289 0.539 0.539 0.539 0.537 0.375	5.52 6.85 6.19 6.19 6.10 2.47 0.75 8.10 1.6 4.3 5.10 5.	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 1 1 1 1 1 1 1 1 1 1 1 1 1			2 1140,7148 2 1465,7581 2 1405,7581 2 1145,7148 2 131,462 2 131,462 2 131,462 2 131,462 2 131,462 2 131,462 2 143,7464 1 143,7546 1 143,7546 2 143,7546 2 1439,7890 1 191,007 2 1086,637 2 1986,637 2 1986,64746 1 1937,7462 2 1431,256 2 1431,456 2 1431,456 2 1431,456 2 1441,455 2 144	130           224           130           281           391           282           311           282           121           283           284           311           282           121           283           284           212           189           213           283           213           284           213           285           215           216           217           218           219           219           219           219           219           219           219           219           205           205           205           205           205           205           205           205           205           205           205           205           205           205           205	138           139           225           139           4001           4005           259           324           139           269           224           234           335           345           324           325           244           421           421           422           217           218           316           3217           218           316           321           421           225           221           336           3270           422           320           221           320           221           320           422           431           432           433           434           432           433           434           432           433           434           434           431
Vimentin - Box taurus (Bovine)     VIME_BOVIN       ATP synthase suburit bets, mitochondisil precursor (EC 3.6.3.14) - Hono sapiens (FATPE_HEAMAN       ATP synthase suburit bets, mitochondisil precursor (EC 3.6.3.14) - Hono sapiens (FATPE_HEAMAN       ATP synthase suburit bets, mitochondisil precursor (EC 3.6.3.14) - Hono sapiens (FATPE_HEAMAN       ATP synthase suburit bets, mitochondisil precursor (EC 3.6.3.14) - Hono sapiens (FATPE_HEAMAN       ATP synthase suburit bets, mitochondisil precursor (EC 3.6.3.14) - Hono sapiens (FATPE_HEAMAN       Attrastic control (Program) - Critectulus griseus (Chinese hemster)     VIME_CRIGR       Catesticulin precursor (CRP55) (Categulin) (M4CBP) (Ebpto) (CALBP) (Calcum-EndeCALR_MAT       Alpha-1-antiproteinase 2 precursor (Alpha-1-antitypsin 2) (Alpha-1-proteinase Inhib ATAT2_HORSE       Alpha-1-antiproteinase 2 precursor (Alpha-1-antitypsin 2) (Alpha-1-proteinase Inhib ATAT2_HORSE	19702 197108 56542,5 56542,5 51831,8 47975 46925,8	100.00% 100.00% 100.00% 100.00%	2 8 10 13 8 6	2 2 14 16 19 14 6	4 0.42% 2 0.21% 27 4.46% 37 12.40% 51 7.46% 19 1.76% 11 0.72% 6 0.56%	A.72% ILABLECK VSLOEHANK     VSLOEHANK     SUBLEATR     SUBLEATR     ZON ANELENTR	化化 化化 用理论用化化化化 的现在分词化化化化化 的现在分词化化的现在分词 化化化化化化化化化化化化化化化化化化化化化	G         99,00%           G         99,00%           G         99,00%           I         99,00%           I         99,00%           J         99,00%           G         99,00%           G         99,00%           G         99,00%           S         99,00%           E         90,00%           K         90,00%           K         90,00%           F         90,00%           G         90,00%           G         90,00%           G         90,00%           G         90,00%           G         90,00%           G         90,00% <th>3.34 3.47 3.47 3.44 3.47 3.44 3.47 3.44 3.47 3.44 3.47 3.44 3.47 3.47</th> <th>0.222 0.922 0.276 0.256 0.277 0.275 0.275 0.275 0.275 0.275 0.275 0.275 0.275 0.275 0.285 0.281 0.281 0.281 0.292 0.292</th> <th>5.52           6.85           6.19           6.13           6.14           6.3           9.7</th> <th>0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0</th> <th>3 1 1 1 1 1 1 1 1 1 1 1 1 1</th> <th></th> <th></th> <th>2 1140,7148 2 1465,7581 2 1465,7581 2 1467,7484 2 131,462 2 131,462 2 131,462 2 131,462 2 131,462 2 145,7581 2 435,7548 1 435,7548 1 435,7548 1 435,7548 1 435,7548 1 435,7548 1 435,7548 1 435,7548 1 435,7548 1 338,1109 2 2056,6972 2 435,7548 1 338,1109 2 2056,6972 2 1455,7548 1 338,1109 2 2056,6972 2 1455,7548 1 338,1109 2 2056,6972 2 1455,7548 1 338,1109 2 1550,8959 1 1016,0578 2 1650,918 1 435,7548 1 435,7548 1 435,7548 1 338,1109 2 1550,8959 1 1016,0578 2 1650,918 1 455,7548 1 455,7548 1 455,9548 1 455,95</th> <th>130           224           130           288           391           288           131           282           112           139           288           242           113           282           213           282           311           282           213           283           295           213           289           172           172           172           172           172           205           205           205           205           206           202           203           204           205           206           207           208           209           200           201           202           203           204           205           206           301           