Table S2.
Subfamily 2A.

KS2-SubA

Type	Sequence	EC Number	Organism	GenBank ID	RefSeq	UniProt	PDB
Eukaryota	Very long-chain fatty acid condensing enzyme 8	2.3.1.-	Arabidopsis thaliana (Mouse-ear cress).	AAD03366.1, AAY56418.1, BAF00913.1	NP_179113.2	Q4V3C9 [T], Q4V3C9.1	
Eukaryota	Putative uncharacterized protein		Arabidopsis lyrata subsp. lyrata.	EFH60138.1	XP_002883879.1	D7L3J1	
Eukaryota	Putative uncharacterized protein		Arabidopsis lyrata subsp. lyrata.	EFH45421.1	XP_002869162.1	D7MF36	
Eukaryota	At4g34250	2.3.1.-	Arabidopsis thaliana (Mouse-ear cress).	ABP88112.1, BAF01126.1, CAB36702.1, CAB80142.1	NP_195151.1	A4VCL7 [T], Q9SYZ0 [T], Q9SYZ0.1	
Eukaryota	3-ketoacyl-CoA synthase		Arabidopsis lyrata subsp. lyrata.	EFH60422.1	XP_002884163.1	D7L154	
Eukaryota	3-ketoacyl-CoA synthase		Lesquerella fendleri (Fendler's bladderpod).	AAU05611.1		Q670P4	
Eukaryota	3-ketoacyl-CoA synthase		Lesquerella fendleri (Fendler's bladderpod).	AAK62348.1		Q93XD5	
Eukaryota	3-ketoacyl-CoA synthase		Cardamine graeca.	ACJ61778.1		C6FDV1 [T]	
Eukaryota	Beta-ketoacyl-CoA synthase		Orychophragmus violaceus (Chinese violet cress) (Brassica violacea).	AAX58618.1		Q56NH7	
Eukaryota	3-ketoacyl-CoA synthase		Teesdalia nudicaulis.	ABM65880.1		A2IB85	
Eukaryota	Beta-ketoacyl-CoA synthase		Sinapis arvensis (Charlock mustard) (Brassica kaber).	AAX58617.1		Q56NH8	
Eukaryota	Beta-ketoacyl-CoA synthase		Sinapis alba (White mustard) (Brassica hirta).	AAX58616.1		Q56NH9	

Eukaryota	Fatty acid elongase 1		Brassica campestris (Field mustard).	CAC79669.1		Q8VXU2	
Eukaryota	3-ketoacyl-CoA synthase		Crambe abyssinica (Abyssinian crambe) (Abyssinian kale).	AAX22298.1		Q32VC2	
Eukaryota	Beta-ketoacyl-CoA synthase		Sinapis arvensis (Charlock mustard) (Brassica kaber).	ACP19737.1		C3VJR0	
Eukaryota	Beta-ketoacyl-CoA synthase FAE1.2		Brassica juncea (Indian mustard) (Sinapis juncea).	CAD90160.1		Q84LN5	
Eukaryota	Fatty acid elongase 1		Brassica campestris (Field mustard).	CAC79670.1		Q8VXU1	
Eukaryota	Fatty acid elongase 1		Brassica oleracea (Wild cabbage).	CAC79671.1		Q8VXT6	
Eukaryota	Fatty acid elongase		Brassica napus (Rape).	AAA96054.1		Q39310 [T]	
Eukaryota	3-ketoacyl-CoA synthase		Brassica campestris (Field mustard).	AAM08352.1		Q8S3A1	
Eukaryota	Beta-ketoacyl-CoA synthase FAE1.1		Brassica juncea (Indian mustard) (Sinapis juncea).	CAD90159.1		Q84MZ6	
Eukaryota	FAE1		Brassica campestris (Field mustard).	ADB85635.1		D3JXE7	
Eukaryota	3-ketoacyl-CoA synthase		Brassica napus (Rape).	AAB72178.1		O23738 [T]	
Eukaryota	Fatty acid elongase		Brassica napus (Rape).	AAK64213.1, ACB55611.1, ADB85629.1		Q93XF0 [T]	
Eukaryota	FAE1		Brassica campestris (Field mustard).	ADB85636.1, ADB85637.1		D3JXE8	

Eukaryota	Beta-ketoacyl-CoA synthase		Brassica napus (Rape).	AAX58620.1		Q56NH5	
Eukaryota	FAE1		Brassica napus (Rape).	AAX58619.1, ADB85630.1		Q56NH6	
Eukaryota	3-ketoacyl-CoA synthase		Brassica napus (Rape).	AAM08353.1		Q8S3A0	
Eukaryota	FAE1		Brassica oleracea (Wild cabbage).	ADB85640.1		D3JXF2	
Eukaryota	FAE1		Brassica oleracea (Wild cabbage).	ADB85641.1		D3JXF3	
Eukaryota	3-ketoacyl-CoA synthase		Brassica napus (Rape).	AAM08350.1		Q8S3A3	
Eukaryota	FAE1		Brassica oleracea (Wild cabbage).	ADB85642.1, ADB85643.1		D3JXF4	
Eukaryota	Beta-ketoacyl-CoA synthase		Brassica napus (Rape).	ABV53972.1		A8D2G7	
Eukaryota	Fatty acid elongase		Brassica napus (Rape).	ACB55612.1, ADB85631.1		B2CQF6	
Eukaryota	Truncated FAE1		Brassica napus (Rape).	ADB85632.1, ADB85634.1		D3JXE4	
Eukaryota	3-ketoacyl-CoA synthase		Brassica oleracea (Wild cabbage).	AAM08351.1		Q8S3A2	
Eukaryota	Truncated FAE1		Brassica napus (Rape).	ADB85633.1		D3JXE5	
Eukaryota	Beta-ketoacyl-CoA synthase		Brassica napus (Rape).	AAX58614.1		Q56NI1	

Eukaryota	Fatty acid elongation 1		Brassica juncea (Indian mustard) (Sinapis juncea).	CAA71898.1		P93058	
Eukaryota	Fatty acid elongase		Brassica campestris (Field mustard).	AAM33539.1		Q8LSC7	
Eukaryota	Fatty acid elongase		Brassica juncea (Indian mustard) (Sinapis juncea).	AAM11648.1, AAM34043.1		Q8S384	
Eukaryota	Putative uncharacterized protein		Arabidopsis lyrata subsp. lyrata.	EFH45401.1	XP_002869142.1	D7MF05	
Eukaryota	Protein FATTY ACID ELONGATION 1	2.3.1.- 2.3.1.119	Arabidopsis thaliana (Mouse-ear cress).	AAA70154.1, CAA18831.1, CAB80169.1	NP_195178.1	Q38860 [P], Q38860.1	

Subfamily 2B.

