SUPPLEMENTAL DATA – GFP-PSMA1 PIG

EMBRYO TRANSFER OUTCOMES

Six embryo transfers were performed, transferring 881 embryos. Eight piglets were recovered at C-Section (six breathed). Five of the eight did not express and one healthy expressing male founder was identified.

<u>#</u>	<u>Day of</u>	
Transferred	Surrogate	<u>Status</u>
214	1	Cycled day 20
142	1	Cycled day 28
140	0	Delivered 5 (4 live) pigs 6/7/10 - none expressed
140	1	Delivered 2 piglets 6/14/10 - one never breathed
120	0	Cycled day 25
		2 piglets delivered 6/29/10 - one never breathed
125	0	and the other died on day 3
	# <u>Transferred</u> 214 142 140 140 120 125	

*Surviving piglet expressed the transgene.

TRANSGENIC OFFSPRING SEMEN ANALYSIS AND IVF

The sperm concentration of GFP offspring was significantly lower than wild type boar (0.4 *vs.* 1.5×10^9 spermatozoa/ml, p<0.05). Also the semen of GFP offspring showed high agglutination (head to head binding; **Suppl. Table 1**). Collected semen was diluted with X-Cell extender and sperm motility was measured during storage. The semen of GFP offspring showed 60-75% motility during storage, and the motility was significantly reduced on day 3 compared to the control wild type boar (87.5%, p<0.05; **Suppl. Table 2**).

There was no significant difference in monospermic fertilization between GFP offspring and wild type boar, however, the percentage of polyspermy was dramatically different (0.0% in GFP offspring *vs.* 63.9% in wild type boar, p<0.05; **Suppl. Table 3**). The percentage of cleaving embryos was significantly higher in wild type boar (68.8%) than in the GFP offspring (33.5%, p<0.05), but there was no significant difference in blastocyst formation rate (3.9% in GFP offspring vs. 3.4% in wild type boar). Additionally, mean cell number per blastocyst was higher in GFP offspring than in that of wild type boar (31.5 vs. 18.5; p<0.05; **Suppl. Table 4**). The expression of GFP was first detected in late 2 cell embryos and increased from 4-cell to blastocyst (56.0%; see **Fig. 3 B** in manuscript). We concluded that the male of GFP offspring was fertile *in vitro*.

Supplemental Table 1: Comparison of semen characteristics between GFP offspring and wild type boars

Boar	Breed	Boar No.	Collected semen volume (ml)	Sperm concentration (x10 ⁹ /ml)	% motile spermatozoa	Notes
GFP offspring	Minnesota mini	G137	117.5±7.5 ^a	0.4±0.1 ^b	75±5.0	High agglutinations
Wild type	Duroc	89-10	50±0.0 ^b	1.5±0.1 ^a	90±5.0	None

FOOTNOTES:

- Semen was collected twice from each boar.
- Mean±SEM for 2 ejaculates from each boar are shown.
- ^{a,b} Means in the same column with different superscripts differ significantly (p<0.05).

Supplemental Table 2: Comparison of sperm motility (%) during storage

Boar	Storage period (day)							
	1	2	3	4				
GFP offspring	75±5.0	75±5.0	65 ± 5.0^{b}	60±5.0				
Wild type	92.5±2.5	92.5±2.5	87.5±2.5 ^a	87.5±2.5				

FOOTNOTES:

- Boar semen was collected twice from each boar, diluted with X-Cell extender and stored at room temperature; sperm motility was assessed under stereomicroscope at 37.5°C.
- Mean±SEM for 2 ejaculates from each boar.
- ^{a,b} Means in the same column with different superscripts differ significantly (p<0.05).

Boar	No. oocyte inseminated	% monospermic oocyte	% polyspermic oocyte	% total fertilization
GFP offspring	49	22.3±6.5	$0.0{\pm}0.0^{ m b}$	22.3±6.5 ^b
Wild type	51	32.6±7.5	63.9±9.7 ^a	96.5±3.6 ^a

Supplemental Table 3: Comparison of fertilization parameters on porcine IVF

FOOTNOTES:

- Experiment was repeated four times, and data indicate Mean±SEM.
- a,b Means in the same column with different superscripts differ significantly (p<0.05).

Supplemental Table 4: Comparison of embryo development after IVF

Boar	No. oocytes inseminated	% cleaving oocytes	% blastocyst	Mean cell no. per blastocyst	% GFP expression from embryos
GFP offspring	56	33.5±3.7 ^b	3.9±2.2	31.5±10.5	56.0±9.7
Wild type	55	68.8±8.1 ^a	3.4±2.0	18.5±1.5	None

FOOTNOTES:

- Experiment was repeated four times, and data indicate Mean±SEM.
- a,b Means in the same column with different superscripts differ significantly (p<0.05).

METHODOLGY FOR SEMEN COLLECTION, IVM, IVF, IMMUNOLFUORESCENCE AND WESTERN BLOTTING

Semen collection and processing

Ejaculates from wild type boar and the *PSMA1-GFP* transgenic Minnesota Mini boars were collected under the guidance of approved Animal Care and Use (ACUC) protocols of the University of Missouri, Columbia (UM). The wild-type boar was placed on a routine weekly collection while the transgenic boars were collected less frequently, as needed. Sperm-rich

fractions of the ejaculates with greater than 85% sperm motility and normal sperm acrosomes were used. Sperm concentrations were estimated using a hemacytometer (Fisher Scientific, Houston, TX, USA). The percentage of motile sperm was estimated at 38.5°C by light microscope at 250 x magnification. Semen was slowly cooled to room temperature (20°C) within 2 hrs after collection. Semen was then transferred into 15 ml tubes, centrifuged at room temperature for 10 min at 800 x g, and the supernatant was removed. The spermatozoa were processed according to each experiment's requirements and stored at -80°C. In order to use the semen for *in vitro* fertilization (IVF), the semen was diluted with X-Cell Extender (Cat. #USA851X, IMV Technologies, Maple Grove, MN; final concentration of 1×10^8 spermatozoa/ml). The diluted semen was stored in a styrofoam box at room temperature for 5 days. Unless otherwise noted, all chemicals used in this study were purchased from Sigma Chemical Co. (St. Louis, MO).