302           203</th> <th>138           139           225           139           406           259           130           260           131           269           225           2441           188           190           229           2441           185           100           224           133           198           199           124           225           243           431           198           198           198           198           198           198           198           198           198           198           198           193           218           219           210           211           212           213           214           404           215           216           404           217           404</th>	3.34 3.47 3.47 3.44 3.47 3.44 3.47 3.44 3.47 3.44 3.47 3.44 3.47 3.47	0.222 0.922 0.276 0.256 0.277 0.275 0.275 0.275 0.275 0.275 0.275 0.275 0.275 0.275 0.285 0.281 0.281 0.281 0.292 0.292	5.52           6.85           6.19           6.13           6.14           6.3           9.7	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 1 1 1 1 1 1 1 1 1 1 1 1 1			2 1140,7148 2 1465,7581 2 1465,7581 2 1467,7484 2 131,462 2 131,462 2 131,462 2 131,462 2 131,462 2 145,7581 2 435,7548 1 435,7548 1 435,7548 1 435,7548 1 435,7548 1 435,7548 1 435,7548 1 435,7548 1 435,7548 1 338,1109 2 2056,6972 2 435,7548 1 338,1109 2 2056,6972 2 1455,7548 1 338,1109 2 2056,6972 2 1455,7548 1 338,1109 2 2056,6972 2 1455,7548 1 338,1109 2 1550,8959 1 1016,0578 2 1650,918 1 435,7548 1 435,7548 1 435,7548 1 338,1109 2 1550,8959 1 1016,0578 2 1650,918 1 455,7548 1 455,7548 1 455,9548 1 455,95	130           224           130           288           391           288           131           282           112           139           288           242           113           282           213           282           311           282           213           283           295           213           289           172           172           172           172           172           205           205           205           205           206           202           203           204           205           206           207           208           209           200           201           202           203           204           205           206           301           302           203	138           139           225           139           406           259           130           260           131           269           225           2441           188           190           229           2441           185           100           224           133           198           199           124           225           243           431           198           198           198           198           198           198           198           198           198           198           198           193           218           219           210           211           212           213           214           404           215           216           404           217           404

Protein disulfide-isomerase A3 precursor (EC 5.3.4.1) (Disulfide isomerase ER-60) (EPDIA3_RAT	56607,5	100,00%	12	26	32 2,72% 30,30% DGEEAGAYDGPR EATNPPIIQEEKPK	R	T 95,00% K 95,00%	2,37 2,85	0,327 0,5	2,8 0 5,1 0	5	0	0 2	1236,5135 1593,8492	108 483	119 496
					ELNDFISYLOR FLQEYFDGNLK	R	E 95,00% R 95,00%	2,06 3,31	D,267 1 D,267 6	19 0 82 0	3	0	0 2	1397,7065 1373,6742	472 352	482 362
					FLQEYFDGNLKR KFISDKDASVVGFFR	R K	Y 95,00% D 95,00%	3,34	0,287 4 0 4	75 0 48 0	1	0	0 2	1529,7753 1715,912	352 147	363 161
					LAPEYEAAATR MDATANDVPSPYEV	R K	L 95,00% G 95,00%	2,63 4,28	0,275 5 0,405 8	32 0 15 0	4	0	0 2	1191,6011 1652,7478	63 434	73 448
					SEPIPETNEGPVK TADGIVSHLK	ĸ	V 95,00% K 95.00%	1,74 C 2.81	,0762 3 0.352 4	14 0 72 0	1	0	0 2	1396,6963 1040.5742	367 120	379 129
					TFSHELSDFGLESTT	GEIPVVAIR K	T 95,00% D 95,00%	2,11 C	,0827 7 0.497	35 0	0	2	0 2	2605,3149 1749,8546	306 380	329 395
Alpha-enolase (EC 4.2.1.11) (2-phospho-D-plycerate hydro-lyase) (Non-neural enolaENOA_RAT	47111	100.00%	15	54	88 2.68% 44.50% AAVPSGASTGIYEAL	ELR R	D 95.00%	4.72	0.501 4	57 0	8	1	0 2	1804.9447	33	50
					AGKYDLDFKSPDDA	SR R ILENK K	Y 95,00%	4,77	D,309	8 0 51 0	2	1	0 2	1784,8458	254 203	269
					DATINVGDEGGFAPN	ILENKEALELLK K	S 95,00%	4,21	D,428 3	25 0	0	1	0 2	2757,3945	203	228
					HIADLAGNEVILEV	PAFNVINGGSHAGNK R	L 95,00%	7,22	D,024 5	51 0	0	4	0 2	3021,5911	133	162
					IGAEVYHNLK	R	N 95,00%	2,96	0,19 1	39 0	3	0	0 2	1143,6163	184	193
					LAMQEFMILPVGASS LAQSNGWGVMVSHI	FR K R K	E 95,00% S 95,00%	3,44 C 2,6	,0674 0 5	3,1 0 41 0	10 4	2	0 2 2	1896,9717 1541,7645	163 359	179 372
					LNVVEQEK LNVVEQEKIDQLMIE	K MDGTENK K	I 95,00% S 95.00%	2,23 C	,0166 4 0.418 3	18 0 85 0	8	0	0 2	958,5209 2608,249	82 82	89 103
					VNQIGSVTESLQACK	ĸ	L 95,00%	3,92	D,288	1,2 0	9	1	0 2	1633,822	344	358
					YITPDQLADLYK	R	S 95,00%	2,42	0,12 5	24 0	11	ō	0 2	1439,7425	270	281
Laminin subunit alpha-1 precursor (Laminin A chain) - Mus musculus (Mouse) LAMA1_MOUSE	338149,2	100,00%	9	10	11 0,65% 3,79% ADNEVICTSYYSK	R	L 95,00%	3,14	D,337 1	36 0	1	0	0 2	1549,6844	183	195
					ALLHAPTGSYSDGG	HSISLVR K	N 95,00%	3,16	D,428 3 D,242 2	59 O	ò	2	0 2	2338,1792	2576	2597
					DLIYVGGLPHSK ITATYOPR	ĸ	A 95,00% A 95,00%	2,43 1,71	0,342 0,6 0,103 2	58 0 42 0	1 2	0	0 2 2	1298,7111 949,5108	2440 2969	2451 2976
