Table S5.

KS5-SubA

Type	Sequence	EC Number	Organism	GenBank ID	RefSeq	UniProt	PDB
Eukaryota	GI19161		Drosophila mojavensis (Fruit fly).	EDW09227.1	XP_002005292.1	B4KQ99	
Eukaryota	GJ22296		Drosophila virilis (Fruit fly).	EDW61875.1	XP_002050682.1	B4LLC3	
Eukaryota	AGAP005512-PA		Anopheles gambiae (African malaria mosquito).	EAA11215.4	XP_315512.4	Q7Q747	
Eukaryota	AGAP005513-PA		Anopheles gambiae (African malaria mosquito).	EAA11161.4	XP_315513.4	Q7Q746	
Eukaryota	Elongase		Culex quinquefasciatus (Southern house mosquito) (Culex pungens).	EDS25728.1	XP_001841775.1	B0VZ85	
Eukaryota	Elongase, putative		Aedes aegypti (Yellowfever mosquito) (Culex aegypti).	EAT34080.1	XP_001663836.1	Q16II6	
Eukaryota	PREDICTED: similar to GA18780-PA		Nasonia vitripennis		XP_001607111.1		
Eukaryota	AGAP005511-PA		Anopheles gambiae (African malaria mosquito).	EAU76464.2	XP_001237679.2	A0NEE5	
Eukaryota	GF13757		Drosophila ananassae (Fruit fly).	EDV38038.1	XP_001961216.1	B3MI28	
Eukaryota	GG20949		Drosophila erecta (Fruit fly).	EDV55128.1	XP_001974728.1	B3NKA6	
Eukaryota	GE13887		Drosophila yakuba (Fruit fly).	EDW91582.1	XP_002091870.1	B4P496	

Eukaryota	AT24031p		Drosophila melanogaster (Fruit fly).	AAL90154.1		Q8T400 [T]	
Eukaryota	CG17821		Drosophila melanogaster (Fruit fly).	AAF57646.3	NP_725820.2	A1ZBD2	
Eukaryota	GM19879		Drosophila sechellia (Fruit fly).	EDW48511.1	XP_002034498.1	B4HP09	
Eukaryota	GD25362		Drosophila simulans (Fruit fly).	EDX07729.1	XP_002082144.1	B4QD24	
Eukaryota	GK20710		Drosophila willistoni (Fruit fly).	EDW72442.1	XP_002061456.1	B4MK03	
Eukaryota	GF13758		Drosophila ananassae (Fruit fly).	EDV38039.1	XP_001961217.1	B3MI29	
Eukaryota	GA15013		Drosophila pseudoobscura pseudoobscura (Fruit fly).	EAL24988.2	XP_001360413.2	Q291X4	
Eukaryota	GL11311		Drosophila persimilis (Fruit fly).	EDW31798.1	XP_002015908.1	B4GA46	
Eukaryota	GE13888		Drosophila yakuba (Fruit fly).	EDW91583.1	XP_002091871.1	B4P497	
Eukaryota	GG20950		Drosophila erecta (Fruit fly).	EDV55127.1	XP_001974727.1	B3NKA5	
Eukaryota	RE06553p		Drosophila melanogaster (Fruit fly).	AAF57647.2, AAR99140.1	NP_611365.2	Q6NN18 [T]	
Eukaryota	GM19880		Drosophila sechellia (Fruit fly).	EDW48510.1	XP_002034497.1	B4HP08	
Eukaryota	GD25363		Drosophila simulans (Fruit fly).	EDX07728.1	XP_002082143.1	B4QD23	

Eukaryota	GH19804		Drosophila grimshawi (Fruit fly) (Idiomyia grimshawi).	EDW02596.1	XP_001987729.1	B4JA09	
Eukaryota	GI20347		Drosophila mojavensis (Fruit fly).	EDW09119.1	XP_002005184.1	B4KPK9	
Eukaryota	GI20343		Drosophila mojavensis (Fruit fly).	EDW09116.1	XP_002005181.1	B4KPK6	
Eukaryota	GJ22069		Drosophila virilis (Fruit fly).	EDW61477.1	XP_002050284.1	B4LJ41	
Eukaryota	GK20708		Drosophila willistoni (Fruit fly).	EDW72444.1	XP_002061458.1	B4MK05	
Eukaryota	GK20709		Drosophila willistoni (Fruit fly).	EDW72443.1	XP_002061457.1	B4MK04	
Eukaryota	GK20706		Drosophila willistoni (Fruit fly).	EDW72445.1	XP_002061459.1	B4MK06	
Eukaryota	GI10225		Drosophila mojavensis (Fruit fly).	EDW15885.1	XP_002000424.1	B4KCN6	
Eukaryota	GJ11026		Drosophila virilis (Fruit fly).	EDW59703.1	XP_002056591.1	B4M4Z2	
Eukaryota	GI10223		Drosophila mojavensis (Fruit fly).	EDW15884.1	XP_002000423.1	B4KCN5	
Eukaryota	GH22831		Drosophila grimshawi (Fruit fly) (Idiomyia grimshawi).	EDV94802.1	XP_001994066.1	B4JSR2	
Eukaryota	GJ11028		Drosophila virilis (Fruit fly).	EDW59705.1	XP_002056593.1	B4M4Z4	
Eukaryota	CG31141		Drosophila melanogaster (Fruit fly).	AAN13958.2	NP_732912.2	Q8IMY2 [T]	

Eukaryota	GD21043		Drosophila simulans (Fruit fly).	EDX14122.1	XP_002104619.1	B4QSC3	
Eukaryota	GM26535		Drosophila sechellia (Fruit fly).	EDW43393.1	XP_002032407.1	B4HG00	
Eukaryota	GE10400		Drosophila yakuba (Fruit fly).	EDW98204.1	XP_002098492.1	B4PNZ4	
Eukaryota	GG11234		Drosophila erecta (Fruit fly).	EDV53951.1	XP_001982081.1	B3P8C7	
Eukaryota	GL23223		Drosophila persimilis (Fruit fly).	EDW24749.1	XP_002013763.1	B4G583	
Eukaryota	GA14209		Drosophila pseudoobscura pseudoobscura (Fruit fly).	EAL27712.2	XP_001358571.2	Q299J0	
Eukaryota	GE24724		Drosophila yakuba (Fruit fly).	EDW96740.1	XP_002097028.1	B4PVG7	
Eukaryota	GG17320		Drosophila erecta (Fruit fly).	EDV49697.1	XP_001980739.1	B3P4P4	
Eukaryota	GH01164p		Drosophila melanogaster (Fruit fly).	AAF54462.1, AAM48321.1	NP_649957.1	Q9VH57 [P]	
Eukaryota	GM26206		Drosophila sechellia (Fruit fly).	EDW42799.1	XP_002031813.1	B4HJC7	
Eukaryota	GD20753		Drosophila simulans (Fruit fly).	EDX13553.1	XP_002104050.1	B4QVX3	
Eukaryota	GF22463		Drosophila ananassae (Fruit fly).	EDV32925.1	XP_001964791.1	B3MUL0	
Eukaryota	GF13996		Drosophila ananassae (Fruit fly).	EDV32547.1	XP_001963326.1	B3MKN4	

Eukaryota	GG17319		Drosophila erecta (Fruit fly).	EDV49696.1	XP_001980738.1	B3P4P3	
Eukaryota	GE24723		Drosophila yakuba (Fruit fly).	EDW96741.1	XP_002097029.1	B4PVG8	
Eukaryota	IP10372p		Drosophila melanogaster (Fruit fly).	AAF54463.2, AAY55750.1, AAY55798.1	NP_649958.2	Q4V3H4 [T]	
Eukaryota	GD20752		Drosophila simulans (Fruit fly).	EDX13552.1	XP_002104049.1	B4QVX2	
Eukaryota	GM26205		Drosophila sechellia (Fruit fly).	EDW42798.1	XP_002031812.1	B4HJC6	
Eukaryota	GF17148		Drosophila ananassae (Fruit fly).	EDV42161.1	XP_001953600.1	B3M1D4	
Eukaryota	GG17318		Drosophila erecta (Fruit fly).	EDV49695.1	XP_001980737.1	B3P4P2	
Eukaryota	GE24722		Drosophila yakuba (Fruit fly).	EDW96742.1	XP_002097030.1	B4PVG9	
Eukaryota	IP10371p		Drosophila melanogaster (Fruit fly).	AAF54464.1, AAY55794.1	NP_731419.1	Q9VH55 [P]	
Eukaryota	GD20751		Drosophila simulans (Fruit fly).	EDX13551.1	XP_002104048.1	B4QVX1	
Eukaryota	GL23222		Drosophila persimilis (Fruit fly).	EDW24750.1	XP_002013764.1	B4G584	
Eukaryota	GA21802		Drosophila pseudoobscura pseudoobscura (Fruit fly).	EAL27713.2	XP_001358572.2	Q299J1	
Eukaryota	GF15498		Drosophila ananassae (Fruit fly).	EDV31725.1	XP_001962504.1	B3MLH6	

Eukaryota	GF15497		Drosophila ananassae (Fruit fly).	EDV31724.1	XP_001962503.1	B3MLH5	
Eukaryota	GD18654		Drosophila simulans (Fruit fly).	EDX13554.1	XP_002104051.1	B4QVX4	
Eukaryota	GM23846		Drosophila sechellia (Fruit fly).	EDW42800.1	XP_002031814.1	B4HJC8	
Eukaryota	GG17214		Drosophila erecta (Fruit fly).	EDV49698.1	XP_001980740.1	B3P4P5	
Eukaryota	GE25994		Drosophila yakuba (Fruit fly).	EDW96738.1	XP_002097026.1	B4PVG5	
Eukaryota	MIP05430p		Drosophila melanogaster (Fruit fly).	ACX53668.1		C9QPA5 [T]	
Eukaryota	CG8534		Drosophila melanogaster (Fruit fly).	AAF54460.1	NP_649955.1	Q9VH59 [T]	
Eukaryota	GM23845		Drosophila sechellia (Fruit fly).	EDW42801.1	XP_002031815.1	B4HJC9	
Eukaryota	GD18652		Drosophila simulans (Fruit fly).	EDX13555.1	XP_002104052.1	B4QVX5	
Eukaryota	PREDICTED: similar to AGAP007264-PA		Tribolium castaneum		XP_973993.2		
Eukaryota	Putative uncharacterized protein GLEAN_15657		Tribolium castaneum (Red flour beetle).	EFA05473.1		D2A678	
Eukaryota	PREDICTED: similar to elongase, putative		Acyrthosiphon pisum		XP_001942907.1		
Eukaryota	PREDICTED: similar to GA19958-PA		Acyrthosiphon pisum		XP_001952377.1		

Eukaryota	ACYPI007931 protein		Acyrthosiphon pisum (Pea aphid).	BAH72041.1		C4WVX1 [T]	
Eukaryota	GK12817		Drosophila willistoni (Fruit fly).	EDW85037.1	XP_002074051.1	B4NJS5	
Eukaryota	GL13809		Drosophila persimilis (Fruit fly).	EDW38920.1	XP_002020108.1	B4GP37	
Eukaryota	GA19958		Drosophila pseudoobscura pseudoobscura (Fruit fly).	EAL26992.1	XP_001357857.1	Q29BK4	
Eukaryota	GF18858		Drosophila ananassae (Fruit fly).	EDV44190.1	XP_001955629.1	B3M000	
Eukaryota	GD20962		Drosophila simulans (Fruit fly).	EDX13945.1	XP_002104442.1	B4R0M2	
Eukaryota	GM26443		Drosophila sechellia (Fruit fly).	EDW43207.1	XP_002032221.1	B4HEP6	
Eukaryota	GG11145		Drosophila erecta (Fruit fly).	EDV54129.1	XP_001982259.1	B3P8N4	
Eukaryota	MIP08184p		Drosophila melanogaster (Fruit fly).	ACT88147.1		C6SV14 [T]	
Eukaryota	LD14839p		Drosophila melanogaster (Fruit fly).	AAF56018.1, AAL28730.1, AAN13910.2, AAN13911.1	NP_651062.3, NP_732761.1, NP_732762.1	Q9VCY7 [T]	
Eukaryota	GE10310		Drosophila yakuba (Fruit fly).	EDW98020.1	XP_002098308.1	B4PMB5	
Eukaryota	elongation of very long chain fatty acids protein, putative		Pediculus humanus corporis USDA	EEB15720.1	XP_002428458.1		

Eukaryota	Putative uncharacterized protein		Tribolium castaneum (Red flour beetle).	EFA10643.1	XP_967030.1	D6X2U5	
Eukaryota	Putative uncharacterized protein		Tribolium castaneum (Red flour beetle).	EFA00083.1		D6WHH9	
Eukaryota	PREDICTED: similar to elongase, putative		Tribolium castaneum		XP_975397.2		
Eukaryota	PREDICTED: similar to GA16297-PA		Acyrthosiphon pisum		XP_001951537.1		
Eukaryota	Elongase		Culex quinquefasciatus (Southern house mosquito) (Culex pungens).	EDS39480.1	XP_001864000.1	B0X2X8	
Eukaryota	Elongase, putative		Aedes aegypti (Yellowfever mosquito) (Culex aegypti).	EAT48780.1	XP_001658888.1	Q17Q14	
Eukaryota	GK11478		Drosophila willistoni (Fruit fly).	EDW80599.1	XP_002069613.1	B4N9N4	
Eukaryota	CG6660		Drosophila melanogaster (Fruit fly).	AAF56072.1	NP_651104.1	Q9VCT3 [P]	
Eukaryota	IP10055p		Drosophila melanogaster (Fruit fly).	AAY55686.1		Q4V3T6 [T]	
Eukaryota	Elongation of very long chain fatty acids protein 4		Culex quinquefasciatus (Southern house mosquito) (Culex pungens).	EDS39481.1	XP_001864001.1	B0X2X9	
Eukaryota	AGAP003197-PA		Anopheles gambiae (African malaria mosquito).	EAL40729.3	XP_562969.3	Q5TTH1	
Eukaryota	AGAP003195-PA		Anopheles gambiae (African malaria mosquito).	EAU77013.1	XP_001237502.1	A0NDA4	
Eukaryota	elongation of very long chain fatty acids protein, putative		Pediculus humanus corporis USDA	EEB15718.1	XP_002428456.1		

