

## Supplementary Information (SI)

**Supplementary Table 1: Phosphatase domains identified in the proteome of *Trichuris trichiura*.**

| S. N o. | Accession ID | InterProScan                                                                                                                                                                        | HMMER                                                                                                                | NCBI CDD                                                                                                                                 |
|---------|--------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------|
| 1.      | A0A077Z0F2   | Calcineurin-like phosphoesterase domain, ApaH type, Metallo-dependent phosphatase-like                                                                                              | Calcineurin-like phosphoesterase                                                                                     | Metallophosphatase superfamily, metallophosphatase domain                                                                                |
| 2.      | A0A077Z4J5   | Calcineurin-like phosphoesterase domain, ApaH type, Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)- tetraphosphatase,                                               | Calcineurin-like phosphoesterase                                                                                     | Metallophosphatase superfamily, metallophosphatase domain                                                                                |
| 3.      | A0A077ZK33   | Tyrosine-specific protein phosphatases domain, Dual specificity phosphatase, catalytic domain, Dual specificity protein phosphatase domain, Protein-tyrosine phosphatase, catalytic | Dual specificity phosphatase, catalytic domain, Cytidylyltransferase family, Putative methyltransferase              | PAP2_like proteins                                                                                                                       |
| 4.      | A0A077ZB21   | Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)- tetraphosphatase, Calcineurin-like phosphoesterase domain, ApaH type                                                | Calcineurin-like phosphoesterase                                                                                     | serine/threonine protein phosphatase                                                                                                     |
| 5.      | A0A077ZHG7   | PPM-type phosphatase-like domain                                                                                                                                                    | Protein phosphatase 2C                                                                                               | PP2Cc                                                                                                                                    |
| 6.      | A0A077ZDG9   | Tyrosine-specific protein phosphatases domain, Tyrosine-specific protein phosphatase, PTPase domain                                                                                 | Protein-tyrosine phosphatase                                                                                         | Protein tyrosine phosphatase, catalytic domain                                                                                           |
| 7.      | A0A077ZH74   | Histidine phosphatase superfamily, Histidine phosphatase superfamily, clade-1                                                                                                       | Histidine phosphatase superfamily                                                                                    | histidine phosphatase family protein                                                                                                     |
| 8.      | A0A077Z6N3   | Histidine phosphatase superfamily, Histidine phosphatase superfamily, clade-2                                                                                                       | Histidine phosphatase superfamily                                                                                    | <i>HP_HAP_like</i>                                                                                                                       |
| 9.      | A0A077Z151   | PPM-type phosphatase-like domain, Leucine-rich repeat                                                                                                                               | Leucine rich repeat, Protein phosphatase 2C                                                                          | RA_PHLPP, Serine/threonine phosphatases, family 2C, catalytic domain, Leucine-rich repeat (LRR) protein, Pleckstrin homology (PH) domain |
| 10.     | A0A077ZDY3   | Phosphoserine phosphatase, N-terminal, DNA recombination and repair protein RecA-like, ATP-binding domain, AAA+ ATPase domain                                                       | Haloacid dehalogenase-like hydrolase, Subunit ChII of Mg-chelatase, AAA domain, Domain of unknown function (DUF5609) | Phosphoserine phosphatase, DNA repair protein RadA                                                                                       |

|     |                |                                                                                                                                              |                                                                                    |                                                                                                                        |
|-----|----------------|----------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------|
| 11. | A0A077Z<br>5T3 | Tyrosine-specific protein phosphatases domain, Tyrosine-specific protein phosphatase, PTPase domain, Protein-tyrosine phosphatase, catalytic | Protein-tyrosine phosphatase                                                       | Protein tyrosine phosphatase, catalytic domain                                                                         |
| 12. | A0A077Z<br>3D1 | Protein serine/threonine phosphatase 2C, C-terminal, PPM-type phosphatase-like domain,                                                       | Protein phosphatase 2C, Protein serine/threonine phosphatase 2C, C-terminal domain | Protein serine/threonine phosphatase 2C, C-terminal domain, Serine/threonine phosphatases, family 2C, catalytic domain |
| 13. | A0A077Z<br>1E1 | Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetraphosphatase, Calcineurin-like phosphoesterase domain, ApaH type          | Calcineurin-like phosphoesterase                                                   | serine/threonine protein phosphatase                                                                                   |
| 14. | A0A077Z<br>HX6 | Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetraphosphatase, Calcineurin-like phosphoesterase domain, ApaH type          | Calcineurin-like phosphoesterase                                                   | serine/threonine protein phosphatase                                                                                   |
| 15. | A0A077Z<br>E66 | Damage-control phosphatase ARMT1-like, metal-binding domain                                                                                  | Damage-control phosphatase ARMT1-like domain                                       | damage-control phosphatase ARMT1 family protein                                                                        |
| 16. | A0A077<br>YZL7 | DnaJ domain, Rhodanese-like domain                                                                                                           | DnaJ domain, Rhodanese-like domain                                                 | DnaJ domain, 3-mercaptopyruvate sulfurtransferase SseA, contains two rhodanese domains                                 |
| 17. | A0A077Z<br>944 | Endonuclease/exonuclease/p phosphatase                                                                                                       | Endonuclease/Exonucleas e/phosphatase family                                       | Exonuclease-Endonuclease-Phosphatase (EEP) domain superfamily                                                          |
| 18. | A0A077Z<br>JP5 | Phosphotyrosyl phosphatase activator, PTPA                                                                                                   | Phosphotyrosyl phosphate activator (PTPA) protein                                  | Phosphotyrosyl phosphatase activator (PTPA)                                                                            |
| 19. | A0A077Z<br>M16 | Endonuclease/exonuclease/p phosphatase                                                                                                       | Endonuclease/Exonucleas e/phosphatase family                                       | Exonuclease-Endonuclease-Phosphatase (EEP) domain superfamily                                                          |
| 20. | A0A077Z<br>FJ3 | PPM-type phosphatase-like domain                                                                                                             | Stage II sporulation protein E (SpoIIE)                                            | Serine/threonine phosphatases, family 2C, catalytic domain                                                             |
| 21. | A0A077Z<br>9P7 | Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetraphosphatase, Calcineurin-like phosphoesterase domain, ApaH type          | Calcineurin-like phosphoesterase                                                   | metallophosphatase superfamily, metallophosphatase domain                                                              |
| 22. | A0A077Z<br>2U9 | Phosphatidic acid phosphatase type 2/haloperoxidase                                                                                          | PAP2 superfamily                                                                   | PAP2_ like Superfamily                                                                                                 |
| 23. | A0A077Z<br>9X3 | Acylphosphatase-like domain                                                                                                                  | Acylphosphatase                                                                    | Acylphosphatase                                                                                                        |

|     |                |                                                                                                                                                                                                        |                                                                                                 |                                                                                                         |
|-----|----------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------|
| 24. | A0A077Z<br>2Z0 | Tyrosine-specific protein phosphatases domain, Tyrosine-specific protein phosphatase, PTPase domain, Protein-tyrosine phosphatase, catalytic                                                           | Protein-tyrosine phosphatase                                                                    | Protein tyrosine phosphatase, catalytic domain                                                          |
| 25. | A0A077Z<br>EU7 | Histidine phosphatase superfamily, clade-1                                                                                                                                                             | Histidine phosphatase superfamily (branch 1)                                                    | Histidine phosphatase domain                                                                            |
| 26. | A0A077Z<br>FQ2 | Histidine phosphatase superfamily                                                                                                                                                                      | Histidine phosphatase superfamily                                                               | Histidine phosphatase domain                                                                            |
| 27. | A0A077Z<br>2W0 | Haloacid dehalogenase-like hydrolase, HAD hydrolase, subfamily IA                                                                                                                                      | Haloacid dehalogenase-like hydrolase                                                            | Haloacid Dehalogenase-like Hydrolases                                                                   |
| 28. | A0A077Z<br>5N7 | Histidine phosphatase superfamily, clade-1                                                                                                                                                             | Histidine phosphatase superfamily (branch 1)                                                    | Histidine phosphatase domain                                                                            |
| 29. | A0A077Z<br>783 | Tyrosine-specific protein phosphatases domain, Tyrosine-specific protein phosphatase, PTPase domain, Protein-tyrosine phosphatase, catalytic, Mitochondrial ABC-transporter, N-terminal five TM domain | Mitochondrial ABC-transporter N-terminal five TM region, Protein-tyrosine phosphatase           | Mitochondrial ABC-transporter N-terminal five TM region, Protein tyrosine phosphatase, catalytic domain |
| 30. | A0A077Z<br>P93 | Haloacid dehalogenase-like hydrolase, HAD hydrolase, subfamily IA, 2-phosphoglycolate phosphatase-like, prokaryotic                                                                                    | Haloacid dehalogenase-like hydrolase                                                            | N-acetylmuramic acid 6-phosphate phosphatase MupP                                                       |
| 31. | A0A077Z<br>292 | Calcineurin-like phosphoesterase domain, ApaH type, Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetrakisphosphate, Serine-threonine protein phosphatase, N-terminal                 | Serine-threonine protein phosphatase N-terminal domain, Calcineurin-like phosphoesterase        | serine/threonine-protein phosphatase                                                                    |
| 32. | A0A077Z<br>DE3 | Tyrosine-specific protein phosphatases domain, Cation/H <sup>+</sup> exchanger, Dual specificity phosphatase, catalytic domain, Dual specificity protein phosphatase domain                            | Sodium/hydrogen exchanger family, Dual specificity phosphatase, catalytic domain                | Dual-specificity phosphatase domain, Sodium/hydrogen exchanger 3                                        |
| 33. | A0A077Z<br>725 | Tyrosine-specific protein phosphatases domain, Tensin-type phosphatase domain, Protein-tyrosine phosphatase, catalytic                                                                                 | Dual specificity phosphatase, catalytic domain                                                  | PTP_DSP_cys Superfamily                                                                                 |
| 34. | A0A077Z<br>CV5 | Calcineurin-like phosphoesterase domain, ApaH type                                                                                                                                                     | Calcineurin-like phosphoesterase                                                                | metallophosphoesterase family protein                                                                   |
| 35. | A0A077<br>YXQ6 | Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetrakisphosphate, PPP domain, PP5, C-terminal metallophosphatase domain, Calcineurin-like phosphoesterase domain, ApaH type            | Calcineurin-like phosphoesterase , PPP5 TPR repeat region, Tetratricopeptide repeat, TPR repeat | PP5 family serine/threonine-protein phosphatase                                                         |

|     |                |                                                                                                                          |                                                                                                                              |                                                                                                                                                                                       |
|-----|----------------|--------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 36. | A0A077<br>YZZ0 | Histidine phosphatase superfamily, clade-1, EGF-like domain, EGF-like calcium-binding domain                             | Histidine phosphatase superfamily (branch 1)                                                                                 | Histidine phosphatase domain, Calcium-binding EGF-like domain                                                                                                                         |
| 37. | A0A077<br>YZW5 | HAD-superfamily hydrolase, subfamily IIB, Phosphomannomutase                                                             | Eukaryotic phosphomannomutase                                                                                                | Haloacid Dehalogenase-like Hydrolases                                                                                                                                                 |
| 38. | A0A077Z<br>F71 | Ppx/GppA phosphatase                                                                                                     | Ppx/GppA phosphatase family                                                                                                  | Guanosine-5'-triphosphate,3'-diphosphate diphosphatase                                                                                                                                |
| 39. | A0A077Z<br>2V2 | P-type ATPase, haloacid dehalogenase domain, Cation-transporting P-type ATPase, C-terminal                               | E1-E2 ATPase, Cation transport ATPase (P-type), haloacid dehalogenase-like hydrolase, Cation transporting ATPase, C-terminus | <i>P-type_ATPase_Na-K_like</i>                                                                                                                                                        |
| 40. | A0A077<br>YVW9 | Protein phosphatase 4 core regulatory subunit R2                                                                         | PPP4R2                                                                                                                       | PPP4R2 superfamily                                                                                                                                                                    |
| 41. | A0A077Z<br>EV3 | Dullard phosphatase domain, eukaryotic, FCP1 homology domain                                                             | NLI interacting factor-like phosphatase                                                                                      | Dullard-like phosphatase domain                                                                                                                                                       |
| 42. | A0A077<br>YZL0 | P-type ATPase, haloacid dehalogenase domain, Cation-transporting P-type ATPase, N-terminal, P5B-type ATPase, N-terminal, | Haloacid dehalogenase-like hydrolase, P5-type ATPase cation transporter, E1-E2 ATPase, Cation transporter/ATPase, N-terminus | Haloacid Dehalogenase-like Hydrolases, P5-type ATPase cation transporter                                                                                                              |
| 43. | A0A077Z<br>KV6 | Protein-tyrosine phosphatase-like                                                                                        | No domain found                                                                                                              | protein-tyrosine phosphatase family protein                                                                                                                                           |
| 44. | A0A077Z<br>CQ0 | P-type ATPase, haloacid dehalogenase domain, P-type ATPase, N-terminal, P-type ATPase, C-terminal                        | Phospholipid-translocating ATPase N-terminal, E1-E2 ATPase, Cation transport ATPase (P-type)                                 | Haloacid Dehalogenase-like Hydrolases, Cation transport ATPase (P-type), Phospholipid-translocating P-type ATPase C-terminal                                                          |
| 45. | A0A077<br>YZB8 | mRNA capping enzyme, C-terminal, mRNA capping enzyme, C-terminal, Protein-tyrosine phosphatase-like                      | mRNA capping enzyme, C-terminal domain, mRNA capping enzyme, catalytic domain                                                | Adenylation domain of GTP-dependent mRNA capping enzymes, mRNA capping enzyme, C-terminal domain, cys-based protein tyrosine phosphatase and dual-specificity phosphatase superfamily |
| 46. | A0A077Z<br>3T8 | Tyrosine-specific protein phosphatases domain, Dual specificity phosphatase, catalytic domain                            | Dual specificity phosphatase, catalytic domain                                                                               | cys-based protein tyrosine phosphatase and dual-specificity phosphatase superfamily                                                                                                   |
| 47. | A0A077Z<br>6F0 | PPM-type phosphatase-like domain                                                                                         | Protein phosphatase 2C                                                                                                       | Serine/threonine phosphatases, family 2C, catalytic domain                                                                                                                            |
| 48. | A0A077Z<br>CU0 | Calcineurin-like phosphoesterase domain, lpxH-type                                                                       | Calcineurin-like phosphoesterase superfamily domain                                                                          | Homo sapiens Vps29 and related proteins, metallophosphatase domain                                                                                                                    |
| 49. | A0A077Z<br>4D3 | dUTPase, trimeric, dUTPase-like                                                                                          | dUTPase                                                                                                                      | Trimeric dUTP diphosphatases                                                                                                                                                          |

