

NnAOX1a	1	M MNSK-LAALLLKQLGSATVRTVTMG---PLNG----ITTESSCFLHAS	41
NnAOX1b	1	M MKGSKMVGP <i>L</i> MQTAPRTFSTATTS---R <i>L</i> VTSEP---L <i>L</i> TGTTSF <i>I</i> YAA	45
AtAOX1a	1	M MITRGGA <i>K</i> AKSLLVAAGPRLFSTV---RTVSSHE--ALSASHILKPGV	45
LeAOX1a	1	M MTTRG-ATRMTRVVMGHMGPRYFSTTVLRNNPGTVGGVAAGLLHGLPA	49
LeAOX1b	1	M NRNAAM-KISGLLM-----RQLRGEFLPRGGM---VQIR--	31
NtAOX1	1	M MTTRG-ATRMTRTVLGHMGPRYFSTAIFRNDAGTGVMSGAVF-MHGVPA	48
VuAOX1	1	M MMMSRSCGN-----RVANAV---MLVAK---CLSCE-----V	26
 NnAOX1a	42	GPVVPGRTWIRFSCL-GV--RNGSTSALNNKEKEEKGVRTSSTVGGANR	88
NnAOX1b	46	AARTSVAS--IRLPVL-GV--RNGSTGALGGDEQTRNGLQTDSTGGTSDS	90
AtAOX1a	46	TSAWI---WTRAPTI-C-GMRFASATITLECEKTPMKEDANQKKTENEST	89
LeAOX1a	50	NPSEKAVVTWVRHFSAMGS--RSASTAAIMDKQQEKESSDKKVENTATAT	97
LeAOX1b	32	---II----WS-----N---MNTSSKTKEEQKTHINQPSIITDA	57
NtAOX1	49	NPSEKAVVTWVRHFPVMGS--RSAMSMALNDKQHDK---K-AENGAAA	91
VuAOX1	27	GGA-----RAF-Y-GGGVRSESTI.VT.PEKEKMEK-----KVGDG--	58
 NnAOX1a	89	PEDKMI-----V-SYWGMPPANLT K KDGSEWKWN S FRPWETY K ADLS	129
NnAOX1b	91	PSDKPKPI-----V-SYWGLVPSKV T KEDGT V WRWN S FRPWETY Q ADLS	133
AtAOX1a	90	GGDAACGNNKGDKGIA S YWGV E PNKIT K EDG S EWKWN C FRPWETY K ADIT	139
LeAOX1a	98	AAVG-NVG---KSVV S YWGV P PSKA T KPD G TEWKWN C FRPWETY E ADMS	143
LeAOX1b	58	TNAAG-DKAK---KTV-SYWGV D PPKTS K FDGT P WKWN S FRPWETY S ADIS	103
NtAOX1	92	TGGGDDGDE---KSVV S YWGV Q PSKV T KEDGT E WKWN C FRPWETY K ADLS	138
VuAOX1	59	-----GNKEQ-KGTV S YWGV E PSK T K EDGT E WKWN C FRPWETY K ADVS	101
		*	
NnAOX1a	130	I DLKKHHSPVT F MD K LAYWTVKALRYPTD I LF Q NRGYGRAM M LETVAAVP	179
NnAOX1b	134	I DLKKHH E PNK F LD K AYWTVK T LRYPTD I LF Q RRYGRAM M LETVAAVP	183
AtAOX1a	140	I DLKKHH V PTT F LD R IA Y WTVK S LRWPTD I LF Q RRYGRAM M LETVAAVP	189
LeAOX1a	144	I DLT K HAP V PT F LD K FA Y WTVK I LRFPTD V EF Q RRYGRAM M LETVAAVP	193
LeAOX1b	104	I D V R K HH M PT N FM D K FA Y WTVK Q SL K Y P TY T EF Q RRHMC I AM I LETVAAVP	153
NtAOX1	139	I DL I K H HA P TT F LD K FA Y WTVK S LRYPTD I LF Q RRYGRAM M LETVAAVP	188
VuAOX1	102	I DL I N K HH A PT T F LD K MA T WTVK T LRYPTD I LF Q RRYGRAM M LETVAAVP	151
		* =	
NnAOX1a	180	G MVG G ML L HL K SL R RF E HSGGWIK T L EEA E NERM H LM T F MEV S QP K WYE	229
NnAOX1b	184	G MVG G ML L HC K SL R RF E HSGGWIK K ALLE E NERM H LM T F MEV S QP K WYE	233
AtAOX1a	190	G MVG G ML L HC K SL R RF E QSGGWIK K ALLE E NERM H LM T F MEV A K P K WYE	239
LeAOX1a	194	G MVG G ML L HC K SL R RF E QSGGWIK K ALLE E NERM H LM T F MEV A K P N WYE	243
