

Figure S7

TGGT1_259640 (100%), 302,321.9 Da
| organism=Toxoplasma_gondii_GT1 | product=nucleoporin autopeptidase | location=TGGT1_chrVIIb:2709338-2721341(-) | length=2894 | sequence_SO=chromosome | SO=protein_coding
32 unique peptides, 53 unique spectra, 89 total spectra, 498/2894 amino acids (17% coverage)

M F S S N T S S S L	T G G G S L F G S S	G G G G G L F G G A	G T Q Q Q Q G G S L	F G G T G G F M S Q	P Q Q Q T Q G R L F	G N A G T T G M S L	F G Q Q Q T T P Q
S G G L F G S S T T	T N S G L F G S A P	Q Q Q T G G L F G S	S G L S Q P Q Q T P	S G G G L F G S T N	T S T L G S S I T G	G G L F G Q Q P Q Q	T G G L F G S S T G
T G T G A A A T G T	G A L G Q Q Q S G S	L F G S S G F G T N	T G G F G T S T L G	T A G Q Q T S G G L	F G S Q P Q G G G L	F G S N T S S F G A	A G T S G T S A F G
T S T F G G G A A T	G S V L G A G S L Q	Q Q Q P F Q P H K T	E E G L L M S I C F	G N L A E V S Q D E	E R W R F Y Q Q R G	G G A M G A S N T P	G T G L F G Q Q T T
Q Q P S G G L F G N	S A G T T T S G G L	F G S T P A S T T G	T G L L G S T P Q T	N Q Q Q S G G L F G	T S T T G G F G G G	L F G S S A T T Q P	S G Q Q Q T G G L F
G N T G G S T T P P	G G G L F G S S T L	G N T T G T G L F G	S T T T P Q Q T Q S	G G L F G Q Q Q Q T	A G S G G L F G S S	S L T G A T N T G G	G L F G S S T P S
T G L F G S T T Q Q	C Q P G A T T T Q T	G G G L F G S T T T	S A T T T G Q A T T	G T G L F G G L S S	G T G A T Q G G G L	F G S G G T A T T G	A T G G G L F G N A
Q Q Q S N L S G G G	L F G S S G G L K L	G T T T T P Q T T P	G A T G T T G G L F	G N T T T T G A S G	G T S L F G S S L G	T S G G G L F G S S	A A K P G E T G G L
F G S S G T S G T S	G S L F G N T T T G	A G T G T G L L G A	A P A S S G T G T S	G G G L F G S S T T	G S G T G L F G G S	G I F G S A Q T I Q	Q O N S A A G G L F
G S T S A G G V G V	G G S T L G S G Q A	N Q T S L F G A I G	S L S G C G A Q G A	P A S A A A A D A Y	G L A S L L G G H V	E V K L T L S A R P	S E S S A Q E S A Q
I F P P R M Q L L D	P C G G T A L G D T	G L L G S V G S S V	W R S G A P A R L C	R G R R F R P L G P	M E G G L S G S Y L	S S G A S N A S F A	L P E V Y I Q K A F
G T S R T A S P L E	D E S K G G Q A N A	L R L L P D G K A F	S A A P W A S T T L	E R S A V E A L L M	Q R R R R K P G R L T	P D Q V S P W S S T	A L Q F M R S N P F
Y R E Q L A E V Q A	S K D T M E N K D R	D T L P P T S Q S A	P A A A G V K E T T	L A S E E V S A P A	S V S C P A V P G V	L P A S A A V P D E	K R G W T A N V E V
S P S A K K L A G L	G I S P I E T F S L	A T P A G S P G T S	P N G S R T G P A E	E C T R W H G A P P	A S G S V A A G L E	S V A A C L P A P E	D L R P V L T R P D
Y E T V P S I E V L	T G M T E Q K L S R	V Q D F S I T R R G	Y G S I R W P G Y T	D L R G I N L D E A	V K I E K L E V T V	Y G N E A P P C G V	G L N K R A V I T L
K N C K P R S V K Y	L D T L T I Q R P E	D E A Y V Q D K Q C	Q Y V T K V R R Y T	E R M G A K F V D L	N L A T G E W T F F	V E H F S T Y R F L	D E D D E N D E E L
E T Q L R Q K A L L	P S T S A H Q P T L	E S P V K V L P A H	A D S F P A S P E N	R T R D F G E A P E	R I T H L F P E R P	A N G Y S S E R S S	F L G V Q K Q V L K
