## **Electronic Supplementary Information (ESI)**

## Reversibility and two state behavior in the thermal unfolding of oligomeric TIM barrel proteins

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**Fig. S1.** Phylogenetic representations of BacTIMs. (a) Cladogram of bacterial supertaxa (according to ref. 1) showing the species from which the indicated TIM sequence was studied. (b) Phylogenetic tree showing the TIMs studied in this work (modified from ref. 2). For AvTIM phylum ( $\gamma$ -Proteobacteria) only an approximate location in the phylogenetic tree is shown.



**Fig. S2.** Far-UV CD spectra of BacTIMs at 25 °C. Data shown are the average of five scans recorded using a protein concentration of 15  $\mu$ M in buffer C (10 mM NaH<sub>2</sub>PO<sub>4</sub> pH 8.0).



Fig. S3. Intrinsic tryptophan fluorescence spectra of BacTIMs. The spectra shown are the average of five scans recorded using a protein concentration of 15  $\mu$ M at 25 °C in buffer C (10 mM NaH<sub>2</sub>PO<sub>4</sub> pH 8.0). The excitation wavelength was 295 nm. The inset shows normalized data.



**Fig. S4.** Dependence of the  $T_m$  with respect to scan rate for BacTIMs. In all experiments, protein concentration was 15  $\mu$ M.



Fig. S5. Far-UV CD spectra of BacTIMs at 80 °C. Data shown are the average of five scans recorded using a protein concentration of 15  $\mu$ M in buffer C (10 mM NaH<sub>2</sub>PO<sub>4</sub> pH 8.0).

