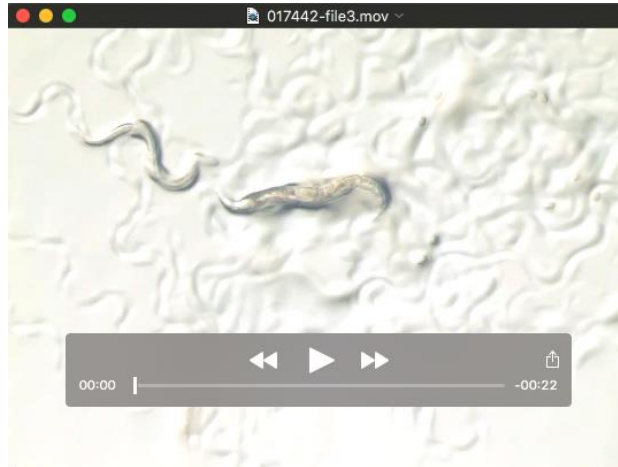


Supplementary Table 1. *C. elegans* strains used in this study

Strain Name	Genotype	Reference
CB444	<i>unc-52(e444) II</i>	(Liu and Sternberg, 1995)
CB1487	<i>him-9(e1487) II</i>	(Hodgkin et al., 1979)
MT3641	<i>osm-10(n1602)</i>	(Hart et al., 1999)
NIN15	<i>him-9(e1487) II; tll-11(tm4059) IV</i>	This study
NIN16	<i>him-9(e1487) II; tll-4(tm3310) III; tll-11(tm4059) IV; tll-5(tm3360) V</i>	This study
NIN20	<i>him-9(e1487) II; tll-4(tm3310) III</i>	This study
NIN21	<i>him-9(e1487) II; tll-5(tm3360) V</i>	This study
NIN23	<i>him-9(e1487) II; tll-9(tm3889) V</i>	This study
NIN24	<i>him-9(e1487); tll-15(tm3871)</i>	This study
NIN40	<i>nIs133 [pkd-2p::GFP] I; him-9(e1487) II</i>	This study; (Schwartz and Horvitz, 2007)
NIN45	<i>nIs133 [pkd-2p::GFP] I; him-9(e1487) II; tll-4(tm3310) III; tll-11(tm4059) IV; tll-5(tm3360) V</i>	This study; (Schwartz and Horvitz, 2007)
OC343	<i>tll-5(tm3360) V</i>	This study
OC422	<i>tll-4(tm3310) III</i>	This study, (Kimura et al., 2010) and (O'Hagan et al., 2011)
OC423	<i>tll-11(tm4059) IV</i>	This study
OC419	<i>tll-9(tm3889) V</i>	This study, (Kimura et al., 2010) and (O'Hagan et al., 2011)
OC504	<i>tll-15(tm3871) V</i>	This study
PS3151	<i>lov-1(sy552) II; him-5(e1490) V</i>	(Barr and Sternberg, 1999)



Movie 1: Wild type male mating behavior.

A *him-9* male executes the response step of male mating. Upon contact with an hermaphrodite, by aligning his tail with her body and initiating a backward motion.



Movie 2: Triple mutants show a defect in the response step of male mating behavior.
A triple mutant male fails to execute the response step of male mating upon contact with an hermaphrodite.

Supplementary Data 1. TLL Protein sequence Alignments and Annotations.

