Relationship between FoxO1 protein levels and follicular development, atresia, and luteinization in the rat ovary

F Shi and P S LaPolt

Department of Biological Sciences, California State University-Los Angeles, 5151 State University Drive, Los Angeles, California 90032, USA

(Requests for offprints should be addressed to P S LaPolt; Email: plapolt@exchange.calstatela.edu)

Abstract

FoxO1 is a transcription factor implicated in a growing number of physiological processes, including apoptosis, cell cycle progression, and insulin signaling. Recent findings indicate that FSH and growth factors influence ovarian functions in part through regulation of FoxO1. The present study utilized immunohistochemical analysis to determine the ovarian localization and regulation of FoxO1 protein levels in neonatal rats, immature rats during gonadotropin-induced follicular development, ovulation, and luteinization, and in spontaneously developing ovarian cysts of aging rats. In postnatal rats, FoxO1 immunoreactivity was very faint in ovaries of 5- and 10-day-old females. In contrast, strong immunoreactivity was observed in granulosa cells of larger developing follicles at 25 days of age. To stimulate follicle development, immature female rats received equine chorionic gonadotropin (eCG) followed 52 h later by an ovulatory dose of human chorionic gonadotropin (hCG). Prior to gonadotropin treatment, moderate FoxO1 immunoreactivity was observed in granulosa cells of small follicles. Subsequently, treatment with eCG markedly decreased FoxO1 protein levels in granulosa cells of healthy antral and preovulatory follicles. Interestingly, FoxO1 staining was observed in cumulus and antral, but not mural granulosa cells of preovulatory follicles. Induction of ovulation and luteinization with hCG further decreased ovarian FoxO1 levels, with no staining evident in corpora lutea. At all time points, the most intensive FoxO1 staining was observed in granulosa cells of atretic follicles, with predominantly nuclear localization. Similarly, while FoxO1 levels were low in granulosa cells of preovulatory follicles in proestrous rats, FoxO1 staining was intense in granulosa cells of spontaneously developing cystic follicles in aged, acyclic females. Together, these findings indicate that FoxO1 is expressed in a regulated, cell-specific manner during ovarian follicular development, atresia and luteinization, suggesting roles in these physiological processes.


Introduction

Ovarian functions are regulated by a number of hormones and autocrine/paracrine factors, acting through diverse signaling pathways. It is clear that the influences of gonadotropins on ovarian function are mediated, to a large part, through increased levels of the second messenger cAMP. While increased cAMP accumulation is known to activate protein kinase A (PKA)-dependent signaling, recent findings indicate that follicle-stimulating hormone (FSH)-stimulated cAMP may also activate protein kinase B (Akt/PKB) in a PKA-independent manner (Gonzalez-Robayna et al. 2000), thus expanding the potential mechanisms through which gonadotropins act on ovarian cells. Among the substrates phosphorylated by Akt/PKB is the forkhead transcription factor, forkhead box protein of the subclass O, member 1 (FoxO1, formerly referred to as FKHR; see Kaestner et al. 2000).

Forkhead transcription factors are implicated in a growing number of physiological processes, including apoptosis, cell cycle progression, and insulin signaling (Nakae et al. 1999, Tang et al. 1999, Nakamura et al. 2000, Alvarez et al. 2001). Phosphorylation of FoxO1 by Akt/PKB results in cytoplasmic, rather than nuclear localization, and inhibits function of this proapoptotic transcription factor, indicating post–translational regulation of FoxO1 activity (Nakae et al. 2000). Potential roles of FoxO1 in influencing ovarian functions are suggested by recent studies by Richards and colleagues (2002). Their findings indicate that FSH and insulin-like growth factor–I (IGF-I) both cause phosphorylation of FoxO1 in cultured granulosa cells (Richards et al. 2002). The ability of FSH and IGF-I to induce phosphorylation of FoxO1 is associated with translocation of protein from nucleus to cytoplasm, and suggests post–translational influences of these factors on as yet undefined activities of FoxO1 in the ovary.