Collection and In Vitro Maturation (IVM) of Porcine Oocyte

Ovaries were collected from prepubertal gilts at a local slaughterhouse and transported to the laboratory in a warm box (25-30°C). Cumulus-oocyte complexes (COCs) were aspirated from antral follicles (3-6 mm in diameter), washed three times in HEPES-buffered Tyrode lactate (TL-HEPES-PVA) medium containing 0.01% (w/v) polyvinyl alcohol (PVA), then washed three times with the maturation medium [1]. Each time, a total of 50 COCs were transferred to 500 μ l of the maturation medium that had been covered with mineral oil in a 4-well multidish (Nunc, Roskilde, Denmark) and equilibrated at 38.5°C, with 5% CO₂ in air. The medium used for oocyte maturation was tissue culture medium (TCM) 199 (Gibco, Grand Island, NY) supplemented with 0.1% PVA, 3.05 mM D-glucose, 0.91 mM sodium pyruvate, 0.57 mM cysteine, 0.5 μ g/ml LH (L5269, Sigma), 0.5 μ g/ml FSH (F2293, Sigma), 10 ng/ml epidermal growth factor (E4127, Sigma), 10% porcine follicular fluid, 75 μ g/ml penicillin G, and 50 μ g/ml streptomycin. After 22 h of culture, the oocytes were washed twice and cultured in TCM199 without LH and FSH for 22 h at 38.5°C, 5% CO₂ in air.

In Vitro Fertilization (IVF) and Culture (IVC) of Porcine Oocytes

After IVM, cumulus cells were removed with 0.1% hyaluronidase in TL-HEPES-PVA medium and ova were washed three times with TL-HEPES-PVA medium and three times with Trisbuffered (mTBM) medium [1] containing 0.2% BSA (A7888, Sigma). Thereafter, 20 oocytes were placed into each of four 100 µl drops of the mTBM medium, which had been covered with mineral oil in a 35 mm polystyrene culture dish. The dishes were allowed to equilibrate in the incubator for 30 min until spermatozoa were added for fertilization. One ml liquid semen preserved in X-Cell Extender was washed twice in PBS containing 0.1% PVA (PBS-PVA) at $800 \times g$ for 5 min, respectively. At the end of the washing procedure, the spermatozoa were resuspended in mTBM medium. After appropriate dilution, 1 µl of this sperm suspension was added to the medium that contained oocytes to give a final sperm concentration of 5×10^5 sperm/ml. Oocytes were co-incubated with spermatozoa for 6 hrs at 38.5° C, 5% CO₂ in air. At 6 hrs after IVF, oocytes were transferred into 500 µl PZM-3 medium [2] containing 0.4% BSA (A6003, Sigma) for further culture during 16-19 hrs or 144 hrs.

Evaluation of Oocyte Fertilization and Embryo Culture

Semen collection, in vitro oocyte maturation and in vitro fertilization were performed using standard methods described in Supplemental Data File. For evaluation of fertilization, oocytes/zygotes or embryos were fixed with 2% formaldehyde for 40 min at room temperature, washed with PBS three times, permeabilized with PBS-TX for 40 min at room temperature, and stained with 2.5 µg/ml DAPI (Molecular Probes, Eugene, OR) for 40 min. Sperm penetration and fertilization status of the zygotes (unfertilized, fertilized-monospermic or fertilizedpolyspermic) or the number of nuclei in embryos/blastocyst were assessed under epifluorescence microscope. Image acquisition was performed on a Nikon Eclipse 800 microscope (Nikon Instruments Inc., Melville, NY) with Cool Snap camera (Roper Scientific, Tucson, AZ) and MetaMorph software (Universal Imaging Corp., Downington, PA). The same imaging system was used for the analysis of tissue fragments collected from stillborn transgenic siblings of the founder boar; microscopic tissue fragments were whole-mounted on ceroscopy slides in TL-HEPES medium with 10% PVP and directly imaged under epifluorescence illumination at the excitation wave length corresponding to peak excitation wavelength of GFP. To assure that the resultant signals were not due to autofluorescence, control acquisitions were also made in the UV and red excitation & emission bands. None of the GFP-patterns described in this study were observed in tissues of non-transgenic offspring.

Immunofluorescence of Boar Spermatozoa

Spermatozoa were affixed to poly-lysine treated microscopy coverslips and fixed in 2% formaldehyde, washed, permeablized in PBS with 0.1% Triton-X-100 (PBS-TX) and and blocked in PBS-TX containing 5% normal goat serum. Spermatozoa were incubated with mouse monoclonal antibody raised against the green fluorescent protein (GFP) from the jellyfish *Aequorea victoria* (1:100 dilution, cat #33-2600; Zymed Laboratories Inc., South San Francisco, CA, USA) overnight. Then they were incubated in PBS-TX containing 1% normal goat serum with goat-anti-mouse (GAM)-IgG-FITC (1:100 dilution; Zymed – Invitrogen) and DAPI (1:100; Molecular Probes - Invitrogen) for 40 min. Image acquisition was performed as described for oocytes.

