

protein construct	aa sequence
SBP-mTFP1	MGSSHHHHHHHSQDPMDEKTTGWRGGHVVEGLAGELEQLRARLEHHHPQGQREPGDPMVSKGEETTMGVIKPDMKIKLKMEGNVNGHAFVIEGEGEGKPYDGTNTINLEVKEGAPLPFSYDILTAFAYGNRAFTKYPDDIPNYFKQSFPEGYSWERTMTFEDKGIVKVKSDISMEEDSFIYEIHLKGENFPPNGPVMQKKTGWDASTERMYVRDGLKGDVKKHLLLEGGGHRVDFKTIYRAKKAVKLPDYHFVDHRIEILNHDKDYNKVTVYESAVARNSTDMDELYK*
His-mTFP1	MGSSHHHHHHHSQDPMVSKGEETTMGVIKPDMKIKLKMEGNVNGHAFVIEGEGEGKPYDGTNTINLEVKEGAPLPFSYDILTAFAYGNRAFTKYPDDIPNYFKQSFPEGYSWERTMTFEDKGIVKVKSDISMEEDSFIYEIHLKGENFPPNGPVMQKKTGWDASTERMYVRDGLKGDVKKHLLLEGGGHRVDFKTIYRAKKAVKLPDYHFVDHRIEILNHDKDYNKVTVYESAVARNSTDMDELYK*
His-1238_E11-FLAG	MRGSHHHHHHHHSGDLGKKLLEAARAGQDDEVRI LMANGADV NATDVGMTPLHLAAWKGHLEIVEVLLKTGADVNAHDVFGTTPHLAAHRGHLEIVEVLLKAGADVNAQDMVGKTPHLHLAAYYGHLEIVEVLLKHGADVNAQDKFGKTPFDLAIDNGNEDIAEVLQKAAKLN DYKDDDDK*
His-1238_G01-FLAG	MRGSHHHHHHHHSGDLGKKLLEAARAGQDDEVRI LMANGADVNAEDWGMATPLHLAAQSGHLEIVEVLLKTGADVNAHDVFGWTPHLAASQGHLEIVEVLLKAGADV NATDMVGRTPHLHLAARRGHLEIVEVLLKHGADVNAQDKFGKTPFDLAIDNGNEDIAEVLQKAAKLN DYKDDDDK*
1238_E11-mCherry	MRGSHHHHHHHHSGDLGKKLLEAARAGQDDEVRI LMANGADV NATDVGMTPLHLAAWKGHLEIVEVLLKTGADVNAHDVFGTTPHLAAHRGHLEIVEVLLKAGADVNAQDMVGKTPHLHLAAYYGHLEIVEVLLKHGADVNAQDKFGKTPFDLAIDNGNEDIAEVLQKAAKLN DYKDDDDK AAAMVSKGEEDNMAI I KEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADI PDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPMQKKTMGWEASSERMPEDGALKGEIKQRLKLDG GHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDY TIVEQYERAEGRHSTGGMDELYK*
1238_E11-YPet	MRGSHHHHHHHHSGDLGKKLLEAARAGQDDEVRI LMANGADV NATDVGMTPLHLAAWKGHLEIVEVLLKTGADVNAHDVFGTTPHLAAHRGHLEIVEVLLKAGADVNAQDMVGKTPHLHLAAYYGHLEIVEVLLKHGADVNAQDKFGKTPFDLAIDNGNEDIAEVLQKAAKLN DYKDDDDK AAAMVSKGEELFTGVVPI LVELDGDVNGHKFSVSGEGEGDATYGKLT LKLLCTTGKLPVPWP TLVTT LGYGVQCFARYPDHMKQHDFFKSAMPEGYVQERTIFFKD DGNYKTRAEVKFEEDTLVNRIELKGI DFKEDGNILGHKLEYNYN SHNVYITADKQKNGIKANFKIRHNIEDG GVLADHYQQNTPIGDGPVLLPDNHLYSYQSALFKDPNEKRDHMLLEFLTAAGITEGMNELYKDI*
1238_G01-mCherry	MRGSHHHHHHHHSGDLGKKLLEAARAGQDDEVRI LMANGADVNAEDWGMATPLHLAAQSGHLEIVEVLLKTGADVNAHDVFGWTPHLAASQGHLEIVEVLLKAGADV NATDMVGRTPHLHLAARRGHLEIVEVLLKHGADVNAQDKFGKTPFDLAIDNGNEDIAEVLQKAAKLN DYKDDDDK AAAMVSKGEEDNMAI I KEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADI PDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPMQKKTMGWEASSERMPEDGALKGEIKQRLKLDG GHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDY TIVEQYERAEGRHSTGGMDELYK*
1238_G01-YPet	MRGSHHHHHHHHSGDLGKKLLEAARAGQDDEVRI LMANGADVNAEDWGMATPLHLAAQSGHLEIVEVLLKTGADVNAHDVFGWTPHLAASQGHLEIVEVLLKAGADV NATDMVGRTPHLHLAARRGHLEIVEVLLKHGADVNAQDKFGKTPFDLAIDNGNEDIAEVLQKAAKLN DYKDDDDK AAAMVSKGEELFTGVVPI LVELDGDVNGHKFSVSGEGEGDATYGKLT LKLLCTTGKLPVPWP TLVTT LGYGVQCFARYPDHMKQHDFFKSAMPEGYVQERTIFFKD DGNYKTRAEVKFEEDTLVNRIELKGI DFKEDGNILGHKLEYNYN SHNVYITADKQKNGIKANFKIRHNIEDG GVLADHYQQNTPIGDGPVLLPDNHLYSYQSALFKDPNEKRDHMLLEFLTAAGITEGMNELYKDI*
1238_E11-YPet-CAAX	MRGSHHHHHHHHSGDLGKKLLEAARAGQDDEVRI LMANGADV NATDVGMTPLHLAAWKGHLEIVEVLLKTGADVNAHDVFGTTPHLAAHRGHLEIVEVLLKAGADVNAQDMVGKTPHLHLAAYYGHLEIVEVLLKHGADVNAQDKFGKTPFDLAIDNGNEDIAEVLQKAAKLN DYKDDDDK AAAMVSKGEELFTGVVPI LVELDGDVNGHKFSVSGEGEGDATYGKLT LKLLCTTGKLPVPWP TLVTT LGYGVQCFARYPDHMKQHDFFKSAMPEGYVQERTIFFKD DGNYKTRAEVKFEEDTLVNRIELKGI DFKEDGNILGHKLEYNYN SHNVYITADKQKNGIKANFKIRHNIEDG GVLADHYQQNTPIGDGPVLLPDNHLYSYQSALFKDPNEKRDHMLLEFLTAAGITEGMNELYK LQGGGRSK LNPPDESGPGCMSCCKVLS*
1238_G01-YPet-CAAX	MRGSHHHHHHHHSGDLGKKLLEAARAGQDDEVRI LMANGADVNAEDWGMATPLHLAAQSGHLEIVEVLLKTGADVNAHDVFGWTPHLAASQGHLEIVEVLLKAGADV NATDMVGRTPHLHLAARRGHLEIVEVLLKHGADVNAQDKFGKTPFDLAIDNGNEDIAEVLQKAAKLN DYKDDDDK AAAMVSKGEELFTGVVPI LVELDGDVNGHKFSVSGEGEGDATYGKLT LKLLCTTGKLPVPWP TLVTT LGYGVQCFARYPDHMKQHDFFKSAMPEGYVQERTIFFKD DGNYKTRAEVKFEEDTLVNRIELKGI DFKEDGNILGHKLEYNYN SHNVYITADKQKNGIKANFKIRHNIEDG GVLADHYQQNTPIGDGPVLLPDNHLYSYQSALFKDPNEKRDHMLLEFLTAAGITEGMNELYK LQGGGRSK LNPPDESGPGCMSCCKVLS*