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While phosphorylation represents one mechanism through which ovarian FoxO1 activity may be regulated, cell-specific expression and regulation of total FoxO1 protein levels also occurs in the ovary (Richards et al. 2002). Ovarian FoxO1 mRNA levels are regulated in a cell-specific manner, with FoxO1 mRNA levels increasing markedly during follicular development (Richards et al. 2002). These findings are perhaps surprising, given previous observations that indicate inhibitory effects of forkhead transcription factors on cell proliferation (Alvarez et al. 2001). However, it is not clear if the pattern of FoxO1 gene expression at the transcriptional level correlates well with FoxO1 protein levels, as no similar studies on FoxO1 protein localization have been reported. Furthermore, the relationship between FoxO1 protein levels and the onset of follicular atresia is not clear. Therefore, the present study utilized immunohistochemical methods to examine the cell-specific localization and regulation of FoxO1 protein levels during postnatal ovarian development, as well as gonadotropin-induced follicular development, ovulation, atresia and luteinization in immature female rats. In addition, we also compared ovarian FoxO1 localization in healthy preovulatory follicles of proestrous females to that in postnatal rat ovaries, and in cystic follicles of middle-aged acyclic, persistent estrous rats.

Materials and Methods

Animals

Intact, immature Sprague–Dawley rats (21 days old; Harlan Sprague–Dawley, Indianapolis, IN, USA) and young (4 months old) and middle-aged (9 months old) Long–Evans retired breeder females (Charles River Laboratories, Wilmington, MA, USA) were obtained from the commercial suppliers indicated. In addition, neonatal rats were obtained by mating of young Long–Evans males and females. Animals were maintained under a 16-h light, 8-h darkness schedule with food and water available ad libitum. Animals were treated in accordance with the NIH Guide for the Care and Use of Laboratory Animals. All protocols had the approval of the Institutional Animal Care and Use Committee, California State University, Los Angeles.

Immature rats received a subcutaneous injection of equine chorionic gonadotropin (eCG; 10 IU), followed 52 h later by an ovulatory dose (30 IU) of human chorionic gonadotropin (hCG). Ovaries were obtained at 0, 24 and 52 h after eCG, and at 4, 24 and 72 h after hCG. One ovary was fixed in 4% paraformaldehyde and processed for immunohistochemical analysis. The remaining ovary was snap-frozen and used for protein extraction and subsequent immunoblot analysis. Similarly, ovaries were collected from neonatal rats at 5, 10, and 25 days of age for immunohistochemical analysis (day of birth is day 1). Estrous cycle patterns were monitored in young and middle-aged Long–Evans female rats. Animals displaying at least 3 consecutive 4-day-long cycles were considered regularly cyclic, while those displaying at least 15 consecutive days of vaginal cornification were considered to be persistently estrous (PE). Ovaries were obtained at approximately 1000 h on the morning of proestrus (young regularly cyclic rats) and from acyclic PE females, fixed in 4% paraformaldehyde, and processed for immunohistochemical analyses of FoxO1 protein levels.

Immunohistochemistry

After fixation, ovaries were embedded in paraffin and 8 µm sections were cut and mounted on slides. The sections were then processed for immunohistochemical analysis using standard procedures (Shi et al. 2000). Sections were then incubated at 16 h at room temperature with a polyclonal sheep immunofluorescent purified antisera directed against the full length FoxO1 protein (0·5 µg/ml IgG; Upstate Cell Signaling Solutions, Waltham, MA, USA). Sections were then incubated in a biotinylated rabbit anti-sheep IgG secondary antibody (diluted 1:1000 in 10 mM sodium phosphate, pH 7·4 containing 0·9% saline and 1% BSA; Vector Labs, Inc, Burlingame, CA, USA), incubated at room temperature for 1 h. FoxO1 immunoreactivity was then visualized using the ABC Kit Elite (Vector Labs Inc., Burlingame, CA, USA) and 0·05% 3,3’-diaminobenzidine tetrachloride (DAB; Sigma Chemical Co., St Louis, MO, USA) in 10 mM PBS-buffered saline containing 0·01% H2O2, using a 5-min incubation. Specificity of the antibody was examined using normal sheep serum instead of primary antibody. To identify structural components and cell types within the ovary, the section was counter-stained with hematoxylin. Relative levels of immunostaining between groups and cell types were evaluated by two independent observers, with at least four ovaries examined per group/time point. Only samples processed at the same time were compared with one another. Results described represent consistently observed patterns of immunostaining.