Western blotting

Sperm were washed in protein-free PBS and sperm concentration was determined using a hemocytometer so that approximately 1 x 10^9 spermatozoa/ml were loaded per lane after extraction. Spermatozoa were washed again in PBS and boiled for 5 min with loading buffer (50 mM Tris (pH 6.8), 150 mM NaCl, 2% SDS, 20% glycerol, 5% β -mercaptoethanol, 0.02% bromophenol blue). Gel electrophoresis of 10 μ l total protein/lane was performed on 4-20% gradient gels (PAGEr Gels, Lonza, Rockland, ME), followed by protein transfer to PVDF

membranes (Immobilon P, Millipore Corp., Billerica, MA) using an Owl wet transfer system (Fisher Scientific, Houston, TX) at a constant 50 V for 4 hrs. The membranes were sequentially incubated with 10% non-fat milk for 1 hr and with one of the following antibodies: mouse monoclonal anti-GFP antibody (1:2000 dilution, cat. # 33-2600; Zymed - Invitrogen), mouse monoclonal anti-GFP antibody (1:2000 dilution, cat. #A11120; Invitrogen), mouse monoclonal anti-PSMA1/α-6 proteasome subunit (1:2000 dilution, cat. #PW9390; Enzo), mouse monoclonal anti-proteasome 20S core subunits alpha-type 1,2,3,5,6, & 7 (1:2,000 dilution, cat. #PW8195; Enzo), mouse monoclonal anti-proteasome 20S core antibodies (1:2,000 dilution, cat. #PW8155; Enzo), or mouse monoclonal anti-MFGE8 antibody (1:1,000 dilution, cat. #D199-3; MBL) overnight. The membranes were washed and incubated with an appropriate species-specific secondary antibody such as the HRP-conjugated goat-anti-mouse (GAM-IgG-HRP), HRP-goatanti-rabbit IgG or goat-anti-Armenian hamster IgG-HRP antibodies (1:10,000 dilution; used to detect anti-MFGE8 antibody) for 1 hr at room temperature in 1% nonfat dry milk in TBS/Tween. The membranes were washed and reacted with 1.5 mL of chemiluminescent substrate (Illuminata Crescendo, Millipore Corp., Billerica, MA) for 5 min prior to being exposed to Kodak BioMax Light film (Kodak, Rochester, NY, USA).

Immunoprecipitation and MALDI-TOF Mass Spectroscopy

Boar sperm extracts were immunoprecipitated with the anti-GFP antibody (catalog no. A11120; Invitrogen) by using the Seize X Protein G Immunoprecipitation Kit (Pierce), separated on 4-20% gradient gels (PAGEr Gels; Lonza) and stained with Coomassie blue. The immunoprecipitated bands were excised carefully from the Coomassie blue-stained gel, destained, reduced with DTT, alkylated with iodoacetamide, and then trypsinized overnight. The digest solutions were recovered from the gel pieces and transferred to Axygen MAXYMum Recovery microtubes. The gel pieces were extracted further, pooled, and lyophilized dry. The dried digests were reconstituted and analyzed by Nano-LCNanospray quadrupole time-of-flight MS plus MS/MS on an Agilent 6520A mass spectrometer. The "MS plus MS/MS" data were analyzed with the "Find Compounds by Auto MS/MS" program in the Agilent Mass Hunter software (version B.04.00) suite. The MALDI-TOF MS spectra peak lists were obtained for the spectra after internal recalibration using trypsin autolysis fragment masses, computer baseline correction, noise removal, and peak de-isotoping. The threshold for generating peak lists was set to 2% of the maximum observed peak area. Data were exported in the Mascot Generic Format (.mgf) for submission to an in-house copy of Matrix Science's Mascot program (www.matrixscience.com). Database searches were performed against the NCBInr Mammalian protein databases (last updated September 19, 2011) and were adjusted for trypsin digestion with no missed cleavage, fixed modification by carbamidomethylation, and variable modification by methionine oxidation. Mowse and Mascott ion scores were used to identify highly probable matches with known amino acid sequences.

Statistical Analysis

Analyses of variance were carried out using the Statistical Analysis Software package in a completely randomized design. Duncan's multiple range test was used to compare values of individual treatment when the F-value was significant (P < 0.05).



Supplemental Figure 1. Histological and immunocytochemical analysis of the gonads and testicular germ cells of the founder PSMA1-GFP boar. (A, B) Histology of adult transgenic male gonads reveals normal testicular (A) and epididymal (B) tissue architecture, normal spermatogenesis in the testis (A) and abundant spermatozoa within the epididymal tubule lumen (B). (C) Live cell imaging of PSMA1-GFP fluorescence in the germ cells of founder boar. Green fluorescence is visible in the nuclei of round spermatids (i), at the base of the nucleus, probably the chromatoid body or the site of flagellum biogenesis (arrows) in the early step elongating spermatids (ii), in the caudal manchette (arrows) of elongated spermatids (iii), and in the cytoplasmic droplets (arrows) of fully differentiated spermatozoa (iv). Green color channel was

contrast-enhanced due to its low intensity. (**D**) Amplification of PSMA1-GFP1 fluorescence by anti-GFP antibody in the fixed, permeabilized testicular cells of the founder boar. Fluorescence is concentrated in the chromatoid bodies (arrows) of secondary spermatocytes (i), in the nuclei (arrows) of round spermatids, in the subacrosomal/inner acrosomal membrane layer (arrows) of an early step elongating spermatid (iii), in the caudal manchette (iii) of the elongated spermatids (iv), and in the acrosomal cap (arrowhead) and cytoplasmic droplet (arrow) of a fully differentiated testicular spermatozoon. The localization of PSMA1-GFP in panels C and D corroborates previous reports of proteasomal subunit localization in the hotspots of spermatid protein recycling such as the nucleus, redundant nuclear envelopes, caudal manchette, acrosomal cap and cytoplasmic droplet [3-6]. Localization of a proteasomal subunit to the chromatoid body is reported for the first time.



Supplemental Figure 2. Comparisons of proteasomal-proteolytic activities in spermatozoa of PSMA1-GFP offspring (GFP) and wild type boars (WT). Proteasomal proteolytic and deubiquitinating activities were measured using specific fluorometric substrates Z-LLE-AMC, Z-LLVY-AMC, and ubiquitin-AMC, respectively. The relative emitted fluorescence (no units) was measured at multiple time points to follow the kinetics of the reaction (ex: 380 nm, em: 460 nm). Experiments were repeated six times (with two different WT boars as a control). Values are expressed as the mean of fluorescence intensity±SEM.