|     |            |                                                                                                                                                                                                                                        |                                                                                                                                                                                                                        |                                                                                                                                                                                                   |
|-----|------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 50. | A0A077Z4F8 | Tyrosine-specific protein phosphatases domain, Tyrosine-specific protein phosphatase, PTPase domain, Protein-tyrosine phosphatase, catalytic, Dual specificity protein phosphatase domain, Dual specificity protein phosphatase domain | Dual specificity phosphatase, catalytic domain                                                                                                                                                                         | cys-based protein tyrosine phosphatase and dual-specificity phosphatase superfamily                                                                                                               |
| 51. | A0A077YWY8 | Protein-tyrosine phosphatase, catalytic, Myotubularin-like, phosphatase domain                                                                                                                                                         | Myotubularin-like phosphatase domain                                                                                                                                                                                   | Myotubularin-like phosphatase domain, Pleckstrin homology-like domain                                                                                                                             |
| 52. | A0A077Z6K1 | Protein phosphatase 2A regulatory subunit PR55                                                                                                                                                                                         | No domain found                                                                                                                                                                                                        | Serine/threonine protein phosphatase 2A, regulatory subunit                                                                                                                                       |
| 53. | A0A077Z3U3 | Calcineurin-like phosphoesterase domain, ApaH type, Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetrakisphosphate, Serine-threonine protein phosphatase, N-terminal                                                 | Calcineurin-like phosphoesterase, Serine-threonine protein phosphatase N-terminal domain                                                                                                                               | PP1, PPKL (PP1 and kelch-like) enzymes, and related proteins, metallophosphatase domain                                                                                                           |
| 54. | A0A077ZNC2 | Endonuclease/exonuclease/p phosphatase                                                                                                                                                                                                 | Endonuclease/Exonuclease/phosphatase family                                                                                                                                                                            | Exonuclease-Endonuclease-Phosphatase (EEP) domain superfamily                                                                                                                                     |
| 55. | A0A077Z172 | Tyrosine-specific protein phosphatases domain, Tyrosine-specific protein phosphatase, PTPase domain, Protein-tyrosine phosphatase, catalytic                                                                                           | Protein-tyrosine phosphatase                                                                                                                                                                                           | Protein tyrosine phosphatase, catalytic domain                                                                                                                                                    |
| 56. | A0A077Z210 | Endonuclease/exonuclease/p phosphatase, Leucine-rich repeat                                                                                                                                                                            | Leucine rich repeat, Endonuclease/Exonuclease/phosphatase family                                                                                                                                                       | C-terminal deadenylase domain of CCR4 and related domains, Leucine-rich repeat (LRR) protein                                                                                                      |
| 57. | A0A077ZGN6 | Cytidyltransferase-like domain, DNA polymerase III delta, N-terminal, DNA polymerase III subunit delta, C-terminal, GH15-like domain, Histidine phosphatase superfamily                                                                | Lipopolysaccharide-assembly, DNA polymerase III, delta subunit, DNA polymerase III, delta subunit, Cytidyltransferase-like, Histidine phosphatase superfamily (branch 1), Ribosomal silencing factor during starvation | adenosylcobalamin/alpha-ribazole phosphatase, Lipopolysaccharide-assembly, DNA polymerase III, delta subunit, ribosome silencing factor, nicotinate (nicotinamide) nucleotide adenylyltransferase |
| 58. | A0A077Z7L5 | Tyrosine-specific protein phosphatases domain, Dual specificity protein phosphatase domain, Dual specificity phosphatase, catalytic domain                                                                                             | Dual specificity phosphatase, catalytic domain                                                                                                                                                                         | cys-based protein tyrosine phosphatase and dual-specificity phosphatase superfamily                                                                                                               |
| 59. | A0A077ZG77 | PPM-type phosphatase-like domain                                                                                                                                                                                                       | Protein phosphatase 2C                                                                                                                                                                                                 | Serine/threonine phosphatases, family 2C, catalytic domain                                                                                                                                        |

|     |                |                                                                                                                                                                                                              |                                                                                                   |                                                                                               |
|-----|----------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------|
| 60. | A0A077Z<br>7D8 | Alkaline-phosphatase-like,<br>core domain superfamily                                                                                                                                                        | Protein of unknown<br>function (DUF229)                                                           | alkaline phosphatases and<br>sulfatases                                                       |
| 61. | A0A077Z<br>D83 | Dullard phosphatase domain,<br>eukaryotic, FCP1 homology<br>domain                                                                                                                                           | NLI interacting factor-like<br>phosphatase                                                        | Dullard-like phosphatase<br>domain                                                            |
| 62. | A0A077Z<br>1S5 | Histidine phosphatase<br>superfamily                                                                                                                                                                         | No domain found                                                                                   | Histidine phosphatase<br>domain, Basic leucine<br>zipper (bZIP) domain                        |
| 63. | A0A077Z<br>5M7 | Sphingomyelin synthase-like<br>domain                                                                                                                                                                        | PAP2 superfamily C-<br>terminal                                                                   | PAP2_like Superfamily                                                                         |
| 64. | A0A077Z<br>0V2 | Serine/threonine-specific<br>protein phosphatase/bis(5-<br>nucleosyl)-tetrakisphosphate,<br>Calcineurin-like<br>phosphoesterase domain,<br>ApaH type                                                         | Calcineurin-like<br>phosphoesterase                                                               | PP2A, PP4, and PP6<br>phosphoprotein<br>phosphatases,<br>metallophosphatase<br>domain         |
| 65. | A0A077Z<br>6D2 | Endonuclease/exonuclease/p<br>phosphatase superfamily                                                                                                                                                        | No domain found                                                                                   | Endonuclease/Exonucleas<br>e/phosphatase family                                               |
| 66. | A0A077Z<br>9E8 | Protein phosphatase 2A,<br>regulatory B subunit, B56                                                                                                                                                         | Protein phosphatase 2A<br>regulatory B subunit (B56<br>family)                                    | Protein phosphatase 2A<br>regulatory B subunit (B56<br>family)                                |
| 67. | A0A077<br>YWG4 | Serine/threonine-specific<br>protein phosphatase/bis(5-<br>nucleosyl)-tetrakisphosphate,<br>Calcineurin-like<br>phosphoesterase domain,<br>ApaH type                                                         | Calcineurin-like<br>phosphoesterase                                                               | Protein phosphatase 2A<br>homologues, catalytic<br>domain                                     |
| 68. | A0A077Z<br>2N2 | SKICH domain, Inositol<br>polyphosphate-related<br>phosphatase,<br>Endonuclease/exonuclease/p<br>phosphatase superfamily                                                                                     | SKICH domain                                                                                      | Exonuclease-<br>Endonuclease-<br>Phosphatase (EEP)<br>domain superfamily,<br>SKICH domain     |
| 69. | A0A077Z<br>283 | Tyrosine-specific protein<br>phosphatases domain, Dual<br>specificity protein<br>phosphatase domain, Dual<br>specificity phosphatase,<br>catalytic domain                                                    | Dual specificity<br>phosphatase, catalytic<br>domain                                              | cys-based protein tyrosine<br>phosphatase and dual-<br>specificity phosphatase<br>superfamily |
| 70. | A0A077Z<br>JM4 | Serine-threonine protein<br>phosphatase, N-terminal,<br>Serine/threonine-specific<br>protein phosphatase/bis(5-<br>nucleosyl)-tetrakisphosphate,<br>Calcineurin-like<br>phosphoesterase domain,<br>ApaH type | Serine-threonine protein<br>phosphatase N-terminal<br>domain, Calcineurin-like<br>phosphoesterase | metallophosphatase<br>superfamily,<br>metallophosphatase<br>domain                            |
| 71. | A0A077Z<br>3P2 | Tyrosine-specific protein<br>phosphatases domain,<br>Tyrosine-specific protein<br>phosphatase, PTPase domain,<br>Protein-tyrosine phosphatase,<br>catalytic                                                  | Protein-tyrosine<br>phosphatase                                                                   | Protein tyrosine<br>phosphatase, catalytic<br>domain                                          |

|     |            |                                                                                                                                                                                                                                                                                |                                                                                                                                 |                                                                                                                                                                          |
|-----|------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 72. | A0A077YZN2 | Tyrosine-specific protein phosphatases domain, Tyrosine-specific protein phosphatase, PTPase domain, Protein-tyrosine phosphatase, catalytic, PDZ domain, Band 4.1 domain, FERM adjacent, FERM central domain, FERM domain, FERM, C-terminal PH-like domain, FERM, N-terminal, | FERM N-terminal domain, FERM central domain , FERM C-terminal PH-like domain, PDZ domain, Protein-tyrosine phosphatase          | catalytic domain of tyrosine-protein phosphatase non-receptor type 21 and type 14 , Band 4.1 homologues, Pleckstrin homology-like domain, PDZ domain, FERM adjacent (FA) |
| 73. | A0A077ZFN2 | Dual specificity phosphatase, catalytic domain                                                                                                                                                                                                                                 | Dual specificity phosphatase, catalytic domain                                                                                  | protein-tyrosine phosphatase family protein                                                                                                                              |
| 74. | A0A077ZG20 | Histidine phosphatase superfamily, clade-1, Phosphoglycerate mutase 1                                                                                                                                                                                                          | Histidine phosphatase superfamily (branch 1)                                                                                    | Phosphoglycerate mutase (BPG-dependent)                                                                                                                                  |
| 75. | A0A077ZJE2 | Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetraphosphatase, Calcineurin-like phosphoesterase domain, ApaH type                                                                                                                                            | Calcineurin-like phosphoesterase                                                                                                | PP2A, PP4, and PP6 phosphoprotein phosphatases, metallophosphatase domain                                                                                                |
| 76. | A0A077ZMR3 | HAD-like superfamily, HAD superfamily                                                                                                                                                                                                                                          | No domain found                                                                                                                 | Haloacid Dehalogenase-like Hydrolases                                                                                                                                    |
| 77. | A0A077ZCU6 | Inositol polyphosphate-related phosphatase, Endonuclease/exonuclease/p phosphatase superfamily                                                                                                                                                                                 | No domain found                                                                                                                 | Exonuclease-Endonuclease-Phosphatase (EEP) domain superfamily                                                                                                            |
| 78. | A0A077Z8R0 | SAC domain, hSac2 domain, Inositol phosphatase                                                                                                                                                                                                                                 | SacI homology domain, Inositol phosphatase                                                                                      | Phosphoinositide polyphosphatase (Sac family), Inositol phosphatase                                                                                                      |
| 79. | A0A077ZKX1 | Tyrosine-specific protein phosphatase, PTPase domain, Protein-tyrosine phosphatase, catalytic                                                                                                                                                                                  | Protein-tyrosine phosphatase                                                                                                    | cys-based protein tyrosine phosphatase and dual-specificity phosphatase superfamily                                                                                      |
| 80. | A0A077Z4E6 | Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetraphosphatase, Prp31 C-terminal, NOSIC, Nop domain, Calcineurin-like phosphoesterase domain, ApaH type                                                                                                       | Calcineurin-like phosphoesterase, snoRNA binding domain, fibrillarin, Prp31 C terminal domain, Calcineurin-like phosphoesterase | metallophosphatase superfamily, metallophosphatase domain, snoRNA binding domain, fibrillarin, Prp31 C terminal domain                                                   |
| 81. | A0A077ZBQ5 | Phosphoserine phosphatase                                                                                                                                                                                                                                                      | haloacid dehalogenase-like hydrolase                                                                                            | Haloacid Dehalogenase-like Hydrolases                                                                                                                                    |
| 82. | A0A077Z308 | FYVE zinc finger, Zinc finger, FYVE-related, Myotubularin-like, phosphatase domain, Myotubularin-related protein 4, FYVE domain                                                                                                                                                | Myotubularin-like phosphatase domain, FYVE zinc finger                                                                          | Myotubularin-like phosphatase domain, FYVE domain, Pleckstrin homology-like domain                                                                                       |
| 83. | A0A077Z0R5 | Haloacid dehalogenase-like hydrolase, HAD hydrolase, subfamily IA                                                                                                                                                                                                              | Haloacid dehalogenase-like hydrolase                                                                                            | Haloacid Dehalogenase-like Hydrolases                                                                                                                                    |

|     |                |                                                                                                                                                                   |                                                                                       |                                                                                                                                  |
|-----|----------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------|
| 84. | A0A077Z<br>EV8 | Tyrosine-specific protein phosphatases domain, Rhodanese-like domain, Dual specificity protein phosphatase domain, Dual specificity phosphatase, catalytic domain | Dual specificity phosphatase, catalytic domain, Rhodanese-like domain                 | cys-based protein tyrosine phosphatase and dual-specificity phosphatase superfamily, Rhodanese Homology Domain (RHOD)            |
| 85. | A0A077Z<br>G23 | Protein-tyrosine phosphatase, catalytic, Tyrosine-specific protein phosphatase, PTPase domain, Tyrosine-specific protein phosphatases domain                      | Protein-tyrosine phosphatase                                                          | Protein tyrosine phosphatase, catalytic domain                                                                                   |
| 86. | A0A077<br>YZX7 | Histidine phosphatase superfamily                                                                                                                                 | Histidine phosphatase domain                                                          | Histidine phosphatase domain                                                                                                     |
| 87. | A0A077Z<br>3W1 | Protein phosphatase 2A, regulatory B subunit, B56                                                                                                                 | Protein phosphatase 2A regulatory B subunit (B56 family)                              | Protein phosphatase 2A regulatory B subunit (B56 family)                                                                         |
| 88. | A0A077Z<br>8U4 | Histidine phosphatase superfamily                                                                                                                                 | Histidine phosphatase superfamily (branch 1)                                          | Histidine phosphatase domain                                                                                                     |
| 89. | A0A077Z<br>IB4 | Histidine phosphatase superfamily                                                                                                                                 | No domain found                                                                       | Histidine phosphatase domain                                                                                                     |
| 90. | A0A077Z<br>5V1 | HAD hydrolase, subfamily IA, Haloacid dehalogenase-like hydrolase                                                                                                 | Haloacid dehalogenase-like hydrolase                                                  | 6-phosphogluconate phosphatase                                                                                                   |
| 91. | A0A077Z<br>DG8 | Protein-tyrosine phosphatase-like                                                                                                                                 | No domain found                                                                       | cys-based protein tyrosine phosphatase and dual-specificity phosphatase superfamily                                              |
| 92. | A0A077Z<br>IC1 | Rhodanese-like domain                                                                                                                                             | Rhodanese-like domain                                                                 | Rhodanese Homology Domain (RHOD)                                                                                                 |
| 93. | A0A077Z<br>JA6 | Rhodanese-like domain, TBC1 domain family member 23, C-terminal domain, Rab-GAP-TBC domain                                                                        | Rhodanese-like domain, Rab-GTPase-TBC domain, TBC1 domain family member 23 C-terminal | Rhodanese Homology Domain (RHOD), Rab-GTPase-TBC domain, C-terminal domain of TBC1 domain family member 23, and similar proteins |
| 94. | A0A077Z<br>H69 | Histidine phosphatase superfamily                                                                                                                                 | Histidine phosphatase superfamily (branch 1)                                          | Histidine phosphatase domain                                                                                                     |
| 95. | A0A077<br>YZA9 | Tyrosine-specific protein phosphatases domain                                                                                                                     | Protein-tyrosine phosphatase                                                          | protein tyrosine phosphatase type IVA family                                                                                     |
| 96. | A0A077Z<br>942 | HAD-superfamily hydrolase, subfamily IIB, Cof family                                                                                                              | Haloacid dehalogenase-like hydrolase                                                  | Sugar phosphate phosphatase                                                                                                      |
| 97. | A0A077Z<br>372 | Metallo-dependent phosphatase-like                                                                                                                                | No domain found                                                                       | metallophosphatase domain                                                                                                        |
| 98. | A0A077Z<br>NV5 | Histidine phosphatase superfamily                                                                                                                                 | Histidine phosphatase superfamily (branch 2)                                          | Histidine phosphatase domain                                                                                                     |
| 99. | A0A077Z<br>L96 | Calcineurin-like phosphoesterase domain, ApaH type                                                                                                                | Calcineurin-like phosphoesterase                                                      | metallophosphatase superfamily, metallophosphatase domain                                                                        |
| 100 | A0A077Z<br>G39 | Phosphatidic acid phosphatase type 2/haloperoxidase                                                                                                               | PAP2 superfamily                                                                      | PAP2, wunen subfamily.                                                                                                           |

