

TB	-----MTEKEDIVQRAKLAEQAERYDDMAAMKKVTEG-----	35
TS	-----MSEKEDIVQRAKLAEQAERYDDMAAMKKVTEG-----	35
HC	-----MADNKDELVQRAKLAEQAERYDDMAQSMKVTEG-----	36
DI	-----MAENKDELVQRAKLAEQAERYDDMAQSMKVTEG-----	36
CE	-----MSDGKEELVNRAKLAEQAERYDDMAASMKVTEG-----	36
BX	-----MSDGKDELVQRAKLAEQAERYDDMAQSMKVTELG-----	36
AM	-----MSVDKEELVQRAKLAEQAERYDDMAAAMKAVTEG-----	36
HV	-----MTDKEEQVQRAKLAEQAERYDDMAAMKKVTESGA-----	35
HS	-----MDKNELVOKAKLAEQAERYDDMAACMKSVTEOGA-----	34
SB	-----MTTSWVLQCKDLSNTLVHIAKLAEQAERYDDMAAMKKRYTEASG-----	45
HM	-----MVDVSSTEWLKDPLLRDRESLVYTAKCQEQAERFDDMAICMKVEVTNFDQ-----	49
EG	-----MAELLSTEWLKDLPLKRDSYVNTAKCQEQAERFDDMAVCMKEVTRFDK-----	49
EM	-----MAAITSWITDSGCKHHASLVSIAKLAEQAERYEDMAVAMKTIAEMGN-----	47
TG	MVSTDIAFSSAKKSTRRPLLVLHRPARDFVFLRFPFFSGHFPSFPLLLSCVPVSTMEEIKNLREYIVYAKLAEQAERYDEMAEAMKNLVENCLDEQ-----	100
ET	-----MIEDIKTLREEHVYRAKLAEQAERYDEMAEAMKNLVENCLDQN-----	43
GI	-----MAEAFTRDYVFVFMQOLNEAERYDEMVETMRKISGMEG-----	38
SM	-----MDEIRERNIVLAKICEQAERYDEMVKAMIEATNTET-----	37
TB	-----ELTNEERNLLSVAYKVVGARRSSWRVISSIEQKTE-----GSEKKQOMAREYREKVEKELRDIRCHDVIGLLDKYLIPKAATPESEVFYLMK-----	122
TS	-----ELTNEERNLLSVAYKVVGARRSSWRVISSIEQKTE-----GSEKKQOMARDYREKVEKELRDIRCHDVIGLLDRYLIPIKATTPESKVVFYLMK-----	122
HC	-----ELSNEERNLLSVAYKVVGARRSSWRVISSIEQKTE-----GSEKKQOMAKEYREKVEKELRDIRCDQVILNLDDKFILPKAGNPESKVVFYLMK-----	123
DI	-----ELSNEERNLLSVAYKVVGARRSSWRVISSIEQKTE-----GSEKKQOMAKEYREKVEKELRDIRCDQVILNLDDKFILPKAGNPESKVVFYLMK-----	123
CE	-----ELSNEERNLLSVAYKVVGARRSSWRVISSIEQKTE-----GSEKKQOMAKEYREKVEKELRDIRCDQVILNLDDKFILPKAGAAESKVVFYLMK-----	123
BX	-----ELSNEERNLLSVAYKVVGARRSSWRVISSIEQKTE-----GSEKKQOMAKEYREKVERELRDIRCHDVIDLLDKFLIPKAGNPESKVVFYLMK-----	123
AM	-----ELSNEERNLLSVAYKVVGARRSSWRVISSIEQKTE-----GSERKQOMAKEYREKVEKELREICYDVGIGLLDKYLIPPKASNAPESKVVFYLMK-----	123
HV	-----ELSNEERNLLSVAYKVVGARRSSWRVISSIEQKTE-----GSERKOTMAREYREKIEKELREICQDVISLLDKYLIPPKASNAPESKVVFYLMK-----	122
HS	-----ELSNEERNLLSVAYKVVGARRSSWRVISSIEQKTE-----GAEKQOMAREYREKIETELRDICNDVILSLLLEKFLIPPNASQAESKVVFYLMK-----	121
SB	-----NLGNEERNLLSVAYKVVGARRSSWRVISSIEQKTE-----NDCTRKKQIAEYRTRMEKELNTICQVIALLEDYLLPNASPDDSKVFFYLMK-----	132
HM	-----ELNNEERNLLSVAFKVVGSRRNSYRVILSSRLSRTT-----DAE-KQNLTKYELEILQKELNDICTDVKIJUDERLYPKCSNAEGKVVFYKKM-----	135
