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Immunolocalization of Vasa, PIWI, and TDRKH proteins in male germ cells during spermatogenesis of the teleost fish Poecilia reticulata

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1	Immunolocalization of Vasa, PIWI, and TDRKH proteins in male germ cells during
2	spermatogenesis of the teleost fish Poecilia reticulata
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#### 35 Abstract

- 36 Vasa, PIWI and TDRKH are conserved components of germ granules that in metazoans are
- 37 involved in germline specification and differentiation, as documented by mutational experiments in
- 38 some model animals. So far, investigations on PIWI during spermatogenesis of fish has been
- 39 limited to a few species, and no information is available for TDRKH, another protein involved in
- 40 the piRNA pathway. In this study, the immunolocalization of these three germline determinants was
- 41 analyzed in male gonads of the teleost fish *Poecilia reticulata* to document their localization pattern
- 42 in the different stages of germ cell differentiation.
- 43 To analyze their distribution pattern during the different stages of spermatogenesis we performed
- 44 immunohistochemistry (IHC) and immunofluorescence (IF) assays using primary polyclonal
- 45 antibodies after testing their specificity with Western Blot. Moreover, sections of testis stained with
- 46 haematoxylin and eosin clarified the structural organization of *P. reticulata* testis, while the use of
- 47 the confocal microscope and the nuclear staining clarified the different stages of germ cell
- 48 differentiation during spermatogenesis.
- 49 The results showed that Vasa, PIWI and TDRKH were specifically immunolocalized in the germ
- 50 cells of *P. reticulata*, with no specific signal detected in Sertoli cells and in other somatic cells of
- 51 the gonad. These markers were detected in all stages of differentiation from early spermatogonia to
- 52 advanced spermatids. Vasa staining was the strongest in spermatogonia, and then decreases
- 53 throughout differentiation. Instead, both PIWI and TDRKH staining increases during
- 54 differentiation, and their distribution pattern, similar to what observed in the mouse, suggests their
- 55 concerted participation in the piRNA pathway also in this fish.
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57 Keywords:

- 58 germline; spermatogenesis; *Poecilia reticulata*; Vasa; PIWI; TDRKH
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#### 69 Introduction

70

71 Spermatogenesis is the process of differentiation of germ cells that leads to the formation of male

- 72 mature gametes. Spermatogenesis begins inside the testis with the mitotic proliferation of diploid
- 73 spermatogonia, proceeds through the two meiotic divisions, and concludes with spermiogenesis,
- during which the haploid spermatids are transformed into spermatozoa (Schulz et al., 2010).
- 75 In fish, spermatogenesis is of the "cystic type" (Schulz et al., 2010). Within the spermatogenic
- tubules, cyst formation initiates when cytoplasmic extensions of Sertoli cells envelope a single,
- clonally and synchronously developing group of germ cells deriving from a single spermatogonium
- 78 (Grier et al., 2005).

79 In *Poecilia reticulata*, the cysts containing spermatogonia in mitotic divisions are restricted to the

- 80 testis periphery while the cysts containing germ cells in meiosis, migrate towards the region of the
- 81 spermatic ducts (efferent ducts) located centrally in the testis, where spermiation occurs and where
- 82 the cysts open to release spermatozoa (Parenti and Grier, 2004).
- 83 Testis of *Poecilia reticulata* can be useful in studying the presence of germline determinants in
- 84 spermatogenic cells because in each cyst germ cells are in the same developmental stage and this
- 85 allows to easily analyze marker localization in specific germ cell stages. Germline determinants are
- 86 components of germ granules both in females and in males (Saffman and Lasco, 1999). In male
- 87 germ cells, these granules can then aggregate to form a chromatoid body (Parvinen, 2005). Later in
- 88 spermiogenesis, at least in mammals, the chromatoid body appears like a ring adjacent to the
- 89 midpiece and takes part in the formation of the residual body (Shang, 2010).
- 90 Homologs of *vasa*, *piwi*, and *tudor* genes are an example of conserved genes expressed in germ
- 91 granules, involved both in germline specification and in germ cell differentiation (Fierro-Constaín
- 92 et al., 2017; Juliano et al., 2010). Moreover, since they are expressed in germ cells (Juliano et al.
- 2010), they are used also to recognize germ cell localization (Cavelier et al., 2017; Cherif-Feildel etal., 2018).
- 95 Vasa, an ATP-dependent RNA helicase belonging to the DEAD (Asp-Glu-Ala-Asp) box protein
- 96 family, is a typical component of germ granules that promotes germline specification by regulating
- 97 mRNA translation in germ cells during development (Seydoux and Braun, 2006). Vasa, given its
- 98 precence from undifferentiated precursors to germ cells in advanced stages of differentiation, can be
- 99 considered one of the best markers to trace germ cells (reviewed in Lasko, 2013). Vasa is conserved
- among metazoans (Linder et al. 1989) and it has been identified as germ cell determinant in several
- 101 species, such as, for example: *Caenorhabditis elegans* (Gruidl et al., 1996), *Xenopus* (Ikenishi and
- 102 Tanaka, 1997), Danio rerio (Yoon et al., 1997), Podarcis sicula (Maurizii et al., 2009; Milani and

103 Maurizii, 2014, 2015), chicken (Tsunekawa et al., 2000), mouse (Fujiwara et al., 1994), humans

104 (Castrillon et al., 2000). A Vasa homolog was also characterized in the germ cells of the striped

105 catfish (*Pangasianodon hypophthalmus*) (Duangkaew et al., 2019), and two Vasa isoforms have

106 been identified in the male and female gonads of tilapia (*Oreochromis aureus*) (Kobayashi et al.,

107 2002), and in medaka (*Oryzias latipes*) (Li et al., 2009; Reunov et al., 2020). The fundamental role

108 of *vasa* for a proper gametogenesis has been pointed out with mutational experiments. In mice,

109 male individuals carrying a mutation of the *vasa* ortholog *mvh* are sterile (Tanaka et al., 2000). In

110 humans, loss of vasa leads to infertility with development of Sertoli cells only (Castrillon et al.,

111 2000). In zebrafish, *vasa* loss-of-function mutations gave rise to sterile males that formed immature

112 testes (Hartung et al., 2014).

113 PIWI proteins are other conserved components of germ granules and are essential for germline

development and gametogenesis in animals (Thomson and Lin, 2009). PIWI proteins, together with

115 PIWI-interacting RNAs (piRNA, generally 26–31 nucleotides in length), forms PIWI-piRNA

116 complexes, which are involved in transposon silencing, protecting genome integrity during germ

117 cell development, and also regulate translation, and guide epigenetic programming in the germline

118 (Kim, 2006; Kim et al., 2009; Juliano et al., 2011). Animals lacking piRNAs exhibit activation of

transposable elements (TEs) and defects in gametogenesis (Carmell et al., 2007). In mammals,

120 PIWI proteins were found to be male specific-(Bak et al., 2011). In mice, there are three members

121 of PIWI-like proteins (PIWII), MILI (PIWII2), MIWI (PIWII1) and MIWI2 (PIWII4), and

122 mutations in any one of these PIWI genes in the mouse caused spermatogenic arrest and ultimately

resulted in male sterility (Deng and Lin, 2002; Kuramochi-Miyagawa et al., 2001, 2004; Carmell et

al., 2007). In zebrafish, the two described PIWI proteins, Ziwi (PIWII1) and Zili (PIWII2) are

125 expressed in both the male and female gonads (Tan et al., 2002; Houwing et al., 2008). Loss of Ziwi

126 led to germ cell apoptosis, while Zili was essential for germ cell meiosis and differentiation

127 (Houwing et al., 2007; 2008). *piwi* homologous genes have been reported also in other species of

128 teleosts, such as the common carp (Cyprinus carpio), Nile tilapia (Oreochromis niloticus), half-

129 smooth tongue sole (Cynoglossus semilaevis), turbot (Scophthalmus maximus), and dark sleeper

130 (Odontobutis potamophila), in which PIWI proteins are considered to play an important role in

131 gonadal development and gametogenesis (Zhou et al., 2012; Xiao et al., 2013; Zhang et al., 2014;

132 Wang et al., 2017, 2018; Zhao et al., 2018).

133 Other factors involved in the piRNA pathway have also been identified in animals (Ishizu et al.,

134 2012). TDRD proteins (Tudor domain-containing proteins) are known to interact with PIWI

proteins by binding to symmetrically dimethylated arginine residues in the N-terminus of PIWII1

and PIWI12 in both mouse and zebrafish (Kirino et al., 2009; Reuter et al., 2009; Vagin et al. 2009).

4

137 TDRKH (also named TDRD2) is a protein containing Tudor and K homology (KH) domains

- 138 (Zhang et al., 2017) required for spermatogenesis and involved in piRNA biogenesis. Specifically,
- in mice, TDRKH interacts directly with PIWI proteins (PIWI-like protein 1 (PIWI11), PIWI12, and
- 140 PIWII4) (Chen et al., 2009; Vagin et al., 2009). In mice, TDRD2/TDRKH was identified as a
- 141 component of the MIWI complex (Chen et al., 2009) involved in primary piRNA biogenesis
- 142 pathway. Mutation of *tdrkh* results in male sterility due to meiotic defects with concurrent loss of
- 143 retrotransposon silencing (Saxe et al., 2013).
- 144 In this study, we analyzed the immunolocalization of the three germline determinants Vasa, PIWI
- and TDRKH in *Poecilia reticulata* male germ cells to document their distribution pattern in the
- 146 different stages of their differentiation, knowledge that at the moment is limited to a few species
- 147 studied with the use of few molecular markers. To do this, we first verified with Western Blot the
- 148 possibility to confidently use antibodies developed against protein homologs of other animals (e.g.
- 149 anti-human PIWI and TDRKH) in this fish, then with anti-Vasa and nuclear staining, and the use of
- 150 the confocal microscope, we identified male germ cells in different stage of differentiation. This
- allowed us to describe and compare the distribution pattern of the piRNA pathway proteins PIWI
- and TDRKH in the different germ cell stages. When possible, we compared our findings with what
- 153 observed in other fish, otherwise we compared them with what documented in other model animals.
- 154 Indeed, this is the first study on TDRKH distribution in fish. *Poecilia reticulata* is an important
- 155 model system for biomonitoring and toxicological studies (Kinnberg et al., 2003; Antunes et al.,
- 156 2017; Souza Trigueiro et al., 2021), making the acquisition of details on its development and cell
- 157 lineage differentiation of basic importance (e.g. Bettini et al., 2012; Bettini et al., 2017). Moreover,
- given the described characteristics of its gonad, it could become a useful model system also to studygermline development and differentiation.
- 160

# 161 Material and Methods

162

## 163 Experimental animals

- 164 In this study, twenty sexually mature males of *Poecilia reticulata* were used: six for
- 165 immunohistochemistry (two animals for each antibody used), six for immunofluorescence (two
- animals for each antibody used), and eight for Western blot. Animals were purchased from a local
- 167 aquarium shop (Bologna, Italy). Once in the lab, fish were immediately sacrificed by decapitation
- 168 after being anaesthetized with 0.1% 3-aminobenzoic acid ethyl ester (MS-222, Sigma, St. Louis,
- 169 MO). All procedures and experiments were conducted in accordance with the European guidelines
- 170 for animal care.

171

# 172 SDS-PAGE

- 173 Testes of *P. reticulata* were removed from their abdominal cavity and homogenized using an Ultra
- 174 Turrax T25 (Janke and Kunkel IKA-labortechnik) in a buffer containing 10mM Tris-HCl, pH 7.5, 1
- 175 mM ethylene glycol-bis(2-aminoethyl ether)-N,N,N0,N0-tetraacetic acid (EGTA) and in the
- 176 presence of the following protease inhibitors: 1 mM PMSF and 1 tablet of protease inhibitor
- 177 cocktail (Complete Mini of Roche) in 5 mL of the buffer. Then samples were centrifuged at 7,500
- 178 xg for 10 minutes at 4°C. The supernatant was stored at  $-80^{\circ}$ C.
- 179 We used different specimens for homogenization to avoid biased results due to individual
- 180 variability in the germline differentiation stage. Proteins in the total homogenate were quantified
- 181 using the Lowry method (Lowry et al., 1951). The same quantity of total proteins was loaded per
- lane (30 µg) and analyzed by SDS-PAGE (Sodium Dodecyl Sulphate-PolyAcrylamide Gel
- 183 Electrophoresis) (Laemmli, 1970), using 8.5% acrylamide gels.
- 184

#### 185 **Protein sequence analyses and antibodies**

- 186 We used ExPaSy (www.expasy.org) to infer the molecular weight (MW) of *P. reticulata* NCBI
- 187 predicted proteins by using the Compute pI/MW tool (Gasteiger et al., 2005), and we used
- 188 InterProScan (Finn et al., 2017) to recognize conserved protein domains in protein sequences.
- 189 The used anti-Vasa was obtained against zebrafish Vasa (Table 1). For Piwi and TDRDKH
- 190 detection, we used antibodies developed against the human protein. Anti-Piwi primary antibody
- 191 was developed against human PIWII2 (NCBI: NP\_060538). The primary antibodies used for
- 192 TDRKH detection were both developed against of *Homo sapiens* (NP\_001077432.1) orthologue
- 193 (Table 1). We used T-Coffee (Notredame et al., 2000) (supplementary material) to align protein
- sequences of Vasa, PIWI and TDRKH from *P. reticulata* with the corresponding ortholog from the
- 195 species used for antibody production (zebrafish, *Homo sapiens* and *Homo sapiens*, respectively).
- 196

#### 197 Western Blot

- 198 For immunoblotting, proteins were transferred to a Hybond-ECL membrane (Amersham
- 199 International, Buckinghamshire, UK). Non-specific protein-binding sites were blocked with 5%
- 200 dried skimmed milk (Bio-Rad Laboratories, Hercules, CA, USA), 3% bovine serum albumin
- 201 (BSA), 0.1% Tween 20 (Tw) (Sigma) in Tris Buffered Saline solution (TBS: 200 mM Trizma base;
- 202 137 mM NaCl), for 1 hour (hr) and 30 min, at room temperature (RT) and subsequently washed
- 203 with TBS-0.1% Tw. Membranes were then incubated with the following primary antibodies
- developed in rabbit and diluted with TBS-0.1%Tw, pH 7,4: anti-Vasa antibody (Abcam), (1:

205 2,000); anti-Piwil2 (Abcam) (1:500), anti-TDRKH (Genetex) (1:1,000) overnight (ON) at 4°C and

- for 1 hr and 15 min at RT. After rinsing, the membranes were incubated with goat anti-rabbit
- 207 secondary antibody, conjugate with horseradish peroxidase (HRP) (Santa Cruz Biotechnology Inc.,
- 208 Santa Cruz, CA, USA) at the dilution of 1:5,000 for 1 hr at RT. The washed membranes were
- 209 treated with ECL Western Blotting Detection Reagents (GE Healthcare) and exposed to Hyperfilm
- ECL (GE Healthcare).
- 211

# 212 Immunoistochemistry (IHC)

213

# 214 Sample processing

Male gonads of P. reticulata were removed from their abdominal cavity and fixed in modified 215 216 Bouin's solution containing a saturated aqueous solution of picric acid and formalin (ratio 3:1), for 217 24 hrs at room temperature. Picric acid was removed by prolonged washing in 0.1 m sodium 218 phosphate buffer (PB), pH 7.4, at room temperature. Specimens were dehydrated in a graded series 219 of ethanol (70, 80, 95, 100%, for 40 min each at RT) and subsequently embedded in Paraplast plus 220 (Sherwood Medical, St. Louis, MO; melting point 55–57°C). Gonads were cut with a Leica 221 RM2145 microtome and 5-µm-thick sections were mounted on silane-coated slides (Sigma) and 222 dried. Adjacent slides were used for histochemical and immunohistochemical processing. For 223 histochemical sample preparation, the entire body was processed with hematoxylin and eosin 224 staining. Xylene deparaffinized sections were hydrated and stained with hematoxylin and eosin for 225 the evaluation of testis morphology. Briefly, sections were stained with Carazzi's hematoxylin 226 (Bio-Optica, Milano, I) for 10 min. Colour change was obtained with immersion in tap water for 5 227 min. The sections were then stained with aqueous 1% eosin Y solution (Bio-Optica) for 2 min. 228 Excess eosin was removed with quick rinse in distilled water. After dehydration with ethanol 229 solutions, sections were cleared with xylene and coverslipped with Permount (Fisher Scientific, 230 Pittsburgh, PA).

231

### 232 Immunostaining

After sections deparaffinisation with xylene and rehydration, endogenous peroxidase activity was

quenched with 1% H<sub>2</sub>O<sub>2</sub> in 0.01 M Phosphate Buffer containing 0.15 M NaCl, pH 7.4, for 25 min.