| EcTIM   | 1MRHPLVMGNWKLN.GSRHMVHELVSNLRKELAGV.AGCAVAIAPPEMYIDMAKREAEGSHIM   | 60  |
|---|---|---|
| EhTIM   | 1. MSARKFVVGGNWKCN. GTLASIETLTKGVAASVDAELAKKVEVIVGVPFIYIPKVQQILAGEANGANIL   | 68  |
| GqTIM   | 1 MAP. RKFFVGGNWKMN. GDKKSLGELIHTLNG AKLS ADTEVVCGAPSIYLDFARQKLDAKIG  | 60  |
| GITIM   | 1. MPARRPFIGGNFKCN, GSLDFIKSHVAAIAAHKIPDSVDVVIAPSAVHLSTAIAANTSKQLR  | 61  |
| GsTIM   |   | 60  |
| HeTIM   |   | 61  |
| 13 T INI  |   | 62  |
| L/////////  |   | 02  |
| MITT I IM   | 1MRHPVVMGNVKLN.GSREMVVDLNGLAAELERV.IGVDVAVAPALFVDLAERILIEAGSAII   | 62  |
| Mt I IM   | 1 MSRKPLIAGNWKMN . LNHYEATALVQKTAF SLPDKYYDRVDVAVTPPFTDLRSVQTLV DGDKLR  | 63  |
| OcTIM   | 1 MAPSRKFFVGGNWKMN . GRKKNLGELITTLNA AKVP ADTEVVCAPPTAYIDFARQKL DPKIA   | 61  |
| PfTIM   | 1 MARKYFVAANWKCN . GTLESIKSLTNSFNN LDFDP SKLDVVVFPVSVHYDHTRKLL QSKFS  | 60  |
| SsTIM   | 1 MAPARKFFVGGNWKMN.GRKNNLGELINTLNAAKLPADTEVVCAPPTAYIDFARQKLDPKIA  | 61  |
| TbTIM   | 1.MSKPQPIAAANWKCN.GSQQSLSELIDLFNSTSINHDVQCVVASTFVHLAMTKERLSHPKFV  | 61  |
| TcTIM   | 1 MASKPQP I AAANWKCN, GSESLLVPLIET LNAATFDHDVQCVVAPTFLHIPMTKARLTNPKFQ   | 62  |
| TsTIM   | 1. MTRKLEVGGNWKMN, GSYSHINTEEDTLOK. ADTD. PNADIVIGVPACYLKYAQDKA. PKGIK  | 59  |
| TyTIM   |   | 59  |
| VITINA  | 1 MADTEEVGCNEKIN CSKOSIKEIVEDINT ASID ENVEVVICEDATVIDVSVSIV KKDOVT  | 60  |
| I LI IIVI   |   | 64  |
| NPTIM   |   | 01  |
| GoTIM   | 1. MPTRKKFVAGNWKMN.ITLAEAKALGAAVAKGVTDDRVTVAVFPPYPWLTAVGEVLKGSPVA   | 61  |
| DrTIM   | 1 MQTLLALNWKMN . KTPTEARSWAEELTT KYAPA EGVDLAVLAPALDLSALAANL PAGIA  | 58  |
| ScTIM   | 1.MTT <mark>R</mark> TPLMAGNWKMN.LNHLEAIAHVQKLAFALADKDYDAVEVAVLAPFTDLRSVQTLVDGDKLK  | 64  |
| СрТІМ   | 1MRTPIIAGNWKMH.YTIDEAVKLVEELKPLVKDAKCEVVVCPTFVCLDAVKKAVEGTNIK   | 59  |
| -   | REEVAGNWKMN G- L LN O VEVVVAPPE LD L OKE  |   |
| Consensus   |   |   |
|   |   |   |
|   | M+PMRKPFVAGNWKMN-GTKAEA+ELVETLNAAKT++-YADVEVVVAPPFVYLDFAQQKLDGPKT+  |   |
|   |   | 124   |
| EcTIM   | M+PMRKPFVaGNWKMN-GTKAEA+ELVETLNAAKT++-YADVEVVVAPPFVYLDFAQQKLDGPKT+<br>61 LGAQNVDLNLSGAFTGETSAAMLKDIGAQYIIIGHSERRTYHKESDELIAKKFAVLKEQGLTPVLCIGETE  | 131   |
| EcTIM<br>EhTIM  | M+PMRKPFVAGNWKMN-GTKAEA+ELVETLNAAKT++-YADVEVVVAPPFVYLDFAQQKLDGPKT+<br>61 LGAQNVDLNLSGAFTGETSAAMLKDIGAQYIIIGHSERRTYHKESDELIAKKFAVLKEQGLTPVLCIGETE<br>69 VSAENAW.TKSGAYTGEVHVGMLVDCQVPYVILGHSERRQIFHESNEQVAEKVKVAIDAGLKVIACIGETE  | 131<br>138  |
| EcTIM<br>EhTIM<br>GgTIM   | M+PMRRPFVAGNWKMN-GTKAEA+ELVETLNAAKT++-YADVEVVVAPPFVYLDFAQQKLDGPKT+<br>61 LGAQNVDLNLSGAFTGETSAAMLKDIGAQYIIIGHSERRTYHKESDELIAKKFAVLKEQGLTPVLCIGETE<br>69 VSAENAW.TKSGAYTGEVHVGMLVDCQVPYVILGHSERRQIFHESNEQVAEKVKVAIDAGLKVIACIGETE<br>61 VAAQNCYKVPKGAFTGEISPAMIKDIGAAWVILGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL  | 131<br>138<br>131   |
| EcTIM<br>GgTIM<br>GgTIM   | M+PMRRPFVAGNWKMN-GTKAEA+ELVETLNAAKT++-YADVEVVVAPPFVYLDFAQQKLDGPKT+<br>61 LGAQNVDLNLSGAFTGETSAAMLKDIGAQYIIIGHSERRTYHKESDELIAKKFAVLKEQGLTPVLCIGETE<br>69 VSAENAW.TKSGAYTGEVHVGMLVDCQVPYVILGHSERRQIFHESNEQVAEKVKVAIDAGLKVIACIGETE<br>61 VAAQNCYKVPKGAFTGEISPAMIKDIGAAWVILGHSERRHVFGESDELIGQKVAHALAEGLQVIACIGEKL<br>62 IAAQNVYLEGNGAWTGETSVEMLQDMGLKHVIVGHSERRRIMGETDEQSAKKAKRALEKGMTVIFCVGETL  | 131<br>138<br>131<br>132  |
| EcTIM<br>EhTIM<br>GgTIM<br>GITIM<br>GsTIM   | M+PMRKPFVAGNWKMN-GTKAEA+ELVETLNAAKT++-YADVEVVVAPPFVYLDFAQQKLDGPKT+<br>61 L GAQNVDLNLSGAFTGETSAAMLKDIGAQYIIIGHSERRTYHKESDELIAKKFAVLKEQGLTPVLCIGETE<br>69 V SAENAW. TKSGAYTGEVHVGMLVDCQVPYVILGHSERRQIFHESNEQVAEKVKVAIDAGLKVIACIGETE<br>61 V AAQNCYKVPKGAFTGEISPAMIKDIGAAWVILGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>62 I AAQNVYLEGNGAWTGETSVEMLQDMGLKHVIVGHSERRRIMGETDEQSAKKAKRALEKGMTVIFCVGETL<br>61 I GAQTMHFADQGAYTGEVSPVMLKDLGVTYVILGHSERRQMFAETDETVNKKVLAAFTRGLIPIICCGESL  | 131<br>138<br>131<br>132<br>131   |
| EcTIM<br>EhTIM<br>GgTIM<br>GITIM<br>GsTIM<br>HsTIM  | M+PMRRPFVAGNWKMN-GTKAEA+ELVETLNAAKT++-YADVEVVVAPPFVYLDFAQQKLDGPKT+<br>61 LGAQNVDLNLSGAFTGETSAAMLKDIGAQYIIIGHSERRTYHKESDELIAKKFAVLKEQGLTPVLCIGETE<br>69 VSAENAW.TKSGAYTGEVHVGMLVDCQVPYVILGHSERRQIFHESNEQVAEKVKVAIDAGLKVTACIGETE<br>61 VAAQNCYKVPKGAFTGEISPAMIKDIGAAWVILGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>62 IAAQNVYLEGNGAWTGETSVEMLQDMGLKHVIVGHSERRRIMGETDEQSAKKAKRALEKGMTVIFCVGETL<br>61 IGAQTMHFADQGAYTGEVSPVMLKDLGVTYVILGHSERRQMFAETDETVNKKVLAAFTRGLIPIICCGESL<br>62 VAAQNCYKVTNGAFTGEISPGMIKDCGATWVVLGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL  | 131<br>138<br>131<br>132<br>131<br>132  |
| EcTIM<br>GgTIM<br>GgTIM<br>GsTIM<br>HsTIM<br>LmTIM  | M+PMRKPFVAGNWKMN-GTKAEA+ELVETLNAAKT++-YADVEVVVAPPFVYLDFAQQKLDGPKT+<br>61 L. GAQNVDLNLSGAFTGETSAAMLKDIGAQYIIIGHSERRTYHKESDELIAKKFAVLKEQGLTPVLCIGETE<br>69 V. SAENAW. TKSGAYTGEVHVGMLVDCQVPYVILGHSERRQIFHESNEQVAEKVKVA IDAGLKVIACIGETE<br>61 V. AAQNCYKVPKGAFTGEISPAMIKDIGAAWVILGHSERRRIMGETDEQSAKKAKRALAEGLGVIACIGEKL<br>62 I. AAQNVYLEGNGAWTGETSVEMLQDMGLKHVIVGHSERRRIMGETDEQSAKKAKRALEKGMTVIFCVGETL<br>61 I. GQTMHFADQGAYTGEVSPVMLKDLGVTYVILGHSERRQMFAETDETVNKKVLAAFTRGLIPIICCGESL<br>62 V. AAQNCYKVTNGAFTGEISPGMIKDCGATWVVLGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>63 I. SAENAI. AKSGAFTGEVSMPILKDIGVHWVILGHSERRTYYGETDEIVAQKVSEACKGGFMVIACIGETL  | 131<br>138<br>131<br>132<br>131<br>132<br>132   |
| EcTIM<br>GgTIM<br>GgTIM<br>GSTIM<br>HSTIM<br>LmTIM<br>MmTIM   | M+PMRKPFVAGNWKMN-GTKAEA+ELVETENAAKT++-YADVEVVVAPPFVYLDFAQQKLDGPKT+<br>61 LGAQNVDLNLSGAFTGETSAAMLKDIGAQYIIIGHSERRTYHKESDELIAKKFAVLKEQGLTPVLCIGETE<br>69 VSAENAW. TKSGAYTGEVHVGMLVDCQVPYVILGHSERRQIFHESNEQVAEKVKVAIDAGLKVIACIGETE<br>61 VAAQNCYKVPKGAFTGEISPAMIKDIGAAWVILGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>62 IAAQNVYLEGNGAWTGETSVEMLQDMGLKHVIVGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>61 IGAQTMHFADQGAYTGEVSPVMLKDLGVTYVILGHSERRRIMGETDEQSAKKAKRALEKGMTVIFCVGETL<br>62 VAAQNCYKVTNGAFTGEISPGMIKDCGATWVVLGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>63 ISAENAI. AKSGAFTGEVSPVMLKDIGVHWVILGHSERRHVFGESDELIQQKVAHALAEGLGVIACIGEKL<br>63 LGAQTTDLNNSGAFTGDMSPAMLKEFGATHIIGHSERREYHAESDEVAKKAFALKKOGTPVLCIGESD   | 131<br>138<br>131<br>132<br>131<br>132<br>132<br>133  |
| EcTIM<br>EhTIM<br>GgTIM<br>GsTIM<br>HsTIM<br>HsTIM<br>MmTIM<br>MMTIM  | M+PMRRPFVAGNWKMN-GTKAEA+ELVETLNAAKT++-YADVEVVVAPPFVYLDFAQQKLDGPKT+<br>61 L GAQNVDLNLSGAFTGETSAAMLKDIGAQYIIIGHSERRTYHKESDELIAKKFAVLKEQGLTPVLCIGETE<br>69 V SAENAW. TKSGAYTGEVHVGMLVDCQVPYVILGHSERRQIFHESNEQVAEKVKVAIDAGLKVIACIGETE<br>61 V AAQNCYKVPKGAFTGEISPAMIKDIGAAWVILGHSERRRIMGETDEQSAKKAKRALAEGUGVIACIGEKL<br>62 I AAQNVYLEGNGAWTGETSVEMLQDMGLKHVIVGHSERRRIMGETDEQSAKKAKRALEKGMTVIFCVGETL<br>61 I GAQTMHFADQGAYTGEVSPVMLKDLGVTYVILGHSERRRIMGETDEQSAKKAKRALEKGMTVIFCVGETL<br>61 I GAQTMHFADQGAYTGEVSPVMLKDLGVTYVILGHSERRRIMGETDETVNKKVLAAFTRGLIPIICCGESL<br>62 V AAQNCYKVTNGAFTGEISPGMIKDCGATWVVLGHSERRTYGETDEIVAQKVSEACKQGFMVIACIGEKL<br>63 I SAENAI. AKSGAFTGEVSMPILKDIGVHWVILGHSERRTYGETDEIVAQKVSEACKQGFMVIACIGETL<br>63 L GAQNTDLNNSGAFTGDMSPAMLKEFGATHIGHSERREYHAESDEFVAKKFAFLKENGLTPVLCIGESD<br>64 LTYGAQDLSPHDSGAYTGDVSGAFLAKLGCSYVVVGHSERRTYHNEDDALVAAKAATALKHGLTPIVCIGEHL   | 131<br>138<br>131<br>132<br>131<br>132<br>132<br>133<br>136   |
| EcTIM<br>EhTIM<br>GgTIM<br>GSTIM<br>HSTIM<br>HSTIM<br>MmTIM<br>MmTIM<br>QcTIM   | M+PMRRPFVAGNWKMN-GTKAEA+ELVETLNAAKT++-YADVEVVVAPPFVYLDFAQQKLDGPKT+<br>61 L GAQNVDLNLSGAFTGETSAAMLKD I GAQY I I I GHSERRTYHK ESDEL I AKK FAVLKEQGLTPVLC I GETE<br>69 V SAENAW. TKSGAYTGEVHVGMLVDCQVPYVI LGHSERRQI FHESNEQVAEKVKVA I DAGLKVI AC I GETE<br>61 V AAQNCYKVPKGAFTGE I SPAMI KD I GAAWVI LGHSERRHVFGESDEL I GQKVAHALAEGLGVI AC I GEKL<br>62 I AAQNVYLEGNGAWTGETSVEMLQDMGLKHVI VGHSERRRIMGETDEQSAKKAKRALEKGMTVI FCVGETL<br>61 I GAQTMHFADQGAYTGEVSPVMLKDLGVTYVI LGHSERRQMFAETDETVNKKVLAAFTRGLI PI I CCGESL<br>62 V AAQNCYKVTNGAFTGE I SPGMI KDCGATWVVLGHSERRHVFGESDEL I GQKVAHALAEGLGVI AC I GEKL<br>63 I SAENAI . AKSGAFTGEVSMPI LKDI GVHWVI LGHSERRTYYGETDE I VAQKVSEACKOGFMVI AC I GEKL<br>63 L GAQNTDLNNSGAFTGDMSPAMLKEFGATH I I GHSERREYHAESDEFVAKKFAFLKENGL TPI VC I GESD<br>64 LTYGAQDLSPHDSGAYTGDVSGAFLAKLGCSYVVVGHSERRTYHNEDDALVAAKAATALKHGLTPI VC I GEHL<br>62 V AAQNCYKVTNGAFTGE I SPGMI KDCGATWVVLGHSERRHVFGESDEL I GQKVAHALSEGLGVI AC I GEKL   | 131<br>138<br>131<br>132<br>131<br>132<br>132<br>133<br>136<br>132  |
| EcTIM<br>EhTIM<br>GgTIM<br>GSTIM<br>HSTIM<br>LmTIM<br>MmTIM<br>MtTIM<br>PFTIM   | M+PMRRPFVAGNWKMN-GTKAEA+ELVETLNAAKT++-YADVEVVVAPPFVYLDFAQQKLDGPKT+<br>61 L. GAQNVDLNLSGAFTGETSAAMLKD IGAQYIIIGHSERRTYHKESDELIAKKFAVLKEQGLTPVLCIGETE<br>69 V. SAENAW. TKSGAYTGEVHVGMLVDCQVPYVILGHSERRQIFHESNEQVAEKVKVA IDAGLKVIACIGETE<br>61 V. AAQNCYKVPKGAFTGE ISPAMIKD IGAAWVILGHSERRRIMGETDEQSAKKAKRALEKGMTVIFCVGETL<br>61 I. AAQNVYLEGNGAWTGETSVEMLQDMGLKHVIVGHSERRRIMGETDEQSAKKAKRALEKGMTVIFCVGETL<br>61 I. GAQTMHFADQGAYTGEVSPVMLKDLGVTYVILGHSERRRIMGETDEQSAKKAKRALEKGMTVIFCVGETL<br>61 I. GAQTMHFADQGAYTGEVSPVMLKDLGVTYVILGHSERRRIMGETDETVNKKVLAAFTRGLIPIICCGESL<br>62 V. AAQNCYKVTNGAFTGE ISPGMIKDCGATWVVLGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>63 I. SAENAI. AKSGAFTGEVSMPILKDIGVHWVILGHSERRTYYGETDEIVAKKVEACKGGFMVIACIGETL<br>63 L. GAQNTDLNNSGAFTGDMSPAMLKEFGATHIIIGHSERRTYHAESDEFVAKKFAFLKENGLTPVLCIGESD<br>64 LTYGAQDLSPHDSGAYTGDVSGAFLAKLGCSYVVYGHSERRTYNEDDALVAKKATALKHGLTPIVCIGEKL<br>67 L. GLDNVSKFGNGSYTGEVSAFLAKLDCVAWVLGHSERRHVFGESDELIGQKVAHALSEGLGVIACIGEKL   | 131<br>138<br>131<br>132<br>131<br>132<br>133<br>136<br>132<br>131  |
| EcTIM<br>GgTIM<br>GgTIM<br>GITIM<br>GSTIM<br>HsTIM<br>LmTIM<br>MmTIM<br>OcTIM<br>SeTIM  | M+PMRRPFVAGNWKMN-GTKAEA+ELVETLNAAKT++-YADVEVVVAPPFVYLDFAQQKLDGPKT+<br>61 L. GAQNVDLNLSGAFTGETSAAMLKDIGAQYIIIGHSERRTYHKESDELIAKKFAVLKEQGLTPVLCIGETE<br>69 V. SAENAW. TKSGAYTGEVHVGMLVDCQVPYVILGHSERRQIFHESNEQVAEKVKVAIDAGLKVIACIGETE<br>61 V. AAQNCYKVPKGAFTGEISPAMIKDIGAAWVILGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>62 I. AAQNVYLEGNGAWTGETSVEMLQDMGLKHVIVGHSERRRIMGETDEQSAKKAKRALEKGMTVIFCVGETL<br>61 I. GAQTMHFADQGAYTGEVSPVMLKDLGVTYVILGHSERRRIMGETDEQSAKKAKRALEKGMTVIFCVGETL<br>61 I. GAQTMHFADQGAYTGEVSPVMLKDLGVTYVILGHSERRRIMGETDEQSAKKAKRALEKGMTVIFCVGETL<br>62 V. AAQNCYKVTNGAFTGEISPGMIKDCGATWVVLGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>63 I. SAENAI. AKSGAFTGEVSMPILKDIGVHWVILGHSERRTYYGETDEIVAQKVSEACKOGFMVIACIGETL<br>63 L. GAQNTDLNNSGAFTGDMSPAMLKEFGATHIIIGHSERREYHAESDEFVAKKFAFLKENGLTPVLCIGESD<br>64 LTYGAQDLSPHDSGAYTGDVSGAFLAKLGCSYVVVGHSERRTYHNEDDALVAAKAATALKHGLTPIVCIGEHL<br>62 V. AAQNCYKVTNGAFTGEISPGMIKDCGATWVVLGHSERRHVFGESDELIGQKVAHALSEGLGVIACIGEKL<br>64 LTYGAQDLSPHDSGAYTGDVSGAFLAKLGCSTVVVGHSERRTYHNEDDALVAAKAATALKHGLTPIVCIGEHL<br>65 V. AAQNCYKVANGAFTGEISPGMIKDCGATWVVLGHSERRHVFGESDELIGQKVAHALSEGLGVIACIGEKL<br>66 LTYGAQDLSPHDSGAYTGDVSGAFLAKLGCSTVVVGHSERRTYHNEDDALVAAKAATALKHGLTPIVCIGEHL<br>67 V. AAQNCYKVANGAFTGEISPGMIKDCGATWVVLGHSERRHVFGESDELIGQKVAHALSEGLGVIACIGEKL<br>67 V. AAQNCYKVANGAFTGEISPGMIKDCGATWVVLGHSERRHVFGESDELIGQKVAHALSEGLGVIACIGEKL  | 131<br>138<br>131<br>132<br>131<br>132<br>133<br>136<br>132<br>131  |
| EcTIM<br>GgTIM<br>GgTIM<br>GsTIM<br>MsTIM<br>LmTIM<br>MmTIM<br>MmTIM<br>OcTIM<br><br>PfTIM<br>TbTTM   | M+PMRRPFVAGNWKMN-GTKAEA+ELVETLNAAKT++-YADVEVVVAPPFVYLDFAQQKLDGPKT+<br>61 L. GAQNVDLNLSGAFTGETSAAMLKD I GAQYIII GHSERRTYHKESDELIAKKFAVLKEQGLTPVLCIGETE<br>69 V. SAENAW. TKSGAYTGEVHVGMLVDCQVPYVILGHSERRQIFHESNEQVAEKVKVA I DAGLKVIAC I GETE<br>61 V. AAQNCYKVPKGAFTGE I SPAMIKD I GAAWVILGHSERRRIMGETDEQSAKKAKRALEKGMTVIFCVGETL<br>62 I. AAQNVYLEGNGAWTGETSVEMLQDMGLKHVIVGHSERRRIMGETDEQSAKKAKRALEKGMTVIFCVGETL<br>64 I. GAQTMHFADQGAYTGEVSPVMLKDLGVTYVILGHSERRRIMGETDEQSAKKAKRALEKGMTVIFCVGETL<br>64 I. GAQTMHFADQGAYTGEVSPVMLKDLGVTYVILGHSERRRIMGETDETVNKKVLAAFTRGLIPIICCGESL<br>62 V. AAQNCYKVTNGAFTGE I SPGMIKDCGATWVVLGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>63 I. SAENAI. AKSGAFTGEVSMPILKDIGVHWVILGHSERRTYNGETDEIVAQKVSEACKQFMVIACIGETL<br>64 LTYGAQDLSPHDSGAYTGDVSGAFLAKLGCSYVVVGHSERRTYHNEDDALVAAKAATALKHGLTPIVCIGEHL<br>65 V. AAQNCYKVTNGAFTGE I SPGMIKDCGATWVVLGHSERRTYHNEDDALVAAKAATALKHGLTPIVCIGEHL<br>66 LTYGAQDLSPHDSGAYTGDVSGAFLAKLGCSYVVVGHSERRTYHNEDDALVAAKAATALKHGLTPIVCIGEHL<br>67 V. AAQNCYKVTNGAFTGE I SPGMIKDCGATWVVLGHSERRTYHNEDDALVAAKAATALKHGLTPIVCIGEHL<br>68 L. GAQNTDLNNSGAFTGEVSAFIAKDLNIEYVIGHSERRTYHNEDDALVAAKAATALKHGLTPIVCIGEHL<br>69 V. AAQNCYKVTNGAFTGE I SPGMIKDCGATWVVLGHSERRTYHNEDDALVAAKAATALKHGLTPIVCIGEHL<br>60 V. AAQNCYKVNGAFTGE I SPGMIKDCGATWVVLGHSERRTYHNEDDALVAAKAATALKHGLTPIVCIGEKL<br>61 T. GIQNVSKFGNGSYTGEVSAEIAKDLNIEYVIGHSERRTYHNEDDALVAAKAATALKHGLTPIVCIGEKL<br>62 V. AAQNCYKVANGAFTGE I SPGMIKDCGATWVVLGHSERRTYHNETDEDVREKLQASLKNNLKAVVCFGESL<br>62 V. AAQNCYKVANGAFTGE I SPGMIKDCGATWVVLGHSERRTYHTETDEDVREKLQASLKNNLKAVVCFGESL<br>62 V. AAQNCYKVANGAFTGE I GPGMIKDLGATWVVLGHSERRTYHTETDEDVREKLAASLKMALKAVCFGESL<br>64 LTYGAQDLSPHDVAAFTGE I GPGMIKDLGATWVVLGHSERRTYHTETDEDVREKLAASLKAATALGCVIACIGEKL<br>65 J. AAQNCYKVANGAFTGE I SPGMIKDLGATWVVLGHSERRTYHTETDEDVREKLAASLKMALAFGEVTACIGEKL<br>65 J. AAQNCYKVANGAFTGE I GPGMIKDLGATWVVLGHSERRTYFGESDELIGQKVAHALAEGUGVIACIGET   | 131<br>138<br>131<br>132<br>131<br>132<br>133<br>136<br>132<br>131<br>132   |
| EcTIM<br>EhTIM<br>GgTIM<br>GSTIM<br>HSTIM<br>MTIM<br>MTIM<br>OcTIM<br>OcTIM<br>   | M+PMRRPFVAGNWKMN-GTKAEA+ELVETENAAKT++-YADVEVVVAPPFVYLDFAQQRLDGPKT+<br>61 L. GAQNVDLNLSGAFTGETSAAMLKDIGAQYIIIGHSERRTYHKESDELIAKKFAVLKEQGLTPVLCIGETE<br>69 V. SAENAW. TKSGAYTGEVHVGMLVDCQVPYVILGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGETE<br>61 V. AAQNCYKVPKGAFTGEISPAMIKDIGAAWVILGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>62 I. AAQNVYLEGNGAWTGETSVEMLQDMGLKHVIVGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>61 I. GAQTMHFADQGAYTGEVSPVMLKDLGVTYVILGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>62 V. AAQNCYKVTNGAFTGEISPCMIKDLGVTYVILGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>63 I. SAENAI.AKSGAFTGEVSMPILKDIGVHVVLGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGETL<br>64 L. GAQNTDLNNSGAFTGDMSPAMLKEFGATHIIIGHSERREYHAESDEFVAKKFAFLKENGLTPVLCIGESD<br>64 LTYGAQUSPHDSGAYTGDVSGAFLAKLGCSYVVVGHSERRTYNEDDALVAAKAATALKHGLTPVLCIGESL<br>64 LTYGAQUSPHDSGAYTGEVSAFIAKLGCSYVVVGHSERRTYNEDDALVAAKAATALKHGLTPVLCIGEKL<br>64 T. GIQNVSKFGNGSYTGEVSAEIAKDLNIEYVIIGHSERRTYFHETDEDVREKLQASLKNNLKAVVCFGESL<br>64 LTYGAQNCYKVANGAFTGEISPGMIKDCGATWVVLGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>65 T. GAQNCYKVANGAFTGEIGPGMIKDLGATWVVLGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>66 T. GIQNVSKFGNGSYTGEVSAEIAKDLNIEYVIIGHSERRTYFHETDEDVREKLQASLKNNLKAVVCFGESL<br>67 C. AAQNCYKVANGAFTGEIGPGMIKDLGATWVVLGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>67 C. AAQNCYKVANGAFTGEIGPGMIKDLGATWVVLGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>68 T. AAQNAI.AKSGAFTGEVSLPILKDFGVNWIVLGHSERRTYFHETDEDVREKLQASLKNNLKAVVCFGESL<br>69 C. AAQNCYKVANGAFTGEIGPGMIKDLGATWVVLGHSERRYFHETDEDVREKLQASLKNNLKAVVCFGESL<br>60 C. AAQNAI.AKSGAFTGEVSLPILKDFGVNWIVLGHSERRAYFGESDELIGQKVAHALAEGLGVIACIGEKL<br>62 J. AAQNAI.AKSGAFTGEVSLPILKDFGVNWIVLGHSERRAYFGESDELIGQKVAHALAEGLGVIACIGETU  | 131<br>138<br>131<br>132<br>132<br>132<br>133<br>136<br>132<br>131<br>132   |
| EcTIM<br>GgTIM<br>GgTIM<br>GsTIM<br>HsTIM<br>MmTIM<br>MmTIM<br>MtTIM<br>OcTIM<br>SsTIM<br>TbTIM<br>TcTIM  | M+PMRRPFVAGNWKMN-GTKAEA+ELVETLNAAKT++-YADVEVVVAPPFVYLDFAQQRLDGPKT+<br>61 L. GAQNVDLNLSGAFTGETSAAMLKD IGAQYIIIGHSERRTYHKESDELIAKKFAVLKEQGLTPVLCIGETE<br>69 V. SAENAW. TKSGAYTGEVHVGMLVDCQVPYVILGHSERRQIFHESNEQVAEKVKVA IDAGLKVIACIGETE<br>61 V. AAQNCYKVPKGAFTGE ISPAMIKD IGAAWVILGHSERRRIMGETDEQSAKKAKRALEKGMTVIFCYGETL<br>61 I. GAQTMHFADQGAYTGEVSPVMLKDLGVTYVILGHSERRRIMGETDEQSAKKAKRALEKGMTVIFCYGETL<br>61 I. GAQTMHFADQGAYTGEVSPVMLKDLGVTYVILGHSERRRIMGETDETVNKKVLAAFTRGLIPIICCGESL<br>62 V. AAQNCYKVTNGAFTGE ISPGMIKDCGATWVVLGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>63 I. SAENAI. AKSGAFTGEVSMPILKDIGVHWVILGHSERRTYYGETDEIVAKKVEAFLKENGLTPVLCIGESL<br>64 LTYGAQDLSPHDSGAYTGDVSGAFLAKLGCSYVVVGHSERRTYHNEDDALVAKKATALKHGLTPIVCIGEHL<br>65 L. GQNVSKGNGSYTGEVSAEIAKLDCGATWVVLGHSERRTYHEDDALVAKKATALKHGLTPIVCIGEKL<br>66 LTYGAQDLSPHDSGAYTGDVSGAFLAKLGCSYVVVGHSERRTYHNEDDALVAKKATALKHGLTPIVCIGEKL<br>67 V. AAQNCYKVNGAFTGE ISPGMIKDCGATWVVLGHSERRTYFHETDEDVRKKLQASLKNNLKAVVCFGESL<br>64 LTYGAQDLSPHDSGAYTGEVSAEIAKLDLNIEYVIIGHSERRTYFHETDEDVREKLQASLKNNLKAVVCFGESL<br>64 LTYGAQDLSPHDSGYTGEVSAEIAKLDLNIEYVIGHSERRTYFHETDEDVREKLQASLKNNLKAVVCFGESL<br>64 LTYGAQDLSPHDSGYTGEVSAEIAKDLNIEYVIGHSERRTYFHETDEDVREKLQASLKNNLKAVVCFGESL<br>64 LTYGAQDLSPHDSGYTGEVSAEIAKDLNIEYVIGHSERRTYFHETDEDVREKLQASLKNNLKAVVCFGESL<br>65 AAQNCYKVNNGAFTGEISPGMIKDCGATWVVLGHSERRTYFHETDEDVREKLQASLKNNLKAVVCFGESL<br>64 LTYGAQDLSPHDSGYTGEVSAEIAKDLNIEYVIGHSERRTYFHETDEDVREKLQASLKNNLKAVVCFGESL<br>65 AAQNCYKVANGAFTGEISPGMIKDCGATWVVLGHSERRTYFHETDEDVREKLQASLKNNLKAVVCFGESL<br>64 LTYGAQALI.AKSGAFTGEVSLPILKDFGVNWIVLGHSERRTYFHETDEDVREKLQASLKNNLKAVVCFGESL<br>65 AAQNAI.AKSGAFTGEVSLPILKDFGVNWIVLGHSERRAYFGESDELIGQKVAHALAEGLGVIACIGEKL<br>65 AAQNAI.AKSGAFTGEVSLPILKDFGVNWIVLGHSERRLYFGENEIVAFTGENETVAGAAAAASGFMVIACIGETL<br>65 AAQNAI.AKSGAFTGEVSLQILKDYGIKWVLGHSERRLYFGENETVAFT   | 131<br>138<br>131<br>132<br>131<br>132<br>133<br>136<br>132<br>131<br>132<br>131  |