|     |             |                                                                                                                                                                            |                                               |                                                                                                                                                                         |
|-----|-------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 101 | A0A077Z8C2  | PPM-type phosphatase-like domain                                                                                                                                           | Protein phosphatase 2C                        | Serine/threonine phosphatases, family 2C, catalytic domain                                                                                                              |
| 102 | A0A077Z1H9  | Tyrosine-specific protein phosphatases domain, Tyrosine-specific protein phosphatase, PTPase domain, Protein-tyrosine phosphatase, catalytic,                              | Protein-tyrosine phosphatase                  | cys-based protein tyrosine phosphatase and dual-specificity phosphatase superfamily                                                                                     |
| 103 | A0A077ZL46  | Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetrakisphosphatase, Metallo-dependent phosphatase-like                                                     | No domain found                               | metallophosphatase superfamily, metallophosphatase domain                                                                                                               |
| 104 | A0A077YZQ2  | Tyrosine-specific protein phosphatases domain, Tyrosine-specific protein phosphatase, PTPase domain, Protein-tyrosine phosphatase, catalytic,                              | Protein-tyrosine phosphatase                  | Protein tyrosine phosphatase, catalytic domain                                                                                                                          |
| 105 | A0A077ZIF8  | Endonuclease/exonuclease /phosphatase, Endonuclease/exonuclease /phosphatase superfamily                                                                                   | Endonuclease/Exonuclease/p phosphatase family | exonuclease/endonuclease /phosphatase family protein                                                                                                                    |
| 106 | A0A077Z761  | Calcineurin-like phosphoesterase domain, ApaH type, Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetrakisphosphatase                                     | Calcineurin-like phosphoesterase              | metallophosphatase superfamily, metallophosphatase domain                                                                                                               |
| 107 | A0A077ZCP7  | EF-Hand 1, calcium-binding site, Serine/threonine-protein phosphatase 2A regulatory subunit B" subunit gamma, EF-hand domain pair                                          | No domain found                               | serine/threonine protein phosphatase 2A regulatory subunit B                                                                                                            |
| 108 | A0A077Z737  | Calcineurin-like phosphoesterase domain, ApaH type, Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetrakisphosphatase, Metallo-dependent phosphatase-like | Calcineurin-like phosphoesterase              | metallophosphatase superfamily, metallophosphatase domain                                                                                                               |
| 109 | A0A077Z FV4 | DEK, C-terminal, Protein-tyrosine phosphatase-like, Protein phosphatase Slingshot-like                                                                                     | DEK C terminal domain                         | N-terminal domain conserved in slingshot (SSH) phosphatases, cys-based protein tyrosine phosphatase and dual-specificity phosphatase superfamily, DEK C terminal domain |

|     |            |                                                                                                                                                                            |                                                                                  |                                                                                                                        |
|-----|------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------|
| 110 | A0A077Z9S3 | Phosphatidic acid phosphatase type 2/haloperoxidase, Phosphatidic acid phosphatase type 2/haloperoxidase superfamily, Glucose-6-phosphatase                                | PAP2 superfamily                                                                 | PAP2 superfamily                                                                                                       |
| 111 | A0A077ZQ26 | Histidine phosphatase superfamily, clade-1, Histidine phosphatase superfamily                                                                                              | Histidine phosphatase superfamily (branch 1)                                     | Histidine phosphatase superfamily (branch 1)                                                                           |
| 112 | A0A077ZC20 | Lariat debranching enzyme, C-terminal, Calcineurin-like phosphoesterase domain, ApaH type, Lariat debranching enzyme, N-terminal metallophosphatase domain                 | Calcineurin-like phosphoesterase, Lariat debranching enzyme, C-terminal domain   | Dbr1 RNA lariat debranching enzyme, N-terminal metallophosphatase domain, Lariat debranching enzyme, C-terminal domain |
| 113 | A0A077ZDX1 | Rhodanese-like domain, Rhodanase, C-terminal, tRNA uridine(34) hydroxylase, N-terminal                                                                                     | Rhodanese-like domain, Rhodanase C-terminal, UPF0176 acylphosphatase like domain | Rhodanese-related sulfurtransferase, Transcriptional regulatory protein, C terminal                                    |
| 114 | A0A077ZEA8 | Endonuclease/exonuclease /phosphatase, Endonuclease/exonuclease /phosphatase superfamily                                                                                   | Endonuclease/Exonuclease/phosphatase family                                      | Exonuclease-Endonuclease-Phosphatase (EEP) domain superfamily                                                          |
| 115 | A0A077ZEI8 | Histidine phosphatase superfamily, clade-2, Histidine phosphatase superfamily, Histidine acid phosphatase active site                                                      | Histidine phosphatase superfamily (branch 2)                                     | Histidine phosphatase domain                                                                                           |
| 116 | A0A077ZHK7 | Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetrakisphosphatase, Calcineurin-like phosphoesterase domain, ApaH type, Metallo-dependent phosphatase-like | Calcineurin-like phosphoesterase                                                 | Protein phosphatase 2A homologues, catalytic domain                                                                    |
| 117 | A0A077Z559 | Endonuclease/exonuclease /phosphatase superfamily, Type I inositol 1,4,5-trisphosphate 5-phosphatase                                                                       | No domain found                                                                  | Exonuclease-Endonuclease-Phosphatase (EEP) domain superfamily                                                          |
| 118 | A0A077YXV9 | Tyrosine-specific protein phosphatase, PTPase domain, Tyrosine-specific protein phosphatases domain, Protein-tyrosine phosphatase, catalytic                               | Protein-tyrosine phosphatase                                                     | Protein tyrosine phosphatase, catalytic domain                                                                         |

|     |                |                                                                                                                                                                                                                                          |                                                                          |                                                                                                     |
|-----|----------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------|
| 119 | A0A077Z<br>MC2 | HAD-superfamily<br>hydrolase, subfamily IIIA,<br>Histidinol-phosphate<br>phosphatase                                                                                                                                                     | HAD-hydrolase-like                                                       | Histidinol phosphatase                                                                              |
| 120 | A0A077Z<br>KM7 | Metallo-dependent<br>phosphatase-like,<br>Calcineurin-like<br>phosphoesterase domain,<br>ApaH type, NUDIX<br>hydrolase domain                                                                                                            | Calcineurin-like<br>phosphoesterase, NUDIX<br>domain                     | NUDIX family, 3',5'-<br>cyclic AMP<br>phosphodiesterase CpdA                                        |
| 121 | A0A077Z<br>F56 | Endonuclease/exonuclease<br>/phosphatase superfamily,<br>Rho GTPase-activating<br>protein domain, OCRL-1/2,<br>ASH domain, Inositol<br>polyphosphate-related<br>phosphatase, Inositol<br>polyphosphate 5-<br>phosphatase OCRL,<br>RhoGAP | RhoGAP domain,<br>Endonuclease/Exonucleas<br>e/phosphatase family        | Exonuclease-<br>Endonuclease-<br>Phosphatase (EEP)<br>domain superfamily,<br>RhoGAP_OCRL1           |
| 122 | A0A077<br>YXF9 | Trehalose-6-phosphate<br>phosphatase, helical<br>bundle domain, Trehalose-<br>6-phosphate phosphatase,<br>C-terminal domain                                                                                                              | Trehalose-6-phosphate<br>phosphatase N-terminal<br>helical bundle domain | Trehalose-6-phosphate<br>phosphatase N-terminal<br>helical bundle domain                            |
| 123 | A0A077Z<br>586 | Histidine phosphatase<br>superfamily, clade-2,<br>Histidine phosphatase<br>superfamily                                                                                                                                                   | Histidine phosphatase<br>superfamily (branch 2)                          | Histidine<br>phosphatase superfamily                                                                |
| 124 | A0A077Z<br>1R2 | Inositol monophosphatase,<br>lithium-sensitive, Inositol<br>monophosphatase,<br>conserved site, Inositol<br>monophosphatase, metal-<br>binding site, Inositol<br>monophosphatase-like,<br>Inositol monophosphatase                       | Inositol monophosphatase<br>family                                       | Archaeal fructose-1,6-<br>bisphosphatase or related<br>enzyme of inositol<br>monophosphatase family |
| 125 | A0A077<br>YWP4 | Histidine phosphatase<br>superfamily, Histidine<br>phosphatase superfamily,<br>clade-2, Histidine acid<br>phosphatase active site                                                                                                        | Histidine phosphatase<br>superfamily (branch 2)                          | Histidine phosphatase<br>domain                                                                     |
| 126 | A0A077<br>YZ15 | Endonuclease/exonuclease<br>/phosphatase                                                                                                                                                                                                 | Endonuclease/Exonucleas<br>e/phosphatase family                          | Exonuclease-<br>Endonuclease-<br>Phosphatase (EEP)<br>domain superfamily                            |
| 127 | A0A077Z<br>DM0 | HAD hydrolase, subfamily<br>IA, Haloacid dehalogenase-<br>like hydrolase, HAD-like<br>superfamily,<br>Phosphoglycolate<br>phosphatase-like, domain<br>2, HAD superfamily                                                                 | Haloacid dehalogenase-<br>like hydrolase                                 | Beta-phosphoglucomutase<br>or related phosphatase,<br>HAD superfamily                               |

|     |            |                                                                                                                                                                                     |                                                                                                              |                                                                                                                |
|-----|------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------|
| 128 | A0A077Z934 | Dual specificity protein phosphatase domain, Dual specificity phosphatase, catalytic domain, Protein-tyrosine phosphatase, catalytic, Tyrosine-specific protein phosphatases domain | Dual specificity phosphatase, catalytic domain                                                               | Dual-specificity phosphatase domain                                                                            |
| 129 | A0A077Z9T8 | Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetraphosphatase, Calcineurin-like phosphoesterase domain, ApaH type                                                 | Calcineurin-like phosphoesterase                                                                             | Metallophosphatase superfamily, Metallophosphatase domain                                                      |
| 130 | A0A077ZJ61 | Endonuclease/exonuclease /phosphatase                                                                                                                                               | Endonuclease/Exonuclease/phosphatase family                                                                  | Exonuclease-Endonuclease-Phosphatase (EEP) domain superfamily, ISXO2-like transposase domain                   |
| 131 | A0A077YXS8 | Rhodanese-like domain, Dual specificity protein phosphatase domain, Dual specificity phosphatase, catalytic domain, Tyrosine-specific protein phosphatases domain                   | Dual specificity phosphatase, catalytic domain, Rhodanese-like domain                                        | Dual specificity phosphatase domain of class II mitogen-activated protein kinase phosphatase, RHOD Superfamily |
| 132 | A0A077YYJ1 | Tyrosine-specific protein phosphatase, PTPase domain, Protein-tyrosine phosphatase, catalytic, Tyrosine-specific protein phosphatases domain                                        | Protein-tyrosine phosphatase                                                                                 | Protein tyrosine phosphatase, catalytic domain                                                                 |
| 133 | A0A077YZX0 | Sphingomyelin synthase-like domain                                                                                                                                                  | PAP2 superfamily C-terminal                                                                                  | PAP2 superfamily C-terminal, Membrane-associated phospholipid phosphatase                                      |
| 134 | A0A077Z7Y2 | Histidine phosphatase superfamily, clade-2, Histidine phosphatase superfamily                                                                                                       | Histidine phosphatase superfamily (branch 2)                                                                 | Histidine phosphatase domain                                                                                   |
| 135 | A0A077Z5I1 | Histidine acid phosphatase, VIP1 family, Histidine phosphatase superfamily, Histidine phosphatase superfamily, clade-2 VIP1, N-terminal, Histidine acid phosphatase active site     | Diphosphoinositol pentakisphosphate kinase 2 N-terminal domain, Histidine phosphatase superfamily (branch 2) | Glutathione synthase/RimK-type ligase                                                                          |
| 136 | A0A077ZKY5 | Inorganic pyrophosphatase superfamily, Inorganic pyrophosphatase                                                                                                                    | Inorganic pyrophosphatase                                                                                    | Inorganic diphosphatase                                                                                        |

|     |                |                                                                                                                                                          |                                                                                                                   |                                                                                                                                           |
|-----|----------------|----------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------|
| 137 | A0A077Z<br>D23 | Histidine phosphatase superfamily, Histidine phosphatase superfamily, clade-1                                                                            | Histidine phosphatase superfamily (branch 1)                                                                      | Histidine phosphatase domain                                                                                                              |
| 138 | A0A077Z<br>8N3 | Dual specificity phosphatase, catalytic domain                                                                                                           | No domain found                                                                                                   | cys-based protein tyrosine phosphatase and dual-specificity phosphatase superfamily                                                       |
| 139 | A0A077Z<br>JA4 | Histidine phosphatase superfamily, Histidine phosphatase superfamily, clade-1                                                                            | Histidine phosphatase superfamily (branch 1)                                                                      | Histidine phosphatase domain                                                                                                              |
| 140 | A0A077Z<br>0L2 | Protein phosphatase 1 regulatory subunit 21, six-helix bundle, Protein phosphatase 1 regulatory subunit 21, C-terminal                                   | Protein phosphatase 1 regulatory subunit 21, six-helix bundle                                                     | Predicted coiled-coil domain-containing protein                                                                                           |
| 141 | A0A077Z<br>BE7 | Myotubularin-like, phosphatase domain                                                                                                                    | Myotubularin-like phosphatase domain                                                                              | PTP_DSP_cys Superfamily, Pleckstrin homology-like domain                                                                                  |
| 142 | A0A077Z<br>0G9 | Rhodanese-like domain, M-phase inducer phosphatase                                                                                                       | Rhodanese-like domain                                                                                             | Rhodanese-related sulfurtransferase                                                                                                       |
| 143 | A0A077Z<br>4A6 | Rhodanese-like domain                                                                                                                                    | Rhodanese-like domain                                                                                             | Rhodanese Homology Domain (RHOD)                                                                                                          |
| 144 | A0A077Z<br>CB2 | HAD-superfamily hydrolase, subfamily IA, YjjG/PynA, HAD hydrolase, subfamily IA                                                                          | Haloacid dehalogenase-like hydrolase                                                                              | FMN phosphatase YigB, HAD superfamily                                                                                                     |
| 145 | A0A077Z<br>9G1 | Histidine phosphatase superfamily, clade-1                                                                                                               | Histidine phosphatase superfamily (branch 1)                                                                      | Histidine phosphatase, Phosphohistidine phosphatase SixA                                                                                  |
| 146 | A0A077Z<br>2Z3 | Tyrosine-specific protein phosphatase, PTPase domain, SH2 domain, Tyrosine-specific protein phosphatases domain, Protein-tyrosine phosphatase, catalytic | Protein-tyrosine phosphatase, SH2 domain                                                                          | PTP_DSP_cys Superfamily, N-terminal Src homology 2 (N-SH2) domain, C-terminal Src homology 2 (C-SH2) domain                               |
| 147 | A0A077<br>YZU0 | Dual specificity protein phosphatase domain, Dual specificity phosphatase, catalytic domain, Tyrosine-specific protein phosphatases domain               | Dual specificity phosphatase, catalytic domain                                                                    | Dual specificity phosphatase domain of class III mitogen-activated protein kinase phosphatase                                             |
| 148 | A0A077Z<br>8D3 | Trehalose-6-phosphate phosphatase, helical bundle domain, Trehalose-6-phosphate phosphatase, C-terminal domain                                           | Trehalose-6-phosphate phosphatase N-terminal helical bundle domain, Glycosyltransferase family 20                 | Trehalose-6-phosphate synthase, Trehalose-6-phosphate phosphatase N-terminal helical bundle domain, Haloacid Dehalogenase-like Hydrolases |
| 149 | A0A077Z<br>CG9 | Phosphotyrosine protein phosphatase I                                                                                                                    | Low molecular weight phosphotyrosine protein phosphatase, Peptidyl-tRNA hydrolase PTH2, DeoC/LacD family aldolase | Low molecular weight protein tyrosine phosphatase, PTH2_family Superfamily, DeoC                                                          |