- For antigen retrieval, tissue sections were immersed in 0.01 M citrate buffer, pH 6.0 and heated in a
- 236 microwave oven (750 W) for two cycles of 5 min each at 98°C. Non-specific background staining
- 237 was reduced by preincubation in PBS containing 10% normal goat serum (NGS; Vector
- Laboratories, Burlingame, CA), 1% bovine serum albumin (BSA; Sigma) and 0.1% Tween 20

239 (Merck, Darmstadt, Germany) for 30 min. Sections were incubated separately ON with the

- following primary antibodies in a moist chamber on a floating plate at 4 °C: the anti-Vasa antibody
- 241 (Abcam), anti-Piwil2 (Abcam) and anti-TDRKH (Genetex), all produced in rabbit and diluted 1:
- 242 200, 1:50, 1:50, respectively, in PBS containing 3% NGS, 1% BSA and 0.1% Tween 20. After
- rinsing in PBS with 0.1% Tween 20, the sections were incubated with HRP-conjugated goat anti-
- rabbit IgG (PI-1000, Vector Laboratories) diluted 1:100 in PBS containing 1% BSA and 0.1%
- Tween 20 for 1 hr at RT. After rinsing in PBS, immunoreaction was visualised using the intensified
- 246 diaminobenzidine method (Adams, 1981). Sections were dehydrated in ethanol, cleared in xylene,
- and coverslipped with Permount (Fisher Scientific, Pittsburgh, PA). Finally, the slides were
- examined using an Olympus BH-2 microscope.
- 249

# 250 Immunofluorescence (IF)

251

# 252 Sample processing

- 253 Testes of adult *P. reticulata* were rapidly removed and fixed with 3.7% paraformaldehyde plus
- 254 0.25% or 0.5% glutaraldehyde (depending on gonads dimension) in a buffer containing 80mM
- 255 KPIPES, 1mM MgCl<sub>2</sub>, 5mM EGTA, and 0.2% Triton X-100 (Tx), pH 6.8, for 4 hrs at RT. Fixed
- testes were washed with phosphate-buffered saline (PBS) (128 mM NaCl, 2 mM KCl, 8 mM
- 257 Na<sub>2</sub>HPO<sub>4</sub>, 2 mM KH<sub>2</sub>PO<sub>4</sub>), pH 7.2, for 1 hr, and embedded in 7% agar. Vibratome sections (Leica
- 258 VT1000 S), were post-fixed with increasing concentrations of methanol (50–100%) and rehydrated
- 259 in PBS or TBS (10 mM Tris–HCl, 155 mM NaCl), pH 7.4. Unreacted aldehydes were reduced with
- 260 70 mM sodium borohydride (NaBH4) in TBS, pH 7.4, for 90 min at room temperature, followed by
- several washes with TBS-0.1%Tx for 2 hrs. Permeabilization was carried out by adding TBS-1%Tx
- to the sections and leaving the tissues ON at 4°C. Then, free-floating sections were processed for
- 263 immunofluorescence as described below.
- 264

# 265 Immunostaining

- 266 Non-specific protein-binding sites were blocked in TBS-0.1%Tx containing 1% BSA, 10% normal
- 267 goat serum (NGS; both from Sigma), pH 7.4 for 1 hr and 30 min at RT. As primary antibodies we
- used the following antibodies produced in rabbit and diluted with 3% BSA in TBS-0.1%Tx, pH 7.4:
- the anti-Vasa antibody (Abcam), diluted 1: 200, anti-Piwil2 (Abcam) diluted 1:50 and anti-TDRKH
- 270 (GeneTex), diluted 1:50, all incubated for 60 hrs at 4°C. After washing, the treated sections were
- 271 incubated with a goat anti-rabbit polyclonal antibody, conjugated with Alexa Fluor 488, diluted
- 1:450 with 1% NGS and 1% BSA in TBS-0.1%Tx for 24 hrs at 4°C and then washed.

273 For alpha-Tubulin Immunostaining see Milani and Maurizii, 2015.

- All the immunostained sections were stained with a nuclear dye, 1  $\mu$ M TO-PRO-3 iodide
- 275 (Molecular Probes), in PBS, pH 7.2, for 10 min at RT and, after washing, mounted in 2.5%
- 276 DABCO (1,4- diazabicyclo [2.2.2] octane (Sigma), 50 mM Tris), pH 8, 90% glycerol. Finally, the
- sections were covered with coverslips, sealed with nail polish and stored at 4°C, in the dark.
- 278 Controls were performed using sections from which the first or the second antibody was replaced
- with 1% normal serum in TBS-0.1%Tx. Sections were examined with a Leica TCS SL confocal
- 280 laser scanning microscope equipped with Ar/He/Ne lasers, employing Leica confocal software.
- 281
- 282 Results
- 283

#### 284 Western blot

285

286 The anti-Vasa antibody detected a single strong band at about 70 kDa (Fig. 1), compatible with the 287 expected MW (Table 1). A band of a molecular weight of about 78 kDa was detected with anti-288 Piwil2 (Fig. 1). Other very light bands of lower or higher MW were visible that can be due to 289 nonspecific signal. For PIWI, the *P. reticulata* expected molecular weight was 116 kDa (Table 1), 290 however if we consider only the functional domains (see Interproscan results; supplementary 291 material) the weight would drop down considerably (up to ~67 kDa for the PAZ domain and the 292 PIWI domain). About TDRKH, of the two isoforms, X1 was 32-AA longer in the N-terminus than 293 X2. InterProScan (supplementary material) found that both the isoform X1 and X2 contain one 294 KH1 and one TUDOR domains (Fig. 1), with the N terminus extension of X1 being not assigned to 295 a specific functional domain. Anti-TDRKH GeneTex antibody detected a strong band compatible 296 with a weight of 63 kDa (Fig. 1), corresponding to the expected weight of the heavier TDRKH 297 isoform.

298

# 299 Histological organization of testis in *Poecilia reticulata*

300

Sections of testis of *P. reticulata* stained with haematoxylin and eosin (HE) show the tubular or "restricted type" organization of the single fused testis (Fig. 2). Cysts move from the periphery to the central region of the gonad where the efferent ducts reside (Fig. 2 a). Cysts containing germ cells in the early stages of spermatogenesis (spermatogonia and spermatocytes) are located near the periphery of the testis (Fig. 2 a). The region immediately beneath the apex of the testis shows cysts of different sizes containing spermatogonia (Fig. 2 b). Numerous and large cysts containing

spermatocytes are recognizable for their smaller size compared to that of spermatogonia (Fig. 2). It 308 is difficult to distinguish cysts containing spermatocytes I from those containing spermatocytes II 309 (Fig. 2). In any case, it must be considered that cysts containing spermatocytes II are seen less 310 frequently than primary spermatocytes as they divide rapidly, after a short interphase between the 2 311 divisions of meiosis. Also, cysts containing only early spermatids are not easily seen (Fig. 2). In 312 fact, spermatids are small cells, spherical in shape with a spherical nucleus with condensed 313 chromatin, that rapidly undergo morphological transformation, becoming spermatozoa through the 314 process called spermiogenesis. Differently, many cysts with numerous spermatids at different stages of spermiogenesis are located deeper, near the efferent ducts (Fig. 2 b, c). In the same region, 315 316 peculiar cysts called "spermatozeugmata", in which spermatozoa are tightly packed (Fig. 2 a, b, c), 317 are also present. Spermatozeugmata show sperm heads oriented towards the Sertoli cells, while 318 flagella are oriented towards the centre of the cyst (Fig. 2D, E). Spermatozeugmata are found also 319 inside the efferent ducts where mature spermatozoa are finally released (Fig. 2 a, f). 320 321 Vasa Immunostaining

322

307

323 Anti-Vasa staining was performed on sections of P. reticulata testis and then Vasa localization 324 pattern was utilized to trace germ cell localization and distribution inside the gonadic tissue.

325

#### IHC 326

327 A strong Vasa immunostaining is evident at the periphery of the testis, in cysts containing 328 spermatogonia and spermatocytes (Fig. 3 a). In testis apical region, spermatogonia inside small 329 cysts show a very strong Vasa staining in the cytoplasm (Fig. 3 b). Vasa appears also abundant in 330 spermatocyte cytoplasm (Fig. 3 b). Furthermore, cysts containing spermatids show a progressively 331 weaker immunostaining as they progress through spermiation (Fig. 3 a, c). In spermatozeugmata, 332 the labelling results dashed and concentrated only at the edges of the cysts, where the sperm heads 333 take contact with the Sertoli cells (Fig. 3 a, c).

334 IF

335 Vasa immunolocalization in testis sections of *P. reticulata* shows the labelling in all cysts

336 containing germ cells at different stages of differentiation (Fig. 4 a). In the apical region, cysts of

337 small size, each containing a generation of spermatogonia according to their different nuclear and

cellular dimensions, are observed (Fig. 4 b). In spermatogonia, Vasa appears localized only in the 338

339 cytoplasm, and particularly abundant to fill the entire cytoplasm. A stronger marking is present

340 around the nucleus, where a deeply fluorescent ring is observed (Fig. 4 b). Unlabeled cells

- 341 positioned between spermatogonia and spermatocyte cysts are probably Sertoli cells not yet
- involved in cyst formation (Fig. 4 b). Also in spermatocytes I, Vasa immunolabeling appears
- 343 cytoplasmatic with a granular distribution (Fig. 4 b). Aggregation of Vasa granules occurs gradually
- in the later stages of spermatogenesis as can be seen in the cytoplasm of spermatocytes II and early
- 345 spermatids (Fig. 4 c). In early spermatids, Vasa aggregates forming a single, big spot located near
- the nucleus (Fig. 4 c inset). In spermatids at different stages of differentiation, Vasa marking is very
- 347 weak with small, stained spots mainly localized in proximity of the nuclei (Fig. 4 c). The
- 348 spermatozoa forming spermatozeugmata result unmarked; the labelling is present only at the
- 349 periphery of the cysts, where sperm heads are in contact with Sertoli cells (Fig. 4 d).
- 350

### 351 **PIWI immunostaining**

#### 352 *IHC*

353 A weak PIWI immunostaining is observed in spermatocytes inside the large cysts located in the 354 apical region and in the spermatids in the different stages of differentiation inside cysts localized 355 both in the periphery and deeper in the testis (Fig. 5 a, b). With this technique, spermatogonia inside small cvsts, typically observed in the apex or in the peripheral region of the testis, result unmarked 356 357 and consequently not recognizable (Fig. 5 a, b). Differently, the immunostaining is well evident in 358 the cysts containing germ cells in the last stages of differentiation. In fact, a dashed marking is 359 observed at the periphery of spermatozeugmata, where the heads of the spermatozoa make contact 360 with the Sertoli cells (Fig. 5 b). Some spermatozeugmata show an additional ring of marking due to 361 the spermatozoa reaching the peripheral region of the cysts (Fig. 5 a, b). Inside some efferent ducts, 362 the peripheral region of spermatozeugmata results marked while in others it appears unmarked 363 (Fig.c). In the former case, the wall of the efferent ducts results clearly immunostained (Fig. 5 c). Mature spermatozoa, after detachment from Sertoli cells, are released into the efferent ducts and 364 365 appear clearly unmarked (Fig. 5 c).

366 *IF* 

367 IF revealed the presence of the PIWI protein in all the cysts containing germ cells in differentiation, 368 but, as shown in Fig. 6 a, the distribution pattern of this protein in germ cells varies in the different 369 differentiation stages. In particular, in spermatogonia, inside small cyst, few labeled granules of the 370 PIWI protein are detected in their cytoplasm; in spermatogonia observed inside a cyst of bigger 371 size, the immunostained granules in their cytoplasm appear increased (Fig. 6 a). In spermatocytes, 372 the presence of PIWI increases when compared to spermatogonia, and numerous marked granules

- are scattered in the cytoplasm (Fig. 6 a). In spermatocytes II, PIWI immunostained granules appear
- to aggregate in the cytoplasm forming bigger spots, while in spermatids a single large granule

appears located on one side of the nucleus (Fig. 6 a). In spermatozeugmata, a dotted marking is
present at the periphery of the cysts, as observed with IHC (Fig. 6 b).

377

# 378 TDRKH Immunostaining

- 379
- 380 *IHC*

381 Anti-TDRKH antibody immunostaining is present in all the cysts that extend from the periphery to 382 the central region of the testis (Fig. 7 a). At higher magnification, the peripheral region shows 383 TDRKH protein in spermatogonia. In cysts containing spermatocytes, the immunostaining is 384 weaker if compared to that of spermatogonia and appears with cytoplasmic localization (Fig. 7 a, b). Differently, the marking is clearly evident in the last stages of germ cells differentiation as for 385 386 example, in cysts containing spermatids in spermiogenesis and in spermatozeugmata, where the 387 immunolabelling is very strong in the peripheral region of the cysts (Fig. 7 b). The wall of some 388 efferent ducts appears clearly immunostained, while the spermatozeugmata inside the efferent ducts 389 results unmarked (Fig. 7 B).

#### 390 *IF*

391 In the cysts containing spermatogonia and spermatocytes at the periphery of the testis TDRKH 392 labeling is detected (Fig. 8 a). In particular, IF reveals that in spermatogonia the immunostained 393 granules are few and scattered in the cytoplasm. In the spermatocytes I, the number of labelled 394 granules increases considerably, and they fill the cytoplasm. In some areas of the cytoplasm, the 395 granules coalesce to form larger aggregates (Fig. 8 a). TDRKH immunolabeling decreases in cysts 396 containing germ cells in more advanced stages of spermatogenesis. In fact, cysts containing 397 spermatocytes II and cysts containing spermatids at different stages of spermiogenesis, show a 398 lower presence of TDRKH (Fig. 8 b). In particular, in the cytoplasm of spermatocytes II and in 399 early spermatids present within the same cyst (Fig. 8 c), the immunostaining appears reduced but 400 numerous granules are scattered in the cytoplasm. Also, a clear TDRKH labelling is observed in the 401 peripheral region of cysts containing spermatozeugmata (Fig. 8 d).

402

#### 403 **Discussion**

404 In this work we highlighted the immunolocalization and distribution pattern of three germline

405 markers, i.e. Vasa, PIWI, and TDRKH proteins, in male germ cells of the fish *P. reticulata*. We

406 used primary polyclonal antibodies in immunoistochemistry (IHC) and immunofluorescence (IF)

407 assays after testing their specificity with Western Blot. To better understand the structural

408 organization of *P. reticulata* testis, a histological study was conducted using sections of testis

- stained with haematoxylin and eosin. Moreover, since the study of germline determinant
- 410 localization requires a clear understanding of the different stages of germ cell differentiation, the
- 411 nuclear dye TO-PRO3 was used at confocal laser scanning microscopy to clarify the differentiation
- 412 stages of male germ cells during spermatogenesis.
- 413 Western blotting with anti-Vasa developed against Vasa zebrafish shows a single marked band of
- 414 about 70-75 kDa, supporting its specificity. Also, this molecular weight corresponds to that
- 415 documented for the marine medaka Oryzias melastigma (Reunov et al., 2020), and only a bit lighter
- 416 than zebrafish Vasa homologue, which is around 80 kDa (Braat et al., 2000). Vasa molecular
- 417 weight in these fish results comparable with that found for Vasa in the mouse *Mus musculus*,
- 418 (MVH), where the molecular weight is around 85 kDa (Toyooka et al., 2000), and in humans, with
- 419 a weigh of 79 kDa (Castrillon et al., 2000). Anti-Piwil2 antibody, developed against the human
- 420 protein, detects a major band of about 78 kDa. The value is lower than the molecular weight of
- 421 PIWI found in zebrafish (Houwing et al., 2007, 2008) and in the mouse (Deng and Lin, 2002). Anti-
- 422 TDRKH developed against TDRKH protein of human shows a strong immunostained band almost
- 423 matching the expected molecular weight of *P. reticulata* TDRKH protein (63.4 kDa the heaviest
- 424 isoform). We did not find in bibliography an observed molecular weight for zebrafish TDRKH,
- however, Western blot analysis of mouse testis shows a highly marked band with anti-TDRKH with
  a molecular weight of approximately 70 kDa (Toyooka et al., 2000).
- To identify germ cells within the testis of *P. reticulata*, we used Vasa as molecular marker given its
  wide spectrum of expression during germ line development (reviewed in Lasko, 2013).
- 429 Vasa immunolocalization is strongest in the peripheral cysts and it is present inside germ cells with
- 430 a cytoplasmatic distribution, evident with both IHC and IF techniques. In particular, cysts
- 431 containing mitotically dividing spermatogonia shows the strongest staining in respect to all other
- 432 germ cells. With IF, we identified two different generations of spermatogonia (Fig. 4 b). The apical
- 433 spermatogonia, with a large nucleus, appears to correspond to type A spermatogonia of mammals
- 434 (Billard, 1984), and similar to other teleosts (Lofts 1968; Billard 1969), and to selachians (Stanley
- 435 1966; Holstein 1968). Instead, spermatogonia of smaller size and with a smaller nucleus (Fig. 4 b)
- 436 appear homologous to type B spermatogonia of mammals that, differently to type A spermatogonia,
- 437 do not mitotically divide but proceed with meiosis (Billard, 1984).
- 438 In spermatogonia and in spermatocytes, the Vasa staining appears granular with the numerous
- 439 stained spots scattered in the cytoplasm (Fig. 4 b). Aggregation of Vasa granules occurs gradually
- 440 in the later stages of spermatogenesis as can be seen in the cytoplasm of spermatocytes II and early
- 441 spermatids (Fig. 4 c). In early spermatids, recognizable in IF for the round nucleus and compacted
- 442 chromatin, Vasa protein aggregates forming a single big spot located near the nucleus (Fig. 4 c,

443 insert). Interestingly, this is similar to Vasa accumulation in the chromatoid body of mammals

444 (Noce et al., 2001; Gustafson and Wessel, 2010), a structure present in sperm cells close to the end

445 of their differentiation. In teleost fishes, the chromatoid body was found in some species, typically

446 in the postmeiotic phase (Yuan et al., 2014 and references therein). However, in some fish, such as

447 *P. reticulata*, no chromatoid body comparable to that of mammals has been described so far (Mattei

and Mattei, 1978; Billard, 1983; Flores and Burns, 1993; Munoz et al., 2002). In this work, IF

showed that spermatid cysts present a progressively weaker marking as they progress through

450 spermiation. Indeed, late spermatids show only some stained spots, preferentially close to the

- 451 elongated nucleus (Fig. 4 d), that probably represent immunostained Vasa contained in the
- 452 cytoplasm of residual bodies.