					LYLGGLPSHYR NGVLIGISSAK	ĸ	A 95,00%	2,03	D,168 1	77 0	1	0	0 2	1275,6851	2845	2855
					TLNADLMTLSHR	R	D 95,00%	0	0 2	96 0	1	0	0 2	1387,7006	240	251
Elongation factor 2 (EF-2) - Cricetulus griseus (Chinese hamster) EF2_CRIGR	95380	100,00%	4	8	10 0,59% 5,48% CLYASVLTAOPR	R	L 95,00%	3,1	D,424 0,8	62 0	5	0	0 2	1378,7154	728	739
					ETVSEESNVLCLSK IMGPNYTPGK	R	S 95,00% K 95,00%	3,99 2,35	0,463 5 0,25 1	66 0 35 0	2	0	0 2	1594,7634 1093,5354	581 429	594 438
					VESGVVSTGLK	R	V 95,00%	3,39	0,36 /	2/ 0	2	0	0 2	1093,6257	416	426
Serotransternin precursor (Transternin) (Siderophilin) (Beta-T metal-binding globulin) Here_HORSE	/80/6,6	100,00%	37	93	166 3,92% 54,80% AAUUUELHNUUAS APNHAVVSR	YGK K R	K 95,00%	1,85	0,582 8 0,401	2,4 0	2	0	0 2	950,5171	609	617
					CACSNHEPYFGYSG	JR K NFK K	C 95,00%	4,51	0,497 5 0,537 5	28 0	3	1	0 2	1994,8165	165	214
					CGLVPVLAENYETR CLADGAGDVAFVK	ĸ	S 95,00% H 95,00%	0	0 5	27 0 41 0	9	0	0 2 2	1603,7793 1305,6152	423 215	436 227
					CLVEKGDVAFVK DCYLASIPSHAVVAR	R	H 95,00%	3,03	0 396 3	3,3 0 42 0	5	0	0 2	1364,725	550	561 275
					DDTQCLANLQPTTT	K R	T 95,00%	5,28	0,492 5	03 0	6	0	0 2	1868,8705	660	675
					DFHLFSSPHGK	ĸ	D 95,00%	2,39	D,386 1	17 0	1	0	0 2	1271,6173	302	312
					DLKSENFK DLLFKDSALGFLR	ĸ	L 95,00% I 95,00%	1,98 3,19 C	D,145 ,0742 3	2,5 0 41 0	2	0	0 2 2 2	980,5054 1494,8323	580 313	587 325
					DILFRDDTOCLANLO	PTTTYK K	T 95,00%	2,79	0,332 2 0,277 0 0	68 0 41 0	0	1	0 2	2513,2349	655 349	675
					FCLFQSATK	ĸ	D 95,00%	2,48	D,235 3	68 0	3	0	0 2	1101,5404	646	654
					HQTVEQNTDGRNPD	DWAK K	D 95,00%	3,13	0,398 3	46 0	3	2	0 2	2110,9544	562	579
					KNSNFQLNQLQGK KSVDEYKDCYLASIP	SHAVVAR R	K 95,00% S 95,00%	2,47 5,18	D,124 2 D,421 0,8	06 0 86 0	1	2	0 2	1518,803 2508,2556	119 254	275
					LLCPDGTR	ĸ	K 95,00%	1,8	0,149 2	57 O	3	0	0 2	931,4673	588	595 705
					LLEACTFHRV	R	- 95,00%	1,81	D,192	1,7 0	3	ō	0 2	1245,6415	697	706
					NSNFQLNQLQGK	ĸ	K 95,00%	3,73	D,321 1	39 0	9	ò	0 2	1390,708	120	131
					SAGWNIPIGLLYWOI	.PEPR R	E 95,00%	4,97	D,117 2 D,475 6	89 0 82 0	4	1	0 2	2210,1765	141	159
					SIVPAPPLVACVK SKDFHLFSSPHGK	ĸ	R 95,00% D 95,00%	2,46 3,85	D,356 4 D,433 4	24 0 55 0	5	0	0 2	1350,7821 1486,7445	45 300	57 312
					SSSDPDLTWNSLK SVDEYKDCYLASIPS	K HAVVAR K	G 95,00% S 95.00%	3,56	0,38 3 0.503 4	82 0 89 0	8	6	0 2	1449,6863 2380,1606	457 255	469 275
					SVDGKEDLIWGLLN TAGWNIDMGLLVSEL	DAQEHFGTEK R	S 95,00%	3,97	0,329 3	16 0	0	1	0 2	2714,3428	276	299
					TAVPNLCOLCVGK	R	G 95,00%	2,7	D,469 5	21 0	9	0	0 2	1459,7404	181	193
					YLTAVANLR	ĸ	Q 95,00%	1,86	D,216 -0,2 D,228 1	08 0	11	0	0 2	1013,4979	682	690
					YYGYTGAFR	R	C 95,00%	1,74	0,316 -0	74 1	6	0	0 2	1097,5056	541	549
Malate dehydrogenase, cytoplasmic (EC 1.1.1.37) (Cytosolic malate dehydrogenase) MDHC_MOUSE	36494,1	100,00%	5	10	14 1,96% 21,60% DLDVAVLVGSMPR FVEGLPINDFSR	ĸ	R 95,00% E 95,00%	3,04 2,24	D,395 D,379 5	5,5 0 66 0	1	0	0 2	1387,7257 1393,7117	80 299	92 310
					GEFITTVQQR NVIIWGNHSSTQYPI	VNHAK K	G 95,00% V 95,00%	3,29	0 6	42 0	4	2	0 2	1178,6172 2280,1162	221 180	230 199
					VIVVGNPANTNCLTA	SK K	S 95,00%	4,51	D,528	12 0	2	0	0 2	1757,922	126	142
8 kDa glucose-regulated protein precursor (GRP 78) (Heat shock 70 kDa protein 5) GRP78_HUMAN	72316,7	100,00%	6	10	13 2,39% 12,70% DAGTIAGLNVMR ITPSYVAFTPEGER	R	L 95,00%	3,19 3,63	0,332 5 0,526 2	96 0 05 0	2	0	0 2	1233,6263 1566,7806	186 61	197 74
					KKELEEIVOPIISK TFAPEEISAMVLTK	ĸ	L 95,00% M 95,00%	3,29 2,95 C	0,119 5 ,0552	19 0 8 0	0	2	0 2 2	1653,9795 1552,7933	620 139	633 152
					TWNDPSVQQDIK	R K	F 95,00%	3,54	0,322 0 1	5,7 O	1	0	0 2	1430,6918	102	113
ropomyosin beta chain (Tropomyosin 2) (Beta-tropomyosin) - Homo sapiens (HumaTPM2_HUMAN	32833.7	100.00%	9	14	20 2.48% 23.20% CKOLEEEOOALOK	R	K 95.00%	3.59	0.442	1.4 0	1	0	0 2	1631.8066	36	48
					CKOLEEEOQALOKK IOLVEEELDR	R	L 95,00%	0	0 4	27 0	0	1	0 2	1759,9016	36	49
					KATDAEADVASLNR	ĸ	R 95,00%	4,25	D,357 7	62 0	2	0	0 2	1460,7346	77	90
					LVILEGELER	ĸ	S 95,00%	2,87	0,21	1,4 0	4	0	0 2	1170,6736	169	178
					RIQLVEEELDR	R	A 95,00%	2,96	0 0,206 4	25 0	4	0	0 2	1326,6544	38	101
					RIQLVEEELDRAQER	R	L 95,00%	3,78	0,404 1	39 0	0	3	0 2	1883,994	91	105
Jesmin - Mesocricetus auratus (Golden hamster) DESM_MESAU	53421,5	100,00%	20	43	53 8,56% 43,50% ADVDAATLAR DGEVVSEATQQQHE	R VL R	- 95,00%	3,98	0,403 6 0,453	89 0 1,6 0	4	0	0 2	1002,522 1768,8356	212 454	221 469
					DNLIDDLOR EEAENNLAAFR	R	L 95,00% A 95,00%	2,41 2,59	u,∠83 4 0,216 6	07 0 01 0	2	0	ປ 2 0 2	1101,5543 1263,5969	180 201	188 211
					EYODLLNVK FASEASGYODNIAR	R	M 95,00% L 95,00%	1,63 4,66	D,193 1 D,529 8	89 0 08 0	1	0	0 2	1121,5845 1528,7031	386 355	394 368
					FASEASGYODNIARL	EEEIR R	H 95,00%	2,6 5.36	D,278 5	03 0 68 0	0	1	0 2	2298,1001 1673 861	355	374 141
					HOUSYTCEIDALK	R	G 95,00%	4,09	0,45 6	14 0	1	5	0 2	1705,8223	325	338
					LOEEIQLR	ĸ	E 95,00%	2,44	D,148	3,5 O	3	0	0 2	1033,7065	193	200
					MALDVEIATYR NISEAEEWYK	к	K 95,00% S 95,00%	3,43 3,27	D,472 6 D,334 4	14 0 13 0	4	0	0 2 2 2	1297,6464 1268,58	395 287	405 296
					QVEVLTNOR TNEKVELOFLNDR	R	A 95,00% F 95,00%	1,91 2.68	D,193 D.279 3	3,5 0 28 0	3	0	0 2	1086,5908 1587,798	164 105	172 117
					VAELYEEEMR	R	E 95,00%	3,22	0,452 4	72 0	2	0	0 2	1268,5834	150	159
					VAELYEEEMRELR VAELYEEEMDELDD	к	- 95,00%	2.21	0,108 3	0 85 0	0	1	0 2	1838.9071	150	162
					PALITELINGLIGG	R	G 73,00%								130	