SubB

Type	Sequence	EC Number	Organism	GenBank ID	RefSeq	UniProt	PDB
Eukaryota	hypothetical protein		Selaginella moellendorffii	EFJ19349.1	XP_002979460.1		
Eukaryota	hypothetical protein		Selaginella moellendorffii	EFJ21203.1	XP_002977865.1		
Eukaryota	Very long-chain fatty acid condensing enzyme 2	2.3.1.- 2.3.1.119	Arabidopsis thaliana (Mouse-ear cress).	CAA18830.1, CAB80168.1	NP_195177.1	O65677 [T], O65677.1	
Eukaryota	3-ketoacyl-CoA synthase 2		Arabidopsis lyrata subsp. lyrata.	EFH45402.1	XP_002869143.1	D7MF06	
Eukaryota	Putative uncharacterized protein		Oryza sativa subsp. indica (Rice).	EAY99068.1		A2Y7K8	
Eukaryota	cDNA clone:J033025C07, full insert sequence		Oryza sativa subsp. japonica (Rice).	AAU10670.1, BAF18268.1, BAG94915.1, BAG99710.1, EEE64728.1	NP_001056354.1	Q688V9 [T]	
Eukaryota	Acyltransferase		Zea mays (Maize).	ACG28710.1	NP_001130522.1	B6SV27 [T]	
Eukaryota	Putative uncharacterized protein Sb09g028860		Sorghum bicolor (Sorghum) (Sorghum vulgare).	EES19964.1	XP_002441534.1	C5YVX8	
Eukaryota	Putative uncharacterized protein		Zea mays (Maize).	ACN30819.1	NP_001168833.1	C0P9H4 [T]	

Eukaryota	Putative uncharacterized protein		Arabidopsis lyrata subsp. lyrata.	EFH60419.1	XP_002884160.1	D7L149	
Eukaryota	Very long-chain fatty acid condensing enzyme 9	2.3.1.-	Arabidopsis thaliana (Mouse-ear cress).	AAD22309.1	NP_179223.1	Q9SIX1 [T], Q9SIX1.1	
Eukaryota	PREDICTED: hypothetical protein isoform 1		Vitis vinifera		XP_002282403.1		
Eukaryota	3-ketoacyl-CoA synthase	2.3.1.119	Camellia oleifera.	ACQ41892.1		C3VPA4 [T]	
Eukaryota	Very long-chain fatty acid condensing enzyme 4	2.3.1.-	Arabidopsis thaliana (Mouse-ear cress).	AAF79428.1, ACE79746.1	NP_173376.1	Q9LN49 [T], Q9LN49.1	
Eukaryota	Putative uncharacterized protein		Arabidopsis lyrata subsp. lyrata.	EFH66600.1	XP_002890341.1	D7KI29	
Eukaryota	Predicted protein		Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa).	EEE99625.1	XP_002321310.1	B9IBF7	
Eukaryota	Acyltransferase, putative		Ricinus communis (Castor bean).	EEF52581.1	XP_002510394.1	B9R7V1	
Eukaryota	3-ketoacyl-CoA synthase		Eranthis hyemalis (Winter aconite).	ABS18382.1		A7L830 [T]	
Eukaryota	Putative uncharacterized protein		Vitis vinifera (Grape).	CAN68997.1		A5AGM3	
Eukaryota	Predicted protein		Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa).	EEE87748.1	XP_002313793.1	B9HRM7	

Eukaryota	Predicted protein		Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa).	EEE85942.1	XP_002305431.1	B9H0R8	
Eukaryota	Acyltransferase, putative		Ricinus communis (Castor bean).	EEF50878.1	XP_002509491.1	B9RBF7	
Eukaryota	Predicted protein		Physcomitrella patens subsp. patens.	EDQ72629.1	XP_001762506.1	A9S896	
Eukaryota	Predicted protein		Physcomitrella patens subsp. patens.	EDQ81858.1	XP_001753229.1	A9RGK9	
Eukaryota	Predicted protein		Physcomitrella patens subsp. patens.	EDQ82178.1	XP_001753137.1	A9RG41	
Eukaryota	Predicted protein		Physcomitrella patens subsp. patens.	EDQ76304.1	XP_001758798.1	A9RXN9	
Eukaryota	Predicted protein		Physcomitrella patens subsp. patens.	EDQ77625.1	XP_001757568.1	A9RTP0	
Eukaryota	hypothetical protein		Selaginella moellendorffii	EFJ35502.1	XP_002963631.1		
Eukaryota	hypothetical protein		Selaginella moellendorffii	EFJ24239.1	XP_002974719.1		
Eukaryota	FAE1		Marchantia polymorpha (Liverwort).	AAP74371.1		Q7XZE7	

Subfamily 2C.

SubC

Type	Sequence	EC Number	Organism	GenBank ID	RefSeq	UniProt	PDB
Eukaryota	Acyltransferase, putative		Ricinus communis (Castor bean).	EEF45199.1	XP_002517036.1	B9RTG7	
Eukaryota	Beta-ketoacyl-coa synthase family protein		Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa).	EEE71322.1	XP_002332626.1	B9NBJ1	
Eukaryota	Beta-ketoacyl-coa synthase family protein		Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa).	EEE71320.1	XP_002332624.1	B9NBI9	
Eukaryota	Putative uncharacterized protein		Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa).	ABK94954.1		A9PF01 [T]	
Eukaryota	Beta-ketoacyl-coa synthase family protein		Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa).	EEE77823.1	XP_002333986.1	B9NFF1	
Eukaryota	Putative fatty acid elongase		Tropaeolum majus (Common nasturtium).	ABD77097.1		Q1ZZJ8	
Eukaryota	Putative fatty acid elongase		Tropaeolum majus (Common nasturtium).	AAL99199.1		Q8RXA6 [T]	
Eukaryota	Beta-ketoacyl-CoA synthase		Simmondsia chinensis (Jojoba) (Buxus chinensis).	AAC49186.1		Q41301 [T]	
Eukaryota	Fatty acid elongase 1-like protein		Limnanthes douglasii (Douglas's meadowfoam).	AAG28600.1		Q9FV67 [T]	
Eukaryota	Very long-chain fatty acid condensing enzyme 19	2.3.1.-	Arabidopsis thaliana (Mouse-ear cress).	AAK59535.1, AAL11613.1, AAN12994.1, BAB11304.1	NP_199189.1	Q9FG87 [T], Q9FG87.1	
Eukaryota	Very long-chain fatty acid condensing enzyme 17	2.3.1.-	Arabidopsis thaliana (Mouse-ear cress).	AAC16740.1, AAL67132.1, AAU95453.1, BAD95022.1	NP_171918.1	Q5XEP9 [T], Q5XEP9.2	
Eukaryota	Putative uncharacterized protein	2.3.1.-	Arabidopsis lyrata subsp. lyrata.	EFH68460.1	XP_002892201.1	D7KDC3	

Eukaryota	Beta-ketoacyl-CoA synthase		Helianthus annuus (Common sunflower).	ACC60973.1		C9VYH7 [T]	
Eukaryota	PREDICTED: hypothetical protein		Vitis vinifera		XP_002283935.1		
Eukaryota	Beta-ketoacyl-CoA synthase		Gossypium hirsutum (Upland cotton) (Gossypium mexicanum).	ABV60087.1		A9XUG6 [T]	
Eukaryota	Acyltransferase, putative		Ricinus communis (Castor bean).	EEF45198.1	XP_002517035.1	B9RTG6	
Eukaryota	Beta-ketoacyl-coa synthase family protein		Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa).	EEE89929.1	XP_002312562.1	B9HKC7	
Eukaryota	Beta-ketoacyl-coa synthase family protein		Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa).	EEF00831.1	XP_002314660.1	B9HUP8	
Eukaryota	Putative uncharacterized protein		Populus trichocarpa x Populus deltoides.	ABK96299.1		A9PIU6 [T]	
Eukaryota	Putative uncharacterized protein Sb09g029260		Sorghum bicolor (Sorghum) (Sorghum vulgare).	EES19987.1	XP_002441557.1	C5YW23	
Eukaryota	Putative uncharacterized protein		Oryza sativa subsp. indica (Rice).	EAY99126.1		A2Y7R6	
Eukaryota	cDNA clone:J023067B12, full insert sequence		Oryza sativa subsp. japonica (Rice).	AAT69586.1, BAF18305.1, BAG92126.1, EEE64780.1	NP_001056391.1	Q6F365 [T]	
Eukaryota	Putative uncharacterized protein		Oryza sativa subsp. japonica (Rice).	EAZ22163.1		A3A4C4	
Eukaryota	Putative uncharacterized protein		Oryza sativa subsp. indica (Rice).	EAY84941.1		A2X281	