TLL-4

CLUSTAL 2.1 multiple sequence alignment

mmTLL4	MASAGTEHYSIGLRRGNSFKQRHPSGTVSASPSEKPEVKVWSQAHQOVKPIWKLEKKHV	60
ceTLL-4	-----	
mmTLL4	GTLNAGLGLVSLGVSQPAYFLCPSTLCSGTTAVIAGHSNPCYLQSLPNLFSNTLLYRR	120
ceTLL-4	-----	
mmTLL4	TNVRQKPYQOLESFCLRSSPSEKRSFSLPQKGLPVSVTANKATSSSTVFPMAQPMATSPTD	180
ceTLL-4	-----	
mmTLL4	PYLSLAAAGENPSRKSLASAIISKIASPLSYKPMNNSFMRPNSTKVPQSQATDGLKPV	240
ceTLL-4	-----	
mmTLL4	SSPKIQPVSWHHSGGTGDCVPQPGDHKVPQNIATVLDDVTAPITPSIPSTLNISTASVTS	300
ceTLL-4	-----MSSGYSSAPSVSH	13
	* : * : . * * :	
mmTLL4	SQCSQSNFRMEAHPCGLDENPDSQSATKEVHFTEAVRKLAEKGLEKMPROGYQFEQACFV	360
ceTLL-4	TSSDIDLNRIDSYDDGAEETDEQ-----	37
	: * : : : : * : * *	
mmTLL4	NPSFQWGLLNRSRRWKPLMGQRFQEDIGLDSAILPGTSDTLGLDSTVFCTKRISIHLLA	420
ceTLL-4	-----	
mmTLL4	SHVHGLNPSACGSAVDLPQVLGEDRAPVPPSSLQPLGVAEVATRLSSVHLDQPGKEPEEA	480
ceTLL-4	-----RMCG-----LS-----ELVTSCLTSSRLK-----	56
	** * . * : : * : * * * :	
mmTLL4	KDLNSCTKGGGSATDLQPNQVEPEDTEDELGDGLEDSCSHDENEEEGDSECSSLSVVSP	540
ceTLL-4	-----AIDEEDEEE---NCNDIEIVGL	75
	: * : : * * * : * : . . . : * :	
mmTLL4	SESVALISRN---CVDLMSKSLPNHEKVVRPALIYSLFPNVPTPTIYFGTRDERVEKLPW	596
ceTLL-4	SKTTTTKVKRSKKVLSCPIVSSSTKENGNAAPFLKSSQFTDVPPTIRFYTKGTKVKTPAR	135
	* : : : : : * . . . : * : * : . . * * * * . : * : * * * * * : * : * * .	
mmTLL4	EQRLLRWKMSTVTPNIVKQTIIGRSHFKISKRNDDWLGCVGHHMKSPPGFRSIREH	656
ceTLL-4	QIARL TWCHNSLLPIVMRQTLAASHFTVVDLSLFYVGYWGRHLKSAQYRALOPH	195
	: : * * . : : * : : * : : * : : * * * * * : : : * : * * * :	
mmTLL4	FPGSFQIGRKDR LRNLSRMQSRFGKKEFSFFPQSFILPODSKLLRKAWESSSRQ KWIVK	716
ceTLL-4	FPGAFHIGRKDR LMHIRKQOERFEG-EFDIMPFTYILPTDRQELLKYLETDASR HVIVK	254
	* * : * : * * * * * * : : * * * * * * * * * * * * : * * * * * * * * * :	
mmTLL4	PPASARGIGIQ VIHKWSQLPKRRPLLV OR YHLHKPYLISGSKF DLRIYVYVTSYDPLRIYL	776
ceTLL-4	PPASARGTGISV TRKPKDFPTTATLVA QH YIERPLTINRAK DLRLYAYVPTFEPLRVYI	314
	* * * * * * * * * * * * * * * * : * . : * : . . * : * * * * : * : * * * * * * * * * * * * * * * :	
mmTLL4	FSDGLVRFASCKYSPSMKSLSNKFMHLTNYSVNKKNTEYQANADETACQGH -KWALKALW	835