|     |            |                                                                                                                                                                             |                                                                                           |                                                                                 |
|-----|------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------|
| 150 | A0A077Z052 | Serine/threonine-protein phosphatase 4 regulatory subunit 3-like, central domain                                                                                            | Phosphatase 4 regulatory subunit 3                                                        | SMK-1                                                                           |
| 151 | A0A077ZKZ1 | 3'(2'),5'-bisphosphate nucleotidase CysQ, Inositol monophosphatase-like                                                                                                     | Inositol monophosphatase family                                                           | Adenosine-3'(2'),5'-bisphosphate nucleotidase                                   |
| 152 | A0A077Z7Q3 | Histidine phosphatase superfamily, clade-1                                                                                                                                  | Histidine phosphatase superfamily (branch 1)                                              | Histidine phosphatase domain                                                    |
| 153 | A0A077YXW5 | Tyrosine-specific protein phosphatase, PTPase domain, Protein-tyrosine phosphatase, catalytic, Tyrosine-specific protein phosphatases domain                                | Protein-tyrosine phosphatase                                                              | Protein tyrosine phosphatase, catalytic domain                                  |
| 154 | A0A077ZBU6 | PPM-type phosphatase-like domain                                                                                                                                            | Stage II sporulation protein E (SpolIE)                                                   | Serine/threonine phosphatases, family 2C, catalytic domain                      |
| 155 | A0A077ZM03 | Histidine phosphatase superfamily, clade-2                                                                                                                                  | No domain found                                                                           | Histidine phosphatase domain                                                    |
| 156 | A0A077YZS8 | Fibronectin type III, PTPRJ, transmembrane domain                                                                                                                           | TM proximal of protein tyrosine phosphatase, receptor type J, Fibronectin type III domain | No domain found                                                                 |
| 157 | A0A077Z562 | Dual specificity protein phosphatase domain, Tyrosine-specific protein phosphatases domain, Dual specificity phosphatase, catalytic domain                                  | Dual specificity phosphatase, catalytic domain                                            | Protein tyrosine phosphatase                                                    |
| 158 | A0A077ZA15 | Tyrosine-specific protein phosphatases domain, Dual specificity protein phosphatase domain, Dual specificity phosphatase, catalytic domain                                  | Dual specificity phosphatase, catalytic domain, PAC2 family                               | Dual-specificity phosphatase domain, PAC2 family                                |
| 159 | A0A077ZH63 | SAC domain                                                                                                                                                                  | SacI homology domain                                                                      | SacI homology domain                                                            |
| 160 | A0A077Z9E7 | Dual specificity phosphatase, catalytic domain, Tyrosine-specific protein phosphatases domain                                                                               | Dual specificity phosphatase, catalytic domain                                            | PTP_DSP_cys Superfamily                                                         |
| 161 | A0A077Z6K7 | Protein-tyrosine phosphatase, catalytic, Myotubularin-like, phosphatase domain, Tyrosine-specific protein phosphatases domain, FYVE zinc finger, Zinc finger, FYVE-related, | FYVE zinc finger, Myotubularin-like phosphatase domain                                    | No domain found                                                                 |
| 162 | A0A077ZCR3 | Rhodanese-like domain, Rab-GAP-TBC domain, Protein kinase domain                                                                                                            | Rhodanese-like domain, Rab-GTPase-TBC domain                                              | Rhodanese-like domain, Rab-GTPase-TBC domain, Protein Kinases, catalytic domain |

|     |                |                                                                                                                                                                                                                          |                                                                                        |                                                                                                                      |
|-----|----------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------|
| 163 | A0A077Z<br>425 | Sphingomyelin synthase-like domain, Sterile alpha motif domain                                                                                                                                                           | SAM domain (Sterile alpha motif), PAP2 superfamily C-terminal                          | SAM_SGMS1-like, PAP2 superfamily C-terminal                                                                          |
| 164 | A0A077Z<br>538 | Rhodanese-like domain                                                                                                                                                                                                    | Rhodanese-like domain                                                                  | Rhodanese-related sulfurtransferase                                                                                  |
| 165 | A0A077Z<br>3S0 | Tyrosine-specific protein phosphatase, Protein-tyrosine phosphatase, catalytic, PTPase domain, Immunoglobulin subtype, Immunoglobulin-like domain, Immunoglobulin subtype 2, Fibronectin type III, Immunoglobulin I-set, | Protein-tyrosine phosphatase, Fibronectin type III domain, Immunoglobulin I-set domain | R-PTPc-LAR-1, PTP_DSP_cys Superfamily, Immunoglobulin domain, Fibronectin type 3 domain, Fibronectin type III domain |
| 166 | A0A077Z<br>832 | Protein-tyrosine phosphatase-like, PTPLA                                                                                                                                                                                 | Protein tyrosine phosphatase-like protein, PTPLA                                       | Protein tyrosine phosphatase-like protein, PTPLA                                                                     |
| 167 | A0A077Z<br>9J9 | Tyrosine-specific protein phosphatase, PTPase domain, Protein-tyrosine phosphatase, catalytic, Tyrosine-specific protein phosphatases domain                                                                             | Protein-tyrosine phosphatase                                                           | PTP_DSP_cys Superfamily                                                                                              |
| 168 | A0A077Z<br>FC8 | Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetraphosphatase, Calcineurin-like phosphoesterase domain, ApaH type                                                                                      | Calcineurin-like phosphoesterase                                                       | Protein phosphatase 2A homologues, catalytic domain                                                                  |
| 169 | A0A077Z<br>4V4 | Inositol monophosphatase-like                                                                                                                                                                                            | Inositol monophosphatase family                                                        | 3'- Phosphoadenosine 5'-phosphosulfate (PAPS) 3'-phosphatase                                                         |
| 170 | A0A077Z<br>EH3 | Histidine phosphatase superfamily, clade-1                                                                                                                                                                               | Histidine phosphatase superfamily (branch 1)                                           | No domain found                                                                                                      |
| 171 | A0A077Z<br>EA0 | Phosphatidic acid phosphatase type 2/haloperoxidase                                                                                                                                                                      | PAP2 superfamily                                                                       | PAP2, wunen subfamily                                                                                                |
| 172 | A0A077Z<br>DA4 | HAD hydrolase, subfamily IA                                                                                                                                                                                              | Haloacid dehalogenase-like hydrolase                                                   | FMN phosphatase YigB, HAD superfamily                                                                                |
| 173 | A0A077Z<br>FZ6 | Calcineurin-like phosphoesterase domain, ApaH type, CpdB, N-terminal metallophosphatase domain                                                                                                                           | Calcineurin-like phosphoesterase                                                       | cpdB Superfamily                                                                                                     |
| 174 | A0A077Z<br>1M2 | Histidine phosphatase superfamily, clade-2                                                                                                                                                                               | Histidine phosphatase superfamily (branch 2)                                           | Histidine phosphatase domain                                                                                         |

|     |                |                                                                                                                                                                      |                                                                   |                                                                                                              |
|-----|----------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------|
| 175 | A0A077Z<br>2W3 | Serine/threonine-specific protein phosphatase/bis(5-nucleosyl)-tetraphosphatase, Calcineurin-like phosphoesterase domain, ApaH type, PP2B, metallophosphatase domain | Calcineurin-like phosphoesterase                                  | PP2B, metallophosphatase domain                                                                              |
| 176 | A0A077Z<br>J29 | Histidine phosphatase superfamily, clade-2                                                                                                                           | Histidine phosphatase superfamily (branch 2)                      | No domain found                                                                                              |
| 177 | A0A077Z<br>4L6 | Tyrosine-specific protein phosphatases domain, Dual specificity protein phosphatase domain, Dual specificity phosphatase, catalytic domain                           | Dual specificity phosphatase, catalytic domain                    | DUSP14-like                                                                                                  |
| 178 | A0A077Z<br>CQ9 | 2-phosphoglycolate phosphatase, eukaryotic, HAD-superfamily hydrolase, subfamily IIA                                                                                 | Haloacid dehalogenase-like hydrolase, HAD-hydrolase-like          | Haloacid Dehalogenase-like Hydrolases                                                                        |
| 179 | A0A077Z<br>5J2 | Protein-tyrosine phosphatase, catalytic, Tyrosine-specific protein phosphatase, PTPase domain, Tyrosine-specific protein phosphatases domain                         | Protein-tyrosine phosphatase                                      | Protein tyrosine phosphatase, catalytic domain                                                               |
| 180 | A0A077Z<br>BJ3 | PPM-type phosphatase-like domain                                                                                                                                     | Protein phosphatase 2C                                            | Serine/threonine phosphatases, family 2C, catalytic domain                                                   |
| 181 | A0A077Z<br>FU8 | Tyrosine-specific protein phosphatases domain, Protein-tyrosine phosphatase, catalytic, Tyrosine-specific protein phosphatase, PTPase domain                         | Protein-tyrosine phosphatase                                      | Protein-tyrosine phosphatase                                                                                 |
| 182 | A0A077Z<br>058 | Inositol polyphosphate-related phosphatase, SAC domain                                                                                                               | Endonuclease/Exonuclease/phosphatase family, SacI homology domain | Exonuclease-Endonuclease-Phosphatase (EEP) domain superfamily, Phosphoinositide polyphosphatase (Sac family) |
| 183 | A0A077Z<br>2A4 | Tyrosine-specific protein phosphatase, PTPase domain, Tyrosine-specific protein phosphatases domain, Protein-tyrosine phosphatase, catalytic                         | Protein-tyrosine phosphatase                                      | Protein tyrosine phosphatase, catalytic domain                                                               |
| 184 | A0A077Z<br>226 | Phosphatidic acid phosphatase type 2/haloperoxidase                                                                                                                  | PAP2 superfamily                                                  | Membrane-associated phospholipid phosphatase                                                                 |
| 185 | A0A077Z<br>BE2 | HAD-superfamily hydrolase, subfamily IIB, Cof family                                                                                                                 | Haloacid dehalogenase-like hydrolase                              | HAD_YbiV-Like                                                                                                |

|     |                |                                                                                                                    |                 |                                                                          |
|-----|----------------|--------------------------------------------------------------------------------------------------------------------|-----------------|--------------------------------------------------------------------------|
| 186 | A0A077<br>YZT4 | Endonuclease/exonuclease<br>/phosphatase superfamily,<br>Type I inositol 1,4,5-<br>trisphosphate 5-<br>phosphatase | No domain found | Exonuclease-<br>Endonuclease-<br>Phosphatase (EEP)<br>domain superfamily |
|     |                | <b>UNCHARACTERIZED PROTEIN</b>                                                                                     |                 |                                                                          |
| 187 | A0A077Z<br>KM0 | HAD-like protein                                                                                                   |                 |                                                                          |

**Supplementary Table 2: Classification of *T. trichiura* phosphatases in their respective families and classes.**

| Phosphatases                  | Class                            | Number | Accession ID                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
|-------------------------------|----------------------------------|--------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Ser/Thr phosphatases          | PPP                              | 44     | A0A077Z0L2, A0A077Z0F2, A0A077Z052, A0A077Z4J5, A0A077ZB21, A0A077Z1E1, A0A077ZHX6, A0A077Z9P7, A0A077Z292, A0A077ZCV5, A0A077ZCU0, A0A077YXQ6, A0A077Z6K1, A0A077Z9E8, A0A077Z3W1, A0A077ZCP7, A0A077Z3U3, A0A077Z0V2, A0A077YWG4, A0A077ZJM4, A0A077ZJE2, A0A077Z4E6, A0A077ZL96, A0A077Z761, A0A077ZJP5, A0A077Z372, A0A077ZL46, A0A077Z737, A0A077ZHK7, A0A077ZKM7, A0A077Z9T8, A0A077ZFC8, A0A077ZFZ6, A0A077Z2W3, A0A077ZDY3, A0A077Z2U9, A0A077Z5M7, A0A077ZG39, A0A077Z9S3, A0A077YZX0, A0A077Z425, A0A077ZEA0, A0A077Z226, A0A077ZC20 |
|                               | PPM                              | 12     | A0A077ZHG7, A0A077Z3D1, A0A077ZFI3, A0A077Z6F0, A0A077ZG77, A0A077Z8C2, A0A077ZBJ3, A0A077ZBU6, A0A077ZE66, A0A077Z1R2, A0A077ZKZ1, A0A077Z4V4                                                                                                                                                                                                                                                                                                                                                                                                 |
|                               | HAD family                       | 21     | A0A077Z2W0, A0A077ZP93, A0A077YZW5, A0A077Z2V2, A0A077YZL0, A0A077ZCQ0, A0A077ZMR3, A0A077ZBQ5, A0A077Z0R5, A0A077Z5V1, A0A077Z942, A0A077ZDM0, A0A077ZCB2, A0A077ZDA4, A0A077ZCQ9, A0A077ZBE2, A0A077ZMC2, A0A077ZKM0, A0A077ZEV3, A0A077ZD83, A0A077Z9X3                                                                                                                                                                                                                                                                                     |
|                               |                                  |        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| Protein Tyrosine Phosphatases | PTPc                             | 32     | A0A077ZDG9, A0A077Z5T3, A0A077Z2Z0, A0A077Z783, A0A077ZKV6, A0A077YZB8, A0A077Z172, A0A077Z3P2, A0A077YZN2, A0A077ZKX1, A0A077ZG23, A0A077ZDG8, A0A077YZA9, A0A077Z1H9, A0A077YZQ2, A0A077ZDV4, A0A077YXV9, A0A077YYJ1, A0A077Z2Z3, A0A077YXW5, A0A077Z3S0, A0A077Z9J9, A0A077Z5J2, A0A077ZFU8, A0A077ZCG9, A0A077Z8R0, A0A077ZH63, A0A077Z2A4, A0A077YZS8, A0A077YXF9, A0A077Z8D3                                                                                                                                                             |
|                               | DSPc                             | 20     | A0A077ZDE3, A0A077Z725, A0A077Z3T8, A0A077Z4F8, A0A077Z7L5, A0A077Z283, A0A077ZFN2, A0A077ZEV8, A0A077Z934, A0A077Z8N3, A0A077YZU0, A0A077Z562, A0A077ZA15, A0A077Z9E7, A0A077Z4L6, A0A077ZK33, A0A077YWY8, A0A077Z308, A0A077ZBE7, A0A077Z6K7                                                                                                                                                                                                                                                                                                 |
|                               | CDC25                            | 9      | A0A077YZL7, A0A077ZIC1, A0A077ZJA6, A0A077ZDX1, A0A077Z0G9, A0A077Z4A6, A0A077ZCR3, A0A077Z538, A0A077YXS8                                                                                                                                                                                                                                                                                                                                                                                                                                     |
|                               | LMWPTPASE                        | 0      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
|                               | Histidine phosphatase            | 28     | A0A077ZH74, A0A077ZEU7, A0A077Z5N7, A0A077YZZ0, A0A077ZG20, A0A077ZQ26, A0A077ZD23, A0A077ZJA4, A0A077Z9G1, A0A077Z7Q3, A0A077ZEH3, A0A077ZFY2, A0A077ZGN6, A0A077Z1S5, A0A077YZX7, A0A077Z8U4, A0A077ZIB4, A0A077ZH69, A0A077Z6N3, A0A077ZEI8, A0A077Z586, A0A077YWP4, A0A077Z7Y2, A0A077Z5I1, A0A077ZM03, A0A077Z1M2, A0A077ZJ29, A0A077ZNV5,                                                                                                                                                                                                |
|                               |                                  |        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| Pyrophosphatase               | Deoxyutp Pyrophosphatase family  | 1      | A0A077Z4D3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
|                               | Inorganic Pyrophosphatase family | 1      | A0A077ZKY5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |

|                                      |  |    |                                                                                                                                                                        |  |
|--------------------------------------|--|----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--|
|                                      |  |    |                                                                                                                                                                        |  |
| Endonuclease/exonuclease/phosphatase |  | 14 | A0A077Z944, A0A077ZM16, A0A077ZNC2, A0A077Z210, A0A077ZIF8, A0A077ZEA8, A0A077Z559, A0A077ZF56, A0A077YZ15, A0A077ZJ61, A0A077Z058, A0A077YZT4, A0A077Z2N2, A0A077ZCU6 |  |
|                                      |  |    |                                                                                                                                                                        |  |
| Ppx/GppA phosphatase family          |  | 1  | A0A077ZF71                                                                                                                                                             |  |
| Alkaline-phosphatase-like            |  | 1  | A0A077Z7D8                                                                                                                                                             |  |