<u>Methodology</u>: Proteasomal-proteolytic activity of boar spermatozoa was measured by a standard fluorometric proteasomal substrate assay as described [7]. Spermatozoa preserved in X-cell Extender were loaded onto a 96-well black plate (final sperm con. $1x10^6$ spermatozoa/ml), and incubated at 37.5°C with Z-LLE-AMC (a specific substrate for 20S chymotrypsin-like peptidyl-glutamylpeptide hydrolyzing [PGPH] activity, final conc. 100 µM; Enzo Life Sciences, Plymouth, PA), Z-LLVY-AMC (a specific substrate for 20S proteasome other chymotrypsin-like proteases and calpains; final con. 100 µM; Enzo), or ubiquitin-AMC (a specific substrate for deubiquitinylating activity; final conc. 300 nM; Enzo). The emitted fluorescence (no units) was measured every 10 min for a period of 1 hr, yielding a curve of relative fluorescence (excitation: 355 nm, emission: 460, Thermo Fluoroskan, ThermoFisher Scientific).

Supplemental Table 5 A: Proteasomal Subunits and Putative Proteasome-Interacting Proteins Co-immunoprecipitated with Anti-GFP-Antibody

Protein annotation	<u>NCBI gi #</u>	<u>Score</u>	<u>%</u> Coverage	$\frac{MW}{(kDa)}$
			Coverage	<u>(KDu)</u>
A- PROTEASOMAL SUBUN	ITS			
Proteasome subunit alpha type-1 like	311248177	440	41	29.5
Proteasome subunit alpha type-3 isoform 1	194034201	985	39	28.4
Proteasome subunit alpha type-3 isoform 2	194034199	985	40	27.6
Proteasome subunit alpha type-4	347300165	1171	59	29.5
Proteasome subunit alpha type-4 isoform 1	347300165	669	64	29.5
Proteasome subunit alpha type-5	222136590	654	55	26.4
Proteasome subunit alpha type-6	8394076	1092	41	27.4
Proteasome subunit alpha type-7-like isoform 1	311259068	601	65	27.9
Proteasome (prosome, macropain) subunit, alpha type (alpha 7)	343887360	467	58	27.8
Proteasome subunit beta type-2 isoform 1	4506195	638	61	22.8
Proteasome subunit beta type-2 isoform 2	315139006	638	69	20.2
Proteasome subunit beta type-5	335292522	2006	59	30.1
Proteasome subunit beta type-6	344259274	566	61	25.4
Full-proteasome subunit beta type-7	194034199	275	39	30
Chain H, Crystal Structure of the Mammalian 20s Proteasome at 2.75 A	21465649	607	65	21.9
Resolution (Proteasome subunit beta type-6)				
B-OTHER SPERM PROTE	INS			
Spermadhesins & Acrosome Associated Proteins				
Spermadhesin AWN	66990208	761	74	16.9
Major Seminal Plasma Glycoprotein PSP-I precursor	47523176	275	46	14.5
Seminal Plasma Sperm Motility Inhibitor	72535165	419	69	15
Seminal Plasma Protein pB1 precursor	47523184	178	43	15.4
Acrosin-binding protein (degradation product)	75052483	940	26	60.5
Seminal Plasma Acrosin Inhibitor A1	123986	177	67	7.6
Disintegrin/ADAM-Family Proteins				
Disintegrin and metalloproteinase domain-containing protein 5	323276507	443	23	45.1
Disintegrin and metalloproteinase domain-containing protein 20-like	311261282	322	26	82.5
Other Sperm Proteins & GFP				
Lactadherin	172072653	1264	49	47.8
Enhanced Green Fluorescent Protein	13194618	713	42	27
Ropporin-1-like	301783203	404	33	23.9

Supplemental Table 5 B: Immunoprecipitation & MS/MS Identification of Proteasome Interacting Sperm Proteins. Identified peptides are shown in red.

Proteasomal Subunits:

Protein	NCBI gi #	<u>gi # Score</u>		<u>% Coverage</u>		<u>MW (kDa)</u>
Proteasome subunit	311248177	440		41		29.5
alpha type-1 like						
1 mfr nq	ydndv tvwspqgrih	qieyameavk	qgsat	vglks	kthavlvalk	raqselaahq
61 k kilh	vdnhi gisiagltad	l arllcnfmrq d	eclds	r fvfd	rplpvsrlvs	ligsk tqipt
121 qrygr	rpygv glliagyddm	gphifqtcps	anyfd	lcrams	igarsqsart	yler hmsefm
181 ecnln	elvk h glralr etlp	aeqdlttknv	sigiv	gk dle	ftiyddddvs	pflegleerp
241 qrkaq	paqpa depaekadep	meh				
D	104024201	005			20	20 4

alpha type-3 i	soform	19	94034201	985			39	28.4	
1	mssig	tgydl	sastfspdgr	vfqveyamka	vensst	taigi	rckdgvvfgv	ek lvlsklye	
61	egsnk	rlfnv	dr hvgmavag	lladar slad	iareea	asnfr	snfgyniplk	hladrvamyv	
121	haytl	ysavr	pfgcsfmlgs	ysvndgaqly	midpso	gvsyg	ywgcaigkar	qaakteiekl	
181	qmkem	tcrdv	vkevak iiyi	vhdevkdkaf	elelsv	wvgei	tk grheivpk	direeaekya	
241	keslk	eedes	dddnm						