453 In the spermatozeugmata, in which spermatozoa are tightly packed, a dashed staining is present 454 only at the edge of the cyst, where the sperm heads are in contact with the Sertoli cells, as observed 455 with both the assays (Figs 3 b and 4 d). This peculiar localization of Vasa immunostaining in 456 spermatozeugmata is probably due to the disposal of the residual bodies of the late spermatids that 457 contained Vasa protein in their cytoplasm (Grier, 1981; Uribe, 2014). In the testis of fish with 458 "restricted type" organization, spermatozeugmata migrate towards the efferent ducts and, within 459 them, mature spermatozoa are released, while the residual bodies are phagocytized by the Sertoli 460 cells. After the detachment of spermatozoa, the Sertoli cells move to the periphery of the efferent 461 duct, where they form the wall of the efferent duct (Grier, 1981; Uribe et al., 2014). According to this, in P. reticulata spermatozeugmata inside the efferent ducts, spermatozoa result unmarked after 462 463 their detachment from the Sertoli cells (Fig. 3 b). The Sertoli cells appear unmarked in non-464 spermatozeugmata cyst; in addition, the confocal microscopy observations of small group of clearly 465 unmarked Sertoli cells not yet organized into cysts reinforces this hypothesis (Fig. 4 b). 466 These findings together indicate that the Vasa protein can be used as a germline marker also in P. 467 reticulata. Also, these results are in accordance with what already known in zebrafish (Danio rerio) 468 (Braat et al., 2000) and in Gibel Carp (Carassius auratus gibelio) (Xu et al., 2005). The Vasa 469 distribution pattern in *P. reticulata* appears exclusively cytoplasmatic, as found in other teleost fish 470 such as zebrafish (Houwing et al., 2008) and Gibel Carp (Carassius auratus gibelio) (Xu et al., 471 2005). Also, in *P. reticulata*, Vasa immunostaining is present in spermatogonia, spermatocytes and 472 early spermatids while no staining was detected in spermatozoa. In the Gibel Carp, Vasa was 473 similarly present in spermatogonia but spermatocytes and spermatids show a low Vasa staining (Xu 474 et al., 2005), while in *P. reticulata* Vasa was highly immunodetected also in spermatocytes. In 475 tilapia (Oreochromis niloticus) testis, Vasa protein was localized in spermatogonia and in primary

- 476 spermatocytes but was not observed in secondary spermatocytes and spermatozoa (Kobayashi et al.,
- 477 2002). This indicates for these fish a similar Vasa distribution pattern with modifications.
- 478 In zebrafish, *vasa* mutant gonads do not develop germ cells in the testis, that results empty and
- 479 containing only somatic cells (Hartung et al., 2014). No data is yet available on the effects of vasa
- 480 mutations in *P. reticulata* and functional analyses are necessary to verify its role in this species. In
- 481 any case, the presence of Vasa protein in all the developmental stages suggests that it can have a
- role in the differentiation process of male germ cells during *P. reticulata* spermatogenesis.
- 483 In *P. reticulata*, PIWI is detected from early to later stages of spermatogenesis but absent in
- 484 spermatozoa. However, IHC does not detect PIWI in spermatogonia in the apical region of the
- 485 testis. This is probably due to the low presence of PIWI in spermatogonia, that was nonetheless
- 486 detected in IF (Fig. 6 a). In more advanced spermatogonia, PIWI immunostaining increases, and the
- 487 granules clearly appear with a cytoplasmic distribution.
- 488 In zebrafish, Zili (PIWII2) is found in cytoplasmic granules around spermatogonia and
- 489 spermatocyte nuclei but is seen also in the nucleus showing a dynamic distribution between the two
- 490 cell districts (Houwing et al. 2008); Zili is not detectable in later stages of zebrafish
- 491 spermatogenesis. The same results were also observed in medaka (Li et al. 2012; Zhao et al. 2012).
- 492 In *P. reticulata* spermatocytes I, the presence of PIWI increases further and IF highlights the
- 493 numerous immunostained granules scattered in the cytoplasm. In spermatocytes II, stained granules
- 494 are aggregated forming bigger spots with a clear cytoplasmic distribution (Fig. 6 a). Therefore, in
- 495 male germ cells of *P. reticulata*, PIWI localization appears only cytoplasmatic, no nuclear marking
- 496 was observed in the analyzed stages.
- 497 In zebrafish, Ziwi (PIWII1) is detectable up to spermatids in the last stages of differentiation, with a
- 498 predominant cytoplasmic distribution (Houwing et al., 2007). In the mouse, Miwi (PIWI11) is a
- 499 cytoplasmic protein present only in the male germline from meiotic spermatocytes to elongating
- 500 spermatids and *miwi* knockout is characterized by a block at the early spermatid stage (Deng and
- 501 Lin, 2002). Also in zebrafish, *piwi* genes has a role in meiotic progression of developing sperm as
- shown by the use of mutants. In general, the role of PIWI-like proteins in meiosis appears to be
- 503 conserved during evolution (Thomson and Lin, 2009). In *ziwi* mutant fish, for example,
- 504 gametogenesis occurs but germ cells undergo increased apoptosis, resulting in loss of all germ cells
- 505 by the time fish reach adulthood (Houwing et al., 2007) and *zili* null animals are agametic
- 506 (Houwing et al., 2008).
- 507 In *P. reticulata* early spermatids, a single anti-PIWI-stained large granule appears located on one
- 508 side of the nucleus (Fig 6 b), as seen in Vasa protein immunolocalization. In the mouse, MIWI has
- 509 been localized to the chromatoid body (Kotaja and Sassone-Corsi, 2007). In zebrafish, germ-cell-

510 specific granules appear to be required for the regulation of translational activity in which the Piwi-511 like proteins appear to be involved (Houwing et al., 2007).

512 In *P. reticulata*, a weak PIWI immunostaining is observed also in elongated spermatids near the

513 nuclei, probably representing immunostained PIWI inside the cytoplasm of residual bodies. Also

514 Ziwi in zebrafish (Houwing et al., 2007), but also Miwi in the mouse (Deng and Lin, 2002), are

515 present in late spermatids. In spermatozeugmata cysts of *P. reticulata*, a dashed and well evident

516 marking is visible at the periphery of the cysts (Fig. 6 b). Moreover, within some

517 spermatozeugmata, an additional ring of Piwi immunostaining is present, probably due to late

518 spermatids (or still immature sperm) reaching the peripheral region of the cysts (Fig. 5), where their

519 heads make contact with the Sertoli cells while the flagella are oriented towards the center of the

520 cyst (Fig. 5 b, f). The IHC analyses show that spermatozoa inside the efferent ducts are unmarked

521 after their release from the Sertoli cells and that the Sertoli cells contribute to the duct walls

522 formation (Fig. 3 c). Similar to what observed for Vasa, the staining observed at the periphery of

523 spermatozeugmata can depend by the presence of PIWI protein in the cytoplasm of the residual

524 bodies of the late spermatids. In support of this, we did not observe staining in spermatozeugmata

525 after the detachment of the spermatozoa from the Sertoli cells, the staining is instead evident in the

526 duct wall (Fig. 3 c). However, the wall of some efferent ducts results unmarked (Fig. 3 c), despite

527 the presence inside them of spermatozoa already released by the Sertoli cells. This can be easily

528 explained in the case of efferent ducts in which Sertoli cells have already phagocytized the residual

529 bodies. In this regard, another aspect to consider is the asynchronous activity of the numerous

530 efferent ducts present in fish testis (Grier, 1981), as also occurs in *P. reticulata* (Fig. 3 a, c). No

531 PIWI signal is detected in Sertoli cells inside the cysts containing differentiating germ cells and in

the somatic cells of the gonad, as also described in zebrafish (Houwing et al., 2007, 2008), and in

533 the mouse (Deng and Lin, 2002).

534 Given the functions of TDRKH protein in germ cell maintenance and transposon silencing together

535 with PIWI, we analyzed the immunolocalization pattern of TDRKH and its cellular distribution

536 during *P. reticulata* spermatogenesis. TDRKH presence in the same differentiation stages as PIWI

537 would have suggest a similar function in the germ cells of this fish.

538 In *P. reticulata* testis, both IHC and IF reveal TDRKH presence from spermatogonia to spermatids

539 in advanced stages of spermiation, while spermatozoa resulted unmarked (Fig.7 b). No data on

540 TDRKH localization pattern in fish has been reported so far. In the mouse, immunofluorescence

541 analyses detected TDRKH in spermatogonia, spermatocytes, and round spermatids, but not in

642 elongating spermatids (Saxe et al., 2013). In *P. reticulata*, IHC detect strongly TDRKH protein in

543 spermatogonia while a lower staining is present in spermatocytes and spermatids. In *P. reticulata*,

- 544 IF detects few TDRKH immunostained granules in the cytoplasm of early spermatogonia while the
- 545 granules increase in the cytoplasm of more advanced spermatogonia inside larger cysts. This
- 546 immunolocalization pattern of TDRKH is similar to that observed for PIWI, but different to what
- 547 we documented for Vasa, which is highly immunostained also in early spermatogonia. In
- 548 spermatocytes I, TDRKH granules increase further in number, and their distribution still appear
- only cytoplasmic, as no nuclear marking is observed in nuclei in all the stages of spermatogenesis
- analyzed. In the mouse, TDRKH staining is present in the cytoplasm of spermatogonia with a
- 551 granular pattern and resulted particularly strong in meiotic primary spermatocytes, correlating with
- the onset of meiosis; in fact, *tdrkh*-null mutants show meiotic arrest at the zygotene stage (Saxe et
- 553 al., 2013; Wang et al., 2020).
- 554 In P. reticulata spermatocytes II, IF detects numerous immunostained granules of TDRKH
- scattered in the cytoplasm and in the round spermatids many granules are visible as well (Fig. 8 c),
- similarly to what described in the mouse (Toyooka et al., 2000; Saxe, 2013). Indeed, in the mouse,
- 557 TDRKH does not aggregate in the chromatoid body, but immunostained granules remain scattered
- 558 in the cytoplasm (Ding et al., 2019; Wang et al., 2020). However, it has been demonstrated that
- 559 TDRKH deficiency affects the localization of MIWI in the chromatoid body and spermiogenesis
- 560 arrests (Meikar et al., 2014; Ding et al., 2019).
- 561 Thus, in *P. reticulata* testis, IHC detects a strong anti-TDRKH staining in spermatogonia, while a
- smaller amount is found in spermatocytes and spermatids. The TDRKH marking observed in
- solution for the second second
- 564 protein in the cytoplasm of residual bodies, as discussed for Vasa and PIWI.
- 565 TDRKH is immunodetected specifically in the germ cells of *P. reticulata* and no specific signal is
- 566 detected in Sertoli cells and in the other somatic cells of the gonad supporting a germ cell-specific
- 567 function of TDRKH as already observed in the mouse (Virant-Klun et al., 2016).
- 568

#### 569 Conclusions

- 570
- 571 The results from the two assays used in this study (IF and IHC) are in accordance with each other,
- with the IF analyses at the confocal microscope allowing, as expected, the observation of a more
- 573 detailed distribution pattern of the proteins in the cytoplasm of germ cells.
- 574 Vasa has the strongest staining in the cytoplasm of early spermatogonia, with the staining that
- 575 decreases throughout differentiation, instead both PIWI and TDRKH staining increases during
- 576 differentiation. Interestingly, Vasa and PIWI granules aggregate forming larger aggregates up to a
- single spot in spermatids, as observed in the mouse (Noce et al., 2001; Gustafson and Wessel, 2010;

578	Kotaja et al., 2006); instead, TDRKH granules are scattered in the cytoplasm and do not appear to
579	aggregate in a single spot, similarly to what observed in the mouse (Ding et al., 2019; Wang et al.,
580	2020). Immunolocalization of PIWI and TDRKH in the same stages of germ cell differentiation and
581	with a distribution pattern similar to that observed in the mouse (Saxe et al., 2013) may suggest
582	their concerted partecipation in the piRNA pathway also in this fish.
583	
584	Author contributions
585	M.G.M. and L.M.: Conceptualization and Supervision; F.C. and M.I.: Formal analysis; L.M., F.C.,
586	M.I., M.L., V.F., M.G.M.: Investigation; L.M., M.L., V.F., M.G.M.: Resources; M.G.M.: Writing -
587	Original Draft; All the authors: Writing - Review & Editing, and Visualization.
588	
589	Availability of data and materials
590	Data and materials are available upon reasonable request. Address to M.G.M.
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592	
593	Conflict of interest
594	None.
595	
596	Figure legends
597	
598	Fig. 1. Western blot. WB with anti-Vasa, anti-PIWI and anti-TDRKH on <i>P. reticulata</i> total protein
599	testis homogenate (30 $\mu$ g). See table 1 for predicted molecular weights. Protein standard molecular
600	weights on the left of each panel.
601	
602	Fig. 2. Sections of <i>P. reticulata</i> testis stained with HE. $\mathbf{a}$ – The section shows the "Restricted type
603	organization" of the testis. The cysts, from the periphery to the central region, contain germ cells in
604	different stages of differentiation. In the central region of the testis, many efferent ducts are present

- 605 (ED). **b** Magnification of Figure 2a showing the cysts in different stages of differentiation
- 606 containing, from the periphery to the central region of testis: spermatogonia (Sg), then
- 607 spermatocytes (Sc) and spermatids at different stages of spermiation (St1, St2, St3). The cysts at
- more advanced phases of spermatogenesis, called spermatozeugmata (Sz), are positioned closer to
- 609 the center of the testis. c Magnification of the region showed in Figure 2b with cysts containing
- 610 spermatids (st) and cysts containing spermatozeugmata (Sz) with different levels of organization of
- 611 spermatozoa inside them. In larger spermatozeugmata, the sperm heads are oriented towards Sertoli

612 cells (SC) arranged at the periphery of the cysts, while flagella facing inwards; in smaller

- 613 spermatozeugmata (\*), the sperm heads they are not all in contact with the Sertoli cells (SC). d –
- 614 High magnification of a portion of spermatozeugmata (Sz) showing sperm heads in contact with the
- 615 Sertoli cells (SC), and flagella oriented towards the inside of the cyst. **e** High magnification of a
- 616 portion of spermatozeugmata in which the TO-PRO-3 nuclear dye shows the sperm heads (in green)
- 617 near the Sertoli cells (SC), while the anti-alpha tubulin stained the flagella (in red) extending
- 618 towards the center of the cyst.  $\mathbf{f}$  Magnification of an efferent duct (ED) with inside many
- 619 spermatozeugmata (Sz). In some of them, the spermatic heads are located in the proximity to Sertoli
- 620 cells (arrow) while in others, the detachment of spermatozoa (\*) from Sertoli cells are visible. [Sg:
- 621 spermatogonia; Sc: spermatocytes; St: spermatids; Sz: spermatozeugmata; SC: Sertoli cells; ED:
- 622 efferent ducts].
- 623

624 Fig. 3. Immunolocalization of Vasa on sections of P. reticulata testis by IHC. a - Immunostained 625 section showing the labelling in the cysts that extend from the periphery to the central region of the 626 section. A more evident marking is present in the cysts with germ cells in the early stages of 627 differentiation (spermatogonia: Sg; spermatocytes: Sc) localized at the periphery of testis.  $\mathbf{b}$  – 628 Magnification of a portion of the section showed in Figure 3a in which spermatogonia (Sg) result 629 strongly marked. An evident immunostaining is also observed in the cysts containing spermatocytes 630 (Sc).  $\mathbf{c}$  – A lower immunomarking is present in the cysts containing early spermatids (St), which is 631 further reduced in those containing spermatids at more advanced stages of spermiation (St1; St2; 632 St3). In spermatozeugmata (Sz), the labelling with anti-Vasa antibody is evident on the periphery of 633 cysts (arrowheads) near Sertoli cells (SC) and appears as dashed labelling. [Sg: spermatogonia; Sc: 634 spermatocytes; St: spermatids; Sz: spermatozeugmata; Sp: spermatozoa; SC: Sertoli cells]. 635

636 Fig. 4. Immunolocalization of Vasa on sections of *P. reticulata* testis by IF. a – Section containing 637 a portion of testis extended from the periphery to the central region. The immunolabeling is most 638 evident in peripheral cysts. Vasa immunostaining is present in cysts containing germ cells at 639 different stages of differentiation (spermatogonia: Sg; spermatocytes: Sc; spermatids: St1,2). b -640 Magnification of peripheral cysts showing a strong Vasa staining in spermatogonia (Sg) and 641 spermatocytes (Sc). In particular, in spermatogonia (Sg1, Sg2) contained in the two small cysts, 642 Vasa results very abundant and spread in their cytoplasm. A fluorescent ring is observed around the 643 nucleus of spermatogonia (arrowheads). The group of unlabeled cells seen between spermatogonia 644 and spermatocyte cysts are probably unmarked Sertoli cells (SC) not yet involved in cyst formation. 645 In spermatocytes I (ScI), the cytoplasmatic Vasa immunolabeling appears with granular

646 distribution.  $\mathbf{c}$  – Higher magnification of some cysts containing germ cells at different stages of 647 differentiation. In spermatocytes II (Sc II) aggregation of Vasa granules occurs in the cytoplasm. In 648 early spermatids (st), Vasa aggregates forming a single big spot (arrowhead) located near the 649 nucleus (inset). In spermatids at advanced stages of differentiation (St3), small stained spots of 650 Vasa localized mainly in proximity of the nuclei (arrowhead). d - In spermatozeugmata (Sz), Vasa 651 immunostaining is detectable at cysts periphery (\*), where sperm heads make contact with Sertoli 652 cells. Inside spermatozeugmata (Sz) some sperm heads and small Vasa-stained spots are observed. 653 [Sg: spermatogonia; Sc: spermatocytes; St: spermatids; Sz: spermatozeugmata; SC: Sertoli cells]. In 654 red Vasa staining, in green TO-PRO-3 nuclear dye.