**Supplementary Table 3: Identification of non-homologous protein phosphatases from *Trichuris trichiura***

| S. No. | Accession Id | Homology analysis | Percentage similarity     |
|--------|--------------|-------------------|---------------------------|
| 1      | A0A077Z0F2   | Homologous        | 38.9%                     |
| 2      | A0A077Z4J5   | Homologous        | 41.47%                    |
| 3      | A0A077ZK33   | Homologous        | 27.54%                    |
| 4      | A0A077ZB21   | Homologous        | 40.29%                    |
| 5      | A0A077ZHG7   | Homologous        | 27.07%                    |
| 6      | A0A077ZDG9   | Homologous        | 33.14%                    |
| 7      | A0A077ZH74   | Homologous        | 37.27%                    |
| 8      | A0A077Z6N3   | Homologous        | 30%                       |
| 9      | A0A077ZDY3   | Homologous        | 31.87%                    |
| 10     | A0A077Z5T3   | Homologous        | 31.34%                    |
| 11     | A0A077Z3D1   | Homologous        | 25.53%                    |
| 12     | A0A077Z1E1   | Homologous        | 38.83%                    |
| 13     | A0A077ZHX6   | Homologous        | 33.65%                    |
| 14     | A0A077ZE66   | Homologous        | 39.78%                    |
| 15     | A0A077YZL7   | Homologous        | 52.94%                    |
| 16     | A0A077Z944   | Homologous        | 41.52%                    |
| 17     | A0A077ZJP5   | Homologous        | 75%                       |
| 18     | A0A077ZM16   | Homologous        | 28.82%                    |
| 19     | A0A077ZPJ3   | Homologous        | 50%                       |
| 20     | A0A077Z9P7   | Homologous        | 52.62%                    |
| 21     | A0A077Z2U9   | Non-Homologous    | 35.06%                    |
| 22     | A0A077Z9X3   | Homologous        | 50%                       |
| 23     | A0A077Z2Z0   | Homologous        | 29.41%                    |
| 24     | A0A077ZEU7   | Non-Homologous    | 29.58%                    |
| 25     | A0A077ZPQ2   | Homologous        | 32.63%                    |
| 26     | A0A077Z2W0   | Homologous        | 47.69%                    |
| 27     | A0A077Z5N7   | Homologous        | 31.91%                    |
| 28     | A0A077Z783   | Homologous        | 32.60%                    |
| 29     | A0A077ZP93   | Homologous        | 31.01%                    |
| 30     | A0A077Z292   | Non-Homologous    | 89.05%                    |
| 31     | A0A077ZDE3   | Homologous        | 50.77%                    |
| 32     | A0A077Z725   | Homologous        | 41.53%                    |
| 33     | A0A077ZCV5   | Non-Homologous    | 38.30%                    |
| 34     | A0A077YXQ6   | Non-Homologous    | 55.44%                    |
| 35     | A0A077YZZ0   | Homologous        | 32.23%                    |
| 36     | A0A077YZW5   | Homologous        | 57.38%                    |
| 37     | A0A077ZF71   | Non-Homologous    | No significant similarity |
| 38     | A0A077Z2V2   | Non-Homologous    | 71.09%                    |
| 39     | A0A077ZEV3   | Homologous        | 26.03%                    |
| 40     | A0A077YZL0   | Homologous        | 39.81%                    |
| 41     | A0A077ZKV6   | Homologous        | 46.67%                    |
| 42     | A0A077ZCQ0   | Homologous        | 28.82%                    |
| 43     | A0A077YZB8   | Homologous        | 44.08%                    |

|    |            |                |                           |
|----|------------|----------------|---------------------------|
| 44 | A0A077Z3T8 | Homologous     | 26.47%                    |
| 45 | A0A077Z6F0 | Homologous     | 22.46%                    |
| 46 | A0A077ZCU0 | Homologous     | 63.69%                    |
| 47 | A0A077Z4D3 | Homologous     | 70.37%                    |
| 48 | A0A077Z4F8 | Homologous     | 35.96%                    |
| 49 | A0A077YWY8 | Non-Homologous | 48.59%                    |
| 50 | A0A077Z6K1 | Homologous     | 68.17%                    |
| 51 | A0A077Z3U3 | Non-Homologous | 84.40%                    |
| 52 | A0A077ZNC2 | Homologous     | 48.84%                    |
| 53 | A0A077Z172 | Homologous     | 31.65%                    |
| 54 | A0A077Z210 | Homologous     | 43.37%                    |
| 55 | A0A077ZGN6 | Homologous     | 34.78%                    |
| 56 | A0A077Z7L5 | Homologous     | 38.89%                    |
| 57 | A0A077ZG77 | Homologous     | 30.27%                    |
| 58 | A0A077Z7D8 | Non-Homologous | No significant similarity |
| 59 | A0A077ZD83 | Homologous     | 47.50%                    |
| 60 | A0A077Z1S5 | Non-Homologous | No significant similarity |
| 61 | A0A077Z5M7 | Non-Homologous | 35.59%                    |
| 62 | A0A077Z0V2 | Non-Homologous | 91.27%                    |
| 63 | A0A077Z9E8 | Non-Homologous | 71.09%                    |
| 64 | A0A077YWG4 | Homologous     | 39.29%                    |
| 65 | A0A077Z2N2 | Homologous     | 27.86%                    |
| 66 | A0A077Z283 | Homologous     | 23.65%                    |
| 67 | A0A077ZJM4 | Homologous     | 38.78%                    |
| 68 | A0A077Z3P2 | Homologous     | 33.99%                    |
| 69 | A0A077YZN2 | Non-Homologous | 40.28%                    |
| 70 | A0A077ZFN2 | Homologous     | 30.58%                    |
| 71 | A0A077ZG20 | Homologous     | 52.36%                    |
| 72 | A0A077ZJE2 | Non-Homologous | 84.82%                    |
| 73 | A0A077ZMR3 | Homologous     | 45.10%                    |
| 74 | A0A077ZCU6 | Homologous     | 30.19%                    |
| 75 | A0A077Z8R0 | Homologous     | 34.70%                    |
| 76 | A0A077ZKX1 | Homologous     | 30.69%                    |
| 77 | A0A077Z4E6 | Non-Homologous | 58.24%                    |
| 78 | A0A077ZBQ5 | Homologous     | 47.27%                    |
| 79 | A0A077Z308 | Homologous     | 42.15%                    |
| 80 | A0A077Z0R5 | Homologous     | 47.65%                    |
| 81 | A0A077ZEV8 | Homologous     | 55.41%                    |
| 82 | A0A077ZG23 | Homologous     | 33.99%                    |
| 83 | A0A077YZX7 | Homologous     | 46.36%                    |
| 84 | A0A077Z3W1 | Non-Homologous | 60.99%                    |
| 85 | A0A077Z8U4 | Homologous     | 27.39%                    |
| 86 | A0A077ZIB4 | Homologous     | 27.39%                    |
| 87 | A0A077Z5V1 | Non-Homologous | No significant similarity |
| 88 | A0A077ZDG8 | Homologous     | 49.60%                    |
| 89 | A0A077ZIC1 | Homologous     | 37%                       |

|     |            |                |                           |
|-----|------------|----------------|---------------------------|
| 90  | A0A077ZJA6 | Homologous     | 40.77%                    |
| 91  | A0A077ZH69 | Homologous     | 45.45%                    |
| 92  | A0A077YZA9 | Homologous     | 28.57%                    |
| 93  | A0A077Z942 | Non-Homologous | No significant similarity |
| 94  | A0A077Z372 | Homologous     | 43.75%                    |
| 95  | A0A077ZNV5 | Homologous     | 34.15%                    |
| 96  | A0A077ZL96 | Homologous     | 40.23%                    |
| 97  | A0A077ZG39 | Homologous     | 31.67%                    |
| 98  | A0A077Z8C2 | Homologous     | 26.29%                    |
| 99  | A0A077Z1H9 | Homologous     | 44.29%                    |
| 100 | A0A077ZL46 | Homologous     | 40.58%                    |
| 101 | A0A077YZQ2 | Homologous     | 32.79%                    |
| 102 | A0A077ZIF8 | Homologous     | 23.90%                    |
| 103 | A0A077Z761 | Homologous     | 38.06%                    |
| 104 | A0A077ZCP7 | Homologous     | 36.11%                    |
| 105 | A0A077Z737 | Homologous     | 36.52%                    |
| 106 | A0A077ZFV4 | Homologous     | 30.99%                    |
| 107 | A0A077Z9S3 | Homologous     | 26.89%                    |
| 108 | A0A077ZQ26 | Homologous     | 25.85%                    |
| 109 | A0A077ZC20 | Homologous     | 36.17%                    |
| 110 | A0A077ZDX1 | Homologous     | 38.64%                    |
| 111 | A0A077ZEA8 | Homologous     | 28.23%                    |
| 112 | A0A077ZEI8 | Homologous     | 28.36%                    |
| 113 | A0A077ZHK7 | Homologous     | 40.98%                    |
| 114 | A0A077Z559 | Homologous     | 24.33%                    |
| 115 | A0A077YXV9 | Homologous     | 24.10%                    |
| 116 | A0A077ZMC2 | Non-Homologous | 33.33%                    |
| 117 | A0A077ZKM7 | Non-Homologous | No significant similarity |
| 118 | A0A077ZF56 | Homologous     | 33.68%                    |
| 119 | A0A077YXF9 | Non-Homologous | No significant similarity |
| 120 | A0A077Z586 | Homologous     | 55.56%                    |
| 121 | A0A077Z1R2 | Homologous     | 51.95%                    |
| 122 | A0A077YWP4 | Homologous     | 58.33%                    |
| 123 | A0A077YZ15 | Non-Homologous | No significant similarity |
| 124 | A0A077ZDM0 | Homologous     | 49.73%                    |
| 125 | A0A077Z934 | Homologous     | 58.33%                    |
| 126 | A0A077Z9T8 | Homologous     | 39.78%                    |
| 127 | A0A077ZJ61 | Non-Homologous | 23.73%                    |
| 128 | A0A077YXS8 | Homologous     | 40.43%                    |
| 129 | A0A077YYJ1 | Homologous     | 35.32%                    |
| 130 | A0A077YZX0 | Homologous     | 25.58%                    |
| 131 | A0A077Z7Y2 | Homologous     | 48.08%                    |
| 132 | A0A077Z5I1 | Homologous     | 51.76%                    |
| 133 | A0A077ZKY5 | Homologous     | 33.75%                    |
| 134 | A0A077ZD23 | Homologous     | 31.37%                    |
| 135 | A0A077Z8N3 | Homologous     | 27.84%                    |

|     |            |                |                           |
|-----|------------|----------------|---------------------------|
| 136 | A0A077ZJA4 | Homologous     | 34.07%                    |
| 137 | A0A077Z0L2 | Homologous     | 29.41%                    |
| 138 | A0A077ZBE7 | Homologous     | 30.73%                    |
| 139 | A0A077Z0G9 | Homologous     | 48.72%                    |
| 140 | A0A077Z4A6 | Homologous     | 28.23%                    |
| 141 | A0A077ZCB2 | Homologous     | 36.22%                    |
| 142 | A0A077Z9G1 | Homologous     | 32.94%                    |
| 143 | A0A077Z2Z3 | Homologous     | 61.93%                    |
| 144 | A0A077YZU0 | Homologous     | 34.03%                    |
| 145 | A0A077Z8D3 | Non-Homologous | No significant similarity |
| 146 | A0A077ZCG9 | Homologous     | 40%                       |
| 147 | A0A077Z052 | Homologous     | 46.51%                    |
| 148 | A0A077ZKZ1 | Homologous     | 25.10%                    |
| 149 | A0A077Z7Q3 | Homologous     | 25.56%                    |
| 150 | A0A077YXW5 | Homologous     | 33.91%                    |
| 151 | A0A077ZBU6 | Homologous     | 47.85%                    |
| 152 | A0A077ZM03 | Homologous     | 30.49%                    |
| 153 | A0A077YZS8 | Non-Homologous | 27.16%                    |
| 154 | A0A077Z562 | Non-Homologous | No significant similarity |
| 155 | A0A077ZA15 | Homologous     | 34.11%                    |
| 156 | A0A077ZH63 | Homologous     | 27.69%                    |
| 157 | A0A077Z9E7 | Homologous     | 28.40%                    |
| 158 | A0A077Z6K7 | Homologous     | 46.26%                    |
| 159 | A0A077ZCR3 | Homologous     | 64.81%                    |
| 160 | A0A077Z425 | Homologous     | 25.74%                    |
| 161 | A0A077Z538 | Homologous     | 38.96%                    |
| 162 | A0A077Z3S0 | Homologous     | 55.32%                    |
| 163 | A0A077Z9J9 | Homologous     | 40.23%                    |
| 164 | A0A077ZFC8 | Homologous     | 39.61%                    |
| 165 | A0A077Z4V4 | Homologous     | 39.37%                    |
| 166 | A0A077ZEH3 | Non-Homologous | No significant similarity |
| 167 | A0A077ZEA0 | Homologous     | 42.86%                    |
| 168 | A0A077ZDA4 | Homologous     | 30.21%                    |
| 169 | A0A077ZFY6 | Non-Homologous | No significant similarity |
| 170 | A0A077Z1M2 | Homologous     | 25%                       |
| 171 | A0A077Z2W3 | Homologous     | 39.19%                    |
| 172 | A0A077ZJ29 | Homologous     | 31.82%                    |
| 173 | A0A077Z4L6 | Homologous     | 35.25%                    |
| 174 | A0A077ZCQ9 | Non-Homologous | 25%                       |
| 175 | A0A077Z5J2 | Homologous     | 33.33%                    |
| 176 | A0A077ZBJ3 | Homologous     | 43.28%                    |
| 177 | A0A077ZFU8 | Homologous     | 35.81%                    |
| 178 | A0A077Z058 | Homologous     | 35.08%                    |
| 179 | A0A077Z2A4 | Homologous     | 40.71%                    |
| 180 | A0A077Z226 | Homologous     | 37%                       |
| 181 | A0A077ZBE2 | Non-Homologous | No significant similarity |

|            |            |                                 |                           |
|------------|------------|---------------------------------|---------------------------|
| <b>182</b> | A0A077YZT4 | Homologous                      | 31.95%                    |
|            |            | <b>Uncharacterized Proteins</b> |                           |
| <b>185</b> | A0A077ZKM0 | Non-homologous                  | No significant similarity |

