**Fig. S1. The domain organization of teneurin-1 and the sequences that were expressed or purified in this study.** The amino acid sequence of human teneurin-1 with the various domains indicated. The expressed protein is underlined, the furin cleavage site is indicated in red, and the GHH toxin domain is in italics. The amino acid sequences of the two human and two chicken CTDs are also shown, with the furin cleavage sites in red and the region corresponding to the GHH toxin domain in italics.

#### Intracellular domain

MEQTDCKPYQPLPKVKHEMDLAYTSSSDESEDGRKPRQSYNSRETLHEYNQELRM NYNSQSRKRKEVEKSTQEMEFCETSHTLCSGYQTDMHSVSRHGYQLEMGSDVDTE TEGAASPDHALRMWIRGMKSEHSSCLSSRANSALSLTDTDHERKSDGENGFKFSP VCCDMEAQAGSTQDVQSSPHNQFTFRPLPPPPPPPAACTCARKPPPAADSLQRRS MTTRSQPSPAAPAPPTSTQDSVHLHNSWVLNSNIPLETRHFLFKHGSGSSAIFSA ASQNYPLTSNTVYSPPPRPLPRSTFSRPAFTFNKPYRCCNWK

#### Transmembrane domain

CTALSATAITVTLALLLAYVIAV

## Beginning of extracellular domain

HLFGLTWQLQPVEGELYANGVSKGNRGTESMDTTYSPIGGKVSDKSEKKVFQKGR AIDTGEVDIGAQVMQTIPPGLFWRFQITIHHPIYLKFNISLAKDSLLGIYGRRNI PPTHTQFDFVKLMDGKQLVKQDSKGSDDTQHSPRNLILTSLQETGFIEYMDQGPW YLAFYNDGKKMEQVFVLTTAIEIM

## EGF-like domains

DDCSTNCNGNGECISGHCHCFPGFLGPDCARDSCPVLCGGNGEYEKGHCVCRHGW KGPECDVPEEQCIDPTCFGHGTCIMGVCICVPGYKGEICEEEDCLDPMCSNHGIC VKGECHCSTGWGGVNCETPLPVCQEQCSGHGTFLLDAGVCSCDPKWTGSDCSTEL CTMECGSHGVCSRGICQCEEGWVGPTCEERSCHSHCTEHGQCKDGKCECSPGWEG DHCTIAHYLDAVRDGCPGLCFGNGRCTLDQNGWHCVCQVGWSGTGCNV

## C-rich domain

VMEMLCGDNLDNDGDGLTDCVDPDCCQQSNCYISPLCQ

GSPDPLDLIQQSQTLFSQHTSRLFYDRIKFLIGKDSTHVIPPEVSFDSRRACVIR GQVVAIDGTPLVGVNVSFLHHSDYGFTISRQDGSFDLVAIGGISVILIFDRSPFL PEKRTLWLPWNQFIVVEKVTMQRVVSDPPSCDISNFISPNPIVLPSPLTSFGGSC PERGTIVPELQVVQEEIPIPSSFVRLSYLSSRTPGYKTLLRILLTHSTIPVGMIK VHLTVAVEGRLTQKWFPAAINLVYTFAWNKTDIYGQKVWGLAEALVSVGYEYETC PDFILWEQRTVVLQGFEMDASNLGGWSLNKHHILNPQSGIIHKGNGENMFISQQP PV

## 6-bladed beta propeller

ISTIMGNGHQRSVACTNCNGPAHNNKLFAPVALASGPDGSVYVGDFNFVRRIFPS GNSVSILELSTSPAHKYYLAMDPVSESLYLSDTNTRKVYKLKSLVETKDLSKNFE VVAGTGDQCLPFDQSHCGDGGRASEASLNSPRGITVDRHGFIYFVDGTMIRKIDE NAVITTVIGSNGLTSTQPLSCDSGMDITQVRLEWPTDLAVNPMDNSLYVLDNNIV LQISENRRVRIIAGRPIHCQ

