

Table S5. List of PFAM domains identified in predicted *V. nonalfalfa* secretome

| PFAM description | PFAM ID | Number of hits |
|--|---------|----------------|
| EFFECTOR-SPECIFIC PFAM | | 66 |
| Calcineurin-like phosphoesterase | PF00149 | 6 |
| Cerato-platanin | PF07249 | 2 |
| CFEM (Common in Fungal Extracellular Membranes) domain | PF05730 | 13 |
| Chitin recognition protein | PF00187 | 1 |
| Chitin recognition protein | PF03067 | 3 |
| CVNH (Cyanovirin-N) domain | PF08881 | 2 |
| Cysteine-rich secretory protein family | PF00188 | 4 |
| Fungal hydrophobin | PF06766 | 4 |
| LysM domain | PF01476 | 9 |
| Lytic transglycolase | PF03330 | 3 |
| Necrosis inducing protein (NPP1) | PF05630 | 6 |
| PAN domain | PF00024 | 1 |
| Hce2 (Homologs of <i>C. fulvum</i> Ecp2 effector) | PF14856 | 5 |
| Ricin-type beta-trefoil lectin domain | PF00652 | 2 |
| Ser-Thr-rich glycosyl-phosphatidyl-inositol-anchored membrane family | PF10342 | 4 |
| Thaumatin family | PF00314 | 1 |
| NO PFAM DOMAIN | | 299 |
| OTHER PFAM DOMAINS | | 3132 |
| [2Fe-2S] binding domain | PF01799 | 1 |
| 14-3-3 protein | PF00244 | 1 |
| 16S rRNA methyltransferase RsmB/F | PF01189 | 1 |
| 2Fe-2S iron-sulfur cluster binding domain | PF13085 | 2 |
| 2Fe-2S iron-sulfur cluster binding domain | PF00111 | 2 |
| 2Fe-2S iron-sulfur cluster binding domain | PF13510 | 1 |
| 2OG-Fe(II) oxygenase superfamily | PF13640 | 1 |
| 2OG-Fe(II) oxygenase superfamily | PF13661 | 1 |
| 2OG-Fe(II) oxygenase superfamily | PF03171 | 4 |
| 2OG-Fe(II) oxygenase superfamily | PF13532 | 2 |
| 2-oxoacid dehydrogenases acyltransferase (catalytic domain) | PF00198 | 1 |

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| 3' exoribonuclease family, domain 1 | PF01138 | 2 |
| 39S mitochondrial ribosomal protein L46 | PF11788 | 1 |
| 3-beta hydroxysteroid dehydrogenase/isomerase family | PF01073 | 5 |
| 3-Oxoacyl-[acyl-carrier-protein (ACP)] synthase III C terminal | PF08541 | 1 |
| 4F5 protein family | PF04419 | 2 |
| 4Fe-4S dicluster domain | PF13534 | 2 |
| 4Fe-4S dicluster domain | PF13183 | 2 |
| 4Fe-4S iron sulfur cluster binding proteins, NifH/frxC family | PF00142 | 1 |
| 50S ribosome-binding GTPase | PF01926 | 4 |
| 56kDa selenium binding protein (SBP56) | PF05694 | 1 |
| 6,7-dimethyl-8-ribityllumazine synthase | PF00885 | 1 |
| 60s Acidic ribosomal protein | PF00428 | 1 |
| 60S ribosome biogenesis protein Rrp14 | PF15459 | 1 |
| 6-phosphofructo-2-kinase | PF01591 | 1 |
| 8-oxoguanine DNA glycosylase, N-terminal domain | PF07934 | 1 |
| AAA ATPase domain | PF13191 | 6 |
| AAA domain | PF13671 | 4 |
| AAA domain | PF13207 | 7 |
| AAA domain | PF13238 | 4 |
| AAA domain | PF13481 | 4 |
| AAA domain | PF13087 | 2 |
| AAA domain | PF13086 | 2 |
| AAA domain | PF13614 | 1 |
| AAA domain | PF13401 | 6 |
| AAA domain | PF13476 | 2 |
| AAA domain | PF13604 | 1 |
| AAA domain (Cdc48 subfamily) | PF07724 | 2 |
| AAA domain (dynein-related subfamily) | PF07728 | 3 |
| AAA domain, putative AbiEii toxin, Type IV TA system | PF13304 | 5 |
| AAA-ATPase Vps4-associated protein 1 | PF08432 | 1 |
| ABC transporter | PF00005 | 8 |
| ABC transporter transmembrane region | PF00664 | 3 |
| ABC transporter transmembrane region 2 | PF06472 | 1 |