| EcTIM<br>GgTIM<br>GgTIM<br>GSTIM<br>HsTIM<br>LmTIM<br>MmTIM<br>MtTIM<br>OcTIM<br>SSTIM<br>TbTIM<br>TcTIM<br>TsTIM   | M+PMRRPFVAGNWKMN-GTKAEA+ELVETENAAKT++-YADVEVVVAPPFVYLDFAQQKLDGPKT+<br>61 L. GAQNVDLNLSGAFTGETSAAMLKD I GAQYI I I GHSERRTYHK ESDEL I AKK FAVLKEQGL TPVLC I GETE<br>69 V. SAENAW. TKSGAYTGEVHVGMLVDCQVPYVI LGHSERRQI FHESNEQVAEKVKVA I DAGLKVI AC I GETE<br>61 V. AAQNCYKVPKGAFTGE I SPAMI KD I GAAWVI LGHSERRHVFGESDEL I GQKVAHALAEGLGVI AC I GETL<br>61 I. AAQNVYLEGNGAWTGETSVEMLQDMG LKHVI VGHSERRRI IMGET DEQSAKKAKRALEKGMT VI FCYGETL<br>61 I. GAQTMHFADQGAYTGEVSPVMLKD LGVTYVI LGHSERRRI MGET DEQSAKKAKRALEKGMT VI FCYGETL<br>62 V. AAQNCYKVTNGAFTGE I SPAMI KD LGATWVVLGHSERRHVFGESDEL I GQKVAHALAEGLGVI AC I GEKL<br>63 I. SAENAI. AKSGAFTGEVSMPI LKD I GVHWVI LGHSERRTYFGET DE I VAQKVSEACKOGFMVI AC I GETL<br>63 L. GAQNTDLNNSGAFTGEVSMPI LKD I GVHWVI LGHSERRTYHAE SDEFVAKKFAFLKENGL TPVLC I GESD<br>64 LTYGAQDLSPHDSGAYTGDVSGAFLAKLGCSYVVVGHSERRTYHNEDDALVAAKAATALKHGLTPI VCI GEHL<br>62 V. AAQNCYKVTNGAFTGE I SPGMI KDCGATWVVLGHSERRHVFGESDEL I GQKVAHALSEGLGVI AC I GEKL<br>64 LTYGAQDLSPHDSGAYTGDVSGAFLAKLGCSYVVGHSERRTYHNEDDALVAAKAATALKHGLTPI VCI GEHL<br>65 V. AAQNCYKVTNGAFTGE I SPGMI KDCGATWVVLGHSERRHVFGESDEL I GQKVAHALSEGLGVI AC I GEKL<br>66 LTYGAQDLSPHDSGAYTGEVSAE I AKDLN I EYVI I GHFERKYFHETDEDVREKLQASLKNN LKAVVC FGESL<br>67 V. AAQNCYKVNGAFTGE I SPGMI KDCGATWVVLGHSERRHVFGESDEL I GQKVAHALSEGLGVI AC I GEKL<br>68 J. AQNNAI. AKSGAFTGEVSLPI LKDFGVNWI VLGHSERRAYGE SDEL I GQKVAHALSEGLGVI AC I GEKL<br>69 J. AAQNCYKVNGAFTGE I SPGMI KDCGATWVVLGHSERRAYGE SDEL I GQKVAHALSEGLGVI AC I GEKL<br>61 J. AAQNAI. AKSGAFTGEVSLPI LKDFGVNWI VLGHSERRAYGE SDEL I GQKVAHALSEGLGVI AC I GEKL<br>62 I. AAQNAI. AKSGAFTGEVSLPI LKDFGVNWI VLGHSERRAYGE SDEL I GQKVAHALAEGLGVI AC I GEKL<br>63 I. AAQNAI. AKSGAFTGEVSLPI LKDFGVNWI VLGHSERRAYGE SDEL I GQKVAHALAEGLGVI AC I GEKL<br>64 I. AAQNAI. AKSGAFTGEVSLPI LKDFGVNWI VLGHSERRAYGE SDEL I GQKVAHALAEGLGVI AC I GEKL<br>65 I. AAQNAI. AKSGAFTGEVSLPI LKDFGVNWI VLGHSERRAYGE SDEL I GQKVAHALAEGLGVI AC I GETL<br>65 I. AAQNAI. TRSGAFTGEVSLPI LKDFGCCEWVI LGHSERRAYGE SDEL I GGKVKHALDSGLNVI PC I GELL   | 131<br>138<br>131<br>132<br>131<br>132<br>133<br>136<br>132<br>131<br>132<br>131<br>132<br>130                                    |
| EcTIM<br>GgTIM<br>GgTIM<br>GSTIM<br>HsTIM<br>HsTIM<br>MmTIM<br>MmTIM<br>OcTIM<br>PfTIM<br>SSTIM<br>TbTIM<br>TcTIM<br>TsTIM<br>TsTIM   | M+PMRRPFVAGNWKMN-GTKAEA+ELVETLNAAKT++-YADVEVVVAPPFVYLDFAQQKLDGPKT+<br>61 L. GAQNVDLNLSGAFTGETSAAMLKD I GAQYIII GHSERRTYHKESDELIAKKFAVLKEQGLTPVLCIGETE<br>69 V. SAENAW. TKSGAYTGEVHVGMLVDCQVPYVILGHSERRQIFHESNEQVAEKVKVA I DAGLKVIAC I GETE<br>61 V. AAQNCYKVPKGAFTGE I SPAMIKD I GAAWVILGHSERRRIMGET DEQSAKKAKRALEKGMTVIFCVGETL<br>62 I. AAQNVYLEGNGAWTGETSVEMLQDMG LKHVIVGHSERRRIMGET DEQSAKKAKRALEKGMTVIFCVGETL<br>63 L. GAQTMHFADQGAYTGEVSPVMLKDLGVTYVILGHSERRRIMGET DEQSAKKAKRALEKGMTVIFCVGETL<br>64 LTYGAQDLSPHDSGATGE I SPAMIKD GATWVVLGHSERRHVFGESDELIGQKVAHALAEGLGVIAC I GETL<br>63 L. GAQTTDLNNSGAFTGEVSMPILKD I GVHWVILGHSERRTYNGET DE I VAQKVSEACKQFFMVIAC I GETL<br>64 LTYGAQDLSPHDSGAYTGDVSGAFLAKLGCSYVVVGHSERRTYHNEDDALVAAKAATALKHGLTPIVCIGEHL<br>65 V. AAQNCYKVTNGAFTGE I SPGMIKDCGATWVVLGHSERRTYHNEDDALVAAKAATALKHGLTPIVCIGEHL<br>66 LTYGAQDLSPHDSGAYTGDVSGAFLAKLGCSYVVVGHSERRTYHNEDDALVAAKAATALKHGLTPIVCIGEHL<br>67 V. AAQNCYKVTNGAFTGE I SPGMIKDCGATWVVLGHSERRTYHNEDDALVAAKAATALKHGLTPIVCIGEHL<br>68 L. GQQNTGDVSGAFLAKLGCSYVVGHSERRTYHNEDDALVAAKAATALKHGLTPIVCIGEHL<br>69 V. AAQNCYKVNGAFTGE I SPGMIKDCGATWVVLGHSERRTYHNEDDALVAAKAATALKHGLTPIVCIGEHL<br>60 V. AAQNCYKVNGAFTGE I GPGMIKDLGATWVVLGHSERRHVFGESDELIGQKVAHALSEGLGVIAC I GEKL<br>61 T. GIQNVSKFGNGSYTGEVSAE I AKDLN I EYVIIGHSERRHVFGESDELIGQKVAHALSEGLGVIAC I GEKL<br>62 I. AAQNAI. AKSGAFTGEVSLPILKDFGVNWIVLGHSERRHVFGESDELIGQKVAHALAEGLGVIAC I GEKL<br>63 I. AAQNAI. AKSGAFTGEVSLPILKDFGVNWIVLGHSERRHVFGESDELIGGKVAHALAEGLGVIAC I GETL<br>63 I. AAQNAI. TRSGAFTGEVSLPILKDFGVNWIVLGHSERRLYTGETNEIVADKVAAAVASGFMVIAC I GETL<br>64 L. AAQNAI. TRSGAFTGEVSLPILKDFGVNWIVLGHSERRLYTGETNEIVADKVAAAVASGFMVIAC I GETL<br>64 L. AAQNAI. TRSGAFTGEVSLPILKDFGVNWIVLGHSERRLYTGETNEIVADACVAAGAGAGAGHVIVCYGETN<br>60 I. AAENCYKVGSGAFTGE I STEMIKDCGCEWVILGHSERRLYTGETNEIVADACAAGAFHVIVCYGETN<br>60 V. SAENVFTKPNGAFTGEVTVPMIKSFGIEWTILGHSERRHIFGESNELIGEKVKHALDSGLNVIPCIGELL<br>60 V. SAENVFTKPNGAFTGEVTVPMIKSFGIEWTILGHSERRDILKEDDEFLAAKAKFALENGMKIIYCGEHL   | 131<br>138<br>131<br>132<br>131<br>132<br>133<br>136<br>132<br>131<br>132<br>131<br>132<br>130<br>130                             |
| EcTIM<br>EhTIM<br>GgTIM<br>GSTIM<br>HSTIM<br>MTIM<br>MTIM<br>OcTIM<br>OCTIM<br>   | M+PMRRPFVAGNWKMN-GTKAEA+ELVETLNAAKT++-YADVEVVVAPPFVYLDFAQQRLDGPKT+<br>61 L. GAQNVDLNLSGAFTGETSAAMLKDIGAQYIIIGAQYIIIGHSERRTYHKESDELIAKKFAVLKEQGLTPVLCIGETE<br>69 V. SAENAW. TKSGAYTGEVHVGMLVDCQVPYVILGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGETE<br>61 V. AAQNCYKVPKGAFTGEISPAMIKDIGAAWVILGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>62 I. AAQNVYLEGNGAWTGETSVEMLQDMGLKHVIVGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>61 I. GAQTMHFADQGAYTGEVSPVMLKDLGVTYVILGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>62 V. AAQNCYKVTNGAFTGEISPOMIKDLGVTYVILGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>63 I. SAENAI.AKSGAFTGEVSPVMLKDLGVTYVILGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGETL<br>64 L. GAQNTDLNNSGAFTGDMSPAMLKEFGATHIIIGHSERREYHAESDEFVAKKFAFLKENGLTPVLCIGESD<br>64 LTYGAQDLSPHDSGAYTGDVSGAFLGKLGGATWVVLGHSERRHVFGESDELIGQKVAHALSEGLGVIACIGEKL<br>61 T. GIQNVSKFGNGSYTGEVSAFIAKLGCSVVVVGHSERRHVFGESDELIGQKVAHALSEGLGVIACIGEKL<br>61 T. GIQNVSKFGNGSYTGEVSAFIAKDCGATWVVLGHSERRHVFGESDELIGQKVAHALSEGLGVIACIGEKL<br>62 V. AAQNCYKVNGAFTGEISPGMIKDCGATWVLGHSERRHVFGESDELIGQKVAHALSEGLGVIACIGEKL<br>63 L. GAQNAI.KHGLTPIVCIGEISPGMIKDCGATWVLGHSERRHVFGESDELIGQKVAHALSEGLGVIACIGEKL<br>64 LTYGAQNAJKKFGNGSYTGEVSAFIAKDLNIEYVIIGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>65 L. AAQNAI.AKSGAFTGEVSLOILKDYGIKWVLGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>66 LTYGAQNAI.KEGNGSYTGEVSAEIAKDLNIEYVIIGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>67 L. AAQNAI.TRSGAFTGEVSLOILKDYGIKWVVLGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGETL<br>68 L. AAQNAI.TRSGAFTGEVSLOILKDYGIKWVVLGHSERRAYFGETNEIVAEKVAQACAAAGSGFWVIACIGETL<br>69 L. AAQNAI.TRSGAFTGEVSLOILKDYGIKWVVLGHSERRAYFGETNEIVAEKVAQACAAAAASGFWVIACIGETL<br>60 L. AAQNAI.TRSGAFTGEVSLOILKDYGIKWVVLGHSERRAYFGETNEIVAEKVAQACAAGAFHVIVCVGETN<br>60 L. AAENVFKKNGSGAFTGEISTEMIKDCGCEWVILGHSERRNIKGDELIGEKKHALDSCLNVVICGELL<br>60 V. SAENVFKKNGSGAFTGENSVDQIKDVGAKWVLGHSERRPIIKSYFHEDDKFIAAKAKFALENGMKIIYCCGEHL<br>61 V. GAQNAYLKASGAFTGENSVDQIKDVGAKWVLGHSERRPIKFEDELIGEKVKHALDSCLNVVICGELL<br>60 V. SAENVFKKAGGAFTGENSVDQIKDVGAKWVLGHSERRPIKFEDELIGEKVKHALDGCNGKIIYCCGEHL  | 131<br>138<br>131<br>132<br>131<br>132<br>133<br>136<br>132<br>131<br>132<br>131<br>132<br>130<br>130<br>131                      |
| EcTIM<br>GgTIM<br>GgTIM<br>GsTIM<br>HsTIM<br>MmTIM<br>MmTIM<br>OcTIM<br>PITIM<br>SSTIM<br>TbTIM<br>TsTIM<br>TvTIM<br>YtTIM<br>YtTIM<br>NpTIM  | M+PMRRPFVAGNWKMN-GTKAEA+ELVETLNAAKT++-YADVEVVVAPPFVYLDFAQQRLDGPKT+<br>61 L. GAQNVDLNLSGAFTGETSAAMLKD IGAQYIIIGHSERRTYHKESDELIAKKFAVLKEQGLTPVLCIGETE<br>69 V. SAENAW. TKSGAYTGEVHVGMLVDCQVPYVILGHSERRQIFHESNEQVAEKVKVA IDAGLKVIACIGETE<br>61 V. AAQNCYKVPKGAFTGE ISPAMIKD IGAAWVILGHSERRRUMGETDEQSAKKAKRALEKGMTVIFCYGETL<br>61 I. GAQTMHFADQGAYTGEVSPVMLKDLGVTYVILGHSERRRUMGETDEQSAKKAKRALEKGMTVIFCYGETL<br>61 I. GAQTMHFADQGAYTGEVSPVMLKDLGVTYVILGHSERRRUMGETDEQSAKKAKRALEKGMTVIFCYGETL<br>61 I. GAQTMHFADQGAYTGEVSPVMLKDLGVTYVILGHSERRRUMFAETDETVNKKVLAAFTRGLIPIICCGESL<br>62 V. AAQNCYKVTNGAFTGE ISPGMIKDCGATWVVLGHSERRHVFGESDEL IGQKVAHALAEGLGVIACIGEKL<br>63 I. SAENAI. AKSGAFTGEVSMPILKDIGVHWVILGHSERRTYNGETDE IVAQKVSEACKQGFMVIACIGETL<br>63 L. GAQNTDLNNSGAFTGDMSPAMLKEFGATHIIIGHSERREYHAESDEFVAKKFAFLKENGLTPVLCIGESD<br>64 LTYGAQDLSPHDSGAYTGDVSGAFLAKLGCSYVVVGHSERRTYNEDDALVAAKAATALKHGLTPIVCIGEHL<br>62 V. AAQNCYKVTNGAFTGE ISPGMIKDCGATWVVLGHSERRTYFHETDEDVREKLQASLKNNLKAVVCFGESL<br>64 LTYGAQDLSPHDSGAYTGEVSAEIAKDLNIEYVIIGHSERRTYFHETDEDVREKLQASLKNNLKAVVCFGESL<br>65 LTYGAQDLSPHDSGAFTGEVSAEIAKDLNIEYVIGHSERRTYFHETDEDVREKLQASLKNNLKAVVCFGESL<br>64 LTYGAQDLSPHDSGAFTGEISPGMIKDCGATWVVLGHSERRTYFHETDEDVREKLQASLKNNLKAVVCFGESL<br>64 LTYGAQDLSPHDSGAYTGEVSAEIAKDLNIEYVIGHSERRTYFHETDEDVREKLQASLKNNLKAVVCFGESL<br>64 LTYGAQDLSPHDSGAFTGEISPGMIKDCGATWVVLGHSERRTYFHETDEDVREKLQASLKNNLKAVVCFGESL<br>64 LTYGAQDLSPHDSGAYTGEVSAEIAKDLNIEYVIGHSERRTYFHETDEDVREKLQASLKNNLKAVVCFGESL<br>65 AAQNCYKVNNGAFTGEISPGMIKDCGATWVLGHSERRTYFHETDEDVREKLQASLKNNLKAVVCFGESL<br>64 LTYGAQDAI. AKSGAFTGEVSLQILKDYGIKWVLGHSERRTYFHETDEDVREKLQASLKNNLKAVVCFGESL<br>65 AAQNAI. AKSGAFTGEVSLQILKDYGIKWVLGHSERRAYGETNE IVADKVAAAVASGFMVIACIGETL<br>63 I. AAQNAI. AKSGAFTGEVSLQILKDYGIKWVLGHSERRLYFGETNE IVADKVAAAVASGFMVIACIGETL<br>64 AAQNAI. TRSGAFTGEVSLQILKDYGIKWVLGHSERRLYFGETNE IVADKVAAAVASGFMVIACIGETL<br>65 ALANYLKASGAFTGENSVDQIKDVGAKWVILGHSERRLYFGETNE IVADKVAAAVASGFMVIACIGETL<br>64 AAQNAI. TRSGAFTGENSVDQIKDVGAKWVILGHSERRNIFGETDATVNLRLRTAQRFGLTPILCVGETK  | 131<br>138<br>131<br>132<br>131<br>132<br>133<br>136<br>132<br>131<br>132<br>130<br>130<br>131<br>132                             |
| EcTIM<br>GgTIM<br>GgTIM<br>GSTIM<br>HSTIM<br>MMTIM<br>MMTIM<br>OCTIM<br>SSTIM<br>SSTIM<br>TSTIM<br>TSTIM<br>TSTIM<br>YtTIM<br>NpTIM<br>GGTIM  | M+PMRRPFVAGNWKMN-GTKAEA+ELVETLNAAKT++-YADVEVVVAPPFVYLDFAQQKLDGPKT+<br>61 L. GAQNVDLNLSGAFTGETSAAMLKD IGAQYIIIGHSERRTYHKESDELIAKKFAVLKEQGLTPVLCIGETE<br>69 V. SAENAW. TKSGAYTGEVHVGMLVDCQVPYVILGHSERRQIFHESNEQVAEKVKVA IDAGLKVIAC IGETE<br>61 V. AAQNCYKVPKGAFTGE ISPAMIKD IGAAWVILGHSERRRIMGETDEQSAKKAKRALEKGMTVIFCYGETL<br>61 I. GAQTMHFADQGAYTGEVSPVMLKDLGVTYVILGHSERRRIMGETDEQSAKKAKRALEKGMTVIFCYGETL<br>62 V. AAQNCYKVTNGAFTGE ISPGMIKDLGVTYVILGHSERRRIMGETDEQSAKKAKRALEKGMTVIFCYGETL<br>63 I. SAENAI. AKSGAFTGEVSPVMLKDLGVTYVILGHSERRRIFVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>63 I. SAENAI. AKSGAFTGEVSMPILKDIGVHWVILGHSERRTYHGETDEIVAKKVERALKAGLTPVLCIGESD<br>64 LTYGAQDLSPHDSGAYTGDVSGAFLAKLGCSYVVVGHSERRTYHNEDDALVAAKAATALKHGLTPVLCIGESD<br>64 LTYGAQDLSPHDSGAYTGDVSGAFLAKLGCSYVVVGHSERRTYHNEDDALVAAKAATALKHGLTPVCIGEHL<br>62 V. AAQNCYKVTNGAFTGE ISPGMIKDCGATWVVLGHSERRTYHNEDDALVAAKAATALKHGLTPVCIGEHL<br>62 V. AAQNCYKVTNGAFTGE ISPGMIKDCGATWVVLGHSERRTYHNEDDALVAAKAATALKHGLTPVCIGEHL<br>62 V. AAQNCYKVTNGAFTGE ISPGMIKDCGATWVVLGHSERRTYHNEDDALVAAKAATALKHGLTVICIGEKL<br>63 L. GQNVSKFGNGSYTGEVSAE IAKDLNIEYVIIGHERRAYFGESDELIGQKVAHALSEGLGVIACIGEKL<br>64 LTYGAQDLSPHDSGAYTGEVSAE IAKDLNIEYVIGHSERRTYHNEDDALVAAKAATALKHGLTVICIGEKL<br>65 V. AAQNCYKVANGAFTGE ISPGMIKDCGATWVVLGHSERRHVFGESDELIGQKVAHALSEGLGVIACIGEKL<br>66 L. AAQNAI. AKSGAFTGEVSLPILKDFGVNWIVLGHSERRHVFGESDELIGQKVAHALAFGLGVIACIGEKL<br>67 AAQNAI. AKSGAFTGEVSLPILKDFGVNWIVLGHSERRAYGETNEIVAGKVAAAVASGFMVIACIGEKL<br>68 J. AAQNAI. AKSGAFTGEVSLQILKDYGIKWVLGHSERRAYGETNEIVAGKVAAAVASGFMVIACIGETL<br>69 V. SAENVFKNGSGAFTGEISTEMIKDCGCEWVILGHSERRAIGETNEIVAGKVAAQACAAGFHVIYCYGETN<br>60 J. AAENCYKVGSGAFTGEISTEMIKDCGCEWVILGHSERRDILKEDDEFLAAKAKFALENGMKII YCCGEHL<br>60 V. SAENVFKNGAFTGENSVDQIKDVGAKWVLGHSERRDILKEDGETDATVNLKLRTAQRGGUTVIPCIGELL<br>61 V. GAQNAYLKASGAFTGENSVDQIKDVGAKWVLGHSERRDILKEDGETDATVNLKLRTAQRGGUTVICIGETL<br>62 L. GAQNIHWEEFGAYTGEISGPMLETGCKYALIGHSERRPIFGETDATVNLRLRTAQRFGLTPILCIGETL<br>62 L. GAQNYSSEKKGAFTGENSVDQIKDVGAKWVLGHSERRDILKGESTATINKKTALDSGLNVICCGETL<br>62 L. GAQNYSSEKKGAFTGENSVDQIKDVGAKWVLGHSERRDILKGESTATINKVHTALEEGLSVVLCMGETL   | 131<br>138<br>131<br>132<br>132<br>133<br>136<br>132<br>131<br>132<br>131<br>132<br>130<br>130<br>131<br>132<br>132               |
| EcTIM<br>GgTIM<br>GgTIM<br>GSTIM<br>HsTIM<br>LmTIM<br>MmTIM<br>OcTIM<br>OcTIM<br>SSTIM<br>TbTIM<br>TbTIM<br>TvTIM<br>TvTIM<br>YtTIM<br>GoTIM<br>DrTIM                                     | M+PMRRPFVAGNWKMN-GTKAEA+ELVETENAAKT++-YADVEVVVAPPFVYLDFAQQRLDGPKT+<br>61 L. GAQNVDLNLSGAFTGETSAAMLKDIGAQYIIIGHSERRTYHKESDELIAKKFAVLKEQGLTPVLCIGETE<br>69 V. SAENAW. TKSGAYTGEVHVGMLVDCQVPYVILGHSERRQIFHESNEQVAEKVKVAIDAGLKVIACIGETE<br>61 V. AAQNCYKVPKGAFTGEISPAMIKDIGAAWVILGHSERRIMGETDEQSAKKAKRALEKGMTVIFCVGETL<br>61 I. GAQTMHFADQGAYTGEVSPVMLKDLGVTYVILGHSERRIMGETDEQSAKKAKRALEKGMTVIFCVGETL<br>61 I. GAQTMHFADQGAYTGEVSPVMLKDLGVTYVILGHSERRMFAETDETVNKKVLAAFTRGLIPIICCGESL<br>62 V. AAQNCYKVTNGAFTGEISPGMIKDCGATWVVLGHSERRHVFGESDELIGQKVAHALAECLGVIACIGEKL<br>63 I. SAENAI. AKSGAFTGEVSPVMLKDLGVTWVILGHSERRTYGETDEIVAKKFAFLKENGLTPVLCIGESD<br>64 LTYGAQDLSPHDSGAYTGDVSGAFLAKLGCSYVVVGHSERRTYHNEDDALVAAKAATALKHGLTPIVCIGEHL<br>62 V. AAQNCYKVTNGAFTGEISPGMIKDCGATWVVLGHSERRTYHNEDDALVAAKAATALKHGLTPIVCIGEHL<br>62 V. AAQNCYKVTNGAFTGEISPGMIKDCGATWVVLGHSERRTYHNEDDALVAAKAATALKHGLTPIVCIGEHL<br>62 V. AAQNCYKVTNGAFTGEISPGMIKDCGATWVVLGHSERRTYHNEDDALVAAKAATALKHGLTPIVCIGEHL<br>62 V. AAQNCYKVTNGAFTGEISPGMIKDCGATWVVLGHSERRTYHNEDDALVAAKAATALKHGLTPIVCIGEHL<br>62 V. AAQNCYKVNGAFTGEISPGMIKDCGATWVVLGHSERRHVFGESDELIGQKVAHALSEGLGVIACIGEKL<br>63 I. AQNAI. AKSGAFTGEVSLPILKDFGVNWIVLGHSERRHVFGESDELIGQKVAHALSEGLGVIACIGEKL<br>64 LTYGAQDLSPHDSGAYTGEVSAEIAKDLNIEYVIGHSERRHVFGESDELIGQKVAHALSEGLGVIACIGEKL<br>65 I. AAQNAI. AKSGAFTGEVSLPILKDFGVNWIVLGHSERRHVFGESDELIGQKVAHALSEGLGVIACIGEKL<br>66 I. AAQNAI. AKSGAFTGEVSLPILKDFGVNWIVLGHSERRHVFGESDELIGQKVAHALSEGLGVIACIGETL<br>67 I. AAQNAI. AKSGAFTGEVSLPILKDFGVWVVIGHSERRLYGETNEIVADKVAQACAAGFHVIVCVGETN<br>60 I. AAENCYKVGSGAFTGEISTEMIKDCGCEWVILGHSERRLYGETNEIVADKVAQACAAGFHVIVCVGETN<br>60 I. AAENCYKVGSGAFTGEISTEMIKDCGCEWVILGHSERRLYGETNEIVADKVAQACAAGFHVIVCVGETN<br>60 I. AAENCYKVGSGAFTGEISTEMIKDCGCEWVILGHSERRSVFHEDDLFIAAKAKFALENGMKIIYCCGEHL<br>61 V. GAQNAYLKASGAFTGEVTVPMIKSFGIEWTILGHSERRVIGESDELIGEKVKHALDSGLNVIPCIGELL<br>62 L. GAQNYLKASGAFTGEVSPAMLLETGCKYAVIGHSERRSVFHEDDKFIADKFIAAKAKFALENGMKIIYCCGEHL<br>64 J. GAQNAYLKASGAFTGEVSPAMLLETGCKYAVIGHSERRVINGSETFINHKVHTALEEGLSVVLCMGETL<br>75 F. GCQDVSAHESGAYTGEISGPMLTESGVFVVGHSERRVVGHSERRVHDESDATVANKARAACAAAAANGLLPIVCYGEN   | 131<br>138<br>131<br>132<br>132<br>133<br>136<br>132<br>131<br>132<br>130<br>130<br>131<br>132<br>132<br>132<br>132               |
| EcTIM<br>GgTIM<br>GgTIM<br>GsTIM<br>HSTIM<br>MmTIM<br>OcTIM<br>OcTIM<br>PTIM<br>TbTIM<br>TbTIM<br>TsTIM<br>TvTIM<br>YvTIM<br>YvTIM<br>SgTIM<br>SgTIM<br>SgTIM<br>SgTIM                    | M+PMRRPFVAGNWKMN-GTKAEA+ELVETENAAKT++-YADVEVVVAPPFVYLDFAQQRLDGPKT+<br>61 L. GAQNVDLNLSGAFTGETSAAMLKD IGAQYI IIGHSERRTYHKESDELIAKKFAVLKEQGLTPVLCIGETE<br>69 V. SAENAW. TKSGAYTGEVHVGMLVDCQVPYVILGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGETE<br>61 V. AAQNCYKVPKGAFTGEISPAMIKD IGAAWVILGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>62 I. AAQNVYLEGNGAWTGETSVEMLQDMGLKHVIVGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>61 I. GAQTMHFADQGAYTGEVSPVMLKDLGVTYVILGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>62 V. AAQNCYKVTNGAFTGEISPGMIKDCGATWVVLGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>63 I. SAENAI.AKSGAFTGEVSMPILKDIGVHWVILGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGETL<br>63 L. GAQNTDLNNSGAFTGDWSPAMLKEFGATHIIIGHSERREYHAESDEFVAKKFAFLKENGLTPVLCIGESD<br>64 LTYGAQDLSPHDSGAYTGDVSGAFLAKLGCSYVVVGHSERRHVFGESDELIGQKVAHALSEGLGVIACIGEKL<br>65 I. GIQNVSKFGNGSYTGDVSGAFLAKLCSYVVVGHSERRHVFGESDELIGQKVAHALSEGLGVIACIGEKL<br>66 LTYGAQDLSPHDSGAYTGDVSGAFLAKLCSYVVVGHSERRHVFGESDELIGQKVAHALSEGLGVIACIGEKL<br>67 . AAQNCYKVNGAFTGEISPGMIKDCGATWVVLGHSERRHVFGESDELIGQKVAHALSEGLGVIACIGEKL<br>68 LTYGAQDLSPHDSGATGEVSLAEIAKDLNIEYVIIGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>69 . AAQNCYKVANGAFTGEIGPGMIKDLGATWVVLGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>61 . AAQNAI.AKSGAFTGEVSLQILKDYGIKWVVLGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGETL<br>62 V. AAQNCYKVANGAFTGEIGPGMIKDLGATWVVLGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGETL<br>63 I. AAQNAI.AKSGAFTGEVSLQILKDYGIKWVVLGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGETL<br>64 L. GAQNAI.AKSGAFTGEVSLQILKDYGIKWVVLGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGETL<br>65 L. GAQNAI.AKSGAFTGEVSVQIKDVGAKWVILGHSERRPITKEDDENEKVAAQACAAGHVIVCVGETN<br>60 I. AAENCYKVASGAFTGEISTEMIKDCGCEWVILGHSERRPITKEDDENELVAKVAAVASGFMVIACIGETL<br>64 L. GAQNAYLKASGAFTGENSVDQIKDVGAKWVILGHSERRPITKESVFHEDDKFIADAKKAADGAAGHVIVCVGETN<br>65 L. GAQNVSEKKGAFTGENSVDQIKDVGAKWVILGHSERRPITKESVFHEDDKFIADAKKAAQACGAAGHVIVCVGETK<br>62 L. GAQNIHWEEFGAYTGEISGPMLTESCVRFVIVGHSERRQYFGETDATVNLKRTAQRFGTTPILCVGETK<br>63 L. GAQNVSEKKGAFTGENSVDQIKDVGAKWVILGHSERRPITGESTFINHKVHAAKARQAQANGLPITVCVGETK<br>64 L. GAQNVSEKKGAFTGENSVDQIKDVGAKWVIGHSERRPITGESTFINHKVAAAKARQAANGLTPILCVGETK<br>65 LKYGADOISAHESGAYTGEISAAMLKDAGASCVVY | 131<br>138<br>131<br>132<br>132<br>133<br>136<br>132<br>131<br>132<br>130<br>130<br>131<br>132<br>132<br>132<br>132               |
| EcTIM<br>GgTIM<br>GgTIM<br>GsTIM<br>HsTIM<br>MmTIM<br>MmTIM<br>OcTIM<br>PTIIM<br>SSTIM<br>TbTIM<br>TsTIM<br>TvTIM<br>YtTIM<br>YtTIM<br>OpTIM<br>CoTIM                                     | M+PMRRPFVAGNWKMN-GTKAEA+ELVETENAAKT++-YADVEVVVAPPFVYLDFAQQRLDGPKT+<br>61 L. GAQNVDLNLSGAFTGETSAAMLKD IGAQYIIIGHSERRTYHKESDELIAKKFAVLKEQGLTPVLCIGETE<br>69 V. SAENAW. TKSGAYTGEVHVGMLVDCQVPYVILGHSERRQIFHESNEQVAEKVKVA IDAGLKVIACIGETE<br>61 V. AAQNCYKVPKGAFTGE ISPAMIKD IGAAWVILGHSERRRUMGETDEQSAKKAKRALEKGMTVIFCYGETL<br>61 I. GAQTMHFADQGAYTGEVSPVMLKDLGVTYVILGHSERRRUMGETDEQSAKKAKRALEKGMTVIFCYGETL<br>61 I. GAQTMHFADQGAYTGEVSPVMLKDLGVTYVILGHSERRRUMGETDEQSAKKAKRALEKGMTVIFCYGETL<br>61 I. GAQTMHFADQGAYTGEVSPVMLKDLGVTYVILGHSERRRUMFGETDETVNKKVLAAFTRGLIPIICCGESL<br>62 V. AAQNCYKVTNGAFTGE ISPGMIKDCGATWVVLGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>63 I. SAENAI.AKSGAFTGEVSMPILKDIGVHWVILGHSERRTYYGETDEIVAQKVSEACKQGFMVIACIGETL<br>63 L. GAQNTDLNNSGAFTGDMSPAMLKEFGATHIIIGHSERREYHAESDEFVAKKFAFLKENGLTPVLCIGESD<br>64 LTYGAQDLSPHDSGAYTGDVSGAFLAKLGCSYVVVGHSERRTYNEDDALVAAKAATALKHGLTPIVCIGEHL<br>62 V. AAQNCYKVNGAFTGE ISPGMIKDCGATWVVLGHSERRTYFHETDEDVREKLQASLKNNLKAVVCFGESL<br>64 LTYGAQDLSPHDSGAYTGEVSAEIAKLDCGATWVVLGHSERRTYFHETDEDVREKLQASLKNNLKAVVCFGESL<br>64 LTYGAQDLSPHDSGAFTGEISPGMIKDCGATWVVLGHSERRTYFHETDEDVREKLQASLKNNLKAVVCFGESL<br>64 LTYGAQDLSPHDSGAYTGEVSAEIAKLDKIEYVIIGHSERRTYFHETDEDVREKLQASLKNNLKAVVCFGESL<br>64 LTYGAQDLSPHDSGAYTGEVSAEIAKDLNIEYVIIGHSERRTYFHETDEDVREKLQASLKNNLKAVVCFGESL<br>65 J. AAQNCYKVNNGAFTGEISPGMIKDCGATWVVLGHSERRTYFHETDEDVREKLQASLKNNLKAVVCFGESL<br>64 LTYGAQDLSPHDSGAYTGEVSAEIAKDLNIEYVIIGHSERRTYFHETDEDVREKLQASLKNNLKAVVCFGESL<br>65 J. AAQNAI.AKSGAFTGEVSLQILKDYGIKWVLGHSERRTYFHETDEDVREKLQASLKNNLKAVVCFGESL<br>64 LYGAQNAI.AKSGAFTGEVSLQILKDYGIKWVLGHSERRLYFGETDEIVAKVAQACAAGFHVIVCVGETN<br>66 J. AAQNAI.TRSGAFTGEVSLQILKDYGIKWVLGHSERRLYFGETDEIVAKVAQACAAGFHVIVCVGETN<br>67 J. GAQNIHWEEFGAYTGEISGPMLKSFGIEWTILGHSERRSVFHEDDKFIAAKKFALENGMKIIYCCGEHL<br>67 J. GAQNVSKKKGAFTGEVSVDQIKDVGAKWVILGHSERRLYFGETDATVNLRLRTAQRFGLTPILCVGETK<br>62 L. GAQNIHWEEFGAYTGEISGPMLTESGVRFVILGHSERREVTHDESDATVAAKARQAQANGLLPIVCVGENL<br>65 IKYGAQDISAHBSGAYTGEISAMLLETGCKYALIGHSERREVTHDESDATVAAKARQAQANGLLPIVCVGENL<br>65 JKYGAQDISAHBGGAYTGEISAMLLETGCKYALIGHSERREVTHDESDATVAAKARQAQANGLLPIVCVGENL<br>65 JKYGAQDISAHBGGATGEISAPNLAKLKCTYAYGHSERRCYFET | 131<br>138<br>131<br>132<br>131<br>132<br>133<br>136<br>132<br>131<br>132<br>130<br>130<br>131<br>132<br>132<br>132<br>137<br>130 |