## YD-repeats and first half of the RHS-domain

VPGIDHFLVSKVAIHSTLESARAISVSHSGLLFIAETDERKVNRIQOVTTNGEIY IIAGAPTDCDCKIDPNCDCFSGDGGYAKDAKMKAPSSLAVSPDGTLYVADLGNVR IRTISRNOAHLNDMNIYEIASPADOELYOFTVNGTHLHTLNLITRDYVYNFTYNS EGDLGAITSSNGNSVHIRRDAGGMPLWLVVPGGOVYWLTISSNGVLKRVSAOGYN LALMTYPGNTGLLATKSNENGWTTVYEYDPEGHLTNATFPTGEVSSFHSDLEKLT **KVELDTSNRENVLMSTNLTATSTIYILKOENTOSTYRVNPDGSLRVTFASGMEIG** LSSEPHILAGAVNPTLGKCNISLPGEHNANLIEWRORKEONKGNVSAFERRLRAH NRNLLSIDFDHITRTGKIYDDHRKFTLRILYDOTGRPILWSPVSRYNEVNITYSP SGLVTFIORGTWNEKMEYDOSGKIISRTWADGKIWSYTYLEKSVMLLLHSORRYI FEYDQPDCLLSVTMPSMVRHSLQTMLSVGYYRNIYTPPDSSTSFIQDYSRDGRLL QTLHLGTGRRVLYKYTKQARLSEVLYDTTQVTLTYEESSGVIKTIHLMHDGFICT IRYRQTGPLIGRQIFRFSEEGLVNARFDYSYNNFRVTSMQAVINETPLPIDLYRY VDVSGRTEQFGKFSVINYDLNQVITTTVMKHTKIFSANGQVIEVQYEILKAIAYW MTIQYDNVGRMVICDIRVGVDANITRYFYEYDADGQLQTVSVNDKTQWRYSYDLN GNINLLSHGKSARLTPLRYDLRDRITRLGEIQYKMDEDGFLRQRGNDIFEYNSNG LLOKAYNKASGWTVOYYDGLGRRVASKSSLGOHLOFFYADLTNPIRVTHLYNHT SSEITSLYYDLOGHLIAMELSSGEEYYVACDNTGTPLAVFSSRGOVIKEILYTPY GDIYHDTYPDFQVIIGFHGGLYDFLTKLVHLGQRDYDVVAGRWTTPNHHIWKQLN LLPKPFNLYSFENNYPVGKIQDVAKYTTDIRSWLELFGFQLHNVLPGFPKPELEN LELTYELLRLQTKTQEWDPGKTILGIQCELQKQLRNFISLDQLPMTPRYNDGRCL EGGKOPRFAAVPSVFGKGIKFAIKDGIVTADIIGVANEDSRRLAAILNNAHYLEN LHFTIEGRDTHYFIKLGSLEEDLVLIGNTGGRRILENGVNVTVSOMTSVLNG

Furin-cleavage site within the RHS-domain (red) and Cterminal domain (GHH Tox domain) in *italics* 

RTRRFADIQLQHGALCFNIRYGTTVE*EEKNHVLEIARQRAVAQAWTKEQRRLQEG* EEGIRAWTEGEKQQLLSTGRVQGYDGYFVLSVEQYLELSDSANNIHFMRQSEIGR R

Expressed human Teneurin-1 C-terminal domain (CTD) sequence (furin cleavage site in red, GHH toxin domain in *italics*):

VTVSQMTSVLNG**RTRR**FADIQLQHGALCFNIRYGTTVE*EEKNHVLEIARQRAVAQ AWTKEQRRLQEGEEGIRAWTEGEKQQLLSTGRVQGYDGYFVLSVEQYLELSDSAN NIHFMR*QSEIGRR

Expressed human Teneurin-2 C-terminal domain (CTD) sequence (furin cleavage site in red, GHH toxin domain in *italics*):

TVSQPTLLVNG**RTRR**FTNIEFQYSTLLLSIRYGLTPDTLD*EEKARVLDQARQRAL* GTAWAKEQQKARDGREGSRLWTEGEKQQLLSTGRVQGYEGYYVLPVEQYPELADS SSNIQFLRQNEMGKR

Purified chicken Teneurin-1 C-terminal domain (CTD) sequence (GHH toxin domain in italics):

FADIQLQHGALCFNVRYGTTVE*EEKNHVLEVARQRAVAQAWTKEQRRLQEGEEGI RAWTDGEKQQLLNTGRVQGYDGYFVLSVEQYLELSDSANNIHFMR*QSEIGRR

Purified chicken Teneurin-2 C-terminal domain (CTD) sequence (GHH toxin domain in italics):

FTNIEFQYSTLLINIRYGLTADTLD*EEKARVLDQARQRALGSAWAKEQQKARDGR* EGSRVWTDGEKQQLLNTGRVQGYEGYYVLPVEQYPELADSSSNIQFLRQNEMGKR

#### Fig. S2. Amino acid identity and similarity between teneurin C-terminal domains and the bacterial GHH toxins. The GHH

domains from three bacterial toxins were aligned with the corresponding amino acids from the C-terminal domains (CTDs) of representative teneurins (TOX) to illustrate the possibility that the teneurin CTD is an endonuclease.