**Supplementary Table 4: Predicted sub-cellular localization, signal peptide and transmembrane helices for the protein phosphatases of *Trichuris trichiura***

| S.No. | Accession ID | DeepLoc               | SignalP | TargetP        | Outcyte       | TMHMM |
|-------|--------------|-----------------------|---------|----------------|---------------|-------|
| 1     | A0A077Z0F2   | Cytoplasm             | Other   | Other          | UPS           | 0     |
| 2     | A0A077Z4J5   | Cytoplasm             | Other   | Other          | Intracellular | 0     |
| 3     | A0A077ZK33   | Endoplasmic-reticulum | Other   | Other          | Intracellular | 11    |
| 4     | A0A077ZB21   | Cytoplasm             | Other   | Other          | UPS           | 0     |
| 5     | A0A077ZHG7   | Nucleus               | Other   | Other          | Intracellular | 0     |
| 6     | A0A077ZDG9   | Cytoplasm             | Other   | Other          | Intracellular | 0     |
| 7     | A0A077ZH74   | Cytoplasm             | Other   | Other          | UPS           | 0     |
| 8     | A0A077Z6N3   | Extracellular         | Other   | Other          | Intracellular | 0     |
| 9     | A0A077ZDY3   | Nucleus               | Other   | Other          | Intracellular | 0     |
| 10    | A0A077Z5T3   | Cytoplasm             | Other   | Other          | Intracellular | 0     |
| 11    | A0A077Z3D1   | Cytoplasm             | Other   | Other          | Intracellular | 0     |
| 12    | A0A077Z1E1   | Cytoplasm             | Other   | Other          | Intracellular | 0     |
| 13    | A0A077ZHX6   | Cytoplasm             | Other   | Other          | Intracellular | 0     |
| 14    | A0A077ZE66   | Cytoplasm             | Other   | Other          | Intracellular | 0     |
| 15    | A0A077YZL7   | Endoplasmic-reticulum | Other   | Other          | Intracellular | 2     |
| 16    | A0A077Z944   | Cytoplasm             | Other   | Other          | UPS           | 0     |
| 17    | A0A077ZJP5   | Cytoplasm             | Other   | Other          | UPS           | 0     |
| 18    | A0A077ZM16   | Nucleus               | Other   | Other          | Intracellular | 0     |
| 19    | A0A077ZFI3   | Mitochondria          | Other   | Other          | UPS           | 0     |
| 20    | A0A077Z9P7   | Cytoplasm             | Other   | Other          | UPS           | 0     |
| 21    | A0A077Z2U9   | Endoplasmic-reticulum | Other   | Other          | UPS           | 5     |
| 22    | A0A077Z9X3   | Mitochondria          | Other   | Other          | Intracellular | 0     |
| 23    | A0A077Z2Z0   | Cytoplasm             | Other   | Other          | Intracellular | 0     |
| 24    | A0A077ZEU7   | Nucleus               | Other   | Other          | Intracellular | 0     |
| 25    | A0A077ZFY2   | Cytoplasm             | Other   | Other          | UPS           | 0     |
| 26    | A0A077Z2W0   | Cytoplasm             | Other   | Other          | Intracellular | 0     |
| 27    | A0A077Z5N7   | Cytoplasm             | Other   | Other          | UPS           | 0     |
| 28    | A0A077Z783   | Cell-membrane         | Other   | Other          | Intracellular | 5     |
| 29    | A0A077ZP93   | Mitochondria          | Other   | Other          | Intracellular | 0     |
| 30    | A0A077Z292   | Cytoplasm             | Other   | Other          | UPS           | 0     |
| 31    | A0A077ZDE3   | Lysosome              | Other   | Signal Peptide | Intracellular | 11    |
| 32    | A0A077Z725   | Cytoplasm             | Other   | Other          | UPS           | 0     |
| 33    | A0A077ZCV5   | Endoplasmic-reticulum | Other   | Other          | UPS           | 1     |
| 34    | A0A077YXQ6   | Cytoplasm             | Other   | Other          | Intracellular | 8     |
| 35    | A0A077YZZ0   | Cell-membrane         | Other   | Other          | UPS           | 1     |
| 36    | A0A077YZW5   | Cytoplasm             | Other   | Other          | UPS           | 0     |
| 37    | A0A077Z7F1   | Cytoplasm             | Other   | Other          | Intracellular | 0     |
| 38    | A0A077Z2V2   | Cell-membrane         | Other   | Other          | Intracellular | 8     |

|    |            |                       |                          |                |               |    |
|----|------------|-----------------------|--------------------------|----------------|---------------|----|
| 39 | A0A077ZEV3 | Golgi apparatus       | Other                    | Other          | UPS           | 0  |
| 40 | A0A077YZL0 | Lysosome              | Other                    | Other          | Intracellular | 10 |
| 41 | A0A077ZKV6 | Cytoplasm             | Other                    | Other          | Intracellular | 0  |
| 42 | A0A077ZCQ0 | Golgi apparatus       | Signal peptide (Sec/SPI) | Other          | Intracellular | 10 |
| 43 | A0A077YZB8 | Cytoplasm             | Other                    | Other          | Intracellular | 0  |
| 44 | A0A077Z3T8 | Cytoplasm             | Other                    | Other          | Intracellular | 0  |
| 45 | A0A077Z6F0 | Mitochondria          | Other                    | Other          | Intracellular | 0  |
| 46 | A0A077ZCU0 | Cytoplasm             | Other                    | Other          | UPS           | 0  |
| 47 | A0A077Z4D3 | Cytoplasm             | Other                    | Other          | UPS           | 0  |
| 48 | A0A077Z4F8 | Cytoplasm             | Other                    | Signal peptide | UPS           | 0  |
| 49 | A0A077YWY8 | Cytoplasm             | Other                    | Other          | Intracellular | 0  |
| 50 | A0A077Z6K1 | Cytoplasm             | Other                    | Other          | Intracellular | 0  |
| 51 | A0A077Z3U3 | Cytoplasm             | Other                    | Other          | Intracellular | 0  |
| 52 | A0A077ZNC2 | Lysosome              | Other                    | Other          | UPS           | 1  |
| 53 | A0A077Z172 | Cytoplasm             | Other                    | Other          | UPS           | 0  |
| 54 | A0A077Z210 | Cytoplasm             | Other                    | Other          | Intracellular | 0  |
| 55 | A0A077ZGN6 | Cytoplasm             | Other                    | Other          | Intracellular | 0  |
| 56 | A0A077Z7L5 | Cytoplasm             | Other                    | Other          | UPS           | 0  |
| 57 | A0A077ZG77 | Cytoplasm             | Other                    | Other          | Intracellular | 0  |
| 58 | A0A077Z7D8 | Golgi apparatus       | Other                    | Other          | Intracellular | 1  |
| 59 | A0A077ZD83 | Endoplasmic-reticulum | Other                    | Other          | Intracellular | 1  |
| 60 | A0A077Z1S5 | Cytoplasm             | Signal peptide (Sec/SPI) | Signal peptide | Intracellular | 0  |
| 61 | A0A077Z5M7 | Endoplasmic-reticulum | Other                    | Other          | Intracellular | 4  |
| 62 | A0A077Z0V2 | Cytoplasm             | Other                    | Other          | UPS           | 0  |
| 63 | A0A077Z9E8 | Cytoplasm             | Other                    | Other          | Intracellular | 0  |
| 64 | A0A077YWG4 | Cytoplasm             | Other                    | Other          | UPS           | 0  |
| 65 | A0A077Z2N2 | Cytoplasm             | Other                    | Other          | Intracellular | 0  |
| 66 | A0A077Z283 | Cytoplasm             | Other                    | Other          | UPS           | 0  |
| 67 | A0A077ZJM4 | Cytoplasm             | Other                    | Other          | Intracellular | 0  |
| 68 | A0A077Z3P2 | Cytoplasm             | Other                    | Other          | UPS           | 0  |
| 69 | A0A077YZN2 | Cytoplasm             | Other                    | Other          | Intracellular | 2  |
| 70 | A0A077ZFN2 | Cytoplasm             | Other                    | Other          | UPS           | 0  |
| 71 | A0A077ZG20 | Cytoplasm             | Other                    | Other          | UPS           | 0  |
| 72 | A0A077ZJE2 | Cytoplasm             | Other                    | Other          | UPS           | 0  |
| 73 | A0A077ZMR3 | Endoplasmic-reticulum | Other                    | Other          | Intracellular | 1  |
| 74 | A0A077ZCU6 | Cytoplasm             | Other                    | Other          | Intracellular | 0  |
| 75 | A0A077Z8R0 | Cytoplasm             | Other                    | Other          | Intracellular | 0  |
| 76 | A0A077ZKX1 | Cytoplasm             | Other                    | Other          | Intracellular | 0  |
| 77 | A0A077Z4E6 | Cytoplasm             | Other                    | Other          | Intracellular | 0  |
| 78 | A0A077ZBQ5 | Cytoplasm             | Other                    | Other          | Intracellular | 0  |
| 79 | A0A077Z308 | Cytoplasm             | Other                    | Other          | Intracellular | 0  |

|     |            |                       |                          |                |               |   |
|-----|------------|-----------------------|--------------------------|----------------|---------------|---|
| 80  | A0A077Z0R5 | Cytoplasm             | Other                    | Other          | UPS           | 0 |
| 81  | A0A077ZEV8 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |
| 82  | A0A077ZG23 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |
| 83  | A0A077YZX7 | Cytoplasm             | Other                    | Other          | UPS           | 0 |
| 84  | A0A077Z3W1 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |
| 85  | A0A077Z8U4 | Cytoplasm             | Other                    | Other          | UPS           | 0 |
| 86  | A0A077ZIB4 | Cell-Membrane         | Other                    | Other          | UPS           | 1 |
| 87  | A0A077Z5V1 | Cytoplasm             | Other                    | Other          | UPS           | 0 |
| 88  | A0A077ZDG8 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |
| 89  | A0A077ZIC1 | Cytoplasm             | Other                    | Other          | UPS           | 0 |
| 90  | A0A077ZJA6 | Cytoplasm             | Signal peptide (Sec/SPI) | Signal peptide | Intracellular | 0 |
| 91  | A0A077ZH69 | Mitochondria          | Signal peptide (Sec/SPI) | Signal peptide | Intracellular | 0 |
| 92  | A0A077YZA9 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |
| 93  | A0A077Z942 | Cytoplasm             | Other                    | Other          | UPS           | 0 |
| 94  | A0A077Z372 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |
| 95  | A0A077ZNV5 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |
| 96  | A0A077ZL96 | Cytoplasm             | Other                    | Other          | UPS           | 0 |
| 97  | A0A077ZG39 | Endoplasmic-reticulum | Other                    | Signal Peptide | UPS           | 5 |
| 98  | A0A077Z8C2 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |
| 99  | A0A077Z1H9 | Cell-Membrane         | Other                    | Signal peptide | Intracellular | 0 |
| 100 | A0A077ZL46 | Cytoplasm             | Other                    | Other          | UPS           | 0 |
| 101 | A0A077YZQ2 | Cytoplasm             | Other                    | Other          | UPS           | 0 |
| 102 | A0A077ZIF8 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |
| 103 | A0A077Z761 | Cytoplasm             | Other                    | Other          | UPS           | 0 |
| 104 | A0A077ZCP7 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |
| 105 | A0A077Z737 | Cytoplasm             | Other                    | Other          | UPS           | 0 |
| 106 | A0A077ZJV4 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |
| 107 | A0A077Z9S3 | Endoplasmic-reticulum | Other                    | Other          | UPS           | 4 |
| 108 | A0A077ZQ26 | Cytoplasm             | Other                    | Other          | UPS           | 0 |
| 109 | A0A077ZC20 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |
| 110 | A0A077ZDX1 | Endoplasmic-Reticulum | Other                    | Other          | Intracellular | 3 |
| 111 | A0A077ZEA8 | Cytoplasm             | Other                    | Signal peptide | UPS           | 0 |
| 112 | A0A077ZEI8 | Cell-Membrane         | Signal peptide (Sec/SPI) | Signal peptide | UPS           | 1 |
| 113 | A0A077ZHK7 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |
| 114 | A0A077Z559 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |
| 115 | A0A077YXV9 | Cytoplasm             | Other                    | Other          | UPS           | 0 |
| 116 | A0A077ZMC2 | Mitochondria          | Other                    | Signal peptide | UPS           | 0 |
| 117 | A0A077ZKM7 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |
| 118 | A0A077ZF56 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |

|     |            |                       |                          |                |               |   |
|-----|------------|-----------------------|--------------------------|----------------|---------------|---|
| 119 | A0A077YXF9 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |
| 120 | A0A077Z586 | Cell-Membrane         | Other                    | Other          | Intracellular | 3 |
| 121 | A0A077Z1R2 | Cytoplasm             | Other                    | Other          | UPS           | 0 |
| 122 | A0A077YWP4 | Extracellular         | Other                    | Other          | UPS           | 0 |
| 123 | A0A077YZ15 | Extracellular         | Signal peptide (Sec/SPI) | Signal peptide | UPS           | 0 |
| 124 | A0A077ZDM0 | Cytoplasm             | Other                    | Other          | UPS           | 0 |
| 125 | A0A077Z934 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |
| 126 | A0A077Z9T8 | Cytoplasm             | Other                    | Other          | UPS           | 0 |
| 127 | A0A077ZJ61 | Nucleus               | Other                    | Other          | UPS           | 0 |
| 128 | A0A077YXS8 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |
| 129 | A0A077YYJ1 | Cytoplasm             | Other                    | Other          | UPS           | 0 |
| 130 | A0A077YZX0 | Endoplasmic-Reticulum | Other                    | Other          | UPS           | 6 |
| 131 | A0A077Z7Y2 | Extracellular         | Other                    | Other          | Intracellular | 0 |
| 132 | A0A077Z5I1 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |
| 133 | A0A077ZKY5 | Cytoplasm             | Other                    | Other          | UPS           | 0 |
| 134 | A0A077ZD23 | Peroxisome            | Other                    | Other          | UPS           | 0 |
| 135 | A0A077Z8N3 | Nucleus               | Other                    | Other          | Intracellular | 0 |
| 136 | A0A077ZJA4 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |
| 137 | A0A077Z0L2 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |
| 138 | A0A077ZBE7 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |
| 139 | A0A077Z0G9 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |
| 140 | A0A077Z4A6 | Cytoplasm             | Other                    | Other          | UPS           | 0 |
| 141 | A0A077ZCB2 | Cytoplasm             | Other                    | Other          | UPS           | 0 |
| 142 | A0A077Z9G1 | Peroxisome            | Other                    | Other          | UPS           | 0 |
| 143 | A0A077Z2Z3 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |
| 144 | A0A077YZU0 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |
| 145 | A0A077Z8D3 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |
| 146 | A0A077ZCG9 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |
| 147 | A0A077Z052 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |
| 148 | A0A077ZKZ1 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |
| 149 | A0A077Z7Q3 | Cytoplasm             | Other                    | Other          | UPS           | 0 |
| 150 | A0A077YXW5 | Cytoplasm             | Other                    | Other          | UPS           | 0 |
| 151 | A0A077ZBU6 | Cytoplasm             | Signal peptide (Sec/SPI) | Signal peptide | UPS           | 0 |
| 152 | A0A077ZM03 | Nucleus               | Other                    | Other          | Intracellular | 0 |
| 153 | A0A077YZS8 | Endoplasmic-Reticulum | Signal peptide (Sec/SPI) | Signal peptide | Intracellular | 3 |
| 154 | A0A077Z562 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |
| 155 | A0A077ZA15 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |
| 156 | A0A077ZH63 | Lysosome              | Other                    | Other          | Intracellular | 0 |
| 157 | A0A077Z9E7 | Cytoplasm             | Other                    | Other          | UPS           | 0 |
| 158 | A0A077Z6K7 | Lysosome              | Other                    | Other          | Intracellular | 0 |
| 159 | A0A077ZCR3 | Cytoplasm             | Other                    | Other          | Intracellular | 0 |

|                                 |            |                       |                          |                                |               |   |
|---------------------------------|------------|-----------------------|--------------------------|--------------------------------|---------------|---|
| 160                             | A0A077Z425 | Endoplasmic-Reticulum | Other                    | Other                          | Intracellular | 4 |
| 161                             | A0A077Z538 | Mitochondria          | Other                    | Mitochondrial transfer peptide | UPS           | 0 |
| 162                             | A0A077Z3S0 | Cytoplasm             | Other                    | Other                          | Intracellular | 1 |
| 163                             | A0A077Z9J9 | Cell-Membrane         | Other                    | Other                          | Intracellular | 1 |
| 164                             | A0A077ZFC8 | Cytoplasm             | Other                    | Other                          | Intracellular | 0 |
| 165                             | A0A077Z4V4 | Cytoplasm             | Other                    | Other                          | Intracellular | 0 |
| 166                             | A0A077ZEH3 | Cytoplasm             | Other                    | Other                          | UPS           | 0 |
| 167                             | A0A077ZEA0 | Endoplasmic-Reticulum | Other                    | Other                          | Intracellular | 6 |
| 168                             | A0A077ZDA4 | Cytoplasm             | Other                    | Other                          | UPS           | 0 |
| 169                             | A0A077ZfZ6 | Extracellular         | Signal peptide (Sec/SPI) | Signal peptide                 | UPS           | 0 |
| 170                             | A0A077Z1M2 | Extracellular         | Other                    | Other                          | Intracellular | 0 |
| 171                             | A0A077Z2W3 | Cytoplasm             | Other                    | Other                          | Intracellular | 0 |
| 172                             | A0A077ZJ29 | Extracellular         | Other                    | Other                          | UPS           | 0 |
| 173                             | A0A077Z4L6 | Cytoplasm             | Other                    | Other                          | Intracellular | 0 |
| 174                             | A0A077ZCQ9 | Cytoplasm             | Other                    | Other                          | UPS           | 0 |
| 175                             | A0A077Z5J2 | Cytoplasm             | Signal peptide (Sec/SPI) | Signal peptide                 | UPS           | 0 |
| 176                             | A0A077ZBJ3 | Cytoplasm             | Other                    | Other                          | Intracellular | 0 |
| 177                             | A0A077ZFU8 | Lysosome              | Other                    | Other                          | Intracellular | 1 |
| 178                             | A0A077Z058 | Cytoplasm             | Other                    | Other                          | Intracellular | 0 |
| 179                             | A0A077Z2A4 | Cytoplasm             | Other                    | Other                          | Intracellular | 0 |
| 180                             | A0A077Z226 | Endoplasmic-Reticulum | Other                    | Other                          | Intracellular | 5 |
| 181                             | A0A077ZBE2 | Nucleus               | Other                    | Other                          | UPS           | 0 |
| 182                             | A0A077YZT4 | Cytoplasm             | Other                    | Other                          | UPS           | 0 |
| <b>Uncharacterized Proteins</b> |            |                       |                          |                                |               |   |
| 183                             | A0A077ZKM0 | Cytoplasm             | Other                    | Other                          | UPS           | 0 |