Eukaryota	ACYPI003344 protein		Acyrthosiphon pisum (Pea aphid).	BAH72780.1		C4WY10 [T]	
Eukaryota	PREDICTED: similar to elongase, putative		Acyrthosiphon pisum		XP_001947506.1		
Eukaryota	PREDICTED: similar to elongase, putative		Acyrthosiphon pisum		XP_001947312.1		
Eukaryota	ACYPI005277 protein		Acyrthosiphon pisum (Pea aphid).	BAH71168.1		C4WTE8 [T]	
Eukaryota	PREDICTED: similar to elongase, putative		Nasonia vitripennis		XP_001599867.1		
Eukaryota	Elongase, putative		Aedes aegypti (Yellowfever mosquito) (Culex aegypti).	EAT40021.1	XP_001659028.1	Q16ZG9	
Eukaryota	Elongation of very long chain fatty acids protein 4		Culex quinquefasciatus (Southern house mosquito) (Culex pungens).	EDS32245.1	XP_001843382.1	B0W3U8	
Eukaryota	elongation of very long chain fatty acids protein, putative		Pediculus humanus corporis USDA	EEB14961.1	XP_002427699.1		
Eukaryota	elongation of very long chain fatty acids protein, putative		Pediculus humanus corporis USDA	EEB15719.1	XP_002428457.1		

KS5-SubB

Type	Sequence	EC Numbe	Organism	GenBank ID	RefSeq	UniProt	PDB
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC04105.1	XP_002409062.1	B7PBY3	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC20289.1	XP_002400747.1	B7QN67	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC20291.1	XP_002400749.1	B7QN69	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC17384.1	XP_002414076.1	B7QEW2	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC04438.1	XP_002410351.1	B7PCW6	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC13956.1	XP_002401424.1	B7Q534	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC01635.1	XP_002406518.1	B7P4W3	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC01636.1	XP_002406519.1	B7P4W4	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC04694.1	XP_002410958.1	B7PDM2	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC20298.1	XP_002400756.1	B7QN76	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC09162.1	XP_002399480.1	B7PRE0	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC18466.1	XP_002414801.1	B7QHZ4	

Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC09160.1	XP_002399478.1	B7PRD8	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC15529.1	XP_002406058.1	B7Q9K7	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC15041.1	XP_002404768.1	B7Q869	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC20302.1	XP_002400760.1	B7QN80	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC20299.1	XP_002400757.1	B7QN77	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC20303.1	XP_002400761.1	B7QN81	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC14591.1	XP_002403442.1	B7Q6W9	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC02854.1	XP_002401846.1	B7P8D2	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC06381.1	XP_002404990.1	B7PIF9	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC02754.1	XP_002400875.1	B7P832	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC02753.1	XP_002400874.1	B7P831	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC02752.1	XP_002400873.1	B7P830	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC12340.1	XP_002407675.1	B7Q0G8	

Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC02750.1	XP_002400871.1	B7P828	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC02749.1	XP_002400870.1	B7P827	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC20292.1	XP_002400750.1	B7QN70	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC20293.1	XP_002400751.1	B7QN71	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC20297.1	XP_002400755.1	B7QN75	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC09159.1	XP_002399477.1	B7PRD7	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC20296.1	XP_002400754.1	B7QN74	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC04697.1	XP_002410961.1	B7PDM5	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC18787.1	XP_002415122.1	B7QIW5	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC08456.1	XP_002435626.1	B7PPD4	
Eukaryota	Fatty acyl-CoA elongase, putative		Ixodes scapularis (Black-legged tick) (Deer tick).	EEC18783.1	XP_002415118.1	B7QIW1	
Eukaryota	Elongation of very long chain fatty acids protein AAEL008004		Lepeophtheirus salmonis (salmon louse).	ACO12429.1		C1BTS6 [T]	
Eukaryota	Elongation of very long chain fatty acids protein AAEL008004		Caligus clemensi.	ACO15214.1		C1C1R1 [T]	

Eukaryota	Elongation of very long chain fatty acids protein AAEL008004		Caligus clemensi.	ACO15291.1		C1C1Y8 [T]	
Eukaryota	Elongation of very long chain fatty acids protein AAEL008004		Caligus rogercresseyi.	ACO10789.1		C1BP36 [T]	

KS5-SubC

Type	Sequence	EC Numb	Organism	GenBank ID	RefSeq	UniProt	PDB
Eukaryota	Zgc:112263		Danio rerio (Zebrafish) (Brachydanio rerio).	AAH95712.1	NP_001019609.1	Q502G0 [T]	
Eukaryota	Novel protein similar to vertebrate elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like (Zgc:112263)		Danio rerio (Zebrafish) (Brachydanio rerio).	CAX13621.1		B8JJK4	
Eukaryota	LOC100135292 protein		Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).	AAI57588.1	NP_001107444.1	A9UMA8 [T]	
Eukaryota	PREDICTED: hypothetical protein		Taeniopygia guttata		XP_002188337.1		
Eukaryota	MGC115163 protein		Xenopus laevis (African clawed frog).	AAH93571.1	NP_001089378.1	Q566F8 [T]	
Eukaryota	PREDICTED: hypothetical protein		Strongylocentrotus purpuratus		XP_001194650.1, XP_797869.2		
Eukaryota	Novel protein similar to vertebrate elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1 (ELOVL1, zgc:103538)		Danio rerio (Zebrafish) (Brachydanio rerio).	CAN88636.1		A5PMD4	
Eukaryota	Novel protein similar to vertebrate elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1 (ELOVL1, zgc:103538)		Danio rerio (Zebrafish) (Brachydanio rerio).	AAH83417.1, CAN88635.1	NP_001005989.1	Q5XJ87 [T]	
Eukaryota	Elongation of very long chain fatty acids protein 1		Osmerus mordax (Rainbow smelt) (Atherina mordax).	ACO09366.1		C1BK13 [T]	
Eukaryota	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1		Homo sapiens	EAX07100.1			
Eukaryota	Elovl1-prov protein		Xenopus laevis (African clawed frog).	AAH42304.1	NP_001080371.1	Q8AVG1 [T]	
Eukaryota	MGC64517 protein		Xenopus laevis (African clawed frog).	AAH54983.1	NP_001079820.1	Q7SY74 [T]	
Eukaryota	Elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1		Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).	CAJ82993.1	NP_001016644.1	Q28IH0 [T]	

Eukaryota	Elovl7a protein		Danio rerio (Zebrafish) (Brachydanio rerio).	AAI55282.1		A9JTC1 [T]	
Eukaryota	Novel protein similar to vertebrate ELOVL family member (Zgc:55879)		Danio rerio (Zebrafish) (Brachydanio rerio).	CAP19505.1		A9C3R2	
Eukaryota	ELOVL family member 7, elongation of long chain fatty acids (Yeast) a		Danio rerio (Zebrafish) (Brachydanio rerio).	AAH45481.1	NP_956169.1	Q7ZVN0 [T]	
Eukaryota	PREDICTED: similar to LOC398440 protein		Taeniopygia guttata		XP_002188325.1		
Eukaryota	PREDICTED: similar to LOC398440 protein		Gallus gallus		XP_429134.2		
Eukaryota	ELOVL family member 7, elongation of long chain fatty acids (Yeast) b		Danio rerio (Zebrafish) (Brachydanio rerio).	AAH51608.1	NP_956072.1	Q7ZTU5 [T]	
Eukaryota	MGC80262 protein		Xenopus laevis (African clawed frog).	AAH72173.1	NP_001085206.1	Q6INU9 [T]	
Eukaryota	ELOVL family member 7, elongation of long chain fatty acids		Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).	AAH74576.1	NP_001005456.1	Q6GLC3 [T]	
Eukaryota	PREDICTED: hypothetical protein		Monodelphis domestica		XP_001381271.1		
Eukaryota	Elongation of very long chain fatty acids protein 7		Bos taurus (Bovine).	AAI26612.1	NP_001071510.1	A0JNC4 [T], A0JNC4.1	
Eukaryota	elongation of very long chain fatty acids protein 7		Bos taurus	DAA17940.1			
Eukaryota	Elongation of very long chain fatty acids protein 7		Mus musculus (Mouse).	AAH05602.1, BAB31310.1, BAC29727.1, BAC33552.1, BAE23454.1, EDL18446.1	NP_083277.3	Q9D2Y9 [T], Q9D2Y9.1	
Eukaryota	Putative uncharacterized protein Elovl7		Rattus norvegicus (Rat).		NP_001178773.1, XP_001065454.1	D4ADY9	

Eukaryota	PREDICTED: elongation of very long chain fatty acids-like 7		Oryctolagus cuniculus		XP_002714040.1		
Eukaryota	Putative uncharacterized protein		Ailuropoda melanoleuca (Giant panda).	EFB24434.1		D2H3V0	
Eukaryota	PREDICTED: similar to ELOVL family member 7, elongation of long chain fatty acids		Canis familiaris		XP_851268.1		
Eukaryota	PREDICTED: similar to elongation of very long chain fatty acids-like 7		Equus caballus		XP_001494543.1		
Eukaryota	PREDICTED: elongation of very long chain fatty acids protein 7-like		Callithrix jacchus		XP_002745002.1		
Eukaryota	PREDICTED: similar to ELOVL family member 7, elongation of long chain fatty acids isoform 1		Pan troglodytes		XP_001137116.1		
Eukaryota	PREDICTED: ELOVL family member 7, elongation of long chain fatty acids isoform 2		Pan troglodytes		XP_001137205.1		
Eukaryota	PREDICTED: LOW QUALITY PROTEIN: elongation of very long chain fatty acids protein 7-like		Pongo abelii		XP_002815632.1		
Eukaryota	Elongation of very long chain fatty acids protein 7		Homo sapiens (Human).	AAI30311.1, AAI30313.1, BAB15697.1, BAD93238.1, CAB70777.1	NP_001098028.1, NP_079206.2	A1L3X0 [T], A1L3X0.1	
Eukaryota	ELOVL family member 7, elongation of long chain fatty acids (yeast), isoform CRA_a		Homo sapiens	EAW55001.1			
Eukaryota	SJCHGC06698 protein		Schistosoma japonicum (Blood fluke).	AAW25886.1, CAX69919.1, CAX82879.1		Q5DE70 [T]	
Eukaryota	Elongation of very long chain fatty acids protein 1		Schistosoma japonicum	CAX69918.1			
Eukaryota	Elongation of fatty acids protein 1		Schistosoma mansoni (Blood fluke).	CAZ28764.1	XP_002572532.1	C4PZV5	

Eukaryota	Fatty acid acyl transferase-related		Schistosoma mansoni (Blood fluke).	CAZ28765.1	XP_002572533.1	C4PZV6	
Eukaryota	Zgc:153394		Danio rerio (Zebrafish) (Brachydanio rerio).	AAI24344.1	NP_001070061.1	Q08C82 [T]	

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Type	Sequence	EC Number	Organism	GenBank ID	RefSeq	UniProt	PDB
Eukaryota	elongation of very long chain fatty acids protein, putative		Pediculus humanus corporis USDA	EEB10552.1	XP_002423290.1		
Eukaryota	GA18780		Drosophila pseudoobscura pseudoobscura (Fruit fly).	EAL26993.1	XP_001357858.1	Q29BK5	
Eukaryota	GF16146		Drosophila ananassae (Fruit fly).	EDV44191.1	XP_001955630.1	B3M001	
Eukaryota	GM23637		Drosophila sechellia (Fruit fly).	EDW43208.1	XP_002032222.1	B4HEP7	
Eukaryota	GD18447		Drosophila simulans (Fruit fly).	EDX13946.1	XP_002104443.1	B4R0M3	
Eukaryota	GG12505		Drosophila erecta (Fruit fly).	EDV54128.1	XP_001982258.1	B3P8N3	
Eukaryota	GE24026		Drosophila yakuba (Fruit fly).	EDW98021.1	XP_002098309.1	B4PMB6	
Eukaryota	CG5278		Drosophila melanogaster (Fruit fly).	AAF56019.1	NP_651063.1	Q9VCY6 [P]	
Eukaryota	GK14432		Drosophila willistoni (Fruit fly).	EDW85036.1	XP_002074050.1	B4NJS4	
Eukaryota	GH19244		Drosophila grimshawi (Fruit fly) (Idiomyia grimshawi).	EDV93327.1	XP_001990265.1	B4JF46	
Eukaryota	GJ23058		Drosophila virilis (Fruit fly).	EDW67476.1	XP_002053956.1	B4M165	
Eukaryota	GI24279		Drosophila mojavensis (Fruit fly).	EDW14471.1	XP_001999010.1	B4K958	

Eukaryota	Elongase, putative		Aedes aegypti (Yellowfever mosquito) (Culex aegypti).	EAT46133.1	XP_001662066.1	Q17HH4	
Eukaryota	AGAP008780-PA		Anopheles gambiae (African malaria mosquito).	EAA10106.4	XP_314908.3	Q7PPN4	
Eukaryota	PREDICTED: similar to elongase, putative		Nasonia vitripennis		XP_001599914.1		
Eukaryota	PREDICTED: similar to CG5278-PA		Apis mellifera		XP_624324.2		
Eukaryota	GA18806		Drosophila pseudoobscura pseudoobscura (Fruit fly).	EAL26994.1	XP_001357859.1	Q29BK2	
Eukaryota	GF16148		Drosophila ananassae (Fruit fly).	EDV44188.1	XP_001955627.1	B3LZZ8	
Eukaryota	GH17398		Drosophila grimshawi (Fruit fly) (Idiomyia grimshawi).	EDV91362.1	XP_001994733.1	B4JV42	
Eukaryota	RH69239p		Drosophila melanogaster (Fruit fly).	AAF56015.1, AAL25486.1, AAN71629.1	NP_651060.1	Q9VCZ0 [T]	
Eukaryota	GG12507		Drosophila erecta (Fruit fly).	EDV54131.1	XP_001982261.1	B3P8N6	
Eukaryota	GI22725		Drosophila mojavensis (Fruit fly).	EDW15549.1	XP_002000088.1	B4K9B7	
Eukaryota	GK14434		Drosophila willistoni (Fruit fly).	EDW85039.1	XP_002074053.1	B4NJS7	
Eukaryota	GJ24664		Drosophila virilis (Fruit fly).	EDW68362.1	XP_002054842.1	B4M0I3	
Eukaryota	Elongase, putative		Aedes aegypti (Yellowfever mosquito) (Culex aegypti).	EAT35432.1	XP_001662545.1	Q16M71	