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| ABC-2 family transporter protein | PF12698 | 3 |
| ABC-2 type transporter | PF01061 | 3 |
| ABC-transporter extracellular N-terminal | PF14510 | 2 |
| Acetokinase family | PF00871 | 1 |
| Acetyltransferase (GNAT) domain | PF13508 | 3 |
| Acetyltransferase (GNAT) domain | PF13673 | 1 |
| Acetyltransferase (GNAT) domain | PF13420 | 1 |
| Acetyltransferase (GNAT) domain | PF13302 | 1 |
| Acetyltransferase (GNAT) family | PF00583 | 3 |
| Aconitase C-terminal domain | PF00694 | 1 |
| Aconitase family (aconitate hydratase) | PF00330 | 1 |
| Actin | PF00022 | 1 |
| Acyl CoA binding protein | PF00887 | 1 |
| Acyl transferase domain | PF00698 | 3 |
| Acyl-CoA dehydrogenase, C-terminal domain | PF00441 | 1 |
| Acyl-CoA dehydrogenase, C-terminal domain | PF08028 | 1 |
| Acyl-CoA dehydrogenase, middle domain | PF02770 | 1 |
| Acyl-CoA dehydrogenase, N-terminal domain | PF02771 | 1 |
| Acyl-CoA reductase (LuxC) | PF05893 | 1 |
| Acylphosphatase | PF00708 | 1 |
| Acyltransferase | PF01553 | 2 |
| Adaptin N terminal region | PF01602 | 2 |
| Adaptor complexes medium subunit family | PF00928 | 1 |
| Adenylate cyclase associated (CAP) C terminal | PF08603 | 1 |
| Adenylate kinase | PF00406 | 2 |
| Adenylate kinase, active site lid | PF05191 | 2 |
| Adenylosuccinate lyase C-terminus | PF10397 | 1 |
| ADP-ribosylation factor family | PF00025 | 3 |
| AFG1-like ATPase | PF03969 | 1 |
| AhpC/TSA family | PF00578 | 2 |
| AICARFT/IMPCHase bienzyme | PF01808 | 1 |
| AIR carboxylase | PF00731 | 2 |
| AKAP7 2'5' RNA ligase-like domain | PF10469 | 1 |

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| Alanine racemase, N-terminal domain | PF01168 | 2 |
| Alcohol acetyltransferase | PF07247 | 1 |
| Alcohol dehydrogenase GroES-like domain | PF08240 | 5 |
| Aldehyde dehydrogenase family | PF00171 | 5 |
| Aldehyde oxidase and xanthine dehydrogenase, a/b hammerhead domain | PF01315 | 1 |
| Aldo/keto reductase family | PF00248 | 6 |
| Aldose 1-epimerase | PF01263 | 2 |
| ALG6, ALG8 glycosyltransferase family | PF03155 | 1 |
| Alginate lyase | PF05426 | 2 |
| Alkaline phosphatase | PF00245 | 3 |
| Allophanate hydrolase subunit 1 | PF02682 | 1 |
| Allophanate hydrolase subunit 2 | PF02626 | 1 |
| Alpha amylase, catalytic domain | PF00128 | 2 |
| Alpha and gamma adaptin binding protein p34 | PF10199 | 1 |
| Alpha/beta hydrolase family | PF12697 | 24 |
| Alpha/beta hydrolase family | PF12695 | 23 |
| alpha/beta hydrolase fold | PF07859 | 16 |
| alpha/beta hydrolase fold | PF00561 | 7 |
| Alpha-L-arabinofuranosidase B (ABFB) domain | PF05270 | 2 |
| Alpha-L-arabinofuranosidase B, catalytic | PF09206 | 1 |
| Alpha-L-arabinofuranosidase C-terminal domain | PF06964 | 1 |
| Alpha-L-rhamnosidase N-terminal domain | PF08531 | 2 |
| Alternative oxidase | PF01786 | 1 |
| Amidase | PF01425 | 4 |
| Amidohydro_5 - Amidohydrolase | PF13594 | 5 |
| Amidohydrolase family | PF01979 | 5 |
| Amidohydrolase family | PF07969 | 4 |
| Amidohydrolase family | PF07908 | 1 |
| Amidohydrolase family | PF13147 | 4 |
| Amino acid kinase family | PF00696 | 1 |
| Amino acid permease | PF00324 | 8 |
| Amino acid permease | PF13520 | 8 |
| Aminotransferase class I and II | PF00155 | 1 |