| EcTIM<br>GgTIM<br>GgTIM<br>GgTIM<br>GSTIM<br>HSTIM<br>MMTIM<br>MMTIM<br>MITIM<br>OCTIM<br>SSTIM<br>TSTIM<br>TSTIM<br>TSTIM<br>TSTIM<br>YtIIM<br>NpTIM<br>GoTIM<br>ScTIM<br>ScTIM<br>CpTIM | M+PMRRPFVAGNWKMN-GTKAEA+ELVETENAAKT++-YADVEVVVAPPFVYLDFAQQRLDGPKT+<br>61 L. GAQNVDLNLSGAFTGETSAAMLKD IGAQYI IIGHSERRTYHKESDELIAKKFAVLKEQGLTPVLCIGETE<br>69 V. SAENAW. TKSGAYTGEVHVGMLVDCQVPYVILGHSERRQIFHESNEQVAEKVKVA IDAGLKVIACIGETE<br>61 V. AAQNCYKVPKGAFTGE ISPAMIKD IGAAWVILGHSERRRIMGETDEQSAKKAKRALEKGMTVIFCYGETL<br>61 I. GAQTMHFADQGAYTGEVSPVMLKDLGVTYVILGHSERRRIMGETDEQSAKKAKRALEKGMTVIFCYGETL<br>62 V. AAQNCYKVTNGAFTGE ISPGMIKDLGVTYVILGHSERRRIVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>63 I. SAENAI. AKSGAFTGEVSPVMLKDLGVTYVILGHSERRRIVFGESDELIGQKVAHALAEGLGVIACIGEKL<br>64 LTYGAQDLSPHDSGAYTGDVSGAFLAKLGCSYVVVGHSERRTYHNEDDALVAAKAATALKHGLTPVLCIGESD<br>64 LTYGAQDLSPHDSGAYTGDVSGAFLAKLGCSYVVVGHSERRTYHNEDDALVAAKAATALKHGLTPVCIGEKL<br>67 V. AAQNCYKVTNGAFTGE ISPGMIKDCGATWVVLGHSERRTYHNEDDALVAAKAATALKHGLTPVCIGEKL<br>68 LTYGAQDLSPHDSGAYTGDVSGAFLAKLGCSYVVVGHSERRTYHNEDDALVAAKAATALKHGLTPVCIGEKL<br>69 V. AAQNCYKVTNGAFTGE ISPGMIKDCGATWVVLGHSERRTYHNEDDALVAAKAATALKHGLTPVCIGEKL<br>60 T. GIQNVSKFGNGSYTGEVSAEIAKDLNIEYVIIGHSERRTYHEGESDELIGQKVAHALSECLGVIACIGEKL<br>61 T. GIQNVSKFGNGSYTGEVSAEIAKDLNIEYVIGHSERRTYHNEDDALVAAKAATALKHGLTPIVCIGESL<br>62 V. AAQNCYKVANGAFTGE ISPGMIKDCGATWVVLGHSERRTYHNEGSSDELIGQKVAHALSECLGVIACIGEKL<br>63 1. AAQNAI. AKSGAFTGEVSLPILKDFGVNWIVLGHSERRTYHEGESDELIGQKVAHALAEGLGVIACIGEKL<br>64 LTYGAQDAI. AKSGAFTGEVSLPILKDFGVNWIVLGHSERRTYHEGESDELIGQKVAHALAEGLGVIACIGEKL<br>65 1. AAQNAI. AKSGAFTGEVSLQILKDYGIKWVVLGHSERRTYHGESSNELIGGKVAHALAEGUVIACIGETL<br>66 V. SAENVFKKNGAFTGEVSLQILKDYGIKWVLGHSERRDILKEDDEFLAAKAKFALENGMKIIYCCYGETN<br>66 1. AAENCYKVGSGAFTGEISTEMIKDCGCEWVILGHSERRDILKEDDEFLAAKAKFALENGMKIIYCCYGETN<br>67 . GQQDVSEKKGAFTGEVSVDQIKDVGAKWVIGHSERRDILKEDDEFLAAKAKFALENGMKIIYCCGEHL<br>68 V. GAQNVSSEKKGAFTGEVSVDQIKDVGAKWVIGHSERRDILKEDDEFLAAKAKFALENGMKIIYCCGEHL<br>69 F. GGQDVSAHESGAYTGE ISAMLKDAGASCVVGHSERREYHDESDATVAAKARQAQANGLLPIVCVGEHL<br>65 IKYGAQOISAHESGAYTGE ISAMLKDAGASCVVGHSERREYHDESDATVAAKARQAQANGLLPIVCVGEHL<br>66 IKYGAQOISAHESGAYTGE ISAMLKDAGASCVVGHSERREYHDESDATVAAKARQAQANGLLPIVCVGEHL<br>67 V. GAQDVSAKKGAFTGE ISAMLKDAGASCVVGHSERREYHDESDATVAAKARQAQANGLLPIVCVGEHL<br>68 V. GAQDVSAHESGAYTGE ISAMLKDAGASCVVGHS | 131<br>138<br>131<br>132<br>131<br>132<br>133<br>136<br>132<br>131<br>132<br>130<br>131<br>132<br>132<br>132<br>132<br>137        |
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| EcTIM   | . 132 AENEAGKTEE <mark>WC</mark> ARQIDAVLKTQGAAAFEGA <mark>VIA</mark> YEPVWAIGTGKSATPAQAQAVHKFIRDHIAK  | V. DAN I 201   |
|---|--|--|
| EhTIM   | . 139 AQRIANQTEE <mark>VV</mark> AAQLKAINNAISKEAWKN <mark>IILAYEPVWAIGTGKTATPDQAQEVHQYIRKWM</mark> TEI   | NISKEV 209   |
| GgTIM   | 132 DEREAG I TEKVVFEQTK <mark>A I</mark> ADNVKDWSKVVLAYEPVWA I GTGKTATPQQAQEVHEK <mark>L</mark> RGWLKSI  | HVSDAV 200   |
| GITIM   | . 133 DERKANRTME <mark>VN</mark> I AQLEALGKELGESKMLWKE <mark>VV I AYEPVWS I GTG</mark> VVATPEQAEEVHV <mark>GLR</mark> KWFAEI   | VCAEG 205  |
| GsTIM   | 132 EEREAGQTNAVVASQVEKALAGLTPEQVKQAVIAYEP IWA IGTGKSSTPEDANSVCGHIRSVVSR  | LFGPEA 202   |
| HsTIM   | . 133 DEREAG I TEK <mark>VV</mark> FEQTK <mark>V I A</mark> DNV KDWSK <mark>VV LA</mark> YEP VWA I GTGK TATPQQAQEVHEKLRGWLKSI  | NVSDAV 201   |
| LmTIM   | "133 QQREANQTAKVVLSQTS <mark>AIAA</mark> KLTKDAWNQ <mark>VVLAYEPVWAIGTGKVATPEQAQEVHLLLRKWV</mark> SEI  | NIGTDV 203   |
| MmTIM   | 134 AQNEAGETMAYCARQLDAY INTQ GVEALEGAT I AYEP IWA IGTGKAATAEDAQR I HAQTRAHTAET   | K.SEAV 203   |
| MtTIM   | . 137 DVREAGNH <mark>VAHNI</mark> EQLRGSLVGLLAEQIGS <mark>VVIAYEPVWAIGTG</mark> RVASAADAQEVCAAIRKELASI   | LASPRI 207   |
| OcTIM   | 133 DEREAG I TEK <mark>VV</mark> FEQTK <mark>V I A</mark> DNV KDWSK <mark>VV LA</mark> YEPVWA I GTGKTATPQQAQEVHEKLRGWLKSI  | VSDAV 201  |
| PfTIM   | 132 EQREQNKTIEVITKOVKAFVDLIDNFDNVILAYEPLWAIGTGKTATPEQAQLVHKEIRKIVKD  | TCGEKQ 200   |
| SsTIM   | . 133 DEREAG I TEKVV FEQTKV I ADNV KDWNKVVLAYEPVWA I GTGKT ATPQQAQEVHEKLRGWLKTI  | IVPEAV 201   |
| TbTIM   | . 132 QERESGRTAVVVLTQIAAIAKKLKKADWAKVVIAYEPVWAIGTGKVATPQQAQEAHALIRSWVSSI   | KIGADV 202   |
| TcTIM   | . 133 EEREAGRTAAVVLTQLAAVAQKLSKEAWAHVVIAYEPVWAIGTGKVATPQQAQEVHELLRRWVRSI   | KLGAD I 203  |
| TsTIM   | . 131 SEREAGKTNDVCFAQMDA I AKNV. PSKEAWDKVV I AYEPVWA I GTGKTATPAQAQEVHKVVRDW I RKI  | HVDAGI 202   |
| TvTIM   | . 131 SEREAGKASEFVSAQIEKMIPAIPAGKWDDVVIAYEPIWAIGTGKVASTQDAQEMCKVIRDILAA  | KVGAD I 201  |
| YtTIM   | 132 EEKKAGKTLDVVERQLNAVLEEVKDWTNVVVAYEPVWAIGTGLAATPEDAQDIHASIRKFLASI   | KLGDKA 200   |
| NpTIM   | 133 QQ <mark>RDAGETESLIALQLDKGLVDIDQNNLVIAYEP IWAIGTG</mark> ETCEAVE <mark>A</mark> NRIIGLIRSQLSN  | <u>.</u> 194   |
| GoTIM   | 133 AERERGLQER <mark>V</mark> FQRQVYAACAGL TDEQFGR <mark>IVIAYEPVWAIGTGKVATPEQAQE</mark> AHAFVRSKLRLI  | LY <mark>G</mark> DKI 203  |
| DrTIM   | . 130 DVRERGEHVPQTLAQLRGSLEGVGADVVVAYEPVWAIGTGKTATADDAEELAAAIRGALRE(   | QY <mark>G</mark> AR . 195   |
| ScTIM   | . 138 DVREAGNHVEHTLAQVEGGLKDL AAEQAESVVIAYEPVWAIGTGKVCGADDAQEVCAAIRGKLAEI  | LYSQEL 208   |
| CpTIM   | 131 EQRENGTTNDV IKAQ I TADLEGL TKEQAEK <mark>VV I AYEP IWA I GTGK</mark> TATSDQANET I AA I RAM <mark>V</mark> AEI  | MFGQEV 201   |
| _   |  |  |
| Consensus   |  |  |
|   | DEREAGNIEEVVTAULKAITTTLTREDWERVVTATEPVWAIGIGNIAIPTUAUEVNATIRTWLAT  | NVGA+V   |
|   |  |  |
| FcTIM   | 202 AFOVI LOVGGSVNASNAAFI FAOPDI DGALVGGASI KADAFAVI VKAAFAAKOA  | 255  |
| EcTIM<br>EbTIM  | 202 AEQVIIQYGGSVNASNAAELFAQPDIDGALVGGASLKADAFAVIVKAAEAAKQA<br>210 AFATRIQYGGSVNPANCNELAKKADIDGELVGGASIDAAKEKTIINSVSEKE   | 255<br>261   |
| EcTIM<br>EhTIM<br>GaTIM   | 202 AEQVIIQYGGSVNASNAAELFAQPDIDGALVGGASLKADAFAVIVKAAEAAKQA<br>210 AEATRIQYGGSVNPANCNELAKKADIDGFLVGGASLDAAKFKTIINSVSEKF<br>201 AQSTRILYGGSVTGGNCKELASQHDVDGFLVGGASLKPF.EVDLINAKH  | 255<br>261<br>248  |
| EcTIM<br>EhTIM<br>GgTIM<br>GITIM  | . 202 AEQVIIQYGGSVNASNAAELFAQPDIDGALVGGASLKADAFAVIVKAAEAAKQA<br>. 210 AEATRIQYGGSVNPANCNELAKKADIDGFLVGGASLDAAKFKTIINSVSEKF<br>. 201 AQSTRIIYGGSVTGGNCKELASQHDVDGFLVGGASLKPE.FVDIINAKH<br>206 AQHIRIIYGGSANGSNCEKIGQCPNIDGFLVGGASLKPE.FMTMIDIITKTRT   | 255<br>261<br>248<br>257   |
| EcTIM<br>EhTIM<br>GgTIM<br>GSTIM  | . 202 AEQVIIQYGGSVNASNAAELFAQPDIDGALVGGASLKADAFAVIVKAAEAAKQA<br>. 210 AEATRIQYGGSVNPANCNELAKKADIDGFLVGGASLDAAKFKTIINSVSEKF<br>   | 255<br>261<br>248<br>257<br>253  |
| EcTIM<br>GgTIM<br>GITIM<br>GITIM<br>HSTIM   | 202 AEQVIIQYGGSVNASNAAELFAQPDIDGALVGGASLKADAFAVIVKAAEAAKQA<br>210 AEATRIQYGGSVNPANCNELAKKADIDGFLVGGASLDAAKFKTIINSVSEKF<br>201 AQSTRIIYGGSVTGGNCKELASQHDVDGFLVGGASLKPE.FVDIINAKH<br>206 AQHIRIIYGGSNGSNCEKLGQCPNIDGFLVGGASLKPE.FMTMIDILTKTRT.<br>203 AEAIRIQYGGSVKPDNIRDFLAQQQIDGPLVGGASLEPASFLQLVEAGRHE<br>202 AQSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ.  | 255<br>261<br>248<br>257<br>253<br>249   |
| EcTIM<br>GgTIM<br>GITIM<br>GSTIM<br>HsTIM<br>I mTIM   | 202 AEQVIIQYGGSVNASNAAELFAQPDIDGALVGGASLKADAFAVIVKAAEAAKQA<br>210 AEATRIQYGGSVNPANCNELAKKADIDGFLVGGASLDAAKFKTIINSVSEKF<br>201 AQSTRIIYGGSVTGGNCKELASQHDVDGFLVGGASLKPE.FVDIINAKH<br>206 AQHIRIIYGGSANGSNCEKLGQCPNIDGFLVGGASLKPE.FMTMIDILTKTRT.<br>203 AEAIRIQYGGSVKPDNIRDFLAQQQIDGPLVGGASLKPE.FMTMIDILTKTRT.<br>202 AQSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ<br>204 AQKIRIIYGGSVNAANAATIYAKPDINGFIVGGASLKPE.FVDIINAKQ  | 255<br>261<br>248<br>257<br>253<br>249<br>251  |
| EcTIM<br>GgTIM<br>GgTIM<br>GSTIM<br>GSTIM<br>HSTIM<br>MmTIM   | 202 AEQVIIQYGGSVNASNAAELFAQPDIDGALVGGASLKADAFAVIVKAAEAAKQA<br>210 AEATRIQYGGSVNPANCNELAKKADIDGFLVGGASLDAAKFKTIINSVSEKF<br>201 AQSTRIIYGGSVTGGNCKELASQHDVDGFLVGGASLKPE.FVDIINAKH<br>206 AQHIRIIYGGSANGSNCEKLGQCPNIDGFLVGGASLKPE.FMTMIDILTKTRT.<br>203 AEAIRIQYGGSVKPDNIRDFLAQQQIDGPLVGGASLKPE.FMTMIDILTKTRT.<br>204 AQSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ<br>204 AAKLRILYGGSVNAANAATLYAKPDINGFLVGGASLKPE.FRDIIDATR<br>204 AKNVV QYGGSVKAENAAATLYAQPDINGALVGGAALDAKSEAAJAKAAAEAKA  | 255<br>261<br>248<br>257<br>253<br>249<br>251<br>251   |
| EcTIM<br>GTIM<br>GTIM<br>GSTIM<br>HSTIM<br>LmTIM<br>MmTIM<br>MmTIM  | 202 AEQVIIQYGGSVNASNAAELFAQPDIDGALVGGASLKADAFAVIVKAAEAAKQA<br>210 AEATRIQYGGSVNPANCNELAKKADIDGFLVGGASLDAAKFKTIINSVSEKF<br>201 AQSTRIIYGGSVTGGNCKELASQHDVDGFLVGGASLKPE.FVDIINAKH<br>206 AQHIRIIYGGSANGSNCEKLGQCPNIDGFLVGGASLKPE.FMTMIDILTKTRT.<br>203 AEAIRIQYGGSVKPDNIRDFLAQQQIDGPLVGGASLEPASFLQLVEAGRHE<br>202 AQSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ<br>204 AAKLRILYGGSVNAANAATLYAKPDINGFLVGGASLKPE.FRDIIDATR<br>204 AKNVVIQYGGSVKPENAAAYFAQPDIDGALVGGAALDAKSFAAIAKAAAEAKA.<br>208 ANVVVIQYGGSVNENAAAYFAQPDIVAQDDVDGGIVGGAALDAKSFAAIAKAAAEAKA.  | 255<br>261<br>248<br>253<br>249<br>251<br>256<br>251   |
| EcTIM<br>GgTIM<br>GgTIM<br>GGTIM<br>GSTIM<br>HSTIM<br>MmTIM<br>OcTIM  | 202 AEQVIIQYGGSVNASNAAELFAQPDIDGALVGGASLKADAFAVIVKAAEAAKQA<br>210 AEATRIQYGGSVNPANCNELAKKADIDGFLVGGASLDAAKFKTIINSVSEKF<br>201 AQSTRIIYGGSVTGGNCKELASQHDVDGFLVGGASLKPE.FVDIINAKH<br>206 AQHIRIIYGGSANGSNCEKLGQCPNIDGFLVGGASLKPE.FMTMIDILTKTRT.<br>203 AEAIRIQYGGSVKPDNIRDFLAQQQIDGPLVGGASLEPASFLQLVEAGRHE<br>202 AQSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ<br>204 AAKLRILYGGSVNAANAATLYAKPDINGFLVGGASLKPE.FRDIIDATR<br>206 AKNVVIQYGGSVKPENAAAYFAQPDIDGALVGGALVGGALDAKSFAAIAKAAAEAKA.<br>207 AZSTRIIYGGSVNAKNVGDIVAQDDVDGFLVGGASLDGEHFATLAAIAAGGPLP<br>208 ADVRVLYGGSVNAKNVGDIVAQDDVDGFLVGGASLDGEHFATLAAIAAGGPLP<br>202 AQSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ.  | 255<br>261<br>248<br>257<br>253<br>249<br>251<br>256<br>266<br>249   |
| EcTIM<br>GgTIM<br>GgTIM<br>GSTIM<br>HSTIM<br>HSTIM<br>LmTIM<br>MtTIM<br>OCTIM<br>PTIM.  | 202 AEQVIIQYGGSVNASNAAELFAQPDIDGALVGGASLKADAFAVIVKAAEAAKQA<br>210 AEATRIQYGGSVNPANCNELAKKADIDGFLVGGASLDAAKFKTIINSVSEKF<br>201 AQSTRIIYGGSVTGGNCKELASQHDVDGFLVGGASLKPE.FVDIINAKH<br>206 AQHIRIIYGGSANGSNCEKLGQCPNIDGFLVGGASLKPE.FMTMIDILTKTRT.<br>203 AEAIRIQYGGSVKPDNIRDFLAQQQIDGPLVGGASLEPASFLQLVEAGRHE<br>204 AQSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ<br>204 AAKLRILYGGSVNAANAATLYAKPDINGFLVGGASLKPE.FRDIIDATR<br>204 AKNVVIQYGGSVKPENAAAYFAQPDIDGALVGGAALDAKSFAAIAKAAAEAKA.<br>208 ADTVRVLYGGSVNAKNVGDIVAQDDVDGGLVGGASLDGEHFATLAAIAAGGPLP<br>202 AQSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ<br>204 AKNVVIQYGSVNAKNVGDIVAQDDVDGGLVGGASLDGEHFATLAAIAAGGPLP<br>202 AQSTRIIYGGSVNAKNZGIVAQDDVDGFLVGGASLKPE.FVDIINAKQ<br>204 ANQIRILYGGSVNAKNZGIVAQDDVDGFLVGGASLKPE.FVDIINAKQ   | 255<br>261<br>248<br>257<br>253<br>249<br>251<br>256<br>261<br>249<br>249  |
| EcTIM<br>EhTIM<br>GgTIM<br>GITIM<br>GITIM<br>HSTIM<br>LmTIM<br>MmTIM<br>MtTIM<br>OCTIM<br>PFTIM<br>SSTIM  | 202 AEQVIIQYGGSVNASNAAELFAQPDIDGALVGGASLKADAFAVIVKAAEAAKQA<br>210 AEATRIQYGGSVNPANCNELAKKADIDGFLVGGASLDAAKFKTIINSVSEKF<br>201 AQSTRIIYGGSVTGGNCKELASQHDVDGFLVGGASLKPE.FVDIINAKH<br>206 AQHIRIIYGGSANGSNCEKLGQCPNIDGFLVGGASLKPE.FMTMIDILTKTRT.<br>203 AEAIRIQYGGSVKPDNIRDFLAQQQIDGPLVGGASLKPE.FVDIINAKQ<br>204 AQSTRIIYGGSVTGATCKELASQHDVDGFLVGGASLKPE.FVDIINAKQ<br>204 AAKLRILYGGSVNAANAATLYAKPDINGFLVGGASLKPE.FVDIIDATR<br>204 AKNVVIQYGGSVKPENAAAYFAQPDIDGALVGGASLKPE.FNDIIDATR<br>208 ADTVRVLYGGSVNAKNVGDIVAQDDVDGFLVGGASLKPE.FVDIINAKQ<br>208 ADTVRVLYGGSVNAKNVGDIVAQDDVDGGLVGGASLDGEHFATLAAIAAGGPLP<br>202 AQSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ<br>204 AKNVVIQYGGSVNAKNVGDIVAQDDVDGGLVGGASLKPE.FVDIINAKA<br>204 AKNVVIQYGGSVNAKNVGDIVAQDDVDGFLVGGASLKPE.FVDIINAKQ  | 255<br>261<br>248<br>257<br>253<br>259<br>251<br>256<br>261<br>249<br>248<br>248   |
| EcTIM<br>EhTIM<br>GJTIM<br>GJTIM<br>GJTIM<br>HSTIM<br>LmTIM<br>MmTIM<br>OCTIM<br>CTIM<br>SSTIM<br>TbTIM   | <ul> <li>202 AEQVIIQYGGSVNASNAAELFAQPDIDGALVGGASLKADAFAVIVKAAEAAKQA</li> <li>210 AEATRIQYGGSVNPANCNELAKKADIDGFLVGGASLDAAKFKTIINSVSEKF</li> <li>201 AQSTRIIYGGSVTGGNCKELASQHDVDGFLVGGASLKPE.FVDIINAKH</li> <li>206 AQHIRIIYGGSVKPDNIRDFLAQQQIDGPLVGGASLKPE.FMTMIDILTKTRT.</li> <li>203 AEAIRIQYGGSVKPDNIRDFLAQQQIDGPLVGGASLKPE.FVDIINAKQ</li> <li>204 AAKLRILYGGSVTGATCKELASQHDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AKLRILYGGSVKPDNIRDFLAQQQIDGPLVGGASLKPE.FVDIINAKQ</li> <li>204 AKNVVIQYGGSVKPENAAAYFAQPDIDGALVGGASLKPE.FRDIDATR</li> <li>208 ADTVRVLYGGSVNAKNVGDIVAQDDVDGFLVGGASLDGEHFATLAAIAAGPLP</li> <li>202 AQSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AKNNVIQYGGSVKPENAAAYFAQPDIDGALVGGASLKPE.FVDIINAKQ</li> <li>204 AKNNVIQGSVNAKNVGDIVAQDDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AKNNVIQGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AKNNVIQGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>205 AQSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AKNVIQGSVNTENCSSLIQEDIDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AGGLRILYGGSVNTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ</li> </ul>  | 255<br>261<br>248<br>257<br>253<br>249<br>251<br>256<br>261<br>249<br>248<br>248<br>248<br>250   |
| EcTIM<br>EhTIM<br>GgTIM<br>GgTIM<br>HSTIM<br>LmTIM<br>MmTIM<br>MtTIM<br>OcTIM<br>PfTIM<br>TbTIM<br>TcTIM.   | <ul> <li>202 AEQVIIQYGGSVNASNAAELFAQPDIDGALVGGASLKADAFAVIVKAAEAAKQA</li> <li>210 AEATRIQYGGSVNPANCNELAKKADIDGFLVGGASLDAAKFKTIINSVSEKF</li> <li>201 AQSTRIIYGGSVTGGNCKELASQHDVDGFLVGGASLKPE.FVDIINAKH</li> <li>206 AQHIRIIYGGSVKPDNIRDFLAQQQIDGFLVGGASLKPE.FMTMIDILTKTRT.</li> <li>202 AQSTRIIYGGSVKDDNIRDFLAQQQIDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AAKLRILYGGSVTGATCKELASQHDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>205 AQSTRIIYGGSVKPDNIRDFLAQQQIDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AAKLRILYGGSVNAANAATLYAKPDINGFLVGGASLKPE.FRDIIDATR</li> <li>208 ADTVRVLYGGSVKAANAATLYAKPDINGFLVGGASLDGEHFATLAAIAAGGPLP</li> <li>202 AQSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AKNVYIQYGGSVKPENAAAYFAQPDIDGALVGGASLDGEHFATLAAIAAGGPLP</li> <li>202 AQSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 ANTRILYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 ANTRILYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>205 AQSTRIIYGGSVKAKNTTATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>206 AQLALKIYGGSVNAKNATLYQQRDVDGFLVGGASLKPE.FVDIINAK</li> <li>207 AQSTRIIYGGSVTGATCKELASQPDVDGFLVGASLKES.FVDIIKSAM</li> <li>208 ADTVRVLYGGSVNAKNATLYQQRDVNGFLVGGASLKPE.FVDIINAK</li> <li>209 AQSTRIIYGGSVTGATCKELASQPDVDGFLVGASLKES.FVDIIKSAM</li> <li>200 AGELRILYGGSVTAKNARTLYQQRDVNGFLVGGASLKPE.FVDIINAK</li> <li>200 AGELRILYGGSVTAKNARTLYQQRDVNGFLVGGASLKPE.FVDIINAK</li> </ul>   | 255<br>261<br>248<br>257<br>253<br>249<br>251<br>256<br>261<br>249<br>248<br>248<br>248<br>251   |
| EcTIM<br>EhTIM<br>GgTIM<br>GSTIM<br>HSTIM<br>LmTIM<br>MnTIM<br>OCTIM<br>PfTIM<br>SSTIM<br>TCTIM<br>TSTIM  | <ul> <li>202 AEQVIIQYGGSVNASNAAELFAQPDIDGALVGGASLKADAFAVIVKAAEAAKQA</li> <li>210 AEATRIQYGGSVNPANCNELAKKADIDGFLVGGASLDAAKFKTIINSVSEKF</li> <li>201 AQSTRIIYGGSVTGGNCKELASQHDVDGFLVGGASLKPE.FVDIINAKH</li> <li>206 AQHIRIIYGGSVKPDNIRDFLAQQQIDGFLVGGASLKPE.FMTMIDILTKTRT.</li> <li>203 AEAIRIQYGGSVKPDNIRDFLAQQQIDGFLVGGASLKPE.FMTMIDILTKTRT.</li> <li>204 AQSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AAKLRILYGGSVNAANAATLYAKPDINGFLVGGASLKPE.FVDIIDATR</li> <li>208 ADTVRVLYGGSVNAANATLYAKPDIDGALVGGASLKPE.FRDIIDATR</li> <li>209 AQSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AKNVVIQYGGSVKPENAAAYFAQPDIDGALVGGASLDGEHFATLAAIAAGCPLP</li> <li>202 AQSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>203 ADTVRVLYGGSVNTENCSSLIQQEDIDGFLVGASLKPE.FVDIINAKQ</li> <li>204 ANTRILYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>205 ADTVRVLYGGSVNTENCSSLIQQEDIDGFLVGASLKPE.FVDIINAKQ</li> <li>206 AQLRILYGGSVNGKNARTLYQQRDVNGFLVGGASLKPE.FVDIINAK</li> <li>207 AQLRILYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAK</li> <li>208 ADTVRVLYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAK</li> <li>209 AQSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAK</li> <li>2004 AAQLRILYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAK</li> <li>2014 AQLRILYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAK</li> <li>2025 AGELRILYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAK</li> <li>203 AGELRILYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAK</li> <li>204 AQLRILYGGSVTAKNARTLYQQRDVNGFLVGGASLKPE.FVDIIAAR</li> </ul>   | 255<br>261<br>248<br>257<br>253<br>249<br>251<br>256<br>261<br>249<br>248<br>248<br>248<br>250<br>251  |
| EcTIM<br>   | <ul> <li>202 AEQVIIQYGGSVNASNAAELFAQPDIDGALVGGASLKADAFAVIVKAAEAAKQA</li> <li>210 AEATRIQYGGSVNPANCNELAKKADIDGFLVGGASLDAAKFKTIINSVSEKF</li> <li>201 AQSTRIIYGGSVTGGNCKELASQHDVDGFLVGGASLKPE.FVDIINAKH</li> <li>206 AQHIRIIYGGSVKPDNIRDFLAQQQIDGPLVGGASLKPE.FMTMIDILTKTRT.</li> <li>203 AEAIRIQYGGSVKPDNIRDFLAQQQIDGPLVGGASLKPE.FVDIINAKQ</li> <li>204 AAKLRILYGGSVNAANAATLYAKPDINGFLVGGASLKPE.FRDIIDATR</li> <li>208 ADTVRVLYGGSVKPDNIACKELASQPDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AAKLRILYGGSVNAANAATLYAKPDINGFLVGGASLKPE.FRDIIDATR</li> <li>205 AQSTRIIYGGSVKPENAAAYFAQPDIDGALVGGASLKPE.FVDIINAKQ</li> <li>206 AQNTRILYGGSVNAANAATLYAKPDINGFLVGGASLKPE.FVDIINAKQ</li> <li>207 AQSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>208 ADTVRVLYGGSVNTENCSSLIQQEDIDGFLVGGASLKPE.FVDIINAKQ</li> <li>209 AQSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>201 ANQIRILYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>202 AQSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIIKSAM</li> <li>203 AGELRILYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAK</li> <li>204 AKNVRILYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAK</li> <li>205 AQSTRIIYGGSVTAKNARTLYQRDVDGFLVGGASLKPE.FVDIINAK</li> <li>206 AQSTRIIYGGSVTASNAKDLGTQPDVDGFLVGGASLKPE.FVDIINAK</li> <li>207 ANKYRILYGGSVTASNAKDLGTQPDVDGFLVGGASLKPE.FVDIINAK</li> <li>208 AQLRILYGGSVTASNAKDLGTQPDVDGFLVGGASLKPE.FVDIIAXA</li> <li>209 AQLRILYGGSVTASNAKDLGTQPDVDGFLVGGASLKPE.FVIIIAATA</li> <li>2002 ANKYRILYGGSVTASNAKDLGTQPDVDGFLVGGASLKPE.FVIIIAATA</li></ul>  | 255<br>261<br>248<br>257<br>253<br>249<br>251<br>256<br>261<br>249<br>248<br>248<br>250<br>251<br>250<br>251   |