1238_E11-YPet-H2B MRGSHHHHHHHH GSDLGKKLLEAARAGQDDEVRI LMANGADV NATDWVGMTPLHLAAWKGHLEIVEVLLKTG
 ADVNAHDVFGTTPHLHLAAHRGHLEIVEVLLKAGADVNAQDMVGKTPHLHLAAYYGHLEIVEVLLKHGADVNAQ
 DKFGKTPFDLAI DNGNEDIAEVLQKAAKLN DYKDDDDK AAAMVSKGEELFTGVVPI LVELDGDVNGHKFSVS
 GEGEGDATY GKLT LKLLCTTGKLPVPWP TLVTT LGYGVQC FARYPDHMKQHDFFKSAMPEGYVQERTIFFKD
 DGNKYTRAEVKFEGDTLVNRIELKGI DFKEDGNILGHKLEYNYN SHNVYITADKQKNGIKANFKIRHNIEDG
 GVQLADHYQQNTPIGDGPVLLPDNHYSYQSALFKDPNEKRDHMVLEFLTAAGITEGMNELYK DIMPEPAK
 SAPAPKKGSKKAVTKAQKGGKKRKR SRKESYSIYVYKVLKQVHPDTGISSKAMGIMNSFVNDIFERIAGEA
 SRLAHYNKRSTITSREIQ TAVRLLLPGELAKHAVSEGTKAITKY TSAK*