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| Aminotransferase class-III | PF00202 | 1 |
| Aminotransferase class-V | PF00266 | 1 |
| AMP-binding enzyme | PF00501 | 9 |
| AMP-binding enzyme C-terminal domain | PF13193 | 5 |
| Amylo-alpha-1,6-glucosidase | PF06202 | 0 |
| Anaphase promoting complex (APC) subunit 2 | PF08672 | 1 |
| Anaphase-promoting complex APC subunit CDC26 | PF10471 | 1 |
| Ankyrin repeat | PF00023 | 9 |
| Ankyrin repeat | PF13606 | 9 |
| Ankyrin repeats (3 copies) | PF12796 | 9 |
| Ankyrin repeats (many copies) | PF13637 | 10 |
| Ankyrin repeats (many copies) | PF13857 | 8 |
| Annexin | PF00191 | 1 |
| Anp1 | PF03452 | 1 |
| Apoptosis antagonizing transcription factor | PF13339 | 1 |
| Apoptosis-antagonizing transcription factor, C-terminal | PF08164 | 1 |
| AraC-like ligand binding domain | PF02311 | 1 |
| ARD/ARD' family | PF03079 | 1 |
| Arginase family | PF00491 | 2 |
| ARID/BRIGHT DNA binding domain | PF01388 | 1 |
| Armadillo/beta-catenin-like repeat | PF00514 | 1 |
| ARP2/3 complex ARPC3 (21 kDa) subunit | PF04062 | 1 |
| Arp2/3 complex, 34 kD subunit p34-Arc | PF04045 | 1 |
| ARS binding protein 2 | PF09441 | 2 |
| Arylsulfotransferase (ASST) | PF14269 | 2 |
| Arylsulfotransferase (ASST) | PF05935 | 2 |
| Asparaginase | PF01112 | 1 |
| Aspartyl protease | PF13650 | 3 |
| AT hook motif | PF02178 | 1 |
| Ataxin-2 C-terminal region | PF07145 | 1 |
| ATP synthase complex subunit h | PF10775 | 1 |
| ATP synthase subunit C | PF00137 | 1 |
| ATP synthase subunit D | PF01813 | 1 |

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| ATP10 protein | PF05176 | 1 |
| ATPase domain predominantly from Archaea | PF01637 | 3 |
| ATPase family associated with various cellular activities (AAA) | PF00004 | 7 |
| ATPase MipZ | PF09140 | 1 |
| ATP-dependent Clp protease adaptor protein ClpS | PF02617 | 1 |
| ATP-dependent protease La (LON) substrate-binding domain | PF02190 | 1 |
| ATP-grasp domain | PF02222 | 3 |
| ATP-grasp domain | PF13535 | 4 |
| Autophagocytosis associated protein, active-site domain | PF03987 | 1 |
| Autophagy protein Apg6 | PF04111 | 1 |
| Autophagy protein Atg8 ubiquitin like | PF02991 | 1 |
| Autophagy-related protein 11 | PF10377 | 1 |
| Autophagy-related protein 13 | PF10033 | 1 |
| Autophagy-related protein 27 | PF09451 | 1 |
| Autophagy-related protein C terminal domain | PF09333 | 1 |
| Bacterial alpha-L-rhamnosidase | PF05592 | 5 |
| Bacterial low temperature requirement A protein (LtrA) | PF06772 | 1 |
| Bacterial transferase hexapeptide (six repeats) | PF00132 | 1 |
| BAH domain | PF01426 | 1 |
| Barwin family | PF00967 | 2 |
| Basic region leucine zipper | PF07716 | 1 |
| B-cell receptor-associated protein 31-like | PF05529 | 2 |
| Berberine and berberine like | PF08031 | 10 |
| Beta/Gamma crystallin | PF00030 | 1 |
| beta-acetyl hexosaminidase like | PF14845 | 1 |
| Beta-Casp domain | PF10996 | 1 |
| Beta-eliminating lyase | PF01212 | 1 |
| Beta-galactosidase jelly roll domain | PF13364 | 2 |
| Beta-galactosidase, domain 2 | PF10435 | 2 |
| Beta-galactosidase, domain 3 | PF13363 | 2 |
| Beta-glucan synthesis-associated protein (SKN1) | PF03935 | 2 |
| Beta-glucosidase (SUN family) | PF03856 | 3 |
| Beta-ketoacyl synthase, C-terminal domain | PF02801 | 2 |

