

Summary of models on the 4 taxa tree.

OrthoDB Group ^a	Gene ^b	Classification	Sites ^c	Global ω ¹	M8 vs M7 ²	Branch-site ³	Clade D ⁴
EOG6JSXPT	abaecin	AMP	46	0.33584			X
EOG6TDZ3C	defensin	AMP	93	0.2081			X
EOG6C2FSC	atg1	Autophagy	476	0.13269			X
EOG644J2Q	atg10	Autophagy	162	0.11878			
EOG6MGQPH	atg16L	Autophagy	160	0.12256			X
EOG6DR7V8	atg18	Autophagy	338	0.01356			
EOG69KD5B	atg2	Autophagy	1983	0.07114			
EOG6D2556	atg4A	Autophagy	482	0.06251			X
EOG602V84	atg4B	Autophagy	371	0.05558			
EOG6P8D0V	atg5	Autophagy	265	0.02194			
EOG6WH726	atg6	Autophagy	430	0.01014			
EOG6W9GKN	atg7	Autophagy	668	0.08236			X
EOG60001Z	atg8	Autophagy	117	1e-04			
EOG6Q574K	atg9	Autophagy	836	0.07233			
EOG6NP5KW	buffy	Autophagy	270	0.06015			
EOG6PC86T	tor	Autophagy	2407	0.01111			
EOG6XPNXB	basket	c-Jun N-terminal kinases	388	0.02014			
EOG680GDM	eiger	c-Jun N-terminal kinases	374	0.12769			
EOG61893B	hemipterous	c-Jun N-terminal kinases	759	0.03338			
EOG6K3JCB	jra	c-Jun N-terminal kinases	196	0.27614			
EOG64B8HP	kayak	c-Jun N-terminal kinases	185	0.019			
EOG64QRG8	tak1	c-Jun N-terminal kinases	407	0.11524			
EOG6N8PNJ	wengen	c-Jun N-terminal kinases	293	0.18255			X
EOG6FBG95	Clect-10	C-type lectin	159	0.14616			X
EOG68W9HQ	Clect-8	C-type lectin	412	0.07825			
EOG66WWRH-1	Clect-GA1	C-type lectin	217	0.02995			
EOG66WWRH-2	Clect-GA2	C-type lectin	216	0.04598			
EOG6W6MC0	Clect-GA3	C-type lectin	230	0.02812			
EOG61VHHT	Clect-SE1	C-type lectin	1095	0.03638			X
EOG6612JX	Clect-SE2	C-type lectin	866	0.06072			
EOG6VX0M3	ark	Caspase	1263	0.1294	X		X
EOG62BVQX	caspase-L1	Caspase	396	0.16633			X
EOG6F1VKC	ice	Caspase	297	0.12397			
EOG6Z8WBN	catalase	Catalase	221	0.10103			
EOG64B8H5	CLIP-A10	CLIP serine protease	816	0.12855	X		
EOG6PRR5Q	CLIP-A30	CLIP serine protease	875	0.1305			X
EOG61NS2P	CLIP-A5	CLIP serine protease	308	0.2122			X
EOG6FJ6RD	CLIP-B13	CLIP serine protease	355	0.26853			X
EOG6QRFKP	CLIP-C1B	CLIP serine protease	350	0.3294			X
EOG6TX97G	CLIP-D1	CLIP serine protease	241	0.22975			
EOG6TX97R	CLIP-D1-like protein	CLIP serine protease	320	0.36655			X
EOG6GHX4B	CLIP-D10	CLIP serine protease	308	0.00845			
EOG6R7SS0	CLIP-D3	CLIP serine protease	569	0.09458			
EOG680GC4	CLIP-D9	CLIP serine protease	503	0.08069			X
EOG6CRJF5	masquerade	CLIP serine protease	603	0.09003			
EOG6RBP1C	persephone	CLIP serine protease	293	0.27289			X
EOG6RJJDH9	scarface	CLIP serine protease	622	0.30015			X
EOG6NCJV4	snake	CLIP serine protease	404	0.26193			
EOG6HX3GG	stubble	CLIP serine protease	695	0.06682			
EOG6N5TBN	galectin-3	Galectin	1290	0.0529			X
EOG634TPR	galectin-5	Galectin	423	0.10772			
EOG6RV16R-1	BGRP-1	GGBP	457	0.2749			X
EOG6RV16R-2	BGRP-2	GGBP	322	0.22745			X
EOG69CNQ4-1	IAP-1A	IAP repeat	401	0.14696			X
EOG69CNQ4-2	IAP-1B	IAP repeat	346	0.24138			X
EOG6Q2BWQ	IAP-2	IAP repeat	515	0.14886			X