HSTENITOX	100%																				
ISTEN2TOX	67.53%	100%																HS	S = Homo	sapiens	
ISTEN3TOX	71.42%	79.22%	100%															5.4		nungaulung	
STEN4TOX	83.11%	70.12%	75.32%	100%														IVI	$v_{I} = iv_{I}u_{S}r$	nusculus	
MTENITOX	93.5%	64.93%	70.12%	80.51%	100%													G	G = Gallus	sallus	
MTEN2TOX	67.53%	100%	79.22%	70.12%	64.93%	100%													o ounu	, gunus	
IMTEN3TOX	71.42%	79.22%	100%	75.32%	70.12%	79.22%	100%											CI	vi = Callor	nincus mili	1
IMTEN4TOX	80.51%	66.23%	71.42%	94.8%	79.22%	66.23%	71.42%	100%										D	m = Droso	nhila mala	nonacte
GTENITOX	96.1%	64.93%	68.83%	80.51%	92.2%	64.93%	68.83%	83.11%	100%										11 - D1030	prilla mela	nogasu
GTEN2TOX	64.93%	94.8%	75.32%	67.53%	64.93%	94.8%	75.32%	68.83%	67.53%	100%											
GTEN3TOX	70.12%	79.22%	97.4%	75.32%	68.83%	79.22%	97.4%	71.42%	67.53%	76.62%	100%										
GTEN4TOX	83.11%	71.42%	77.92%	92.2%	81.81%	71.42%	77.92%	89.61%	83.11%	71.42%	76.62%	100%									
MTEN2TOX	63.63%	\$3.11%	79.22%	64.93%	62.33%	83.11%	79.22%	61.03%	61.03%	79.22%	77.92%	67.53%	100%								
MTENJTOX	64.93%	79.22%	90.9%	70.12%	63.63%	79.22%	90.9%	66.23%	62.33%	75.32%	90.9%	71.42%	75.32%	100%							
MTEN4TOX	79.22%	72.72%	75.32%	87.01%	77.92%	72.72%	75.32%	84.41%	76.62%	70.12%	75.32%	89.61%	67.53%	74.02%	100%						
MTENITOX	62.33%	50.64%	57.14%	59.74%	62.33%	50.64%	57.14%	58.44%	61.03%	49.35%	54.54%	59.74%	49.35%	53.24%	59.74%	100%					
MTENMTOX	36.36%	38.96%	44.15%	38.96%	36.36%	38.96%	44.15%	37.66%	35.06%	37.66%	42.85%	38.96%	37.66%	41.55%	38.96%	38,96%	100%				
mTENATOX	27.27%	32.46%	33.76%	33.76%	27.27%	32.46%	33.76%	33.76%	27.27%	32.46%	33.76%	32.46%	37.66%	32.46%	32.46%	27.27%	32.46%	100%			
BrevibacillusbrevisGHHTOX	23.37%	18.18%	20.77%	22.07%	24.67%	18.18%	20.77%	20.77%	22.07%	16.88%	20.77%	20.77%	18.18%	20.77%	22.07%	19.48%	16.25%	18.18%	100%		
BacilluscytotoxicusGHHTOX	14.28%	10.38%	12.98%	14.28%	16.88%	10.38%	12.98%	14.28%	14.28%	10.38%	12.98%	14.28%	10.38%	12.98%	12.98%	16.88%	8.75%	12.98%	65.43%	100%	
Pacillusthuringionris GUUTOX	33 7686	37 66%	37 6695	35.06%	36 3694	37 6695	37 66%	35.0685	33 7695	37 6696	37 6696	33 7686	22 7684	36 368	22 768/	20 9795	25.0685	21 1685	10.49%	16 9994	100%

HSTENITOX HSTENITOX HSTENITOX BATENATOX MMTENITOX MMTENITOX MMTENITOX MMTENITOX GGTENITOX GGTENITOX GGTENITOX GGTENITOX GGTENITOX CMTENITOX CMTENITOX CMTENITOX DmTENATOX DmTENATOX BrenhacilladoreisGHHTOX Bacillus

