

NP_568270.3	1	MTEGIRARGPRSSSVNSVPLILDIEDFKGDFSFDALFGNLVNDLLPSFLDEEADSGDGHG	60
AK222187	1	MTEGIRARGPRSSSVNSVPLILDIEDFKGDFSFDALFGNLVNDLLPSFLDEEADSGDGHG	60
AF479280	1	MTERIRARGPRSSSVNSVPLILDIEDFKGDFSFDALFGNLVNDLLPSFLDEEADSGDGHG	60
NP_568270.3	61	NIAGVDGLTNGHLRGQSAPLSSAPFFPEVDGLLSLFKDACKELVDLRKQVDGRLNTLKKE	120
AK222187	61	NIAGVDGLTNGHLRGQSAPLSSAPFFPEVDGLLSLFKDACKELVDLRKQVDGRLNTLKKE	120
AF479280	61	NIAGVDGLTNGHLRGQSAPLSSAPFFPEVDGLLSLFKDACKELVDLRKQVDGRLNTLKKE	120
NP_568270.3	121	VSTQDSKHKRTLTEIEKGVDGLFESFARLDGRISSVGQTAAKIGDHLQSADAQRETASQT	180
AK222187	121	VSTQDSKHKRTLTEIEKGVDGLFESFARLDGRISSVGQTAAKIGDHLQSADAQRETASQT	180
AF479280	121	VSTQDSKHKRTLTEIEKGVDGLFESFARLDGRISSVGQTAAKIGDHLQSADAQRETASQT	180
NP_568270.3	181	IDLIKYLMEFNGSPGDLMELSALFSDDSRVAAEASIAQKLRSFAEEDIGRQGASAAAGNA	240
AK222187	181	IDLIKYLMEFNGSPGDLMELSALFSDDSRVAAEASIAQKLRSFAEEDIGRQGASAAAGNA	240
AF479280	181	IDLIKYLMEFNGSPGDLMELSALFSDDSRVAAEASIAQKLRSFAEEDIGRQGASTAAGNA	240
NP_568270.3	241	TPGRGLEVAVANLQDYCNELENRLLSRFDAASQRRDLSTMSECAKILSQFNRGTSAMQHY	300
AK222187	241	TPGRGLEVAVANLQDYCNELENRLLSRFDAASQRRDLSTMSECAKILSQFNRGTSAMQHY	300
AF479280	241	TPGRGLEVAVANLQDYCNELENRLLSRFDAASQRRDLSTMSECAKILSQFNRGTSAMQHY	300
NP_568270.3	301	VATRPMFIDVEVMNSDIRLVLGDHGSGQSPSNVARGLSALFKEITDVRKEAATITAVFP	360
AK222187	301	VATRPMFIDVEVMNSDIRLVLGDHGSGQSPSNVARGLSALFKEITDVRKEAATITAVFP	360
AF479280	301	VATRPMFIDVEVMNSDIRLVLGDHGSGQSPSNVARGLSALFKEITDVRKEAATITAVFP	360
NP_568270.3	361	TPNEVMAILVQRVLEQRVTGILDKILAKPSLMSPPPVQEGGLLYLRMLAVAYERTQELA	420
AK222187	361	TPNEVMAILVQRVLEQRVTGILDKILAKPSLMSPPPVQEGGLLYLRMLAVAYERTQELA	420
AF479280	361	TPNEVMAILVQRVLEQRVTGILDKILAKPSLMSPPPVQEGGLLYLRMLAVAYERTQELA	420
NP_568270.3	421	KDLRAVGCGDLVDVLDLTSLSFSSHKDEYPEHERASLKQLYQAKMEELRAESQQVSESSGT	480
AK222187	421	KDLRAVGCGDLVDVLDLTSLSFSSHKDEYPEHERASLKQLYQAKMEELRAESQQVSESSGT	480
AF479280	421	KDLRAVGCGDLVDVLDLTSLSFSSHKDEYPEHERASLKQLYQAKMEELRAESQQVSESSGT	480
NP_568270.3	481	IGRSKGASISSSLQQISVTVVTD FVRWNEEAITRCTLFSSQPATLAANVKAIFTCLLDQV	540
AK222187	481	IGRSKGASISSSLQQISVTVVTD FVRWNEEAITRCTLFSSQPATLAANVKAIFTCLLDQV	540
AF479280	481	IGRSKGASISSSLQQISVTFVTE FVRWNEEAITRCTLFSSQPATLAANVKAIFTCLLDQV	540
NP_568270.3	541	SVYITEGLERARDSLSEAAALRERFVLG RRVAAAAASAAEAAAAAGESSFKSFMVA	596
AK222187	541	SVYITEGLERARDSLSEAAALRERFVLG RRVAAAAASAAEAAAAAGESSFKSFMVA	596
AF479280	541	SVYITEGLERARDSLSEAAALRERFVLGTSVSRVAAAAASAAEAAAAAGESSFKSFMVA	600
NP_568270.3	597	VQRCGSSVAIVQQYFANSISRLLLPVDGAHAASCEEMSTALSKAEAAAYKGLQQCIETVM	656
AK222187	597	VQRCGSSVAIVQQYFANSISRLLLPVDGAHAASCEEMSTALSKAEAAAYKGLQQCIETVM	656
AF479280	601	VQRCGSSVAIVQQYFANSISRLLLPVDGAHAASCEEMSTALSKAEAAAYKGLQQCIETVM	660
NP_568270.3	657	AEVDRLLSSEQKSTDYRSDDG IASDHRPTNACIRVVAYLSRVLESFAFTALEGLNKQAF L	716
AK222187	657	AEVDRLLSSEQKSTDYRSDDG IASDHRPTNACIRVVAYLSRVLESFAFTALEGLNKQAF L	716
AF479280	661	AEVDRLLSSEQKSTDYRSPDDG IASDHRPTNACIRVVAYLSRVLESFAFTALEGLNKQAF L	720
NP_568270.3	717	TELGNRLEKLLLTHWQKFTFNPSGGLRLKRDLNEYVGFVKSFSGAPSVDEKFELLG I IANV	776
AK222187	717	TELGNRLEKLLLTHWQKFTFNPSGGLRLKRDLNEYVGFVKSFSGAPSVDEKFELLG I IANV	776
AF479280	721	TELGNRLEKLLLTHWQKFTFNPSGGLRLKRDLNEYVGFVKSFSGAPSVDEKFELLG I IANV	780
NP_568270.3	777	FIVAPDSLPTLFEGSPSIRKDAQRF IQLREDYKSAKLATKLSSLWPSLS	825
AK222187	777	FIVAPDSLPTLFEGSPSIRKDAQRF IQLREDYKSAKLATKLSSLWPSLS	825
AF479280	781	FIVAPDSLPTLFEGSPSIRKDAQRF IQLREDYKSAKLATKLSSLWPSLS	829

Figure S3. Alignment of predicted SEC10a and SEC10b protein sequences.

An alignment of predicted protein sequences of the AK222187 cDNA (*SEC10a*), AF479280 cDNA (*SEC10b*), and a conceptual protein NP_568270.3 based on the reference cDNA sequence NM_121275.4, corresponding to *SEC10a* by its coding sequence.