

The 30 slowest evolving genes on the 5 taxa tree as determined by the M0 model

OrthoDB group ^a	Gene ^b	Classification	Global ω ^c	Tree Length ^d
EOG6XPNXB	basket	c-Jun N-terminal kinases	0.00469	0.9624
EOG6VX0M4	rm62-I	Small RNA regulatory pathway members	0.00638	1.8385
EOG69W0XF	ran	Small RNA regulatory pathway members	0.00899	2.0558
EOG6PC86T	tor	Autophagy	0.00972	1.8615
EOG6GHX4B	CLIP-D10	CLIP serine protease	0.01051	1.5225
EOG634TNR	pellino	Toll pathway	0.01095	1.3130
EOG6WH726	atg6	Autophagy	0.01267	1.6741
EOG6J9KDP	Duox	Peroxidase	0.01440	1.7390
EOG6W9GK1-2	rm62-H	Small RNA regulatory pathway members	0.01533	26.8464
EOG641NSQ	stat	JAK/STAT pathway	0.01591	1.9244
EOG6K3JCB	jra	c-Jun N-terminal kinases	0.01599	1.9814
EOG6931ZS-4	TLR-8	Toll receptor	0.01807	2.0594
EOG6CRJF5	masquerade	CLIP serine protease	0.01809	2.4697
EOG6NVX17	argonaute-1	Small RNA regulatory pathway members	0.01837	1.1468
EOG6612K2	rm62-A	Small RNA regulatory pathway members	0.01941	1.5797
EOG634TMW	ranbp-21	Small RNA regulatory pathway members	0.02043	1.4494
EOG6W9GK1-3	rm62-B1	Small RNA regulatory pathway members	0.02174	12.2854
EOG60001Z	atg8	Autophagy	0.02379	0.9714
EOG6X3FG7	tudor-SN	Small RNA regulatory pathway members	0.02586	1.6953
EOG6P8D0V	atg5	Autophagy	0.02650	1.7760
EOG6KKWJ6	fmr1	Small RNA regulatory pathway members	0.02706	0.7046
EOG66WWRH-1	Clect-GA1	C-type lectin	0.02727	15.4043
EOG66DJHX-1	dscam-like protein	Immunoglobulin	0.02775	39.7524
EOG6W9GK1-1	rm62-J	Small RNA regulatory pathway members	0.02782	14.5619
EOG6931ZS-1	TLR-7	Toll receptor	0.02839	1.6509
EOG64B8HP	kayak	c-Jun N-terminal kinases	0.02866	1.1186
EOG6K6DKF	cactin	Toll pathway	0.03088	2.3047
EOG6KD521	chorion peroxidase	Peroxidase	0.03149	16.4281
EOG6DR7V8	atg18	Autophagy	0.03276	1.0310
EOG6TTF0B	spatzle-6	Spatzle	0.03401	1.7632

^a Group identifiers are from OrthoDB 6 (<http://cegg.unige.ch/orthodb6>).^b Unless otherwise specified, gene names are taken from the *A. mellifera* or *D. melanogaster* orthologs.^c Maximum likelihood estimate across all sites and branches.^d Tree length in synonymous substitutions per synonymous sites.