ceTTL-4	YDQGLVRFASVPYSHSVSTISNKYMHLTNYSINK ----- LAEADGVANKPVPKWTLHHLW	369
	:.:***** ** *.:.:****:*****:** *:* .* : **:* **	
mmTTL4	NYLSQKGINSDAIWEKIKDVVVKTIISSEPYVTNLLKLYVRRPYSCHELF GFD IMLDENL	895
ceTTL-4	EHFDEMVDREKIQREIEEVIIKAFISTEKP IREHMSRFLEQEFICYELF GIDI IILDEDY	429
	:.:. : * : : * .:****:****:* : : . : . : : * :****:****:****:	
mmTTL4	KPWVLEVNISPSL HNSPLDISIKQMIRDLLNLAGFVLPN MEDI ISSSSPSSSSGSST	955
ceTTL-4	KPWVLEVNISPSL HSGTPLDVSVKAPLAKDVLNLAGVYVP----- PSFDKLSDA	478
	:**.:****:*. : :*:*****. :* ** .. *.:	
mmTTL4	SLPSSPRDKCQMTPEHF TAQMKKAYYL TQKIPDQDFYASVLDVLT PDDVRLVEMEDEF	1015
ceTTL-4	DYSTRPRNGRKNREQLIKEASWVAAYKDQLGVIDN ---- RIFKRLTPEDTRALVEFEDEL	534
	. .: **: : : :. . ** : * : :. : **:*.*.***:***:	
mmTTL4	SRRGQFERIFPSRIS SRYLRFQPRYFNILTTQWEQKYHGKGLKGVDLLRNWCYKGFHT	1075
ceTTL-4_	ERIGDFKLVFPTAHTSHYQKYFAETIYMNILLQWQIAQEDDRSIGINRLEQLCRQKHMQ	594
	. * **:* :***: **:* :* :. *:* ** : . : : * : * : * : .	
mmTTL4	GIVSDSAPLWSLPTSLMTTSTKGDGTPNSASKSRKKSASEGTTLSSEDRSTPKSKKSQAGL	1135
ceTTL-4_	---SDQE-----TSF-----	601
	** . **:	
mmTTL4	SPISRKTLSSRSNENTSKQSKRSTPGLPVLKYSQSSRLSAASASQSVTDSRLTAVSS	1193
ceTTL-4_	-----	

Key:

- DOMAIN NOT INCLUDED
- Predicted Substrate Interacting Domains
- ATP & Mg²⁺ Interacting Domains
- Essential ATP-Binding Residues
- Cationic MT Binding Domain
- Extended TTL-Domain
- Core TTL-Domain
- Deletion