| EcTIM<br>EhTIM<br>GgTIM<br>GgTIM<br>GSTIM<br>HSTIM<br>LmTIM<br>MtTIM<br>OCTIM<br>PfTIM<br>SSTIM<br>TbTIM<br>TcTIM<br>TvTIM<br>YtTIM   | <ul> <li>202 AEQVI I QYGGSVNASNAAEL FAQPD I DGALVGGASLKADAFAVI VKAAEAAKQA</li> <li>210 AEATR I QYGGSVNPANCNELAKKAD I DGFLVGGASLDAAKFKT I INSVSEKF</li> <li>201 AQSTRI I YGGSVTGGNCKELASQHDVDGFLVGGASLKPE.FVD I INAKH</li> <li>206 AQHIRII YGGSVKPDN IRDFLAQQQI DGPLVGGASLKPE.FVD I INAKH</li> <li>203 AEAIR I QYGGSVKPDN IRDFLAQQQI DGPLVGGASLEPASFLQUVEAGRHE</li> <li>204 AAKLR I LYGGSVTGATCKELASQHDVDGFLVGGASLKPE.FVD I INAKQ</li> <li>204 AAKLR I LYGGSVNAANAATLYAKPD INGFLVGGASLKPE.FND I IDATR</li> <li>208 ADTVRVLYGGSVKPENAAAYFAQPD I DGALVGGASLCPE.FRD I IDATR</li> <li>209 AQSTRI I YGGSVTGATCKELASQPDVDGFLVGGASLKPE.FND I IDATR</li> <li>204 AKNVV I QYGGSVKPENAAAYFAQPD I DGALVGGASLCPE.FVD I INAKQ</li> <li>204 AKNVV I QYGGSVKPENAAAYFAQPD I DGALVGGASLKPE.FVD I INAKA</li> <li>208 ADTVRVLYGGSVNAKNYGD I VAQDDVDGGLVGGASLKPE.FVD I INAKQ</li> <li>204 AQSTRI I YGGSVTGATCKELASQPD VDGFLVGGASLKPE.FVD I INAKQ</li> <li>204 ANNVV I QYGGSVKPENAAAYFAQPD I DGALVGGASLKPE.FVD I INAKA</li> <li>205 AQSTRI I YGGSVTGATCKELASQPD VDGFLVGGASLKPE.FVD I INAKQ</li> <li>206 ADTVRVLYGGSVTGATCKELASQPD VDGFLVGGASLKPE.FVD I INAK</li> <li>207 ANSTRI I YGGSVTGATCKELASQPD VDGFLVGGASLKPE.FVD I INAK</li> <li>208 ADTVRVLYGGSVTAKNARTLYQQRD VNGFLVGGASLKPE.FVD I INAK</li> <li>209 AQSTRI LYGGSVTAKNARTLYQQRD VNGFLVGGASLKPE.FVD I INAK</li> <li>200 ANKVRI LYGGSVTAKNARTLYQQRD VNGFLVGGASLKPE.FVD I INAK</li> <li>201 AAQLRI LYGGSVTASNAKDLGTQPD VDGFLVGGASLKPE.FVD I INARN</li> <li>202 ANKVRI LYGGSVATASNAKDLGTQPD VDGFLVGGASLKPE.FVD I INARN</li> <li>202 ANKVRI LYGGSVATASNAKDLGTQPD VDGFLVGGASLKPE.FVD I INARN</li> <li>203 ADKVRI LYGGSANGSNAVTFKDKADVDGFLVGGASLEPG.FIN INNSNHSK</li> <li>204 ANKVRI LYGGSANGSNAVTFKDKADVDGFLVGGASLEPG.FIN INNSNHSK</li></ul>   | 255<br>261<br>248<br>257<br>253<br>251<br>251<br>256<br>261<br>249<br>248<br>248<br>250<br>251<br>250<br>252<br>248  |
| EcTIM<br>EhTIM<br>GgTIM<br>GGTIM<br>GGTIM<br>HSTIM<br>LmTIM<br>MtTIM<br>OCTIM<br>PFTIM<br>SSTIM<br>TbTIM<br>TcTIM<br>TsTIM<br>YtTIM<br>YtTIM  | <ul> <li>202 AEQVIIQYGGSVNASNAAELFAQPDIDGALVGGASLKADAFAVIVKAAEAAKQA</li> <li>210 AEATRIQYGGSVNPANCNELAKKADIDGFLVGGASLDAAKFKTIINSVSEKF</li> <li>201 AQSTRIIYGGSVTGGNCKELASQHDVDGFLVGGASLKPE.FVDIINAKH</li> <li>206 AQHIRIIYGGSVNPANCNELAQQQIDGPLVGGASLKPE.FMTMIDILTKTRT</li> <li>203 AEAIRIQYGGSVKPDNIRDFLAQQQIDGPLVGGASLKPE.FVDIINAKH</li> <li>204 AQSTRIIYGGSVTGATCKELASQHDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AAKLRILYGGSVNAANAATLYAKPDINGFLVGGASLKPE.FNDIIDATR</li> <li>208 ADTVRVLYGGSVKPENAAAYFAQPDIDGALVGGASLKPE.FNDIIDATR</li> <li>209 AQSTRIIYGGSVKPENAAAYFAQPDIDGALVGGASLKPE.FNDIIDATR</li> <li>201 ANQIRILYGGSVNGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>202 AQSTRIIYGGSVKDENAAAYFAQPDIDGALVGGASLKPE.FVDIINAKQ</li> <li>203 AGLTRILYGGSVNGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AKNVVIQGSVKPENAAAYFAQPDIDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AKNVVIQGSVNENCSSLIQQEDIDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AQSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AQLRILYGGSVNENCSSLIQQEDIDGFLVGGASLKPE.FVDIINAK</li> <li>203 AGELRILYGGSVTAKNARTLYQQRDVNGFLVGGASLKPE.FVDIINAK</li> <li>204 AAQLRILYGGSVTAKNARTLYQQRDVNGFLVGGASLKPE.FVDIINAK</li> <li>205 ADKVRILYGGSVTASNAKDLGTQPDVDGFLVGGASLKPE.FVDIINARR</li> <li>206 ANKVRILYGGSVATASNAKDLGTQPDVDGFLVGGASLKPE.FVDIINAR</li> <li>207 ANKVRILYGGSVATASNAKDLGTQPDVDGFLVGGASLKPE.FVDIINAR</li> <li>208 ANKVRILYGGSVATASNAKDLGTQPDVDGFLVGGASLKPE.FVDIINAR</li> <li>209 ANKVRILYGGSVATASNAKDLGTQPDVDGFLVGGASLKPE.FVDIINAR</li> <li>201 ASELRILYGGSVATASNAKDLGTQPDVDGFLVGGASLKPE.FVDIINAR</li> <li>202 ANKVRILYGGSVATASNAKDLGTQPDVDGFLVGGASLKPE.FVDIINAR</li> <li>203 ADKVRILYGGSANGSNAVTFKDKADVDGFLVGGASLKPE.FVDIINAR</li> <li>204 ANVYNILYGGSVAASNAKDLGTQPDVDGFLVGGASLKPE.FVDIINAR</li></ul>  | 255<br>261<br>248<br>257<br>253<br>249<br>251<br>256<br>261<br>249<br>248<br>248<br>250<br>251<br>250<br>251<br>252<br>248<br>243                                    |
| EcTIM<br>EhTIM<br>GgTIM<br>GgTIM<br>GGTIM<br>HSTIM<br>LmTIM<br>MmTIM<br>MmTIM<br>OcTIM<br>PTIM<br>SSTIM<br>TSTIM<br>TcTIM<br>TsTIM<br>TvTIM<br>YTIM<br>GGTIM                                      | <ul> <li>202 AEQVIIQYGGSVNASNAAELFAQPDIDGALVGGASLKADAFAVIVKAAEAAKQA</li> <li>210 AEATRIQYGGSVNPANCNELAKKADIDGFLVGGASLDAAKFKTIINSVSEKF</li> <li>201 AQSTRIIYGGSVTGGNCKELASQHDVDGFLVGGASLKPE.FVDIINAKH</li> <li>206 AQHIRIIYGGSVKPDNIRDFLAQQQIDGPLVGGASLKPE.FMTMIDILTKTRT.</li> <li>203 AEAIRIQYGGSVKPDNIRDFLAQQQIDGPLVGGASLKPE.FVDIINAKQ</li> <li>204 AQSTRIIYGGSVTGATCKELASQHDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AAKLRILYGGSVNAANAATLYAKPDINGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AKNVVIQYGGSVKPENAAAYFAQPDIDGALVGGASLKPE.FVDIINAKQ</li> <li>204 AKNVVIQYGGSVKPENAAAYFAQPDIDGALVGGASLKPE.FVDIINAKQ</li> <li>204 AKNVVIQYGGSVKPENAAAYFAQPDIDGALVGGASLKPE.FVDIINAKQ</li> <li>204 AKNVVIQGSVNAKNVGDIVAQDDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AKNVVIQGSVNAKNVGDIVAQDDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AKNVVIQGSVNAKNVGDIVAQDDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AKNVVIQGSVNAKNVGDIVAQDDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AKNVVIQGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AQSTRIIYGGSVTAKNARTLYQQRDVNGFLVGGASLKPE.FVDIINAKQ</li> <li>205 AQSTRIIYGGSVTAKNARTLYQQRDVNGFLVGGASLKPE.FVDIINAK</li> <li>206 AQLRILYGGSVTAKNARTLYQQRDVNGFLVGGASLKPE.FVDIINAK</li> <li>207 AQSTRIIYGGSVTAKNARTLYQQRDVNGFLVGGASLKPE.FVDIINAK</li> <li>208 ADKVRILYGGSVTAKNARTLYQMRDINGFLVGGASLKPE.FVDIINAK</li> <li>209 AQKVRILYGGSVKANNCNELAACPDVDGFLVGGASLKPE.FVDIINSNNYHSK</li> <li>201 ASELRILYGGSVKANNCNELAACPDVDGFLVGGASLKPE.FVDIINSNNYHSK</li> <li>202 ANKVRILYGGSVKANN IDEIMAQPEIDGVLVGGASLEPESFARIVNFHLV</li> <li>204 ADSTPIVYGGSVKPNN IDEIMAQPEIDGVLVGGASLEPESFARIVNFHLV</li> <li>204 ADSTPIVYGGSVKPNNTGELAGCDVDGFLVGGASLEPESFARIVNFHLV</li> <li>204 ADSTPIVYGGSVFPNTYGLMSQPDVDGALVGGASLEPESFARIVNFHLV</li> </ul>   | 255<br>261<br>248<br>257<br>253<br>249<br>251<br>256<br>261<br>249<br>248<br>248<br>250<br>251<br>250<br>252<br>248<br>243<br>252                                    |
| EcTIM<br>EhTIM<br>GGTIM<br>GGTIM<br>HSTIM<br>LmTIM<br>MRTIM<br>MRTIM<br>OCTIM<br>PFTIM<br>SSTIM<br>TbTIM<br>TbTIM<br>TsTIM<br>TvTIM<br>YtTIM<br>NpTIM<br>GGTIM<br>DrTIM.                          | <ul> <li>202 AEQVIIQYGGSVNASNAAELFAQPDIDGALVGGASLKADAFAVIVKAAEAAKQA</li> <li>210 AEATRIQYGGSVNPANCNELAKKADIDGFLVGGASLDAAKFKTIINSVSEKF</li> <li>201 AQSTRIIYGGSVTGGNCKELASQHDVDGFLVGGASLKPE.FVDIINAKH</li> <li>206 AQHIRIIYGGSVKPDNIRDFLAQQQIDGFLVGGASLKPE.FMTMIDILTKTRT.</li> <li>203 AEAIRIQYGGSVKPDNIRDFLAQQQIDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AQSTRIIYGGSVTGATCKELASQHDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AAKLRILYGGSVNAANAATLYAKPDINGFLVGGASLKPE.FVDIINAKQ</li> <li>208 ADTVRVLYGGSVKPENAAAYFAQPDIDGALVGGASLKPE.FVDIIDATR</li> <li>204 AKNVVIQYGSSVKPENAAAYFAQPDIDGALVGGASLKPE.FVDIINAKQ</li> <li>204 AKNVVIQGSSVKPENAAAYFAQPDIDGALVGGASLKPE.FVDIINAKQ</li> <li>204 AKNVVIQGSSVKPENAAAYFAQPDIDGALVGGASLKPE.FVDIINAKQ</li> <li>204 AKNVVIQGSSVKPENAAAYFAQPDIDGALVGGASLKPE.FVDIINAKQ</li> <li>204 AKNVVIQGSSVKPENAAAYFAQPDIDGALVGGASLKPE.FVDIINAKQ</li> <li>204 AKNVVIQGSSVKPENAAAYFAQPDINGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AKNVVIQGSSVKBAKAKNVGDIVAQDDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AKNVIQGSSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 ANSTRIIYGGSSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAK</li> <li>203 AGERILYGGSVTAKNARTLYQMRDINGFLVGGASLKPE.FVDIINAK</li> <li>204 AAQLRILYGGSVTAKNARTLYQMRDINGFLVGGASLKPE.FVDIINAK</li> <li>205 ADKVRILYGGSVKPNNCNELAACPDVDGFLVGGASLKPE.FVDIINAK</li> <li>206 ADKVRILYGGSVKPNNCNELAACPDVDGFLVGGASLKPE.FVDIINSNNHSK</li> <li>207 ANKVRILYGSSVASNAKDLGTQPDVDGFLVGGASLKPE.FVDIINSNNHSK</li> <li>208 ADKVRILYGSSVASNAYTFKDKADVDGFLVGGASLKPE.FVDIINSNNHSK</li> <li>201 ASELRILYGSSNASNAVTFKDKADVDGFLVGGASLKPE.FVDIINSN</li> <li>202 ANKVRILYGSSVFPNNIDEIMAQPEIDCVLGGASLKPE.FVDIINSNN</li></ul>   | 255<br>261<br>248<br>257<br>253<br>249<br>251<br>256<br>261<br>248<br>248<br>250<br>251<br>250<br>252<br>248<br>243<br>252<br>244                                    |
|   | <ul> <li>202 AEQVIIQYGGSVNASNAAELFAQPDIDGALVGGASLKADAFAVIVKAAEAAKQA</li> <li>210 AEATRIQYGGSVNPANCNELAKKADIDGFLVGGASLDAAKFKTIINSVSEKF</li> <li>201 AQSTRIIYGGSVTGGNCKELASQHDVDGFLVGGASLKPE.FVDIINAKH</li> <li>206 AQHIRIIYGGSVKPDNIRDFLAQQQIDGFLVGGASLKPE.FMTMIDILTKTRT.</li> <li>203 AEAIRIQYGGSVKPDNIRDFLAQQQIDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AQSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AAKLRILYGGSVNAANAATLYAKPDINGFLVGGASLKPE.FRDIIDATR</li> <li>208 ADTVRVLYGGSVKPENAAAYFAQPDIDGALVGGASLDGEHFATLAAIAAGGPLP</li> <li>202 AQSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AKNVYIQYGSVSVGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AKNVYIQYGSVNAKNVGDIVAQDDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AKNVYIQGSVNAKNVGDIVAQDDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AKNVYLYGGSVNAKNVGDIVAQDDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AKNVYLYGGSVNAKNVGDIVAQDDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AQSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AQUSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAKQ</li> <li>204 AQUSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAK</li> <li>205 ADTVRVLYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAK</li> <li>206 ADTVRVLYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAK</li> <li>207 AQSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPE.FVDIINAK</li> <li>208 ADTVRVLYGGSVTAKNARTLYQMRDINGFLVGGASLKPE.FVDIINAK</li> <li>209 ANKVRILYGGSVTANAKDLGTQPDVDGFLVGGASLKPE.FVDIINAK</li> <li>201 ASELRILYGGSANGSNAVTFKDKADVDGFLVGGASLKPE.FVDIINSRN</li> <li>202 ANKVRILYGGSVTPNNCNELAACPDVDGFLVGGASLKPE.FVDIINSRN</li> <li>204 ANKVRILYGGSVTPNTVGLMAQPEIDCVLVGGASLKPE.FVDIINSRN</li> <li>205 ANKVRILYGGSVKPNNIDE IAACPDVDGFLVGGASLKPE.FVDIINSRN</li> <li>206 ANKVRILYGGSVKPNNIDE IAACPDVDGFLVGGASLKPE.FVDIINSRN</li> <li>207 ANKVRILYGGSVKPNNIDE IAACPDVDGFLVGGASLKPE.FVDIINSRN</li> <li>208 ANKVRILYGGSVKPNNIDE IAACPDVDGFLVGGASLKPE.FVDIINSRN</li> <li>204 ANKVRILYGGSVKPNIAEINAAPDIDGALVGGASLKVPIVLGMLDAR</li></ul>   | 255<br>261<br>248<br>257<br>253<br>249<br>251<br>256<br>261<br>249<br>248<br>250<br>251<br>250<br>252<br>248<br>243<br>252<br>244<br>254<br>254                      |
| EcTIM<br>EhTIM<br>GgTIM<br>GgTIM<br>GGTIM<br>HSTIM<br>LmTIM<br>MmTIM<br>OCTIM<br>PFTIM<br>SSTIM<br>TbTIM<br>TcTIM<br>TvTIM<br>YtTIM<br>QGTIM<br>CoTIM<br>CoTIM<br>CoTIM                           | <ul> <li>202 AEQVI I QYGGSVNASNAAEL FAQPD I DGALVGGASLKADAFAVI VKAAEAAKQA</li> <li>210 AEATR I QYGGSVNPANCNELAKKAD I DGFLVGGASLDAAKFKT I INSVSEKF</li> <li>201 AQSTRI I YGGSVTGGNCKELASQHDVDGFLVGGASLKPE. FVDI INAKH</li> <li>206 AQHIRII YGGSVKPDN IRDFLAQQQI DGPLVGGASLKPE. FVDI INAKH</li> <li>203 AEAIR I QYGGSVKPDN IRDFLAQQQI DGPLVGGASLEPASFLQUVEAGRHE</li> <li>204 AAKLR I LYGGSVNAANAATLYAKPD INGFLVGGASLKPE. FVDI INAKQ</li> <li>204 AKLR I LYGGSVNAANAATLYAKPD INGFLVGGASLKPE. FNDI IDATR</li> <li>205 AQSTRI I YGGSVKPENAAAYFAQPD I DGALVGGASLKPE. FNDI IDATR</li> <li>206 AQNTVL YGGSVNAKNQD I VAQDDVDGLVGGASLKPE. FNDI IDATR</li> <li>207 AQSTRI I YGGSVTGATCKELASQPD VDGFLVGGASLKPE. FVDI INAKQ</li> <li>208 ADTVRVL YGGSVNAKNYGD I VAQDDVDGGLVGGASLKPE. FVDI INAKQ</li> <li>209 AQSTRI I YGGSVTGATCKELASQPD VDGFLVGGASLKPE. FVDI INAKQ</li> <li>201 ANQIRILYGGSVNAKNYGD I VAQDDVDGFLVGGASLKPE. FVDI INAKQ</li> <li>202 AQSTRI I YGGSVTGATCKELASQPD VDGFLVGGASLKPE. FVDI INAKQ</li> <li>203 AGELRI LYGGSVNGKNARTLYQQRD VNGFLVGGASLKPE. FVDI INAK</li> <li>204 AAQLRI LYGGSVTAKNARDLGTQPD VDGFLVGGASLKPE. FVDI INAK</li> <li>205 ADKVRI LYGGSVTAKNARTLYQQRD VNGFLVGGASLKPE. FVDI INAK</li> <li>204 AAQLRI LYGGSVTAKNARTLYQQRD VNGFLVGGASLKPE. FVDI INAK</li> <li>205 ADKVRI LYGGSVTAKNARDLGTQPD VDGFLVGGASLKPE. FVDI INAK</li> <li>206 ADKVRI LYGGSVTASNAKDLGTQPD VDGFLVGGASLKPE. FVDI INARR</li> <li>207 ANKVRI LYGGSVTASNAKDLGTQPD VDGFLVGGASLKPE. FVDI INARR</li> <li>208 ADKVRI LYGGSVKPNN IDE IMAQPE IDGVLVGGASLEPESFARI VNFHLV</li> <li>204 ADSTP IVYGGSVKPNN IDE IMAQPE IDGVLVGGASLEPESFARI VNFHLV</li> <li>204 ADSTP IVYGGSVKPNN IAE IGKPNNGALVGGASLKDGASLKADSFLAIVKAAG</li> <li>205 ADKVRI QYGGSVKPNI IAE ICGKPNNGALVGGASLKDSPLAIVKIARG</li> <li>206 ADKVRI QYGGSVKPNI IAE IGAKPNNGALVGGASLKDSPLAIVKIRARGAL</li> <li>207 ADKVRI QYGGSVKPNI IAE IGAKPNNGALVGGASLKADSFLAIVKAAG</li></ul>  | 255<br>261<br>248<br>257<br>253<br>249<br>251<br>256<br>261<br>249<br>248<br>248<br>250<br>251<br>250<br>252<br>248<br>243<br>252<br>244<br>252<br>244<br>254<br>254 |
| EcTIM<br>EhTIM<br>GgTIM<br>GgTIM<br>GgTIM<br>HSTIM<br>LmTIM<br>MmTIM<br>MtTIM<br>OCTIM<br>PFTIM<br>SSTIM<br>TbTIM<br>TcTIM<br>TcTIM<br>TyTIM<br>NpTIM<br>GoTIM<br>DrTIM<br>ScTIM<br>CpTIM         | 202 AEQVI I QYGGSVNASNAAEL FAQPD I DGALVGGASLKADAFAVI VKAAEAAKQA<br>210 AEATR I QYGGSVNPANCNELAKKAD I DGFLVGGASLDAAKFKT I INSVSEKF<br>201 AQSTRI I YGGSVTGGNCKELASQHDVDGFLVGGASLKPE. FVDI I NAKH<br>206 AQHIRI I YGGSVNGNCEKLGQCPN I DGFLVGGASLKPE. FVDI I NAKH<br>207 AEAIR I QYGGSVKPDN I RDFLAQQQI DGPLVGGASLKPE. FVDI I NAKH<br>208 AAIR I QYGGSVKPDN I RDFLAQQQI DGPLVGGASLKPE. FVDI I NAKQ<br>209 AQSTRI I YGGSVTGATCKELASQPDVDGFLVGGASLKPE. FVDI I NAKQ<br>204 AKLRI L YGGSVNAANAATLYAKPD I NGFLVGGASLKPE. FVDI I NAKQ<br>204 AKNVV I QYGGSVKPENAAAYFAQPD I DGALVGGASLDGEH FATLAAIAAGGPLP<br>202 AQSTRI I YGGSVNGATCKELASQPDVDGFLVGGASLDGEH FATLAAIAAGGPLP<br>202 AQSTRI I YGGSVNGATCKELASQPDVDGFLVGGASLKPE. FVDI I NAKQ<br>204 AKNVV I QYGGSVKPENAAAYFAQPD I DGALVGGASLDGEH FATLAAIAAGGPLP<br>202 AQSTRI I YGGSVNGATCKELASQPDVDGFLVGGASLKPE. FVDI I NAKQ<br>204 AKNV I QYGGSVNGFNATLYQQPD VDGFLVGGASLKPE. FVDI I NAKA<br>205 AHSTRI I YGGSVTGATCKELASQPDVDGFLVGGASLKPE. FVDI I NAK<br>206 AGLRI L YGGSVNGKNARTLYQQRDVNGFLVGGASLKPE. FVDI I NAK<br>207 AGLRI L YGGSVTAKNARTLYQQRDVDGFLVGGASLKPE. FVDI I NAK<br>208 AGLRI L YGGSVTAKNARTLYQQRDVDGFLVGGASLKPE. FVDI I NAK<br>209 ADKVRI L YGGSVTAKNARTLYQQRDVDGFLVGGASLKPE. FVDI I NAK<br>200 ANKVRI L YGGSVTAKNARTLYQQRDVDGFLVGGASLKPE. FVDI I NAK<br>201 ASELRI L YGGSVATAKNARTLYQQRDVDGFLVGGASLKPE. FVDI I NAKK<br>202 ANKVRI L YGGSVATAKNARTLYQQRDVDGFLVGGASLKPE. FVDI I NARR<br>203 ADKVRI L YGGSVATASNAKDLGT QPDVDGFLVGGASLKPE. FVDI I NARR<br>204 ADSTPI VYGGSVTPDNTVGLMAQPE VDGFLVGGASLKPE. FVDI I NARR<br>205 ANKVRI L YGGSVATASNAKDLGT QPDVDGFLVGGASLKPE. FVDI I NARR<br>206 ANKVRI L YGGSVATASNAKDLGT QPDVDGFLVGGASLKPE. FVDI I NSRN<br>207 ANKVRI L YGGSVATASNAKDLGT PDVDGFLVGGASLKPE. FVDI I NSRN<br>208 ANKVRI L YGGSVATASNAKDLGT PDVDGFLVGGASLKPE. FVDI I NSRN<br>209 ADKVRI QYGGSVKPNN I DE I MAQPE I DCVLVGGASLKADSFLAI VKAAG<br>200 ADKVRI QYGGSVKPNN I DE I MACPE I DCVLVGGASL VADFAN VNFKLDALR<br>200 ADKVRI QYGGSVKPNN I DE I MACPE I DCALVGGASL VADFAN VNFK VNFRDQ<br>202 ADKVRI QYGGSV | 255<br>261<br>248<br>257<br>253<br>249<br>249<br>248<br>248<br>250<br>251<br>250<br>252<br>248<br>243<br>252<br>244<br>258<br>243                                    |
| EcTIM<br>EhTIM<br>GgTIM<br>GgTIM<br>GGTIM<br>HSTIM<br><br>MMTIM<br><br>MMTIM<br><br>MMTIM<br>OCTIM<br>SSTIM<br>ToTIM<br>ToTIM<br><br>ToTIM<br><br>YtTIM<br><br>OTIM<br><br>CoTIM<br><br>Consensus | 202 AEQVI I QYGGSVNASNAAEL FAQPD I DGALVGGASLKADAFAVI VKAAEAAKQA<br>210 AEATR I QYGGSVNPANCNELAKKAD I DGFLVGGASLDAAKFKT I INSVSEKF<br>201 AQSTRI I YGGSVTGGNCKELASQHDVDGFLVGGASLKPE. FVDI INAKH<br>206 AQHIRI I YGGSVNGANCEKLGQCPN I DGFLVGGASLKPE. FVDI I NAKH<br>207 AQSTRI I YGGSVNGANCKLGQCPN I DGFLVGGASLKPE. FVDI I NAKH<br>208 AQHIRI I YGGSVNGANCKLGQCPN I DGFLVGGASLKPE. FVDI I NAKQ<br>202 AQSTRI I YGGSVTGATCKELASQPDVDGFLVGGASLKPE. FVDI I NAKQ<br>204 AKLRI L YGGSVNAANAATLYAKPD I NGFLVGGASLKPE. FVDI I NAKQ<br>204 AKNVVI QYGGSVKPENAAAYFAQPD I DGALVGGAALDAKSFAAIAKAAAEAKA.<br>208 ADTVRVL YGGSVNAKNVGDI VAQDDVDGGLVGGASLDGEHFATLAAIAAGGPLP<br>202 AQSTRI I YGGSVTGATCKELASQPDVDGFLVGGASLKPE. FVDI I NAKQ<br>204 AKNVVI QYGGSVKPENAAAYFAQPD I DGALVGGASLKPE. FVDI I NAKQ<br>204 AKNVVI QYGGSVNGGNCKLASQPDVDGFLVGGASLKPE. FVDI I NAKQ<br>204 AKNVVI QYGGSVNGGNACKLASQPDVDGFLVGGASLKPE. FVDI I NAKQ<br>204 AKNVVI QYGGSVNGGNACKLASQPDVDGFLVGGASLKPE. FVDI I NAKQ<br>204 AQSTRI I YGGSVTGATCKELASQPDVDGFLVGGASLKPE. FVDI I NAKK<br>203 AGELRI L YGGSVNGKNARTLYQQRDVNGFLVGGASLKPE. FVDI I NAKK<br>204 AAQLRI L YGGSVTAKNARTLYQQRDVNGFLVGGASLKPE. FVDI I NAKK<br>205 ADKVRI L YGGSVKPNNCNELAACPDVDGFLVGGASLKPE. FVDI I NARR<br>206 AAQLRI L YGGSVNFNCNELAACPDVDGFLVGGASLKPE. FVDI I NARR<br>207 ADKVRI L YGGSVKPNN I DE I MAQPE I DGYLVGGASLKPE. FVDI I NSRN<br>208 ADKVRI L YGGSVKPNN I DE I MAQPE I DGYLVGGASLKPE. FVDI I NSRN<br>209 ADKVRI L YGGSVKPNN I DE I MAQPE I DGYLVGGASLKPE. FVDI I NSRN<br>204 ADSTPI VYGGSVKPNN I DE I MAQPE I DGYLVGGASLKPE FVDI I NSRN<br>205 PNVS QYGGSVKPNN I DE I MAQPE I DGYLVGGASLKPE FVDI I NSRN<br>206 ADSTPI VYGGSVKPNN I DE I MAQPE I DGYLVGGASLKADSFLAI VKAAG<br>207 ADKVRI QYGGSVKSGNVAE I MAKPDI DGALVGGASLKADSFLAI VKAAG<br>208 ADKVRI QYGGSVKSPN I AE I CGKPNNNGALVGGASLKADSFLAI VKAADFAQI VNY<br>209 ADKVRI QYGGSVKSPN I AE I CGKPNNNGALVGGASLKADFLAI VKAADFAQI VNY<br>200 ADKVRI QYGGSVKSPN I AE I CGKPNNGALVGGASLKADFLAI VKAADFAQI VNY<br>200 ADKVRI QYGGSVKSPN I AE I DGYLVGGASLKADFLAI VXADFA        | 255<br>261<br>248<br>257<br>253<br>249<br>251<br>256<br>261<br>249<br>248<br>248<br>250<br>251<br>250<br>251<br>250<br>252<br>248<br>243<br>252<br>244<br>258<br>244 |