vinientin (ringment) - crieetaras graeda (crimese narrater)	VIME_CRIGR	51831,8	100,00%	21	04	87	4,56%	53,40% DGUVINETSUHHDDLE	ĸ	-	42,00%	3,2	0,266	3,7	0	2	0	0	2 1030,0002	433	440
								EEAESTLQSFR	R	0	95.00%	2.44	0.453	5.41	0	4	0	0	2 1296.6072	179	189
								ETMI ESI DI VIDTUSK	P	P	95.00%	2 14	0.211	2 77	0	2	0	0	2 1692 9602	407	421
								ETHELSE EVENTION	R.		13,0070	4,17	0,211	A., / /		- ÷			2 1002,0002	407	44.1
								EYODLLNVK	R	M	95,00%	1,93	0,292	1,44	0	3	0	0	2 1121,5845	364	372
								FADLSEAANR	К	N	95.00%	2.2	0.312	2.52	0	5	0	0	2 1093.5278	277	286
								EADVIDK	P	V	95.00%	2 11	0.11	1.49	2	0	0	0	2 971 4202	0.6	102
								TADTIDK ELEMENT P			75,0075		0,11	1,40					2 071,4202	70	102
								FADYIDKVR	к	F	42,00%	3,14	0,24	4,18	0	2	U	0	2 1126,5898	90	104
								ILLAELEQLK	ĸ	G	95,00%	2,65	0,229	4,28	0	5	0	0	2 1169,7148	112	121
								ILLAFLEOLKGOGK	ĸ	s	95.00%	3 79	0.405	6.6	0	3	0	0	2 1539 9114	112	125
								ICI DI DNICCCI NI D			OF OOK	2,02	0,205	1.00	-	-	-	-	3 1570 0057	202	101
								ISCPLPINESSCINCK	R	E	95,00%	2,03	0,295	1,07	0	2	0		2 1370,6937	373	400
								KVESLQEEIAFLK	R	ĸ	95,00%	4,15	0,288	0,244	0	2	4	0	2 1533,8529	205	217
								KVESLQEEIAFLKK	R	L	95.00%	3.18	0.398	2.89	0	1	0	0	2 1661.9479	205	218
								LCDI VEEEMP	P	F	95 00%	2 22	0.464	5 22	0		0	0	2 1270 5427	129	127
								1005101010		-		0.00			-			-			
								LUDEIUNIK	к	E	95,00%	2,12	0,149	2,47	0		U	0	2 1134,5466	347	355
								LODEIQNMKEEMAR	R	н	95,00%	1,96	0	4,55	0	0	1	0	2 1766,8054	347	360
								LOEEMLOR	К	E	95.00%	2.57	0.0424	1.8	0	1	0	0	2 1062.5255	171	178
								LOFFAR ODFFAFETLOFFD	~	0	OF ODBY	2.24	0.200	6.00				0	2 2240 1142	171	100
								LUEENILUREEAESILUSFR		4	95,00%	3,24	0,308	0,02	0	0	1	0	2 2340,1143	171	167
								MALDIEIATYR	ĸ	ĸ	95,00%	3,7	0,429	3,77	0		U	0	2 1311,662	3/3	383
								NLQEAEEWYK	ĸ	S	95,00%	2,68	0,224	4,89	0	5	0	0	2 1309,6066	265	274
								ODVIDNIASLAD	P		95.00%	2 71	0.295	6.07	0	7	0	0	2 1099 5227	100	100
								OUDOL TNDKAD			05,00%	£,//i	0,505	0,01		-			2 1000,0007	140	150
								UVDUL INDIAR	R	v	95,00%	0	0	4	0	-	0	0	2 1270,0394	142	132
								QVQSLTCEVDALK	R	G	95,00%	0	0	4,07	0	1	0	0	2 1473,7262	304	316
								OVOSLTCEVDALKGTNESLER	R	0	95.00%	0	0	5.43	0	4	1	0	2 2360.1404	304	324
								SLYSSSDCCAVVTD	D	e	95.00%	2.05	0.254	11.2	0	0	0	0	2 1444 707	22	46
								JET JJJJ GOATVIK	R.	2	13,0070	4,75	0,000						2 1444,707		40
								INEKVELUELNDR	к	F	95,00%	3,62	0,358	6,8	0	3		0	2 1587,798	83	42
								TVETRDGQVINETSQHHDDLE	ĸ		95,00%	2,88	0,22	1,27	0	0	3	0	2 2423,1072	428	448
								VELOFLNDR	ĸ	F	95.00%	2 57	0.114	37	0	2	0	0	2 1115 5698	87	95
Manualia (Communit) Colonialia aniana (Chinasa komputer)	VILLE COLOR	F3033.0	100.000/	21		(0	E OFW	ALOOK DOOLINETEOLINDDIE	0		OF OOW	2.55	0.245	4.75	0		1	0	2 1026 0002	433	440
Vimentin (Fragment) - Cricetulus griseus (Chinese hamster)	VIME_CRIGR	51831,8	100,00%	21	46	60	5,95%	44,00% DGQVINETSOHHDDLE	R		95,00%	3,55	0,345	4,25	0	4	1	0	2 1836,8002	433	448
Vimentin (Fragment) - Cricetulus griseus (Chinese hamster)	VIME_CRIGR	51831,8	100,00%	21	46	60	5,95%	44,00% DGOVINETSOHHDDLE EEAESTLQSFR	R	Q	95,00% 95,00%	3,55 2,46	0,345	4,25 2,18	0	4	1 0	0	2 1836,8002 2 1296,6072	433 179	448 189
Vimentin (Fragment) - Cricetulus griseus (Chinese hamster)	VIME_CRIGR	51831,8	100,00%	21	46	60	5,95%	44,00% DGQVINETSOHHDDLE EEAESTLQSFR EEAESTLQSFRODVDNASLAR	R R R	Q L	95,00% 95,00% 95,00%	3,55 2,46 0	0,345 0,289 0	4,25 2,18 7,08	0	4	1 0 1	0	2 1836,8002 2 1296,6072 2 2366,1221	433 179 179	448 189 199
Vimentin (Fragment) - Cricetulus griseus (Chinese hamster)	VIME_CRIGR	51831,8	100,00%	21	46	60	5,95%	44,00% DGOVINETSOHHDDLE EEAESTLOSFR EEAESTLOSFRODVDNASLAR ETNI ERIP UNTVIKK	R R R	C L	95,00% 95,00% 95,00%	3,55 2,46 0	0,345 0,289 0	4,25 2,18 7,08 4,41	0	4	1 0 1	0	2 1836,8002 2 1296,6072 2 2366,1221 2 1692,8602	433 179 179 407	448 189 199 421
Vimentin (Fragment) - Cricetulus griseus (Chinese hamster)	VIME_CRIGR	51831,8	100,00%	21	46	60	5,95%	44,00% DGQVINETSOHHDDLE EEAESTLOSFR EEAESTLOSFRODVDNASLAR ETNLESJPLVDTHSK	R R R	C L R	95,00% 95,00% 95,00% 95,00%	3,55 2,46 0 3,54	0,345 0,289 0 0,42	4,25 2,18 7,08 6,41	0	4 1 0 1	1 0 1 0	0	2 1836,8002 2 1296,6072 2 2366,1221 2 1682,8602	433 179 179 407	448 189 199 421
Vimentin (Fragment) - Cricetulus griseus (Chinese hamster)	VIME_CRIGR	51831,8	100,00%	21	46	60	5,95%	44,00% DGQVINETSQHHDDLE EEAESTLQSFR EEAESTLQSFRODVDNASLAR ETNLESLPLVDTHSK EYQDLLNVK	R R R R	Q L R M	95,00% 95,00% 95,00% 95,00% 95,00%	3,55 2,46 0 3,54 2,06	0,345 0,289 0 0,42 0,261	4,25 2,18 7,08 6,41 3,42	0 0 0 0	4 1 0 1 2	1 0 1 0 0	0 0 0 0	2 1836,8002 2 1296,6072 2 2366,1221 2 1682,8602 2 1121,5845	433 179 179 407 364	448 189 199 421 372
Vimentin (Fragment) - Cricetulus griseus (Chinese hamster)	VIME_CRIGR	51831,8	100,00%	21	46	60	5,95%	44,00% DGOVINETSOHHDDLE EEAESTLOSFR EEAESTLOSFRODVDNASLAR ETNLESJPLVDTHSK EYODLINVK FADLSEAANR	R R R K	C L R M N	95,00% 95,00% 95,00% 95,00% 95,00% 95,00%	3,55 2,46 0 3,54 2,06 3,05	0,345 0,289 0 0,42 0,261 0,147	4,25 2,18 7,08 6,41 3,42 5,28		4 1 0 1 2 4	1 0 1 0 0		2 1836,8002 2 1296,6072 2 2366,1221 2 1682,8602 2 1121,5845 2 1093,5278	433 179 179 407 364 277	448 189 199 421 372 286