TTL-5
 CLUSTAL 2.1 multiple sequence alignment

```

mmTTL5 -----MPVVMARDL 9
ceTTL5-5 MKPKNVPREIFNPFTNKTSLGTRREGLFLCKRLKLRPDNYLEEYCADLEVIDIMAPIRPA 60
          :. *

mmTTL5 EETASSEDEDLANQEDHPCIMWTGG-CRRIPVLVFHAEAILTKDNNIRV-----IGER 62
ceTTL5-5 DETERCPPTSTSDDEAGDYLVSRNKKSRNSDYMLFSSDALVHIAHDAKVSEKYTWLGER 120
          : ** .. . : ** : : . *. : * : : : : : : * : **
          :

mmTTL5 YHLSYKIVRTDSRLVRSILTAHGFEVHPSSTDYNLMWTGSHLKPFLRLTLSEAQKVNHF 122
ceTTL5-5 LRLTFKMMRSDSRLIRTMCHSHCFMQCSSKNPSVNVIVWCAPVKSVMRELMPWQRLNOF 180
          : * : : : : : : * : : : : : * : * : * : * : * : * : *
          :

mmTTL5 PRSYELTRKDRLYKNIIRMQHTHGKFAHILPQTFLLLPAEYAEFCNSYSKDR----- 174
ceTTL5-5 PRSTELTKKDRLYENIERSKSIK-ESFDIFIPEFYVTPRENRMENAFVVRVAKEIAAAGG 239
          * * * : * : * : * : * : * : * : * : * : * : * : * : *
          :

mmTTL5 -----GPWIVKPVASSRGRGVYLINPNQISLEENILVSRVINNPLLIDDFKFDVRLYLVL 229
ceTTL5-5 ELCFPGEFIVKPTNSRQCKGIFFANSMADIPAECPILLVSRYLKDPYLVNNHKFDLRIYVA 299
          * : * * * . * : * : : : : * . : * . * : * * * : * : * : * : * : *
          :

mmTTL5 VTSYDPLVIYLYEGLARFATVRYDOGSKNIR-NQFMHLTNYSVNKKSVDYVSCDDPEVE 288
ceTTL5-5 VTSFYPLVAVVYSEGLARLASRPYDTSASSADSNEYVHLTNYSINKNSTSFVRNESMSSE 359
          * * : * * * : * . * * : * : * * * : * : * : * : * : *
          :

mmTTL5 DYGNKWSMSAMRLRYLKQEGKDTTALMAHVEDLIKTIISAELAIATACTFVPHRSSCFE 348
ceTTL5-5 DLCHKWTLGALLRYVENECKDAKLMLRIEDLIVKSLLSIQNSVATASRTNLRFACTNFE 419
          * * : * : : : * : * : : * * : * : * : * : * : * : * : *
          :

mmTTL5 LYGFDVLIIDNTLKPWLLLEVNLSPSLACDAPLDLKIKASMISDMFTVVGFVCQDPAQRTSN 408
ceTTL5-5 LFCFDVLDQALKPWLLLEVNLSPSLACDAPLDSLLKTRLIADLLNLA---CVPLLDRKII 476
          * : * * * : * : * * * * * * * * * * * * * * * * * * * * * * *
          :

mmTTL5 RSIYPSFESSRRNPFQKQRTPLSASDAEMKNLVAAREKVPGLGGSVLGLSMEEIK- 467
