## Evolutionary Considerations in Sexual Reproduction

## **More Rotifer Strangeness**

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Gene ID, name	Contig ID	Introns	AI	% Identity to best hit	Best hit, E-value	Best hit, metazoan	Best hit, taxonomy	Definition
AV10027_ <i>XynB</i>	Av212A	0	460	63	0.00E+00	No hits	Bacteria; Bacteroidetes	Xylosidase/arabinosidase
AV10001_ <i>NRPS</i>	Av110A	10	460	32	0.00E+00	No hits	Bacteria; (Proteobacteria/ Cyanobacteria)	Nonribosomal peptide synthetase
AV10134_PheA	161F07	0	400	61	1.00E-174	No hits	(Fungi; Bacteria)	Monooxygenase, FAD dependent
AV10002_ <i>TrkA</i>	Av110A	0	379	54	1.00E-175	4.00E-11	Bacteria; Proteobacteria	Monooxygenase, NAD dependent
PR10002_ <i>MviM</i>	182F10	0	327	67	1.00E-149	2.00E-07	Bacteria; (Acidobacteria/ Chloroflexi)	Oxidoreductase
PR10010_ <i>DAP2</i>	182F10	0	310	27	1.00E-140	1.00E-05	Bacteria; (Acidobacteria/ Proteobacteria)	Prolyl oligopeptidase*
V10104_Dur3	AvTelL.B	1	243	44	1.00E-132	4.00E-27	Eukaryota; Fungi	Urea active transporter*
PR10012_RamA	182]17	0	246	31	1.00E-107	No hits	(Bacteria; Fungi)	α-L-Rhamnosidase
AV10121_NRPS	9907	4	237	30	1.00E-103	No hits	Bacteria; Cyanobacteria	Nonribosomal peptide synthetase
AV10153_ <i>XghA</i>	210B3	0	212	50	1.00E-108	2.00E-16	Eukaryota; Fungi	Endo-xylogalacturonan hydrolase
AV10042_HemK	Av240B	1	199	56	2.00E-91	1.00E-04	Bacteria; Proteobacteria	HemK-like methyltransferase
AV10092_β-Gal	AvTelL.A	0	153	33	1.00E-105	4.00E-39	Eukaryota; Viridiplantae	β-D-Galactosidase
AV10044_ <i>Alr</i>	Av240B	1	152	38	1.00E-67	No hits	Bacteria; Bacteroidetes	Alanine racemase
AV10025_AMH	Av212A	1	150	52	8.00E-77	2.00E-11	Eukaryota; Fungi	Amidohydrolase
AV10045_ <i>Ddl</i>	Av240B	1	138	40	1.00E-60	No hits	Bacteria; Bacteroidetes	D-Alanine-D-alanine ligase
AV10140_ <i>PLDc</i>	193E18	2	126	31	1.00E-55	No hits	Eukaryota; Fungi	Phospholipase-D active site motif protein*
AV10016_ <i>FabG</i>	Av212A	0	98	58	1.00E-74	8.00E-32	Bacteria	Short-chain dehydrogenase/reductase
AV10109_ <i>FabG</i>	AvTelL.B	0	92	57	4.00E-73	5.00E-33	Bacteria	Short-chain dehydrogenase/reductase
AV10011_ <i>FabG</i>	Av212A	0	88	54	6.00E-67	2.00E-28	Bacteria	Short-chain dehydrogenase/reductase
AV10071_ <i>HAL</i>	AvTelK.A	0	77	48	2.00E-61	1.00E-27	Bacteria	Histidine ammonia-lyase
V10095_GCN5	AvTelL.A	0	59	35	2.00E-27	No hits	Bacteria; Proteobacteria	GCN5-related N-acetyltransferase+/*
AV10158 FabG	210B3	2	46	41	2.00E-39	2.00E-19	Bacteria	Short-chain dehydrogenase/reductase