Eukaryota	cDNA clone:J013127I02, full insert sequence		Oryza sativa subsp. japonica (Rice).	BAD16019.1, BAD38439.1, BAF08164.1, BAG90658.1	NP_001046250.1	Q6Z6C7 [T]	
Eukaryota	Putative uncharacterized protein Sb04g007190		Sorghum bicolor (Sorghum) (Sorghum vulgare).	EES06493.1	XP_002453517.1	C5XXY2	
Eukaryota	Fatty acid elongase		Zea mays (Maize).	ACG43464.1	NP_001151591.1	B6U281 [T]	
Eukaryota	Putative uncharacterized protein		Zea mays (Maize).	ACR36808.1		C4J6K8 [T]	
Eukaryota	Putative uncharacterized protein		Oryza sativa subsp. japonica (Rice).	BAD32939.1, BAF19910.1, EAZ37545.1	NP_001057996.1	Q69X62	
Eukaryota	Putative uncharacterized protein		Oryza sativa subsp. indica (Rice).	EAZ01557.1		A2YEP6	
Eukaryota	Putative uncharacterized protein Sb10g023290		Sorghum bicolor (Sorghum) (Sorghum vulgare).	EER88601.1	XP_002437234.1	C5Z5K2	
Eukaryota	Fatty acid elongase		Zea mays (Maize).	ACG36525.1		B6THE2 [T]	
Eukaryota	Putative fatty acid elongase		Zea mays (Maize).	CAC01441.1	NP_001105135.1	Q9FXZ8 [T]	
Eukaryota	Very long-chain fatty acid condensing enzyme 11		Arabidopsis thaliana (Mouse-ear cress).	AAB95298.1, AAO41904.1, AAO64112.1	NP_180232.1	O48780 [P], O48780.1	
Eukaryota	Putative uncharacterized protein	2.3.1.- 2.3.1.119	Arabidopsis lyrata subsp. lyrata.	EFH55253.1	XP_002878994.1	D7LE90	
Eukaryota	Beta-ketoacyl-CoA synthase		Helianthus annuus (Common sunflower).	ACC95444.1		C6ES40 [T]	

Eukaryota	Beta-ketoacyl-coa synthase family protein		Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa).	EEF02841.1	XP_002324276.1	B9IKT4	
Eukaryota	Beta-ketoacyl-coa synthase family protein		Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa).	EEE92165.1	XP_002308642.1	B9H9R8	
Eukaryota	PREDICTED: hypothetical protein		Vitis vinifera		XP_002284751.1		
Eukaryota	Putative uncharacterized protein		Vitis vinifera (Grape).	CAN67313.1	XP_002284986.1	A5AYN9	
Eukaryota	Whole genome shotgun sequence of line PN40024, scaffold_16.assembly12x		Vitis vinifera (Grape).	CBI28145.3		D7TBW0	
Eukaryota	CM0216.300.nc protein		Lotus japonicus.	BAF98214.1		B0BLH8	
Eukaryota	Putative uncharacterized protein		Medicago truncatula (Barrel medic).	ACJ85761.1		B7FLX8 [T]	
Eukaryota	Acyltransferase, putative		Ricinus communis (Castor bean).	EEF33033.1	XP_002529366.1	B9STP7	
Eukaryota	Fatty acid elongase		Pistacia chinensis.	ACY78677.1		D1LFJ9 [T]	

Subfamily 2D.

			SubD				
Type	Sequence	EC Numbe	Organism	GenBank ID	RefSeq	UniProt	PDB
Eukaryota	Putative uncharacterized protein		Picea sitchensis (Sitka spruce).	ADE77445.1		D5AD26 [T]	
Eukaryota	Putative uncharacterized protein		Picea sitchensis (Sitka spruce).	ABK24632.1		A9NVH1 [T]	
Eukaryota	Putative FIDDLEHEAD very long chain fatty acid condensing enzyme FDH		Hordeum vulgare (Barley).	ABG35745.1, ABV22580.1, ABV22581.1, ABV22587.1		A7YA55 [T], A9L9S2 [T]	
Eukaryota	Similar to Fiddlehead protein		Oryza sativa subsp. japonica (Rice).	ABF94315.1, BAF11084.1, BAG87571.1, BAG87863.1, BAG94008.1, BAG99590.1	NP_001049170.1	Q10QW1 [T]	
Eukaryota	Putative uncharacterized protein		Oryza sativa subsp. indica (Rice).	EAY88792.1		A2XD82	
Eukaryota	Putative fiddlehead-like protein		Oryza sativa subsp. japonica (Rice).	AAN65442.1		Q8H7L2	
Eukaryota	Fiddlehead, putative, expressed		Oryza sativa subsp. japonica (Rice).	ABF94313.1		Q10QW0	
Eukaryota	Putative uncharacterized protein		Oryza sativa subsp. japonica (Rice).	EEE58439.1		B9F5I5	
Eukaryota	Similar to Fiddlehead protein		Oryza sativa subsp. japonica (Rice).	ABF94314.1, BAG87572.1, BAG87864.1, BAG94009.1, BAG99591.1		Q10QV9 [T]	
Eukaryota	Fiddlehead, putative, expressed		Oryza sativa subsp. japonica (Rice).	ABF94316.1		Q10QV8	

Eukaryota	Fiddlehead-like protein		Zea mays (Maize).	ACG35345.1	NP_001149405.1	B6TE12 [T]	
Eukaryota	Putative uncharacterized protein		Zea mays (Maize).	ACN25771.1		C0HFG8 [T]	
Eukaryota	Putative uncharacterized protein Sb01g045150		Sorghum bicolor (Sorghum) (Sorghum vulgare).	EER95395.1	XP_002468397.1	C5WVS4	
Eukaryota	PREDICTED: hypothetical protein isoform 1		Vitis vinifera		XP_002282234.1		
Eukaryota	PREDICTED: hypothetical protein isoform 2		Vitis vinifera		XP_002282282.1		
Eukaryota	Whole genome shotgun sequence of line PN40024, scaffold_8.assembly12x		Vitis vinifera (Grape).	CBI20747.3		D7STZ8	
Eukaryota	Predicted protein		Arabidopsis lyrata subsp. lyrata.	EFH57030.1	XP_002880771.1	D7LCV5	
Eukaryota	Protein FIDDLEHEAD	2.3.1.-	Arabidopsis thaliana (Mouse-ear cress).	AAC14526.1, AAF73973.1, AAF73974.1, AAF73975.1, AAF73976.1, AAF73977.1, AAF73978.1, AAF73979.1, AAF73980.1, AAF73981.1, AAG60062.1, AAK62618.1, AAN31115.1, AAN86193.1, BAD94049.1, CAA09311.1	NP_180193.1	Q570B4 [P], Q570B4.2	