A G F A E A D R E T	P A Y L G G G V A E	N L V N P E F L K N	V S L A E S V N R H	C Q Q R W R P L Y V	S G E A P S R G L K	R V S Y N S G K T V	E A V H D L K E K A
L P G G E R W E A T	G V S G G R M V W E	P Q V N G V E A S H	R G V Q R F Q D E K	T E D K G V Q D T E	R R D G G A A A S L	R L E D G T G G S V	R A V P P G R P C E
D T R S S S A S F P	H L Q Q R R H C P Y	P V R C A P V I S R	D G L M A L P L L S	L P V S L E G I T T	A S L P G S L V Q L	A H L S P L L R E E	E M P V Q N G G I S
S S V G S L E G G S	A G L E A P V Q P S	P M W T V G E V P D	E S V S R E E E E E	K Q A L S M A A Q R	Y V Q P L R E A K G	A P S L T A A S L P	L A D V S P A L V A
A S R L R P F Q A D	L A T S G A P Y T N	Q S P T E Q L S L V	R D G C R V R R T L	G A S A M P L V L S	A F L E E V V K E N	G E S E L Q S R E E	D S Q Q S E S S A R
A D A T Q E F L P A	L T P A P E V A E M	G K E G R R G R R S	K G E A G S S G D S	N R R R F R S Q Q S	E W W L L T E L C R	Q E S H A L E K S R	R S K S V K T L N A
F P S S G L V Q R L	L L R L L A F F E Q	Q T R V Y S G C M S	P T S S V S V G N S	K C S L P L S S Q P	F L Q S A P V S S A	H P P D V P E A S Y	L A P Y M L Q T W Q
L L V A L M L S S P	E Q E E S V F T A P	S G L F S Q R D I S	P E A I L E S Q R Q	S R L L E W L L R E	S G R E V T A L L Q	R A A A L R A S P P	F S T S E G L S L D
R G E S L C G A T E	L C R Q R G A A Q N	P A I T R L G A N A	L F R L A G T A G Q	R A L Q I A M A A D	H D E E R K L L A V	F H L A A A G Q L Y	D A V E L L L N S R
P G E P Y Y P H L A	L C L A A H V Q Q Q	V G R E F L Y Y N L	F R A T A P S F L T	P P P G I A R L Y R	L L T P C S T R A S	P S P G S A S V K A	K E G E K R K R S I
S P G V V E P A E A	S R C A S P S K R H	A G A T D R N S G A	K H E S T H A L S L	H A S W K S G E T T	E A N S V S G M G L	E H F V S W R H Q L	T A S L V F S S A S
P L E D P R V L S T	G A V V S S G G N A	E K K V D S V D E G	E K A A A C T Q E D	T V T Q T K G E G S	A A D V D M F O R I	R T E L T P P P Q A	A D A P R E L R R A
L L Q F E H R L R F	R E N G D A S Q S G	V E F A V P A S P A	P L Y R Q Q D E D G	E T Q K D R M H D G	L Q G A T S N I F D	L Q Y G L L R M H A	G L A Q P S L S I F
D P S S H T P Y G L	D F F F A W T A G V	V T L L H R G S A R	A R V R L L K Q T E	S E G T E A A E A I	D A E D G L E Q E E	A R Q L H R L T V A	F A A E L E C L P G
C W P W A C A A L L	F T P F C G R A L Q	G M R A L I G R H A	A E F T C T G V G P	R Q S G K E S Q G L	Q A F P E K A A F E	E R R R E I L R V L	L E E V G V A Q W W
L D E A D G L Y A L	S Q R K F M Q A A F	L F Y W A Y L R L R	L P L V R G F L G S	P V A A P L R E E L	L N L W S P T G A M	E R H L L R H A G R	A L L Q C L P G F L
L A V L L Q Q I Q H	V E K E T R V S R M	R R A L E K C E R L	T G S V T S G T T R	A L S D E L R A Y E	R Q E R R E E P T E	V C D E M G S M P S	V L I L S T E A K M
R L L L Q I L E A I	R V K L A G G L P D	L S Q D A N G T D G	S R K G V E K D I L	A S C V V G G E C R	S A K F P V D L A R	L A C M E K A L R W	L L K K Q M R K Q K
Q H N R T E Q R T S	P G S A R V P S S D	A K L S G A T A K S	S L E E D G D R V D	A D F S A A L L R E	V E K Q T K H V E A	M S D A N R G F F P	T D I S P D E P A F
W I A L K T A L L E	E R R E						