655

Fig. 5. Immunolocalization of Piwi on sections of P. reticulata testis by IHC. a –Section showing 656 657 apical and central regions of the testis. A weak immunostaining is observed inside apical cysts 658 containing spermatocytes (Sc). Cysts containing spermatogonia typically located in the peripheral 659 region result unmarked. The peripheral region (\*) of spermatozeugmata (Sz) shows a strong and 660 dotted marking. In the central region many efferent ducts (ED) are present, with marked and 661 unmarked spermatozeugmata inside.  $\mathbf{b}$  – Magnification of a portion of testis showing a weak 662 labeling in cysts containing spermatocytes and spermatids (spermatocytes: Sc; spermatids: St). The 663 spermatozeugmata cysts (Sz) are at different stages of formation. In some spermatozeugmata, the 664 immunostaining is present only at the periphery of the cyst (\*) while in others an additional marked 665 ring is observed inside the cyst (Arrowhead).  $\mathbf{c}$  – Deep region of testis showing many efferent ducts 666 (ED) with unmarked spermatozeugmata (Sz) inside. The wall of the efferent ducts shows evident 667 marking (Arrows). [Sg: spermatogonia; Sc: spermatocytes; St: spermatids; Sz: spermatozeugmata; 668 SC: Sertoli cells].

669

670 Fig. 6. Immunolocalization of PIWI on sections of *P. reticulata* testis by IF. a – PIWI localization 671 in germ cells at different development stages. In spermatogonia inside small cyst (Sg1), few 672 immunolabeled spots are visible in their cytoplasm; inside a bigger cyst, spermatogonia (Sg2) show 673 an increased number of the immunostained granules in their cytoplasm. In spermatocytes I (Sc I), 674 numerous marked granules are scattered in the cytoplasm. Bottom left, a portion of a cyst with 675 spermatocytes II (ScII) showing numerous immunostained granules (see also inset). **b** – PIWI 676 localization in germ cells at advanced stages of differentiation. In the inset, magnification of a 677 portion of cyst containing early spermatids (St) with only a big spot near the nucleus (arrowhead). 678 In spermatozeugmata (Sz), the dotted marking results at the periphery of the cysts (\*). [Sg:

- spermatogonia; Sc: spermatocytes; St: spermatids; Sz: spermatozeugmata; SC: Sertoli cells]. In
  magenta, anti-PIWI staining, in green TO-PRO-3 nuclear dye.
- 681

682 Fig. 7. Immunolocalization of TDRKH on sections of *P. reticulata* testis by IHC. a – Portion of 683 section showing the labelling in cysts that extend from the periphery to the central region of the 684 testis. A more evident marking is present in spermatogonia (Sg) contained in small cysts and in 685 germ cells at more advanced stages of differentiation (Sz). In the central region, the wall of some 686 efferent ducts (ED), transversely sectioned, is strongly marked. **b** – Portion of a section showing 687 spermatogonia (Sg) and spermatocytes (Sc) clearly marked. A strong immunostaining is observed at 688 the periphery (\*) of spermatozeugmata (Sz). Inside the efferent ducts (ED) unmarked spermatozeugmata (Sz) are present. Wall portion of some efferent ducts results strongly 689 690 immunostained (arrows). Below in the section, the large efferent duct (ED) shows unmarked wall. 691 Inside, unmarked spermatozeugmata (Sz) are present. [Sg: spermatogonia; Sc: spermatocytes; St: 692 spermatids; Sz: spermatozeugmata; SC: Sertoli cells; ED: efferent ducts]. 693 694 Fig. 8. Immunolocalization of TDRKH on sections of *P. reticulata* testis by IF. a – TDRKH 695 immunostaining in the cysts containing spermatogonia and spermatocytes at the periphery of the 696 testis. Bottom right, spermatogonia (Sg) show few immunostained granules in the cytoplasm. In 697 spermatocytes I (ScI), the labelled granules increase compared to spermatogonia and they fill the 698 cytoplasm. In some areas of the cytoplasm, the granules coalesce to form larger aggregates 699 (arrowhead). **b** – Cysts containing immunostained germ cells at different stages of differentiation: 700 (Sg: spermatogonia; ScI: spermatocytes I; ScII: spermatocytes II; St: spermatids; Sz: 701 spermatozeugmata).  $\mathbf{c}$  – Portion of section showing cysts containing germ cells at advanced stage of 702 differentiation. On the top, the large cyst contains both spermatocytes II (\*) and spermatids 703 (arrowhead). Inset: immunostained granules of TDRKH are visible in the cytoplasm of 704 spermatocytes II (\*) and round spermatids (arrowhead).). d – In spermatids at advanced stage of 705 spermiogenesis (St3), immunostained spots show a prevalent localization near the nucleus (see 706 inset). In spermatozeugmata (Sz), the labelling is present in the peripheral region of the cyst (\*) [Sg: 707 spermatogonia; Sc: spermatocytes; St: spermatids; Sz: spermatozeugmata]. In red anti-TDRKH 708 staining, in green TO-PRO-3 nuclear dye. 709

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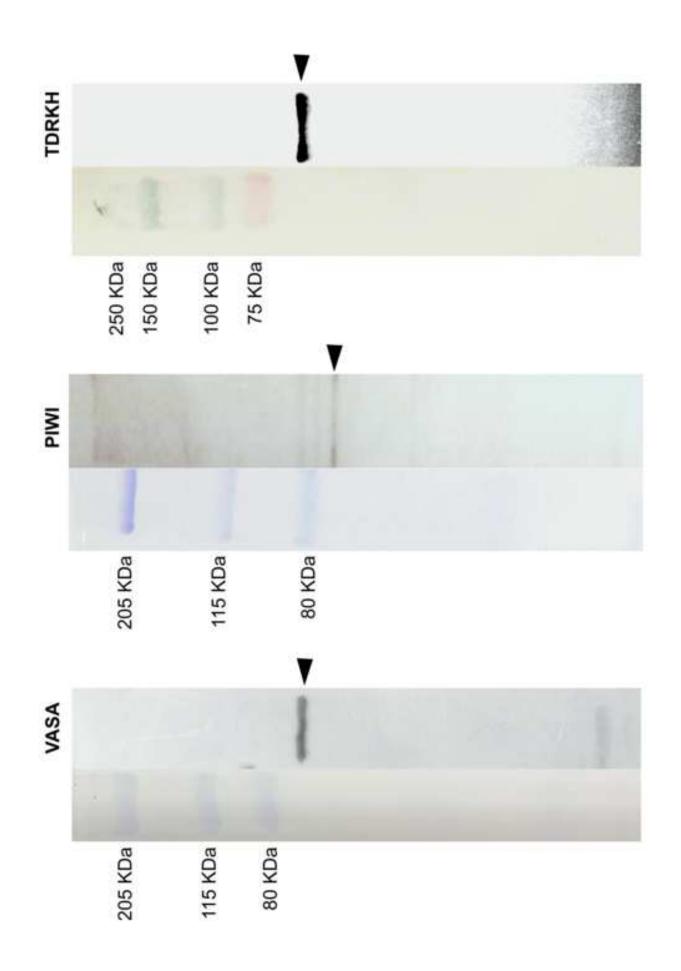
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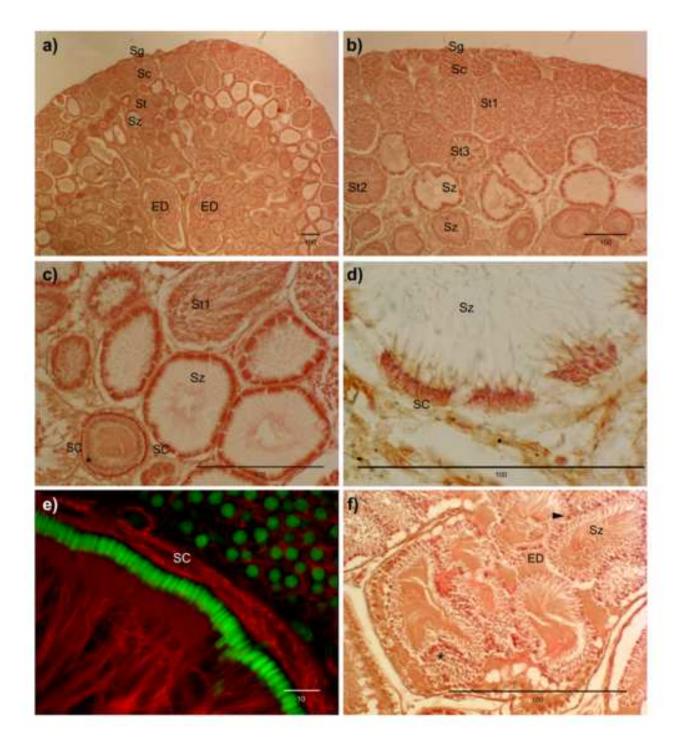
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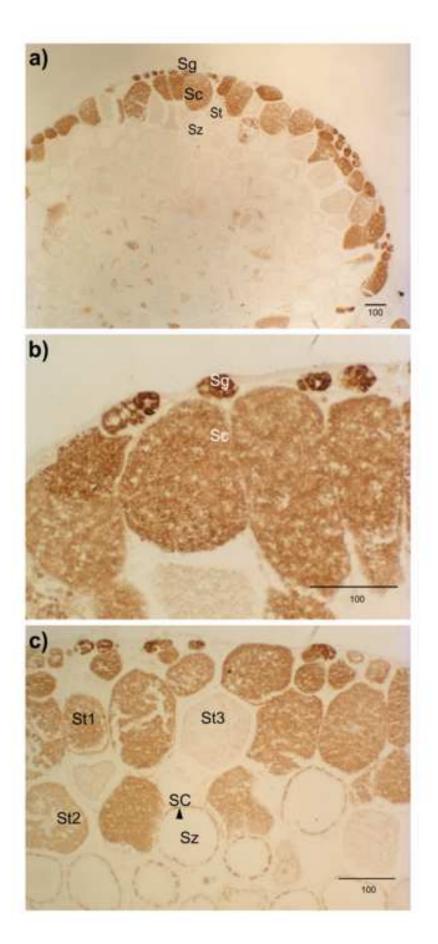
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- 946 carp (*Cyprinus carpio*) ovaries. Gen. Comp. Endocrinol. 176, 126-131.
- 947
- 948
- 949 **Table 1.** Predicted and observed (WB) protein molecular weight and list of primary antibodies
- 950 used.

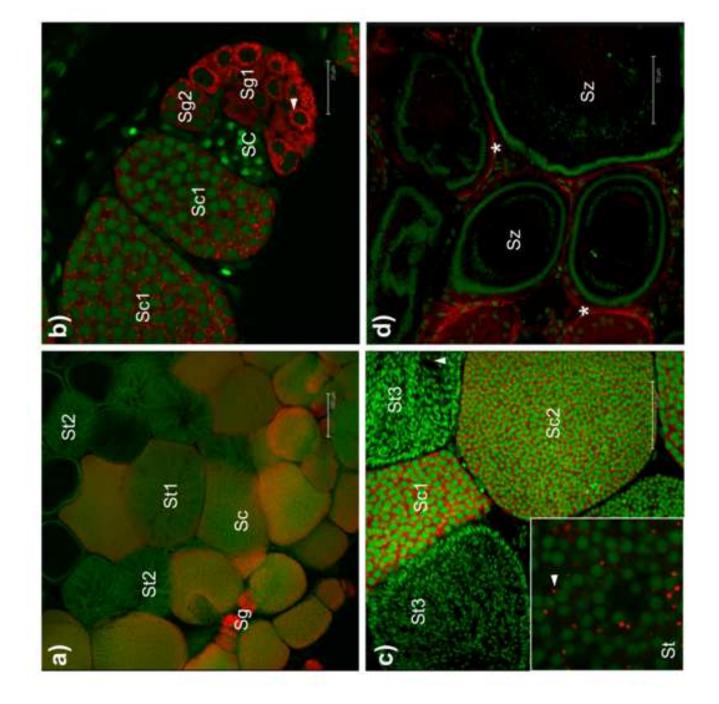
Predicted protein [Poecilia reticulata]	NCBI	MW predicted
ATP-dependent RNA helicase DDX4	XP_008428196.1	70 kDa
Piwi-like protein 2	XP_008415818.1	116 kDa
Tudor and KH domain-containing protein	XP_008436386.1 (isoform X1)	63.4 kDa
	XP_008436387.1 (isoform X2)	59.9 kDa
	Ab1	MW observed
Anti-VASA	Abcam, ab209710 (1:2,000)	~ as predicted
Anti-PIWI12	Abcam, ab98852 (1:500)	~ 78 kDa
Anti-TDRKH	GeneTex, GTX129795 (1:1,000)	~ as predicted