**Fig. S6.** Sequence alignment of diverse TIMs used for comparison. The conserved residues in these TIMs are shown on the *consensus line* and represented from blue light to dark in accordance to increase conservation. In red squares are shown the residues (both internal and boundary) involved in the formation of the biggest cavity in these structures, except for *Np*TIM, *Ss*TIM and *Ts*TIM for which there is not structural data reported.

Table S1. Thermodynamic parameters for the irreversible thermal unfolding of *Np*TIM and *Go*TIM.

|  | Bacteri            | al TIMs      |                            | Eukaryotic TIMs            |                            |                            |                            |  |  |
|--|--------------------|--------------|----------------------------|----------------------------|----------------------------|----------------------------|----------------------------|--|--|
| Thermodynamic parameter  | NpTIM              | GoTIM        | <i>GI</i> TIM <sup>a</sup> | <i>Hs</i> TIM <sup>a</sup> | <i>Lm</i> TIM <sup>b</sup> | <i>Tb</i> TIM <sup>b</sup> | <i>Tc</i> TIM <sup>b</sup> |  |  |
| Activation free energy (kJ mol <sup>-1</sup> ) from<br>average of individual fits to DSC thermograms<br>(Eqs. (3) and (4)) | $368 \pm 46$       | 716 ± 63     | NR                         | NR                         | 312 ± 5                    | 397 ± 5                    | $809 \pm 7$                |  |  |
| Activation free energy (kJ mol <sup>-1</sup> ) from<br>Arrhenius plot (Eq. (2))  | 368 ± 17           | 716 ± 25     | $367 \pm 7$                | $361 \pm 4$                | $315 \pm 3$                | $398 \pm 5$                | 793 ± 18                   |  |  |
| Activation free energy (kJ mol <sup>-1</sup> ) from<br>consistency test using several scanning rates<br>(Eq. (5))          | 343 ± 21           | 715 ± 88     | NR                         | NR                         | $347 \pm 39$               | $420 \pm 55$               | 715 ± 137                  |  |  |
| Activation free energy average (kJ mol <sup>-1</sup> )   | $360 \pm 25$       | $715 \pm 46$ | NR                         | NR                         | $325 \pm 21$               | $406\pm29$                 | $774 \pm 75$               |  |  |
| $m^{\ddagger}(kJ mol^{-1} M^{-1})$   | 1.67               | 8.12         | 3.94                       | 2.77                       | 1.47                       | 1.69                       | 8.32                       |  |  |
| $m_{eq}$ (kJ mol <sup>-1</sup> M <sup>-1</sup> )   | 27.95 <sup>c</sup> | 27.77        | 30.02                      | 30.09                      | 30.80                      | 30.35                      | 30.67                      |  |  |
| $m^{t}/m_{eq}$   | 0.06               | 0.29         | 0.13                       | 0.09                       | 0.05                       | 0.06                       | 0.27                       |  |  |
| Number of residues unfolded<br>in the transition state <sup>d</sup>  | 30                 | 148          | 67                         | 45                         | 24                         | 28                         | 136                        |  |  |