1238_G01-YPet-H2B MRGSHHHHHHHH GSDLGKKLLEAARAGQDDEVRI LMANGADVNAEDWGMATPLHLAAQSGHLEIVEVLLKTG
 ADVNAHDVFGTTPHLHLAASQGHLEIVEVLLKAGADV NATDMVGRTPHLHLAARRGHLEIVEVLLKHGADVNAQ
 DKFGKTPFDLAI DNGNEDIAEVLQKAAKLN DYKDDDDK AAAMVSKGEELFTGVVPI LVELDGDVNGHKFSVS
 GEGEGDATY GKLT LKLLCTTGKLPVPWP TLVTT LGYGVQC FARYPDHMKQHDFFKSAMPEGYVQERTIFFKD
 DGNKYTRAEVKFEGDTLVNRIELKGI DFKEDGNILGHKLEYNYN SHNVYITADKQKNGIKANFKIRHNIEDG
 GVQLADHYQQNTPIGDGPVLLPDNHYSYQSALFKDPNEKRDHMVLEFLTAAGITEGMNELYK DIMPEPAK
 SAPAPKKGSKKAVTKAQKGGKKRKR SRKESYSIYVYKVLKQVHPDTGISSKAMGIMNSFVNDIFERIAGEA
 SRLAHYNKRSTITSREIQ TAVRLLLPGELAKHAVSEGTKAITKY TSAK*

H2B-mTFP1 MPEPAKSAPAPKKGSKKAVTKAQKGGKKRKR SRKESYSIYVYKVLKQVHPDTGISSKAMGIMNSFVNDIFE
 RIAGEASRLAHYNKRSTITSREIQ TAVRLLLPGELAKHAVSEGTKAITKY TSAKDPMVSKGEETTMGVIKPD
 mTFP1-CAAX MVSKGEETTMGVIKPDMKIKLMEGNVNGHAFVIEGEGEKPYDGTNTINLEVKEGAPLPFSYDILTTFAY
 GNRAFTKY PDDIPNYFKQSFPEGYSWERTMTFEDKGI VVKVSDI SMEEDSFIYEIHLKGENFPNGPVMQKK
 TTGWDASTERMYVRDGV LKGDVKHKLLEGGGHRVDFKTIYRAKAVKLPDYHFVDHRIEILNHDKDYNKV
 TVYESAVARNSTDGMDELYKLQGGGRSKLNPPDESGPGCMSCKCVLS*

mito-mTFP1 MSLTSSSSVRVEWIAAVTIAAGTAAIGYLAYKRFYVKDHRNKAMINLHIQKDNPKIVHAGSLPVAEFGMVSK
 GEETTMGVIKPDMKIKLMEGNVNGHAFVIEGEGEKPYDGTNTINLEVKEGAPLPFSYDILTTFAYGNRA
 FTKY PDDIPNYFKQSFPEGYSWERTMTFEDKGI VVKVSDI SMEEDSFIYEIHLKGENFPNGPVMQKKTGW
 DASTERMYVRDGV LKGDVKHKLLEGGGHRVDFKTIYRAKAVKLPDYHFVDHRIEILNHDKDYNKVTVYE
 SAVARNSTDGMDELYKGGGAAADR SITRATMTSFVQSGPEELLSKNYHLENEVARLKKTAVNIWIDHNTRV
 *

mTFP1-Rab5c MVSKGEETTMGVIKPDMKIKLMEGNVNGHAFVIEGEGEKPYDGTNTINLEVKEGAPLPFSYDILTTFAY
 GNRAFTKY PDDIPNYFKQSFPEGYSWERTMTFEDKGI VVKVSDI SMEEDSFIYEIHLKGENFPNGPVMQKK
 TTGWDASTERMYVRDGV LKGDVKHKLLEGGGHRVDFKTIYRAKAVKLPDYHFVDHRIEILNHDKDYNKV
 TVYESAVARNSTDGMDELYKVV TMAGRGGPARTNGAAPVGNKICQFKLVLLGESAVGKSSLVLRVFKGFHE
 YQESTIGAAFLTQTLCLDDTTVKFEIWDTAGQERYHSLAPMYRGAQA AIVVYDITNTDFTTRAKNWKELQ
 RQASPNIVIALAGNKADLAN KRAVDFQEAQAYADDNSLLFMETS AKTAMNVNEIFMAI AKKLPKSEPQGGAG
 SGGRRAGGVDLQETAPQGRSGQCCGGGN*