Proteasome s	ubunit	19	94034199	985		40		27.6
alpha type-3 i	soform							
2								
1	mssig	tgydl	sastfspdgr	vfqveyamka	venssta	igi rckdg	vvfgv	ek lvlsklye
61	egsnk	rlfnv	dr hvgmavag	lladar slad	iareeas	nfr snfgy	niplk	hladrvamyv
121	haytl	ysavr	pfgcsvndga	qlymidpsgv	sygywgca	aig karqa	aktei	eklqmkemtc
181	rdvvk	evak <mark>i</mark>	iyivhdevkd	kafelelswv	geitkgrh	nei vpkdi	reeae	kyakeslkee
241	desdd	dnm						

Proteasome s	ubunit	34	7300165	1171		59		29.5
alpha type	alpha type-4							
1	msrry	dsr tt	<pre>ifspegrlyq</pre>	veyameaigh	agtclg	ilan dgv	/llaaerr	nihk lldevf
61	fseki	yk lne	dmacsvagit	sdanvltnel	r liaqr	yllq yqe	pipceql	vtalcdik qa
121	ytqfg	gk rpf	gvsllyigwd	khygfqlyqs	dpsgny	ggwk ato	cignnsaa	avsmlkqdyk
181	egemt	lksal	alaik vlnkt	mdvsk lsaek	veiatl	tr en gkt	zvirvlk <mark>q</mark>	keveqlikk h
241	eeeea	kaere	kkekeqkekd	k				

Proteasome subunit alpha type-4 isoform 1	347300165	669		64	29.5
1 msrry	dsrtt ifspegr ly	y veyameaigh	agtclgilan	dgvllaaer r	nihk lldevf
61 fsek i	yk lne dmacsvagit	sdanvltnel	r liaqr yllq	yqepipceql	vtalcdik qa
121 ytqfg	gk rpf gvsllyigw	l khygfqlyqs	dpsgnyggwk	atcignnsaa	avsmlkqdyk
181 egemt	lksal alaik vlnkt	mdvsk lsaek	veiatltr en	gktvirvlkq	keveqlikkh
241 eeeea	kaere kkekeqkeko	l k			

Proteasome su	easome subunit 22		2136590	654		55		26.4
alpha type	alpha type-5							
1	mfltr	seydr	gvntfspegr	lfqveyaiea	iklgs	staigi	qtsegvclav	v ekritsplme
61	pssie	k ivei	dahigcamsg	liadaktlid	karve	etqnhw	ftynetmtve	e svtqavsnla
121	lqfge	edadp	gamsrpfgva	llfggvdek <mark>g</mark>	pqlfl	mdpsg	tfvqcdarai	. gsasegaqss
181	lqevy	hksmt	lk eaik ssli	ilk qvmeek l	natni	ielatv	qpgqnfhmft	: keeleevikd
241	i							

Proteasome s	ubunit	8	3394076	1092			41	27.4
alpha type	e-6							
1	msrgs	sagfd	rhitifspeg	rlyqveyafk	ainq	ggltsv	avr gkdcavi	l vtqkkvpdkl
61	ldsst	vthlf	k itenigcvm	tgmtadsr sq	vqra	ryeaan	wkyk ygyei	vdmlckriad
121	isqvy	tqnae	mrplgccmil	igideeqgpq	vyk c	dpagyy	cgfkataagv	/ k qtestsfle
181	kk vkk	kfdwt	feqtvetait	clstvlsidf	kpse:	ievgvv	tvenpkfril	l teaeidahlv
241	alaer	d						

	Proteasome subunit alpha type-7-like isoform 1	311259068	601		65	27.9	
L	1 masry 61 vr kic 121 tqsng 181 daian 241 aek kk	dr ait vfspdghlfg alddh vcmafaglta grrpfg isalivgfdd adneai klairallev sskkta	<pre>veyaqeavkk darvvinrar dgiprlyqtd vqsggkniel</pre>	gstavair gt vecqshk ltv psgtyhawk a aiirr nqplk	divvlgvekk edpvtveyit naigrsaktv mfsak eielc	svaklqdert rfiatlkqky refleknyte vneiekekee	-

Proteasor	ne	34	43887360	467		58	27.8
(prosom	e,						
macropain) su	ıbunit,						
alpha typ	be						
1	msydr	aitvf	spdghlfqve	yaqeavkk gs	tavgvr grdi	vvlgvekksv	v arlqdertvr
61	k ical	ddnvc	mafagltada	r ivinrarve	cqshr ltved	pvtveyitry	/ iaslkqrytq
121	sngr r	pfgis	alivgfdfdg	tprlyqtdps	gtyhawkana	igrgaksvre	e flek nytdea
181	ietdg	ltikl	vik allevvq	sggk nielav	mrrdqplk il	npeeiekyva	eiek ekeene
241	kkkqk	kas					

Proteasome subunit	4506195	638		61	22.8
1					
1 meyl:	igiqgp dyvlvasdrv	v aasnivqmkd	dhdkmfkmse	k illlcvgea	gdtvqfaeyi
61 ak nya	ylykmr ngyelspta a	anftrrnlad	clrsr tpyhy	nlllagydeh	eopalvymdy

61 qknvqlykmr ngyelsptaa anftrrnlad clrsrtpyhv nlllagydeh egpalyymdy 121 laalakapfa ahgygafltl sildryytpt isreravell rkcleelqkr filnlptfsv 181 riidkngihd ldnisfpkqg s

Proteasome subunit	3	15139006	638		69	20.2
beta type-2 isoform						
2						
1 meyl	idhdkm	fkmsek illl	cvgeagdtvq	faeyiqk nvq	lykmr ngyel	. sptaaanftr
61 rnla	dclrsr	tpyhvnllla	gydehegpal	yymdylaala	kapfaahgyg	afltlsildr
121 yyt	tisr er	avellrkcle	elqk rfilnl	ptfsvriidk	ngihdldnis	fpk qgs