Eukaryota	Elongase, putative		Aedes aegypti (Yellowfever mosquito) (Culex aegypti).	EAT33534.1	XP_001648181.1	Q16H16	
Eukaryota	AGAP011812-PA		Anopheles gambiae (African malaria mosquito).	EAA00350.4	XP_320705.4	Q7PZA2	
Eukaryota	PREDICTED: similar to CG5326-PA, isoform A		Apis mellifera		XP_001120442.1		
Eukaryota	PREDICTED: similar to AGAP011812-PA, partial		Tribolium castaneum		XP_967207.2		
Eukaryota	Putative uncharacterized protein		Tribolium castaneum (Red flour beetle).	EFA10641.1		D6X2U7	
Eukaryota	PREDICTED: similar to GA18806-PA		Nasonia vitripennis		XP_001599838.1		
Eukaryota	Elongation of very long chain fatty acids protein 2		Culex quinquefasciatus (Southern house mosquito) (Culex pungens).	EDS29827.1	XP_001843008.1	B0W2S4	
Eukaryota	AGAP007134-PA		Anopheles gambiae (African malaria mosquito).	EAA04155.4	XP_308627.4	Q7QIY7	
Eukaryota	Elongation of very long chain fatty acids protein 4		Culex quinquefasciatus (Southern house mosquito) (Culex pungens).	EDS40638.1	XP_001845514.1	B0W9Y0	
Eukaryota	Elongase, putative		Aedes aegypti (Yellowfever mosquito) (Culex aegypti).	EAT45640.1	XP_001663163.1	Q17GE6	
Eukaryota	PREDICTED: similar to elongation of very long chain fatty acids protein 4		Tribolium castaneum		XP_968636.1		
Eukaryota	PREDICTED: similar to CG31522 CG31522-PA		Acyrthosiphon pisum		XP_001950768.1		
Eukaryota	PREDICTED: similar to CG31522-PB, isoform B		Apis mellifera		XP_001120770.1		

Eukaryota	PREDICTED: similar to CG33110-PA		Nasonia vitripennis		XP_001599942.1		

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Type	Sequence	EC Number	Organism	GenBank ID	RefSeq	UniProt	PDB
Eukaryota	elongation of very long chain fatty acids protein, putative		Pediculus humanus corporis USDA	EEB16888.1	XP_002429626.1		
Eukaryota	PREDICTED: similar to Elongation of very long chain fatty acids protein AAEL008004		Tribolium castaneum		XP_968706.1		
Eukaryota	Elongation of very long chain fatty acids protein AAEL008004		Lepeophtheirus salmonis (salmon louse).	ACO12890.1		C1BV37 [T]	
Eukaryota	Elongation of very long chain fatty acids protein AAEL008004		Caligus clemensi.	ACO14746.1		C1C0E3 [T]	
Eukaryota	Elongation of very long chain fatty acids protein AAEL008004		Caligus rogercresseyi.	ACO10630.1		C1BNM7 [T]	
Eukaryota	Similar to CG31523-PA		Papilio xuthus.	BAG30735.1		B2DBH6 [T]	
Eukaryota	GK13749		Drosophila willistoni (Fruit fly).	EDW83699.1	XP_002072713.1	B4NIB7	
Eukaryota	GF18505		Drosophila ananassae (Fruit fly).	EDV43467.1	XP_001954906.1	B3M2T7	
Eukaryota	GH18532		Drosophila grimshawi (Fruit fly) (Idiomyia grimshawi).	EDV92976.1	XP_001989914.1	B4JI95	
Eukaryota	GI22068		Drosophila mojavensis (Fruit fly).	EDW16724.1	XP_002001263.1	B4KA49	
Eukaryota	GJ24117		Drosophila virilis (Fruit fly).	EDW67386.1	XP_002053866.1	B4M0X5	
Eukaryota	GL22347		Drosophila persimilis (Fruit fly).	EDW34630.1	XP_002017530.1	B4GDW9	
Eukaryota	GA16298		Drosophila pseudoobscura pseudoobscura (Fruit fly).	EAL28742.1	XP_001359592.1	Q295H0	
Eukaryota	GE25346		Drosophila yakuba (Fruit fly).	EDW95669.1	XP_002095957.1	B4PTT6	

Eukaryota	GD19675		Drosophila simulans (Fruit fly).	EDX11613.1	XP_002102110.1	B4QVI8	
Eukaryota	GH09808p		Drosophila melanogaster (Fruit fly).	AAL25306.1, AAN13323.1, AAN13324.1, AAN13325.1, AAN13326.2	NP_649474.1, NP_730846.1, NP_730847.1, NP_730848.2	Q95T98 [P]	
Eukaryota	GG11532		Drosophila erecta (Fruit fly).	EDV47789.1	XP_001978831.1	B3P216	
Eukaryota	GM10700		Drosophila sechellia (Fruit fly).	EDW54839.1	XP_002038302.1	B4I3P6	
Eukaryota	PREDICTED: similar to CG31523 CG31523-PA		Acyrthosiphon pisum		XP_001952817.1		
Eukaryota	PREDICTED: similar to CG31523-PA, isoform A		Apis mellifera		XP_397228.2		
Eukaryota	PREDICTED: similar to elongase, putative		Nasonia vitripennis		XP_001600017.1		
Eukaryota	Putative uncharacterized protein		Tribolium castaneum (Red flour beetle).	EFA09796.1	XP_971544.1	D6X365	
Eukaryota	Putative uncharacterized protein		Tribolium castaneum (Red flour beetle).	EFA09795.1	XP_971599.1	D6X366	
Eukaryota	elongation of very long chain fatty acids protein, putative		Pediculus humanus corporis USDA	EEB19473.1	XP_002432211.1		
Eukaryota	PREDICTED: similar to CG31522-PA, isoform A, partial		Apis mellifera		XP_623221.1		
Eukaryota	PREDICTED: similar to Elongation of very long chain fatty acids protein AAEL008004		Acyrthosiphon pisum		XP_001943200.1		
Eukaryota	Putative uncharacterized protein		Tribolium castaneum (Red flour beetle).	EFA09483.1	XP_968784.1	D6X1G2	
Eukaryota	GH22993p		Drosophila melanogaster (Fruit fly).	AAN13319.2, AAN13320.2, AAO25056.1	NP_730841.2, NP_730842.2	Q8IPL8 [T]	

Eukaryota	GK13751		Drosophila willistoni (Fruit fly).	EDW83701.1	XP_002072715.1	B4NIB9	
Eukaryota	LD14383p		Drosophila melanogaster (Fruit fly).	AAF52122.3, AAX33543.1	NP_730843.2	Q9VN29 [T]	
Eukaryota	GE25348		Drosophila yakuba (Fruit fly).	EDW95666.1	XP_002095954.1	B4PTT3	
Eukaryota	GH18533		Drosophila grimshawi (Fruit fly) (Idiomyia grimshawi).	EDV92975.1	XP_001989913.1	B4JI94	
Eukaryota	GI22070		Drosophila mojavensis (Fruit fly).	EDW16723.1	XP_002001262.1	B4KA48	
Eukaryota	elongation of very long chain fatty acids protein, putative		Pediculus humanus corporis USDA	EEB19470.1	XP_002432208.1		
Eukaryota	PREDICTED: similar to CG31522-PB, isoform B		Apis mellifera		XP_393136.2		
Eukaryota	PREDICTED: similar to CG31522-PA		Nasonia vitripennis		XP_001599996.1		
Eukaryota	GH18531		Drosophila grimshawi (Fruit fly) (Idiomyia grimshawi).	EDV92977.1	XP_001989915.1	B4JI96	
Eukaryota	GI22067		Drosophila mojavensis (Fruit fly).	EDW16725.1	XP_002001264.1	B4KA50	
Eukaryota	GJ24115		Drosophila virilis (Fruit fly).	EDW67384.1	XP_002053864.1	B4M0X3	
Eukaryota	RH49985p		Drosophila melanogaster (Fruit fly).	AAM51033.1		Q8MS02 [T]	
Eukaryota	GE25754		Drosophila yakuba (Fruit fly).	EDW96310.1, EDX00181.1	XP_002086779.1, XP_002096598.1	B4IUW7	
Eukaryota	GD19443		Drosophila simulans (Fruit fly).	EDX12048.1	XP_002102545.1	B4R0C3	
Eukaryota	CG2781	2.4.1.34	Drosophila melanogaster (Fruit fly).	AAF54172.2	NP_649754.1	Q9VHX7 [T]	

Eukaryota	GG24795		Drosophila erecta (Fruit fly).	EDV48203.1	XP_001979245.1	B3NYU0	
Eukaryota	GM10441		Drosophila sechellia (Fruit fly).	EDW55290.1	XP_002038753.1	B4I4Z7	
Eukaryota	GK13951		Drosophila willistoni (Fruit fly).	EDW84092.1	XP_002073106.1	B4NKN1	
Eukaryota	GF16560		Drosophila ananassae (Fruit fly).	EDV43365.1	XP_001954804.1	B3M241	
Eukaryota	GL23546		Drosophila persimilis (Fruit fly).	EDW24136.1	XP_002013150.1	B4G2U1	
Eukaryota	GA15460		Drosophila pseudoobscura pseudoobscura (Fruit fly).	EAL28161.2	XP_001359018.2	Q297P4	

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Type	Sequence	EC Number	Organism	GenBank ID	RefSeq	UniProt	PDB
Eukaryota	PREDICTED: similar to elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4 (predicted)		Hydra magnipapillata		XP_002158269.1		
Eukaryota	PREDICTED: similar to elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4 (predicted)		Hydra magnipapillata		XP_002160705.1		
Eukaryota	GF10549		Drosophila ananassae (Fruit fly).	EDV40517.1	XP_001957711.1	B3M4U3	
Eukaryota	GA23552		Drosophila pseudoobscura pseudoobscura (Fruit fly).	EDY73516.1	XP_002134889.1	B5DPB4	
Eukaryota	GL24915		Drosophila persimilis (Fruit fly).	EDW40393.1	XP_002021237.1	B4GRK8	
Eukaryota	GK12306		Drosophila willistoni (Fruit fly).	EDW79983.1	XP_002068997.1	B4N6J4	
Eukaryota	GD12826		Drosophila simulans (Fruit fly).	EDX10036.1	XP_002084451.1	B4QPP5	
Eukaryota	GM24775		Drosophila sechellia (Fruit fly).	EDW41050.1	XP_002030064.1	B4HDW0	
Eukaryota	IP08602p		Drosophila melanogaster (Fruit fly).	AAN11899.2, AAY55350.1, AAY55470.1, CAI40769.1	NP_729666.2	Q5JZZ4 [T]	
Eukaryota	Elongase 68beta, isoform B		Drosophila melanogaster (Fruit fly).	ABW08521.1	NP_001097580.1	A8JNR0	
Eukaryota	GM24776		Drosophila sechellia (Fruit fly).	EDW41049.1	XP_002030063.1	B4HDV9	
Eukaryota	GD12827		Drosophila simulans (Fruit fly).	EDX10035.1	XP_002084450.1	B4QPP4	
Eukaryota	GE20239		Drosophila yakuba (Fruit fly).	EDW94080.1	XP_002094368.1	B4PEL4	
Eukaryota	GG13940		Drosophila erecta (Fruit fly).	EDV51369.1	XP_001972343.1	B3NCS2	

Eukaryota	PREDICTED: elongation of very long chain fatty acids-like 4-like, partial		Saccoglossus kowalevskii		XP_002733844.1		
Eukaryota	Elongase, putative		Aedes aegypti (Yellowfever mosquito) (Culex aegypti).	EAT44716.1	XP_001648136.1	Q17E22	
Eukaryota	Elongation of very long chain fatty acids protein 4		Culex quinquefasciatus (Southern house mosquito) (Culex pungens).	EDS35408.1	XP_001861291.1	B0WV69	
Eukaryota	elongation of very long chain fatty acids protein, putative		Pediculus humanus corporis USDA	EEB16673.1	XP_002429411.1		
Eukaryota	Putative uncharacterized protein		Tribolium castaneum (Red flour beetle).	EEZ97311.1	XP_966527.1	D6X467	
Eukaryota	PREDICTED: similar to ENSANGP00000016884		Nasonia vitripennis		XP_001600743.1		
Eukaryota	PREDICTED: similar to elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4		Apis mellifera		XP_395160.2		
Eukaryota	Putative uncharacterized protein		Branchiostoma floridae (Florida lancelet) (Amphioxus).	EEN64591.1	XP_002608581.1	C3Y558	
Eukaryota	Zgc:73341		Danio rerio (Zebrafish) (Brachydanio rerio).	AAH59658.1	NP_957090.1	Q6PBM2 [T]	
Eukaryota	PREDICTED: elongation of very long chain fatty acids-like 4-like		Danio rerio		XP_002664825.1		
Eukaryota	Very long-chain fatty acids elongase-like 4 protein		Rachycentron canadum (cobia).	ADG59898.1		D6QZA6 [T]	
Eukaryota	Chromosome 14 SCAF14660, whole genome shotgun sequence.		Tetraodon nigroviridis (Green puffer).	CAG01780.1		Q4SC52	
Eukaryota	Elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4		Danio rerio (Zebrafish) (Brachydanio rerio).	AAH60897.1	NP_956266.1	Q6P978 [T]	
Eukaryota	Elovl4 protein		Danio rerio (Zebrafish) (Brachydanio rerio).	AAI52204.1		A7MCJ3 [T]	
Eukaryota	elongation of very long chain fatty acids-like 4		Salmo salar	ADJ95235.1	NP_001182481.1		
Eukaryota	PREDICTED: elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4		Taeniopygia guttata		XP_002188735.1		