951 Note: ExPaSy (www.expasy.org) predicted the molecular weight (MW) of the analyzed proteins.

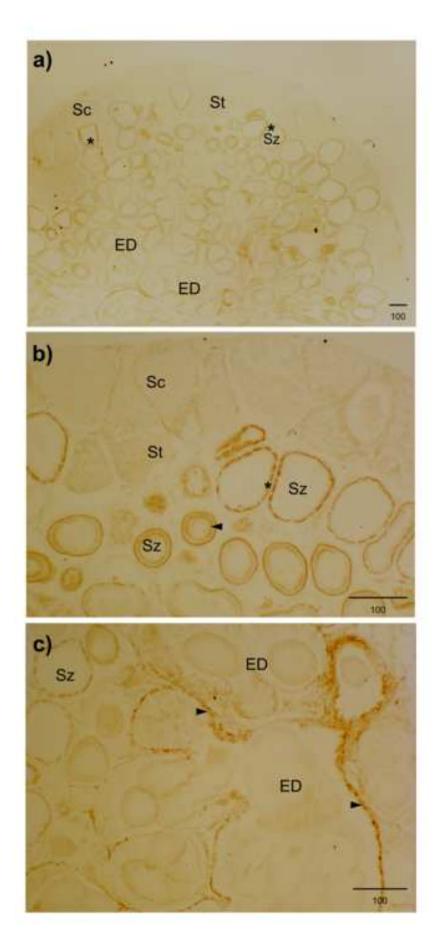


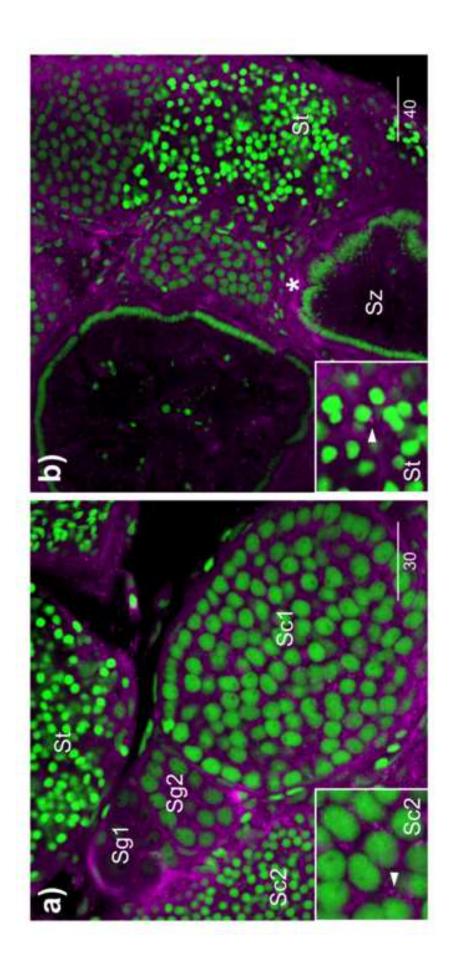


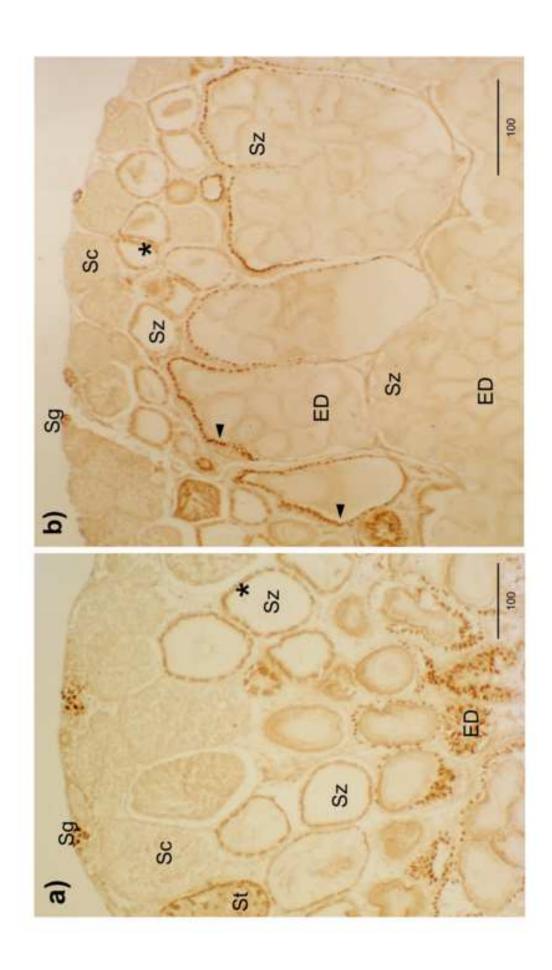


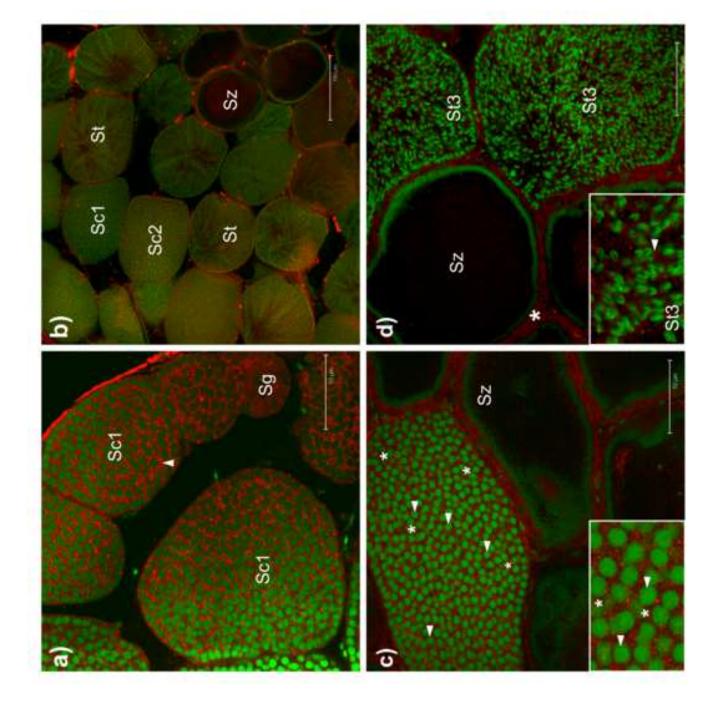












# **Supplementary Materials**

Analysis	Signature accession	n Signature description	Start	Stop	e	-value	InterPro accession	InterPro description
MobiDBLite ProSitePatterns		consensus disorder prediction DEAD-box subfamily ATP-dependent helicases signature.		5 <b>2</b> :	174 - 370 -		- IPR000629	- ATP-dependent RNA helicase DEAD-box, conserved s
PANTHER SMART	PTHR47958:SF11 SM00490	ATP-DEPENDENT RNA HELICASE DDX4-RELATED helicmild6			598 553	0 8.30E-35	- IPR001650	- Helicase, C-terminal
MobiDBLite	mobidb-lite	consensus disorder prediction			108 -	0.502 55	-	-
Pfam	PF00271	Helicase conserved C-terminal domain				4.00E-31	IPR001650	Helicase, C-terminal
MobiDBLite	mobidb-lite	consensus disorder prediction	:	27	43 -		-	-
PANTHER	PTHR47958	ATP-DEPENDENT RNA HELICASE DBP3	1	74 !	598	0	-	-
ProSiteProfiles	PS51195	DEAD-box RNA helicase Q motif profile.			234	11.11268	IPR014014	RNA helicase, DEAD-box type, Q motif
MobiDBLite	mobidb-lite	consensus disorder prediction		59	75 -		-	-
Pfam	PF00270	DEAD/DEAH box helicase					IPR011545	DEAD/DEAH box helicase domain
Gene3D ProSiteProfiles	G3DSA:3.40.50.300 PS51194	- Superfamilies 1 and 2 helicase C-terminal domain profile.			597 593		IPR027417 IPR001650	P-loop containing nucleoside triphosphate hydrolase Helicase, C-terminal
MobiDBLite	mobidb-lite	consensus disorder prediction			595 639 -	24.3000	-	-
MobiDBLite	mobidb-lite	consensus disorder prediction			160 -		-	-
ProSiteProfiles	PS51192	Superfamilies 1 and 2 helicase ATP-binding type-1 domain profile.				31.82966	IPR014001	Helicase superfamily 1/2, ATP-binding domain
CDD	cd18787	SF2_C_DEAD	4	33 !	562	7.05E-60	-	-
Gene3D	G3DSA:3.40.50.300	-			424	2.40E-81	IPR027417	P-loop containing nucleoside triphosphate hydrolase
SMART	SM00487	ultradead3				5.50E-64	IPR014001	Helicase superfamily 1/2, ATP-binding domain
MobiDBLite	mobidb-lite	consensus disorder prediction			628 -		-	-
CDD	cd18052	DEADc_DDX4			427	0	-	-
MobiDBLite SUPERFAMILY	mobidb-lite SSF52540	consensus disorder prediction		11 84 !	26 -	4 615 72	- IPR027417	- D loop containing publication triphosphoto hudrolase
Gene3D	G3DSA:2.170.260.10	P-loop containing nucleoside triphosphate hydrolases paz domain				1.10E-38		P-loop containing nucleoside triphosphate hydrolase
MobiDBLite	mobidb-lite	consensus disorder prediction			145 -	1.102 50	-	-
Pfam	PF02170	PAZ domain				4.60E-32	IPR003100	PAZ domain
PANTHER	PTHR22891:SF111	PIWI-LIKE PROTEIN 2			055	0		-
SMART	SM00950	Piwi_a_2			041 9	0.00E-123	IPR003165	Piwi domain
MobiDBLite	mobidb-lite	consensus disorder prediction			263 -		-	-
CDD	cd02845	PAZ_piwi_like				9.18E-55		-
CDD	cd04658	Piwi_piwi-like_Euk			038	0		-
SUPERFAMILY	SSF101690	PAZ domain					IPR036085	PAZ domain superfamily
ProSiteProfiles Gene3D	PS50821	PAZ domain profile.				21.01985 2.40E-31	IPR003100	PAZ domain
PANTHER	G3DSA:3.40.50.2300 PTHR22891	EUKARYOTIC TRANSLATION INITIATION FACTOR 2C			055	2.40E-51		-
SMART	SM00949	PAZ_2_a_3					IPR003100	PAZ domain
Gene3D	G3DSA:3.30.420.10						IPR036397	Ribonuclease H superfamily
ProSiteProfiles	PS50822	Piwi domain profile.					IPR003165	Piwi domain
Pfam	PF02171	Piwi domain	7!	50 10	040	9.20E-82	IPR003165	Piwi domain
SUPERFAMILY	SSF53098	Ribonuclease H-like					IPR012337	Ribonuclease H-like superfamily
CDD	cd00105	KH-I Region of a membrane-bound protein predicted to be embedded in the	1	54 2	219	7.16E-14	-	-
Phobius	TRANSMEMBRANE	membrane.		44	62 -		-	-
Pfam	PF00013	KH domain					IPR004088	K Homology domain, type 1
Gene3D	G3DSA:3.30.310.210	-				2.80E-16		-
Gene3D SUPERFAMILY	G3DSA:2.30.30.140 SSF54791	- Eukaryotic type KH-domain (KH-domain type I)				1.20E-66	- IPR036612	- K Homology domain, type 1 superfamily
SMART	SM00322	kh_6					IPR004087	K Homology domain
		Region of a membrane-bound protein predicted to be outside the						
Phobius	NON_CYTOPLASMIC_	Imembrane, in the extracellular region.	ſ	53 !	578 -		-	-
PANTHER	PTHR22948:SF18	TUDOR AND KH DOMAIN-CONTAINING PROTEIN			566 1	.10E-114	-	-
Pfam	PF00567	Tudor domain	32	28 4	450	6.90E-25	IPR002999	Tudor domain
		Region of a membrane-bound protein predicted to be embedded in the						
	TRANSMEMBRANE	membrane.		12	32 -		-	-
Phobius		Design of a membrane bound protein and distribute be extended of						
		Region of a membrane-bound protein predicted to be outside the		13	<b>D</b> 3		-	_
Phobius		A membrane, in the cytoplasm.		33 80 4	43 - 439	10.28092	- IPR002999	- Tudor domain
Phobius ProSiteProfiles	CYTOPLASMIC_DOMA PS50304 PTHR22948	A membrane, in the cytoplasm. Tudor domain profile.	38	80 4	439		- IPR002999 -	- Tudor domain -
Phobius	PS50304	A membrane, in the cytoplasm.	38	80 4 43 !	439 566 1	10.28092 1.10E-114 5.19E-22	-	- Tudor domain - -
Phobius ProSiteProfiles PANTHER	PS50304 PTHR22948	A membrane, in the cytoplasm. Tudor domain profile. TUDOR DOMAIN CONTAINING PROTEIN	38	80 4 43 5 56 4 52 2	439 566 1 451 218	10E-114 5.19E-22 16.14333	-	- Tudor domain - - -
Phobius ProSiteProfiles PANTHER SUPERFAMILY ProSiteProfiles Gene3D	PS50304 PTHR22948 SSF63748 PS50084 G3DSA:2.40.50.90	A membrane, in the cytoplasm. Tudor domain profile. TUDOR DOMAIN CONTAINING PROTEIN Tudor/PWWP/MBT Type-1 KH domain profile.	38 35 15 33	80 4 43 5 56 4 52 2 34 5	439 566 1 451 218 519	1.10E-114 5.19E-22 16.14333 1.20E-66	- - - IPR035437	- - - SNase-like, OB-fold superfamily
Phobius ProSiteProfiles PANTHER SUPERFAMILY ProSiteProfiles Gene3D SMART	PS50304 PTHR22948 SSF63748 PS50084 G3DSA:2.40.50.90 SM00333	A membrane, in the cytoplasm. Tudor domain profile. TUDOR DOMAIN CONTAINING PROTEIN Tudor/PWWP/MBT Type-1 KH domain profile. TUDOR_7	38 35 15 33	80 4 43 5 56 4 52 2 34 9 79 4	439 566 1 451 218 519 437	1.10E-114 5.19E-22 16.14333 1.20E-66 1.10E-04	- - - IPR035437 IPR002999	- - Svase-like, OB-fold superfamily Tudor domain
Phobius ProSiteProfiles PANTHER SUPERFAMILY ProSiteProfiles Gene3D	PS50304 PTHR22948 SSF63748 PS50084 G3DSA:2.40.50.90	A membrane, in the cytoplasm. Tudor domain profile. TUDOR DOMAIN CONTAINING PROTEIN Tudor/PWWP/MBT Type-1 KH domain profile. - TUDOR_7 TUDOR	38 35 15 33	80 4 43 5 56 4 52 2 34 9 79 4	439 566 1 451 218 519 437	1.10E-114 5.19E-22 16.14333 1.20E-66 1.10E-04	- - - IPR035437	- - - SNase-like, OB-fold superfamily
Phobius ProSiteProfiles PANTHER SUPERFAMILY ProSiteProfiles Gene3D SMART CDD	PS50304 PTHR22948 SSF63748 PS50084 G3DSA:2.40.50.90 SM00333 cd04508	Amembrane, in the cytoplasm. Tudor domain profile. TUDOR DOMAIN CONTAINING PROTEIN Tudor/PWWP/MBT Type-1 KH domain profile. TUDOR, 7 TUDOR Region of a membrane-bound protein predicted to be outside the	38 39 19 33 31 31 31 38	80 4 43 5 56 4 52 2 34 9 79 4 84 4	439 566 1 451 218 519 437 431	1.10E-114 5.19E-22 16.14333 1.20E-66 1.10E-04	- - - IPR035437 IPR002999	- - Svase-like, OB-fold superfamily Tudor domain
Phobius ProSiteProfiles PANTHER SUPERFAMILY ProSiteProfiles Gene3D SMART CDD Phobius	PS50304 PTHR22948 SSF63748 PS50084 G3DSA:2.40.50.90 SM00333 cd04508 NON_CYTOPLASMIC_	A membrane, in the cytoplasm. Tudor domain profile. TUDOR DOMAIN CONTAINING PROTEIN Tudor/PWWP/MBT Type-1 KH domain profile. TUDOR_7 TUDOR Region of a membrane-bound protein predicted to be outside the Imembrane, in the extracellular region.	38 39 19 33 31 31 31 31	80 4 43 9 56 4 52 2 34 9 79 4 84 4	439 566 1 451 218 519 437 431	1.10E-114 5.19E-22 16.14333 1.20E-66 1.10E-04 2.48E-11	- - - IPR035437 IPR002999 -	- - SNase-like, OB-fold superfamily Tudor domain Tudor domain -
Phobius ProSiteProfiles PANTHER SUPERFAMILY ProSiteProfiles Gene3D SMART CDD	PS50304 PTHR22948 SSF63748 PS50084 G3DSA:2.40.50.90 SM00333 cd04508	A membrane, in the cytoplasm. Tudor domain profile. TUDOR DOMAIN CONTAINING PROTEIN Tudor/PWWP/MBT Type-1 KH domain profile. TUDOR_7 TUDOR Region of a membrane-bound protein predicted to be outside the Imembrane, in the extracellular region. Tudor domain	38 39 19 33 31 31 31 31	80 4 43 9 56 4 52 2 34 9 79 4 84 4	439 566 1 451 218 519 437 431	1.10E-114 5.19E-22 16.14333 1.20E-66 1.10E-04 2.48E-11	- - - IPR035437 IPR002999	- - Svase-like, OB-fold superfamily Tudor domain
Phobius ProSiteProfiles PANTHER SUPERFAMILY ProSiteProfiles Gene3D SMART CDD Phobius	PS50304 PTHR22948 SSF63748 PS50084 G3DSA:2.40.50.90 SM00333 cd04508 NON_CYTOPLASMIC_	A membrane, in the cytoplasm. Tudor domain profile. TUDOR DOMAIN CONTAINING PROTEIN Tudor/PWWP/MBT Type-1 KH domain profile. TUDOR_7 TUDOR Region of a membrane-bound protein predicted to be outside the Imembrane, in the extracellular region.	38 39 19 33 31 38 29	80 4 43 9 56 4 52 2 34 9 79 4 84 4	439 566 1 451 218 519 437 431	1.10E-114 5.19E-22 16.14333 1.20E-66 1.10E-04 2.48E-11	- - - IPR035437 IPR002999 -	- - SNase-like, OB-fold superfamily Tudor domain Tudor domain -
Phobius ProSiteProfiles PANTHER SUPERFAMILY ProSiteProfiles Gene3D SMART CDD Phobius Pfam	PS50304 PTrR22948 SSF63748 PS50084 G3DSA:2.40.50.90 SM00333 cd04508 NON_CYTOPLASMIC_ PF00567	A membrane, in the cytoplasm. Tudor domain profile. TUDOR DOMAIN CONTAINING PROTEIN Tudor/PWWP/MBT Type-1 kH domain profile. TUDOR, 7 TUDOR, 7 TUDOR Region of a membrane-bound protein predicted to be outside the Imembrane, in the extracellular region. Tudor domain Region of a membrane-bound protein predicted to be embedded in the	38 39 19 33 33 31 38 29	80 4 43 9 56 4 52 2 33 2 1 1 1 1 1 1 1 1	439 566 1 451 218 519 437 431 <u>11 -</u> 418 30 -	1.10E-114 5.19E-22 16.14333 1.20E-66 1.10E-04 2.48E-11	- IPR035437 IPR002999 IPR002999 - IPR002999 -	- - SNase-like, OB-fold superfamily Tudor domain Tudor domain -
Phobius ProSiteProfiles PANTHER SUPERFAMILY ProSiteProfiles Gene3D Phobius Pfam TMHMM Gene3D PANTHER	PS50304 PTHR22948 SSF63748 PS50084 G3DSA:2.40.50.90 SM00333 cd04508 NON_CYTOPLASMIC PF00567 TMhelix G3DSA:3.30.310.210 PTHR22948:SF18	A membrane, in the cytoplasm. Tudor domain profile. TUDOR DOMAIN CONTAINING PROTEIN Tudor/PWWP/MBT Type-1 KH domain profile. TUDOR, 7 TUDOR, 7 TUDOR, 7 TUDOR Region of a membrane-bound protein predicted to be outside the Imembrane, in the extracellular region. Tudor domain Tudor domain Tudor And mathrane-bound protein predicted to be embedded in the membrane. TUDOR AND KH DOMAIN-CONTAINING PROTEIN	33 33 19 33 33 33 34 29 29	80         4           443         9           556         4           552         2           334         9           779         4           884         4           1         1           13         568           11         9	439 566 1 451 218 519 437 431 <u>11 -</u> 418 30 - 195 534 1	.10E-114 5.19E-22 16.14333 1.20E-66 1.10E-04 2.48E-11 6.30E-25 2.50E-16 L.00E-114	- IPR035437 IPR02999 IPR002999 - IPR002999 - -	- - SNase-like, OB-fold superfamily Tudor domain Tudor domain -
Phobius ProSiteProfiles PANTHER SUPERFAMILY ProSiteProfiles Gene3D SMART CDD Phobius Pfam TMHMM Gene3D	PS50304 PTHR22948 SSF63748 PS50084 G3D5A:2.40.50.90 SM00333 cd04508 NON_CYTOPLASMIC_ PF00567 TMhelix G3DSA:3.30.310.210	A membrane, in the cytoplasm. Tudor domain profile. TUDOR DOMAIN CONTAINING PROTEIN Tudor/PWWP/MBT Type-1 KH domain profile. 	33 33 19 33 33 33 34 29 29	80         4           443         9           556         4           552         2           334         9           779         4           884         4           1         1           13         568           11         9	439 566 1 451 218 519 437 431 <u>11 -</u> 418 30 - 195 534 1	1.10E-114 5.19E-22 16.14333 1.20E-66 1.10E-04 2.48E-11 6.30E-25 2.50E-16	- IPR035437 IPR02999 IPR002999 - IPR002999 - -	- - SNase-like, OB-fold superfamily Tudor domain Tudor domain -
Phobius ProSiteProfiles PANTHER SUPERFAMILY ProSiteProfiles Gene3D SMART COD Phobius Pfam TMHMM Gene3D PANTHER SUPERFAMILY	PS50304 PTHR22948 SSF63748 PS50084 G3D5A:2.40.50.90 SM00333 cd04508 NON_CYTOPLASMIC_ PF00567 TMhelix G3DSA:3.30.310.210 PTHR22948:SF18 SSF63748	A membrane, in the cytoplasm. Tudor domain profile. TUDOR DOMAIN CONTAINING PROTEIN Tudor/PWWP/MBT Type-1 KH domain profile. TUDOR_7 TUDOR_ Region of a membrane-bound protein predicted to be outside the Imembrane, in the extracellular region. Tudor domain Region of a membrane-bound protein predicted to be embedded in the membrane. TUDOR AND KH DOMAIN-CONTAINING PROTEIN Tudor/PWWP/MBT Region of a membrane-bound protein predicted to be embedded in the	33 35 15 33 33 31 29 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	80         4           443         9           56         4           52         2           34         9           79         4           84         4           1         1           13         568           11         9           24         4	439           5566         1           451         218           519         437           431         11           11         -           418         30           195         534           534         1           419         1	.10E-114 5.19E-22 16.14333 1.20E-66 1.10E-04 2.48E-11 6.30E-25 2.50E-16 L.00E-114	- IPR035437 IPR02999 IPR002999 - IPR002999 - -	- - SNase-like, OB-fold superfamily Tudor domain Tudor domain -
Phobius ProSiteProfiles PANTHER SUPERFAMILY ProSiteProfiles Gene3D Phobius Pfam TMHMM Gene3D PANTHER SUPERFAMILY Phobius	PS50304 PTHR22948 SSF63748 PS50084 G3D5A:2.40.50.90 SM00333 cd04508 NON_CYTOPLASMIC_ PF00567 TMhelix G3D5A:3.30.310.210 PTHR22948:SF18 SSF63748 TRANSMEMBRANE	A membrane, in the cytoplasm. Tudor domain profile. TUDOR DOMAIN CONTAINING PROTEIN Tudor/PWWP/MBT Type-1 KH domain profile. 	33 39 19 33 31 31 32 4 4 4 32 32	80         4           43         9           56         4           52         2           34         9           79         4           1         1           96         4           13         68           11         9           24         4           12         12	30         -           439         -           5566         1           451         -           218         -           519         -           437         -           437         -           431         -           11         -           4418         -           30 -          -           30 -          -	1.10E-114 5.19E-22 16.14333 1.20E-66 1.10E-04 2.48E-11 6.30E-25 2.50E-16 1.00E-114 4.74E-22	- IPR035437 IPR002999 IPR002999 - IPR002999 - - - - - -	- - SNase-like, OB-fold superfamily Tudor domain Tudor domain -
Phobius ProSiteProfiles PANTHER SUPERFAMILY ProSiteProfiles Gene3D SMART COD Phobius Pfam TMHMM Gene3D PANTHER SUPERFAMILY	PS50304 PTHR22948 SSF63748 PS50084 G3D5A:2.40.50.90 SM00333 cd04508 NON_CYTOPLASMIC_ PF00567 TMhelix G3DSA:3.30.310.210 PTHR22948:SF18 SSF63748	A membrane, in the cytoplasm. Tudor domain profile. TUDOR DOMAIN CONTAINING PROTEIN Tudor/PWWP/MBT Type-1 KH domain profile TUDOR_ Region of a membrane-bound protein predicted to be outside the Imembrane, in the extracellular region. Tudor domain Region of a membrane-bound protein predicted to be embedded in the membrane TUDOR AND KH DOMAIN-CONTAINING PROTEIN Tudor/PWWP/MBT Region of a membrane-bound protein predicted to be embedded in the membrane TUDOR AND KH DOMAIN-CONTAINING PROTEIN Tudor/PWWP/MBT Region of a membrane-bound protein predicted to be embedded in the membrane	33 39 19 33 31 31 32 4 4 4 32 32	80         4           43         9           56         4           52         2           34         9           79         4           1         1           96         4           13         68           11         9           24         4           12         12	30         -           439         -           5566         1           451         -           218         -           519         -           437         -           437         -           431         -           11         -           4418         -           30 -          -           30 -          -	.10E-114 5.19E-22 16.14333 1.20E-66 1.10E-04 2.48E-11 6.30E-25 2.50E-16 L.00E-114	- IPR035437 IPR002999 IPR002999 - IPR002999 - - - - - -	- - SNase-like, OB-fold superfamily Tudor domain Tudor domain -
Phobius ProSiteProfiles PANTHER SUPERFAMILY ProSiteProfiles Gene3D SMART CDD Phobius Pfam TMHIMM Gene3D PANTHER SUPERFAMILY Phobius Gene3D	PS50304 PTHR22948 SSF63748 PS50084 G3D5A:2.40.50.90 SM00333 cd04508 NON_CYTOPLASMIC_ PF00567 TMhelix G3DSA:3.30.310.210 PTHR22948:SF18 SSF63748 TRANSMEMBRANE G3DSA:2.30.30.140	Amembrane, in the cytoplasm. Tudor domain profile. TUDOR DOMAIN CONTAINING PROTEIN Tudor/PWWP/MBT Type-1 KH domain profile. TUDOR_7 TUDOR_ Region of a membrane-bound protein predicted to be outside the Imembrane, in the extracellular region. Tudor domain Region of a membrane-bound protein predicted to be embedded in the membrane. TUDOR AND KH DOMAIN-CONTAINING PROTEIN Tudor/PWWP/MBT Region of a membrane-bound protein predicted to be embedded in the membrane. Region of a membrane-bound protein predicted to be embedded in the membrane. Region of a membrane-bound protein predicted to be embedded in the membrane. Region of a membrane-bound protein predicted to be embedded in the membrane.	33 33 33 33 34 29 29 29 29 29 29 29 29 29 29 29 29 29	80         4           413         9           56         4           52         2           34         9           34         9           84         4           11         9           13         68           11         9           224         4           12         31	39           439           566           451           218           519           437           431           11 -           418           30 -           534           419           30 -           403	1.10E-114 5.19E-22 16.14333 1.20E-66 1.10E-04 2.48E-11 6.30E-25 2.50E-16 1.00E-114 4.74E-22	- IPR035437 IPR002999 IPR002999 - IPR002999 - - - - - -	- - SNase-like, OB-fold superfamily Tudor domain Tudor domain -