**Supplementary table 5: Predicted physicochemical properties of the protein phosphatases of *Trichuris trichiura***

| Accession Id | Amino acids | Molecular weight (Da) | Theoretical PI | Extinction coefficient (M <sup>-1</sup> cm <sup>-1</sup> ) | Instability Index |                | Aliphatic Index | Grand average of Hydropathicity (GRAVY) |
|--------------|-------------|-----------------------|----------------|------------------------------------------------------------|-------------------|----------------|-----------------|-----------------------------------------|
|              |             |                       |                |                                                            | Computed          | Classification |                 |                                         |
| A0A077ZB59   | 783         | 86730.20              | 8.60           | 60290                                                      | 58.89             | Unstable       | 70.78           | -0.592                                  |
| A0A077Z0F2   | 286         | 32558.81              | 5.59           | 30160                                                      | 35.68             | Stable         | 87.24           | -0.225                                  |
| A0A077Z4J5   | 299         | 33805.51              | 5.17           | 46005                                                      | 36.75             | Stable         | 83.81           | -0.149                                  |
| A0A077Z1G5   | 430         | 49603.89              | 9.33           | 29505                                                      | 51.05             | Unstable       | 100.44          | -0.176                                  |
| A0A077ZK33   | 1855        | 208021.62             | 6.83           | 325770                                                     | 39.58             | Stable         | 102.94          | 0.005                                   |
| A0A077ZB21   | 300         | 34596.27              | 8.93           | 46005                                                      | 46.06             | Unstable       | 89.97           | -0.192                                  |
| A0A077ZHG7   | 635         | 70234.07              | 7.06           | 74130                                                      | 53.18             | Unstable       | 81.75           | -0.403                                  |
| A0A077ZDG9   | 389         | 44868.73              | 9.50           | 58495                                                      | 45.33             | Unstable       | 74.16           | -0.505                                  |
| A0A077ZH74   | 300         | 34460.93              | 7.67           | 47120                                                      | 43.44             | Unstable       | 61.13           | -0.649                                  |
| A0A077Z6N3   | 372         | 42763.69              | 5.28           | 67520                                                      | 41.10             | Unstable       | 83.87           | -0.284                                  |
| A0A077ZDY3   | 748         | 80682.24              | 5.92           | 55390                                                      | 37.18             | Stable         | 102.49          | 0.065                                   |
| A0A077Z5T3   | 620         | 72003.74              | 8.70           | 97930                                                      | 38.74             | Stable         | 88.90           | -0.261                                  |
| A0A077Z3D1   | 415         | 45373.14              | 4.80           | 30535                                                      | 45.01             | Unstable       | 89.95           | -0.225                                  |
| A0A077Z1E1   | 302         | 34371.32              | 5.50           | 34755                                                      | 32.30             | Stable         | 93.25           | -0.090                                  |
| A0A077ZHX6   | 356         | 40272.54              | 6.27           | 39015                                                      | 32.34             | Stable         | 92.50           | -0.098                                  |
| A0A077ZE66   | 482         | 55120.75              | 6.90           | 79465                                                      | 40.42             | Unstable       | 100.62          | -0.016                                  |
| A0A077YZL7   | 642         | 74216.46              | 8.60           | 115920                                                     | 46.11             | Unstable       | 88.24           | -0.325                                  |
| A0A077Z944   | 257         | 29542.71              | 8.07           | 53330                                                      | 31.03             | Stable         | 75.80           | -0.296                                  |
| A0A077ZJP5   | 248         | 28474.72              | 5.69           | 37150                                                      | 56.25             | Unstable       | 84.48           | -0.020                                  |
| A0A077ZM16   | 462         | 52071.83              | 8.76           | 53955                                                      | 48.63             | Unstable       | 81.84           | -0.201                                  |
| A0A077ZPJ3   | 326         | 35691.62              | 8.77           | 26400                                                      | 52.79             | Unstable       | 86.17           | -0.077                                  |
| A0A077Z9P7   | 293         | 33162.12              | 6.23           | 48400                                                      | 36.81             | Stable         | 81.19           | -0.053                                  |
| A0A077Z2U9   | 338         | 38790.78              | 9.11           | 91370                                                      | 33.75             | Stable         | 115.06          | 0.472                                   |
| A0A077Z9X3   | 111         | 12472.96              | 7.99           | 12490                                                      | 42.46             | Unstable       | 61.44           | -0.467                                  |
| A0A077Z2Z0   | 351         | 40426.85              | 8.75           | 57130                                                      | 58.84             | Unstable       | 89.66           | -0.265                                  |

|                |      |               |      |        |       |          |        |        |
|----------------|------|---------------|------|--------|-------|----------|--------|--------|
| A0A077ZEU<br>7 | 191  | 21515.5<br>0  | 8.35 | 30730  | 59.79 | Unstable | 88.38  | -0.442 |
| A0A077ZFQ<br>2 | 327  | 37098.5<br>9  | 8.24 | 47120  | 49.68 | Unstable | 75.81  | -0.385 |
| A0A077Z2W<br>0 | 233  | 26636.9<br>9  | 6.71 | 17670  | 51.98 | Unstable | 83.69  | -0.266 |
| A0A077Z5N<br>7 | 266  | 29785.3<br>8  | 5.42 | 55390  | 40.25 | Unstable | 79.89  | -0.219 |
| A0A077Z783     | 519  | 59701.4<br>9  | 7.52 | 94030  | 43.03 | Unstable | 99.09  | 0.115  |
| A0A077ZP93     | 141  | 15052.1<br>8  | 4.66 | 7450   | 34.85 | Stable   | 99.65  | -0.060 |
| A0A077Z292     | 316  | 36081.5<br>6  | 7.45 | 29630  | 39.86 | Stable   | 81.46  | -0.250 |
| A0A077ZDE<br>3 | 891  | 100526.<br>65 | 8.53 | 126055 | 38.04 | Stable   | 103.37 | 0.304  |
| A0A077Z725     | 164  | 18818.4<br>9  | 6.58 | 20775  | 51.48 | Unstable | 80.73  | -0.216 |
| A0A077ZCV<br>5 | 240  | 27708.1<br>6  | 8.20 | 60765  | 43.91 | Unstable | 94.54  | 0.159  |
| A0A077YXQ<br>6 | 516  | 58485.0<br>9  | 5.96 | 49780  | 36.76 | Stable   | 85.62  | -0.220 |
| A0A077YZZ<br>0 | 705  | 80497.3<br>4  | 6.14 | 104385 | 36.10 | Stable   | 66.44  | -0.437 |
| A0A077YZ<br>W5 | 250  | 29016.5<br>0  | 6.09 | 19410  | 52.84 | Unstable | 86.48  | -0.311 |
| A0A077ZF71     | 421  | 46326.2<br>5  | 5.91 | 31315  | 37.39 | Stable   | 104.32 | -0.004 |
| A0A077Z2V<br>2 | 979  | 108729.<br>76 | 5.82 | 110460 | 36.81 | Stable   | 94.31  | 0.064  |
| A0A077ZEV<br>3 | 277  | 31509.2<br>5  | 6.22 | 36035  | 36.49 | Stable   | 97.04  | -0.089 |
| A0A077YZL<br>0 | 1186 | 132547.<br>28 | 8.38 | 138155 | 39.05 | Stable   | 103.42 | 0.276  |
| A0A077ZKV<br>6 | 455  | 50045.2<br>8  | 8.35 | 32150  | 61.11 | Unstable | 74.55  | -0.532 |
| A0A077ZCQ<br>0 | 1024 | 115424.<br>02 | 8.29 | 127795 | 36.02 | Stable   | 106.12 | 0.242  |
| A0A077YZB<br>8 | 612  | 70618.5<br>7  | 8.99 | 96105  | 44.92 | Unstable | 88.48  | -0.256 |
| A0A077Z3T8     | 191  | 22433.6<br>4  | 7.08 | 35660  | 43.85 | Unstable | 77.02  | -0.478 |
| A0A077Z6F0     | 432  | 48816.6<br>3  | 6.83 | 49905  | 42.82 | Unstable | 88.52  | -0.159 |
| A0A077ZCU<br>0 | 158  | 18173.9<br>4  | 6.29 | 16055  | 36.36 | Stable   | 100.38 | -0.152 |
| A0A077Z4D<br>3 | 144  | 15558.7<br>2  | 5.82 | 10680  | 16.20 | Stable   | 88.06  | -0.099 |
| A0A077Z4F8     | 241  | 27389.6<br>1  | 8.26 | 40045  | 40.31 | Unstable | 79.67  | -0.146 |
| A0A077YW<br>Y8 | 673  | 77948.4<br>6  | 9.06 | 88905  | 46.35 | Unstable | 81.50  | -0.258 |
| A0A077Z6K<br>1 | 456  | 53032.7<br>4  | 6.15 | 63995  | 52.72 | Unstable | 78.44  | -0.525 |
| A0A077Z3U<br>3 | 333  | 38021.7<br>8  | 6.54 | 42245  | 46.86 | Unstable | 82.31  | -0.341 |
| A0A077ZNC<br>2 | 148  | 16937.3<br>3  | 6.78 | 30160  | 24.24 | Stable   | 87.57  | -0.080 |

|                |      |               |       |        |       |          |        |        |
|----------------|------|---------------|-------|--------|-------|----------|--------|--------|
| A0A077Z172     | 295  | 33702.9<br>8  | 9.02  | 34880  | 59.19 | Unstable | 90.92  | -0.415 |
| A0A077Z210     | 562  | 63328.1<br>7  | 7.03  | 60945  | 45.49 | Unstable | 96.09  | -0.047 |
| A0A077ZGN6     | 957  | 107590.<br>81 | 5.48  | 128060 | 40.63 | Unstable | 98.81  | -0.221 |
| A0A077Z7L5     | 142  | 16123.6<br>3  | 10.16 | 8480   | 48.85 | Unstable | 94.65  | 0.002  |
| A0A077ZG77     | 506  | 55444.3<br>5  | 4.51  | 46255  | 47.25 | Unstable | 73.85  | -0.396 |
| A0A077Z7D8     | 1418 | 161505.<br>91 | 9.10  | 146595 | 40.59 | Unstable | 83.53  | -0.221 |
| A0A077ZD83     | 271  | 31506.7<br>1  | 7.68  | 41620  | 43.25 | Unstable | 107.42 | 0.095  |
| A0A077Z1S5     | 547  | 60583.0<br>6  | 8.92  | 36675  | 50.98 | Unstable | 89.63  | -0.094 |
| A0A077Z5M7     | 264  | 30882.6<br>3  | 9.23  | 59400  | 39.23 | Stable   | 104.47 | 0.387  |
| A0A077Z0V2     | 311  | 35668.2<br>1  | 5.00  | 53455  | 34.65 | Stable   | 77.36  | -0.386 |
| A0A077Z9E8     | 508  | 59599.5<br>0  | 5.53  | 66155  | 52.09 | Unstable | 86.77  | -0.428 |
| A0A077YW<br>G4 | 336  | 38218.3<br>7  | 5.87  | 33265  | 39.45 | Stable   | 100.62 | -0.077 |
| A0A077Z2N2     | 573  | 65906.9<br>9  | 7.50  | 86470  | 44.53 | Unstable | 77.10  | -0.186 |
| A0A077Z283     | 189  | 22309.5<br>9  | 8.85  | 63495  | 38.62 | Stable   | 80.48  | -0.375 |
| A0A077ZJM4     | 300  | 35366.0<br>9  | 8.86  | 41870  | 51.72 | Unstable | 79.90  | -0.309 |
| A0A077Z3P2     | 302  | 34700.4<br>6  | 9.00  | 43485  | 38.50 | Stable   | 91.95  | -0.198 |
| A0A077YZN2     | 887  | 100429.<br>04 | 8.41  | 97400  | 42.78 | Unstable | 84.72  | -0.244 |
| A0A077ZFN2     | 191  | 22266.6<br>4  | 8.81  | 40255  | 42.01 | Unstable | 80.10  | -0.353 |
| A0A077ZG20     | 244  | 27658.2<br>8  | 5.05  | 46410  | 44.41 | Unstable | 87.54  | -0.561 |
| A0A077ZJE2     | 309  | 35406.2<br>0  | 4.91  | 49110  | 40.27 | Unstable | 83.53  | -0.272 |
| A0A077ZMR3     | 138  | 16092.1<br>3  | 7.84  | 21095  | 50.86 | Unstable | 120.65 | 0.259  |
| A0A077ZCU6     | 413  | 46915.0<br>9  | 5.41  | 43025  | 47.37 | Unstable | 81.65  | -0.349 |
| A0A077Z8R0     | 878  | 98238.9<br>2  | 8.49  | 99710  | 35.30 | Stable   | 85.23  | -0.258 |
| A0A077ZKX1     | 522  | 58103.0<br>9  | 7.16  | 40170  | 58.02 | Unstable | 80.69  | -0.370 |
| A0A077Z4E6     | 1128 | 127280.<br>61 | 6.45  | 123340 | 48.44 | Unstable | 86.99  | -0.178 |
| A0A077ZBQ5     | 254  | 28044.1<br>1  | 6.09  | 28795  | 39.52 | Stable   | 82.13  | -0.053 |
| A0A077Z308     | 982  | 110682.<br>67 | 6.11  | 137385 | 52.38 | Unstable | 80.08  | -0.291 |
| A0A077Z0R5     | 232  | 26165.3<br>7  | 8.29  | 16180  | 40.56 | Unstable | 86.16  | -0.267 |
| A0A077ZEV8     | 374  | 42445.9<br>0  | 9.62  | 29505  | 48.06 | Unstable | 82.33  | -0.359 |