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| Beta-ketoacyl synthase, N-terminal domain | PF00109 | 3 |
| Beta-lactamase | PF00144 | 2 |
| Beta-lactamase superfamily domain | PF12706 | 2 |
| Beta-lactamase superfamily domain | PF13483 | 1 |
| Biotin carboxylase C-terminal domain | PF02785 | 1 |
| Biotin carboxylase, N-terminal domain | PF00289 | 1 |
| Biotin/lipoate A/B protein ligase family | PF03099 | 1 |
| Biotin-lipoyl like | PF13533 | 1 |
| Biotin-requiring enzyme | PF00364 | 2 |
| Blastomyces yeast-phase-specific protein | PF04681 | 1 |
| Blt1 N-terminal domain | PF12754 | 1 |
| BNR repeat-like domain | PF13088 | 2 |
| BNR/Asp-box repeat | PF02012 | 2 |
| BRCA1 C Terminus (BRCT) domain | PF00533 | 2 |
| Brix domain | PF04427 | 1 |
| BRO1-like domain | PF03097 | 1 |
| Bromodomain | PF00439 | 1 |
| Bromodomain associated | PF07524 | 1 |
| BTB/POZ domain | PF00651 | 2 |
| BUD22 | PF09073 | 1 |
| bZIP Maf transcription factor | PF03131 | 1 |
| bZIP transcription factor | PF00170 | 1 |
| C2 domain | PF00168 | 1 |
| C2 domain in Dock180 and Zizimin proteins | PF14429 | 1 |
| C2H2-type zinc finger | PF13894 | 4 |
| CAAX protease self-immunity | PF02517 | 1 |
| CAF1 family ribonuclease | PF04857 | 1 |
| Calcineurin-like phosphoesterase | PF00149 | 6 |
| Calpain family cysteine protease | PF00648 | 1 |
| Calponin homology (CH) domain | PF00307 | 2 |
| Calreticulin family | PF00262 | 1 |
| Calsequestrin | PF01216 | 1 |
| Candida agglutinin-like (ALS) | PF05792 | 1 |

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| Carbamoyl-phosphate synthase L chain, ATP binding domain | PF02786 | 2 |
| Carbohydrate binding domain X2 | PF03442 | 1 |
| Carbon-nitrogen hydrolase | PF00795 | 2 |
| Carboxylesterase family | PF00135 | 20 |
| Carboxypeptidase regulatory-like domain | PF13620 | 1 |
| CAS/CSE protein, C-terminus | PF03378 | 1 |
| Casein kinase II regulatory subunit | PF01214 | 1 |
| Caspase domain | PF00656 | 1 |
| Catalase | PF00199 | 4 |
| Catalase-related immune-responsive | PF06628 | 4 |
| Cation efflux family | PF01545 | 1 |
| Cation transport ATPase (P-type) | PF13246 | 4 |
| Cation transporter/ATPase, N-terminus | PF00690 | 2 |
| Cation transporting ATPase, C-terminus | PF00689 | 2 |
| CBS domain | PF00571 | 1 |
| CCAAT-binding transcription factor (CBF-B/NF-YA) subunit B | PF02045 | 1 |
| CDC24 Calponin | PF06395 | 1 |
| Cdc37 C terminal domain | PF08564 | 1 |
| Cdc37 Hsp90 binding domain | PF08565 | 1 |
| Cdc37 N terminal kinase binding | PF03234 | 1 |
| CDP-alcohol phosphatidyltransferase | PF01066 | 1 |
| CDR ABC transporter | PF06422 | 3 |
| Cell division protein anillin | PF08174 | 1 |
| Cellulase (glycosyl hydrolase family 5) | PF00150 | 14 |
| Centromere protein H (CENP-H) | PF05837 | 1 |
| Centromere protein Scm3 | PF10384 | 1 |
| Centrosome localisation domain of PPC89 | PF14197 | 1 |
| Centrosome microtubule-binding domain of Cep57 | PF06657 | 1 |
| Centrosomin N-terminal motif 1 | PF07989 | 1 |
| CFEM domain | PF05730 | 13 |
| ChaC-like protein | PF04752 | 1 |
| Chalcone and stilbene synthases, C-terminal domain | PF02797 | 1 |
| Chalcone and stilbene synthases, N-terminal domain | PF00195 | 1 |