Eukaryota	PREDICTED: hypothetical protein		Gallus gallus		XP_419868.2		
Eukaryota	PREDICTED: similar to ELOVL4		Ornithorhynchus anatinus		XP_001512185.1		
Eukaryota	PREDICTED: hypothetical protein		Monodelphis domestica		XP_001366145.1		
Eukaryota	PREDICTED: similar to elongation of very long chain fatty acids-like 4		Equus caballus		XP_001503697.1		
Eukaryota	ELOVL4 protein		Bos taurus (Bovine).	AAI42460.1, DAA26375.1	NP_001092520.1	A5PKE6 [T]	
Eukaryota	PREDICTED: similar to elongation of very long chain fatty acids-like 4		Sus scrofa		XP_001925804.1		
Eukaryota	PREDICTED: elongation of very long chain fatty acids protein 4-like		Callithrix jacchus		XP_002746802.1		
Eukaryota	PREDICTED: similar to elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4		Canis familiaris		XP_539015.1		
Eukaryota	Putative uncharacterized protein		Ailuropoda melanoleuca (Giant panda).	EFB14596.1	XP_002916342.1	D2H3V6	
Eukaryota	Putative uncharacterized protein Elovl4		Rattus norvegicus (Rat).	EDL77659.1	NP_001178725.1, XP_001062735.1	D4ACH5	
Eukaryota	Putative uncharacterized protein		Mus musculus (Mouse).	AAG47667.1, AAH37030.1, BAC26274.1, CAD80158.4, EDL26470.1	NP_001139446.1, NP_683743.2	Q8JZV3 [T], Q9EQC4 [T], Q9EQC4.1	
Eukaryota	Elongation of very long chain fatty acids protein 4		Macaca mulatta (Rhesus macaque).	AAZ95094.1	NP_001035509.1	Q3S8M4	
Eukaryota	PREDICTED: elongation of very long chain fatty acids-like 4		Oryctolagus cuniculus		XP_002714591.1		
Eukaryota	PREDICTED: LOW QUALITY PROTEIN: elongation of very long chain fatty acids protein 4-like		Pongo abelii		XP_002817130.1		
Eukaryota	PREDICTED: elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4		Pan troglodytes		XP_518601.2		

Eukaryota	Elongation of very long chain fatty acids protein 4		Homo sapiens (Human).	AAG47668.1, AAG47669.1, AAH38506.1, AAK68639.1, BAB70895.1, BAG35412.1, CAI20320.1, CAI23374.1, EAW48701.1	NP_073563.1	Q9GZR5 [T], Q9GZR5.1	

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Type	Sequence	EC Number	Organism	GenBank ID	RefSeq	UniProt	PDB
Eukaryota	PREDICTED: similar to predicted protein		Hydra magnipapillata		XP_002155036.1		
Eukaryota	PREDICTED: similar to predicted protein, partial		Hydra magnipapillata		XP_002154976.1		
Eukaryota	PREDICTED: similar to CG31522 CG31522-PB, partial		Hydra magnipapillata		XP_002160924.1		
Eukaryota	Predicted protein		Nematostella vectensis (Starlet sea anemone).	EDO48664.1	XP_001640727.1	A7RI99	
Eukaryota	Putative uncharacterized protein		Branchiostoma floridae (Florida lancelet) (Amphioxus).	EEN41768.1	XP_002585757.1	C4A0A9	
Eukaryota	Polyunsaturated fatty acid elongase elvol5		Gadus morhua (Atlantic cod).	AAT81406.1, ADA70325.1		Q68YU1 [T]	
Eukaryota	Polyunsaturated fatty acid elongase		Danio rerio (Zebrafish) (Brachydanio rerio).	AAH55137.1, AAN77156.2, CAX14512.1	NP_956747.1	Q8AX86 [T]	
Eukaryota	Fatty acid elongase		Clarias gariepinus (Sharptooth catfish) (African catfish).	AAT81405.1		Q68YU2 [T]	
Eukaryota	Elongation of very long chain fatty acids protein 5		Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).	AAH87826.1	NP_001011248.1	Q5M8U1 [T], Q5M8U1.1	
Eukaryota	MGC114802 protein		Xenopus laevis (African clawed frog).	AAI00191.1	NP_001089650.1	Q498J8 [T]	
Eukaryota	Elongation of very long chain fatty acids protein 5		Xenopus laevis (African clawed frog).	AAI08604.1	NP_001089883.1	Q32NI8 [T], Q32NI8.1	
Eukaryota	PREDICTED: similar to elongation of very long chain fatty acids-like 2		Taeniopygia guttata		XP_002195568.1		
Eukaryota	Elongation of very long chain fatty acids-like 2 protein		Meleagris gallopavo (Common turkey).	ADD65339.1		D4N2R0	
Eukaryota	PREDICTED: similar to Elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2		Gallus gallus		XP_426204.2		
Eukaryota	PREDICTED: similar to Elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2		Ornithorhynchus anatinus		XP_001511544.1		

Eukaryota	PREDICTED: hypothetical protein		Monodelphis domestica		XP_001364339.1		
Eukaryota	PREDICTED: similar to fatty acid elongase 1		Equus caballus		XP_001499220.2		
Eukaryota	Fatty acid elongase 1		Rattus norvegicus (Rat).	BAB69887.1	NP_599209.1	Q920L7 [T], Q920L7.1	
Eukaryota	Elongation of very long chain fatty acids protein 5		Mus musculus (Mouse).	AAH22911.1, BAC26105.1, BAC32290.1, BAC34682.1, BAC39499.1, BAC39509.1, BAC40176.1, BAE36925.1, BAE40787.1, EDL26357.1	NP_599016.2	Q8BHI7 [P], Q8BHI7.1	
Eukaryota	PREDICTED: elongation of very long chain fatty acids protein 5-like isoform 2		Callithrix jacchus		XP_002746702.1		
Eukaryota	Elongation of very long chain fatty acids protein 5		Pongo abelii (Sumatran orangutan).	CAH89442.1	NP_001127147.1	Q5RFL5 [T], Q5RFL5.1	
Eukaryota	Elongation of very long chain fatty acids protein 5		Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).	BAE01809.1		Q4R516 [T], Q4R516.1	
Eukaryota	cDNA FLJ52813, highly similar to Homo sapiens ELOVL family member 5, elongation of long chain fatty acids, mRNA		Homo sapiens (Human).	BAG64104.1		B4DZJ2 [T]	
Eukaryota	Fatty acid elongase 1		Homo sapiens (Human).	AAF70631.1, AAH17270.2, AAH67123.2, AAM00193.1, BAC11178.1, BAC11270.1, BAD93035.1, CAB66873.1, CAI21530.1, EAX04416.1, EAX04418.1, EAX04421.1, EAX04422.1	NP_068586.1	Q9NYP7 [P], Q9NYP7.1	
Eukaryota	PREDICTED: homolog of yeast long chain polyunsaturated fatty acid elongation		Pan troglodytes		XP_527417.2		

Eukaryota	cDNA FLJ43108 fis, clone CTONG2021289, highly similar to Homo sapiens ELOVL family member 5, elongation of long chain fatty acids, mRNA		Homo sapiens (Human).	BAG54141.1		B3KWH9 [T]	
Eukaryota	PREDICTED: elongation of very long chain fatty acids-like 5		Oryctolagus cuniculus		XP_002714555.1		
Eukaryota	PREDICTED: similar to homolog of yeast long chain polyunsaturated fatty acid elongation		Canis familiaris		XP_852962.1		
Eukaryota	Elongase		Sus scrofa (Pig).	ACE80202.2		B3VHV3 [T]	
Eukaryota	Elongation of very long chain fatty acids protein 5		Bos taurus (Bovine).	AAI05392.1, DAA16564.1	NP_001040062.1	Q2KJD9 [T], Q2KJD9.1	
Eukaryota	ELOVL family member 5		Capra hircus (Goat).	BAF49682.1		A4PBF5 [T]	
Eukaryota	Fatty acid elongase		Anguilla japonica (Japanese eel).	ACI32414.1		D3TJK6 [T]	
Eukaryota	Fatty acid elongase		Siniperca chuatsi (Chinese perch).	ACH53603.1		D3TJH7 [T]	
Eukaryota	Putative polyunsaturated fatty acid elongase		Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).	AAO13174.2		Q8AWE8 [T]	
Eukaryota	Polyunsaturated fatty acid elongase elovl5b		Salmo salar (Atlantic salmon).	ACI62499.1	NP_001130024.1	B6V6V0 [T]	
Eukaryota	Polyunsaturated fatty acid elongase elvol5a		Salmo salar (Atlantic salmon).	AAO13175.2, ADA70324.1	NP_001117039.1	Q8AWE7 [T]	
Eukaryota	Putative polyunsaturated fatty acid elongase		Oncorhynchus masou (Cherry salmon) (Masu salmon).	AAY79352.1		Q4PLF1 [T]	
Eukaryota	Polyunsaturated fatty acid elongase		Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).	AAV67803.1	NP_001118108.1	Q5SE05 [T]	
Eukaryota	Fatty acid elongase		Epinephelus coioides (Orange-spotted grouper) (Epinephelus nebulosus).	ACJ26847.1		D3TJK3 [T]	
Eukaryota	Polyunsaturated fatty acid elongase		Psetta maxima (Turbot) (Pleuronectes maximus).	AAL69984.2		Q8UVB9 [T]	
Eukaryota	Fatty acid elongase		Sparus aurata (Gilthead sea bream).	AAT81404.1		Q68YU3 [T]	

Eukaryota	Polyunsaturated fatty acid elongase		Nibea mitsukurii (Nibe croaker).	ACR47973.1		C5ILA7 [T]	
Eukaryota	Fatty acyl elongase		Thunnus maccoyii (southern bluefin tuna).	ACZ55930.1		D2IFF5 [T]	
Eukaryota	Putative fatty acyl elongase		Thunnus maccoyii (southern bluefin tuna).	ACH86120.1		B5U1I5 [T]	
Eukaryota	Fatty acyl elovl5 elongase		Lates calcarifer (Barramundi).	ACS91459.1, ACY25090.1		D0U1T1 [T]	
Eukaryota	Polyunsaturated fatty acid elongase		Rachycentron canadum (cobia).	ACJ65150.1		B7U6V2 [T]	
Eukaryota	PREDICTED: similar to MGC84669 protein		Gallus gallus		XP_418947.2		
Eukaryota	Putative elongation of very long chain fatty acids-like 2 variant 1		Taeniopygia guttata (Zebra finch) (Poephila guttata).	ACH46005.1		B5G3Z4 [T]	
Eukaryota	Putative elongation of very long chain fatty acids-like 2 variant 1		Taeniopygia guttata (Zebra finch) (Poephila guttata).	ACH46004.1		B5G3Z3 [T]	
Eukaryota	PREDICTED: elongation of very long chain fatty acids-like 2		Taeniopygia guttata		XP_002186815.1		
Eukaryota	MGC84669 protein		Xenopus laevis (African clawed frog).	AAH80108.1	NP_001087564.1	Q68EU2 [T]	
Eukaryota	Elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2		Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).	AAI35163.1, CAJ83102.1	NP_001016159.1	Q28FK3 [T]	
Eukaryota	PREDICTED: similar to Elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2		Monodelphis domestica		XP_001377373.1		
Eukaryota	Elongation of very long chain fatty acids-like 2		Bos taurus	DAA16044.1			
Eukaryota	ELOVL2 protein		Bos taurus (Bovine).	AAI14787.1	NP_001076986.1	A4FUF2 [T]	
Eukaryota	PREDICTED: similar to elongation of very long chain fatty acids-like 2		Sus scrofa		XP_001924876.1		
Eukaryota	PREDICTED: similar to elongation of very long chain fatty acids-like 2		Sus scrofa		XP_001924743.1		

Eukaryota	Putative uncharacterized protein Elovl2		Rattus norvegicus (Rat).	EDL98219.1, EDL98220.1	NP_001102588.1	D4A612	
Eukaryota	Elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2, isoform CRA_a		Mus musculus mixed	EDL40970.1			
Eukaryota	Elongation of very long chain fatty acids protein 2		Mus musculus (Mouse).	AAF72373.1, AAH98215.1, BAB29559.1, BAC26646.1, BAC32079.1, BAC34236.1, EDL40971.1	NP_062296.1	Q543J1 [T], Q9JLJ4 [T], Q9JLJ4.1	
Eukaryota	PREDICTED: elongation of very long chain fatty acids-like 2		Oryctolagus cuniculus		XP_002714222.1		
Eukaryota	Elongation of very long chain fatty acids protein 2		Homo sapiens (Human).	AAH50278.2, AAH60809.1, BAA91096.1, CAI22076.1, EAW55291.1, EAW55292.1	NP_060240.3	Q9NXB9 [T], Q9NXB9.2	
Eukaryota	PREDICTED: elongation of very long chain fatty acids protein 2-like		Callithrix jacchus		XP_002746274.1		
Eukaryota	PREDICTED: elongation of very long chain fatty acids protein 2		Macaca mulatta		XP_001091337.1		
Eukaryota	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2, isoform CRA_a		Homo sapiens	EAW55290.1			
Eukaryota	PREDICTED: similar to elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2		Canis familiaris		XP_545341.2		
Eukaryota	Putative uncharacterized protein		Ailuropoda melanoleuca (Giant panda).	EFB16677.1		D2H2W1	
Eukaryota	Polyunsaturated fatty acid elongase elov12		Salmo salar (Atlantic salmon).	ACI62500.1	NP_001130025.1	B6V6V1 [T]	
Eukaryota	Elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2		Danio rerio (Zebrafish) (Brachydanio rerio).	AAI15093.1	NP_001035452.1	Q1RM84 [T]	
Eukaryota	Elovl2 protein		Danio rerio (Zebrafish) (Brachydanio rerio).	AAI34116.1		A3KP14 [T]	
Eukaryota	Elovl2 protein		Danio rerio (Zebrafish) (Brachydanio rerio).	AAH95785.1		Q502A7 [T]	