Eukaryota	Fiddlehead-like protein		Pisum sativum (Garden pea).	ABU75309.2		A7X6P9 [T]	
Eukaryota	Putative beta-ketoacyl-CoA synthase		Antirrhinum majus (Garden snapdragon).	CAC84082.1		Q8S2R3	
Eukaryota	Acyltransferase, putative		Ricinus communis (Castor bean).	EEF46169.1	XP_002516167.1	B9RQZ8	
Eukaryota	Fiddlehead-like protein		Tropaeolum majus (Common nasturtium).	AAO47729.1, AAP14903.1		Q84K36 [T]	
Eukaryota	Beta-ketoacyl-coa synthase family protein		Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa).	EEE92974.1	XP_002309451.1	B9HCP2	
Eukaryota	Fiddlehead-like protein		Gossypium hirsutum (Upland cotton) (Gossypium mexicanum).	AAL67993.1		Q8VWP9 [T]	
Eukaryota	Very long-chain fatty acid condensing enzyme 15	2.3.1.-	Arabidopsis thaliana (Mouse-ear cress).	AAM61287.1, ABE66011.1, CAB41336.1	NP_190784.1	Q9SUY9 [T], Q9SUY9.1	
Eukaryota	Very long-chain fatty acid condensing enzyme 15	2.3.1.-	Arabidopsis thaliana (Mouse-ear cress).	AAM61287.1, ABE66011.1, CAB41336.1	NP_190784.1	Q9SUY9 [T], Q9SUY9.1	
Eukaryota	Putative uncharacterized protein		Arabidopsis thaliana (Mouse-ear cress).	ABK28598.1		A0MF23 [T]	
Eukaryota	Beta-ketoacyl-CoA synthase family protein		Arabidopsis lyrata subsp. lyrata.	EFH54104.1	XP_002877845.1	D7LU31	
Eukaryota	Acyltransferase, putative		Ricinus communis (Castor bean).	EEF32005.1	XP_002530372.1	B9SWK3	
Eukaryota	PREDICTED: hypothetical protein		Vitis vinifera		XP_002273798.1		

Subfamily 2E.

SubE

Type	Sequence	EC Number	Organism	GenBank ID	RefSeq	UniProt	PDB
Eukaryota	Predicted protein		Physcomitrella patens subsp. patens.	EDQ76154.1	XP_001759085.1	A9RY07	
Eukaryota	Predicted protein		Physcomitrella patens subsp. patens.	EDQ65326.1	XP_001769764.1	A9STT5	
Eukaryota	Putative uncharacterized protein		Arabidopsis lyrata subsp. lyrata.	EFH56520.1	XP_002880261.1	D7LF81	
Eukaryota	3-ketoacyl-coA synthase 13 KCS13		Arabidopsis halleri subsp. halleri.	CAZ68133.1		D4HU18	
Eukaryota	Very long-chain fatty acid condensing enzyme 14	2.3.1.-	Arabidopsis thaliana (Mouse-ear cress).	AAF02814.1	NP_187639.1	Q9SS39 [T], Q9SS39.1	
Eukaryota	Protein HIGH CARBON DIOXIDE	2.3.1.-	Arabidopsis thaliana (Mouse-ear cress).	AAC69929.1, AAG24644.1, AAG24645.1	NP_182195.1	Q9ZUZ0 [T], Q9ZUZ0.1	
Eukaryota	Senescence-associated protein 15		Hemerocallis sp. (Daylily).	AAC34858.1		O81658 [T]	
Eukaryota	Putative uncharacterized protein Sb01g041190		Sorghum bicolor (Sorghum) (Sorghum vulgare).	EER92561.1	XP_002465563.1	C5WQZ2	
Eukaryota	Senescence-associated protein 15, putative, expressed		Oryza sativa subsp. japonica (Rice).	ABF94942.1, BAF11454.1, EAY89235.1, EAZ26253.1	NP_001049540.1	A2XEH5, Q10P61	
Eukaryota	Putative uncharacterized protein Sb01g025820		Sorghum bicolor (Sorghum) (Sorghum vulgare).	EER91722.1	XP_002464724.1	C5WNZ0	
Eukaryota	Putative uncharacterized protein		Oryza sativa subsp. japonica (Rice).	EEE50594.1		B9G7K9	
Eukaryota	Putative senescence-associated protein 15		Oryza sativa (Rice).	AAK95678.1, ABB46794.2		Q33AY1, Q94GT5	
Eukaryota	Os10g0158100 protein		Oryza sativa subsp. japonica (Rice).	BAF26110.2	NP_001064196.2	Q0IYV5	

Eukaryota	Putative uncharacterized protein		Oryza sativa subsp. indica (Rice).	EEC66585.1		B8BFS6	
Eukaryota	Chalcone and stilbene synthases, N-terminal		Medicago truncatula (Barrel medic).	ABD32702.1		Q2HTC9	
Eukaryota	Fatty acid elongase 3-ketoacyl-CoA synthase		Brassica napus (Rape).	AAT65207.1		Q6DUV5	
Eukaryota	Fatty acid elongase 3-ketoacyl-CoA synthase		Brassica napus (Rape).	AAT65206.1		Q6DUV6 [T]	
Eukaryota	3-ketoacyl-CoA synthase 1		Arabidopsis lyrata subsp. lyrata.	EFH65642.1	XP_002889383.1	D7KQB2	
Eukaryota	AT1G01120 protein		Arabidopsis thaliana (Mouse-ear cress).	BAH20305.1		B9DHT8 [T]	
Eukaryota	Very long-chain fatty acid condensing enzyme 1	2.3.1.- 2.3.1.119	Arabidopsis thaliana (Mouse-ear cress).	AAC99312.1, AAF26470.1, AAL66982.1, AAM20218.1, BAD95286.1	NP_171620.2	Q9MAM3 [P], Q9MAM3.1	
Eukaryota	Putative fatty acid elongase 3-ketoacyl-CoA synthase 1		Arabidopsis thaliana (Mouse-ear cress).	BAE98925.1		Q0WVC3 [T]	
Eukaryota	Acyltransferase, putative		Ricinus communis (Castor bean).	EEF32418.1	XP_002529975.1	B9SVF6	
Eukaryota	3-ketoacyl-CoA synthase 10		Gossypium hirsutum (Upland cotton) (Gossypium mexicanum).	ABX10440.1		A9XU46 [T]	
Eukaryota	Predicted protein		Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa).	EEE80709.1	XP_002301436.1	B9GRP8	
Eukaryota	Putative uncharacterized protein		Vitis vinifera (Grape).	CAN77062.1		A5BMG1	
Eukaryota	Whole genome shotgun sequence of line PN40024, scaffold_48.assembly12x		Vitis vinifera (Grape).	CBI38700.3		D7U818	

Eukaryota	PREDICTED: hypothetical protein		Vitis vinifera		XP_002264721.1		

Subfamily 2F.