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| CHD5-like protein | PF04420 | 2 |
| Chitin recognition protein | PF00187 | 1 |
| Chitin synthase | PF03142 | 2 |
| Chitin synthase | PF01644 | 1 |
| Chitin synthase N-terminal | PF08407 | 1 |
| Chloramphenicol phosphotransferase-like protein | PF07931 | 1 |
| Chlorophyllase enzyme | PF12740 | 1 |
| Choline/ethanolamine kinase | PF01633 | 1 |
| Chondroitinase B | PF14592 | 3 |
| CHORD | PF04968 | 1 |
| Chorismate synthase | PF01264 | 1 |
| Chromatin associated protein KTI12 | PF08433 | 1 |
| Chromatin modification-related protein EAF7 | PF07904 | 1 |
| Cid1 family poly A polymerase | PF03828 | 1 |
| CLASP N terminal | PF12348 | 1 |
| Clr5 domain | PF14420 | 1 |
| Clustered mitochondria | PF13236 | 1 |
| CO dehydrogenase flavoprotein C-terminal domain | PF03450 | 1 |
| CoA binding domain | PF13380 | 1 |
| CoA-transferase family III | PF02515 | 1 |
| CobQ/CobB/MinD/ParA nucleotide binding domain | PF01656 | 2 |
| CobW/HypB/UreG, nucleotide-binding domain | PF02492 | 2 |
| Coenzyme A transferase | PF01144 | 2 |
| Cofilin/tropomyosin-type actin-binding protein | PF00241 | 1 |
| Common central domain of tyrosinase | PF00264 | 5 |
| Complex 1 protein (LYR family) | PF05347 | 2 |
| Complex1_LYR-like | PF13232 | 2 |
| Condensation domain | PF00668 | 3 |
| Conserved hypothetical ATP binding protein | PF03029 | 1 |
| Copper amine oxidase, enzyme domain | PF01179 | 2 |
| Copper amine oxidase, N2 domain | PF02727 | 2 |
| Copper amine oxidase, N3 domain | PF02728 | 2 |
| Coproporphyrinogen III oxidase | PF01218 | 1 |

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| CorA-like Mg ²⁺ transporter protein | PF01544 | 3 |
| Core histone H2A/H2B/H3/H4 | PF00125 | 2 |
| Cortical protein marker for cell polarity | PF12768 | 1 |
| CPL (NUC119) domain | PF08144 | 1 |
| CPSF A subunit region | PF03178 | 1 |
| CRAL/TRIO domain | PF00650 | 1 |
| Creatinase/Prolidase N-terminal domain | PF01321 | 1 |
| CrtC N-terminal lipocalin domain | PF07143 | 1 |
| CS domain | PF04969 | 2 |
| C-terminal, D2-small domain, of ClpB protein | PF10431 | 1 |
| Ctf8 | PF09696 | 2 |
| CTLH/CRA C-terminal to LisH motif domain | PF10607 | 1 |
| CTP synthase N-terminus | PF06418 | 2 |
| Ctr copper transporter family | PF04145 | 1 |
| CUE domain | PF02845 | 1 |
| Cupin | PF00190 | 4 |
| Cupin domain | PF07883 | 4 |
| Cutinase | PF01083 | 14 |
| Cyclic nucleotide-binding domain | PF00027 | 1 |
| Cyclin, C-terminal domain | PF02984 | 1 |
| Cyclin, N-terminal domain | PF00134 | 4 |
| Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD | PF00160 | 2 |
| Cys/Met metabolism PLP-dependent enzyme | PF01053 | 1 |
| Cytidyltransferase-like | PF01467 | 1 |
| Cytochrome b5-like Heme/Steroid binding domain | PF00173 | 3 |
| Cytochrome c/c1 heme lyase | PF01265 | 1 |
| Cytochrome C1 family | PF02167 | 1 |
| Cytochrome oxidase complex assembly protein 1 | PF08695 | 1 |
| Cytochrome P450 | PF00067 | 8 |
| Cytoplasmic tRNA 2-thiolation protein 2 | PF10288 | 2 |
| DAHP synthetase I family | PF00793 | 1 |
| D-ala D-ala ligase C-terminus | PF07478 | 4 |
| D-arabinono-1,4-lactone oxidase | PF04030 | 1 |