<sup>*a*</sup> From Ref. 18. <sup>*b*</sup> From Ref. 19. <sup>*c*</sup> Because the structure of NpTIM is not known, the  $\Delta$ ASA value used for the calculation of  $m_{eq}$  is the average of  $\Delta$ ASA from all three-dimensional structures employed for structural comparison (57388 ± 1365 A<sup>2</sup>; Table 4). <sup>*d*</sup> Calculed from: N<sub>r</sub>( $m^{\ddagger}/m_{eq}$ ), where N<sub>r</sub> is the total number of residues in the dimeric protein, and  $m^{\ddagger}/m_{eq}$  is the degree of unfolding as estimated from the urea *m* values. NR: value not reported.

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| Data collection <sup>a</sup> |                        |                        |                        |                        |  |  |  |  |  |  |  |
|------------------------------|------------------------|------------------------|------------------------|------------------------|--|--|--|--|--|--|--|
|                              | GoTIM                  | DrTIM                  | ScTIM                  | <i>Cp</i> TIM          |  |  |  |  |  |  |  |
| PDB ID                       | 4Y96                   | 4Y90                   | 4Y9A                   | 4Y8F                   |  |  |  |  |  |  |  |
| Resolution range (Å)         | 36.36-1.58 (1.64-1.58) | 36.13-2.09 (2.17-2.09) | 43.03-2.29 (2.37-2.29) | 37.59-1.54 (1.59-1.54) |  |  |  |  |  |  |  |
| Space group                  | P 65 2 2               | R 3 2                  | P 4 <sub>3</sub>       | C 1 2 1                |  |  |  |  |  |  |  |
| Unit cell dimensions         |                        |                        |                        |                        |  |  |  |  |  |  |  |
| a, b, c, (Å)                 | 124.8, 127.8, 134.2    | 169.6, 169.6, 202.3    | 86.1, 86.1, 134.0      | 75.3, 49.6, 71.5       |  |  |  |  |  |  |  |
| α, β, γ, (°)                 | 90.0, 90.0, 120.0      | 90.0, 90.0, 120.0      | 90.0, 90.0, 90.0       | 90.0, 120.0, 90.0      |  |  |  |  |  |  |  |
| Total reflections            | 779530 (107888)        | 261090 (36321)         | 128420 (19245)         | 142402 (17348)         |  |  |  |  |  |  |  |
| Unique reflections           | 81335 (8192)           | 64962 (6342)           | 43475 (4241)           | 33930 (3130)           |  |  |  |  |  |  |  |
| Multiplicity                 | 9.6 (9.0)              | 4.0 (3.9)              | 3.0 (3.1)              | 4.2 (3.7)              |  |  |  |  |  |  |  |
| Completeness (%)             | 99.3 (97.1)            | 99.7 (98.6)            | 99.7 (98.1)            | 99.2 (94.4)            |  |  |  |  |  |  |  |
| Mean I / sigma (I)           | 29.0 (4.8)             | 11.0 (2.9)             | 10.0 (3.0)             | 14.6 (3.1)             |  |  |  |  |  |  |  |
| R-merge                      | 0.040 (0.487)          | 0.097 (0.464)          | 0.071 (0.371)          | 0.062 (0.448)          |  |  |  |  |  |  |  |
|                              | Refinenment statistics |                        |                        |                        |  |  |  |  |  |  |  |
|                              | GoTIM                  | DrTIM                  | ScTIM                  | <i>Cp</i> TIM          |  |  |  |  |  |  |  |
| $R_{work} / R_{free}$ (%)    | 17.8 / 20.1            | 13.8 / 18.6            | 23.1 / 28.2            | 14.8 / 18.1            |  |  |  |  |  |  |  |
| Average B-value ( $Å^2$ )    | 24.9                   | 25.9                   | 35.8                   | 16.6                   |  |  |  |  |  |  |  |
| Protein                      | 23.1                   | 24.8                   | 35.9                   | 14.1                   |  |  |  |  |  |  |  |
| Ligand                       | 32.8                   | 49.3                   |                        | 31.5                   |  |  |  |  |  |  |  |
| Solvent                      | 35.2                   | 33.2                   | 32.7                   | 29.5                   |  |  |  |  |  |  |  |
| Number of atoms              | 4446                   | 8069                   | 7943                   | 2362                   |  |  |  |  |  |  |  |
| Protein                      | 3777                   | 7142                   | 7690                   | 1977                   |  |  |  |  |  |  |  |
| Ligand                       | 14                     | 87                     |                        | 11                     |  |  |  |  |  |  |  |
| Water                        | 639                    | 832                    | 250                    | 372                    |  |  |  |  |  |  |  |
| Protein residues             | 500                    | 976                    | 1018                   | 251                    |  |  |  |  |  |  |  |
| RMS (bonds) (Å)              | 0.007                  | 0.011                  | 0.009                  | 0.010                  |  |  |  |  |  |  |  |
| RMS (angles) (°)             | 1.11                   | 1.30                   | 1.33                   | 1.24                   |  |  |  |  |  |  |  |
| Ramachandran favored (%)     | 98.43                  | 97.74                  | 96.15                  | 98.47                  |  |  |  |  |  |  |  |
| Ramachandran allowed (%)     | 1.18                   | 1.85                   | 3.56                   | 1.15                   |  |  |  |  |  |  |  |
| Ramachandran outliers (%)    | 0.39                   | 0.41                   | 0.30                   | 0.38                   |  |  |  |  |  |  |  |
| Clashcore                    | 1.83                   | 1.25                   | 5.41                   | 1.76                   |  |  |  |  |  |  |  |