Vimentin (Fragment) - Cricelulus griseus (Chinese hamster)	VIME_CRIGR	51831,8	100,00%	21	46	60	5,95%	44,00% DGOVINETSOHHDDLE EEAESTLOSSR EEAESTLOSSRODVDNASLAR ETNLESSPLVDTHSK EYODLINVK FADLSEAANR ILLAELEOLK	R R R K K	C L R M G	95,00% 95,00% 95,00% 95,00% 95,00% 95,00%	3,55 2,46 0 3,54 2,06 3,05 3,61	0,345 0,289 0,42 0,261 0,147 0,217	4,25 2,18 7,08 6,41 3,42 5,28 4,24		4 1 0 1 2 4 2	1 0 0 0 0		2 1836,8002 2 1296,6072 2 2366,1221 2 1682,8602 2 1121,5845 2 1093,5278 2 1169,7148	433 179 179 407 364 277 112	448 189 199 421 372 286 121
Vimentin (Fragment) - Cricetolus griseus (Chinese hamster)	VIME_CRIGR	51831,8	100,00%	21	46	60	5,95%	44,00%. DGOVINETSOHHDDLE EEAESTLOSFR EEAESTLOSFROVDONASLAR ETNLESJPLVDTHSK EYODLLNVK FADLSEAANR ILLAELEOLK III JEFERKGOGK	R R R R K K K	U L R M S S	95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00%	3,55 2,46 0 3,54 2,06 3,05 3,61 2,39	0,345 0,289 0,42 0,261 0,147 0,217 0,217	4,25 2,18 7,08 6,41 3,42 5,28 4,24 4,24 4,14		4 1 0 1 2 4 2 0	1 0 0 0 0 3		2 1836,8002 2 1296,6072 2 2366,1221 2 1682,8602 2 1121,5845 2 1093,5278 2 1169,7148 2 1539,9114	433 179 179 407 364 277 112 112	448 189 199 421 372 286 121 125
Wimentin (Fragment) - Cricetolus griseus (Chinese hamster)	VIME_CRIGR	51831,8	100,00%	21	46	60	5,95%	44.00% DGOVINETSCHHIDDLE EEAESTLOSFROVUONASLAR ETALESLIOSFROVUONASLAR ETALESLIVUOTHSK EYODLINVK FADISEAANR ILLAELEOKKOOGK ILLAELEOKKOOGK	R R R R K K K	- L R M G S	95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00%	3,55 2,46 0 3,54 2,06 3,05 3,61 2,39	0,345 0,289 0,42 0,261 0,147 0,217 0,126	4,25 2,18 7,08 6,41 3,42 5,28 4,24 4,14 4,14		4 1 2 4 2	1 0 0 0 0 0 3		2 1836,8002 2 1296,6072 2 2366,1221 2 1682,8402 2 1121,5845 2 1093,5278 2 1169,7148 2 1539,9114	433 179 179 407 364 277 112 112	448 189 199 421 372 286 121 125
Mmentin (Fragment) - Cricetulus griseus (Chinese hamster)	VIME_CRIGR	51831,8	100,00%	21	46	60	5,95%	44,00% DGOVINETSOHHDDLE EEAESTLOSFROUVDNASLAR ETNLESLPUVDTHSK EYODLINVK FADLSEANAR ILLAELEOLK ILLAELEOLK ILLAELEOLK ILLAELEOLK	R R R R K K K R	- L R M S S E	95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00%	3,55 2,46 0 3,54 2,06 3,05 3,61 2,39 1,67	0,345 0,289 0,42 0,261 0,147 0,217 0,126 0,144	4,25 2,18 7,08 6,41 3,42 5,28 4,24 4,14 2,52		4 1 2 4 2 0 3	1 0 0 0 0 3 0		2 1836,8002 2 1296,6072 2 2366,1221 2 1682,8602 2 1121,5845 2 1093,5278 2 1169,7148 2 1539,9114 2 1539,9174	433 179 179 407 364 277 112 112 393	448 189 199 421 372 286 121 125 406
Mmentin (Fragment) - Cricetulus griseus (Chinese hamster)	VIME_CRIGR	51831,8	100,00%	21	46	60	5,95%	44,00% DEGWINETSCHHDDLE EEASTLOSFR EEASTLOSFROMMASLAR ETNLESLPLUTHSK EYDDLINK HILALEOLK HILALEOLK ILLALEOLKOGOK ISLPLINFSSIAR KVESLOELAFLK	R R R R K K K R R	- L R M G S E K	95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00%	3,55 2,46 0 3,54 2,06 3,05 3,61 2,39 1,67 5,21	0,345 0,289 0,42 0,261 0,147 0,217 0,126 0,144 0,369	4,25 2,18 7,08 6,41 3,42 5,28 4,24 4,14 4,14 2,52 8,35		4 1 2 4 2 0 3 1	1 0 0 0 0 3 0 2		2 1836,8002 2 1296,6072 2 2366,1221 2 1682,8602 2 1121,5845 2 1093,5278 2 1169,7148 2 1539,9114 2 1570,8957 2 1533,8529	433 179 179 407 364 277 112 112 393 205	448 189 199 421 372 286 121 125 406 217
Wimentin (Fragment) - Cricetulus griseus (Chinese hamster)	VIME_CRIGR	51831,8	100,00%	21	46	60	5,95%	44,00% DEGWINETSCHHDDLE EEAISTLOSR ETALSTLOSR TYDELINK FYDELINK FYDELINK FADLSEAMR ILLAFLECKC ILLAFLECKCOCK ISJPINYSSIN R GODYEEMR	R R R R R K K K R R R	- L R M S S E K E	95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00%	3,55 2,46 0 3,54 2,06 3,05 3,61 2,39 1,67 5,21 0	0,345 0,289 0,261 0,147 0,217 0,126 0,144 0,369 0	4,25 2,18 7,08 6,41 3,42 5,28 4,24 4,24 4,14 2,52 8,35 5,34		4 1 2 4 2 0 3 1 3	1 0 0 0 3 0 2 0		2 1836,8002 2 1296,6072 2 2366,1221 2 1682,8602 2 1121,5845 2 1093,5278 2 1169,7148 2 1539,9114 2 1570,8957 2 1533,8529 2 1254,5679	433 179 179 407 364 277 112 112 393 205 128	448 189 199 421 372 286 121 125 406 217 137
(Vimentin (Fragment) - Cricetulus griseus (Chinese hemoter)	VIME_CRIGR	51831,8	100,00%	21	46	60	5,95%	44,00% DEGVINE ISOHHDDLE EASISTICSFROUVDINGLAR ETHLISTICSFROUVDINGLAR ETHLISTICSFROUVDING FADLSEAMR HALEEGLKOGOK ISUPURYSSING KVESLOGELAFLK LGDVEEDR	R R R R R K K K R R R R R R	- C L R M N G S E K E P	95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00%	3,55 2,46 0 3,54 2,06 3,05 3,61 2,39 1,67 5,21 0	0,345 0,289 0,42 0,261 0,147 0,217 0,126 0,144 0,369 0 0,144	4,25 2,18 7,08 6,41 3,42 5,28 4,24 4,14 2,52 8,35 5,34 4,22		4 1 2 4 2 0 3 1 3	1 0 0 0 3 0 2 0 2		2 1836,8002 2 1296,6072 2 2366,1221 2 1682,8602 2 1121,5845 2 1093,5278 2 1169,7148 2 1530,9114 2 15570,8957 2 1553,8529 2 1254,5679 2 1254,5679	433 179 179 407 364 277 112 112 393 205 128	448 189 199 421 372 286 121 125 406 217 137 140
Mmentin (Fragment) - Cricetalus griseus (Chinese hamsler)	VIME_CRIGR	51831,8	100,00%	21	46	60	5,95%	44,00% DEGWINETSCHHDDLE EEASTLOSFR EEASTLOSFROPUNASLAR ETNELSLPLUTINSK FYDLESLPLUTINSK HLAELEOLK HLAELEOLKOGOK ISLPLPNFSSLN.R KVESLOELAFLK LGDLYEELARL LGDLYEELARLE	R R R R K K K R R R R R R R R R R R R R	- C L R M N G S E K E R	95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00%	3,55 2,46 0 3,54 2,06 3,61 2,39 1,67 5,21 0 1,99	0,345 0,289 0 0,42 0,261 0,147 0,217 0,126 0,144 0,369 0 0,166	4,25 2,18 7,08 6,41 3,42 5,28 4,24 4,14 2,52 8,35 5,34 4,33 5,34		4 1 2 4 2 0 3 1 3 0	1 0 1 0 0 3 0 2 0 2 2		2 1836,8002 2 12%,6072 2 23%,61221 2 1682,8602 2 1121,5845 2 1093,5278 2 1093,5278 2 1539,9114 2 1570,8957 2 1533,8529 2 1254,5679 2 1254,5679	433 179 179 407 364 277 112 112 112 393 205 128 128 128	448 189 199 421 372 286 121 125 406 217 137 140