Type	Sequence	EC Number	Organism	GenBank ID	RefSeq	UniProt	PDB
Eukaryota	Putative uncharacterized protein		Vitis vinifera (Grape).	CAN63425.1		A5BF22	
Eukaryota	PREDICTED: hypothetical protein		Vitis vinifera		XP_002271250.1		
Eukaryota	3-ketoacyl-CoA synthase II		Triticum aestivum (Wheat).	ABY82172.1		B6CEY0 [T]	
Eukaryota	3-ketoacyl-CoA synthase I		Triticum aestivum (Wheat).	ABY82171.2		B6CEX9 [T]	
Eukaryota	Putative very long chain fatty acid condensing enzyme CUT1		Hordeum vulgare (Barley).	ABG35744.1		A9L9S1 [T]	
Eukaryota	cDNA clone:J013074H08, full insert sequence		Oryza sativa subsp. japonica (Rice).	ABF94686.1, BAF11320.1, BAG90041.1, BAG96897.1, BAG97602.1, EAY89070.1, EAZ26093.1	NP_001049406.1	A2XE10, Q10PV5 [T]	
Eukaryota	Putative uncharacterized protein Sb01g042600		Sorghum bicolor (Sorghum) (Sorghum vulgare).	EER92628.1	XP_002465630.1	C5WSP8	
Eukaryota	Putative uncharacterized protein		Zea mays (Maize).	ACF87925.1, ACN34702.1		B4G0N2 [T]	
Eukaryota	Putative uncharacterized protein		Zea mays (Maize).	ACF78737.1	NP_001130497.1	B4F9E4 [T]	
Eukaryota	PREDICTED: hypothetical protein		Vitis vinifera		XP_002282526.1		

Eukaryota	Putative uncharacterized protein		Arabidopsis lyrata subsp. lyrata.	EFH64929.1	XP_002888670.1	D7KWD3	
Eukaryota	Cuticular protein 1	2.3.1.-	Arabidopsis thaliana (Mouse-ear cress).	AAD37122.1, AAG52390.1, AAL50069.1, AAM16230.1, BAD94789.1	NP_177020.1	Q9XF43 [T], Q9XF43.1	
Eukaryota	Very-long-chain fatty acid condensing enzyme CUT1		Arabidopsis thaliana (Mouse-ear cress).	AAM65060.1		Q8LAZ1 [T]	
Eukaryota	Uncharacterized protein At1g68530.2		Arabidopsis thaliana (Mouse-ear cress).		NP_849861.1	Q3ECG1	
Eukaryota	Putative uncharacterized protein		Arabidopsis lyrata subsp. lyrata.	EFH66948.1	XP_002890689.1	D7KAI4	
Eukaryota	Very long-chain fatty acid condensing enzyme 5	2.3.1.-	Arabidopsis thaliana (Mouse-ear cress).	AAG50800.1, AAM67234.1, AAO42223.1	NP_173916.1	Q9C6L5 [T], Q9C6L5.1	
Eukaryota	CER6		Solanum tuberosum (Potato).	ACF17125.1		B7SSK0	
Eukaryota	CER6		Solanum lycopersicum (Tomato) (Lycopersicon esculentum).	ACT21783.1		C6KH60	
Eukaryota	Putative uncharacterized protein		Vitis vinifera (Grape).	CAN74750.1	XP_002283730.1	A5BLZ4	
Eukaryota	3-ketoacyl-CoA synthase		Gossypium hirsutum (Upland cotton) (Gossypium mexicanum).	ABA01490.1		Q2QCW7 [T]	
Eukaryota	Predicted protein		Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa).	EEE88824.1	XP_002311457.1	B9HJ26	
Eukaryota	Putative uncharacterized protein		Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa).	ABK94727.1, EEF02113.1	XP_002315942.1	A9PEC4 [T]	

Subfamily 2G.

Type	Sequence	EC Number	Organism	GenBank ID	RefSeq	UniProt	PDB
Eukaryota	Putative uncharacterized protein Sb02g030230		Sorghum bicolor (Sorghum) (Sorghum vulgare).	EER97063.1	XP_002460542.1	C5X618	
Eukaryota	Acyltransferase		Zea mays (Maize).	ACG30367.1	NP_001148270.1	B6SZT4 [T]	
Eukaryota	Long-chain fatty acid condensing enzyme		Oryza brachyantha.	ABG73470.1		A6MCZ1	
Eukaryota	Putative very-long-chain fatty acid condensing enzyme		Oryza sativa subsp. japonica (Rice).	BAD46681.1		Q650T6	
Eukaryota	Putative very-long-chain fatty acid condensing enzyme		Oryza sativa subsp. japonica (Rice).	BAD46682.1, EAZ45400.1		Q650T5	
Eukaryota	Very long-chain fatty acid condensing enzyme 20	2.3.1.-	Arabidopsis thaliana (Mouse-ear cress).	BAB10089.1	NP_199718.1	Q9FH27 [T], Q9FH27.1	
Eukaryota	Beta-ketoacyl-CoA synthase family protein		Arabidopsis lyrata subsp. lyrata.	EFH41960.1	XP_002865701.1	D7MN62	
Eukaryota	Whole genome shotgun sequence of line PN40024, scaffold_42.assembly12x		Vitis vinifera (Grape).	CBI29070.3		D7TEZ7	
Eukaryota	Acyltransferase, putative		Ricinus communis (Castor bean).	EEF45554.1	XP_002516940.1	B9RT71	
Eukaryota	Beta-ketoacyl-coa synthase family protein		Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa).	EEE95431.1	XP_002319508.1	B9I7H3	
Eukaryota	Beta-ketoacyl-CoA synthase family protein		Arabidopsis lyrata subsp. lyrata.	EFH65082.1	XP_002888823.1	D7KYS2	
Eukaryota	Very long-chain fatty acid condensing enzyme 7	2.3.1.-	Arabidopsis thaliana (Mouse-ear cress).	AAG51695.1, AAT71956.1	NP_177272.1	Q9C992 [T], Q9C992.1	

Eukaryota	Beta-ketoacyl-coa synthase family protein		Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa).	EEE82976.1	XP_002298171.1	B9GEW1	
Eukaryota	Putative uncharacterized protein		Vitis vinifera (Grape).	CAN66110.1		A5BX65	
Eukaryota	Acyltransferase, putative		Ricinus communis (Castor bean).	EEF33117.1	XP_002529285.1	B9STG6	
Eukaryota	PREDICTED: hypothetical protein		Vitis vinifera		XP_002270917.1		
Eukaryota	Whole genome shotgun sequence of line PN40024, scaffold_22.assembly12x		Vitis vinifera (Grape).	CBI24529.3		D7T239	
Eukaryota	PREDICTED: hypothetical protein		Vitis vinifera		XP_002267475.1		
Eukaryota	Whole genome shotgun sequence of line PN40024, scaffold_22.assembly12x		Vitis vinifera (Grape).	CBI24530.3	XP_002267424.1	D7T240	
Eukaryota	Putative uncharacterized protein		Vitis vinifera (Grape).	CAN79857.1		A5CAA5	
Eukaryota	Predicted protein		Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa).	EEF05987.1	XP_002321860.1	B9ICY9	
Eukaryota	Acyltransferase, putative		Ricinus communis (Castor bean).	EEF51488.1	XP_002510886.1	B9R9L1	
Eukaryota	Acyltransferase, putative		Ricinus communis (Castor bean).	EEF51487.1	XP_002510885.1	B9R9L0	

Subfamily 2H.