Phobius ProSiteProfiles PANTHER SUPERFAMILY ProSiteProfiles Gene3D Phobius Pfam TMHMM Gene3D PANTHER SUPERFAMILY Phobius	PS50304 PTHR22948 SSF63748 PS50084 G3D5A:2.40.50.90 SM00333 cd04508 NON_CYTOPLASMIC_ PF00567 TMhelix G3D5A:3.30.310.210 PTHR22948:SF18 SSF63748 TRANSMEMBRANE G3D5A:2.30.30.140 NON_CYTOPLASMIC_	A membrane, in the cytoplasm. Tudor domain profile. TUDOR DOMAIN CONTAINING PROTEIN Tudor/PWWP/MBT Type-1 KH domain profile	33 33 33 33 33 34 29 29 29 29 29 29 29 20 29 20 20 20 20 20 20 20 20 20 20 20 20 20	80         4           443         9           56         4           52         2           34         9           779         4           96         4           11         9           12         1           12         31           31         9	$\begin{array}{c} 439 \\ 439 \\ 566 \\ 1 \\ 451 \\ 218 \\ 519 \\ 437 \\ 431 \\ \hline \\ 111 \\ - \\ 418 \\ 30 \\ - \\ 195 \\ 534 \\ 19 \\ 30 \\ - \\ 403 \\ 30 \\ - \\ 403 \\ 546 \\ - \\ \end{array}$	1.10E-114 5.19E-22 16.14333 1.20E-66 1.10E-04 2.48E-11 6.30E-25 2.50E-16 1.00E-114 4.74E-22 1.00E-66	- IPR035437 IPR002999 IPR002999 - IPR002999 - - - - - - - - -	SNase-like, OB-fold superfamily Tudor domain Tudor domain
Phobius ProSiteProfiles PANTHER SUPERFAMILY ProSiteProfiles Gene3D Phobius Pfam TMHMM Gene3D PANTHER SUPERFAMILY Phobius Gene3D	PS50304 PTHR22948 SSF63748 PS50084 G3DSA:2.40.50.90 SM00333 cd04508 NON_CYTOPLASMIC_ PF00567 TMhelix G3DSA:3.30.310.210 PTHR22948:SF18 SSF63748 TRANSMEMBRANE G3DSA:2.30.30.140 NON_CYTOPLASMIC_ SSF54791	Amembrane, in the cytoplasm. Tudor domain profile. TUDOR DOMAIN CONTAINING PROTEIN Tudor/PWWP/MBT Type-1 KH domain profile. TUDOR_7 TUDOR_ Region of a membrane-bound protein predicted to be outside the Imembrane, in the extracellular region. Tudor domain Region of a membrane-bound protein predicted to be embedded in the membrane. TUDOR AND KH DOMAIN-CONTAINING PROTEIN Tudor/PWWP/MBT Region of a membrane-bound protein predicted to be embedded in the membrane. Region of a membrane-bound protein predicted to be embedded in the membrane. Region of a membrane-bound protein predicted to be embedded in the membrane. Region of a membrane-bound protein predicted to be embedded in the membrane.	38 33 19 33 38 38 29 4 4 4 4 4 33 32 33 33 33 33 33 33 33 33 33 33 33	80         4           413         9           56         4           52         2           34         9           779         4           1         1           13         5           13         2           14         1           15         1           16         1           17         1           18         1           12         1           12         1           131         9           11         9           12         1           131         9           11         9           12         1	$\begin{array}{c} 339 \\ 439 \\ 566 \\ 1 \\ 451 \\ 218 \\ 519 \\ 437 \\ 431 \\ 111 \\ - \\ 437 \\ 431 \\ 111 \\ - \\ 418 \\ 30 \\ - \\ 195 \\ 534 \\ 19 \\ 30 \\ - \\ 30 \\ - \\ 192 \\ 102 \\ - \\ 192 \\ - \\$	1.10E-114 5.19E-22 16.14333 1.20E-66 1.10E-04 2.48E-11 6.30E-25 2.50E-16 1.00E-114 4.74E-22 1.00E-66 2.78E-15	- IPR035437 IPR002999 IPR002999 - IPR002999 - - - - - -	- SNase-like, OB-fold superfamily SNase-like, OB-fold superfamily Tudor domain - Tudor domain 
Phobius ProSiteProfiles PANTHER SUPERFAMILY ProSiteProfiles Gene3D Phobius Pfam TMHMM Gene3D PANTHER SUPERFAMILY Phobius Gene3D Phobius	PS50304 PTHR22948 SSF63748 PS50084 G3D5A:2.40.50.90 SM00333 cd04508 NON_CYTOPLASMIC_ PF00567 TMhelix G3D5A:3.30.310.210 PTHR22948:SF18 SSF63748 TRANSMEMBRANE G3D5A:2.30.30.140 NON_CYTOPLASMIC_	A membrane, in the cytoplasm. Tudor domain profile. TUDOR DOMAIN CONTAINING PROTEIN Tudor/PWWP/MBT Type-1 KH domain profile. 	38 33 19 33 38 38 29 4 4 4 4 4 33 32 33 33 33 33 33 33 33 33 33 33 33	80         4           443         9           56         4           52         2           34         9           779         4           1         1           13         5           13         2           14         4           15         1           16         4           17         12           18         1           19         2	$\begin{array}{c} 339 \\ 439 \\ 566 \\ 1 \\ 451 \\ 218 \\ 519 \\ 437 \\ 431 \\ 111 \\ - \\ 437 \\ 431 \\ 111 \\ - \\ 418 \\ 30 \\ - \\ 195 \\ 534 \\ 19 \\ 30 \\ - \\ 30 \\ - \\ 192 \\ 102 \\ - \\ 192 \\ - \\$	1.10E-114 5.19E-22 16.14333 1.20E-66 1.10E-04 2.48E-11 6.30E-25 2.50E-16 1.00E-114 4.74E-22 1.00E-66 2.78E-15	- - IPR035437 IPR002999 - IPR002999 - - - - - - - - - - - - -	SNase-like, OB-fold superfamily Tudor domain Tudor domain
Phobius ProSiteProfiles PANTHER SUPERFAMILY ProSiteProfiles Gene3D Phobius Pfam TMHMM Gene3D PANTHER SUPERFAMILY Phobius Gene3D	PSS034 PTHR22948 SSF63748 PSS0084 G3DSA:2.40.50.90 SM00333 cd04508 NON_CYTOPLASMIC_ PF00567 TMhelix G3DSA:3.30.310.210 PTHR22948:SF18 SSF63748 TRANSMEMBRANE G3DSA:2.30.30.140 NON_CYTOPLASMIC_ SSF54791 PF00013	Amembrane, in the cytoplasm. Tudor domain profile. TUDOR DOMAIN CONTAINING PROTEIN Tudor/PWWP/MBT Type-1 KH domain profile TUDOR, 7 TUDOR, 7 TUDOR, 7 TUDOR, 7 TUDOR of a membrane-bound protein predicted to be outside the Imembrane, in the extracellular region. Tudor domain Region of a membrane-bound protein predicted to be embedded in the membrane Region of a membrane-bound protein predicted to be embedded in the membrane Region of a membrane-bound protein predicted to be embedded in the membrane Region of a membrane-bound protein predicted to be embedded in the membrane Region of a membrane-bound protein predicted to be embedded in the membrane Region of a membrane-bound protein predicted to be outside the Imembrane, in the extracellular region. Eukaryotic type KH-domain (KH-domain type I) KH domain	38 39 39 33 30 30 29 29 30 30 33 31 33 31 33 31 31 11 12	80         43         9           56         45         52         2           34         9         5         4         4           13         1         1         1         1           13         58         2         1         1           13         24         4         4         1           12         24         4         1         1         1           131         2         2         4         1	$\begin{array}{c} 339 \\ 439 \\ 566 \\ 1 \\ 451 \\ 218 \\ 519 \\ 437 \\ 431 \\ 111 \\ - \\ 437 \\ 431 \\ 111 \\ - \\ 418 \\ 30 \\ - \\ 195 \\ 534 \\ 19 \\ 30 \\ - \\ 30 \\ - \\ 192 \\ 102 \\ - \\ 192 \\ - \\$	1.10E-114 5.19E-22 16.14333 1.20E-66 1.10E-04 2.48E-11 6.30E-25 2.50E-16 1.00E-114 4.74E-22 1.00E-66 2.78E-15	- - IPR035437 IPR002999 - IPR002999 - - - - - - - - - - - - -	- SNase-like, OB-fold superfamily SNase-like, OB-fold superfamily Tudor domain - Tudor domain 
Phobius ProSiteProfiles PANTHER SUPERFAMILY ProSiteProfiles Gene3D Phobius Pfam TMHMM Gene3D PANTHER SUPERFAMILY Phobius Gene3D Phobius SUPERFAMILY Phobius	PSS034 PTHR22948 SSF63748 PSS0084 G3DSA:2.40.50.90 SM00333 cd04508 NON_CYTOPLASMIC_ PF00567 TMhelix G3DSA:3.30.310.210 PTHR22948:SF18 SSF63748 TRANSMEMBRANE G3DSA:2.30.30.140 NON_CYTOPLASMIC_ SSF54791 PF00013	A membrane, in the cytoplasm. Tudor domain profile. TUDOR DOMAIN CONTAINING PROTEIN Tudor/PWWP/MBT Type-1 KH domain profile. 		80     43       43     9       56     4       52     3       334     9       1     9       13     5       58     2       11     9       12     4       13     1       14     1       15     1       16     2       17     1       18     2       19     2       19     2       11     1	439           5566           451           218           519           437           431           11           418           30           534           403           546           192           188           11	1.10E-114 5.19E-22 16.14333 1.20E-66 1.10E-04 2.48E-11 6.30E-25 2.50E-16 1.00E-114 4.74E-22 1.00E-66 2.78E-15	- - IPR035437 IPR002999 - IPR002999 - - - - - - - - - - - - -	- SNase-like, OB-fold superfamily SNase-like, OB-fold superfamily Tudor domain - Tudor domain 
Phobius ProSiteProfiles PANTHER SUPERFAMILY ProSiteProfiles Gene3D Phobius Pfam TMHMM Gene3D PANTHER SUPERFAMILY Phobius Gene3D Phobius Gene3D Phobius SUPERFAMILY Phobius SUPERFAMILY Phobius SUPERFAMILY Phobius ProSiteProfiles ProSiteProfiles	PS50304 PTHR22948 SSF63748 PS50084 G3DSA:2.40.50.90 SM00333 cd04508 NON_CYTOPLASMIC_ PF00567 TMhelix G3DSA:3.30.310.210 PFHR2294S:F18 SSF63748 TRANSMEMBRANE G3DSA:2.30.30.140 NON_CYTOPLASMIC_ SSF54791 PF00013 CYTOPLASMIC_DOMA PS500304	Amembrane, in the cytoplasm. Tudor domain profile. TUDOR DOMAIN CONTAINING PROTEIN Tudor/PWWP/MBT Type-1 KH domain profile. 	333 31 31 31 31 33 33 33 33 33 33 34 25 25 25 25 25 33 34 34 25 25 25 25 25 25 25 25 25 25 25 25 25	80     43       43     9       56     4       52     2       34     9       54     4       96     4       13     58       13     58       12     24       12     23       19     22       21     23       12     23       12     23       12     23       12     23       23     24       48     448	439           566         1           451         218           519         437           431         11           11         -           418         30           195         534           30         -           403         -           546         -           192         188           111         -           188         -           111         -           186         -           111         -           186         -           187         -	1.10E-114 5.19E-22 16.14333 1.20E-66 1.10E-04 2.48E-11 6.30E-25 2.50E-16 1.00E-114 4.74E-22 1.00E-66 2.78E-15 6.00E-14 16.14333 10.28092	- - IPR035437 IPR002999 - IPR002999 - - - - - - - - - - - - -	
Phobius ProSiteProfiles PANTHER SUPERFAMILY ProSiteProfiles Gene3D SMART COD Phobius Pfam TMHMM Gene3D PANTHER SUPERFAMILY Phobius Gene3D Phobius SUPERFAMILY Phobius SUPERFAMILY Phobius SUPERFAMILY Phobius SUPERFAMILY	PS50304 PTHR22948 SSF63748 PS50084 G3DSA:2.40.50.90 SM00333 cd04508 NON_CYTOPLASMIC_ PF00567 TMhelix G3DSA:3.30.310.210 PTHR22948:SF18 SSF63748 TRANSMEMBRANE G3DSA:2.30.30.140 NON_CYTOPLASMIC_ SSF54791 PF00013 CYTOPLASMIC_DOM/ PS50304 PS50304	A membrane, in the cytoplasm. Tudor domain profile. TUDOR DOMAIN CONTAINING PROTEIN Tudor/PWWP/MBT Type-1 KH domain profile. 	34 34 34 31 35 35 35 36 37 37 37 37 37 37 37 37 37 37 37 37 37	80	439           439           5566           1           451           218           519           437           431           11           413           30           5534           419           30           403           403           546           192           188           111           186           407           405	L10E-114 5.19E-22 16.14333 1.20E-66 1.10E-04 2.48E-11 6.30E-25 2.50E-16 L00E-114 4.74E-22 1.00E-66 2.78E-15 6.00E-14 16.14333 10.28092 1.10E-04	 IPR035437 IPR002999 - IPR002999 - - IPR002999 - - - - - - - - - - - - -	
Phobius ProSiteProfiles PANTHER SUPERFAMILY ProSiteProfiles Gene3D Phobius Phobius Gene3D PANTHER SUPERFAMILY Phobius SUPERFAMILY Phobius SUPERFAMILY Phobius ProSiteProfiles SMART	PS50304 PTHR22948 SSF63748 PS50084 G3D5A:2.40.50.90 SM00333 cd04508 NON_CYTOPLASMIC_ PF00567 TMhelix G3D5A:3.30.310.210 PTHR22948:SF18 SSF63748 TRANSMEMBRANE G3D5A:2.30.30.140 NON_CYTOPLASMIC_ SSF54791 PF0013 CYTOPLASMIC_DOM/ PS50304 SM00333 PTHR22948	Amembrane, in the cytoplasm. Tudor domain profile. TUDOR DOMAIN CONTAINING PROTEIN Tudor/PWWP/MBT Type-1 KH domain profile. 	333 393 313 333 333 333 333 333 333 333	80         -           43         :           55         -           52         :           52         :           52         :           52         :           52         :           52         :           52         :           52         :           1         :           10         :           58         :           58         :           58         :           12         :           231         :           233         :           1         :           20         :           48	439           439           5566           1           451           218           519           437           431           11           413           30           5534           419           30           403           546           192           188           11           186           4007           405           534	10E-114 5.19E-22 16.14333 1.20E-66 1.10E-04 2.48E-11 6.30E-25 2.50E-16 0.00E-114 4.74E-22 1.00E-66 2.78E-15 6.00E-14 16.14333 10.28092 1.10E-04 1.00E-14	- - - - IPR002999 - - - - - - - - - - - - -	- SNase-like, OB-fold superfamily Tudor domain 
Phobius ProSiteProfiles PANTHER SUPERFAMILY ProSiteProfiles Gene3D Phobius Pfam TMHMM Gene3D PANTHER SUPERFAMILY Phobius Gene3D Phobius SUPERFAMILY Phobius SUPERFAMILY Phobius SUPERFAMILY Phobius SUPERFAMILY Phobius SUPERFAMILY Phobius SUPERFAMILY Phobius SUPERFAMILY Phobius SUPERFAMILY Phobius SUPERFAMILY Phobius Phobius SUPERFAMILY Phobius SUPERFAMILY Phobius SUPERFAMILY Phobius SUPERFAMILY Phobius Phobius SUPERFAMILY Phobius Phobius Phobius SUPERFAMILY Phobiu	PS50304 PTHR22948 SSF63748 PS50084 G3DSA:2.40.50.90 SM00333 cd04508 NON_CYTOPLASMIC_ PF00567 TMhelix G3DSA:3.30.310.210 PTHR22948:SF83748 TRANSMEMBRANE G3DSA:2.30.30.140 NON_CYTOPLASMIC_ SSF54791 PF00013 CYTOPLASMIC_DOMA PS50034 SM00333 PTHR22948 G3DSA:2.40.50.90	Amembrane, in the cytoplasm. Tudor domain profile. TUDOR DOMAIN CONTAINING PROTEIN Tudor/PWWP/MBT Type-1 KH domain profile. - TUDOR Region of a membrane-bound protein predicted to be outside the Imembrane, in the extracellular region. Tudor domain Region of a membrane-bound protein predicted to be embedded in the membrane. - TUDOR AND KH DOMAIN-CONTAINING PROTEIN Tudor/PWWP/MBT Region of a membrane-bound protein predicted to be embedded in the membrane. - TUDOR AND KH DOMAIN-CONTAINING PROTEIN Tudor/PWWP/MBT Region of a membrane-bound protein predicted to be outside the Imembrane, - Region of a membrane-bound protein predicted to be outside the Imembrane, in the extracellular region. Eukaryotic type KH-domain (KH-domain type I) KH domain Region of a membrane-bound protein predicted to be outside the Amembrane, in the cytoplasm. Type-1 KH domain profile. TUDOR_7 TUDOR DOMAIN CONTAINING PROTEIN	34 4 33 33 33 34 22 22 22 22 21 33 34 34 34 34 34 34 34 34 34	80         -           43         -           55         -           52         -           52         -           52         -           13         -           13         -           13         -           13         -           12         -           131         -           122         -           131         -           122         -           131         -           123         -           1         -           1         -           1         -           1         -           23         -           24         -           447         -           202         -	439         439           5566         1           451         218           519         30           11         -           4418         30           30         -           403         -           5534         1           403         -           546         -           1186         -           1186         -           5534         1           403         -           546         -           1186         -           547         -           407         -           407         -           4087         -	1.10E-114 5.19E-22 1.10E-06 1.10E-04 2.48E-11 2.48E-11 2.50E-16 0.00E-114 4.74E-22 1.00E-66 0.07E-14 4.74E-22 1.00E-66 0.07E-14 1.00E-66 1.10E-04 1.00E-14 1	 IPR035437 IPR002999        	
Phobius ProSiteProfiles PANTHER SUPERFAMILY ProSiteProfiles Gene3D Phobius Phobius Gene3D PANTHER SUPERFAMILY Phobius SUPERFAMILY Phobius SUPERFAMILY Phobius ProSiteProfiles SMART	PS50304 PTHR22948 SSF63748 PS50084 G3D5A:2.40.50.90 SM00333 cd04508 NON_CYTOPLASMIC_ PF00567 TMhelix G3D5A:3.30.310.210 PTHR22948:SF18 SSF63748 TRANSMEMBRANE G3D5A:2.30.30.140 NON_CYTOPLASMIC_ SSF54791 PF0013 CYTOPLASMIC_DOM/ PS50304 SM00333 PTHR22948	A membrane, in the cytoplasm. Tudor domain profile. TUDOR DOMAIN CONTAINING PROTEIN Tudor/PWWP/MBT Type-1 KH domain profile. 	313 313 313 313 313 313 313 313 313 313	880	439         439           5566         1           451         218           519         437           411         -           418         30           30         -           4419         -           300         -           403         -           546         -           1186         -           1186         -           407         -           5534 1         -           4407         -           564         -           1186         -           407         -           5534 1         -           487         -	1.10E-114 5.19E-22 1.10E-06 1.10E-04 2.48E-11 2.48E-11 2.50E-16 0.00E-114 4.74E-22 1.00E-66 0.07E-14 4.74E-22 1.00E-66 0.07E-14 1.00E-66 1.10E-04 1.00E-14 1	 IPR035437 IPR002999 - IPR002999 - IPR002999 - - - - - - - - - - - - -	- SNase-like, OB-fold superfamily SNase-like, OB-fold superfamily Tudor domain - Tudor domain 