Eukaryota	Elovl2 protein		Danio rerio (Zebrafish) (Brachydanio rerio).	AAI29269.1		A1L1Y7 [T]	

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Type	Sequence	EC Number	Organism	GenBank ID	RefSeq	UniProt	PDB
Eukaryota	Polyunsaturated fatty acids delta-5-elongase		Thraustochytrium sp. FJN-10.	ABC18313.1		Q2PWB8 [T]	
Eukaryota	Delta-6 polyunsaturated fatty acid elongase		Parietochloris incisa.	ACK99719.1		B8YJJ0 [T]	
Eukaryota	Fatty acid elongase	2.3.1.119	Parietochloris incisa.	ACO71191.1		C1KKV1	
Eukaryota	Polyunsaturated fatty acids elongase		Parietochloris incisa.	ACF60496.1		B5AFK8 [T]	
Eukaryota	Delta-6 elongase		Pyramimonas cordata.	ACR53359.1		D7NLL0 [T]	
Eukaryota	Polyunsaturated fatty acid elongase 1 (ISS)		Ostreococcus tauri.	AAV67797.1, CAL52008.1		Q5SE78	
Eukaryota	Predicted protein		Micromonas pusilla CCMP1545.	EEH55768.1	XP_003059816.1	C1MVV4	
Eukaryota	Polyunsaturated fatty acid elongase		Marchantia polymorpha (Liverwort).	AAT85662.1		Q696V7	
Eukaryota	Polyunsaturated fatty acid specific elongation enzyme 1		Physcomitrella patens (Moss).	AAL84174.1, BAE71131.1, EDQ54842.1	XP_001780388.1	A9TP48, Q8S4Q5 [T]	
Eukaryota	Delta5-elongase		Marchantia polymorpha (Liverwort).	BAE71129.1, BAE71130.1		Q2PEN5 [T]	
Eukaryota	Predicted protein		Physcomitrella patens subsp. patens.	EDQ56051.1	XP_001779105.1	A9TKH5	
Eukaryota	Predicted protein		Physcomitrella patens subsp. patens.	EDQ58622.1	XP_001776634.1	A9TDC6	

Eukaryota	Long chain polyunsaturated fatty acid elongation enzyme-like protein		Leishmania braziliensis.	CAM42926.1	XP_001567488.1	A4HKA3	
Eukaryota	Long chain polyunsaturated fatty acid elongation enzyme-like protein		Leishmania infantum.	CAM70869.1	XP_001467802.1	A4I7T3	
Eukaryota	Long chain polyunsaturated fatty acid elongation enzyme-like protein		Leishmania major.	CAJ08636.1	XP_001685432.1	Q4Q5G6	
Eukaryota	Delta-6 elongase		Mortierella alpina (Mortierella renispora).	ADE06662.1		D5KSD4 [T]	
Eukaryota	Long chain polyunsaturated fatty acid elongation enzyme		Mortierella alpina (Mortierella renispora).	AAF70417.1		Q9P4D7 [T]	
Eukaryota	Polyunsaturated fatty acid elongation enzyme		Mortierella alpina (Mortierella renispora).	ACD31685.1, BAF97073.1		A9ZLZ4 [T]	
Eukaryota	Fatty acid elongase		Ectocarpus siliculosus (Brown alga).	CBJ26568.1		D7FYS6	
Eukaryota	Delta-6-elongase		Phaeodactylum tricornutum.	ABQ18315.1		A5HML5	
Eukaryota	Polyunsaturated fatty acid elongase 1		Thalassiosira pseudonana (Marine diatom).	AAV67799.1		Q5SE76	
Eukaryota	Probable microsomal very long chain fatty acid elongase		Thalassiosira pseudonana (Marine diatom).	EED93917.1	XP_002288481.1	B8BYM9	

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Type	Sequence	EC Number	Organism	GenBank ID	RefSeq	UniProt	PDB
Eukaryota	Putative uncharacterized protein		Aspergillus flavus (strain ATCC 200026 / FGSC A1120 / NRRL 3357 / JCM 12722 / SRRC 167).	EED52530.1	XP_002377694.1	B8NAK7	
Eukaryota	Fatty acid elongase		Mortierella alpina (Mortierella renispora).	BAI40363.1		C8KHM6	
Eukaryota	Putative uncharacterized protein		Candida tropicalis (strain ATCC MYA-3404 / T1) (Yeast).	EER33690.1	XP_002548211.1	C5M7Y6	
Eukaryota	Potential fatty acid elongase		Candida albicans (Yeast).	EAL04355.1, EAL04510.1	XP_723068.1, XP_723215.1	Q5AN96	
Eukaryota	Putative uncharacterized protein		Candida albicans (Yeast).	EEQ44568.1		C4YNQ9	
Eukaryota	Elongation of fatty acids protein, putative		Candida dubliniensis (strain CD36 / CBS 7987 / NCPF 3949 / NRRL Y-17841) (Yeast).	CAX43027.1	XP_002419433.1	B9WEB6	
Eukaryota	Whole genome shotgun sequence assembly, scaffold_50, strain Mel28		Tuber melanosporum (Perigord truffle).	CAZ84657.1	XP_002840466.1	D5GJG4	
Eukaryota	Predicted CDS Pa_7_6910		Podospora anserina.	CAP68722.1	XP_001908049.1	B2AWE8	
Eukaryota	Whole genome shotgun sequence assembly, scaffold_29		Sordaria macrospora.	CBI55186.1		D1ZG36	
Eukaryota	Putative uncharacterized protein		Neurospora crassa.	EAA29768.1	XP_959004.1	Q7S2Z3	

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Type	Sequence	EC Number	Organism	GenBank ID	RefSeq	UniProt	PDB
Eukaryota	unnamed protein product		Blastocystis hominis	CBK22771.2			
Eukaryota	Putative uncharacterized protein		Malassezia globosa (strain ATCC 96807 / CBS 7966) (Dandruff-associated fungus).	EDP42299.1	XP_001729513.1	A8Q9S0	
Eukaryota	Putative elongation of fatty acids protein 2		Schizosaccharomyces pombe (Fission yeast).	CAB55288.2	NP_592859.2	Q7LKX0, Q7LKX0.2	
Eukaryota	Elongation of fatty acids protein		Schizosaccharomyces japonicus (strain yFS275 / FY16936) (Fission yeast).	EEB07778.1	XP_002174071.1	B6K1F7	
Eukaryota	Putative uncharacterized protein		Ustilago maydis (Smut fungus).	EAK85103.1	XP_760105.1	Q4P7F5	
Eukaryota	Putative uncharacterized protein		Cryptococcus neoformans (Filobasidiella neoformans).	AAW42062.1, EAL21675.1	XP_569369.1, XP_776322.1	Q5KLB1	
Eukaryota	hypothetical protein		Schizophyllum commune H4-8	EFJ03723.1	XP_003038625.1		
Eukaryota	Fatty acid elongase		Coprinopsis cinerea (strain Okayama-7 / 130 / FGSC 9003) (Inky cap fungus) (Hormographiella aspergillata).	EAU93111.2	XP_001828716.2	A8N1G7	
Eukaryota	Elongase of fatty acids, ELO		Laccaria bicolor (strain S238N-H82) (Bicoloured deceiver) (Laccaria laccata var. bicolor).	EDR14987.1	XP_001873195.1	B0CPT7	
Eukaryota	Elongation of fatty acids protein		Schizosaccharomyces japonicus (strain yFS275 / FY16936) (Fission yeast).	EEB06313.1	XP_002172606.1	B6K0G3	
Eukaryota	Putative elongation of fatty acids protein 1		Schizosaccharomyces pombe (Fission yeast).	CAB61470.1	NP_593930.1	Q9UTF7 [P], Q9UTF7.1	
Eukaryota	Fatty acid elongase isoform II		Mucor rouxii.	ACJ23176.1		C6F130	
Eukaryota	Fatty acid elongase		Mortierella alpina (Mortierella renispora).	BAH02594.1		B6ZK38	
Eukaryota	Long chain fatty acid elongation enzyme		Mortierella alpina (Mortierella renispora).	AAF71789.1		Q9P8G1 [T]	

Eukaryota	Fatty acid elongase isoform I		Mucor rouxii.	ACJ23175.1		C6F129	
Eukaryota	YJL196Cp-like protein		Saccharomyces cerevisiae (strain AWRI1631) (Baker's yeast).	EDZ71398.1		B5VKZ6	
Eukaryota	Elongase		Saccharomyces cerevisiae (strain RM11-1a) (Baker's yeast).	EDN63193.1, EDV12585.1		A6ZQE1, B3LPT2	
Eukaryota	Elo1p		Saccharomyces cerevisiae (strain Lalvin EC1118 / Prise de mousse) Baker's yeast).	CAA54764.1, CAA89491.1, CAY80591.2	NP_012339.1	C8ZB25, P39540 [P], P39540.1	
Eukaryota	Elo1p		Saccharomyces cerevisiae (strain JAY291) (Baker's yeast).	EEU06413.1		C7GS17	
Eukaryota	Elongation of fatty acids protein, putative		Penicillium marneffei (strain ATCC 18224 / CBS 334.59 / QM 7333).	EEA26663.1	XP_002143178.1	B6Q7C1	
Eukaryota	Elongation of fatty acids protein, putative		Talaromyces stipitatus (strain ATCC 10500 / CBS 375.48 / QM 6759 / NRRL 1006) (Penicillium stipitatum).	EED19044.1, EED19045.1	XP_002479478.1, XP_002479479.1	B8M644	
Eukaryota	Putative fatty acid elongase protein		Aureobasidium pullulans.	ABL63519.2		A1ED48	
Eukaryota	YALI0B20196p		Yarrowia lipolytica (Candida lipolytica).	CAG83378.1	XP_501125.1	Q6CDY7	
Eukaryota	Putative uncharacterized protein		Sclerotinia sclerotiorum (strain ATCC 18683 / 1980 / Ss-1) (White mold) (Whetzelinia sclerotiorum).	EDN99048.1	XP_001585048.1	A7F8H7	
Eukaryota	Putative uncharacterized protein		Botryotinia fuckeliana (strain B05.10) (Noble rot fungus) (Botrytis cinerea).	EDN18918.1	XP_001548467.1	A6SJT3	
Eukaryota	Putative uncharacterized protein		Aspergillus nidulans FGSC A4.		XP_664039.1	C8V0F1	
Eukaryota	Elongation of fatty acids protein, putative		Talaromyces stipitatus (strain ATCC 10500 / CBS 375.48 / QM 6759 / NRRL 1006) (Penicillium stipitatum).	EED15705.1	XP_002485658.1	B8MJ43	
Eukaryota	Elongation of fatty acids protein 3		Pyrenophora tritici-repentis (strain Pt-1C-BFP) (Wheat tan spot fungus) (Drechslera tritici-repentis).	EDU43942.1	XP_001941223.1	B2WLN2	
Eukaryota	Whole genome shotgun sequence assembly, scaffold_1, strain Mel28		Tuber melanosporum (Perigord truffle).	CAZ79212.1	XP_002835091.1	D5G3W9	

Eukaryota	Putative fatty acid elongase A		Hortaea werneckii.	ACF19588.1		B3LEU1	
Eukaryota	Pc21g18830 protein		Penicillium chrysogenum (strain ATCC 28089 / DSM 1075 / Wisconsin 54-1255) (Penicillium notatum).	CAP96780.1	XP_002568874.1	B6HI82	
Eukaryota	Elongation of fatty acids protein, putative		Aspergillus flavus (strain ATCC 200026 / FGSC A1120 / NRRL 3357 / JCM 12722 / SRRC 167).	EED55977.1	XP_002374759.1	B8N1U5	
Eukaryota	Fatty acyl-CoA elongase/Polyunsaturated fatty acid specific elongation enzyme		Aspergillus oryzae.	BAE57737.1	XP_001819739.1	Q2UL28	
Eukaryota	hypothetical protein MGG_07280		Magnaporthe oryzae 70-15		XP_367355.1		
Eukaryota	hypothetical protein FG07347.1		Gibberella zeae PH-1		XP_387523.1		
Eukaryota	Predicted protein		Nectria haematococca (strain 77-13-4 / FGSC 9596 / MPVI) (Fusarium solani subsp. pisi).	EEU44339.1	XP_003050052.1	C7YU27	
Eukaryota	Predicted CDS Pa_2_11530		Podospora anserina.	CAP73794.1	XP_001911966.1	B2B7L6	
Eukaryota	Putative uncharacterized protein		Chaetomium globosum (Soil fungus).	EAQ86504.1	XP_001225413.1	Q2GW97	
Eukaryota	Whole genome shotgun sequence assembly, scaffold_64		Sordaria macrospora.	CBI57612.1		D1ZNH8	
Eukaryota	Probable fatty acid elongase (FEN1)		Neurospora crassa.	CAD70918.1, EAA31773.1	XP_961009.1	Q871S5	
Eukaryota	Putative uncharacterized protein		Sclerotinia sclerotiorum (strain ATCC 18683 / 1980 / Ss-1) (White mold) (Whetzelinia sclerotiorum).	EDN96471.1	XP_001597203.1	A7E7W9	
Eukaryota	Elongation of fatty acids protein 3		Nannizzia otae (strain CBS 113480) (Microsporum canis) (Arthroderma otae).	EEQ28868.1	XP_002848753.1	C5FHN8	
Eukaryota	Putative uncharacterized protein		Trichophyton verrucosum (strain HKI 0517).	EFE41259.1	XP_003021877.1	D4DAA8	
Eukaryota	Putative uncharacterized protein		Arthroderma benhamiae (strain CBS 112371) (Trichophyton mentagrophytes).	EFE34314.1	XP_003014954.1	D4ARH1	