Type	Sequence	EC Number	Organism	GenBank ID	RefSeq	UniProt	PDB
Eukaryota	Putative uncharacterized protein Sb10g009490		Sorghum bicolor (Sorghum) (Sorghum vulgare).	EER89567.1	XP_002438200.1	C5Z837	
Eukaryota	Putative uncharacterized protein Sb10g009450		Sorghum bicolor (Sorghum) (Sorghum vulgare).	EER89562.1	XP_002438195.1	C5Z829	
Eukaryota	Putative very-long-chain fatty acid condensing enzyme CUT1		Oryza sativa subsp. japonica (Rice).	BAD54091.1, BAD54353.1, BAF19245.2, EAZ36552.1	NP_001057331.2	Q5Z6R6	
Eukaryota	Putative very long chain fatty acid condensing enzyme CUT1		Hordeum vulgare (Barley).	ABF51010.1		A9L9N2 [T]	
Eukaryota	Putative uncharacterized protein Sb10g009410		Sorghum bicolor (Sorghum) (Sorghum vulgare).	EER89559.1	XP_002438192.1	C5Z823	
Eukaryota	Putative very-long-chain fatty acid condensing enzyme CUT1		Oryza sativa subsp. japonica (Rice).	BAD54186.1, BAF19243.1, EAZ36546.1	NP_001057329.1	Q5Z7C8	
Eukaryota	Putative uncharacterized protein		Oryza sativa subsp. indica (Rice).	EEC80356.1		B8B0C3	
Eukaryota	Putative uncharacterized protein		Oryza sativa subsp. indica (Rice).	EEC80357.1		B8B0C4	
Eukaryota	Putative very-long-chain fatty acid condensing enzyme CUT1		Oryza sativa subsp. japonica (Rice).	BAD54084.1, BAD54346.1, BAF19244.1	NP_001057330.1	Q5Z6S3	
Eukaryota	Putative uncharacterized protein		Oryza sativa subsp. japonica (Rice).	EEE65482.1		B9FSM1	
Eukaryota	Putative very-long-chain fatty acid condensing enzyme CUT1		Oryza sativa subsp. japonica (Rice).	BAD54167.1, BAF19241.1, EAZ36543.1	NP_001057327.1	Q5Z7E7	
Eukaryota	Putative uncharacterized protein		Oryza sativa subsp. indica (Rice).	EAZ00421.1		A2YBG0	

Eukaryota	Putative uncharacterized protein		Oryza sativa subsp. indica (Rice).	EAY87409.1		A2X999	
Eukaryota	cDNA, clone: J065136G23, full insert sequence		Oryza sativa subsp. japonica (Rice).	BAD15940.1, BAD16133.1, BAF09937.2, BAH00996.1, EAZ24509.1	NP_001048023.2	Q6Z2K7 [T]	
Eukaryota	Putative uncharacterized protein		Oryza sativa subsp. indica (Rice).	EAY87408.1		A2X998	
Eukaryota	Putative uncharacterized protein		Zea mays (Maize).	ACL53765.1, ACN28136.1	NP_001146356.1	B8A0R6 [T]	
Eukaryota	G14a		Zea mays (Maize).	ACO72623.1		D2DWN9	
Eukaryota	G14a		Zea mays (Maize).	ACO72625.1		D2DWP1	
Eukaryota	Truncated g14a		Zea mays (Maize).	ACO72627.1		D2DWP3	
Eukaryota	Putative uncharacterized protein		Zea mays (Maize).	ACF78938.1, ACF84285.1	NP_001130638.1	B4F9Z5 [T]	
Eukaryota	G14a		Zea mays (Maize).	ACO72624.1		D2DWP0	
Eukaryota	Putative uncharacterized protein Sb10g009460		Sorghum bicolor (Sorghum) (Sorghum vulgare).	EER88189.1	XP_002436822.1	C5Z830	
Eukaryota	Putative uncharacterized protein Sb10g009462		Sorghum bicolor (Sorghum) (Sorghum vulgare).	EER88190.1	XP_002436823.1	C5Z831	
Eukaryota	Putative uncharacterized protein Sb06g001920		Sorghum bicolor (Sorghum) (Sorghum vulgare).	EES10442.1	XP_002446114.1	C5YCC2	

Eukaryota	OSJNBb0050O03.6 protein		Oryza sativa subsp. japonica (Rice).	CAE01716.2		Q7XT16	
Eukaryota	cDNA clone:002-183-G08, full insert sequence		Oryza sativa subsp. japonica (Rice).	BAG99811.1		B7F5B4 [T]	
Eukaryota	Putative uncharacterized protein		Oryza sativa subsp. japonica (Rice).	EEE60402.1		B9FD38	
Eukaryota	Putative uncharacterized protein		Zea mays (Maize).	ACF84501.1	NP_001140738.1	B4FQV8 [T]	
Eukaryota	Putative uncharacterized protein Sb03g023131		Sorghum bicolor (Sorghum) (Sorghum vulgare).	EES03073.1	XP_002457953.1	C5XM86	
Eukaryota	Os01g0529800 protein		Oryza sativa subsp. japonica (Rice).	BAF05149.1	NP_001043235.1	Q0JM79	
Eukaryota	Putative uncharacterized protein		Oryza sativa subsp. indica (Rice).	EAY74376.1		A2WQY0	
Eukaryota	Putative very-long-chain fatty acid condensing enzyme CUT1		Oryza sativa subsp. japonica (Rice).	BAB91850.1		Q8LQT7	
Eukaryota	Putative uncharacterized protein Sb03g022990		Sorghum bicolor (Sorghum) (Sorghum vulgare).	EES00849.1	XP_002455729.1	C5XM80	
Eukaryota	3-ketoacyl-CoA synthase		Zea mays (Maize).	ACG35539.1	NP_001149469.1	B6TEK6 [T]	

Subfamily 2I.

Type	Sequence	EC Number	Organism	GenBank ID	RefSeq	UniProt	PDB
Eukaryota	Putative fatty acid elongase 3-ketoacyl-CoA synthase		Oryza sativa (Rice).	AAG16863.1, AAL31025.1, AAP54239.1, BAF26745.1, BAG99955.1	NP_001064831.1	Q7XDH2 [T], Q9FW59	
Eukaryota	Putative uncharacterized protein		Zea mays (Maize).	ACG30081.1, ACN30933.1	NP_001148181.1	B6SYZ8 [T]	
Eukaryota	Putative uncharacterized protein		Zea mays (Maize).	ACF84426.1, ACG47636.1	NP_001152441.1	B4FQN3 [T]	
Eukaryota	Putative uncharacterized protein Sb01g019520		Sorghum bicolor (Sorghum) (Sorghum vulgare).	EER94093.1	XP_002467095.1	C5WYI0	
Eukaryota	Putative uncharacterized protein		Oryza sativa subsp. japonica (Rice).	EAZ27141.1		A3AIK2	
Eukaryota	Putative fatty acid elongase		Oryza sativa subsp. japonica (Rice).	AAR96223.1, BAH92176.1	NP_001173448.1	Q75M84	
Eukaryota	Putative uncharacterized protein		Oryza sativa subsp. japonica (Rice).	EAZ27142.1		A3AIK3	
Eukaryota	Os03g0383600 protein		Oryza sativa subsp. japonica (Rice).	ABF96286.1, BAF12160.1	NP_001050246.1	Q10KI1	
Eukaryota	Putative uncharacterized protein		Oryza sativa subsp. indica (Rice).	EAY90260.1		A2XHF0	
Eukaryota	Putative uncharacterized protein		Oryza sativa subsp. japonica (Rice).	BAD21655.1, BAD22394.1, BAF10400.1, EAZ25051.1	NP_001048486.1	Q6K3E6	
Eukaryota	Putative uncharacterized protein		Oryza sativa subsp. indica (Rice).	EAY87986.1		A2XAX6	

