

Consensus	1	10	20	30	40	50	60	70	80	90	100	MVPDVLREAXXLXXDAKLVAPQAEPWKFQJSYTNVVI FGYLHJXG IYGLXFCVSKAHWATJFFSFILLXASVIGV TAGAHRLWSHRSYKANLPLQ IILMLXXSLSG
												+ intron 1 (1)
Cobl_desat3	MVPDVLREAE	ERLHEDAKLVAPQAEPWKFQ	ISYTNVVI FGYLHLAG	IYGLLFCVSKAHWATL	FFSFILLVASVIGV TAGAHRLWSHRSYKANLPLQ	IILMLFHSLSG						
Poct_desat3	MVPDVLREAD	DPLQADAKLVAPQAEPWKFQ	ISYTNVVI FGYLHLSG	IYGLLFCVSKAHWATL	FFSFILLIASVIGV TAGAHRLWSHRSYKANLPLQ	IILMLMQSLSG						
PexcS_desat3	MVPDVLREAE	ERLQDDAKLVAPQAEPWKFQ	LSYTNVVI FGYLHISG	IYGLLFCVSKAHWATI	FFSFILLVASVIGV TAGAHRLWSHRSYKANLPLQ	IILMLFHSLSG						
Pnot_desat3	MVPDVLREAE	ERLQDDAKLVAPQAEPWKFQ	LSYTNVVI FGYLHISG	IYGLLFCVSKAHWATI	FFSFILLVASVIGV TAGAHRLWSHRSYKANLPLQ	IILMLFHSLSG						
Consensus	110	120	130	140	150	160	170	180	190	200	210	QYTA FNWARDHRLH HKYS DTDADPHNATR GFFYSHIGWLLVVKHP EVXXRGEXIDLS D LLRN PVLTFQRKNVVL I LXLXC YIMP TXVPMXFWG E T FHXAWH IMA LR
												+ intron 2 (2)
												+ intron 3 (2)
Cobl_desat3	QYTA FNWARDHRLH HKYS DTDADPHNATR GFFYSHIGWLLVVKHP EVKR	RGEA IDLS D LLRN PVLTFQRKNVVL I LSLV	LCYIMP T TVPMF	FWG E T FHTAWH IMA LR								
Poct_desat3	QYTA FNWARDHRLH HKYS DTDADPHNATR GFFYSHIGWLLVVKHP EVRKR	RGEA IDLS D LLRN PVLTFQRKNVVL I LALV	LCYIMP T AVPMY	FWG E T FHNAWH IMA LR								
PexcS_desat3	QYTA FNWARDHRLH HKYS DTDADPHNATR GFFYSHIGWLLVVKHP EVRKR	RGEA IDLS D LLRN PVLTFQRKNVVL I LALV	LCYIMP T AVPMY	FWG E T FHNAWH IMA LR								
Pnot_desat3	QYTA FNWARDHRLH HKYS DTDADPHNATR GFFYSHIGWLLVVKHP EVRKR	GET IDLS D LLRN PVLTFQRKNVVL I LSLV	LCYIMP T AVPMY	FWG E T FHNAWH IMA LR								
Consensus	220	230	240	250	260	270	280	290	300	310	FVLC LNF XSLINSAAH XFGXKP YDKXIMP TQ NMSVTLATL GEGFHNYHHVFPFDYRAA ELGNNTFNL TTKFIDFFA XIGWA XXLK TVGXES IXRRAZR TGDGS XXW	
Cobl_desat3	FVLC LNFVSLINSAAH TFGTKPYDKN	IMP TQ NMSVTLATL GEGFHNYHHVFPFDYRAA ELGNNTFNL TTKFIDFFA	LIGWASDLK TVGQES	IVRRAERTGDGS GSW								
Poct_desat3	FVLC LNFISLINSAAH TFGNKPYDKS	IMP TQ NMSVTLATL GEGFHNYHHVFPFDYRAA ELGNNTFNL TTKFIDFFA	MIGWATA LK TVGHES	ILRRAQRTGDGS LTW								
PexcS_desat3	FVLC LNFISLINSAAH TFGNKPYDKS	IMP TQ NMSVTLATL GEGFHNYHHVFPFDYRAA ELGNNTFNL TTKFIDFFA	MIGWATA LK TVGHES	IARRAQRTGDGS LTW								
Pnot_desat3	FVLC LNFVSLINSAAH AFGNKPYDKN	IMP TQ NMSVTLATL GEGFHNYHHVFPFDYRAA ELGNNTFNL TTKFIDFFA	MIGWATDLK TVGRES	ILRRAQRTGDGS LSW								
Consensus	320	330	333	XXXC XVV XG XXXSG *								
Cobl_desat3	KEECKVVP	GGLKSG *										
Poct_desat3	ESDCEVVP	GGFQSG *										
PexcS_desat3	KSDCEVVP	GGLKSG *										
Pnot_desat3	KSDCEVVS	GVLKSG *										