

ST7. Gastropod orthology analysis. Conserved domains associated with the main OGs exclusively contributed by euthyneuran taxa (number of proteins per species). The list is reduced to OGs containing at least 18 sequences, and present in at least 5 of 6 euthyneuran taxa (*R. auricularia* was a posteriori discarded, see text for explanation).

conserved domain	OG_14Gastropoda	Euthyneuran taxa													
		<i>Lymnaea stagnalis</i>	<i>Biomphalaria glabrata</i>	<i>Bulinus truncatus</i>	<i>Elysia chlorotica</i>	<i>Candidula unificiata</i>	<i>Aplysia californica</i>	TOTAL-EUTHYNEURA	<i>Littorina saxatilis</i>	<i>Potamopyrgus antipodarum</i>	<i>Pomacea canaliculata</i>	<i>Batillaria attramentaria</i>	<i>Lottia gigantea</i>	<i>Gigantopelta aegis</i>	<i>Haliotis rubra</i>
CLECT	OG0000086	46	35	24	1	0	19	125	0	0	0	0	0	0	0
7tmA_FMRFamide_R-like	OG0000164	20	28	17	6	13	23	107	0	0	0	0	0	0	0
7tmA_FMRFamide_R-like	OG0000194	35	18	8	4	23	10	98	0	0	0	0	0	0	0
BTB, BACK,Kelch-like	OG0000263	57	9	10	0	3	2	81	0	0	0	0	0	0	0
P450_cycloAA_1	OG0000313	7	18	32	4	1	6	68	0	0	0	0	0	0	0
Aerolysin	OG0000438	12	25	14	1	0	9	61	0	0	0	0	0	0	0
7tmA_NTSTR-like	OG0000474	7	22	12	1	7	10	59	0	0	0	0	0	0	0
Galactosyltransferase	OG0000590	16	14	8	0	5	11	54	0	0	0	0	0	0	0
BIR	OG0000641	17	17	9	1	1	4	49	0	0	0	0	0	0	0
IG_like	OG0000779	7	8	7	21	1	3	47	0	0	0	0	0	0	0
OATP	OG0000504	6	15	9	2	9	6	47	0	0	0	0	0	0	0
LRR_8	OG0000760	9	16	3	0	4	13	45	0	0	0	0	0	0	0
7tmA_ET_R-like	OG0000843	12	13	3	4	9	3	44	0	0	0	0	0	0	0
7tmA_FMRFamide_R-like	OG0000969	1	4	3	19	0	14	41	0	0	0	0	0	0	0
Amelogenin / Glutenin	OG0001218	23	7	5	1	2	0	38	0	0	0	0	0	0	0
7tm_classA_rhodopsin-like	OG0001291	31	1	4	0	1	0	37	0	0	0	0	0	0	0
TNFR	OG0001290	12	8	9	2	3	0	34	0	0	0	0	0	0	0
MFS_1	OG0001548	3	5	6	4	10	3	31	0	0	0	0	0	0	0
SGL / atrophin_1	OG0001383	4	8	5	2	9	2	30	0	0	0	0	0	0	0
TNF	OG0001622	8	14	5	1	1	1	30	0	0	0	0	0	0	0
no domain	OG0001447	6	10	6	3	3	0	28	0	0	0	0	0	0	0
7tmA_FMRFamide_R-like	OG0002416	7	9	4	0	1	6	27	0	0	0	0	0	0	0
7tmB3_Methuselah-like	OG0002357	1	7	6	10	2	1	27	0	0	0	0	0	0	0
CBM_14 / Glutenin_hmw / VWA	OG0002345	5	14	5	2	0	1	27	0	0	0	0	0	0	0
Fasciclin	OG0001545	6	5	6	6	0	4	27	0	0	0	0	0	0	0
no domain	OG0001574	7	10	2	5	0	3	27	0	0	0	0	0	0	0
SH3_and_anchor / DNA_pol3_γ3	OG0001940	11	8	6	0	1	1	27	0	0	0	0	0	0	0
MATH_TRAF_C	OG0002388	3	10	6	2	1	4	26	0	0	0	0	0	0	0
7tmA_FMRFamide_R-like	OG0002778	5	4	3	1	4	8	25	0	0	0	0	0	0	0
UBQ	OG0002344	2	3	3	0	4	13	25	0	0	0	0	0	0	0
no domain	OG0003169	1	19	2	1	0	1	24	0	0	0	0	0	0	0
Trypsin	OG0002794	2	6	7	2	1	6	24	0	0	0	0	0	0	0
HtrL_YibB	OG0003057	5	2	4	2	8	2	23	0	0	0	0	0	0	0
IG_like	OG0002826	4	13	3	1	1	1	23	0	0	0	0	0	0	0
EFh	OG0003457	1	5	7	5	3	1	22	0	0	0	0	0	0	0
no domain	OG0003800	4	5	11	1	0	1	22	0	0	0	0	0	0	0
Globin	OG0003205	5	8	4	2	1	0	20	0	0	0	0	0	0	0
MFS	OG0004044	1	1	1	15	0	2	20	0	0	0	0	0	0	0
Cyt_c_Oxidase_VIIC	OG0005628	3	7	6	1	1	0	18	0	0	0	0	0	0	0
HLH	OG0004461	5	7	1	2	2	1	18	0	0	0	0	0	0	0