Proteasome subunit	335292522	2006		59	30.1
beta type-5					
1 mfwrv	vpfpl ldmalasvle	e rplavnrrgf	fgfggradll	dlgpgspgdg	g lslvapswgv
61 peepr	iemlh gtttlafk <mark>f</mark>	L hgvivaadsr	atagayiasq	tvkkviein	o yllgtmagga
121 adcsf	werll arqcriyel	nkerisvaaa	sk llanmvyq	ykgmglsmg	t micgwdkrgp
181 glyyv	dsegn risgatfsvo	j sgsvyaygvm	drgysydlev	eqaydlar ra	a iyqatyr day
241 sggsv	nlyhv redgwirvs:	s dnvadlhdky	sestp		
Proteasome subunit	344259274	553		61	25.4
beta type-6					
1 maatl	vaarg aglapawghe	e aitpdwenre	vstgttimav	qfdggvvlga	a dsrtttgsyi
61 anrvt	dkltp ihdrifccr	s gsaadtqava	davtyqlgfh	sielnepply	v htaaslfk em
121 cyr yr	edlma giivagwdpo	q eggqvysvpm	ggmmvrqafa	iggsgssyi	y gyvdatyreg
181 mtkee	clqft analalame	dgssggvirl	aaiaesgver	qvllgdqipl	c ftiatlppp
Full-proteasome	160419232	275		39	30
Full-proteasome subunit beta type-7	160419232	275		39	30
Full-proteasome subunit beta type-7 1 maavs	160419232 vyerp vggfsfdnci	275 rnaileadfa	kkgyklptar	39 ktgttiagvv	30 v yk dgivlgad
Full-proteasome subunit beta type-7 1 maavs 61 tr ate	160419232 vyerp vggfsfdnc: gmvva dkncskihf:	275 rnaileadfa spniyccgag	kkgyklptar taadtdmttq	39 ktgttiagvv lissnlelhs	30 v yk dgivlgad s lstgrlprvv
Full-proteasome subunit beta type-7 1 maavs 61 tr ate 121 tanrm	160419232 wyerp vggfsfdnci gmvva dkncskihf: ilk qml fryqgyiga a	275 r rnaileadfa i spniyccgag a lvlggvdvtg	kkgyklptar taadtdmttq phlysiyphg	39 ktgttiagvv lissnlelhs stdklpyvt	30 v yk dgivlgad s lstgrlprvv n gsgslaamav
Full-proteasome subunit beta type-7 1 maavs 61 tr ate 121 tanrm 181 fedkf	160419232 wyerp vggfsfdnc gmvva dkncskihf: ilk qml fryqgyiga rpeme eeeak qlvse	275 rnaileadfa spniyccgag lvlggvdvtg aiaagifndl	kkgyklptar taadtdmttq phlysiyphg gsgsnidlcv	39 ktgttiagvv lissnlelhs stdklpyvtr iskskldfl:	30 v yk dgivlgad s lstgrlprvv n gsgslaamav r pysvpnkkgt
Full-proteasome subunit beta type-7 1 maavs 61 trate 121 tanrm 181 fedkf 241 rfgry	160419232 svyerp vggfsfdncr gmvva dkncskihf: ilk qml fryqgyiga rpeme eeeak qlvse grcekg ttavltek v	275 r rnaileadfa spniyccgag a lvlggvdvtg e aiaagifndl aldievleet	kkgyklptar taadtdmttq phlysiyphg gsgsnidlcv vqtmdts	39 ktgttiagvv lissnlelh: stdklpyvtr iskskldfl:	30 y yk dgivlgad s lstgrlprvv n gsgslaamav r pysvpnkkgt
Full-proteasome subunit beta type-7 1 maavs 61 trate 121 tanrm 181 fedkf 241 rfgry	160419232 svyerp vggfsfdncr gmvva dkncskihf: alk qml fryqgyiga grpeme eeeak qlvse prcekg ttavltek v	275 rnaileadfa spniyccgag alvlggvdvtg aiaagifndl aldievleet	kkgyklptar taadtdmttq phlysiyphg gsgsnidlcv vqtmdts	39 ktgttiagvv lissnlelh: stdklpyvtr iskskldfl:	30 v yk dgivlgad s lstgrlprvv n gsgslaamav r pysvpnkkgt
Full-proteasome subunit beta type-7 1 maavs 61 tr ate 121 tanrm 181 fedkf 241 rfgry Chain H, Crystal	160419232 wyerp vggfsfdncr gmvva dkncskihf: alk qml fryqgyiga rpeme eeeak qlvse rcekg ttavltek <mark>v</mark> 21465649	275 rnaileadfa spniyccgag alvlggvdvtg aiaagifndl aldievleet 607	kkgyklptar taadtdmttq phlysiyphg gsgsnidlcv vqtmdts	39 ktgttiagvv lissnlelhs stdklpyvtr iskskldfl: 65	30 v yk dgivlgad s lstgrlprvv n gsgslaamav r pysvpnkkgt 21.9
Full-proteasome subunit beta type-7 1 maavs 61 tr ate 121 tanrm 181 fedkf 241 rfgry Chain H, Crystal Structure of the	160419232 avyerp vggfsfdncr gmvva dkncskihf: alk qml fryqgyiga frpeme eeeak qlvse grcekg ttavltek v 21465649	275 r rnaileadfa spniyccgag a lvlggvdvtg e aiaagifndl c aldievleet 607	kkgyklptar taadtdmttq phlysiyphg gsgsnidlcv vqtmdts	39 ktgttiagvy lissnlelhs stdklpyvtr iskskldfl: 65	30 v yk dgivlgad s lstgrlprvv n gsgslaamav r pysvpnkkgt 21.9
Full-proteasome subunit beta type-7 1 maavs 61 tr ate 121 tanrm 181 fedkf 241 rfgry Chain H, Crystal Structure of the Mammalian 20s	160419232 avyerp vggfsfdncr gmvva dkncskihf: alk qml fryqgyiga grpeme eeeak qlvse grcekg ttavltek v 21465649	275 c rnaileadfa i spniyccgag a lvlggvdvtg e aiaagifndl c aldievleet 607	kkgyklptar taadtdmttq phlysiyphg gsgsnidlcv vqtmdts	39 ktgttiagvv lissnlelhs stdklpyvtr iskskldfl: 65	30 v yk dgivlgad s lstgrlprvv n gsgslaamav r pysvpnkkgt 21.9
Full-proteasome subunit beta type-71maavs61trate121tanrm181fedkf241rfgryChain H, Crystal Structure of the Mammalian 20s Proteasome at 2.75	160419232 wyerp vggfsfdncr gmvva dkncskihf: alk qml fryqgyiga rpeme eeeak qlvse grcekg ttavltek v 21465649	275 c rnaileadfa i spniyccgag a lvlggvdvtg e aiaagifndl c aldievleet 607	kkgyklptar taadtdmttq phlysiyphg gsgsnidlcv vqtmdts	39 ktgttiagvv lissnlelhs stdklpyvtr iskskldfl: 65	30 v yk dgivlgad s lstgrlprvv n gsgslaamav r pysvpnkkgt 21.9
Full-proteasome subunit beta type-71maavs61trate121tanrm181fedkf241rfgryChain H, CrystalStructure of the Mammalian 20sProteasome at 2.75 A Resolution	160419232 vyerp vggfsfdnc: gmvva dkncskihf: lk qml fryqgyiga rpeme eeeak qlvse rcekg ttavltek <mark>v</mark> 21465649	275 r rnaileadfa spniyccgag a lvlggvdvtg e aiaagifndl c aldievleet 607	kkgyklptar taadtdmttq phlysiyphg gsgsnidlcv vqtmdts	39 ktgttiagvv lissnlelhs stdklpyvtr iskskldfl: 65	30 v yk dgivlgad s lstgrlprvv n gsgslaamav r pysvpnkkgt 21.9
Full-proteasome subunit beta type-7 1 maavs 61 trate 121 tanrm 181 fedkf 241 rfgry Chain H, Crystal Structure of the Mammalian 20s Proteasome at 2.75 A Resolution 1 ttima	160419232 vyerp vggfsfdnc: gmvva dkncskihf: lk qml fryqgyiga rpeme eeeak qlvse rcekg ttavltek v 21465649	275 r rnaileadfa spniyccgag lvlggvdvtg e aiaagifndl aldievleet 607 ttgsyianrv	kkgyklptar taadtdmttq phlysiyphg gsgsnidlcv vqtmdts tdkltpihdr	39 ktgttiagvv lissnlelhs stdklpyvtr iskskldfl: 65	30 v ykdgivlgad s lstgrlprvv n gsgslaamav r pysvpnkkgt 21.9 a dtqavadavt