ceTTL5-5 DSVTPALRKSMSNSQESSESETDDELDPMCAKTLKRRPVGLKRSVLNKKIVSGSTSLIPN 536
          * : * : * . * .. : * * * * . * . * * . * . * : * . *
          :

mmTTL5 -----VLRVKEENDRRGGFIRIFPTSETWEIYGSYLEHKTSMNYMLATRLFQDRGNP 520
ceTTL5-5 NEKKFDQIVRKAELEDGRRGDFIRVFPNCTWCMYSPVMEDLCNED----- 582
          : * : : : * : * * . * * : * . : * . : :
          :

mmTTL5 RRSLLTGRARVSTEGAPELKVESMNSKAKLHAALYERKLLSLEVRKRRRRSGLRAMRPK 580
ceTTL5-5 -----FDERLFDEVVTKKNTKNSSGSSKASS 608
          : : : * : . * * : . . : . .
          :

mmTTL5 YPVIAQPAEMNIKTETESEEEEVGLDNDDEEQEASQEEASAGSLGENQAKYTPSLTVIVE 640
ceTTL5-5 SSASASSSSSMHIEDLSDLFHEVMMQCDKYSS-----IA 643
          .. * . . . . : : * * : . * : : * . .
          :

mmTTL5 NSPRDNAMKVAEWTNKGEPCKKIEAQEPESKFNLMQILQDNGNLSKVQARLAFSAYLQHV 700
ceTTL5-5 DVPIEIREIISPWYEEASEYTKKITQECETYACKLPVIRSTARLR---TKSCAEFYEV 699
          : * : : : * : : . * : * * : : : : * * : : : :
          :

mmTTL5 QIRLTKDSSGQTLSPSWAAKEDQOMELVVRFLKRASSNLOHSLRMVLPSTRRLALLERRRI 760
ceTTL5-5 KVQLAK---KKESEAMASKENEPVILQAVVAKRI----- 730
    
```

:::*** :. * : *::** : * . . **

mmTTL5 ceTTL5-5	LAHQLGDFIGVYNKETEQMAEKSKKKLEEEEDGVNAESFQEFIRQASEAELEEVLTIFY	820
mmTTL5 ceTTL5-5	TQKNKSASVFLGTHSKSSKNSSSYSDSGAKGDHPETIQEVKIKQPKQQQATEIHADKLSR	880
mmTTL5 ceTTL5-5	FTTSSGKEAKLVYTNCSFCSPAVLLQRLPSSHLSSVITTSALSAGPGHSHASLSQIPPA	940
mmTTL5 ceTTL5-5	VPSPHQPALLLSPVPDNAPPSIHSGTQNVSPAGLPRCRSGSYTIGPFSSFQSAHIYSQ	1000
mmTTL5 ceTTL5-5	KLSRPSSAKAAGSCHPHKHHSGIAKTQKEGEDVSLNRRYNQSLVTAELQRLAEKQAAARQY	1060
mmTTL5 ceTTL5-5	SPASHISLLTQQVTNLNLASSVINRSSASTPPTLRPVISPSGPTWSIQPDLHASETHSSP	1120
mmTTL5 ceTTL5-5	PGSRSLQTTGGFAWEGEVENNAYSKTTGVVPOHKYHPTAGSYQLHFALQOLEQOKLQSRQL	1180
mmTTL5 ceTTL5-5	LDQSRARHQAIFGSQTLPNSSLWTMNGPGCRISSATTGGQKPNLTPQKVVAPPNSSTLV	1240
mmTTL5 ceTTL5-5	SKPASNHKQVLRKQPASQRASKGSSAEGQLNGLQSSLNPAAFMPITNSTGSLEAPQVIFAR	1300
mmTTL5 ceTTL5-5	SKPLPTQSGALATVIGQRKSKSVKSGTI	1328