Eukaryota	hypothetical protein CIMG_06474		Coccidioides immitis RS		XP_001242578.1		
Eukaryota	Elongation of fatty acids protein 2 , putative		Coccidioides posadasii (strain C735) (Valley fever fungus).	EER27629.1	XP_003069774.1	C5P4I9	
Eukaryota	Elongation of fatty acids protein 2		Uncinocarpus reesii (strain UAMH 1704).	EEP79098.1	XP_002544427.1	C4JM86	
Eukaryota	Elongation of fatty acids protein		Paracoccidioides brasiliensis (strain Pb03).	EEH23225.1		C0SCN1	
Eukaryota	Elongation of fatty acids protein		Paracoccidioides brasiliensis (strain Pb18).	EEH49672.1		C1GER5	
Eukaryota	Elongation of fatty acids protein		Paracoccidioides brasiliensis (strain ATCC MYA-826 / Pb01).	EEH36829.1	XP_002790710.1	C1H906	
Eukaryota	V-SNARE		Ajellomyces capsulata (strain ATCC 26029 / G186AR / H82 / RMSCC 2432) Darling's disease fungus) (Histoplasma capsulatum).	EEH05298.1		C0NTD7	
Eukaryota	Fatty acid elongase		Ajellomyces dermatitidis (strain ER-3) (Blastomyces dermatitidis).	EEQ89366.1		C5GIA9	
Eukaryota	Fatty acid elongase		Ajellomyces dermatitidis (strain SLH14081) (Blastomyces dermatitidis).	EEQ73235.1	XP_002628557.1	C5JFN4	
Eukaryota	Fatty acid elongase (Gns1), putative		Talaromyces stipitatus (strain ATCC 10500 / CBS 375.48 / QM 6759 / NRRL 1006) (Penicillium stipitatum).	EED17748.1	XP_002481740.1	B8MAQ8	
Eukaryota	Fatty acid elongase (Gns1), putative		Penicillium marneffei (strain ATCC 18224 / CBS 334.59 / QM 7333).	EEA24074.1	XP_002147585.1	B6QF39	
Eukaryota	Putative uncharacterized protein		Aspergillus nidulans FGSC A4.		XP_681386.1	C8V6M8	
Eukaryota	Putative uncharacterized protein		Aspergillus terreus (strain NIH 2624 / FGSC A1156).	EAU30381.1	XP_001217866.1	Q0CAP0	
Eukaryota	Fatty acyl-CoA elongase/Polyunsaturated fatty acid specific elongation enzyme		Aspergillus oryzae.	BAE61449.1	XP_001822582.1	Q2UAG6	
Eukaryota	Remark: FEN1 S. cerevisiae is involved in the synthesis of 1		Aspergillus niger (strain CBS 513.88 / FGSC A1513).	CAK37859.1	XP_001400119.1	A2QE98	

Eukaryota	Fatty acid elongase (Gns1), putative		Aspergillus clavatus.	EAW14829.1	XP_001276255.1	A1C561	
Eukaryota	Fatty acid elongase (Gns1), putative		Aspergillus fumigatus (Sartorya fumigata).	EAL86028.1, EDP51127.1	XP_748066.1	B0Y2F7, Q4WEE9	
Eukaryota	Fatty acid elongase (Gns1), putative		Neosartorya fischeri (strain ATCC 1020 / DSM 3700 / FGSC A1164 / NRRL 181) (Aspergillus fischerianus).	EAW24358.1	XP_001266255.1	A1D038	
Eukaryota	Putative uncharacterized protein		Vanderwaltozyma polyspora (strain ATCC 22028 / DSM 70294) Kluyveromyces polysporus).	EDO18980.1	XP_001646838.1	A7TFG6	
Eukaryota	Similar to uniprot|P25358 Saccharomyces cerevisiae YCR034w V-SNARE bypass mutant		Candida glabrata (Yeast) (Torulopsis glabrata).	CAG61210.1	XP_448249.1	Q6FNE5	
Eukaryota	Putative uncharacterized protein		Vanderwaltozyma polyspora (strain ATCC 22028 / DSM 70294) Kluyveromyces polysporus).	EDO18546.1	XP_001646404.1	A7TGT3	
Eukaryota	ZYRO0C17842p		Zygosaccharomyces rouxii (strain ATCC 2623 / CBS 732 / IFO 1130 / NBRC 1623 / NCYC 568) (Candida mogii).	CAQ43550.1, CAR27480.1	XP_002496413.1	B2G4P1, C5DUL9	
Eukaryota	KLTH0F03740p		Lachancea thermotolerans (strain CBS 6340) (Yeast) (Kluyveromyces thermotolerans).	CAR23935.1	XP_002554372.1	C5DKD4	
Eukaryota	AFR624Wp		Ashbya gossypii (Yeast) (Eremothecium gossypii).	AAS53995.1	NP_986171.1	Q752F2	
Eukaryota	KLLA0C03542p		Kluyveromyces lactis (Yeast) (Candida sphaerica).	CAH01205.1	XP_452354.1	Q6CUN5	
Eukaryota	Fen1p		Saccharomyces cerevisiae (strain JAY291) (Baker's yeast).	AAB21260.1, AAB87766.1, CAA40226.1, CAA42301.1, EDN62154.1, EDV09734.1, EDZ73515.1, EEU07101.1	NP_009963.1	A6ZTL5, B3LUA3, B5VEX8, C7GQ21, P25358 [P], P25358.1	
Eukaryota	Fen1p		Saccharomyces cerevisiae (strain Lalvin EC1118 / Prise de mousse) Baker's yeast).	CAY78240.1		C8Z4C4	
Eukaryota	Similar to uniprot|P25358 Saccharomyces cerevisiae YCR034w GNS1		Candida glabrata (Yeast) (Torulopsis glabrata).	CAG62102.1	XP_449132.1	Q6FKW2	
Eukaryota	FEN1		Kluyveromyces delphensis (Yeast).	AAO25600.1		Q874N5	

Eukaryota	Fatty acid elongase		Pichia angusta (Yeast) (Hansenula polymorpha).	BAF47261.1		A2V729	
Eukaryota	Fatty acid elongase		Pichia pastoris (strain GS115) (Yeast).	CAY70649.1	XP_002492828.1	C4R513	
Eukaryota	Elongation of fatty acids protein 2		Candida tropicalis (strain ATCC MYA-3404 / T1) (Yeast).	EER33138.1	XP_002549266.1	C5MBX1	
Eukaryota	Fatty acid elongase, putative		Candida dubliniensis (strain CD36 / CBS 7987 / NCPF 3949 / NRRL Y-17841) (Yeast).	CAX45552.1	XP_002417837.1	B9W9R7	
Eukaryota	Likely fatty acid elongase		Candida albicans (Yeast).	EAK92337.1, EAK92407.1, EEQ41969.1	XP_711561.1, XP_711629.1	Q59PF0	
Eukaryota	Fatty acyl-CoA elongase/Polyunsaturated fatty acid specific elongation enzyme		Pichia stipitis (Yeast).	EAZ62909.1	XP_001386932.1	A3GI09	
Eukaryota	Putative uncharacterized protein		Pichia guilliermondii (Yeast) (Candida guilliermondii).	EDK38670.1	XP_001485039.1	A5DHL7	
Eukaryota	Elongation of fatty acids protein 2		Lodderomyces elongisporus (Yeast) (Saccharomyces elongisporus).	EDK45395.1	XP_001525646.1	A5E1T7	
Eukaryota	DEHA2G10054p		Debaryomyces hansenii (Yeast) (Torulaspora hansenii).	CAG90454.1	XP_461984.1	Q6BII7	
Eukaryota	Putative uncharacterized protein		Clavispora lusitaniae (strain ATCC 42720) (Yeast) (Candida lusitaniae).	EEQ40576.1	XP_002615822.1	C4Y927	
Eukaryota	Elongation of fatty acids protein 2		Candida tropicalis (strain ATCC MYA-3404 / T1) (Yeast).	EER34319.1	XP_002546874.1	C5M5P9	
Eukaryota	Likely fatty acid elongase		Candida albicans (Yeast).	EAL02338.1, EEQ45755.1	XP_721147.1	Q5AHL5	
Eukaryota	Likely fatty acid elongase		Candida albicans (Yeast).	EAL02212.1	XP_721027.1	Q5AH88	
Eukaryota	Elongation of fatty acids protein 2, putative (Gns1 protein, putative) (V-snare bypass mutant gene 2 protein, putative)		Candida dubliniensis (strain CD36 / CBS 7987 / NCPF 3949 / NRRL Y-17841) (Yeast).	CAX43576.1	XP_002418276.1	B9WB06	
Eukaryota	Fatty acid elongase		Pichia angusta (Yeast) (Hansenula polymorpha).	BAD98251.1		Q50L63	

Eukaryota	ZYRO0B07458p		Zygosaccharomyces rouxii (strain ATCC 2623 / CBS 732 / IFO 1130 / NBRC 1623 / NCYC 568) (Candida mogii).	CAR26340.1	XP_002495273.1	C5DRC9	
Eukaryota	Elongase		Pichia pastoris (strain GS115) (Yeast).	CAY70261.1	XP_002492452.1	C4R3Y7	
Eukaryota	Putative uncharacterized protein		Clavispora lusitaniae (strain ATCC 42720) (Yeast) (Candida lusitaniae).	EEQ37452.1	XP_002618116.1	C4Y043	
Eukaryota	Elongation of fatty acids protein 3		Lodderomyces elongisporus (Yeast) (Saccharomyces elongisporus).	EDK43130.1	XP_001528788.1	A5DVC2	
Eukaryota	Predicted protein		Pichia stipitis (Yeast).	ABN64295.2	XP_001382324.2	A3LNA0	
Eukaryota	hypothetical protein PGUG_02923		Meyerozyma guilliermondii ATCC 6260		XP_001485194.1		
Eukaryota	Putative uncharacterized protein		Pichia guilliermondii (Yeast) (Candida guilliermondii).	EDK38825.2		A5DI22	
Eukaryota	DEHA2G05478p		Debaryomyces hansenii (Yeast) (Torulaspora hansenii).	CAG90243.2	XP_461784.2	Q6BJ37	
Eukaryota	AFR586Wp		Ashbya gossypii (Yeast) (Eremothecium gossypii).	AAS53957.1	NP_986133.1	Q752I9	
Eukaryota	Putative uncharacterized protein		Vanderwaltozyma polyspora (strain ATCC 22028 / DSM 70294) Kluyveromyces polysporus).	EDO15473.1	XP_001643331.1	A7TQH2	
Eukaryota	Strain CBS138 chromosome G complete sequence		Candida glabrata (Yeast) (Torulopsis glabrata).	CAG59498.1	XP_446571.1	Q6FT73	
Eukaryota	Sur4p		Saccharomyces cerevisiae (strain JAY291) (Baker's yeast).	EEU06458.1		C7GRW5	
Eukaryota	v-SNARE bypass mutant gene 1 protein		Saccharomyces cerevisiae (Baker's yeast).	AAA35134.1, AAB67563.1, AAC28398.1, CAA55129.1, CAA57553.1, EDZ70433.1	NP_013476.1	B5VNR0, P40319 [P], P40319.1	
Eukaryota	Elongase		Saccharomyces cerevisiae (strain YJM789) (Baker's yeast).	EDN59277.1		A7A1P9	

Eukaryota	Sur4p		Saccharomyces cerevisiae (strain Lalvin EC1118 / Prise de mousse) Baker's yeast).	CAY81598.1		C8ZDY2	
Eukaryota	Elongation of fatty acids protein 3		Saccharomyces cerevisiae (strain RM11-1a) (Baker's yeast).	EDV08683.1		B3RHN9	
Eukaryota	KLLA0B07777p		Kluyveromyces lactis (Yeast) (Candida sphaerica).	CAH02269.1	XP_451876.1	Q6CW13	
Eukaryota	KLTH0D13596p		Lachancea thermotolerans (strain CBS 6340) (Yeast) (Kluyveromyces thermotolerans).	CAR22863.1	XP_002553301.1	C5DFA8	

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Type	Sequence	EC Number	Organism	GenBank ID	RefSeq	UniProt	PDB
Eukaryota	Putative uncharacterized protein		Toxoplasma gondii VEG.	EEE29738.1		B9QJ09	
Eukaryota	Putative uncharacterized protein		Toxoplasma gondii.	EEE21454.1		B9PWS5	
Eukaryota	GNS1/SUR4 family domain-containing protein		Toxoplasma gondii ME49.	EEB02303.1	XP_002369443.1	B6KNM0	
Eukaryota	GNS1/SUR4 domain containing protein		Plasmodium vivax.	EDL45005.1	XP_001614732.1	A5K6R4	
Eukaryota	Fatty acid elongase, putative		Plasmodium knowlesi (strain H).	CAQ39243.1	XP_002258471.1	B3L2L7	
Eukaryota	Long chain fatty acid elongation enzyme, putative		Plasmodium falciparum (isolate 3D7).	CAX64222.1	XP_002808941.1	C0H545	
Eukaryota	30 kDa glycoprotein		Plasmodium yoelii yoelii.	EAA17248.1	XP_725683.1	Q7RE21	
Eukaryota	Putative uncharacterized protein		Branchiostoma floridae (Florida lancelet) (Amphioxus).	EEN44779.1	XP_002588768.1	C3ZRH9	
Eukaryota	PREDICTED: similar to elongase, putative		Strongylocentrotus purpuratus		XP_001202838.1, XP_794194.2		
Eukaryota	Protein F56H11.3a, partially confirmed by transcript evidence		Caenorhabditis elegans.	CAA92960.2	NP_501691.2	Q20904 [T]	
Eukaryota	C. briggsae CBR-ELO-7 protein		Caenorhabditis briggsae.	CAP37155.1	XP_002633947.1	A8XWY6	
Eukaryota	C. briggsae CBR-ELO-5 protein		Caenorhabditis briggsae.	CAP37101.1	XP_002633893.1	A8XWT2	