EG	-----ELNNEERNLLSVAFKVVGSRRNSYRVILSSRLARTQ-----DPE-KQALTREYLDILOKELNAICSDVQIILERLYPSCSNAEGKVVFYKKM-----	135
EM	-----ELNNEERNLLSVAYKVVGARRSSWRIMSSIAKQ-----GTP-LADQTDIYLKRVEEELTKICNDVIALLSKNLTEKIGAEAKIIFYYKM-----	133
TG	-----QPK-DELSVEERNLLSVAYKNAVGRARRASWRIISSVEQKELSK-----QHMQNKAIAAEYRQKVEEELNKICHDDIIQLTDKLIPTSDSESKVYYKM-----	193
ET	-----NSPPGAKGD-ELTVEERNLLSVAYKNAVGRARRASWRIISSVEQKELANR-----NHMANAKALAASYRQKVENELNKICQEIILITDKLLPRTTDSESRVFYFKM-----	141
GI	-----ELSKERNLLSVAYKVNIGPRRAAWRIVSSTIAKEKGRQKPNAKRIEQIRVYRQKIEKELSDICNDIHKLLQEQFVPRSTNADAKVFYYKM-----	129
SM	-----ELTVEERNLLSVAYKVNIGARRSSWRITINSKEQSDE-----AKGSDEIHIKTRFRKEVEKELDEICTSIIINLLDNCLLPKAVSDESKVFLNK-----	125
TB	KGDYYRYLAEVATGDDRTNIVENSONAQYQEAFLDVAKSQMPHTPIRLGLALNYSVFFYEILNSPDRACOLAKQAFDDATAELDTLNEDSYKDSTLIMQLL-----	222
TS	KGDYYRYLAEVATGDDRNNSIVENSOSAQYQEAFLDVAKSQMPHTPIRLGLALNFSVFFYEILNSPDRACOLAKQAFDDATAELDTLNEDSYKDSTLIMQLL-----	222
HC	KGDYYRYLAEVASGEDRDSVVVDKSQSQYQEAQFDIAKDKQMPTHPIRLGLALNFSVFFYEILNAPDKACOLAKQAFDDATAELDTLNEDSYKDSTLIMQLL-----	223
DI	KGDYYRYLAEVASGDDRNVVVEKSQSQYQEAQFDIAKDKQMPTHPIRLGLALNFSVFFYEILNAPDKACOLAKQAFDDATAELDTLNEDSYKDSTLIMQLL-----	223
CE	KGDYYRYLAEVASGDDRNSSVVEKSQSQYQEAQFDIAKDKQMPTHPIRLGLALNFSVFFYEILNAPDKACOLAKQAFDDATAELDTLNEDSYKDSTLIMQLL-----	223
BX	KGDYYRYLAEVATGDRNAVVEKSQSQYQEAQFDIAKDKQMPTHPIRLGLALNFSVFFYEILNAPDKACOLAKQAFDDATAELDTLNEDSYKDSTLIMQLL-----	223
AM	KGDYYRYLAEVATGETRNAVVEKSQSQYQEAQFDIAKDKQMPTHPIRLGLALNFSVFFYEILNAPDKACOLAKQAFDDATAELDTLNEDSYKDSTLIMQLL-----	223
HV	KGDYYRYLAEVATGDNRTAVIDDQSQSQYQEAQFDIAKDKQMPTHPIRLGLALNFSVFFYEILNAPDKACOLAKQAFDDATAELDTLNEDSYKDSTLIMQLL-----	222
HS	KGDYYRYLAEVAAGDDKKGIVDQSQSQYQEAQFEISKKEMQPTHPIRLGLALNFSVFFYEILNAPDKACOLAKQAFDDATAELDTLNEDSYKDSTLIMQLL-----	221
SB	QGDYYRYLAEVATDDARTEVVQKSLDAYTKATTAEN-LPTTHPIRLGLALNFSVFFYEILNAPDKACOLAKQAFDDATAELDTLNEDSYKDSTLIMQLL-----	231
HM	IGDYYRYKAENAKGEEHKAVVEASRLAYEDATKIA-ESLSCTHPIRLGLALNYSVFFYEIMNSPDRACOLAKKAFDDAVSDVDNAEEESYKDSTLIMQLL-----	234
EG	MGDYYRYKAENAKGEEHDHKQVVEASLKAYEEATEIANEKLSCTHPIRLGLALNYSVFFYEIMNSPDRACOLAKKAFDDAVSDVDSANDDSYKDSTLIMQLL-----	235
EM	MGDYYRYLAEVQEGEONDKSTEAAEEAYQKATSLAEALSVTHPIRLGLALNFSVFFYEIKNMPEKACSLAKAAFDAITEVDSIKDETYKDSTLIMQLL-----	233
TG	KGDYYRYIISEFSGEKGKQAADQAEQSYQKATEAEELPSTHPIRLGLALNYSVFFYEILNLPOQACEMAKRAFDDAITEFDNVSEDSYKDSTLIMQLL-----	293