SIMILARITY RESULTS

HSTEN1TOX	100%																				
HSTEN2TOX	76.62%	100%																			
HSTEN3TOX	81.81%	87.01%	100%																		
HSTEN4TOX	92.2%	83.11%	87.01%	100%																	
MMTENITOX	93.5%	76.62%	80.51%	85.71%	100%																
MMTEN2TOX	76.62%	100%	87.01%	83.11%	76.62%	100%															
MMTEN3TOX	81.81%	87.01%	100%	87.01%	80.51%	87.01%	100%														
MMTEN4TOX	89.61%	79.22%	83.11%	96.1%	84.41%	79.22%	83.11%	100%													
GGTENITOX	98.7%	75.32%	80,51%	90.9%	93.5%	75.32%	80.51%	90.9%	100%												
GGTEN2TOX	75.32%	98.7%	85.71%	81.81%	76.62%	98.7%	85.71%	80.51%	76.62%	100%											
GGTEN3TOX	80.51%	88.31%	97.4%	87.01%	79.22%	88.31%	97.4%	83.11%	79.22%	87.01%	100%										
GGTEN4TOX	90.9%	81.81%	87.01%	96.1%	87.01%	81.81%	87.01%	94.8%	92.2%	83.11%	85.71%	100%									
CMTEN2TOX	76.62%	90.9%	85.71%	79.22%	75.32%	90.9%	85.71%	75.32%	75.32%	89.61%	84.41%	79.22%	100%								
CMTEN3TOX	77.92%	\$8.31%	92.2%	84.41%	75.32%	88.31%	92.2%	80.51%	76.62%	87.01%	92.2%	83.11%	84.41%	100%							
CMTEN4TOX	87.01%	80.51%	83.11%	93.5%	81.81%	80.51%	83.11%	92.2%	85.71%	79.22%	84.41%	93.5%	76.62%	83.11%	100%						
CMTENITOX	71.42%	66.23%	70.12%	70.12%	68.83%	66.23%	70.12%	68.83%	71.42%	66.23%	67.53%	70.12%	62.33%	66.23%	67.53%	100%					
DmTENMTOX	49.35%	50.64%	54.54%	51.94%	49.35%	50.64%	54.54%	53.24%	50.64%	51.94%	53.24%	53.24%	49.35%	51.94%	51.94%	51.94%	103.89%				
DmTENATOX	45.45%	46.75%	50.64%	48.05%	44.15%	46.75%	50.64%	48.05%	45.45%	46.75%	49.35%	46.75%	49.35%	48.05%	46.75%	44.15%	51.94%	100%			
BrevibacillusbrevisGHHTOX	28.57%	25.97%	27.27%	27.27%	29.87%	25.97%	27.27%	25.97%	27.27%	24.67%	27.27%	24.67%	24.67%	28.57%	27.27%	27.27%	24.67%	31.16%	105.19%		
BacilluscytotoxicusGHHTOX	20.77%	20.77%	23.37%	22.07%	23.37%	20.77%	23.37%	22.07%	20.77%	20.77%	23.37%	20.77%	19.48%	24.67%	20.77%	25.97%	20.77%	22.07%	74.02%	105.19%	
BacillusthuringiensisGHHTOX	42.85%	48.05%	49.35%	46.75%	45.45%	48.05%	49.35%	48.05%	44.15%	49.35%	48.05%	46.75%	44.15%	46.75%	45.45%	49.35%	49.35%	48.05%	25.97%	24.67%	100%

HSTENITOX HSTENITOX HSTENITOX MATENITOX MATENITOX MATENITOX MATENITOX MATENITOX GGTENITOX GGTENITOX GGTENITOX GGTENITOX CATENITOX CATENITOX CATENITOX Datenative selection between the static selection of the static selectis selection of the static selection of the static

**Fig. S3. Purification of recombinant proteins.** Lanes from Coomassie blue-stained polyacrylamide gels showing the purified CTDs of chicken teneurin-1 and teneurin-2 used for cell culture and nuclease activity studies. The size ladder indicates apparent molecular weights in kDa.