Eukaryota	Fatty acid elongation protein 5		Caenorhabditis elegans.	AAK29808.1	NP_500793.1	Q20300 [P]	
Eukaryota	C. briggsae CBR-ELO-2 protein		Caenorhabditis briggsae.	CAP21889.1	XP_002632413.1	A8WN34	
Eukaryota	Protein F11E6.5, confirmed by transcript evidence		Caenorhabditis elegans.	CAB02921.1	NP_503114.1	Q9XVQ9 [T]	
Eukaryota	Predicted protein		Monosiga brevicollis (Choanoflagellate).	EDQ92757.1	XP_001742519.1	A9UNT8	
Eukaryota	Fatty acid elongase, putative		Leishmania braziliensis.	CAM37538.1	XP_001563360.1	A4H7M7	
Eukaryota	Fatty acid elongase, putative		Leishmania braziliensis.	CAM37536.1	XP_001563359.1	A4H7M6	
Eukaryota	Fatty acid elongase, putative		Leishmania infantum.	CAM66720.1	XP_001464338.1	A4HW97	
Eukaryota	Fatty acid elongase, putative		Leishmania major.	CAJ02986.1	XP_001687668.1	Q4QFR6	
Eukaryota	Fatty acid elongase, putative		Leishmania infantum.	CAM66631.1	XP_001464252.1	A4HW11	
Eukaryota	Fatty acid elongase, putative		Trypanosoma cruzi.	EAN96213.1	XP_818064.1	Q4DUK4	
Eukaryota	Fatty acid elongase, putative		Trypanosoma cruzi.	EAN87793.1	XP_809644.1	Q4D5J7	
Eukaryota	Fatty acid elongase, putative		Leishmania braziliensis.	CAM37541.1	XP_001563363.1	A4H7N0	
Eukaryota	Fatty acid elongase, putative		Leishmania infantum.	CAM66638.1	XP_001464259.1	A4HW18	

Eukaryota	Fatty acid elongase, putative		Leishmania major.	CAJ03035.1	XP_001687675.1	Q4QFQ9	
Eukaryota	Fatty acid elongase, putative		Trypanosoma brucei.	AAX70673.1, AAZ12480.1	XP_846039.1	Q57UP6	
Eukaryota	Fatty acid elongase, putative		Trypanosoma brucei gambiense DAL972.	CBH12548.1		C9ZT13	
Eukaryota	Fatty acid elongase, putative		Trypanosoma cruzi.	EAN96212.1	XP_818063.1	Q4DUK5	
Eukaryota	Fatty acid elongase, putative		Trypanosoma cruzi.	EAN92119.1	XP_813970.1	Q4DHY3	
Eukaryota	Fatty acid elongase, putative		Leishmania braziliensis.	CAM37533.1	XP_001563356.1	A4H7M3	
Eukaryota	Fatty acid elongase, putative		Leishmania major.	CAJ02967.1	XP_001687665.1	Q4QFR9	
Eukaryota	Fatty acid elongase, putative		Leishmania infantum.	CAM66627.1	XP_001464249.1	A4HW08	
Eukaryota	Fatty acid elongase, putative		Leishmania braziliensis.	CAM37532.1	XP_001563355.1	A4H7M2	
Eukaryota	Fatty acid elongase, putative		Leishmania major.	CAJ02963.1	XP_001687664.1	Q4QFS0	
Eukaryota	Fatty acid elongase, putative		Leishmania infantum.	CAM66626.1	XP_001464248.1	A4HW07	
Eukaryota	Fatty acid elongase, putative		Leishmania braziliensis.	CAM37535.1	XP_001563358.1	A4H7M5	
Eukaryota	Fatty acid elongase, putative		Leishmania major.	CAJ02982.1	XP_001687667.1	Q4QFR7	

Eukaryota	Fatty acid elongase, putative		Leishmania infantum.	CAM66630.1	XP_001464251.1	A4HW10	
Eukaryota	Fatty acid elongase, putative		Trypanosoma brucei gambiense DAL972.	CBH12551.1		C9ZT16	
Eukaryota	Fatty acid elongase, putative		Trypanosoma brucei.	AAX70671.1, AAZ12482.1	XP_846041.1	Q57UP8	
Eukaryota	Fatty acid elongase, putative		Trypanosoma cruzi.	EAN96210.1	XP_818061.1	Q4DUK7	
Eukaryota	Fatty acid elongase, putative		Trypanosoma cruzi.	EAN92121.1	XP_813972.1	Q4DHY1	
Eukaryota	Fatty acid elongase, putative		Trypanosoma brucei gambiense DAL972.	CBH12550.1		C9ZT15	
Eukaryota	Fatty acid elongase, putative		Trypanosoma brucei.	AAX70672.1, AAZ12481.1	XP_846040.1	Q57UP7	
Eukaryota	Fatty acid elongase, putative		Trypanosoma cruzi.	EAN92120.1	XP_813971.1	Q4DHY2	
Eukaryota	Fatty acid elongase, putative		Trypanosoma cruzi.	EAN96211.1	XP_818062.1	Q4DUK6	
Eukaryota	Fatty acid elongation protein, GNS1/SUR4 family, putative		Plasmodium falciparum (isolate 3D7).	CAD49051.1	XP_001351023.1	Q8I251	
Eukaryota	Elongation of very long chain fatty acids protein 3, putative		Plasmodium vivax.	EDL43812.1	XP_001613539.1	A5K9S4	
Eukaryota	Integral membrane protein, gns1/sur4 family,putative		Plasmodium knowlesi (strain H).	CAQ38052.1	XP_002257716.1	B3KZI4	
Eukaryota	Fatty acid elongase		Labyrinthula sp. ND50.	ACM17823.1		B9VJL2 [T]	

Eukaryota	Fatty-acyl elongase		Cryptosporidium hominis.	EAL36110.1	XP_666343.1	Q5CHM8	
Eukaryota	7 pass integral membrane proteinwith FLHWFHH motif shared with fatty-acyl elongase		Cryptosporidium parvum Iowa II.	EAK89598.1	XP_627348.1	Q5CVC1	
Eukaryota	Putative fatty-acyl elongase		Cryptosporidium parvum.	AAO34582.1		Q86LT1	
Eukaryota	Beta-ketoacyl-CoA synthase, putative		Cryptosporidium muris (strain RN66).	EEA05127.1	XP_002139476.1	B6AA86	
Eukaryota	Fatty acid elongase	2.3.1.-	Ectocarpus siliculosus Ec 32	CBN78890.1			
Eukaryota	Putative uncharacterized protein		Toxoplasma gondii VEG.	EEB00626.1, EEE20374.1, EEE30738.1	XP_002367766.1	B6KIC1, B9Q055, B9QF85	
Eukaryota	Fatty-acyl elongase, putative		Perkinsus marinus ATCC 50983.	EER07285.1	XP_002775469.1	C5L723	
Eukaryota	Fatty-acyl elongase, putative		Perkinsus marinus ATCC 50983.	EER03348.1	XP_002771532.1	C5LIE5	
Eukaryota	Fatty-acyl elongase, putative		Perkinsus marinus ATCC 50983.	EER03347.1	XP_002771531.1	C5LIE4	
Eukaryota	Fatty-acyl elongase, putative		Perkinsus marinus ATCC 50983.	EER07286.1	XP_002775470.1	C5L724	
Eukaryota	Fatty-acyl elongase, putative		Perkinsus marinus ATCC 50983.	EER19589.1	XP_002787793.1	C5K7Q4	
Eukaryota	Fatty-acyl elongase, putative		Perkinsus marinus ATCC 50983.	EER13032.1	XP_002781237.1	C5KR61	
Eukaryota	Elongation of very long chain fatty acids protein, putative		Phytophthora infestans T30-4.	EEY61162.1	XP_002908079.1	D0MT65	

Eukaryota	Fatty acid elongase		Nannochloropsis oculata.	ACV21066.1		D2DPY9 [T]	
Eukaryota	Predicted protein		Phaeodactylum tricornutum CCAP 1055/1.	EEC43716.1	XP_002184657.1	B7GC51	
Eukaryota	Predicted protein		Phaeodactylum tricornutum CCAP 1055/1.	EEC43799.1	XP_002184740.1	B7GC46	
Eukaryota	Long chain fatty acid elongase		Thalassiosira pseudonana (Marine diatom).	EED89131.1	XP_002293395.1	B8CBI0	
Eukaryota	Putative uncharacterized protein		Branchiostoma floridae (Florida lancelet) (Amphioxus).	EEN63427.1	XP_002607417.1	C3Y8J0	
Eukaryota	GNS1/SUR4 family protein		Brugia malayi (Filarial nematode worm).	EDP31843.1	XP_001899035.1	A8PY71	
Eukaryota	Protein F56H11.3b, confirmed by transcript evidence		Caenorhabditis elegans.	AAF70462.1, CAA92958.1, CBJ25081.1	NP_501689.1	D3KFU0, Q20901 [T]	
Eukaryota	C. briggsae CBR-ELO-1 protein		Caenorhabditis briggsae.	CAP37153.1	XP_002633945.1	A8XWY4	
Eukaryota	Fatty acid elongation protein 3, putative		Brugia malayi (Filarial nematode worm).	EDP39371.1	XP_001891832.1	A8NFQ6	
Eukaryota	C. briggsae CBR-ELO-6 protein		Caenorhabditis briggsae.	CAP37099.1	XP_002633891.1	A8XWT0	
Eukaryota	Fatty acid elongation protein 6		Caenorhabditis elegans.	AAK29807.1	NP_500797.1	Q20303 [T]	
Eukaryota	Putative uncharacterized protein		Trichoplax adhaerens.	EDV26039.1	XP_002112072.1	B3RVR2	
Eukaryota	PREDICTED: baldspot-like		Saccoglossus kowalevskii		XP_002730580.1		

Eukaryota	PREDICTED: elongation of very long chain fatty acids-like 6-like		Saccoglossus kowalevskii		XP_002730581.1		
Eukaryota	Putative uncharacterized protein		Branchiostoma floridae (Florida lancelet) (Amphioxus).	EEN48619.1	XP_002592608.1	C3ZFL1	
Eukaryota	Putative uncharacterized protein		Trichoplax adhaerens.	EDV25299.1	XP_002111332.1	B3RUA6	
Eukaryota	PREDICTED: baldspot-like		Saccoglossus kowalevskii		XP_002740723.1		
Eukaryota	Hypothetical 34.1 kDa protein C40H1.4 in chromosome III, putative		Brugia malayi (Filarial nematode worm).	EDP34257.1	XP_001896896.1	A8PJ45	
Eukaryota	Protein Y53F4B.2, confirmed by transcript evidence		Caenorhabditis elegans.	CAB61069.1	NP_497086.1	Q9NAC6	
Eukaryota	C. briggsae CBR-ELO-9 protein		Caenorhabditis briggsae.	CAP37831.1	XP_002631698.1	A8XYW4	
Eukaryota	GNS1/SUR4 family protein		Brugia malayi (Filarial nematode worm).	EDP30657.1	XP_001900443.1	A8Q745	
Eukaryota	C. briggsae CBR-ELO-4 protein		Caenorhabditis briggsae.	CAP29621.1	XP_002641772.1	A8XAF3	
Eukaryota	Putative fatty acid elongation protein 4		Caenorhabditis elegans.	CAA79555.1	NP_499056.1	Q03574 [T], Q03574.1	
Eukaryota	PREDICTED: elongation of very long chain fatty acids-like 6-like		Saccoglossus kowalevskii		XP_002734639.1		
Eukaryota	PREDICTED: hypothetical protein		Strongylocentrotus purpuratus		XP_001187222.1, XP_781194.1		
Eukaryota	PREDICTED: similar to ELOVL family member 6, elongation of long chain fatty acids (yeast)		Strongylocentrotus purpuratus		XP_001202419.1, XP_790118.1		

Eukaryota	C. briggsae CBR-ELO-3 protein		Caenorhabditis briggsae.	CAP26513.1	XP_002633120.1	A8X1K3	
Eukaryota	Putative fatty acid elongation protein 3		Caenorhabditis elegans.	AAA82288.2	NP_501147.2	P49191 [P], P49191.2	
Eukaryota	PREDICTED: baldspot-like		Saccoglossus kowalevskii		XP_002740724.1		
Eukaryota	PREDICTED: elongation of very long chain fatty acids-like 6-like		Saccoglossus kowalevskii		XP_002739878.1		
Eukaryota	PREDICTED: elongation of very long chain fatty acids-like 6-like		Saccoglossus kowalevskii		XP_002739877.1		
Eukaryota	Putative uncharacterized protein		Branchiostoma floridae (Florida lancelet) (Amphioxus).	EEN61466.1	XP_002605456.1	C3YEF8	
Eukaryota	PREDICTED: similar to elongase, putative		Strongylocentrotus purpuratus		XP_001180089.1, XP_789064.1		
Eukaryota	PREDICTED: elongation of very long chain fatty acids-like 6-like		Saccoglossus kowalevskii		XP_002736035.1		
Eukaryota	PREDICTED: similar to elongase, putative		Strongylocentrotus purpuratus		XP_001186899.1, XP_001186991.1, XP_001198074.1, XP_795994.1		
Eukaryota	ELOVL family member 6, elongation of long chain fatty acids		Acyrthosiphon pisum		NP_001156725.1		
Eukaryota	Elongase, putative		Aedes aegypti (Yellowfever mosquito) (Culex aegypti).	EAT34657.1	XP_001656366.1	Q16K45	
Eukaryota	AGAP006520-PA		Anopheles gambiae (African malaria mosquito).	EAU76616.2	XP_001237830.2	A0NEU5	
Eukaryota	Long chain fatty acid elongase		Glossina morsitans morsitans (Savannah tsetse fly).	ADD19917.1		D3TQD9 [T]	