Key:

Predicted Substrate Interacting Domains

ATP & Mg²⁺ Interacting Domains

Essential ATP-Binding Residues

Extended TTL-Domain

Core TTL-Domain

Cationic MT Binding Domain

~~Predicted Frameshift~~

TTL-9
CLUSTAL 2.1 multiple sequence alignment

```

mmTTL9          ---MSRQKNQNSKGGHGVSKGKEREQRTLIRFKTTLLMNTLMDVLRHRPGWVEVKDEGEWDF 57
ceTTL9          MSSISNELSVTSSQNVISNSKE-QRKKKILFKCALTNTISDVLTNREGWAQTQGD-DWQF 58
                :*.: . *. : :*:.* :.:. * ** :* **: *** :* **.:.: :*:
mmTTL9          YWCDVSWLRENFHDHYMDEHVRISHFRNHYELTRKNYMKNLKRFRKYLERESGKTEAAK 117
ceTTL9          FWVTREWMTTCYDKHKFSEKQMICFRNDFELTRKDFLIKNYKKARKAKEK-SGIDVVSE 117
                :*  .*:  :*:  :*:  *.*.*.:*.*.:.:** *: ** *: **  .:
mmTTL9          CDFFPKTFEMPCEYHLFVEEFRKNP-GITWIMKPVARSOGKGIFLFRRLKDIMDWRKGTS 176
ceTTL9          FNFLPSSYVLPTEYHLFVEEFRKYPNDTIWIMKPVAGAOCKGIFLFRKLKHVQENKK--- 174
                :*.*.: :* *.*.*.*.*.* * . *.*.*. :*.*.*.*.*.*.:*.: :*:
mmTTL9          GKKPTGVETQPARANMNPSGSHDRSSDDQKDDLPVENYVAQRYVENPYLIGRKFDLRV 236
ceTTL9          -KDSSGSEALP-----YVVQCYVHNPYLVGKKFDVRI 206
                *..:* *: * **.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*
mmTTL9          YVLVMSYIPLRAWLYRDGFARFSNTRFTLNSIDDHYVHLTNVAVQKTSPDYHLKKGCKWM 296
ceTTL9          YVLVTSFRPLNAWVHREGFARFSHSRVSTDSVDDAFVHLTNVAVAKTAADYDPERGLKWS 266
                **** *: **.*.:*:*.*.*.*.:*.: :*.* :*.*.*.*.*.*.*.*.*.:* **
mmTTL9          LQRFROYLASKHGPKAVETLFSDMNIFIKLSQSVQKVIISDKHCFELYGYDILIDQDLK 356
ceTTL9          LPKLFRFFKSVHGOSKLSKTMNDLTNVIESLKSVQNLIIQDNHCFELYCYDILFDENLK 326
                * :. :. :* ** . . . . :*.: *:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*
mmTTL9          PWLLEVNASPSLTASSQEDYELKTCLEDTLHVVDMEARLTGKEKRVGGFDLMWNDGPVS 416
ceTTL9          PWLLEVNASPSLTASSQEDFELKYRILNHMIDVLDIEKKLIGNENEVGGFDLLIKN---S 383
                *.*.*.*.*.*.*.*.*.*:*.* :*.: .*::*:* :* *:*.*.*.*.*.: : : *
mmTTL9          REDGPSDLSGMGNFVTNTHLGCVNDRKEQLRQLFRSLQAQRKAPS 461
ceTTL9          K---PVELCKV-DFHTQPFFG-----TQFNLRLGDYVEATPMP- 417
                : * :*. : :* *.*.:* * *.*. : . *
```

Key:
 Predicted Substrate Interacting Domains
 ATP & Mg²⁺ Interacting Domains
 Essential ATP-Binding Residues
 Extended TTL-Domain
 Core TTL-Domain
 Predicted Frameshift