LeAOX1b	154	G MVG G ML L HC K SL R RF E HSGGWIK K ALLE E NERM H LM T F IEL S N P K WYE	203
NtAOX1	189	G MVG G ML L HC K SL R RF E QSGGWIK T L EEA E NERM H LM T F MEV A K P N WYE	238
VuAOX1	152	G MVG G ML L HL K SL R RF E HSGGWIK K ALLE E NERM H LM T F MEV A K P K WYE	201
		= =	
NnAOX1a	230	R ALVVAVQGVFFNTYFLGYLISPRFAHRVVGYLEEEE I HSYTEFL K ELDK	279
NnAOX1b	234	R ALV T VQGFFNAYFLAYLISPKL A HRVGYLEEEE I HSYTEFL K ELDK	283
AtAOX1a	240	R ALV T VQGVFFNAYFLGYLISPK A HRVGYLEEEE I HSYTEFL K ELDK	289
LeAOX1a	244	R ALVFAVQGVFFNAYFAAYLISPKL A HRVGYLEEEE V HSYTEFL K ELDN	293
LeAOX1b	204	R ALVFAVQGVFVNAYFIAYLASPKL A HRVGYLEEEE V HSYTEFL I DI E K	253
NtAOX1	239	R ALVFAVQGVFFNAYFV T YLLSPK A HRVGYLEEEE I HSYTEFL K ELDK	288
VuAOX1	202	R ALV T VQGVFFNAYFLGYMISPK A HRVGYLEEEE I HSYTEFL K ELDK	251
		= =	
NnAOX1a	280	G NI Q N V PAP A IA I D Y W Q LP P D S TL R D V V M V V R A DE A HH R D V N H F AS D I H D	329
NnAOX1b	284	G NI E N V PAP A IA I D Y W U LP P D S TL R D V V L V R A DE A HH R D V N H F AS D I H F	333
AtAOX1a	290	G NI E N V PAP A IA I D Y W R LP A D A TL R D V V M V V R A DE A HH R D V N H F AS D I H Y	339
LeAOX1a	294	G NI F N V PAP A IA I D Y W R LP K D A TL R D V V T V R A DE A HH R D V N H F AS D I H Y	343
LeAOX1b	254	G LF E N S PAP A IA I D Y W R LP A D A TL K D V V T V R A DE A HH R D I N H F AS D I QC	303
NtAOX1	289	G NI F N V PAP A IA I D Y W C RL P K D S TL D V V V V R A DE A HH R D V N H F AS D I H Y	338
VuAOX1	252	G NI E N V PAP A IA I D Y W Q LP P D S TL K D V V T V R A DE A HH R D V N H F AS D I H Y	301
		= =	
NnAOX1a	330	Q GYELKES P AP I GYH	344
NnAOX1b	334	Q QFLRE T P AP I GYH	348
AtAOX1a	340	Q GRELKE A P I GYH	354
LeAOX1a	344	Q QQLKD S P I GYH	358
LeAOX1b	304	Q CHELKG Y P I GYH	318
NtAOX1	339	Q QQLKD S P T GYH	353
VuAOX1	302	Q GREL R A P I GYH	316
		= =	

Supplemental Figure S1. Sequence alignment of NnAOX1a, NnAOX1b and AOX1 proteins from other dicot species. Bold characters highlight residues conserved across all of the AOX sequences in the alignment. The putative structural features are shown as described in the legend of Fig. 3.
Abbreviations and data sources: AtAOX1a, *Arabidopsis thaliana* AOX1a (NP_188876); LeAOX1a, *Lycopersicon esculentum* AOX1a (AAK58482); LeAOX1b, *L. esculentum* AOX1b (AAK58483); NtAOX1, *Nicotiana tabacum* AOX1 (AAC60576); VuAOX1, *Vigna unguiculata* AOX1 (AAZ09196).