Immunoblot analysis

Whole ovary protein from gonadotropin-treated rats was extracted using radioimmunoprecipitation (RIPA) lysis buffer (50 mM Tris–HCl, pH 8·0 containing 0·15 M NaCl, 0·5% nonidet P40, 20% glycerol, 25 mM benzamidine, 0·5 µg/ml leupeptin, 0·7 µg/ml pepstatin A, 10 µg/ml trypsin inhibitor and 2 µg/ml aprotinin) in a Dounce homogenizer. After homogenization, samples were incubated for 30 min on ice, vortexed, and centrifuged for 5 min at 14 000g. The supernatant was separated and protein concentration was determined by a modification of the Bradford method (Biorad Laboratories, Hercules, CA, USA) using BSA standards and microplate
absorbance readings at 595 nm. Determination of FoxO1 protein levels was performed by immunoblot analysis. Briefly, the proteins were resolved by 7.5% polyacrylamide SDS gel electrophoresis under reducing conditions. In each experiment, equal quantities of protein (20 µg) were loaded for each sample. Protein was then transferred electrophoretically from the gel onto nitrocellulose membranes. Filters were blocked with 5% milk in TBST (Tris buffered saline with 0.05% Tween 20), followed by washing and incubation with the polyclonal sheep immunofluorescence purified antiserum against FoxO1 (1:1000 dilution in TBST containing 1% BSA, incubated for 16 h at 4°C). Blots were then washed and incubated at room temperature for one hour with a 1:25 000 dilution of horseradish peroxidase-conjugated polyclonal rabbit anti-sheep IgG secondary antibody (Pierce Biotechnology, Rockford, IL, USA). After washing in TBST, membranes were incubated in a luminol/enhancer-stable peroxide substrate solution (Pierce Biotechnology) at room temperature for 5–15 min to allow chemiluminescent detection of signals, and blots were then used to expose X-ray film. Resulting autoradiograms were then digitally analyzed using a computerized image analysis system (ImagePC, Scion Corp, Frederick, MD, USA), and the results were subjected to one-way analysis of variance, followed by Tukey’s post-hoc test to determine which groups differed significantly. A confidence level of P<0.05 was considered statistically significant.

Results

FoxO1 immunoreactivity during postnatal ovarian follicle development and luteinization

To examine the relationship between postnatal follicular growth and FoxO1 expression, we collected ovaries from neonatal rats at 5, 10, and 25 days of age. Ovaries of five-day-old females contained only primordial follicles, while those of 10-day-old rats contained primordial, primary, and small secondary follicles (Fig. 1A and B respectively). In these early stages of follicular development, FoxO1 immunoreactivity in the ovary was very faint in granulosa cells. In contrast, by 25 days of age follicles had reached the small and medium antral stages (up to 460 µm in diameter; Fig. 1C) and exhibited high levels of FoxO1 staining in granulosa, but not thecal or stromal cells. Specificity of immunoreactivity was confirmed by the use of normal sheep serum (NSS) in place of primary antibody, which resulted in the absence of reaction product (see Fig. 2F).

FoxO1 immunoreactivity during ovarian follicle development, atresia, and luteinization in gonadotropin-primed immature rats

We next determined whether the levels of FoxO1 protein were regulated in granulosa cells during gonadotropin-induced follicular development, atresia and luteinization in immature rats. Prior to gonadotropin treatment, FoxO1 immunoreactivity was strong in the granulosa layer of healthy preantral, small antral, and large antral follicles (Figs 2A and 3A). Within the granulosa layer, however,
FoxO1 staining was heterogeneous, being low in the layer of granulosa cells immediately surrounding the oocyte, but high in the remaining granulosa cells (Fig. 3E). This heterogeneous pattern was consistently observed from preantral to small antral follicles (100–350 µm), but less evident in larger antral follicles. At 24 h after eCG, FoxO1 levels were decreased in granulosa cells of healthy large antral follicles (Fig. 3B). However, FoxO1 levels were minimal in larger antral follicles (Fig. 3B) and in preovulatory follicles 52 h after eCG (Fig. 3C). In addition, FoxO1 levels were very low in corpora lutea at 24 h (D) and 72 h (E) after receiving an ovulatory dose of hCG. In control experiments, no significant immunoreactivity was observed when normal sheep serum was used instead of primary antibody (F). Bar = 200 µm.

