

Table S1. Proteins identified in the membrane and supernatant fractions of purified yolk platelets

Identified proteins	GI number	YP membranes or supernatant?	Description
Yolk platelets			
Vitellogenin A2	gi 4388696	Both	Major yolk protein, estrogen inducible (liver)
Vitellogenin B1	gi 33563034	Both	Major yolk protein, estrogen inducible (liver)
Plasma			
Ep45	gi 259142	Both	Protein found in <i>X. laevis</i> plasma and eggs, estrogen inducible (liver)
MGC64276	gi 32766455	YP membranes	Homolog of human complement component C9
Pon1-prov	gi 28422437	YP membranes	Homolog of paraoxonase, hydrolyzes oxidized lipids in LDL
MGC82702	gi 49256138	YP supernatant	Homolog of alpha globin, subunit of hemoglobin
LOC448844	gi 51895923	YP supernatant	Serum albumin
Lysosome			
LOC432087	gi 71051360	YP membranes	Predicted alpha-L-1 fucosidase
Manba-prov	gi 50417768	YP supernatant	Predicted beta-mannosidase
MGC64382, dipeptidyl-peptidase IV	gi 111185523, gi 147907306	YP supernatant	Dipeptidyl-peptidase IV, serine protease, hydrolyzes N-terminus dipeptides
LOC446948	gi 71681246	YP supernatant	Predicted galactocerebrosidase
Ctsc-prov	gi 33417162	YP supernatant	Dipeptidyl aminopeptidase I, cysteine protease, hydrolyzes N-terminus dipeptides
Endoplasmic reticulum			
LOC495169	gi 54038199	YP membranes	Homolog of human ERp72, a protein disulfide isomerase
Grp58-prov	gi 28302197	Both	Homolog of human ERp57, a protein disulfide isomerase, associates with ApoB100
P4hb	gi 28436918	Both	Homolog of human PDI, a protein disulfide isomerase
MGC79068	gi 50418205	YP membranes	Homolog of human P5, a protein disulfide isomerase
MGC52808, MGC52894	gi 28277278, gi 28175644	YP membranes	Predicted Ribophorin I
MGC53764	gi 28436786	YP membranes	Predicted Ribophorin II
MGC84282, LOC495100	gi 49522162, gi 54038026	YP membranes	Homolog of human ERLIN2, prohibitin family member
MGC68448, heat shock protein gp96	gi 37805387, gi 148223467	YP supernatant	Predicted Hsp90 chaperone
Hspa5	gi 27370850	Both	Nearly identical to <i>X. laevis</i> BiP, Hsp70 chaperone
Mitochondria			
MGC82638	gi 49256557	YP membranes	Predicted hydroxyacyl-Coenzyme A dehydrogenase
Atp5b	gi 28436792	YP membranes	Predicted ATP synthase, mitochondrial F1 complex, beta subunit precursor
Atp5a1	gi 32766606	YP membranes	Predicted ATP synthase, mitochondrial F1 complex, alpha subunit
MGC82361, MGC82400, MGC82361	gi 47682284, gi 46329495, gi 47682284	YP membranes	Predicted ATP synthase, mitochondrial F0 complex, subunit d
Thiolase-prov	gi 28280033	YP membranes	Predicted hydroxyacyl-Coenzyme A dehydrogenase
Mitochondrial malate dehydrogenase	gi 50882324	YP membranes	Mitochondrial malate dehydrogenase 2a
MGC114756	gi 62826006	YP membranes	Predicted voltage-dependent anion-selective channel protein
MGC79025	gi 50417418	YP membranes	Predicted Prohibitin 2
Hspd1, MGC53106	gi 47938737, gi 28436902	Both	Predicted Hsp60 chaperone
Location not classified			
MGC68676	gi 37747702	YP supernatant	Predicted phospholipase D3, involved in signalling pathways
MGC82953	gi 148228657	YP supernatant	Predicted VAT1, a vesicle amine transport protein
MGC81039	gi 46249838	YP membranes	Homolog of yeast Yop1, binds to Rab proteins
Rheb-prov	gi 27695152	YP membranes	Predicted Rheb, GTPase, growth regulator upstream of TOR
MGC64421	gi 32450604	YP membranes	Homolog of human thrombin inhibitor, an intracellular serpin
Cytoplasm			
MGC53952	gi 28374367	Both	Nearly identical to <i>X. laevis</i> Hsc70, constitutively expressed Hsp70 protein
LOC443576	gi 48734658	YP membranes	Predicted inosine monophosphate synthase, de novo purine biosynthesis
Pgm2-prov	gi 27881782	YP membranes	Predicted phosphoglucomutase, glycogen metabolism
MGC69114	gi 33585659	YP membranes	Predicted transketolase, pentose phosphate pathway
Cct3-prov	gi 29477224	YP membranes	Predicted subunit of CCT chaperonin

Cct8-prov	gi 27924345	YP membranes	Predicted subunit of CCT chaperonin
PKM2	gi 51258124	YP membranes	Predicted pyruvate kinase, glycolysis
MGC53997	gi 27695233	YP membranes	Predicted beta-tubulin
Eno1-prov	gi 32450571	YP membranes	Predicted enolase, glycolysis
MGC64329	gi 32484263	YP membranes	Predicted elongation factor 1 gamma
Actin	gi 1334642	YP membranes	Predicted beta-actin
MGC53030	gi 28302293	YP membranes	Predicted fructose bisphosphate aldolase
Ckb-prov	gi 27503418	YP membranes	Predicted creatine kinase
Gapd-prov	gi 27882192	YP membranes	Predicted glyceraldehyde 3-phosphate dehydrogenase, glycolysis
NM23	gi 1655706	YP membranes	Nucleoside diphosphate kinase
Cofilin-1, Cofilin-2	gi 148232082, gi 1168995	YP membranes	Actin regulation
MGC82306	gi 46329492	YP membranes	Predicted 40S ribosomal protein S18
Rpl27-prov	gi 34193964	YP membranes	Predicted 60S ribosomal protein L27
Ferritin heavy chain	gi 33331485	YP membranes	Forms iron storage complexes
14-3-3 zeta, Ywhaz- prov	gi 1360640, gi 27370992	YP membranes	14-3-3 protein
Ppib-prov, LOC495270	gi 32484306, gi 54261578	YP membranes	Predicted peptidylprolyl isomerase B

The GI number of each identification by the Mascot software and the associated protein name are listed. If the protein has not been assigned a function in *X. laevis*, as in the great majority of cases, BLAST searches were used to assign homologs and predicted functions. When highly similar (>95% amino acid identity) proteins were identified by mass spectrometry, they were assumed to be pseudo-alleles and are listed in the same row, separated by a comma.