Affyprobes	logFC	FC	AveExpr	t	P.Value	adj.P.Val	geneID	Gene name
7903592	-0.72145	0.606487	7.354426	<b>-</b> 12 <b>.</b> 5757	5.03E-08	8.33E-05	NM_020775	KIAA1324
7906878	-0.67236	0.627478	7.214012	-9.72767	7.41E-07	0.000403	NM_001014796	DDR2
7909610	-0.6658	0.630338	7.822956	-10.525	3.29E-07	0.000272	NM 001040619	ATF3
7914923	-0.67225	0.627527	8.664322	-8.30028	3.67E-06	0.000768	NM 145047	OSCP1
7918504	-0.76381	0.588938	8.79511	-8.34036	3.50E-06	0.000768	NM 002557	OVPG1
7919606	-0.69246	0.618796	9.119708	-5.54779	0.000153	0.004596	NM 001024599	HIST2H2BF
7921916	-0.59982	0.659835	7.830591	-9.63692	8.16E-07	0.000406	NM 003617	RGS5
7927305	1.503777	2.835841	9.252199	3.594072	0.003997	0.027026	NM_001144000	AGAP5
7934979	-1.16012	0.447475	8.087316	-15.8307	4.18E-09	1.38E-05	NM_014391	ANKRD1
7937257	-0.71473	0.609319	9.36582	-3.5064	0.004675	0.029707	NM_145651	SCGB1C1
7937696	-1.17705	0.442256	8.674062	-19.0097	5.59E-10	2.78E-06	NM_001004325	KRTAP5-2
7938263	-0.87302	0.546001	8.173645	-6.09672	6.72E-05	0.002971	NM_003754	EIF3F
7948332	-0.5969	0.661171	8.843283	-7.0881	1.69E-05	0.001556	NM 004811	LPXN
7949124	-0.71169	0.610605	8.297349	-7.01971	1.85E-05	0.001598	NM 005609	PYGM
7959102	-0.7667	0.587759	6.783417	-8.20601	4.10E-06	0.000801	NM_014365	HSPB8
7985450	-0.65561	0.634809	8.042572	-3.68078	0.003425	0.024381	NM 198181	GOLGA6L9
7986250	-0.64639	0.638877	10.61057	-9.15753	1.37E-06	0.000593	NM 001271	CHD2
7990391	-0.93391	0.523439	7.239254	-12.1247	7.42E-08	9.41E-05	NM 000499	CYP1A1
8012951	-0.97986	0.50703	8.099792	-8.85831	1.92E-06	0.000709	NM 006382	CDRT1
8018902	-1.63346	0.322315	8.372967	-26.4478	1.41E-11	1.40E-07	NM 173628	DNAH17
8034512	-0.66339	0.631394	12.72709	-3.14155	0.009025	0.043986	NR 002751	SNORD41
8044450	-0.64022	0.641617	8.976154	-9.88059	6.31E-07	0.000376	NM 198581	ZC3H6
8044669	-0.74997	0.594617	6.139221	-3.92222	0.002236	0.018966	NM 013412	RABL2A
8073015	0.590598	1.505871	8.841807	8.056205	4.92E-06	0.000858	NM 006855	KDELR3
8076612	-0.76622	0.587957	7.321342	-10.2007	4.55E-07	0.000337	NM 022785	EFCAB6
8087145	-0.67592	0.625934	7.738101	-8.44067	3.11E-06	0.000768	NM 001407	CELSR3
8090509	0.621983	1.538989	8.029379	3.589539	0.004029	0.027123	NM_004637	RAB7A
8110032	-0.59103	0.663869	8.910183	-7.19709	1.46E-05	0.001474	NM_153607	CREBRF
8113103	-0.77638	0.583831	7.527023	-10.8112	2.48E-07	0.000247	NM_001145678	KIAA0825
8113483	-0.92081	0.528211	8.496886	-10.5983	3.06E-07	0.000272	NM_001039763	TMEM232
8116532	-0.58961	0.664521	9.988008	-4.7771	0.000522	0.008636		SNORD95
8124448	-0.80405	0.572738	11.50295	-12.6511	4.72E-08	8.33E-05	NM_003543	HIST1H4H

# Table S1. Transcriptional profiling of HEK293 cells expressing the teneurin-2 CTD.

Affyprobes	logFC	FC	AveExpr	t	P.Value	adj.P.Val	geneID	Gene name
8128001	-0.81901	0.566831	6.542142	-14.1864	1.38E-08	3.42E-05	NM_000735	CGA
8133314	-0.78137	0.581813	6.560076	-4.64017	0.000655	0.009589	NM_000265	NCF1
8140211	-0.66516	0.630617	9.648513	-4.05341	0.001778	0.016774	NR_003664	SPDYE8P
8156160	-1.61451	0.326575	7.891629	-7.61267	8.53E-06	0.001162	NM_017576	KIF27
8159259	-0.65752	0.633968	8.34969	-8.54771	2.74E-06	0.000757	NM_014582	OBP2A
8163505	0.634357	1.552246	9.225563	7.482806	1.01E-05	0.001236	NM_031219	HDHD3
8164766	-0.72428	0.605298	8.047926	-12.1016	7.57E-08	9.41E-05	NM_152572	AK8
8165496	0.649239	1.568341	10.8664	4.995579	0.000366	0.006937	NM_006088	TUBB4B
8165672	-1.20723	0.433099	6.809187	-3.32621	0.006464	0.036244	L23320	RFC