Eukaryota	Putative uncharacterized protein Sb04g036880		Sorghum bicolor (Sorghum) (Sorghum vulgare).	EES07735.1	XP_002454759.1	C5XV97	
Eukaryota	cDNA, clone: J065198N05, full insert sequence		Oryza sativa subsp. japonica (Rice).	AAR96244.1, ABF96278.1, BAF12157.1, BAH01093.1	NP_001050243.1	Q75M74 [T]	
Eukaryota	Putative uncharacterized protein		Oryza sativa subsp. japonica (Rice).	EAZ27140.1		A3AIK1	
Eukaryota	Putative uncharacterized protein Sb01g033910		Sorghum bicolor (Sorghum) (Sorghum vulgare).	EER94777.1	XP_002467779.1	C5WYK5	
Eukaryota	Acyltransferase		Zea mays (Maize).	ACG29982.1	NP_001148161.1	B6SYP9 [T]	
Eukaryota	Putative uncharacterized protein		Zea mays (Maize).	ACF82788.1		B4FKZ5 [T]	
Eukaryota	Acyltransferase		Zea mays (Maize).	ACG47900.1	NP_001152498.1	B6UEW7 [T]	
Eukaryota	Putative uncharacterized protein		Vitis vinifera (Grape).	CAN60802.1	XP_002282219.1	A5B0J1	
Eukaryota	Beta-ketoacyl-CoA synthase family protein		Arabidopsis lyrata subsp. lyrata.	EFH49413.1	XP_002873154.1	D7LXK1	
Eukaryota	Very long-chain fatty acid condensing enzyme 21	2.3.1.-	Arabidopsis thaliana (Mouse-ear cress).	AAO63450.1, BAC41850.1, CAB85559.1	NP_196073.1	Q9LZ72 [T], Q9LZ72.1	
Eukaryota	Beta-ketoacyl-coa synthase family protein		Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa).	EEF01427.1	XP_002315256.1	B9HTX8	
Eukaryota	Beta-ketoacyl-coa synthase family protein		Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa).	EEE74009.1	XP_002327204.1	B9MW17	
Eukaryota	Beta-ketoacyl-coa synthase family protein		Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa).	EEE74006.1	XP_002327201.1	B9MW14	

Eukaryota	Beta-ketoacyl-coa synthase family protein		Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa).	EEE74010.1	XP_002327205.1	B9MW20	
Eukaryota	Beta-ketoacyl-coa synthase family protein		Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa).	EEF00412.1	XP_002326030.1	B9IQR0	
Eukaryota	Acyltransferase, putative		Ricinus communis (Castor bean).	EEF35589.1	XP_002526783.1	B9SLB4	
Eukaryota	Acyltransferase, putative		Ricinus communis (Castor bean).	EEF35590.1	XP_002526784.1	B9SLB5	
Eukaryota	PREDICTED: hypothetical protein		Vitis vinifera		XP_002276028.1		
Eukaryota	Putative uncharacterized protein		Vitis vinifera (Grape).	CAN62551.1		A5AJT6	
Eukaryota	PREDICTED: hypothetical protein		Vitis vinifera		XP_002284511.1		
Eukaryota	Acyltransferase, putative		Ricinus communis (Castor bean).	EEF28222.1	XP_002534162.1	B9T7E3	
Eukaryota	Beta-ketoacyl-coa synthase family protein		Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa).	EEE83185.1	XP_002298380.1	B9GET3	
Eukaryota	Putative uncharacterized protein		Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa).	ABK95107.1		A9PFF4 [T]	
Eukaryota	Beta-ketoacyl-coa synthase family protein		Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa).	EEE87410.1	XP_002313455.1	B9HPL4	
Eukaryota	3-ketoacyl-CoA synthase 6		Gossypium hirsutum (Upland cotton) (Gossypium mexicanum).	ABX10441.1		A9XU47 [T]	
Eukaryota	3-ketoacyl-CoA synthase 3		Gossypium hirsutum (Upland cotton) (Gossypium mexicanum).	ABX10439.1		A9XU45 [T]	

Eukaryota	Very long-chain fatty acid condensing enzyme 3	2.3.1.-	Arabidopsis thaliana (Mouse-ear cress).	AAF75082.1, AAL16279.1, AAL32778.1, AAM91194.1	NP_172251.1	Q9LQP8 [T], Q9LQP8.2	
Eukaryota	Beta-ketoacyl-CoA synthase family protein		Arabidopsis lyrata subsp. lyrata.	EFH68673.1	XP_002892414.1	D7KH50	
Eukaryota	Beta-ketoacyl-CoA synthase family protein		Arabidopsis lyrata subsp. lyrata.	EFH57258.1	XP_002880999.1	D7LJM8	
Eukaryota	Very long-chain fatty acid condensing enzyme 12	2.3.1.-	Arabidopsis thaliana (Mouse-ear cress).	AAD24372.1, AAL07019.1, AAM14134.1, AAM61290.1	NP_180431.1	Q9SIB2 [T], Q9SIB2.1	
Eukaryota	PREDICTED: hypothetical protein		Vitis vinifera		XP_002263429.1		
Eukaryota	Putative FAE1		Oryza sativa subsp. japonica (Rice).	BAD23320.1, BAF24892.1	NP_001062978.1	Q6K558	
Eukaryota	Putative uncharacterized protein		Oryza sativa subsp. indica (Rice).	EAZ08784.1		A2Z0C3	
Eukaryota	Putative uncharacterized protein		Oryza sativa subsp. japonica (Rice).	EAZ44446.1		A3BY07	
Eukaryota	Putative uncharacterized protein		Zea mays (Maize).	ACF79160.1, ACN28898.1, ACN29014.1, ACN34671.1	NP_001130803.1	B4FAL7 [T]	
Eukaryota	Putative uncharacterized protein		Zea mays (Maize).	ACF87791.1		B4G098 [T]	
Eukaryota	Putative uncharacterized protein Sb02g022830		Sorghum bicolor (Sorghum) (Sorghum vulgare).	EER98791.1	XP_002462270.1	C5XAM8	

Subfamily 2J.

Type	Sequence	EC Number	Organism	GenBank ID	RefSeq	UniProt	PDB
Eukaryota	hypothetical protein		Volvox carteri f. nagariensis Eve	EFJ47586.1	XP_002951410.1		
Eukaryota	Fatty acid elongase 1		Giardia intestinalis ATCC 50581.	EET00530.1		C6LTY1	
Eukaryota	Fatty acid elongase 1		Giardia lamblia ATCC 50803.	EDO80427.1	XP_001708101.1	A8BBZ1	
Eukaryota	Putative uncharacterized protein		Perkinsus marinus ATCC 50983.	EEQ98033.1	XP_002765316.1	C5LZ24	
Eukaryota	Delta9-elongating activity protein		Perkinsus marinus.	ABF58686.1		A2T1W6 [T]	
Eukaryota	Putative uncharacterized protein		Perkinsus marinus ATCC 50983.	EEQ98028.1	XP_002765311.1	C5LZ19	
Eukaryota	3-ketoacyl-CoA synthase, putative	2.3.1.156	Entamoeba dispar SAW760.	EDR26861.1	XP_001736858.1	B0EF12	
Eukaryota	Fatty acid elongase, putative		Entamoeba histolytica.	EAL49013.1	XP_654403.1	C4M5I2	
Eukaryota	3-ketoacyl-CoA synthase, putative	2.3.1.74	Entamoeba dispar SAW760.	EDR28353.1	XP_001735448.1	B0EAU3	
Eukaryota	Fatty acid elongase, putative		Entamoeba histolytica.	EAL44771.2	XP_650157.2	C4M2E3	
Eukaryota	3-ketoacyl-CoA synthase, putative	2.3.1.74	Entamoeba dispar SAW760.	EDR30038.1	XP_001733822.1	B0E601	
Eukaryota	Fatty acid elongase, putative		Entamoeba histolytica.	EAL49183.1	XP_654571.1	C4LUY4	