EOG6ZCRN2	IAP-5	IAP repeat	145	0.09251			X
EOG61ZCRN	IAP-6	IAP repeat	3255	0.04459			X
EOG66T1GW	caspar	IMD pathway	614	0.03108			
EOG6ZW3V0	fadd	IMD pathway	144	0.22926			
EOG6DV43B	immune deficiency	IMD pathway	256	0.20362			
EOG64J10C	ird5	IMD pathway	560	0.19261			X
EOG679CP4	POSH	IMD pathway	866	0.05316			X
EOG66DJHX-2	dscam	Immunoglobulin	777	0.05496	X		X
EOG66DJHX-1	dscam-like protein	Immunoglobulin	1847	0.02561		X	X
EOG666T1W	domeless	JAK/STAT pathway	1490	0.10803			X
EOG6FN2ZK	hopscotch	JAK/STAT pathway	1088	0.10446			X
EOG641NSQ	stat	JAK/STAT pathway	774	0.01621			X
EOG6FBG9K	npc2a	MD-2-related lipid recognition	149	0.17968			
EOG6NVX30	npc2b	MD-2-related lipid recognition	127	0.00435			
EOG6QRFJX	draper	Nimrod	945	0.16982			X
EOG6ZPC96	nimrod-C2	Nimrod	1802	0.12496		X	X
EOG6J3TZ2	cardinal	Peroxidase	1203	0.08436	X		X
EOG6KD521	chorion peroxidase	Peroxidase	482	0.0574			X
EOG6VX0M1-1	DBLOX	Peroxidase	944	0.01738			X
EOG6VX0M1-2	DBLOX-like protein	Peroxidase	699	0.04801			X
EOG6J9KDP	Duox	Peroxidase	1458	0.18854			
EOG6J6Q5V	peroxidasin	Peroxidase	1100	0.07237			X
EOG6XKSQD	peroxiredoxin-1	Peroxidase	208	0.05024			X
EOG693216-1	peroxiredoxin-4	Peroxidase	220	0.12329			X
EOG693216-2	peroxiredoxin-5	Peroxidase	220	0.05527			
EOG60GB73-2	PHGPx2A	Peroxidase	166	0.09657			
EOG60GB73-1	PHGPx2B	Peroxidase	198	0.2249			X
EOG6VX0NG-1	PGRP-LF	PRGP	190	0.06285			
EOG6VX0NG-3	PGRP-S1	PRGP	103	0.11065			
EOG6VX0NG-2	PGRP-S2	PRGP	117	0.16311			
EOG6DFN3J	PPO-6	Prophenol oxidase	673	0.19318			X
EOG6VDNFR	dorsal	Relish	476	0.05633		X	X
EOG659ZWS	relish	Relish	613	0.109			X
EOG634TN8	croquemort	Scavenger receptor	487	0.17554			X
EOG6JQ2CF	LOC100642575 (B. terr)	Scavenger receptor	924	0.07198	X		X
EOG608KPT	LOC100642932 (B. terr)	Scavenger receptor	1893	0.11229			X
EOG6D254M	SCR-AC1	Scavenger receptor	2816	0.08879			X
EOG6CNP6K-1	SCR-B3	Scavenger receptor	569	0.16667			X
EOG6W0VV6	SCR-B5	Scavenger receptor	494	0.21578			
EOG6X3FGJ	SCR-B6	Scavenger receptor	437	0.07868			X
EOG6CNP6K-2	SCR-B9	Scavenger receptor	387	0.11332			X
EOG6HHMH6	serpin-23	Scavenger receptor	2066	0.09921	X	X	X
EOG6BG7B9	snmp1	Scavenger receptor	484	0.1691			X
EOG66Q57J	LOC100642902 (B. terr)	Serine protease inhibitor	1327	0.29567		X	X
EOG6XWDDG-1	serpin-10A	Serine protease inhibitor	385	0.21958		X	X
EOG6XWDDG-3	serpin-10B	Serine protease inhibitor	307	0.17517			X
EOG6M37R0	serpin-27A	Serine protease inhibitor	406	0.03255			
EOG6WDBSW	serpin-28D	Serine protease inhibitor	601	0.2977			X
EOG6XWDDG-2	serpin-9	Serine protease inhibitor	365	0.25778			X
EOG6NVX17	argonaute-1	Small RNA regulatory pathway members	886	0.02329			
EOG6KKWHX	argonaute-2	Small RNA regulatory pathway members	896	0.12628	X	X	X
EOG62Z354	argonaute-3	Small RNA regulatory pathway members	814	0.21295			X
EOG62547K	armitage	Small RNA regulatory pathway members	1054	0.14429			X