**Figure 2** Ovarian localization of FoxO1 protein levels during gonadotropin-induced follicular development, ovulation, and luteinization in immature female rats. FoxO1 immunoreactivity was low in theca cells but high in granulosa cells of small and medium antral follicles at 0 and 24 h after eCG (A and B respectively). However, FoxO1 levels were minimal in larger antral follicles (B, C) and in preovulatory follicles 52 h after eCG (C). In addition, FoxO1 levels were very low in corpora lutea at 24 h (D) and 72 h (E) after receiving an ovulatory dose of hCG. In control experiments, no significant immunoreactivity was observed when normal sheep serum was used instead of primary antibody (F). Bar = 200 µm.

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During gonadotropin-induced follicle development, strong FoxO1 immunoreactivity was consistently observed in granulosa cells of follicles undergoing atresia. In such follicles, the cellular localization of FoxO1 appeared to be primarily nuclear, obscuring hematoxylin-stained nuclei (Fig. 3F). In contrast, FoxO1 localization in granulosa cells of neighboring healthy follicles appeared to be primarily cytoplasmic, with clearly visible nuclei (Fig. 3F).
Immunoblot analysis of FoxO1 protein during ovarian follicle development and luteinization

Western blot analysis of FoxO1 protein levels was performed following gel fractionation of ovarian protein extracts obtained from immature female rats treated with eCG and hCG, as in Figs 2 and 3 above. Using the FoxO1 antiserum, a band with an apparent molecular mass of approximately 75 kDa was identified (Fig. 4), consistent with previous reports (Durham et al. 1999). Whole ovarian FoxO1 levels were readily detectable between 0 and 52 h of eCG treatment. Subsequently, whole ovarian FoxO1 protein levels decreased to very low levels by 24 and 72 h after hCG, indicating down-regulation of FoxO1 in the luteal ovary.

Autoradiograms were subjected to digital image analysis to provide a more quantitative evaluation of ovarian FoxO1 protein levels during gonadotropin treatments (Fig. 5). Relative levels of FoxO1 in whole ovarian homogenates were highest prior to and 24 h after eCG administration, and decreased significantly ($P<0.001$) by 52 h after eCG treatment. A further decline ($P<0.001$) in FoxO1 levels was evident at 24 h after administration of hCG, with these lower levels persisting at 72 h after hCG.

Figure 3 Higher magnification views of FoxO1 immunoreactivity in developing follicles and corpora lutea of gonadotropin-treated immature rats. Prior to eCG treatment, FoxO1 protein levels were high in small, medium, and large developing follicles (A). However, 24 h after eCG, FoxO1 staining remained high in smaller follicles, but was decreased in larger follicles (B). At 52 h after eCG, FoxO1 immunoreactivity in preovulatory follicles was limited to cumulus cells and the most antral layer of granulosa (C). At 72 h after an ovulatory dose of hCG, FoxO1 staining was absent in corpora lutea, but strong in follicles undergoing atresia (D). In small developing follicles, the granulosa layer nearest the oocyte was typically devoid of FoxO1 staining (E). While FoxO1 localization in granulosa cells of healthy developing follicles (h) was primarily cytoplasmic, that in atretic follicles (a) was primarily nuclear (F). Bar=50 μm.
FoxO1 levels in preovulatory follicles versus cystic follicles of middle-aged female rats

The high levels of FoxO1 expression in atretic follicles in ovaries of immature rats is consistent with the proapoptotic function of this transcription factor. To further examine the relationship between FoxO1 levels and cell survival, we performed immunohistochemical comparisons of FoxO1 immunoreactivity in healthy preovulatory follicles of young proestrous rats versus developing and established cystic follicles of middle-aged acyclic, PE rats respectively. FoxO1 levels were low in granulosa cells of healthy preovulatory follicles (900 µm in diameter) of cyclic rats, with immunoreactivity limited to cumulus and antral granulosa cells (Fig. 6A). In PE ovaries, however, developing cystic follicles undergoing atresia exhibited high levels of FoxO1 in the entire granulosa layer (Fig. 6B,C;
In fully formed cystic follicles, the granulosa layer was thin or non-existent, and subsequently little FoxO1 immunoreactivity was observed (Fig. 6B; follicle labeled C). Small numbers of preovulatory-like follicles could be observed in PE rats, with patterns of FoxO1 expression (limited to cumulus and antral granulosa cells) similar to that in preovulatory follicles of immature gonadotropin-treated and young cyclic females (Fig. 6C; follicle labeled POL).