Eukaryota	3-ketoacyl-CoA synthase, putative	2.3.1.41	Entamoeba dispar SAW760.	EDR25014.1	XP_001738646.1	B0EKC7	
Eukaryota	Fatty acid elongase, putative		Entamoeba histolytica.	EAL49265.1	XP_654651.1	C4LZ15	
Eukaryota	3-ketoacyl-CoA synthase, putative	2.3.1.41	Entamoeba dispar SAW760.	EDR27894.1	XP_001733313.1	B0EC46	
Eukaryota	Fatty acid elongase, putative		Entamoeba histolytica.	EAL50716.1	XP_656100.1	C4M9M6	
Eukaryota	Putative uncharacterized protein		Perkinsus marinus ATCC 50983.	EER09322.1	XP_002777506.1	C5L1S3	
Eukaryota	Putative uncharacterized protein		Perkinsus marinus ATCC 50983.	EER07757.1	XP_002775941.1	C5L6D0	
Eukaryota	3-ketoacyl-CoA synthase		Ectocarpus siliculosus Ec 32	CBN73964.1			
Eukaryota	Beta-ketoacyl-coa synthase		Thalassiosira pseudonana (Marine diatom).	EED92958.1	XP_002289421.1	B8BZW4	
Eukaryota	Condensing enzyme		Phaeodactylum tricornutum.	AAW70160.1, EEC49201.1	XP_002179378.1	B7FWF7, Q2TNU6 [T]	
Eukaryota	Fatty acid elongase 3-ketoacyl-CoA synthase		Polysphondylium pallidum PN500.	EFA74550.1		D3BVP7	
Eukaryota	Probable 3-oxoacyl-acyl-carrier protein synthase	2.3.1.41	Dictyostelium discoideum (Slime mold).	AAQ98882.1, EAL65577.1	XP_638938.1	Q6TMJ4	

KS2 outliers

Outliers

Type	Sequence	EC Number	Organism	GenBank ID	RefSeq	UniProt	PDB
Eukaryota	3-ketoacyl-CoA synthase		Dianthus caryophyllus (Carnation) (Clove pink).	BAI94499.1		D4QD77 [T]	
Eukaryota	Beta-ketoacyl-coa synthase family protein		Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa).	EEE94616.1	XP_002307620.1	B9H8F7	
Eukaryota	PREDICTED: hypothetical protein		Vitis vinifera		XP_002275067.1		
Eukaryota	Putative uncharacterized protein		Vitis vinifera (Grape).	CAN83354.1		A5BKV5	
Eukaryota	PREDICTED: hypothetical protein		Vitis vinifera		XP_002275004.1		
Eukaryota	Predicted protein		Physcomitrella patens subsp. patens.	EDQ55232.1	XP_001779915.1	A9TMU0	
Eukaryota	Putative uncharacterized protein		Picea sitchensis (Sitka spruce).	ADE76365.1		D5A9Z6 [T]	
Eukaryota	Beta-ketoacyl-CoA synthase		Dunaliella salina.	AAK11266.1		Q9AXE6 [T]	
Eukaryota	hypothetical protein		Volvox carteri f. nagariensis Eve	EFJ53061.1	XP_002946066.1		
Eukaryota	Predicted protein		Chlamydomonas reinhardtii.	EDP00465.1	XP_001697210.1	A8J6G8	
Eukaryota	Putative uncharacterized protein		Oryza sativa subsp. japonica (Rice).	EAZ16080.1		A3C4R7	
Eukaryota	Fatty acid elongase, putative, expressed		Oryza sativa subsp. japonica (Rice).	AAP53764.1		Q7XEM4	

Eukaryota	Fatty acid elongase		Zea mays (Maize).	ACG33906.1	NP_001149035.1	B6T9X3 [T]	
Eukaryota	Putative uncharacterized protein Sb01g021910		Sorghum bicolor (Sorghum) (Sorghum vulgare).	EER91618.1	XP_002464620.1	C5X1L0	
Eukaryota	Putative uncharacterized protein Sb01g046290		Sorghum bicolor (Sorghum) (Sorghum vulgare).	EER95458.1	XP_002468460.1	C5WWX3	
Eukaryota	Putative uncharacterized protein		Oryza sativa subsp. indica (Rice).	EAY88655.1		A2XCU5	
Eukaryota	Putative fatty acid elongase		Oryza sativa subsp. japonica (Rice).	AAN06858.1, ABF94124.1		Q8H7Z0	
Eukaryota	hypothetical protein		Selaginella moellendorffii	EFJ29917.1	XP_002968801.1		
Eukaryota	hypothetical protein		Selaginella moellendorffii	EFJ25133.1	XP_002974178.1		
Eukaryota	hypothetical protein		Selaginella moellendorffii	EFJ28141.1	XP_002970815.1		
Eukaryota	hypothetical protein		Selaginella moellendorffii	EFJ29634.1	XP_002969546.1		
Eukaryota	hypothetical protein		Selaginella moellendorffii	EFJ15018.1	XP_002984006.1		
Eukaryota	hypothetical protein		Selaginella moellendorffii	EFJ37673.1	XP_002960134.1		
Eukaryota	Putative uncharacterized protein Sb05g025040		Sorghum bicolor (Sorghum) (Sorghum vulgare).	AAD27560.1, AAM94300.1, EES08876.1	XP_002449888.1	Q9XEP1	
Eukaryota	Predicted protein		Physcomitrella patens subsp. patens.	EDQ79046.1	XP_001756180.1	A9RPU2	

Eukaryota	Predicted protein		Physcomitrella patens subsp. patens.	EDQ77204.1	XP_001757962.1	A9RVB4	
Eukaryota	FAE3		Marchantia polymorpha (Liverwort).	AAP74370.1		Q7XZE8	
Eukaryota	Putative uncharacterized protein		Oryza sativa subsp. indica (Rice).	EAY97658.1		A2Y3J8	
Eukaryota	Putative uncharacterized protein		Oryza sativa subsp. japonica (Rice).	EAZ18954.1		A3CCZ1	
Eukaryota	Os11g0591200 protein		Oryza sativa subsp. japonica (Rice).	BAF28547.1	NP_001068184.1	Q0IRW8	
Eukaryota	Beta-ketoacyl-CoA synthase, putative, expressed		Oryza sativa subsp. japonica (Rice).	ABA94525.1		Q2R1V7	
Eukaryota	Beta-ketoacyl-CoA-synthase		Marchantia polymorpha (Liverwort).	AAO48425.1		Q84VI8	
Eukaryota	Predicted protein		Physcomitrella patens subsp. patens.	EDQ56389.1	XP_001778803.1	A9TJJ8	
Eukaryota	hypothetical protein		Selaginella moellendorffii	EFJ14869.1, EFJ38351.1	XP_002960812.1, XP_002983857.1		

KS2 phylogenetic tree.