Mmentin (Fragment) - Cricetalus griseus (Chinese hamster)	VIME_CRIGR	51831,8	100,00%	21	46	60	5,95%	44,00% DGOVINETSCHHDDLE ERASTLOSP ETRASTLOSP ETRASTLOSP ETRASTLOSP FOR SEVOTHSK FOR SEVOTHSK FOR SEVOTHSK FLAREGK ILLAREGK ILLAREGK ILLAREGK ILLAREGK ILLAREGK ILLAREGK ILLARESK ILLARESK	R R R R R K K K R R R R K	- C L R M N G S E K E R I	95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00%	3,55 2,46 0 3,54 2,06 3,05 3,61 2,39 1,67 5,21 0 1,99 2,54	0,345 0,289 0,42 0,261 0,147 0,217 0,126 0,144 0,369 0 0,166 0,122	4,25 2,18 7,08 6,41 3,42 5,28 4,24 4,14 2,52 8,35 5,34 4,33 3,55		4 1 2 4 2 0 3 1 3 0 2	1 0 0 0 0 3 0 2 0 2 0 2 0 2 0		2 1836,8002 2 1296,6072 2 2366,1221 2 1682,8602 2 1121,5845 2 1093,5278 2 1169,7148 2 1530,9114 2 1530,9114 2 1530,9114 2 1530,957 2 1533,8529 2 1254,5679 2 1668,7905 2 932,4689	433 179 179 407 364 277 112 393 205 128 128 385	448 189 199 421 372 286 121 125 406 217 137 140 392
(Vimentin (Fragment) - Cricetulus griseus (Chinese hemster)	VIME_CRIGR	51831,8	100,00%	21	46	60	5,95%	44.00% DGOVINETSCHHDDLE EALSTICGSR ETALSTICGSR ETALSTICGSR ETALSTICHT ETALSTICHT FOLLSAARR ILLATECXX SARARR ILLATECXX ISJPHINSSIGR KVESLOELAFLK LCDAVEENR LCDAVEENR LCDAVEENR MALDIELATAR	R R R R R K K K R R R K K	- Q L R M N G S E K E R I K	95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00%	3,55 2,46 0 3,54 2,06 3,05 3,61 2,39 1,67 5,21 0 1,99 2,54 1,84	0,345 0,289 0 0,42 0,241 0,147 0,126 0,144 0,369 0 0,166 0,122 0	4,25 2,18 7,08 6,41 3,42 5,28 4,24 4,14 2,52 8,35 5,34 4,33 3,55 2,8		4 1 2 4 2 0 3 1 3 0 2 3 3	1 0 0 0 3 0 2 0 2 0 2 0 0		2 1836,8002 2 1296,6072 2 2366,1221 2 1662,8602 2 1121,5845 2 1093,5278 2 1166,7148 2 1539,9114 2 1539,9114 2 1539,9114 2 1538,529 2 1254,5679 2 1666,7905 2 932,4689 2 1311,662	433 179 179 364 277 112 393 205 128 128 128 385 373	448 189 199 421 372 286 121 125 406 217 137 140 392 383
(Vimentin (Fragment) - Cricetulus griseus (Chinese hamsler)	VIME_CRIGR	51831,8	100,00%	21	46	60	5,95%	44.00% BCGWINE FEDERADLE EALSTIC SEPT EALSTIC SEPT ENLISTIC SEPT FOR LIVY FILLE FLATE SEPT FILLE ILLATE EXCOME INFORMATION CONVERSION LOD VEENER LICE SEP MADDELIATION	R R R R K K K R R R K K K	- O L R M N G S E K E R I K S	95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00%	3,55 2,46 0 3,54 2,06 3,05 3,61 2,39 1,67 5,21 0 1,99 2,54 1,84 2,71	0,345 0,289 0 0,42 0,261 0,147 0,147 0,126 0,126 0,126 0,144 0,369 0 0,166 0,122 0 0,446	4,25 2,18 7,08 6,41 3,42 5,28 4,24 4,14 2,52 8,35 5,34 4,33 3,55 2,8 5,55		4 0 1 2 4 2 0 3 1 3 0 2 3 5	1 0 0 0 3 0 2 0 2 0 0 0 0 0 0 0		2 1836,8002 2 1296,6072 2 2366,1221 2 1662,8602 2 1121,5845 2 11093,5278 2 1169,7148 2 1539,9114 2 1570,9857 2 1533,8529 2 1254,5679 2 1254,5679 2 1264,5679 2 1311,662 2 932,4689 2 1311,662	433 179 179 407 364 277 112 112 393 205 128 325 373 373 265	448 189 199 421 372 286 121 125 406 217 137 140 392 383 274
(Vimentin (Fragment) - Cricetulus griseus (Chinese hamster)	VIME_CRIGR	51831,8	100,00%	21	46	60	5,95%	44.000 BOOMINE MOMPHOLE EAASTICOSPE EAASTICOSPE ENASTICOSPECTUARIA ETINISE PUDTISK EVELLINK ILALEED ILALEED EXAMPLE EXAMPLE ILALEED EXAMPLE IL	R R R R K K K R R R K K K P	- O L R M N G S E K E R I K S	95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00%	3,55 2,46 0 3,54 2,06 3,05 3,61 2,39 1,67 5,21 0 1,99 2,54 1,84 2,71 2,24	0,345 0,289 0 0,42 0,261 0,147 0,126 0,144 0,144 0,144 0,144 0,146 0,166 0,166 0,122 0 0,0406	4,25 2,18 7,08 6,41 3,42 5,28 4,24 4,14 4,14 4,14 4,14 4,14 4,252 8,35 5,53 4,33 3,55 2,8 5,55 2,27		4 1 2 4 2 0 3 1 3 0 2 3 5 7	1 0 0 0 0 3 0 2 0 2 0 0 0 0 0 0 0 0 0 0 0		2 1836,8002 2 1296,6072 2 2366,1221 2 1662,8602 2 1121,5845 2 1093,5278 2 11667,7148 2 1537,9114 2 1577,08957 2 1234,5679 2 1234,5679 2 1234,5679 2 1234,5679 2 1311,662 2 1337,6667	433 179 179 407 364 277 112 112 393 205 128 128 128 325 373 265	448 189 199 421 225 125 125 125 125 125 125 1
(Vimentin (Fragment) - Cricetulus griseus (Chinese hemster)	VIME_CRIGR	51631,8	100,00%	21	46	60	5,95%	44.000 BOOMINE SCHENDLE EAASTLOSPF EAASTLOSPF EINLISU/DUTHAK FILLISU/DUTHAK FILLISU/DUTHAK FILLISU/DUTHAK BOOMINE LILICURA COLORISAN KONSTONELIAN LILICURA LILICURA MALDELIAN MALDELIAN COLONISAR	R R R R K K K R R R R K K K R	- O L R M N G S E K E R I K S L .	95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00%	3,55 2,46 0 3,54 2,06 3,05 3,61 2,39 1,67 5,21 0 1,99 2,54 1,84 2,71 2,34	0,345 0,289 0 0,42 0,261 0,147 0,147 0,126 0,126 0,126 0,144 0,369 0,166 0,122 0 0,466 0,355	4,25 2,18 7,08 6,41 3,42 5,28 4,24 4,14 2,52 8,35 5,34 4,33 3,55 2,8 5,55 3,77		4 1 2 4 2 0 3 1 3 0 2 3 5 7 7	1 0 0 0 3 0 2 0 2 0 0 0 0 0 0 0 0 0		2 1836,8002 2 1296,6072 2 2366,1221 2 1662,860,1221 2 1121,5843 2 1126,7148 2 1597,9414 2 1597,9495 2 1537,8529 2 1254,5679 2 1626,7905 2 932,4689 2 1399,6066 2 1088,5337	433 179 179 407 364 277 112 112 393 205 128 385 373 265 190	448 189 421 372 286 121 122 406 217 137 140 392 383 274 179