ET	KGDYYRYIISEFSNEECKKASAEQAEYSKRTDTAEELPSTHPIRLGLALNYSVFFYEILNQPOQACEMAKLAFFDAITEFDVSSEDSYKDSTLIMQLL-----	241
GI	QGDYYRYLAEYSSGEDKEKIAGSAINALNSAFEIS-QQLFPTHPIRLGLALNFSVFFYEILASPDRACELARKAFDAITDLDKLITEESYKDSTLIMQLL-----	228
SM	RGDYHRYRAEYSVGNCNRKDAENSCLAYKKAAEDEK-LPVTHPIRLGLALNFSVFFYEILNNSEQACKCARVAFDSAIELDTLSEESYKDSTIIMQLL-----	224
TB	RDNLTILWTTDAGGDEGGGDQDTAAQG-----	250
TS	RDNLTILWTTDNAGDEGGGEQDAPTGQ-----	250
HC	RDNLTILWTSDDAAADDQDAGEQGEGEGAN-----	249
DI	RDNLTILWTSDDADDQGQEPDDNN-----	251
CE	RDNLTILWTSDDADDQGQEPDDNN-----	248
BX	RDNLTILWTSDDTAGEEQEGNETGETGGN-----	251
AM	RDNLTILWTSDDQGDADEAQEGGDN-----	247
HV	RDNLTILWTSDDATADDQGQEPDDNN-----	246
HS	RDNLTILWTSDDQGDEAEEGEGGEN-----	245
SB	RDNLTILWASDQTAECLEVENDG-----	252
HM	RDNLTILWTSDEEEIENDGAE-----	255
EG	RDNLTILWTSDEETNTTEGAE-----	256
EM	RDNLTILWTSNSECET-----	248
TG	RDNLTILWTSDDQADQQQ-----EGGEKPAAEQADQ-----	323
ET	RDNLTILWTSDDQADQQQ-----EGGEKPAAEQADQ-----	277
GI	RDNLTILWTSNSECET-----	248
SM	RDNLTILWTSNSECET-----TASPKGDKK-----	249

**Supplementary Figure 1.** Sequence of *T. britovi* 14-3-3 aligned with selected 14-3-3 protein isoforms. 14-3-3 in nematodes (magenta) shows 88-96% conservation of sequence. 14-3-3 isoforms in Platyhelminthes (green) and protozoa (orange) share 63-67% and 54-66% similarity with Tb14-3-3, while human (blue), bee (yellow) and barley (brown) 14-3-3 zeta share 86%, 89% and 91% similarity with Tb14-3-3, respectively. TB - *Trichinella britovi* (clade I), TS - *Trichuris suis* (clade I) KFD65230.1, HC - *Haemonchus contortus* (clade V) CDJ94531.1, DI - *Dirofilaria immitis* (clade III) AHJ1155.1, CE - *Caenorhabditis elegans* (clade V) NP\_509939.1, BX - *Bursaphelenchus xylophilus* (clade IV) ACZ13351.1, AM - *Apis mellifera* XP\_006566159.1, HV - *Hordeum vulgare* BAJ95666.1, HS - *Homo sapiens* NP\_001129171.1, SB - *Schistosoma bovis* (zeta) AAT39382.1, HM - *Hymenolepis microstoma* (zeta) CDS31680.1, EG - *Echinococcus granulosus* (zeta) XP\_024353113.1, EM - *Echinococcus multicularis* AAM94864.1, TG - *Toxoplasma gondii* XP\_002365409.1, ET - *Eimeria tenella* AAD02687.1, GI - *Giardia intestinalis* AAZ91664.1, SM - *Schistosoma mansoni* (epsilon) XP\_018645303.1.