**Discussion**

Findings from the present study demonstrate the regulated, cell-specific localization of FoxO1 protein in the ovaries of neonatal, immature gonadotropin-treated, and adult rats. While much attention has focused on the role of Akt/PKB in post-translational regulation of forkhead transcription factor activities, the present studies and others (Richards et al. 2002) demonstrate that ovarian FoxO1 expression is regulated in a highly cell-specific manner. The presence of FoxO1 immunostaining in granulosa, but not stromal, thecal, or healthy luteal cells is consistent with previous findings on FoxO1 message levels (Richards et al. 2002). While the exact roles of this transcription factor in the ovary are not known, the highly regulated pattern of localization likely reflects important actions of FoxO1 on ovarian functions such as follicle growth, differentiation, and/or atresia, and may indicate influences on and/or regulation by the oocyte. Furthermore, data from the present study reveal additional complexity in the regulation of FoxO1 expression, in that there is apparently a high degree of translational and/or post-translational control of protein levels.

The differential pattern of FoxO1 expression in different ovarian cells may provide insight into the functional role(s) of FoxO1 in granulosa cells. In nongonadal cells, it is clear that FoxO1 is a proapoptotic transcription factor (Tang et al. 1999, Nakamura et al. 2000). The high level of FoxO1 we observed in apoptotic granulosa cells but not theca cells of atretic follicles and developing cysts may coincide and contribute to observed differences in the onset and mechanisms controlling apoptosis in these cell types (Tilly et al. 1992, Palumbo & Yeh 1994, Porter et al. 2001). Significantly, while the subcellular distribution of FoxO1 protein in healthy granulosa cells was primarily cytoplasmic, that in granulosa cells of atretic follicles was predominantly nuclear (see Fig. 3F). This nuclear staining corresponds to the functional localization of FoxO1 as a proapoptotic transcription factor (Nakae et al. 2000), indicating a causal relationship between follicular atresia and increased nuclear FoxO1 protein levels. The decreased levels of FoxO1 in the luteal ovary observed by immunohistochemistry and immunoblot analyses are consistent with a previous report on FoxO1 message (Richards et al. 2002). Since the present study did not include analysis of regressing corpora lutea, it is not known whether levels of FoxO1, or other forkhead transcription factors (such as FoxO3a and FoxO4) increase in luteal cells during luteal demise.

The presence of FoxO1 in granulosa cells of small antral follicles, but not in those in large follicles, theca cells or luteal cells, may also reflect the functionally undifferentiated state of granulosa cells in small follicles, suggesting that FoxO1 is down-regulated during gonadotropin-induced cell maturation. Consistent with this hypothesis, both FSH and IGF-I, factors that augment granulosa cell differentiation, act post-translationally to phosphorylate FoxO1 (Richards et al. 2002), resulting in cytoplasmic localization and, presumably, loss of transcriptional activity. Together, the decrease in protein content and post-translational inhibition of protein activity induced by FSH suggest that decreased FoxO1 activity is an important step in gonadotropin-induced granulosa cell differentiation. However, in stark contrast, FoxO1 mRNA and protein levels are induced by cAMP analogs in human endometrial stromal cells, and FoxO1 interacts with the CCAAT/enhancer-binding protein beta to facilitate protein kinase A-dependent gene expression during differentiation (Christian et al. 2002). In these endometrial cells, treatment with cAMP results in nuclear, rather than cytoplasmic localization of FoxO1 (Christian et al. 2002). It is thus clear that regulation of FoxO1 expression and action is complex, and highly tissue-specific. Further studies are required to elucidate any role of FoxO1 in the modulation of ovarian cell differentiation.