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| DASH complex subunit Dad3 | PF08656 | 1 |
| Dcp2, box A domain | PF05026 | 1 |
| DDE superfamily endonuclease | PF03184 | 1 |
| DDHD domain | PF02862 | 1 |
| DEAD/DEAH box helicase | PF00270 | 4 |
| DegT/DnrJ/EryC1/StrS aminotransferase family | PF01041 | 1 |
| Dehydratase family | PF00920 | 1 |
| Deuterolysin metalloprotease (M35) family | PF02102 | 5 |
| DExH-box splicing factor binding site | PF12656 | 1 |
| DHH family | PF01368 | 1 |
| Diacylglycerol acyltransferase | PF03982 | 1 |
| Dienelactone hydrolase family | PF01738 | 3 |
| Dihydroorotate dehydrogenase | PF01180 | 1 |
| Dihydrouridine synthase (Dus) | PF01207 | 2 |
| Dioxygenase | PF00775 | 2 |
| Dip2/Utp12 Family | PF04003 | 2 |
| Dipeptidyl peptidase IV (DPP IV) N-terminal region | PF00930 | 1 |
| Disintegrin | PF00200 | 1 |
| D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain | PF00389 | 1 |
| D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain | PF02826 | 2 |
| DJ-1/PfpI family | PF01965 | 2 |
| DNA mismatch repair protein, C-terminal domain | PF01119 | 1 |
| DNA polymerase alpha subunit p180 N terminal | PF12254 | 1 |
| DNA Polymerase alpha zinc finger | PF08996 | 1 |
| DNA polymerase family B | PF00136 | 1 |
| DNA polymerase family B, exonuclease domain | PF03104 | 1 |
| DNA polymerase III, delta subunit | PF13177 | 2 |
| DNA polymerase III, delta subunit | PF06144 | 1 |
| DNA polymerase Ligase (LigD) | PF13298 | 1 |
| DNA repair metallo-beta-lactamase | PF07522 | 1 |
| DNA topoisomerase | PF01131 | 1 |
| DnaB-like helicase C terminal domain | PF03796 | 1 |
| DnaJ C terminal domain | PF01556 | 0 |

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| DnaJ central domain | PF00684 | 0 |
| DnaJ domain | PF00226 | 3 |
| Dock homology region 2 | PF06920 | 1 |
| Domain of unknown function (DUF1899) | PF08953 | 1 |
| Domain of unknown function (DUF1929) | PF09118 | 2 |
| Domain of unknown function (DUF1961) | PF09224 | 1 |
| Domain of unknown function (DUF1966) | PF09260 | 1 |
| Domain of unknown function (DUF1996) | PF09362 | 4 |
| Domain of unknown function (DUF2405) | PF10293 | 1 |
| Domain of unknown function (DUF2427) | PF10348 | 1 |
| Domain of unknown function (DUF2431) | PF10354 | 1 |
| Domain of unknown function (DUF3328) | PF11807 | 1 |
| Domain of unknown function (DUF3395) | PF11875 | 1 |
| Domain of unknown function (DUF3453) | PF11935 | 1 |
| Domain of unknown function (DUF3492) | PF11997 | 1 |
| Domain of unknown function (DUF3535) | PF12054 | 1 |
| Domain of unknown function (DUF3554) | PF12074 | 1 |
| Domain of unknown function (DUF3635) | PF12330 | 1 |
| Domain of unknown function (DUF3844) | PF12955 | 1 |
| Domain of unknown function (DUF4110) | PF13422 | 1 |
| Domain of unknown function (DUF4112) | PF13430 | 1 |
| Domain of unknown function (DUF4149) | PF13664 | 1 |
| Domain of unknown function (DUF4188) | PF13826 | 1 |
| Domain of unknown function (DUF4360) | PF14273 | 3 |
| Domain of unknown function (DUF4414) | PF14377 | 2 |
| Domain of unknown function (DUF4470) | PF14737 | 1 |
| Domain of unknown function (DUF814) | PF05670 | 1 |
| Domain of unknown function UPF0086 | PF01868 | 1 |
| DOMON domain | PF03351 | 1 |
| Dual specificity phosphatase, catalytic domain | PF00782 | 2 |
| DUF4066 - Putative amidotransferase | PF13278 | 2 |
| D-xylulose 5-phosphate/D-fructose 6-phosphate phosphoketolase | PF03894 | 1 |
| Dynamitin | PF04912 | 1 |