61 yqlgfhsiel nepplvhtaa slfkemcyry redlmagiii agwdpqeggq vysvpmggmm 121 vrqsfaiggs gssyiygyvd atyregmtke eclqftanal alamerdgss ggvirlaaia

181 esgverqvll gdqipkfava tlppa

Spermadhesins & Other Acrosome-Associated Proteins:

Spermadhesin	AWN	6	6990208	761			74	16.9
1 61 121	mklgs fhvvl aspfh	ailwa aippl iyyya	lllstatlvs nlscgkeyve dpegplpfpy	gawnrrsrsc 11dgppgsei ferqtiiate	ggvl: igki knip	rdppgk cggisl	ifnsdgpqk vfrsssnia	d cvwtikvkph t ikylrtsgqr

Major Seminal	47523176	275		46	14.5
Plasma Glycoprotein					
PSP-I precursor					
1 mklgs	aipwa llfstatlis	tgwgldyhac	ggrltddygt	iftykgpkte	cvwtlqvdpk
61 ykllv	siptl nltcgk eyve	<pre>ilegapgsks</pre>	lgk fceglsi	lnr gssgmtv	kykr dsghpa
121 spyei	iflr d sqg				

Seminal Plasma	72535165	419	69	15
Sperm Motility				
Inhibitor				

1 mklgsaipwa lllstatlvs taqnkgsddc ggflk**nysgw isyykalttn cvwtiemkpg** 61 **hk**iilqilpl nltcgkeyle vrdqr**agpdn flkvcggttf vyqsssnvat vk**ysr**dshhp**

121 assfnvyfyg ipqgaka

Sp32 Acrosin- binding protein (degradation product)	75052483	940		26	60.5
l qlaag 61 rathg 121 csqpv 181 slslg 241 glgad	gsilsi ikvilipiag gernpt lvqldqyen ysilsp nslkevdtss ggqeqg qehkqehkqe dsepkf gsefysspa	apaqdansas glvpdgavcs evpittmtsp ggqehkqdeg	tpgsplspte dlpyaswfes vsshitatgr qeqeeqeeeq stommmenig	yerffalltp fcqftqyrcs qvfqpwperl eeegkqeegq elirsagemd	twkaettcrl nhvyyakrvr nnnveellqs gteesleams
301 iwr a q 361 rhlaa 421 r fygl 481 ycafk	<pre>issepsi qservssipi ispgsl lqlphvdall icslcd fcslkleqch .dlygg lrmdfwcar issqqcm mrnrdrkvs</pre>	<pre>sttp://leve vlcysivent setnlqrqqc atkgcednrv mrclqnetyt</pre>	cvitptakaw dnshktpfis aswlqtefls vltqaksedl	qyledetlgf pllasqsmsi fqdgdfptki vlrwsqefst	gksvcdslgr gtqigtlksg cdteyvqypn ltlgqag

Seminal Plasma123986177677.6Acrosin Inhibitor A11 trkqpncnvy rshlffctrq mdpicgtngk syanpcifcs ekglrnqkfd fghwghcrey