<sup>*a*</sup> Statistics for the highest-resolution shell are shown in parentheses.

|           | RMSD values    |          |               |               |               |       |               |               |          |               |               |               |               |               |               |               |               |       |          |       |       |               |       |
|-----------|----------------|----------|---------------|---------------|---------------|-------|---------------|---------------|----------|---------------|---------------|---------------|---------------|---------------|---------------|---------------|---------------|-------|----------|-------|-------|---------------|-------|
| IrrevTIMs |                |          |               |               |               |       |               |               |          |               | RevTIMs       |               | Is            |               |               |               |               |       |          |       |       |               |       |
|           |                | EcTIM    | <i>Eh</i> TIM | <b>G</b> gTIM | <i>GI</i> TIM | GsTIM | <i>Hs</i> TIM | <i>Lm</i> TIM | MmTIM    | <i>Mt</i> TIM | <b>O</b> cTIM | <i>Рf</i> TIM | <i>Ss</i> TIM | <i>Tb</i> TIM | <i>Tc</i> TIM | <i>Ts</i> TIM | <i>Tv</i> TIM | YtTIM | NpTIM    | GoTIM | DrTIM | <b>S</b> cTIM | СрТІМ |
|           | <i>Ec</i> TIM  |          | 1.51          | 1.30          | 1.53          | 1.48  | 1.39          | 1.13          | 1.24     | 1.10          | 1.50          | 1.27          |               | 1.41          | 1.48          |               | 1.24          | 1.08  |          | 1.49  | 1.37  | 1.36          | 1.46  |
|           | <i>Eh</i> TIM  | 41       |               | 0.83          | 1.50          | 1.16  | 0.97          | 1.09          | 1.65     | 1.15          | 0.93          | 1.04          |               | 0.82          | 1.07          |               | 0.90          | 1.21  |          | 1.51  | 1.20  | 0.87          | 1.07  |
|           | <b>G</b> gTIM  | 45       | 50            |               | 1.01          | 0.92  | 0.40          | 0.65          | 1.20     | 1.05          | 0.34          | 0.85          |               | 0.61          | 0.73          |               | 0.62          | 0.68  |          | 1.36  | 1.00  | 0.87          | 1.22  |
|           | <i>GI</i> TIM  | 40       | 43            | 44            |               | 1.21  | 1.01          | 1.05          | 1.09     | 1.37          | 0.98          | 1.30          |               | 1.10          | 0.88          |               | 1.04          | 1.12  |          | 0.86  | 1.49  | 1.45          | 1.52  |
|           | GsTIM          | 39       | 41            | 39            | 38            |       | 0.99          | 1.49          | 1.51     | 1.20          | 0.94          | 1.30          |               | 1.13          | 1.30          |               | 1.11          | 1.24  |          | 1.33  | 1.07  | 0.88          | 0.78  |
|           | <i>Hs</i> TIM  | 44       | 49            | 90            | 45            | 38    |               | 0.93          | 1.26     | 1.06          | 0.22          | 0.96          | ND            | 0.69          | 0.79          | ND            | 0.64          | 0.87  | ND       | 1.13  | 1.29  | 0.91          | 1.17  |
|           | LmTIM          | 42       | 51            | 50            | 46            | 43    | 50            |               | 1.16     | 1.13          | 0.91          | 0.84          |               | 0.46          | 0.51          |               | 1.03          | 0.92  |          | 1.46  | 1.05  | 1.23          | 1.39  |
|           | <i>Mm</i> TIM  | 65       | 41            | 40            | 35            | 41    | 40            | 38            |          | 1.42          | 1.33          | 1.36          |               | 1.40          | 1.17          |               | 1.17          | 0.99  |          | 1.31  | 1.39  | 1.44          | 1.26  |
| ĪM        | <i>Mt</i> TIM  | 41       | 36            | 37            | 38            | 43    | 37            | 38            | 41       |               | 1.11          | 0.93          |               | 1.11          | 1.25          |               | 1.15          | 1.10  |          | 1.49  | 0.61  | 0.70          | 1.40  |
| Tvə.      | 0cTIM          | 44       | 49            | 89            | 45            | 38    | 98            | 50            | 40       | 37            |               | 1.10          |               | 0.76          | 0.87          |               | 0.63          | 0.86  |          | 1.14  | 1.13  | 0.92          | 1.11  |
| Irr       | РfTIM          | 39       | 44            | 43            | 40            | 37    | 42            | 45            | 38       | 35            | 42            |               | _             | 0.87          | 0.93          |               | 1.07          | 1.01  |          | 1.52  | 1.10  | 1.01          | 1.42  |
|           | <b>S</b> sTIM  | 43       | 48            | 87            | 44            | 37    | 93            | 49            | 39       | 35            | 93            | 42            |               |               | 1             |               |               | Ν     | JD       |       |       |               |       |
|           | <i>Tb</i> TIM  | 42       | 43            | 51            | 44            | 40    | 52            | 69            | 38       | 38            | 51            | 43            | 39            |               | 0.47          | ND            | 0.89          | 0.98  | ND       | 1.48  | 1.07  | 0.96          | 1.35  |
|           | TcTIM          | 42       | 45            | 50            | 46            | 41    | 52            | 68            | 39       | 39            | 51            | 43            | 50            | 74            |               |               | 0.91          | 0.88  |          | 1.38  | 1.49  | 1.17          | 1.48  |
|           | TSTIM          | 49       | 48            | 61            | 47            | 39    | 59            | 46            | 39       | 38            | 59            | 41            | 58            | 47            | 50            |               |               | 1.02  |          | ND    | 1.01  | 0.00          | 0.05  |
|           |                | 40       | 44            | 48            | 41            | 43    | 47            | 43            | 40       | 39            | 47            | 38            | 46            | 42            | 42            | 48            |               | 1.02  | ND       | 1.15  | 1.01  | 0.89          | 0.95  |
|           | Yt I IM        | 20       | 43            | 23            | 48            | 38    | 52            | 46            | 42       | 39            | 52            | 42            | 25            | 48            | 46            | 49            | 46            |       |          | 1.49  | 1.27  | 1.15<br>D     | 1.4/  |
|           |                | 39       | 38            | 37            | 33            | 47    | 30            | 30            | 43       | 40            | 36            | 33            | 35            | 34            | 32            | 34<br>45      | 38            | 35    |          |       | N     | D             | 1.44  |
| , so      | GOTIM<br>DeTIM | 40       | 41            | 40            | 39<br>36      | 40    | 40            | 27<br>27      | 45<br>30 | 44            | 45<br>37      | 40            | 43<br>37      | 41            | 40            | 40            | 39            | 40    | 58<br>40 | 40    | 1.23  | 0.76          | 1.44  |
| IIM       | Setim          | 30<br>42 | 54<br>40      | 30<br>38      | 30            | 41    | 30<br>37      | 37<br>40      | 39<br>40 | 40<br>65      | 37            | 33            | 36            | 37            | 39            | 30<br>40      | 39<br>13      | 37    | 40       | 40    | 40    | 0.70          | 0.04  |
| Rev]      | CoTIM          | 45       | 42            | 41            | 38            | 55    | 40            | 42            | 44       | 41            | 40            | 40            | 40            | 40            | 40            | 41            | 43            | 40    | 48       | 44    | 42    | 52            |       |

Table S3. Matrix with identity sequence percentage (below) and average RMSD values (top) for IrrevTIMs and RevTIMs.<sup>a</sup>

<sup>a</sup> ND: average RMSD value not determined because there is no structural data for NpTIM, SsTIM and TsTIM.

Identity sequence percentage

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| Table S4. | Amino | acidic | composition | used i | n the | sequence | comparison | of IrrevTIMs | and |
|-----------|-------|--------|-------------|--------|-------|----------|------------|--------------|-----|
| RevTIMs.  |       |        |             |        |       |          |            |              |     |

| Structural property               | <b>D</b> rTIM | ScTIM      | <i>Cp</i> TIM | Average<br>RevTIMs | Average<br>IrrevTIMs |  |  |  |  |  |  |
|-----------------------------------|---------------|------------|---------------|--------------------|----------------------|--|--|--|--|--|--|
| Amino acid composition (%)        |               |            |               |                    |                      |  |  |  |  |  |  |
| Alanine (A)                       | 17.0          | 13.6       | 12.4          | $14.3\pm2.0$       | $12.0 \pm 3.1$       |  |  |  |  |  |  |
| Cysteine (C)                      | 1.2           | 1.6        | 2.4           | $1.7 \pm 0.5$      | $1.5 \pm 0.4$        |  |  |  |  |  |  |
| Aspartic acid (D)                 | 4.9           | 7.4        | 4.8           | $5.7 \pm 1.2$      | $4.4 \pm 1.4$        |  |  |  |  |  |  |
| Glutamic acid (E)                 | 8.1           | 7.4        | 9.6           | $8.3\pm0.9$        | $7.2 \pm 1.3$        |  |  |  |  |  |  |
| Phenylalanine (F)                 | 0.4           | 1.6        | 2.8           | $1.6 \pm 1.0$      | $3.2\pm0.9$          |  |  |  |  |  |  |
| Glycine (G)                       | 10.9          | 8.9        | 7.2           | $9.0 \pm 1.5$      | $8.8 \pm 1.4$        |  |  |  |  |  |  |
| Histidine (H)                     | 2.0           | 3.1        | 2.0           | $2.4 \pm 0.5$      | $2.3 \pm 0.6$        |  |  |  |  |  |  |
| Isoleucine (I)                    | 3.2           | 5.0        | 8.0           | $5.4 \pm 1.9$      | $6.9 \pm 1.2$        |  |  |  |  |  |  |
| Lysine (K)                        | 3.6           | 7.0        | 7.6           | $6.1 \pm 1.7$      | $6.9 \pm 1.8$        |  |  |  |  |  |  |
| Leucine (L)                       | 10.1          | 8.5        | 4.8           | $7.8 \pm 2.2$      | $7.1 \pm 1.3$        |  |  |  |  |  |  |
| Methionine (M)                    | 1.6           | 1.9        | 3.2           | $2.2 \pm 0.7$      | $1.6 \pm 0.7$        |  |  |  |  |  |  |
| Asparagine (N)                    | 3.2           | 2.3        | 4.8           | $3.4 \pm 1.0$      | $4.0 \pm 1.2$        |  |  |  |  |  |  |
| Proline (P)                       | 4.0           | 2.3        | 2.8           | $3.1 \pm 0.7$      | $3.5 \pm 0.9$        |  |  |  |  |  |  |
| Glutamine (Q)                     | 2.8           | 3.9        | 3.6           | $3.4 \pm 0.4$      | $4.0 \pm 1.1$        |  |  |  |  |  |  |
| Arginine (R)                      | 4.9           | 3.5        | 2.8           | $3.7 \pm 0.9$      | $3.6 \pm 0.8$        |  |  |  |  |  |  |
| Serine (S)                        | 4.9           | 3.9        | 2.4           | $3.7 \pm 1.0$      | $5.1 \pm 1.1$        |  |  |  |  |  |  |
| Threonine (T)                     | 4.5           | 4.3        | 7.2           | $5.3 \pm 1.3$      | $5.1\pm0.9$          |  |  |  |  |  |  |
| Valine (V)                        | 8.9           | 9.7        | 8.8           | $9.1\pm0.4$        | $9.2 \pm 1.1$        |  |  |  |  |  |  |
| Tryptophan (W)                    | 1.2           | 0.8        | 0.8           | $0.9\pm0.2$        | $1.5 \pm 0.5$        |  |  |  |  |  |  |
| Tyrosine (Y)                      | 2.4           | 3.5        | 2.4           | $2.8\pm0.5$        | $2.0\pm0.6$          |  |  |  |  |  |  |
| Physic                            | cochemical a  | amino acid | properties    | s (%)              |                      |  |  |  |  |  |  |
| Charged (DEHKR)                   | 23.5          | 28.3       | 26.7          | $26.2 \pm 2.0$     | $24.4 \pm 1.9$       |  |  |  |  |  |  |
| Positively charged (HKR)          | 10.5          | 13.6       | 12.4          | $12.1 \pm 1.2$     | $12.7 \pm 1.3$       |  |  |  |  |  |  |
| Negatively charged (DE)           | 13.0          | 14.7       | 14.3          | $14.0\pm0.8$       | $11.6 \pm 1.4$       |  |  |  |  |  |  |
| Aliphatic (AGILPV)                | 54.3          | 48.1       | 43.8          | $48.7 \pm 4.3$     | $47.5 \pm 3.3$       |  |  |  |  |  |  |
| Aromatic (FHWY)                   | 6.1           | 8.9        | 8.0           | $7.7 \pm 1.2$      | $9.0 \pm 0.8$        |  |  |  |  |  |  |
| Polar (DEKNQR)                    | 27.5          | 31.4       | 33.1          | $30.7 \pm 2.3$     | $30.1 \pm 2.4$       |  |  |  |  |  |  |
| Neutral, polar (CNQSTY)           | 19.0          | 19.4       | 22.7          | $20.4 \pm 1.7$     | $21.8 \pm 2.7$       |  |  |  |  |  |  |
| Neutral, non-polar<br>(AFGILMPVW) | 57.5          | 52.3       | 50.6          | $53.5\pm2.9$       | $53.8\pm2.9$         |  |  |  |  |  |  |
| Hydrophobic (CFILMVW)             | 26.7          | 29.1       | 30.7          | $28.8\pm1.6$       | $31.0 \pm 1.4$       |  |  |  |  |  |  |
| Small size (ACGSTV)               | 47.4          | 41.9       | 40.2          | $43.2 \pm 3.1$     | $41.8 \pm 3.0$       |  |  |  |  |  |  |
| Medium size (DEHILMNPQ)           | 40.1          | 41.9       | 43.4          | $41.8 \pm 1.4$     | $41.0\pm2.9$         |  |  |  |  |  |  |
| Large size (FKRWY)                | 12.6          | 16.3       | 16.3          | $15.1 \pm 1.8$     | $17.2 \pm 2.1$       |  |  |  |  |  |  |

| Structural property                | DrTIM       | ScTIM       | <i>Cp</i> TIM | Average<br>RevTIMs | Average<br>IrrevTIMs |  |  |  |  |  |  |
|------------------------------------|-------------|-------------|---------------|--------------------|----------------------|--|--|--|--|--|--|
| Secondary structure elements (%)   |             |             |               |                    |                      |  |  |  |  |  |  |
| α-helix                            | 44          | 48          | 43            | $45.0 \pm 2.2$     | $44.9 \pm 2.1$       |  |  |  |  |  |  |
| β-strand                           | 21          | 20          | 21            | $20.7\pm0.5$       | $21.8\pm1.0$         |  |  |  |  |  |  |
| Random coil                        | 35          | 32          | 36            | 34.3 ± 1.7         | 33.3 ± 1.8           |  |  |  |  |  |  |
|                                    | Stabilizing | g interacti | ons           |                    |                      |  |  |  |  |  |  |
| Total H-bonds of the oligomer      | 490         | 503         | 510           | 501 ± 8            | 521 ± 24             |  |  |  |  |  |  |
| Interface H-bonds                  | 27          | 19          | 24            | $23 \pm 3$         | $28\pm5$             |  |  |  |  |  |  |
| Total salt bridges of the oligomer | 37          | 50          | 44            | $44 \pm 5$         | $34\pm7$             |  |  |  |  |  |  |
| Interface salt bridges             | 2           | 2           | 12            | 5 ± 5              | $6 \pm 3$            |  |  |  |  |  |  |

**Table S5.** Secondary structure elements and stabilizing interactions for IrrevTIMs andRevTIMs.

Table S6. Dimeric TIM PDB files used in the structural comparison of IrrevTIMs and RevTIMs.

| Organism                           | Code          | PDB  | Resolution | Spacial  | Asymmetric        | Conform<br>active s | Reference |           |  |
|------------------------------------|---------------|------|------------|--|-------------------|---------------------|-----------|-----------|--|
| Of gamsin                          | Couc          | ID   | (Å)        | group  | unit <sup>a</sup> | Subunit A           | Subunit B |           |  |
| Clostridium perfringens            | <i>Cp</i> TIM | 4Y8F | 1.54       | C 1 2 1  | Monomer           | Open                | Open      | This work |  |
| Deinococcus radiodurans            | DrTIM         | 4Y90 | 2.10       | R 3 2  | Tetramer          | Open                | Open      | This work |  |
| Entamoeba histolytica              | <i>Eh</i> TIM | 1M6J | 1.50       | $P 2_1 2_1 2$                                  | Dimer             | Open                | Open      | 3         |  |
| Escherichia coli                   | <i>Ec</i> TIM | 4K6A | 1.80       | $P 2_1 2_1 2_1$                                | Dimer             | Open                | Open      | 4         |  |
| Gallus gallus                      | GgTIM         | 1TPH | 1.80       | P 21 21 21                                     | Dimer             | Closed              | Closed    | 5         |  |
| Gemmata obscuriglobus              | GoTIM         | 4Y96 | 1.58       | P 65 2 2                                       | Dimer             | Closed              | Open      | This work |  |
| Geobacillus stearotermophilus      | GsTIM         | 1BTM | 2.80       | P 21 21 2                                      | Dimer             | Closed              | Closed    | 6         |  |
| Giardia lamblia                    | <i>Gl</i> TIM | 2DP3 | 2.10       | I 2 2 2  | Monomer           | Closed              | Open      | 7         |  |
| Homo sapiens                       | HsTIM         | 2JK2 | 1.70       | $P 2_1 2_1 2_1$                                | Dimer             | Open                | Open      | 8         |  |
| Leishmania mexicana                | <i>Lm</i> TIM | 1AMK | 1.83       | C 1 2 1  | Monomer           | Closed              | Closed    | 9         |  |
| Moritella marina                   | <i>Mm</i> TIM | 1AW2 | 2.65       | P 1 2 <sub>1</sub> 1                           | Dimer             | Open                | Open      | 10        |  |
| Mycobacterium tuberculosis         | <i>Mt</i> TIM | 3TA6 | 1.41       | C 1 2 1  | Dimer             | Open                | Open      | 11        |  |
| Oryctolagus cuniculus              | <i>Oc</i> TIM | 1R2R | 1.50       | $P 2_1 2_1 2_1$                                | Dimer             | Open                | Open      | 12        |  |
| Plasmodium falciparum              | <i>Pf</i> TIM | 1YDV | 2.20       | C 1 2 1  | Dimer             | Open                | Open      | 13        |  |
| Saccharomyces cerevisiae           | <i>Yt</i> TIM | 1NF0 | 1.60       | P 21 21 21                                     | Dimer             | Open                | Closed    | 14        |  |
| Streptomyces coelicolor            | ScTIM         | 4Y9A | 2.30       | P 4 <sub>3</sub>                               | Dimer             | Open                | Open      | This work |  |
| Trichomonas vaginalis <sup>b</sup> | <i>Tv</i> TIM | 3QSR | 2.05       | P 2 2 <sub>1</sub> 2 <sub>1</sub>              | Monomer           | Open                | Open      | 15        |  |
| Trypanosoma brucei                 | <i>Tb</i> TIM | 5TIM | 1.83       | P 2 <sub>1</sub> 2 <sub>1</sub> 2 <sub>1</sub> | Dimer             | Open                | Closed    | 16        |  |
| Trypanosoma cruzi                  | <i>Tc</i> TIM | 1TCD | 1.83       | P 2 <sub>1</sub> 2 <sub>1</sub> 2 <sub>1</sub> | Dimer             | Closed              | Open      | 17        |  |

<sup>*a*</sup> The number of molecules in asymmetric unit was determined by the Matthews coefficient analysis by solvent content percentage in the crystal.

<sup>b</sup> Structural comparison of *Tv*TIM was realized with the three-dimensional structure of its dimeric Ile45 variant.

Electronic Supplementary Information (ESI) S16

## **References for Electronic Supplementary Information**

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