|            |     |          |      |       |       |          |        |        |
|------------|-----|----------|------|-------|-------|----------|--------|--------|
| A0A077ZG23 | 356 | 40357.63 | 5.80 | 49765 | 50.61 | Unstable | 79.07  | -0.496 |
| A0A077YZX7 | 310 | 35741.94 | 8.99 | 47035 | 41.48 | Unstable | 73.94  | -0.468 |
| A0A077Z3W1 | 512 | 59148.23 | 8.02 | 55725 | 47.96 | Unstable | 87.97  | -0.391 |
| A0A077Z8U4 | 281 | 32174.90 | 9.08 | 60890 | 40.81 | Unstable | 81.21  | -0.503 |
| A0A077ZIB4 | 430 | 48549.55 | 6.94 | 71445 | 46.42 | Unstable | 89.81  | -0.160 |
| A0A077Z5V1 | 221 | 24664.32 | 5.12 | 25690 | 35.52 | Stable   | 87.38  | 0.018  |
| A0A077ZDG8 | 145 | 16892.48 | 9.13 | 22710 | 72.73 | Unstable | 65.17  | -0.659 |
| A0A077ZIC1 | 286 | 32997.12 | 6.00 | 28225 | 54.64 | Unstable | 68.50  | -0.497 |
| A0A077ZJA6 | 628 | 70732.06 | 5.54 | 52465 | 55.93 | Unstable | 92.56  | -0.098 |
| A0A077ZH69 | 268 | 31166.10 | 9.13 | 42650 | 56.39 | Unstable | 63.36  | -0.644 |
| A0A077YZA9 | 214 | 24435.41 | 9.19 | 21680 | 56.64 | Unstable | 86.07  | -0.342 |
| A0A077Z942 | 270 | 29721.14 | 5.11 | 19495 | 25.59 | Stable   | 99.37  | -0.002 |
| A0A077Z372 | 445 | 50088.87 | 7.86 | 43735 | 43.19 | Unstable | 67.66  | -0.571 |
| A0A077ZNV5 | 174 | 20588.78 | 9.66 | 30035 | 34.32 | Stable   | 79.60  | -0.178 |
| A0A077ZL96 | 231 | 26428.62 | 5.89 | 16095 | 39.37 | Stable   | 90.30  | -0.099 |
| A0A077ZG39 | 261 | 29754.02 | 9.53 | 47120 | 21.84 | Stable   | 111.26 | 0.468  |
| A0A077Z8C2 | 456 | 50063.74 | 4.70 | 47995 | 46.67 | Unstable | 89.34  | -0.112 |
| A0A077Z1H9 | 414 | 47179.05 | 8.32 | 58370 | 44.74 | Unstable | 81.86  | -0.297 |
| A0A077ZL46 | 125 | 13975.10 | 7.67 | 10220 | 35.80 | Stable   | 86.48  | -0.048 |
| A0A077YZQ2 | 348 | 39330.66 | 9.68 | 63745 | 23.94 | Stable   | 85.94  | -0.275 |
| A0A077ZIF8 | 569 | 64715.68 | 5.63 | 59580 | 41.75 | Unstable | 89.49  | -0.173 |
| A0A077Z761 | 332 | 38163.95 | 5.21 | 52995 | 35.93 | Stable   | 90.09  | -0.110 |
| A0A077ZCP7 | 422 | 48762.07 | 4.75 | 45060 | 34.89 | Stable   | 81.82  | -0.295 |
| A0A077Z737 | 308 | 35391.86 | 5.61 | 33850 | 42.09 | Unstable | 88.93  | -0.013 |
| A0A077ZFV4 | 351 | 40570.08 | 5.97 | 67965 | 42.06 | Unstable | 83.56  | -0.418 |
| A0A077Z9S3 | 315 | 35839.87 | 8.60 | 81610 | 24.92 | Stable   | 104.89 | 0.357  |
| A0A077ZQ26 | 212 | 23705.89 | 6.49 | 32680 | 39.80 | Stable   | 87.41  | -0.208 |
| A0A077ZC20 | 416 | 47044.53 | 5.76 | 50225 | 40.68 | Unstable | 85.79  | -0.308 |
| A0A077ZDX1 | 495 | 57105.06 | 4.89 | 62020 | 30.89 | Stable   | 93.54  | -0.278 |

|            |     |           |      |        |       |          |        |        |
|------------|-----|-----------|------|--------|-------|----------|--------|--------|
| A0A077ZEA8 | 375 | 42394.76  | 6.27 | 57715  | 41.44 | Unstable | 89.68  | -0.068 |
| A0A077ZEI8 | 395 | 44399.52  | 6.19 | 54360  | 28.58 | Stable   | 98.68  | 0.129  |
| A0A077ZHK7 | 349 | 39581.80  | 8.75 | 42775  | 48.48 | Unstable | 91.63  | -0.142 |
| A0A077Z559 | 379 | 44195.67  | 5.19 | 57090  | 49.00 | Unstable | 77.12  | -0.439 |
| A0A077YXV9 | 337 | 38757.51  | 9.18 | 71975  | 44.79 | Unstable | 87.63  | -0.374 |
| A0A077ZMC2 | 152 | 16921.36  | 5.53 | 22585  | 24.29 | Stable   | 79.01  | -0.331 |
| A0A077ZKM7 | 497 | 55966.49  | 5.32 | 67755  | 40.89 | Unstable | 92.27  | -0.185 |
| A0A077ZF56 | 695 | 79588.00  | 6.03 | 80300  | 40.24 | Unstable | 92.56  | -0.193 |
| A0A077YXF9 | 420 | 46935.01  | 5.22 | 54025  | 26.53 | Stable   | 88.88  | -0.050 |
| A0A077Z586 | 390 | 44907.24  | 8.84 | 57465  | 39.48 | Stable   | 98.51  | 0.046  |
| A0A077Z1R2 | 276 | 30180.82  | 5.80 | 20315  | 31.22 | Stable   | 102.07 | 0.064  |
| A0A077YWP4 | 377 | 43043.76  | 5.89 | 63300  | 38.13 | Stable   | 78.62  | -0.339 |
| A0A077YZ15 | 353 | 40527.88  | 6.34 | 132935 | 46.38 | Unstable | 81.73  | -0.304 |
| A0A077ZDM0 | 228 | 25896.94  | 6.16 | 13325  | 43.44 | Unstable | 81.18  | -0.240 |
| A0A077Z934 | 191 | 21678.84  | 8.88 | 15150  | 54.26 | Unstable | 100    | -0.042 |
| A0A077Z9T8 | 321 | 37235.87  | 5.33 | 62965  | 50.84 | Unstable | 94.14  | -0.112 |
| A0A077ZJ61 | 338 | 38125.53  | 5.38 | 33180  | 48.63 | Unstable | 93.08  | -0.073 |
| A0A077YXS8 | 499 | 54419.40  | 6.76 | 36370  | 61.73 | Unstable | 82.51  | -0.256 |
| A0A077YYJ1 | 335 | 38387.63  | 8.87 | 37400  | 39.33 | Stable   | 93.58  | -0.071 |
| A0A077YZX0 | 342 | 39090.65  | 8.85 | 54360  | 60.80 | Unstable | 109.44 | 0.234  |
| A0A077Z7Y2 | 416 | 47712.26  | 6.92 | 83475  | 41.88 | Unstable | 73.53  | -0.456 |
| A0A077Z5I1 | 901 | 103992.34 | 8.82 | 97860  | 44.65 | Unstable | 88.07  | -0.351 |
| A0A077ZKY5 | 176 | 19731.61  | 5.03 | 23045  | 38.40 | Stable   | 91.42  | -0.269 |
| A0A077ZD23 | 264 | 30704.92  | 8.41 | 51715  | 35.85 | Stable   | 67.50  | -0.542 |
| A0A077Z8N3 | 366 | 42018.14  | 9.20 | 41745  | 48.50 | Unstable | 72.38  | -0.471 |
| A0A077ZJA4 | 358 | 40507.17  | 8.95 | 51715  | 45.46 | Unstable | 68.10  | -0.544 |
| A0A077Z0L2 | 501 | 57488.56  | 5.60 | 22890  | 44.51 | Unstable | 85.71  | -0.566 |
| A0A077ZBE7 | 365 | 41477.21  | 8.71 | 70900  | 41.59 | Unstable | 88.68  | 0.037  |
| A0A077Z0G9 | 188 | 22207.69  | 9.45 | 29590  | 62.32 | Unstable | 75.74  | -0.597 |

|            |      |           |      |        |       |          |        |        |
|------------|------|-----------|------|--------|-------|----------|--------|--------|
| A0A077Z4A6 | 215  | 24146.37  | 6.10 | 20775  | 34.08 | Stable   | 84.79  | -0.424 |
| A0A077ZCB2 | 200  | 22201.15  | 4.98 | 29575  | 31.54 | Stable   | 95.15  | -0.153 |
| A0A077Z9G1 | 276  | 31672.65  | 9.10 | 51255  | 35.27 | Stable   | 76.30  | -0.378 |
| A0A077Z2Z3 | 676  | 77839.51  | 8.36 | 92095  | 55.28 | Unstable | 77.25  | -0.434 |
| A0A077YZU0 | 654  | 71803.36  | 8.65 | 54525  | 54.03 | Unstable | 69.59  | -0.374 |
| A0A077Z8D3 | 1257 | 141933.58 | 5.51 | 151385 | 48.34 | Unstable | 82.15  | -0.344 |
| A0A077ZCG9 | 555  | 62749.75  | 5.36 | 61935  | 36.86 | Stable   | 89.93  | -0.187 |
| A0A077Z052 | 662  | 76267.87  | 5.38 | 55655  | 42.29 | Unstable | 96.42  | -0.086 |
| A0A077ZKZ1 | 246  | 27150.87  | 5.46 | 45170  | 30.67 | Stable   | 85.65  | -0.222 |
| A0A077Z7Q3 | 285  | 32832.26  | 9.16 | 46785  | 40.25 | Unstable | 94.70  | -0.236 |
| A0A077YXW5 | 303  | 34784.39  | 9.28 | 58370  | 47.56 | Unstable | 83.27  | -0.374 |
| A0A077ZBU6 | 261  | 28322.13  | 4.67 | 21805  | 38.54 | Stable   | 91.11  | 0.003  |
| A0A077ZM03 | 597  | 68107.90  | 8.76 | 76500  | 46.24 | Unstable | 73.12  | -0.682 |
| A0A077YZS8 | 779  | 87558.09  | 7.46 | 102650 | 38.59 | Stable   | 97.88  | -0.003 |
| A0A077Z562 | 341  | 38112.45  | 9.06 | 25035  | 64.21 | Unstable | 79.15  | -0.294 |
| A0A077ZA15 | 406  | 45839.22  | 5.66 | 41090  | 60.94 | Unstable | 103.99 | 0.137  |
| A0A077ZH63 | 850  | 96812.92  | 8.61 | 117005 | 45.97 | Unstable | 86.47  | -0.227 |
| A0A077Z9E7 | 193  | 22003.33  | 7.59 | 30285  | 37.68 | Stable   | 76.22  | -0.298 |
| A0A077Z6K7 | 679  | 77244.02  | 6.66 | 121625 | 43.08 | Unstable | 81.84  | -0.276 |
| A0A077ZCR3 | 891  | 102003.39 | 6.92 | 129050 | 41.34 | Unstable | 107.09 | 0.076  |
| A0A077Z425 | 436  | 50376.96  | 6.20 | 88725  | 45.05 | Unstable | 95.69  | 0.107  |
| A0A077Z538 | 196  | 22438.96  | 8.46 | 12045  | 47.16 | Unstable | 86.58  | -0.177 |
| A0A077Z3S0 | 2159 | 243169.38 | 7.08 | 329060 | 42.05 | Unstable | 82.83  | -0.349 |
| A0A077Z9J9 | 751  | 85595.15  | 5.29 | 117285 | 53.30 | Unstable | 77.10  | -0.517 |
| A0A077ZFC8 | 326  | 38002.97  | 9.26 | 59735  | 48.57 | Unstable | 79.20  | -0.406 |
| A0A077Z4V4 | 317  | 34387.42  | 6.11 | 37275  | 22.28 | Stable   | 93.53  | -0.188 |
| A0A077ZEH3 | 300  | 34058.76  | 7.53 | 48525  | 43.13 | Unstable | 93.63  | -0.103 |
| A0A077ZEA0 | 395  | 45888.12  | 8.96 | 77405  | 54.16 | Unstable | 81.92  | 0.091  |
| A0A077ZDA4 | 243  | 28267.97  | 4.95 | 33920  | 49.23 | Unstable | 91.81  | -0.440 |

|                                 |     |           |      |        |       |          |        |        |
|---------------------------------|-----|-----------|------|--------|-------|----------|--------|--------|
| A0A077ZFZ6                      | 247 | 27160.18  | 5.82 | 26360  | 16.62 | Stable   | 94.33  | -0.1   |
| A0A077Z1M2                      | 350 | 40128.28  | 9.45 | 56185  | 35.88 | Stable   | 81.66  | -0.307 |
| A0A077Z2W3                      | 560 | 62909.10  | 6.30 | 53705  | 51.10 | Unstable | 78.21  | -0.247 |
| A0A077ZJ29                      | 243 | 27535.69  | 6.90 | 29255  | 34.09 | Stable   | 88.23  | -0.227 |
| A0A077Z4L6                      | 292 | 32966.80  | 9.64 | 22265  | 53.36 | Unstable | 88.36  | -0.304 |
| A0A077ZCQ9                      | 263 | 29505.66  | 7.75 | 22265  | 32.65 | Stable   | 86.31  | -0.283 |
| A0A077Z5J2                      | 297 | 33642.05  | 8.37 | 49430  | 37.90 | Stable   | 88.32  | -0.134 |
| A0A077ZBJ3                      | 424 | 47275.36  | 5.36 | 40545  | 51.77 | Unstable | 86.98  | -0.258 |
| A0A077ZFU8                      | 713 | 82517.68  | 5.80 | 123160 | 37.45 | Stable   | 81.26  | -0.329 |
| A0A077Z058                      | 922 | 102377.91 | 6.76 | 128155 | 37.76 | Stable   | 88.89  | -0.061 |
| A0A077Z2A4                      | 425 | 47424.34  | 5.45 | 38110  | 39.70 | Stable   | 70.73  | -0.471 |
| A0A077Z226                      | 267 | 30609.54  | 8.97 | 51255  | 33.11 | Stable   | 105.24 | 0.270  |
| A0A077ZBE2                      | 264 | 29629.72  | 4.64 | 18910  | 34.82 | Stable   | 93.48  | -0.208 |
| A0A077YZT4                      | 262 | 29857.33  | 6.49 | 28920  | 45.22 | Unstable | 88.47  | -0.094 |
| <b>Uncharacterized Proteins</b> |     |           |      |        |       |          |        |        |
| A0A077ZKM0                      | 147 | 16766.41  | 8.54 | 45950  | 31.50 | Stable   | 92.38  | -0.355 |

**Supplementary table 6: Identification of druggable targets among the non-homologous protein phosphatases of *Trichuris trichiura***

| S. No.                  | Accession Id | Presence in Drug Bank | Druggability analysis |
|-------------------------|--------------|-----------------------|-----------------------|
| 1.                      | A0A077Z2U9   | No                    | Novel target          |
| 2.                      | A0A077ZEU7   | Yes                   | Druggable             |
| 3.                      | A0A077Z292   | Yes                   | Druggable             |
| 4.                      | A0A077ZCV5   | Yes                   | Druggable             |
| 5.                      | A0A077YXQ6   | Yes                   | Druggable             |
| 6.                      | A0A077ZF71   | Yes                   | Druggable             |
| 7.                      | A0A077Z2V2   | Yes                   | Druggable             |
| 8.                      | A0A077YWY8   | No                    | Novel target          |
| 9.                      | A0A077Z6K1   | Yes                   | Druggable             |
| 10.                     | A0A077Z7D8   | No                    | Novel target          |
| 11.                     | A0A077Z1S5   | Yes                   | Druggable             |
| 12.                     | A0A077Z5M7   | No                    | Novel target          |
| 13.                     | A0A077Z0V2   | Yes                   | Druggable             |
| 14.                     | A0A077Z9E8   | Yes                   | Druggable             |
| 15.                     | A0A077YZN2   | Yes                   | Druggable             |
| 16.                     | A0A077ZJE2   | Yes                   | Druggable             |
| 17.                     | A0A077Z4E6   | Yes                   | Druggable             |
| 18.                     | A0A077Z3W1   | Yes                   | Druggable             |
| 19.                     | A0A077Z5V1   | Yes                   | Druggable             |
| 20.                     | A0A077Z942   | Yes                   | Druggable             |
| 21.                     | A0A077ZMC2   | No                    | Novel target          |
| 22.                     | A0A077ZKM7   | Yes                   | Druggable             |
| 23.                     | A0A077YXF9   | No                    | Novel target          |
| 24.                     | A0A077YZ15   | No                    | Novel target          |
| 25.                     | A0A077ZJ61   | No                    | Novel target          |
| 26.                     | A0A077Z8D3   | Yes                   | Druggable             |
| 27.                     | A0A077YZS8   | Yes                   | Druggable             |
| 28.                     | A0A077Z562   | No                    | Novel target          |
| 29.                     | A0A077ZEH3   | No                    | Novel target          |
| 30.                     | A0A077ZFY6   | Yes                   | Druggable             |
| 31.                     | A0A077ZCQ9   | Yes                   | Druggable             |
| 32.                     | A0A077ZBE2   | Yes                   | Druggable             |
| Uncharacterized Protein |              |                       |                       |
| 33.                     | A0A077ZKM0   | No                    | Novel Target          |