(Vimentin (Fragment) - Cricetulus griseus (Chinese hamster)	VIME_CRIGR	51831,8	100,00%	21	46	60	5,95%	44.00% DOOMER FORHOLE EASTS COSP EASTS COSP ENDER FINLSEVUTHSK PROLLWK FOLLWK FOLLWK ILLALEGLKGOR ISP, PROSSAR KYSLOFELIALK ILLALEGLKGOR ISP, PROSSAR KYSLOFELIALK ILGESS MALDELATR MALDEL	R R R R R K K K R R R R K K K R R	- Q L R M N G S E K E R I K S L N	95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00%	3,55 2,46 0 3,54 2,06 3,05 3,61 2,39 1,67 5,21 0 1,99 2,54 1,84 2,71 2,34 0	0,345 0,289 0 0,42 0,261 0,147 0,217 0,126 0,126 0,126 0,126 0,166 0,122 0 0,406 0,355 0	4,25 2,18 7,08 6,41 3,42 5,28 4,24 4,14 4,14 2,52 8,35 5,54 4,33 3,55 5,34 4,33 3,55 2,8 5,55 3,77 3,46		4 1 2 4 2 0 3 1 3 0 2 3 5 7 2	1 0 0 0 0 3 0 2 0 2 0 2 0 0 0 0 0 0 0 0 0		2 1836,8002 2 1296,6072 2 2366,1221 2 1662,8602 2 1121,5845 2 1093,5278 2 1169,7148 2 1539,9114 2 1570,8957 2 1533,8529 2 1254,5679 2 1254,5679 2 1264,5679 2 1311,662 2 1309,6066 2 1309,6066	433 179 179 407 364 277 112 112 393 205 128 128 385 373 265 190 256	448 189 199 421 372 286 121 125 406 217 140 392 383 274 199 264
(Vimentin (Fragment) - Cricetalus griseus (Chinese hamsler)	VIME_CRIGR	51831.8	100,00%	21	46	60	5,95%	44.000 DOCIMUME YEARHODUL EARISTICOSPIE ERAISTICOSPIE ENAISTICOSPIE VICTORIA ENAISTICOSPIE ILAILEOLK ILAILEOLK ILAILEOLK COD VICEOR ILAILEOLK COD VICEOR COD VICEOR	R R R R K K K R R R R K K K R R	- O L R M N G S E K E R I K S L N G	95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00%	3,55 2,46 0 3,54 2,06 3,05 3,61 2,39 1,67 5,21 0 1,99 2,54 1,84 2,71 2,34 0 3,68	0,345 0,289 0,42 0,261 0,147 0,217 0,126 0,144 0,369 0 0,166 0,122 0 0,166 0,355 0 0,406	4,25 2,18 7,08 6,41 3,42 5,28 4,24 4,14 2,52 8,35 5,34 4,33 3,55 2,8 5,55 3,77 3,46 6		4 1 2 4 2 0 3 1 3 0 2 3 5 7 2 4	1 0 0 0 0 0 2 2 0 0 0 0 0 0 0 0 0 0 0 0		2 1836,8002 2 1296,6072 2 2366,1221 2 1662,8602 2 1121,5845 2 1093,527 2 1167,148 2 1537,9114 2 1537,9114 2 1537,8859 2 1648,7905 2 1638,7905 2 1638,7905 2 1638,7905 2 1329,4689 2 1311,662 2 1309,6066 2 1096,5337 2 1006,4845 2 1096,7527	433 179 407 364 277 112 393 205 128 385 373 265 190 256 304	448 189 199 421 222 226 121 125 426 217 137 140 392 383 274 399 264 316
(Vimentin (Fragment) – Cricetalus griseus (Chinese hamster)	VIME_CRIGR	51831,8	100,00%	21	46	60	5,95%	44.000 HOOMINE HOMPOOL EAASTICOSPE EAASTICOSPE TENESEN UN HOMPO TENESEN HILAIEEDAS HILAI	R R R R R K K K R R R R K K K R R R R	- OL R M N G S E K E R I K S L N G O	95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00%	3,55 2,46 0 3,54 2,06 3,61 2,39 1,67 5,21 0 1,99 2,54 1,84 2,71 2,34 0 3,68 2,88	0,345 0,289 0 0,42 0,261 0,147 0,217 0,126 0,126 0,126 0,126 0,166 0,122 0 0,466 0,355 0 0,425 0 0,425 0	4,25 2,18 7,08 6,41 3,42 5,28 4,24 4,14 2,52 8,35 5,34 5,34 4,33 3,55 2,8 5,55 3,77 3,46 6 1,66		4 1 2 4 2 0 3 1 3 0 2 3 5 7 7 2 4 0	1 0 0 0 0 3 0 2 0 2 0 0 0 0 0 0 0 0 0 0 0		2 1836,8002 2 12%,6072 2 2366,1221 2 1662,801,1221 2 1662,801,1221 2 1662,801,1221 2 1692,912 2 1592,9114 2 1592,9114 2 1592,9114 2 1592,9114 2 1592,9114 2 1592,9114 2 1592,8529 2 1307,6066 2 10056,45316 2 10057,4537 2 10057,4557 2 10057,557 2 1	433 179 407 364 277 112 112 393 205 128 128 385 373 265 373 265 190 256 304 304	448 189 199 421 372 286 121 125 406 217 137 140 392 383 274 199 244 316 374
(Vimentin (Fragment) - Cricetulus griseus (Chinese hemoter)	VIME_CRIGR	51831.8	100,00%	21	46	60	5,95%	44.00% DOWNER FORHELE EAASTICOSPECTOR EAASTICOSPECTOR ETAISTICOSPECTOR FOLLEW FORLIWK FOLLEWAR ILALEELKOOK ISJPHYSSIAR KYSSIGELAFIK LOEVERMER LEGEESR MALDELATYR NCLEAR OVOSITCEVAAK OVOSITCEVAAK OVOSITCEVAAK	R R R R R K K K R R R R R R R R R R R R	- OLRMNGSEKERIKSLNGO	95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00%	3,55 2,46 0 3,54 2,06 3,05 3,61 2,39 1,67 5,21 0 1,99 2,54 1,84 2,71 2,34 0 3,68 2,88	0,345 0,289 0,42 0,261 0,147 0,217 0,126 0,144 0,369 0,166 0,122 0 0,406 0,355 0 0,425 0,346	4,25 2,18 7,08 4,41 3,42 5,28 4,24 4,14 2,52 8,35 5,34 4,33 3,55 2,8 5,55 3,77 3,46 1,66		4 1 2 4 2 0 3 1 3 0 2 3 5 7 2 4 0	1 0 0 0 0 0 2 2 0 2 0 0 0 0 0 0 0 0 0 0		2 1836,8002 2 12%,6073 2 2366,1612 2 1121,5845 2 1093,5278 2 1164,7148 2 1539,9114 2 1539,9114 2 1539,9114 2 1539,9114 2 1532,88529 2 1254,5537 2 1632,4659 2 1311,662 2 1309,6026 2 1309,6026 2 1309,6026 2 1309,6026	433 179 407 364 277 112 112 393 205 128 385 373 265 373 265 190 256 304 304	448 199 421 372 286 121 125 406 211 125 406 211 125 406 211 127 140 392 383 274 199 264 316 324 -
Winentin (Fragment) - Cricetulus griseus (Chinese hamsler)	VIME_CRIGR	51831.8	100,00%	21	46	60	5,95%	44.00 HOOVINE HOMPADIL EALSTLOSF EALSTLOSF ENLIST E	R R R R K K K R R R R R R R R R R R R R	- O L R M N G S E K E R I K S L N G O F	95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00% 95,00%	3,55 2,46 0 3,54 2,06 3,05 2,39 5,21 0 1,99 2,54 1,84 2,71 2,34 0 3,68 2,88 2,5	0,345 0,289 0,42 0,261 0,147 0,217 0,126 0,144 0,369 0,166 0,122 0 0,406 0,355 0,425 0,346 0,198	4,25 2,18 7,08 6,41 3,42 5,28 4,24 4,14 2,52 8,35 5,34 4,33 3,55 2,8 5,55 3,77 3,46 6 1,66 0,444		4 1 2 4 2 0 3 1 3 0 2 3 5 7 2 4 0 0	1 0 1 0 0 0 3 0 2 0 0 2 0 0 0 0 0 0 0 0 0 0 0		2 11236,8002 2 1256,6072 2 2266,2072 2 2266,2072 2 1622,8602 2 1121,5845 2 1039,5278 2 1166,7148 2 1539,9117 2 1133,8529 2 1245,4549 2 1245,4549 2 1311,662 2 1327,6667 2 1311,662 2 1309,6667 2 1311,662 2 1309,6667 2 1309,6667 2 1309,7527 2 1257,167 2 1587,798	433 179 407 364 277 112 393 205 128 385 373 265 190 256 304 304 83	448 189 199 421 372 286 123 135 405 405 405 405 405 405 405 40

Target	5'-Primer	TaqMan Probe ( 5'-FAM, 3'-TAMRA)	3'-Primer
GAPDH	AAC TCC CTC AAG ATT GTC AGC AA	ATG GAC TGT GGT CAT GAG CCC TTC CA	CAG TCT TCT GAG TGG CAG TGA TG
