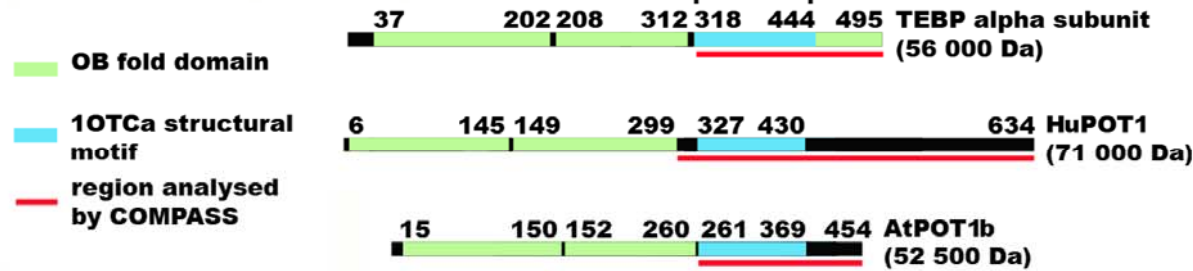


TEBP αL...I..K.....P.....H.....TL....T..EVT.....V...V..AY.....K.C.L....E.....L.L.....L.D.T.R.H....DDC
 HuPOT1 E.....L.....H..L..TPL...LK..K.P..YRIRA.LR.....KPRR.....VK.....C.K.C..L..VP.E.....ILQ.....L...S.Y....T...C
 AtPOT1L..TEI..KM..LPITPL..L..N..T..E.....R...TQF.V.KI.P..V...VKAYD.K.KK..SLK..PG.G..E.I.QVQFLVK..AST.LND.TYRI.LYTHD..G
 10CTa N..AVVL..TEVDKKHAALPSTSLQDLFHHADSDKELQAQDTFR...TQFYVTKIEPSDVKEWVKGYDRKTKKSSSLKGASGKG..DNIFQVQFLVK.dASTOLNNNTYRVLLYTQDGLG

Amino acids identities in 10TCa motifs of C-terminal regions from TEBP alpha subunit, HuPOT1 and AtPOT1b



A

Query	Subject	Smith-Waterman score	E value score
TEBP α subunit		329	3.90e-52
HuPOT1	10TCa	166	4.90e-15
AtPOT1b		119	4.25e-09

B

Supplementary Figure 1. Schematic depiction of amino acid identities in 10TCa motifs of three representative POT1-like proteins (A) and their structural similarity to 10TCa evaluated by COMPASS sequence profile program (Sadreyev and Grishin, 2003).