#### Table S1. Transcriptional profiling of HEK293 cells expressing the teneurin-2 CTD. (cont.)

#### Table S2. FASTA files used for sequence analyses.

>HSTEN1TOX EKNHVLEIARQRAVAQAWTKEQRRLQEGEEGIRAWTEGEKQQLLSTGRVQGYDGYFVLSVEQYL ELSDSANNIHFMR

>HSTEN2TOX EKARVLDQARQRALGTAWAKEQQKARDGREGSRLWTEGEKQQLLSTGRVQGYEGYYVLPVEQYP ELADSSSNIQFLR

>HSTEN3TOX EKARILEQARQRALARAWAREQQRVRDGEEGARLWTEGEKRQLLSAGKVQGYDGYYVLSVEQYP ELADSANNIQFLR

>HSTEN4TOX EKARVLELARQRAVRQAWAREQQRLREGEEGLRAWTEGEKQQVLSTGRVQGYDGFFVISVEQYP ELSDSANNIHFMR

>MMTEN1TOX EKNHVLEMARQRAVAQAWTQEQRRLQEGEEGTRVWTEGEKQQLLGTGRVQGYDGYFVLSVEQYL ELSDSANNIHFMR

>MMTEN2TOX EKARVLDQARQRALGTAWAKEQQKARDGREGSRLWTEGEKQQLLSTGRVQGYEGYYVLPVEQYP ELADSSSNIQFLR

>MMTEN3TOX EKARILEQARQRALARAWAREQQRVRDGEEGARLWTEGEKRQLLSAGKVQGYDGYYVLSVEQYP ELADSANNIQFLR

>MMTEN4TOX EKVRVLELARQRAVRQAWAREQQRLREGEEGLRAWTDGEKQQVLNTGRVQGYDGFFVTSVEQYP ELSDSANNIHFMR

>GGTEN1TOX EKNHVLEVARQRAVAQAWTKEQRRLQEGEEGIRAWTDGEKQQLLNTGRVQGYDGYFVLSVEQYL ELSDSANNIHFMR

>GGTEN2TOX EKARVLDQARQRALGSAWAKEQQKARDGREGSRVWTDGEKQQLLNTGRVQGYEGYYVLPVEQYP ELADSSSNIQFLR

>GGTEN3TOX EKARILEQARQRALSSAWAREQQRVRDGEEGARLWTEGEKRQLLSAGKVQGYDGYYVLSVEQYP ELADSANNIQFLR

>GGTEN4TOX

EKARVLELARQRAVAQAWAREQQRLRDGEEGIRSWTEGEKQQVLNTGRVQGYDGYFVISVEQYP ELSDSANNIHFMR

>CMTEN2TOX

EQARLLEQARLRALANAWTREQQKARDGKEGGRLWTEGEKQQLLSAGRIQGYEGYYVLPVEQYP ELADSSTNIQFLR

>CMTEN3TOX

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>CMTEN1TOX

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>DmTENMTOX

ERHRILKHAHKRAVERAWELEKQLVAAGFQGRGDWTEEEKEELVQHGDVDGWNGIDIHSIHKYP QLADDPGNVAFQRDAK

>DmTENATOX EQQRLMHHAKLTAVRKAWHREKEALRSGLTTALEWSQQETDEILKQSYANNYEGEYIHDVNLYP ELAEDPYNIKFVK

>BrevibacillusbrevisGHHTOX EWNRRLAKRRDAGVKEFWKQEKRRIKNGEPTTRNWTQEQKDAILSNQVPTFNGKPITGHHAYSV SKYPHLANRGEIIYPVT

>BacilluscytotoxicusGHHTOX EWNKKFAKRWDKGVKEFWYQEQQRILNNEPLTREWSQEQLKDILAGKTPKFDGKPIAGHHSYSA AKYPHLADKGEIIYPVT

>BacillusthuringiensisGHHTOX LTDKQFSALRQKAVRHAWRQEKELIKKTGKGTRDWTPAEKLELLQTGKVKGYEGQHMKSANEYP DFAGEPDNIQFLK