The dynamic regulation of FoxO1 in granulosa cells during follicular development may further suggest roles of this transcription factor in the regulation of granulosa cell proliferation. During initial stages of gonadotropin-independent growth, granulosa cells of small preantral follicles exhibit low levels of FoxO1, as is evident in early postnatal ovaries (Fig. 1A,B). However, FoxO1 immunoreactivity is higher in granulosa cells of larger preantral and small antral follicles, containing oocytes of increased size, at 25 days of age, prior to treatment with eCG (Fig. 1C; note change in scale). Interestingly, treatment with gonadotropin to stimulate further follicular growth resulted in a marked down-regulation of granulosa FoxO1 levels. In this regard, forkhead transcription factors reportedly inhibit cell cycle progression, via increased levels of the cell-cycle inhibitor p27 kip1 (Medema et al. 2000) and down-regulation of cyclin B (Alvarez et al. 2001). In this regard, cyclin B and p27 kip1 have been implicated in the hormonal regulation of granulosa cell proliferation (Chaffin et al. 2001). Surprisingly, the down-regulation of FoxO1 protein content that we observed in developing follicles is not accompanied by a decline in follicular FoxO1 mRNA levels (Richards et al. 2002). This indicates that the regulation of FoxO1 protein levels during follicular development is mediated not only by transcriptional regulation of mRNA levels, but also by translational and/or post-translational mechanisms.
The regulation of FoxO1 protein levels differed markedly within the granulosa layer at various stages of development. In preantral and small antral follicles, FoxO1 was expressed throughout the granulosa compartment, with the distinct exception of the single layer of granulosa cells immediately surrounding the oocyte (see Fig. 3E). In contrast, in larger developing and preovulatory follicles, the granulosa layer was devoid of FoxO1 immunoreactivity, with the exception of the cumulus and most of the antral granulosa layer (Fig. 3C). The functional significance of this heterogeneous distribution of FoxO1 protein within the granulosa compartment is not clear. It is well recognized, however, that the oocyte produces factors that influence gene expression in neighboring granulosa cells (Elvin et al. 1999, Joyce et al. 1999, 2001), providing a basis for observed differences between mural and cumulus cell expression. However, a potential basis for differences in FoxO1 expression between mural and the most antral layer of granulosa cells is less apparent. Further studies are clearly required to understand the heterogeneous pattern of FoxO1 expression observed within the granulosa layer.

While FoxO1 expression is decreased in the granulosa layer of healthy preovulatory follicles, the absence of an ovulatory gonadotropin surge in acyclic middle-aged PE rats results in the formation of follicular cysts. PE females display follicular growth, but preovulatory follicles fail to ovulate due to impaired neuroendocrine control of luteinizing hormone secretion (Anzalone et al. 1998, Chern et al. 2000, LaPolt & Lu 2001). Thus, as observed in this study, ovaries of PE rats may contain healthy Graafian (or preovulatory-like) follicles (Fig. 6C). However, these fail to ovulate due to the absence of normal neuroendocrine function, resulting in the formation and accumulation of follicular cysts with degenerating granulosa layers. Healthy preovulatory-like follicles of PE females exhibited the same pattern of low FoxO1 expression in the granulosa layer as preovulatory follicles in immature gonadotropin–treated (Fig. 2C) and young proestrous rats (Fig. 6A). However, FoxO1 immunoreactivity was increased in the granulosa layer of unovulated follicles developing into cysts, presumably reflecting the reported role of FoxO1 in the induction of apoptosis (Datta et al. 1999, Tang et al. 1999, Nakae et al. 2000, Burgering & Kops 2002). As cyst development progressed, the granulosa layer became thin or nonexistent, and FoxO1 immunoreactivity was lower than that in developing cysts. These temporal changes in FoxO1 protein levels strengthen the proposed role of FoxO1 as a mediator of apoptosis in granulosa cells. Furthermore, the dynamic regulation of granulosa cell FoxO1 levels as follicles progress from small antral (high, primarily cytoplasmic FoxO1 levels) to healthy preovulatory follicles (FoxO1 immunoreactivity restricted to cumulus and antral granulosa cells) to an atretic, cystic state (high, primarily nuclear staining) likely reflects multiple functions and complex regulation of this forkhead transcription factor in the ovary.

Future studies are required to reveal the molecular mechanisms regulating FoxO1 protein levels and activity, and the various influences of FoxO1 on ovarian function.

**Funding**

This work was supported by the National Institutes of Health MBRS SCORE Program grant GM08110 (to P S L).

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Regulation of ovarian FoxO1 protein levels · F Shi and P S Lapolt


Received 29 May 2003
Accepted 23 July 2003