(A) SEQUENCE COVERAGE OF Cm_FTL1

MPRNRDPLVVGRVIGDVVDSFSRSISIRVVYDSREVNNGCELKPSQAVNKPRVEIGGTDLRTFFTLVMVDPDAPSPSDPNLREYLHWLVTDIPATTEATFGQEIVCYENPRPTVGIHRFVLVLFRQLGRQTVYAPGWRQNFNTRHFAELYNLGSPVAAVYFNCQRENGSGGRRRAGDECS

Amino acid sequence coverage: 31.7%
Peptide observed:

Sequence	charge	Xcorr	ΔCn
DPLVVGR	2	2.55	0.88
VEIGGTDLR	2	2.80	0.79
VEIGGTDLR	1	1.60	0.90
QTVYAPGWR	2	2.25	-
VIGDVVDSFSR	2	2.16	-
TFFTLVMoxVDPDAPSPSDPNLR	3	3.81	-
TFFTLVMoxVDPDAPSPSDPNLR	2	4.27	-
TFFTLVMVDPDAPSPSDPNLR	2	3.86	-
TFFTLVMVDPDAPSPSDPNLR	3	3.13	-

(B) SEQUENCE COVERAGE OF Cm_FTL2

MPRDRDPLVVGRVIGDVIDSFTKSISIRATYNNREISNGCELKPSQVVNQPRVEIGGTDLRTFFTLVMVDPDAPSPSDPNLREYLHWLVTDIPATTGANFGQEIVCYESPRPTVGIHRLVLVLFRQLGRQTVYAPGRQNFNTRDFAELYNLGLPVAAVYFNCQRESGSGGRRRTQDDF

Amino acid sequence coverage: 74.9%
Peptide observed:

Sequence	charge	Xcorr	ΔCn
DPLVVGR	2	2.55	0.88
DRDPLVVGR	2	2.74	0.37
EISNGCELKPSQVVNQPR	3	4.26	-
EISNGCELKPSQVVNQPR	2	4.55	-
VEIGGTDLR	2	2.85	0.86
VEIGGTDLR	1	1.63	0.83
QTVYAPGWR	2	2.25	-
VIGDVIDSFTK	2	3.44	0.38
TFFTLVMoxVDPDAPSPSDPNLR	3	3.81	-
TFFTLVMoxVDPDAPSPSDPNLR	2	4.27	-
LVLVLFR	1	1.67	0.96
TFFTLVMVDPDAPSPSDPNLR	2	3.86	-
TFFTLVMVDPDAPSPSDPNLR	3	3.13	-
EYLHWLVTDIPATTGANFGQEIVCYESPR	3	4.28	-
DFAELYNLGLPVAAVYFNCQR	3	7.52	0.99
DFAELYNLGLPVAAVYFNCQR	2	4.46	-

Supplemental Figure 5: Typical sequence coverage and identified peptides for Cm_FTL1 and Cm_FTL2 from LC-MS/MS data analysis. SEQUEST search was performed with Xcorr cut-off values of 1.5, 2.0, and 2.5 for singly, doubly, and triply charged ions. All the matched tandem MS spectra were subjected to manual validation. Sequence coverage of 74.9% and 31.7% was obtained for Cm_FTL1 and Cm_FTL2, respectively.