Eukaryota	GM24378		Drosophila sechellia (Fruit fly).	EDW41789.1	XP_002030803.1	B4HJR2	
Eukaryota	GD12451		Drosophila simulans (Fruit fly).	EDX10758.1	XP_002085173.1	B4QMW6	
Eukaryota	Transmembrane protein Noa		Drosophila melanogaster (Fruit fly).	AAF49430.2, AAF75771.1, AAG02080.1, AAL28669.1, AAN11736.2	NP_648909.1, NP_730187.2	Q9VV87 [T]	
Eukaryota	GG15860		Drosophila erecta (Fruit fly).	EDV52055.1	XP_001973029.1	B3NDJ3	
Eukaryota	GK25673		Drosophila willistoni (Fruit fly).	EDW79237.1	XP_002068251.1	B4N3N2	
Eukaryota	GH16451		Drosophila grimshawi (Fruit fly) (Idiomyia grimshawi).	EDV96780.1	XP_001984432.1	B4J008	
Eukaryota	GF10511		Drosophila ananassae (Fruit fly).	EDV40449.1	XP_001957643.1	B3M4F5	
Eukaryota	GL12717		Drosophila persimilis (Fruit fly).	EDW34783.1	XP_002026972.1	B4H7Z3	
Eukaryota	GA17812		Drosophila pseudoobscura pseudoobscura (Fruit fly).	EAL30565.1	XP_001353064.1	Q29D49	
Eukaryota	GJ12451		Drosophila virilis (Fruit fly).	EDW68851.1	XP_002046509.1	B4LCZ0	
Eukaryota	GI16709		Drosophila mojavensis (Fruit fly).	EDW17115.1	XP_002011984.1	B4L9R7	
Eukaryota	PREDICTED: similar to elongation of very long chain fatty acids-like 6		Ciona intestinalis		XP_002123698.1		
Eukaryota	PREDICTED: hypothetical protein		Gallus gallus		XP_001234271.1		

Eukaryota	PREDICTED: similar to elongation of very long chain fatty acids-like 6-like		Ciona intestinalis		XP_002127892.1		
Eukaryota	Elongation of very long chain fatty acids protein 6		Danio rerio (Zebrafish) (Brachydanio rerio).	AAH59459.1	NP_955826.1	Q6PC64 [T], Q6PC64.1	
Eukaryota	Chromosome 20 SCAF14744, whole genome shotgun sequence.		Tetraodon nigroviridis (Green puffer).	CAG04622.1		Q4S410	
Eukaryota	elongation of very long chain fatty acids-like 6		Xenopus (Silurana) tropicalis		NP_001017257.2		
Eukaryota	MGC139109 protein		Bos taurus (Bovine).	AAI48955.1, DAA28878.1	NP_001095625.1	A6QNQ7 [T]	
Eukaryota	Elongation of long chain fatty acids		Sus scrofa (Pig).	BAI47786.1		D0G6S8 [T]	
Eukaryota	PREDICTED: similar to elongation of very long chain fatty acids-like 6		Equus caballus		XP_001502932.1		
Eukaryota	PREDICTED: hypothetical protein		Monodelphis domestica		XP_001367859.1		
Eukaryota	Elongation of very long chain fatty acids protein 6		Gallus gallus (Chicken).	CAG32025.1	NP_001026710.1	Q5ZJR8 [T], Q5ZJR8.1	
Eukaryota	PREDICTED: elongation of very long chain fatty acids-like 6		Taeniopygia guttata		XP_002195282.1		
Eukaryota	PREDICTED: elongation of very long chain fatty acids protein 6 isoform 5		Macaca mulatta		XP_001089527.1, XP_001089649.1, XP_001089764.1		
Eukaryota	Long-chain fatty-acyl elongase		Homo sapiens (Human).	AAH01305.1, AAY40928.1, BAB15632.1, BAC11225.1, EAX06259.1, EAX06260.1	NP_001124193.1, NP_076995.1	Q9H5J4 [T], Q9H5J4.1	

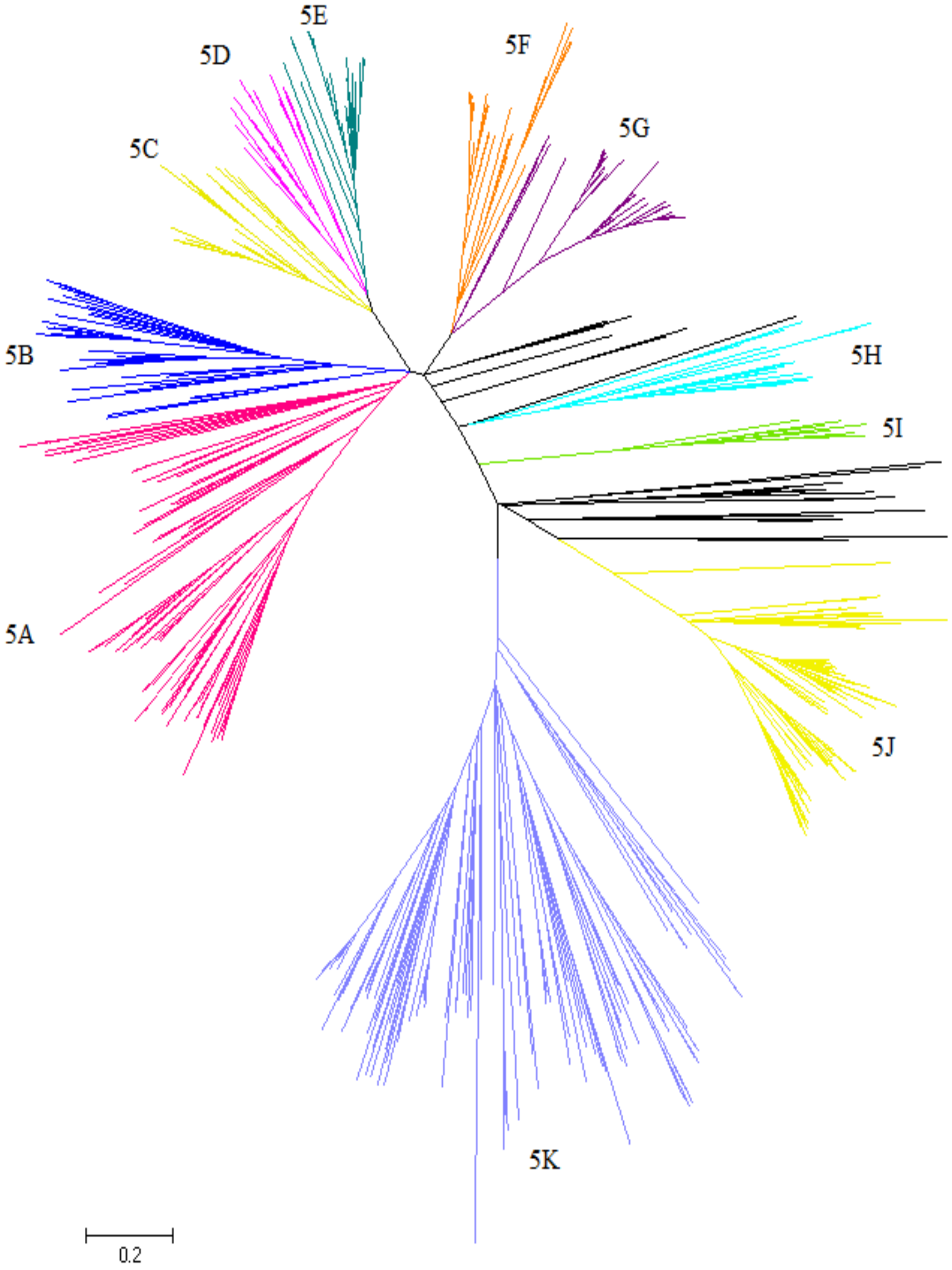
Eukaryota	PREDICTED: elongation of very long chain fatty acids protein 6-like isoform 4		Callithrix jacchus		XP_002745528.1, XP_002745529.1, XP_002745530.1, XP_002745531.1		
Eukaryota	Myelin-associated SUR4 protein		Mus musculus (Mouse).	AAH51041.1, AAH98492.1, AAI00577.1, AAL14239.1, AAM13450.1, BAB68544.1, BAC26252.1, BAE39469.1, EDL12240.1, EDL12241.1	NP_569717.1	Q920L5 [T], Q920L5.1	
Eukaryota	Long-chain fatty-acyl elongase		Rattus norvegicus (Rat).	BAB69888.1, EDL82174.1, EDL82176.1	NP_599210.1	Q920L6 [T], Q920L6.1	
Eukaryota	Putative uncharacterized protein		Ailuropoda melanoleuca (Giant panda).	EFB22375.1	XP_002917561.1	D2H706	
Eukaryota	PREDICTED: elongation of very long chain fatty acids-like 6		Oryctolagus cuniculus		XP_002717168.1		
Eukaryota	PREDICTED: similar to ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)		Canis familiaris		XP_545023.2		
Eukaryota	Chromosome 17 SCAF14760, whole genome shotgun sequence		Tetraodon nigroviridis (Green puffer).	CAG05092.1		Q4S2P0	
Eukaryota	ELOVL family member 6, elongation of long chain fatty acids like		Danio rerio (Zebrafish) (Brachydanio rerio).	AAH46901.1, AAI64614.1	NP_958908.1	Q802X6 [T]	
Eukaryota	ELOVL family member 6, elongation of long chain fatty acids like		Danio rerio (Zebrafish) (Brachydanio rerio).	CAX14332.1		B8JK95	
Eukaryota	Zgc:92749		Danio rerio (Zebrafish) (Brachydanio rerio).	AAH76227.1	NP_001002570.1	Q6DGW0 [T]	

Eukaryota	Zgc:92749		Danio rerio (Zebrafish) (Brachydanio rerio).	AAH95172.1, AAI64609.1		Q503U9 [T]	
Eukaryota	Chromosome 2 SCAF14705, whole genome shotgun sequence.		Tetraodon nigroviridis (Green puffer).	CAG03017.1		Q4S8L5	
Eukaryota	PREDICTED: elongation of very long chain fatty acids like 3		Oryctolagus cuniculus		XP_002718621.1		
Eukaryota	Putative uncharacterized protein		Ailuropoda melanoleuca (Giant panda).	EFB27646.1	XP_002913927.1	D2GXV8	
Eukaryota	PREDICTED: elongation of very long chain fatty acids like 3		Pan troglodytes		XP_001171055.1		
Eukaryota	Cold-inducible glycoprotein of 30 kDa		Homo sapiens (Human).	AAG17875.1, AAH34344.1, CAH71623.1, EAW49711.1	NP_689523.1	Q9HB03 [T], Q9HB03.2	
Eukaryota	PREDICTED: elongation of very long chain fatty acids protein 3-like		Pongo abelii		XP_002821134.1		
Eukaryota	PREDICTED: similar to Elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 3		Monodelphis domestica		XP_001379069.1		
Eukaryota	PREDICTED: similar to olfactory receptor MOR103-7		Ornithorhynchus anatinus		XP_001511055.1		

OUTLIERS

Type	Sequence	EC Number	Organism	GenBank ID	RefSeq	UniProt	PDB	
Eukaryota	Putative uncharacterized protein		Branchiostoma floridae (Florida lancelet) (Amphioxus).	EEN64590.1	XP_002608580.1	C3Y557		Between Subfamilies 5G and 5H
Eukaryota	PREDICTED: elongation of very long chain fatty acids-like 4-like		Saccoglossus kowalevskii		XP_002733299.1			
Eukaryota	PREDICTED: elongation of very long chain fatty acids-like 4-like		Saccoglossus kowalevskii		XP_002732296.1			
Eukaryota	Predicted protein		Monosiga brevicollis (Choanoflagellate).	EDQ85417.1	XP_001749828.1	A9VAQ9		
Eukaryota	GNS1/SUR4 family protein		Dictyostelium discoideum (Slime mold).	EEU04154.1	XP_002649204.1	C7FZW5		
Eukaryota	GNS1/SUR4 family protein		Polysphondylium pallidum PN500.	EFA83001.1		D3B6N1		
Eukaryota	Predicted protein		Monosiga brevicollis (Choanoflagellate).	EDQ87885.1	XP_001747418.1	A9V3Y1		
Eukaryota	Polyunsaturated fatty acids delta-6-elongase		Ectocarpus siliculosus (Brown alga).	CBJ26764.1		D7G1F6		Between Sub
Eukaryota	Polyunsaturated fatty acids delta-6-elongase		Thraustochytrium sp. FJN-10.	ABC18314.1		Q2PWB7 [T]		
Eukaryota	GNS1/SUR4 membrane family protein		Arabidopsis lyrata subsp. lyrata.	EFH58732.1	XP_002882473.1	D7L5I3		
Eukaryota	F24P17.3 protein		Arabidopsis thaliana (Mouse-ear cress).	AAF08569.1	NP_187298.1	Q9SQV0		
Eukaryota	GNS1/SUR4 membrane protein		Medicago truncatula (Barrel medic).	ABD32385.2		Q2HTN1		
Eukaryota	Long chain fatty acid elongation enzyme		Gossypium hirsutum (Upland cotton) (Gossypium mexicanum).	CAE75664.1		Q5K4I1 [T]		
Eukaryota	Predicted protein		Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa).	EEE78137.1	XP_002303158.1	B9GZG1		
Eukaryota	Predicted protein		Physcomitrella patens subsp. patens.	EDQ52371.1	XP_001782794.1	A9TW15		

Eukaryota	GNS1/SUR4 family protein		Dictyostelium discoideum (Slime mold).	EAL68656.2	XP_642582.2	Q7KWQ5		families 5I and 5J
Eukaryota	GNS1/SUR4 family protein		Polysphondylium pallidum PN500.	EFA77110.1		D3BPA0		
Eukaryota	Predicted protein		Naegleria gruberi (Amoeba).	EFC46498.1	XP_002679242.1	D2V9N5		
Eukaryota	Fatty acid elongase A		Dictyostelium discoideum (Slime mold).	ACJ09597.1, EAL60997.1	XP_629422.1	Q54CJ4 [T], Q54CJ4.1		
Eukaryota	Protein SRE1 homolog		Dictyostelium discoideum (Slime mold).	EAL66470.1	XP_640460.1	Q54TC9 [T], Q54TC9.1		
Eukaryota	Steroid isomerase		Polysphondylium pallidum PN500.	EFA85325.1		D3B201		
Eukaryota	Predicted protein		Naegleria gruberi (Amoeba).	EFC39165.1	XP_002671909.1	D2VVU2		
Eukaryota	Predicted protein		Naegleria gruberi (Amoeba).	EFC39392.1	XP_002672136.1	D2VUW7		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