Functional domains predicted with InterProScan in *Poecilia reticulata* proteins Vasa (XP\_008428196.1), PIWI (XP\_008415818.1), TDRKH isoform X1 (XP\_008436386.1) and TDRKH isoform X2 (XP\_008436387.1). Highlighted rows indicate predicted domain (with e-value < 0.05) included in the antibody binding regions.

# MSA

The multiple sequence alignment result as produced by T-coffee.

T-COFFEE, Version_11.00 (Version_11.00) Cedric Notredame SCORE=936				
BAD AVG GOOD				
GeneTex XP_008436386.1 cons	: 92 : 91 : 93			
GeneTex XP_008436386.1	MSTERTSWTSLSTIQKIALGLGIPASATVAYILYRRYR MDVGVSKSRVFVSYSSQVLLSKCSIPLSVRYVMDAVKDGPRGKMVALAAGLSVGATIGYIVYRHIS			
cons	*			
GeneTex XP_008436386.1	ESREERLTFVGEDDIEIEMRVPQEAVKLIIGRQGANIKQLRKQTGARIDVDTEDVGDERVLL NASSSQEPDTEESKIILPIEVYRNISRCYATFLDVASQKSGAHVRVASYSEETGHKAAVCVQ			
cons	::: . * * :: :* *. : * .: :. :::**:: * :*:.*: :			
GeneTex XP_008436386.1	ISGFPVQVCKAKAAIHQILTENTPVSEQLSVPQRSVGRIIGRGGETIRSICKASGAKITCDKESEG IQGSKEQVLLARCVLENLATDCEPTVEVLEVPQNAFGRVIGRGGEGLKLITRSTGAKIVCSREKKH			
cons	* * ** * * * * * *** ** ******* * ******			
GeneTex XP_008436386.1	TLLLSRLIKISGTQKEVAAAKHLILEKVSEDEELRKRIAHSAETRVPRKQPISVRREDMTEPGGAG NPGGKGSVTITGSKQEVKQAKEMILERVGADAVVRSKISQSSALRQKRGHKVV			
cons	· · · * · * · · · * * * · * * · * · * ·			
GeneTex XP_008436386.1	EPALWKNTSSSMEPTAPLVTPPPKGGGDMAVVVSKEGSWEKPSDDSFQKSEA NPDPCCMEPKCPVGLNNNGPVSYTEKNGLVQSKEATAERLLLEMKGLKGTDEQEEESSIST			
cons	*******			
GeneTex XP_008436386.1	QAIPEMPMFEIPSPDFSFHADEYLEVYVSASEHPNHFWIQIVGSRSLQLDKLVNEMTQHYENSVPE DTLSEVSKFEIPSPDLSFQPDEHLEVYVSASENPNHFWIQILGVRSLQLDKLTEEMNNFYTNENPT			
cons	···*· ********************************			
GeneTex XP_008436386.1	DLTVHVGDIVAAPLPTNGSWYRARVLGTLENGNLDLYFVDFGDNGDCPLKDLRA EQRMDSILVGDIVAAPYRDYNKWNRARVLGFLRSGLVDLYYVDFGDNGEFSRDILRPLRSDFLSLP			
cons	*****			
GeneTex XP_008436386.1 cons	FQAIECSLAGVRPKGEAWTEAALDIFEQLTYCANWRPLQAKLCSYSHSEVSSWPSVKLYDNSKGKA			
GeneTex XP_008436386.1 cons	VDIGEELIRLGHAVSFQETFNEKVEGDNLGCLQRMLDDVIGATSELSLSCISLSEAASVSGSVDDG			
GeneTex XP_008436386.1 cons	VEDELL			

T-Coffee alignment of TDRKH isoform X1 of *P. reticulata* (XP\_008436386.1; 579 amino acids) and TDRKH GeneTex antibody binding site (406 amino acids).

#### MSA

The multiple sequence alignment result as produced by T-coffee.

me multiple sequence all				
T-COFFEE, Version_11.00 (Version_11.00) Cedric Notredame SCORE=960				
BAD AVG GOOD				
* XP 008428196.1 tr 042107 04210 cons	: 94 : 91 : 96			
XP_008428196.1	MDEWEEEETKASTFTAA-SYSSNDAAGRDSWKSDHGEFGRGR			
tr 042107 04210	MDDWEEDQSPVVSCSSGFGLGSNGSDGGFKSFYTGGAGNDKSNSEGTEGSSWKMT-GDSFRGR			
cons	**:***::::::::::::::::::::::::::::::::			
XP_008428196.1	GGKGRGRGGFWNSSADGDSRDSNEDGERHGF			
tr[042107 04210	GGRGGSRGGRGGFSGFKSEIDENGSDGGWNGGESRGRGRGGFRGGFRSGSRDENDENRNDDGW			
cons	**: *: *: ::*: : *: *: *: *: *: *: *: *:			
XP_008428196.1	SGRVGRGRGRG-FNRMNSDGFSEDGDGAHENG			
tr 042107 04210	KGGESRGRGGFGGFGGSFRGGFRDGGNEDTGRRGFGRENNENGNDEG BEGRGRGGFRGGFRD			
cons	.* .***** *** :			
XP_008428196.1	DAEQGGRGGFRGGYRGKDEEAFSPGEDQGPVKD-DPDSDKPRVTYVPPTLPEDEDSIFSHY			
tr[042107 04210	GGGDESGKRGFGRGGFRGRNEEVFSKVTTADKLDQEGSENAGPKVVYVPPPPPEEESSIFSHY			
cons	* * ** *** *** *** *** *** *** ********			
XP_008428196.1	KSGINFDKYDDILVDISGTNPPRAIITFDEAALCESLRKNISKSGYVKPTPVQKHGIPIISAG			
tr 042107 04210	ATGINFDKYDDILVDVSGSNPPKAIMTFEEAGLCDSLSKNVSKSGYVKPTPVQKHGIPIISAG			
cons	·**************			
XP_008428196.1	RDLMACAQTGSGKTAAFLLPILQQLMTDGVAASRFSETQEPEAVIVAPTRELINQIYLEARKF			
tr 042107 04210	RDLMACAQTGSGKTAAFLLPILQRFMTDGVAASKFSEIQEPEAIIVAPTRELINQIYLEARKF			
cons	************************			
XP_008428196.1	AHGTCVRPVVVYGGVSTGYQIREILKGCNVVCGTPGRLLDMIGRGKVGLSKVRYLVLDEADRM			
tr]042107 04210	AYGTCVRPVVVYGGINTGYTIREVLKGCNVLCATPGRLHDLIGRGKIGLSKVRYLVLDEADRM			
cons	*:************:.*** ***:****:*			
XP_008428196.1	LDMGFEPDMRRLVGSPGMPSKENRQTLMFSATYPEDIQRMAADFLKPDYLFLAVGIVGGACSD			
tr 042107 04210	LDMGFEPEMRKLVASPGMPSKEERQTLMFSATYPEDIQRMAADFLKVDYIFLAVGVVGGACSD			
cons	******:**:**:**:**:**			
XP_008428196.1	VEQKFVQVTKFSKREQLLDIL			
tr 042107 04210	VEQTVVQVDQYSKRDQLLELLRATGNERTMVFVETKRQADFIAVFLCQEKVPTTSIHGDREQR			
cons	****** ::***:***:***:****************			
XP_008428196.1 tr 042107 04210 cons	ERELALTDFRSGKCPVLVATSVAARGLDIPDVQHVVNFDLPKDIDEYVHRIGRTGRCGNVGRA EREKALSDFRLGHCPVLVATSVAARGLDIEQVQHVVNFDMPSSIDEYVHRIGRTGRCGNTGRA			
XP_008428196.1	VSFFDPEADGGLARSLVTVLSKAQQEVPPWLEESAFSSHG-AGFNPK-KTFGSTDSRKTGSFQ			
tr 042107 04210	VSFFNPESDTPLARSLVKVLSGAQQVVPKWLEEVAFSAHGTTGFNPRGKVFASTDSRKGGSFK			
cons	****:**:* ******.*** *** ** *** ***:** :***:**			
XP_008428196.1	ENSGPSQPAAQAAADDEEWE			
tr 042107 04210	SDEPPPSQTSAPSAAAAADDEEWE			
cons	.:. * * *:* *******			
20110				

T-Coffee alignment of Vasa from *P. reticulata* (XP\_008428196.1; 640 amino acids) and *Danio rerio* (tr|042107|042107\_DANRE; 716 amino acids). Red box indicates anti-VASA binding site.