61 tsars

Seminal Plasma	47523184	178	43	15.4
Protein pB1				
precursor				

1 maprlgifll wagvsvflpl dpvngdqhlp gr**fltpaits ddkcvfpfiy k**gnlyfdctl 61 hdstyywcsv ttyymkrwry crstdyar**ca lpfifrgkey dscikegsvf skywcpvtpn**

121 **ydqdr**awryc

Disintergins (ADAM Family) Proteins:

Disintegrin and metalloproteinase	323276507	443		23	45.1
domain-containing					
protein 5					
1 mhsgo	yvkdfs tcslddfkyf	aahsgltclh	silldepvyk	qrrricgngi	leqgeqcdcg
61 tlenc	thkhc cdprtcrrkr	nkqcgsgecc	tqdck irpan	<pre>vicrksadec</pre>	dfieycngty
121 shcva	dtfar ngqscesgsa	ycyggrcrsf	tkqcr nligg	estgasfscf	deinsr kdrf
181 gncgr	eycny phllcgklvc	nwphkylisr	anlsviyshv	reqmcvstfl	naek ipr dti
241 ttvqf	pgdrd rtfvqdgtvc	gpemfclnfs	cveikyrvny	gecnssrhcn	angvcnnfnh
301 chck	gfvpp dcnvgngfgs	iddghqsk vg	prrlwegkvl	pskhrfqlif	yislpvliia
361 ttaii	ikqnk irelcyrget	esegsvsees	ssssklsptv	snsl	

Disintegrin and		31	1261282	322		26		82.5
metalloproteinase								
domain-containing								
protein 20-like								
1	mgpas	aqaql	rgdpclpllw	lflgpiccsy	appgwrf	ftas	eiviprkvsh	rvstaeiqgq
61	lsyki	rfggq	rhvvhmrvkk	sllprhfpvi	tdndqga	amqe	dypfvprdcy	yygylegvpg
121	smgtl	dtchg	glrgmlqvdd	ftyeikplea	sskfehv	visl	lvtqktpged	ekckiggedt
181	nqade	ealla	empr agpvym	wwphrkyikl	lytvahs	syfl	lnpnqtsvie	nvvimnnilh
241	siyfq	aglev	cir vlciwna	gdgmrldiwr	dggslvt	tr fg	lwkmqrwqgm	iphdtavllt
301	gr rfg	ndryy	ahrggicnpn	wgasfvcvgn	nhiflas	stla	ahtlghmigc	rhdgpgcrcf
361	rrdkc	vmape	tglldmlsnc	syvtlhevvh	rwdpcls	stsn	vpynnfpyva	nrcgdkklda
421	reecd	cgtmk	dcaedpccen	sciltlgstc	segscci	vgcn	yaqpgrmcrd	vlgicdlpey
481	ctglt	htcpd	dsyiqdgtpc	splavcvkgn	csdrdmo	qcqa	lfgfnvkeaa	picyr tlnmr
541	gdrfg	ncgvr	virgggkpvk	ceeddimcgm	lhcanvo	qk ip	gggehttfrh	ivvhdvtpk t
601	cfgfd	ahfgt	ltpqlglvvd	gascgpgqfc	k dqnctf	fypd	lnfscdvstc	nfrgvcnnrr
661	hchcq	qgwkp	pncdvegggg	svdsgpppdk	r ketrał	kir <mark>m</mark>	svnievalll	arfallcisg
721	iigsl	fhlre	vvdqryeeta	sekl				

Other Sperm Proteins & eGFP:

Lactadherin	172072653	1264	49		47.8
1 mpgpr.	lltai cgallcasgl	fafsgdfcds	sqclnggtcl	ldqdpqnpfh	clcpegftgl
61 icnet	ekgpc fpnpchndae	ceviddahr g	dvftqyickc	phgytgihce	iicnaplgme
121 tgaia	dfqis assmhlgfmg	lqrwapelar	lhr agivnaw	tasnydrnpw	<pre>iqvnllrrmr</pre>
181 vtgvv	tqgas ragsaeyikt	fkvayssdgr	kfqfiqgaee	sgdkifmgnl	dnsglkvnlf
241 evple	vqyvr lvpiichrgc	tlr fellgce	lsgcaeplgl	kdntipnkqi	tassfyrtwg
301 lsafs	wypfy arldnqgkfn	awtaqsnsas	ewlqidlgsq	<pre>rvtgiitqg</pre>	ar dfghiqyv
361 aaykv a	aysdd gvswteyrdq	galegk ifpg	nldnnshkkn	mfetpfltrf	vr ilpvawhn
421 r itlr	vellg c				

Enhanced Green	Enhanced Green 13194618		713		42	27
Fluorescent Prote	ent Protein GenBank:					
	AA	K15492.1				
1 mvs	kgeelft	gvvpilveld	gdvnghkfsv	sgegegda	ty gkltlkfic	t tgklpvpwpt
61 lvt	tltygvq	cfsrypdhmk	qhdffk samp	egyvqert	if fkddgnyk t	r aevk fegdtl
121 vnr	ielk gid	fkedgnilgh	kleynynshn	vyimadko	<mark>[k</mark> n gikvnfkir	h niedgsvqla
181 dhy	qqntpig	dgpvllpdnh	ylstqsalsk	dpnekrdh	mv llefvtaag	i tlgmdelyk

Ropporin-1-like	3017832	783203 404		33		33	23.9
1 mpqt	dk qici ppe l	pellk q ftka	aairtqp	qdlic	qwaady	fgamshgeip	pvrerser va
61 lsnw	aeltpe llki	lhsrva grl:	iihadel	aqmwk	cvlslp	tdlfnsvmnv	gr fteeiewl
121 k fla	lacssl gvti	aktlk <mark>i vce</mark> v	vlssdhd	ggppr	ipfst	fqflytyiae	vdgeisashv
181 sr ml	nyieqe vigp	dglikv ndf	tqnprvr	le			

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