CSQ2	TTT CTG ACG GAG ACG TTC AGG	TGG CTG CCT ACA GTA CGC TGG GAA C	TAG CAG GAC AGA GAG GGT GCA
α-cd actin	TGA TGC TCC CAG AGC TGT CTT	CCA CGC CAC CAG GGT GTC ATG GTA	GAT GCC TCG CTT GCT CTG AG
α-sk actin	TAT GAG GGT TAT GCC CTG CC	AAT CTC ACG TTC AGC TGT GGT CAC GAA GG	GCT TCT CTT TGA TGT CGC GC
α-MHC	ACA GAG TGC TTC GTG CCT GAT	ACA GTC ACC GTC TTG CCG TTT TCA GT	CGA ATT TCG GAG GGT TCT GC
β-ΜΗC	GCC TAC AAG CGC CAG GCT	TTC ATT CAG GCC CTT GGC GCC AAT	CAT CCT TAG GGT TGG GTA GCA
bax	ATC CAC CAA GAA GCT GAG CG	ATC AGC AAT CAT CCT CTG CAG CTC CA	ACG GAA GAA GAC CTC TCG GG
Bcl-2	CCT GGT GGA CAA CAT CGC T	AAC GGA GGC TGG GAT GCC TTT GTG	AAT CAA ACA GAG GTC GCA TGC
VEGF-A	ACT GCT GTA CCT CCA CCA TGC	AAG TGG TCC CAG GCT GCA CCC A	AAG ATG TCC ACC AGG GTC TCA
Collagen $\alpha 1(I)$	TGG TCC TCA AGG TTT CCA AG	TGG CGG TTC AGG TCC AAT GG	TTA CCA GCT TCC CCA TCA TC
Collagen a1(III)	AAT GGT GGC TTT CAG TTC AGC T	TGG AAA GAA GTC TGA GGA AGG CCA GCT G	TGT AAT GTT CTG GGA GGC CC
MMP-2	CCGAGGACTATGACCGGGATAA	TCTGCCCCGAGACCGCTATGTCCA	CTTGTTGCCCAGGAAAGTGAAG
MMP-3	CCGTTTCCATCTCTCTCAAGATGA	AGATGGTATTCAATCCCTCTATGGACCTCC	CAGAGAGTTAGATTTGGTGGGTACCA
MMP-13	GGAAGACCCTCTTCTTCTCA	TCTGGTTAGCATCATCATAACTCCACACGT	TCATAGACAGCATCTACTTTGTC
MMP-14	GAACTTTGACACCGTGGCCAT	CAGAACCATCGCTCCTTGAAGACAAACATC	CCGTCCATCACTTGGTTATTCCT
TIMP-1	TCCTCTTGTTGCTATCATTGATAGCTT	TTCTGCAACTCGGACCTGGTTATAAGG	CGCTGGTATAAGGTGGTCTCGAT
TIMP-2	GCTGGACGTTGGAGGAAAGA	TCTCCTTCCGCCTTCCCTGCAATTAGA	GCACAATAAAGTCACAGAGGGTAAT



Online Figure I. Quantification of cardiomyocytes and fibroblasts during EHT culture by flow cytometry. Representative plots identify distinct a-actinin- (A) and vimentin-positive cell populations (B) at the indicated days of EHT culture. Panels resemble overlays of individual dot plots: in red cell pools labeled for actinin (A) or vimentin (B); in grey cell pools exposed to secondary antibody only.

## **Online Figure II**



**Online Figure II. DNA content in mononucleated cardiomyocytes and fibroblasts during EHT culture assessed by FACS. A**, Representative plots of DNA content in mononucleated cardiomyocytes (actinin-positive, red) and non-myocytes (actinin-negative, dark grey) at day 0 and day 12 of EHT culture. **B**, Fractions of mononucleated cardiomyocyte (top panel) and non-myocyte (lower panel) populations at day 0 (n=6) and day 12 (n=4) of EHT culture with 2N, 4N, and 8N DNA content.



**Online Figure III.** Surrogate parameters suggesting hypertrophic growth in EHTs. A, RNA/DNA ratio in EHTs on culture days 0 (n=18), 3 (n=19), 7 (n=10), and 12 (n=16). **B**, <sup>3</sup>H-phenylalanine incorporation during EHT culture days 0-3 (n=7), 3-7 (n=8), and 7-12 (n=5). \*P< 0.05 vs. EHT day 0 (**A**) and EHT days 0-3 (**B**); ANOVA and Bonferroni's multiple comparison test.

**Online Figure IV** 



**Online Figure IV**. **Cell death in EHT and monolayer (2D) culture. A**, Analysis of DNA content in EHT- and 2D culturederived cells (n=3 each). Sub-G1 fraction (green) denotes dead/apoptotic cells with condensed nuclei. **B**, Trypan-blue exclusion in EHT- and 2D culture-derived cells at culture day 1 (n=5 [EHT], n=4 [2D]). **C**, Comparison of CSQ2 transcript abundance The EHT- (black-bars) vs. 2D culture (white bars), n=5-6/time-point. \**P*<0.05 vs. day 0 (grey bar); ANOVA and Bonferroni's multiple comparison test.

**Online Figure V** 



**Online Figure V. Molecular markers of maturation in 2D vs. EHT culture. A**, ANP transcripts per GAPDH transcript; **B**, skeletal actin transcripts per GAPDH transcript in isolated neonatal heart cells at day 0 (black bars; n=5), 2D cultured cells at day 12 (blue bars; n=6), and EHT at day 12 (green bars; n=5). **D**, Correlation of cardiac and skeletal actin transcript abundance in freshly isolated neonatal heart cells (d0; black), in 2D culture (culture days 3,7, and 12 [left panel]) and EHT culture (culture days 3, 7, and 12 [middle panel]) - black arrows denote the trend in expression pattern change in 2D and EHT culture; right panel: direct comparison of 12 day 2D vs. EHT cultures and neonatal cardiomyocytes. \*P<0.05 2D vs. EHT; Student's t-test..

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**Online Figure VI. ECM restructuring during EHT-development. A**, matrix metalloprotease-2 (MMP-2; n=8-10); **B**, MMP-14 (n=7-10); tissue inhibitor of matrix metalloprotease-1 (**C**, TIMP-1; n=7-10), and TIMP-2 (**D**; n=7-10) transcripts per GAPDH transcript in EHT and native rat heart tissue. \**P*<0.05 vs. EHT day 0; ANOVA followed by Bonferroni's multiple comparison test.



**Online Figure VII. Development of a cardiomyocyte-specific qPCR assay to allow approximation of cardiomyocyte content in mixed cell populations.** Detection of CSQ2 (NCBI accession#: AF001334; squares) and GAPDH (NCBI accession#: NC005103; circles) transcripts in 2.5x10<sup>6</sup> cells containing the indicated cardiomyocyte fraction by qPCR. High Ct-values indicate low transcript abundance. Symbols indicate individual Ct-values. Bars indicate the respective means. A Ct-value difference of 3.3 ideally represents a 10-fold difference in transcript abundance. Similar data could be obtained using alternative primer-probe pairs for muscle specific CSQ2 (Ensemble accession#: ENSRNOG00000016243) or 18S-RNA (NCBI accession#: V01270).