TLL-11
 CLUSTAL 2.1 multiple sequence alignment

```

mmTLL11      MRRSSPEKKPEAEWEADAAAAAATAAATESLPAETEKQQGV DAGAAGDPERLELEE QPK 60
ceTLL-11    --MGCKISTEFCS DNPVGSISTSKVHPTDLSTPSYAIKPV E FYEEPLKDDQLFYKVALAK 58
      ..  ..  ..  .:  .:  :::  .  :  *  *  :  *  .  .  *  :  :  .  *

mmTLL11      DVGRIPTPTRRHAP EEGEARVVRRLPPALPLAQPRP--AAR ALSQLVKARGRSRSRVYRRS 119
ceTLL-11    KEYREKEKDKKEQLSSNR RVSLQVEPNKLP IPLTRSSSLSSIMENRPPSGISNSSFIRSR 118
      .  *      :.:  ....  ::  *  **:  .  .*  :  :  :  .  *  *.  .  *

mmTLL11      AGSMRPVTV DSSKARTSLDALKISLRQLRWKEFPFGR--RLPCDIYWHGV SFRDSDILSG 177
ceTLL-11    NTASRRFTIDTSRAKSNQYV VSLCSKKIGIIEYPDGRSDKQPCDVYWHNVVLSDMNKI VT 178
      :  *  .*:  *:  *:  :.:  .....  :::  *:*  **  :  ***:  ***.*  :  *  :  :

mmTLL11      ----QVNKFPGMTEMVRKV TLSRALRIMQNLFP EEFYPRSWILPEEFQLFVSVQVQTVK 233
ceTLL-11    SPQSRVNKFPGMTE LAKKISLTHSISSMQKLPDEYAFY PNSWFLPAHLADFHAFYRKAQ 238
      :*****:  .:  *:  *:  :.:  **:*  **  **  **:*  **  .:  *  :  :.:

mmTLL11      EGDPSWKPTFIVK PDSGCQGDGIYLIKDPDGRLTGTLHNRPAV VQEIYRKPLLI-DK LK 292
ceTLL-11    ALG-KTEMWFI VKPDEGAOCTGIVLINS PNOIRNVDQRO---LVQEVVADPLIMNDK LK 293
      .  .  :  *****.*  **  *****:  *  :  *  ..  :  :*****:  .***:  ****

mmTLL11      FDIRLYVLLKSLDPLEIYIAKDGLSRFCTEPYQEPNPQNLH HVMHLTNYSLNIHSGKFV 352
ceTLL-11    FDFRVYGVIKSINPLSIYVAREGMARFCTEKYEKPDSSNFKNLYAHLTNYSLNKANEAYV 353
      **:  *:  *  :*:  :*:  **  *:  *:  :*:  :*:  *****  *:*  :  .:  :*:  :*:  *****  .  :  *

mmTLL11      HS---DSASTGSKRTFSSILCRLSSKGV DIKKVWSDIISLVIKTVIALTP ELKVFYQSDI 409
ceTLL-11    HSNTLQDQTRGSKRLLS TVFHQLESRGVKT KRLWHDIKLILVKTTLAMLPEIMLHYEHF 413
      **  :.  :  ****  :*:  :*:  :*.  :*.  *  ::*  **  :*:  *:  :*:  :*:  **  :.  *:  .:

mmTLL11      PTGRPGPTCFQILGFDILLMKNLKPMLLEVNANPSM RIEHEYELSPGVFEN---IPSLV 465
ceTLL-11    YDS-TGPOCFQIMGFDVMIRE DGTPIILLEVNAAPSL TADHIVPHPGRTLLEGGQVRVSIV 472
      .  .*  ****:  ***:  :.:  :.  :*****  **  :  :*  .  .:  :  :  :  *:*

mmTLL11      DEEVKVAVIRD TRLMDPLKKKKEIHFPDIYMDRKHRI PPVSDRMSSWKHKGSSLSIVRS 525
ceTLL-11    DEVIKIPLVRDTLLLV LGLMEEYQNN-----SLKGETKSLDDM 511
      **  :*:  :*:  :***  *  :  *  :.:  :  :  :  :  :  .  **.:  :  *

mmTLL11      QQMEKSFTSKEDLNCDPTGGDSEPNPEAHLPSIC LKQVFPKYAKQFN YLRLVDRMANLFI 585
ceTLL-11    QTIKQ-----RRKPHLSEIFP-----TRYGAHSGHLLFLDKAMYIYM 548
      *  :.:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

mmTLL11      RFLGIKGMTKLGPTGFRTFIRNCKLSSSSLSMAAVDILY IDITRRWNSVTVDQRDSGMCL 645
ceTLL-11    QFVQLRSNVNITNAGLKQFVRKCNLID-IIPVHVDAKVSE INYYFTGEKRTN-GNGLPF 606
      *:  :*:  :*:  :*:  :*:  :*:  *  :.:  .  **  :*.  :..  .  :  .*:  :  :

mmTLL11      QAFVEAFFFLAQRKFKLQ-PLHEQVASLIDLCEYHLSVLDEKRLLCHRGRPLQRN----- 699
ceTLL-11    HAFLMFLFFIAEKKFVLENDLLSKVQRLLSFCDM SLRRYGVR SARLRRAEVDSTIGNVEI 666
      **:  :  :*:  *:  *:  *  :  *  .:*  *:  *:  *  .  :  :  :*  .  .

mmTLL11      ---PPQMN RPEHSATG-----SSAPR VIGASKLSQS- 727
ceTLL-11    YMLPSRMARNRSGTNGR KQNFTDDNNPNPNSFAHLPKINERL 707
      *.:  *  *  .  .:  *  .....  .  .  *.:  :
    
```

