



D

PTBP2	1	MDGIVTEVAVGVKRGSDLLSGSVLSPNSNMSSMVVTANGNDSKKFKGEDKMDGAPSRV	60
PTBP1	1	MDGIV++AVG-KRGSDLL-S-V+P-S+...ANGNDSKKFKG++-G-PSRV	60
PTBP2	61	LRHKLPGEVETEVIALGLPFGKVTNIMLKGKQAFLELATEAAITMVNYSAVTPH	120
PTBP1	61	LRHKLPGIDVTEGEVISLGLPFGKVTNIMLKGKQAFIEMNTEEAANTMVNYTSVTFV	120
PTBP2	121	LRNQPPIYIQSNHKLKTDNTLNQRAQAVLQA-VTAQTAN--TPLSGTTVSESAVTPAQ	177
PTBP1	121	LRNQPPIYIQSNHKLKTDSSPNQARAQALQAVNSVQSGNLALAASAAVDAGMAMAGQ	180
PTBP2	178	SPVLRIRIINDMYYPVTLDLVHQIFSKFGVLKIIITFTKNNQFQALLQYQDPVNAQAQAKLA	237
PTBP1	181	SPVLRIRIIVENLFYPVTLDLVHQIFSKFGVLKIIITFTKNNQFQALLQYADVPVSAQHAQKLS	240
PTBP2	238	LDGQNIYNACCTLRIDFSKLVNLNVKYNNDKSRDYTRPDLPSGDGQPALDPAIAAFAKE	297
PTBP1	241	LDGQNIYNACCTLRIDFSKLVNLNVKYNNDKSRDYTRPDLPSGDGQPALDPAIAAFAKE	300
PTBP2	298	TSLLAPE--GALSP--LAIPNAAAAAAGRVGMP-----GVSAG	335
PTBP1	301	GIISAPYAGAGFPPTFAIPQAAGLVNPNVHGALAPLAIPSAAGRAIIPGLAGA	360
PTBP2	336	GNTVLLVSNLNEEMVTPQSLFTLFGVIGDVQVRVKILYNKKDSALIQADGNQSGLAMNHL	395
PTBP1	361	GNTVLLVSNLNEEMVTPQSLFTLFGVIGDVQVRVKILYNKKDSALIQADGNQSGLAMNHL	420
PTBP2	396	NGQRMKGKIRIVTLKSHQTVLPREGLDQGLTKDFGNSPLHRFKKPGSKNFQNIFFPPSA	455
PTBP1	421	NGHKLHGKPIRITLSKHQVQLPREGQEDQGLTKDYGNSSPLHRFKKPGSKNFQNIFFPPSA	480
PTBP2	456	TLHLSNIPPSVAEEDLRLTFANTGVTGKFAKFFQ-DHKMALLQMATVEEAQALIDLHNY	514
PTBP1	481	TLHLSNIPPSVAEEDLRLTFANTGVTGKFAKFFQ-DHKMALLQMATVEEAQALIDLHNY	540
PTBP2	515	NLGENHHLRVFSKSTI	531
PTBP1	541	DLGENHHLRVFSKSTI	557