EOG66DJHQ	aubergine	Small RNA regulatory pathway members	787	0.03453	X		X
EOG6W3R35	belle	Small RNA regulatory pathway members	683	0.05737		X	X
EOG6TTDZQ	dicer-1	Small RNA regulatory pathway members	1908	0.01077			X
EOG634TMX	dicer-2	Small RNA regulatory pathway members	1334	0.16362			X
EOG634TN0	droscha	Small RNA regulatory pathway members	1304	0.02405			X
EOG6KKWJ6	fmr1	Small RNA regulatory pathway members	377	0.02037			X
EOG6ZCRKS	loquacious	Small RNA regulatory pathway members	332	0.03403			X
EOG6GXD37	pasha	Small RNA regulatory pathway members	638	0.02071			
EOG6RJJDHD	r2d2	Small RNA regulatory pathway members	325	0.05218			X
EOG69W0XF	ran	Small RNA regulatory pathway members	128	0.02393			
EOG634TMW	ranbp-21	Small RNA regulatory pathway members	1217	0.11061			
EOG6612K2	rm62-A	Small RNA regulatory pathway members	725	0.14078			X
EOG6W9GK1-3	rm62-B1	Small RNA regulatory pathway members	431	0.03383	X		X
EOG6XWDCW	rm62-C	Small RNA regulatory pathway members	526	0.02738			X
EOG6ZPC9T	rm62-F	Small RNA regulatory pathway members	546	0.06871			X
EOG6W9GK1-2	rm62-H	Small RNA regulatory pathway members	549	0.05434			
EOG6VX0M4	rm62-I	Small RNA regulatory pathway members	713	0.22813			X
EOG6W9GK1-1	rm62-J	Small RNA regulatory pathway members	708	0.00691			X
EOG6W9GK1-4	rm62-J1	Small RNA regulatory pathway members	402	0.01879			
EOG6BG79T	spindle-E	Small RNA regulatory pathway members	1273	0.25716		X	X
EOG6X3FG7	tudor-SN	Small RNA regulatory pathway members	872	0.03453			X
EOG6KWH93	vig	Small RNA regulatory pathway members	411	0.22524			X
EOG6QNKCB	spatzle-1B	Spaetzle	169	0.05277		X	X
EOG61C5BT	spatzle-3	Spaetzle	401	0.17389			
EOG679CPZ	spatzle-5	Spaetzle	277	0.183			
EOG6TTF0B	spatzle-6	Spaetzle	395	0.18222			
EOG68SF83	tep23	Thioester-containing protein	1694	0.09047		X	X
EOG6X0K76	tep3	Thioester-containing protein	1379	0.10134			X
EOG6X95Z0	tepA	Thioester-containing protein	1585	0.15891			
EOG6K6DKF	cactin	Toll pathway	569	0.11892			
EOG6RBP1B	cactus	Toll pathway	357	0.22611			X
EOG6X0K8Q	myd88	Toll pathway	275	0.21105			X
EOG6T1G2P	pelle	Toll pathway	414	0.04759			X
EOG634TNR	pellino	Toll pathway	431	0.02026	X		X
EOG64F4RN	traf6	Toll pathway	409	0.31941			X
EOG6866VT	tube	Toll pathway	298	0.01657		X	X
EOG6H8R8C	TLR-1	Toll receptor	496	0.03138			X
EOG6931ZS-2	TLR-10	Toll receptor	1280	0.04607			
EOG6931ZS-3	TLR-6	Toll receptor	1217	0.03131			
EOG6931ZS-1	TLR-7	Toll receptor	1344	0.08263			X
EOG6931ZS-4	TLR-8	Toll receptor	1184	0.02863			

^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 Total number of codons in the alignment after trimming with Gblocks.¹ Across the whole phylogeny using M0 model.² Positive selection across the whole phylogeny.³ Positive selection on the branch between *Bombus* and *Apis*.⁴ Different selective pressures between *Bombus* and *Apis*.

Using FDR < 0.05 on all tests.