Key:

DOMAIN NOT INCLUDED

Predicted Substrate Interacting Domains

ATP & Mg²⁺ Interacting Domains

Essential ATP-Binding Residues

Extended TTL-Domain

Core TTL-Domain

Cationic MT Binding Domain

TTL-15
CLUSTAL 2.1 multiple sequence alignment

```

mmTTL5      MPVVMARDLEETASSEDEEDLANQEDHPCIMWTGGCRRIPVLVFAEAILTKDNNIRVIG 60
ceTTL5-15  MGLLDSKLCMMILAVSVLIIDINFEARIGTFDFLRLRTSYFKKSSPLLSDSEEDLNY 60
            * :: ::      : *      * * :    :: * .   : : .*:: :

mmTTL5      ERYHLSYKIVRTDSRLVRSILTAHGFEVHPSSTDYNLMWTGSHLKPFLLRTLSEAQKVN 120
ceTTL5-15  LSKHEDKRPVAIVTGSYESAHTCHMMHIREMFEHTCYKIVTKNELSLDTKKWVMMWHHEYS 120
            * . : *   :   .* ** :* . .       : * ..* .   : :: .

mmTTL5      HFPRSYELTRKDRLYKNIIRMQHTHGFKAFHI-----LPQTFLLPAEYAEFCNSY 170
ceTTL5-15  FTQEPFKTLIKNASPNQIVNHVPCSCFYTSKVQLATSDLSNCVPKAFQLPAEKSKLLEYA 180
            . .::: * :   ::* .    ** : ::        :*: * **** :: :

mmTTL5      SKDRGPWIVKPVASSRGRGVYLINNPNOISLEEN-ILVSRVINNPILLIDDFKFDVRLYLVL 229
ceTTL5-15  EKNPDVLVWVOKDNTHRN---TKIKSTNDMDLSKNSFVOKFVDNPLLIDNKKFDIGIYTV 237
            .*: .   * :   : *.    * ..* : * : * * * : * : * * * : * : * : * :

mmTTL5      VTSYDPLVIYLYEEG-LARFATVRYDQGSKNIRNQFMHLTNYSVNKKSGDYVSCDDPEVE 288
ceTTL5-15  VTSLLPLRVYIYDGDVLIRFCPEDYHPFDANNVDKYVVGDDYTPIWEINSLKKYFNTQKM 297
            *** ** :*: * : . * * .. * . . * : : : : * :   : .. . : :

mmTTL5      DYGNKWSMSAMRLRYLKQEGKDTTALMAHVEDLIIKTIISAELAIATACTFVPHRSSCFE 348
ceTTL5-15  SFK----STIDSYLGMQMDTSKIWLQIRNIGEVFRTOOTKMLMSLONLKLN-POYFE 351
            . :      * : : * * * : * : * : : : : : : : : : : : : : : : . . * *

mmTTL5      LYGFDVLDINTLKPWLLEVNLSPSLACDAPLDLKIKASMISDMFTVVGFVCQDPAQRTSN 408
ceTTL5-15  LSRFDVVDDQLNVFLMEANMSPNLSSG---HFKQNQILYEQVLMNIFSLTGISTPITKE 408
            * ** . : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * :

mmTTL5      RSIYPSFESSRRNPFQKQTRPLSASDAEMKNLVASAREKVPGKLGGSVGLGSMEEIKV 468
ceTTL5-15  ADILFKSRTSEQNPLVSRDIN--LPLKFCVENKCESCDEAPECQLCG--HCMNTETRKI 464
            . * . . : * : * * : : : . . . : * * . * : * * . . * * :

mmTTL5      LRRVKEENDRRGGFIRIFPTSETWEIYGSYLEHKTSMNYMLATRLFQDRGNPRRSLTGR 528
ceTTL5-15  LEQTFVENSNRKQMKRIQFD---YENHHPLTKEDHLLTLWLSTKCQLDNTWC----- 513
            * : . . * * . * : * *      * : . . . . . : * : * : * .

mmTTL5      ARVSTEGAPELKVESMNSKAKLHAALYERKLLSLEVRKRRRRSGRLRAMRKYPVIAQPA 588
ceTTL5-15  -----

mmTTL5      EMNIKTETESEEEEEVGLDNDDEEQEASQEESAGSLGENQAKYTPSLTVIVENSPRDNAM 648
ceTTL5-15  -----

mmTTL5      KVAEWTNKGEPCKKIEAQEPESKFNLMQILQDNGNLSKVQARLAFSAYLQHVQIRLTKDS 708
ceTTL5-15  -----

mmTTL5      GGQTLSPSWAAKEDEQMELVVRFLKRASSNLQHSLRMVLPSRRLLALLERRRILAHQLGDF 768
ceTTL5-15  -----

mmTTL5      IGVYNKETEQMAEKKSKKLEEEEDGVNAESFOEFIRQASEAELEEVLTFYTQKNKSAS 828
ceTTL5-15  -----

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mmTTL5 ceTTL5-15	VFLGTHSKSSKNSSSYSDSGAKGDHPETIQEVKIKQPKQQQATEIHADKLSRFTTSSGKE -----	888
mmTTL5 ceTTL5-15	AKLVYTNCSFCSPPAAVLLQRLPSSHLSSVITTSALSAGPGHHSLSQIPPAVPSLPHQP -----	948
mmTTL5 ceTTL5-15	ALLLSPVPDNAPPSIHSGTQNVSPAGLPRCRSGSYTIGPFSSFQSAHIYSQKLSRPSSA -----	1008
mmTTL5 ceTTL5-15	KAAGSCHPHKHHSGIAKTQKEGEDVSLNRRYNQSLVTAELQRLAEKQAARQYSPASHISL -----	1068
mmTTL5 ceTTL5-15	LTOQVTNLNLASSVINRSSASTPPTLRPVISPSGPTWSIQPDLHASETHSSPPGSRSLQT -----	1128
mmTTL5 ceTTL5-15	GGFAWEGEVENNAYSKTTGVVPQHKYHPTAGSYQLHFALQOLEQOKLQSRQLLDQSRARH -----	1188
mmTTL5 ceTTL5-15	QAIFGSQTLPNSSLWTMNNPGPCRISSTATTGGQKPNLTPQKVVAPPNSSTLVSKPASNHK -----	1248
mmTTL5 ceTTL5-15	QVLRKPASQRASKGSSAEGQLNGLQSSLNPAAFMPITNSTGSLEAPQVIFARSKPLPTQS -----	1308
mmTTL5 ceTTL5-15	GALATVIGQRKSKSVKSGTI -----	1328

Key:

DOMAIN NOT INCLUDED

Predicted Substrate Interacting Domains

ATP & Mg²⁺ Interacting Domains

Essential ATP-Binding Residues

Extended TTL-Domain

Core TTL-Domain

Cationic MT Binding Domain

Deletion