T.COFFEE, Version, 11.00 (Version, 11.00)           VEX.000000000000000000000000000000000000	MSA The multiple sequence	alignment result as produced by T-coffee.
	T-COFFEE, Versio Cedric Notredamo	on 11.00 (Version 11.00)
NP. 060538.2         94           XP. 0605138.1         NPDREXPED	* BAD AVG GOOD	
NP_060538.2         MPDFPPSFRQSPIH/PSOCQAVRMPCC/WPQASKPLDPALGRG         A           Cons         ************************************	NP_060538.2	: 94
NP_000415818.1       PAGROVLPSTAPERGELLVOPDEVGVGRANGLLLPSAEPRVGVSNGAVLPRLEONHEOKHLETP         Cons       AGGGNPGKKPEEPSTORCTP         XP_000415818.1       ASAGDPAAPRGEEVSAPPCGOGSTUVSNFRGGVTSNGCTP         XP_000415818.1       ASAGDPAAPRGEEVSAPPCGOSTUVSNFRGGVTSNGCTP         Cons       Cons         XP_000415818.1       REGUSTRONGUSTALUSTRAGUSTNGCTP         NP_00033.2       Cons         XP_000415818.1       REGUSTRONGUSTALSTRAGUSTNGCTP         NP_00033.2       VORGOALLSALPSGOTKPVSTSDPOTAPLSPPHPEGVLKVVPTTOD.PVPLSSAOPKKEHTNEAV         NP_00033.2       VORGOALLSALPSGOTKPVSTSDPOTAPLSPPHPEGVLKVVPTTOD.PVPLSSAOPKKEHTNEAV         NP_000415818.1       VORGOALLSALPSGOTKPVSTSDPOTAPLSPPHPEGVLKVVPTTOD.PVPLSSAOPKKEHTNEAV         NP_000415818.1       TTUKTGTKGAP TT GGNINTVVSKUEMVVYTTTPNVESNMFEGURKONGTTUKTAROUGHAATGENTAROUGHAAT		
NP_660538.2         P	cons	*** :*. *: :*:: *:**.
NP_000415010.1       ASADDPAAPRGEEVSAPPCGOGST.USMPRGMCUTSMGRGTPAVGREESG.         NP_000415010.1       CGEVKV005LVGLTAMOGACHRGDSSLCPGMVVULGRALIP.0LG         NP_000415010.1       REELSPTTMDPK/LAGOSTMAETSVOMS         NP_000415010.1       REELSPTTMDPK/LAGOSTMAETSVOMS         NP_000415010.1       REELSPTTMDPK/LAGOSTMAETSVOMS         NP_000415010.1       VGRGQALLSALPSGOIKPVSPTSDP0TAPLSPHPEGVLKVVPMT0DLPVPLSSAQPKKEMTMEAY         NP_000415010.1       VGRGQALLSALPSGOIKPVSPTSDP0TAPLSPHPEGVLKVVPMT0DLPVPLSSAQPKKEMTMEAY         NP_000415010.1       HTP1INTGTKGAPTTIGSHHJWSCKNEWYQYHVTFTPMVSSMARFGMWKDHRSTTGEVTAPDG         cons	NP_060538.2	PAGRGHVFGKPEEPSTQR
NP_060538.2 XP_008415818.1 NP_060538.2 XP_008415818.1 VGRGQALLSALPSGDIKPVSPTSDP0TAPLSPPHPEGVLKVYPHTQDLPVPLSSADPKKEHTNEAY MP_060538.2 VGRGQALLSALPSGDIKPVSPTSDP0TAPLSPPHPEGVLKVYPHTQDLPVPLSSADPKKEHTNEAY MP_060538.2 XP_008415818.1 HTP:INTCTTKGAPTITGSHITVVSCKHEAVYQYHVTFTPNVESKAMRFCMWKDHRSTTGEVVAFDG SILVLPVKLKBCPKLKSSRRTDNGETELXQMTKTLPPNCEKSMRFCMWKDHRSTTGEVVAFDG SILVLPVKLKBCPKLKSSRRTDNGETELXQMTKTLPPNVESKMRFCMWKDHRSTTGEVAFDG SILVLPVKLKBCPKLKSSRRTDNGETELXQMTKTLPPNVESKMRFCMWKDHRSTTGEVAFDG SILVLPVKLBSRRTDNGETELXQMTKTLPPNVESKMRFCMWKDHRSTTGEVAFDG SILVLPVKLBSRTDNGETELXQMTKTLPPNVESKMRFCMWKDHRSTTGEVAFDG SILVLPVKLBSRTDNGETELXQMTKTLPPNVESKMRFCMWKDHRSTTGEVAFDG SILVLPVKLBSRTDNGETELXQMTKTLPPNVESKMRFCMWKDHRSTTGEVAFDG SILVLPVKLBSRTDNGETELXQMTKTLPPNVESKMRFCMWKDHRSTTGEVAFDG SILVLPVKLBSRTDNGETELXQMTKTLPPNVESKMRFCMWKDHRSTTGEVAFDG SILVLPVKLBSRTDNGETELXQMTKTLPPNVESKMRFCMWKDHRSTGEVAFDG SILVLPVKLBSRTDNGETELXQMTKTLPPNVESKMRFCMWKDHRSTGEVAFDG SILVLPVKLBSRTDNGETELXQMTKTLPPNVESKMRFCMWKDHRSTGEVAFDG SILVLPVKLBSRTDNGETELXQMTKTLPPNVESKMRFCMWKDHRSTGEVAFDG SILVLPVKLBSRTDNGETELXQMTKTLPPNVESKMRFCMWKDHRSTGEVAFDG SILVLPVKLBSRTDNGETELXQMTKTRDSGLFHSDGSFHSDGKETTFLEYSKNRGTHKELTMHTYSSEDQHLLH CONS XP_008415818.1 HYDPESAVUEKGRLQVWFGYATATKRTDSGLFHSDGKETTFLEYSKNRGTHKELLGVARM NP_660538.2 SSNPESVKELSRWGLEIGSELLYDGKTLPLETCLOTSLIPTADVKWRTKKGLLLQWFGYATATKRTDGGFHSDGKETTFLEYYSKNRGTHKELLCHTN SSNPESVKELSRWGLEIGSELLYDGKTLPLETCLOTSLIPTADVSWSREVVRDTSISSVPLNT ANRAATNELRRWGLRLQADVHKIEGRVLPHERNLMKKTSFTGSQLMUSKEVRDTSISSVPLNT ANRAATNELRRWGLRLQADVHKIEGRVLPHERNLMKKTSFTGSQLMUSKEVRDTSISSVPLNT NP_660538.2 XP_008415818.1 NLPGKVDNVHDFSKGANGARELVMHRGKLGVGFPLSQLMURATIGQTRLSVAGKLLQMVKEVTADSISSVFLNT SSNPESVKELSRWGLEIGSELLYDGKTLPHERTNLKMTSFTSQDMKLKSGGELHTVNTTVKEEDQF SSNPESVKELSRWGLEIGSELLYDGKTLPHERTNLKMTSFTSQDMKLKGGELHTVNTTVKETADJSSVFLVT CONS XP_008415818.1 NLPGKVDNVHDFSKGMGARELVMHRGKGRUPPHDELWFLTVKSINGLKLCUVGKKGELHTVNTTVKETAD SSNPESVKELSRWGLEIGSELLYTFKKVGFTPDGIKCFETFSVKSHKMFLTUNGKKGRETNVGATSTNLYAANSNFG CONS XP_008415818.1 NP_660538.2 TFFRGTVDMATTK	cons	
NP_060538.2       REELSPTFWDPKVLAAQDSKWAETSVOWS       RTLGRGSSDAS       LLPLGRAAGGISRE         cons       ****       :***       ::****       ::*****         XP_008415818.1       VGRGQALLSALPSGOTAPUSPTSDPUTAPLSPPHPEOVLKVVPHTODLPVPLSSAQPKKEMTHEAV         NP_060538.2       VDRPCTFFTSRSRPD105       SPLISPDRPLVTUPUSSAQPKKEMTHEAV         cons       ************************************	NP_060538.2	GPAQRESVGLVSMFRGLGIETVSKTPLKREMLPSGRGILGRGLSANLVRKD
NP_060538.2       REELSPTFWDPKVLAAODSKWAETSVOWS       RTLGRGSSDAS'-LLPLGRAAGGISRE         cons       ****       ::****       ::******         XP_008415818.1       VGRGQALLSALPSGOTAPUSPTSDPOTAPLSPHPEQVLKVVPHTODLPVPLSSAOPKKENTTHEAV         NP_060538.2       VDVPCFTSTSRGPPLOTAPLSPHLPG       SPLHSPDRPLVLTVEKKEKEL         cons       ************************************		
NP_060538.2       V0KPPCTFSTPSRGPQLSSPPALPQ       SPLHSPDRPLVLTVEHKEKEL         cons       *::::::::::::::::::::::::::::::::::::	NP_060538.2	REELSPTFWDPKVLAAGDSKMAETSVGWSRTLGRGSSDASLLPLGRAAGGISRE
NP_060538.2       V0KPPCTFSTPSRGPQLSSPPALPQ       SPLHSPDRPLVLTVEHKEKEL         cons       *::::::::::::::::::::::::::::::::::::	XP 008415818.1	VGRGOALLSALPSGOIKPVSPTSDPOTAPLSPPHPEGVLKVVPMTODLPVPLSSAOPKKEMTMEAV
NP_060538.2	-	
XP       008415818.1       SILVLPVKLPEVLLKSSRRTDNQETEIKIOMTKILPPNCDLCIPFYNVVFRRVMKIIG, KUVARN         XP       008415818.1       SILVLPVKLPVKLUKSSRRTDNQETEIKIOMTKILPPNCDLCIPFYNVVFRRVMKIIG, KUVARN         XP       008415818.1       HYDPESAVVLEKORLOVWPGYATAIKRTDGGLYLLSVEVTHKVLONDSVLDLMMMLYROSKENFODZ         cons		
NP_060538.2       SILYLPVLLQVLELKSORKTDSAEISIKIQMTKILEPCSDLCIPFYNVVFRRVMKLLDMLLVGRN         cons       ************************************	-	
cons*********************************		
NP_060538.2FYDPTSAMVLQQHRLQIWPGYAASIRRTDGGLFLLADVSHKVIRNDCVLDVMHAIYQQNKEHFQDEcons*********************************	_	
cons       .*****:*::****:****:******************		
NP_060538.2CTKLLVGNIVITRYNNRTYRIDDVDWNKTPKDSFTMSDGKEITFLEYYSKNYGITVKEEDQPLLIHcons*********************************	cons	*** ** ** ** **************************
XP_008415818.1RPKERSRPGGK0IITGEILLVPELSFLTGIPEKMRKDMRAMKELTNHINVSSEQHTNSIKOLLKNIcons**.**.*::**********************************	NP_060538.2	CTKLLVGNIVITRYNNRTYRIDDVDWNKTPKDSFTMSDGKEITFLEYYSKNYGITVKEEDQPLLIH
NP_060538.2RPSERQDNHG-MLLKGEILLLPELSFMTGIPEKMKKDFRAMKDLAQQINLSPKQHHSALECLLQRIcons**.**. * ::.***************************		
NP_060538.2AKNEAATNELMRWGLRLQKDVHKIEGRVLPMERINLKNTSFITSQELNWVKEVTRDPSILTIPMHFcons:.* :.:** ****: ::::**:*****::::**:****:::******	NP_060538.2	RPSERQDNHG-MLLKGEILLLPELSFMTGIPEKMKKDFRAMKDLAQQINLSPKQHHSALECLLQRI
NP_060538.2AKNEAATNELMRWGLRLQKDVHKIEGRVLPMERINLKNTSFITSQELNWVKEVTRDPSILTIPMHFcons:.* :.:** ****: ::::**:*****::::**:****:::******		
NP_060538.2WALFYPKRAMDQARELVNMLEKIAGPIGMRMSPPAWVELKDDRIETYVRTIQSTLGAEGKIQMVVCcons**:***.*.*****************************	NP_060538.2	AKNEAATNELMRWGLRLQKDVHKIEGRVLPMERINLKNTSFITSQELNWVKEVTRDPSILTIPMHF
NP_060538.2WALFYPKRAMDQARELVNMLEKIAGPIGMRMSPPAWVELKDDRIETYVRTIQSTLGAEGKIQMVVCcons**:***.*.*****************************		WAIFYPSRCADQAEELVSTFKKVAGPIGVRMARPIRVELRDDRTETYVKSIHSHLTSEPNLQLVVC
XP_008415818.1       IMVGNRDDLYSAIKKLCCVKSPIPSQAINIRTISQQMKLKSVAQKILLQVNSKLGGELWTVNIPLK IIMGPRDDLYGAIKKLCCVQSPVPSQVVNVRTIGQPTRLRSVAQKILLQINCKLGGELWGVDIPLK         cons       *::**********************************	-	
NP_060538.2IIMGPRDDLYGAIKKLCCVQSPVPSQVVNVRTIGQPTRLRSVAQKILLQINCKLGGELWGVDIPLKcons*::**********************************	cons	
NP_060538.2       QLMVIGMDVYHDPSRGMRSVVGFVASINLTLTKWYSRVVFQMPHQEIVDSLKLCLVGSLKKFYEVN         cons       :***:*:*:*:*::*::*:*:****************	NP_060538.2	IIMGPRDDLYGAIKKLCCVQSPVPSQVVNVRTIGQPTRLRSVAQKILLQINCKLGGELWGVDIPLK
NP_060538.2       QLMVIGMDVYHDPSRGMRSVVGFVASINLTLTKWYSRVVFQMPHQEIVDSLKLCLVGSLKKFYEVN         cons       :***:*:*:*:*::*::*:*:****************	XP 008415818.1	NLMVVGVDVHHDTSKSHOSVMGFVASVNSSLTRWYSRVTFOTPSFEI THGFRVCI I AAI OKYHFTN
NP_060538.2       HCLPEKIVVYRDGVSDGQLKTVANYEIPQLQKCFEAFENYQPKMVVFVVQKKISTNLYLAAPQNFV         cons       ************************************	NP_060538.2	QLMVIGMDVYHDPSRGMRSVVGFVASINLTLTKWYSRVVFQMPHQEIVDSLKLCLVGSLKKFYEVN
cons       * ***********************************		
NP_060538.2       TPTPGTVVDHTITSCEWVDFYLLAHHVRQGCGIPTHYVCVLNTANLSPDHMQRLTFKLCHMYWNWP         cons       **.****:***: *******:*****: ******: ******: ******	-	
XP_008415818.1 GTIRVPAPCKYAHKLAFLSGQYLHSEPAIQLSDKLFFL NP_060538.2 GTIRVPAPCKYAHKLAFLSGHILHHEPAIQLCENLFFL		TPTPGTVVDHTITSCEWVDFYLLAHHVRQGCGIPTHYVCVLNTANLSPDHMQRLTFKLCHMYWNWP
NP_060538.2 GTIRVPAPCKYAHKLAFLSGHILHHEPAIQLCENLFFL	cons	** **** *** * ****** **** **** **** ****
CONS ************************************	NP_060538.2	GTIRVPAPCKYAHKLAFLSGHILHHEPAIQLCENLFFL
	cons	******

T-Coffee alignment of PIWI from *P. reticulata* (XP\_008415818.1; 1056 amino acids) and *Homo sapiens* (NP\_060538.2; 974 amino acids). Red box indicates anti-PIWI binding site.

# MSA

The multiple sequence alignment result as produced by T-coffee.

The multiple sequence alignment result as produced by T-coffee.				
T-COFFEE, Version_11.00 (Version_11.00) Cedric Notredame SCORE=947 *				
BAD AVG GOOD				
XP 008436386.1 NP_001077432.1 cons	: 92 : 93 : 94			
XP_008436386.1 NP_001077432.1	MDVGVSKSRVFVSYSSQVLLSKCSIPLSVRYVMDAVKDGPRGKMVALAAGLSVGATIGYIVYRHIS MSTERTSWTSLSTIQKIALGLGIPASATVAYILYRRYR			
cons	* : :**. *:**:**:			
XP_008436386.1 NP_001077432.1	NASSSQEPDTEESKIILPIEVYRNISRCYATFLDVASQKSGAHVRVASYSEETGHKAAVCVQ ESREERLTFVGEDDIEIEMRVPQEAVKLIIGRQGANIKQLRKQTGARIDVDTEDVGDERVLL			
cons	:: <mark> * * :: :</mark> * * <mark>: * . : : :: :*</mark> *:: * :*:.*.: : :			
XP_008436386.1 NP_001077432.1	IQGSKEQVLLARCVLENLATDCEPTVEVLEVPQNAFGRVIGRGGEGLKLITRSTGAKIVCSREKKH ISGFPVQVCKAKAAIHQILTENTPVSEQLSVPQRSVGRIIGRGGETIRSICKASGAKITCDKESEG *.* ** *:::: *: *. *.*:*::**:****** :: * :::****.*			
cons				
XP_008436386.1 NP_001077432.1	NPGGKGSVTITGSKQEVKQAKEMILERVGADAVVRSKISQSSALRQKRGHKVV			
cons	:.*:*::** **.:***:* * :*::*: * * : <mark>:</mark>			
XP_008436386.1 NP_001077432.1	NPDPCCMEPKCPVGLNNNGPVSYTEKNGLVQSKEATAERLLLEMKGLKGTDEQEEESSIST EPALWKNTSSSMEPTAPLVTPPPKGGGDMAVVVSKEGSWEKPSDDSFQKSEA			
cons	· · · · *** · · · · · · · · · · · · · ·			
XP_008436386.1 NP_001077432.1	DTLSEVSKFEIPSPDLSFQPDEHLEVYVSASENPNHFWIQILGVRSLQLDKLTEEMNNFYTNENPT QAIPEMPMFEIPSPDFSFHADEYLEVYVSASEHPNHFWIQIVGSRSLQLDKLVNEMTQHYENSVPE			
cons	***************************************			
XP_008436386.1 NP_001077432.1 cons	EQRMDSILVGDIVAAPYRDYNKWNRARVLGFLRSGLVDLYYVDFGDNGEFSRDILRPL DLTVHVGDIVAAPLPTNGSWYRARVLGTLENGNLDLYFVDFGDNGDCPLKDLRAL : ********* ****** ** :***:*******: ***			
XP 008436386.1	FQAIECSLAGVRPKGEAWTEAALDIFEQLTYCANWRPLQAKLCSYSHSEVSSWPSVKLYDNSKGKA			
NP_001077432.1	FQAIECSLAGVKPKGEAWTEAALDIFEQLITEQLITEQAWKPLQAKLCSTSHSEVSSWPSVKLTDNSKGKA			
cons	******* * * * * * * * *** * *** ** ** *			
XP_008436386.1 NP_001077432.1	VDIGEELIRLGHAVSFQETFNEKVEGDNLGCLQRMLDDVIGATSELSLSCISLSE LDIGLELVHKGYAIELPEDIEENRAVPDMLKDMATETDASLSTLLTETKKSSGEITHTLSCLSLSE			
cons	:*** **:: *:*:: * ::*: :*** **:: :::*: * ::*:			
XP_008436386.1 NP_001077432.1	AASVSGSVDDGVEDE - LL AASMSG DDNLEDDYLL			
cons	*** ** ** **			

T-Coffee alignment of TDRKH from *P. reticulata* (XP\_008436386.1; 579 amino acids) and *Homo sapiens* (NP\_001077432.1; 562 amino acids). Red box indicates anti-TDRKH binding sites.