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| Dynein light chain type 1 | PF01221 | 1 |
| E1-E2 ATPase | PF00122 | 4 |
| e3 binding domain | PF02817 | 1 |
| EamA-like transporter family | PF00892 | 1 |
| Ecdysteroid kinase | PF02958 | 1 |
| EF hand | PF00036 | 4 |
| EF hand | PF13202 | 1 |
| EF-1 guanine nucleotide exchange domain | PF00736 | 1 |
| EF-hand domain | PF14658 | 1 |
| EF-hand domain | PF13405 | 3 |
| EF-hand domain pair | PF13499 | 4 |
| EF-hand domain pair | PF13833 | 3 |
| EGF-like domain | PF07974 | 1 |
| eIF-6 family | PF01912 | 1 |
| Elongation factor Tu C-terminal domain | PF03143 | 1 |
| Elongation factor Tu domain 2 | PF03144 | 3 |
| Elongation factor Tu GTP binding domain | PF00009 | 5 |
| Emopamil binding protein | PF05241 | 1 |
| emp24/gp25L/p24 family/GOLD | PF01105 | 6 |
| Endomembrane protein 70 | PF02990 | 1 |
| Endonuclease/Exonuclease/phosphatase family | PF03372 | 4 |
| Endoplasmic reticulum protein ERp29, C-terminal domain | PF07749 | 0 |
| Endoribonuclease L-PSP | PF01042 | 2 |
| Enolase C-terminal domain-like | PF13378 | 1 |
| Enoyl-(Acyl carrier protein) reductase | PF13561 | 9 |
| Enoyl-CoA hydratase/isomerase | PF00378 | 3 |
| ER lumen protein retaining receptor | PF00810 | 1 |
| Ergosterol biosynthesis ERG4/ERG24 family | PF01222 | 1 |
| Esterase PHB depolymerase | PF10503 | 5 |
| ETC complex I subunit conserved region | PF04800 | 1 |
| EthD domain | PF07110 | 2 |
| Eukaryotic aspartyl protease | PF00026 | 19 |
| Eukaryotic elongation factor 1 beta central acidic region | PF10587 | 1 |

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| Eukaryotic porin | PF01459 | 1 |
| Eukaryotic translation initiation factor 3 subunit 7 (eIF-3) | PF05091 | 1 |
| Eukaryotic translation initiation factor 4G1 | PF12152 | 1 |
| Eukaryotic translation initiation factor eIF2A | PF08662 | 3 |
| Eukaryotic-type carbonic anhydrase | PF00194 | 2 |
| Exocyst complex subunit Sec15-like | PF04091 | 1 |
| Exonuclease | PF00929 | 3 |
| Exosome complex exonuclease RRP4 N-terminal region | PF14382 | 1 |
| FAD binding domain | PF01565 | 21 |
| FAD binding domain | PF01494 | 10 |
| FAD binding domain | PF00890 | 15 |
| FAD binding domain | PF00667 | 1 |
| FAD binding domain in molybdopterin dehydrogenase | PF00941 | 1 |
| FAD dependent oxidoreductase | PF01266 | 19 |
| FAD dependent oxidoreductase | PF12831 | 4 |
| FAD-binding domain | PF08022 | 1 |
| FAD-NAD(P)-binding | PF13454 | 5 |
| FAE1/Type III polyketide synthase-like protein | PF08392 | 1 |
| Fasciclin domain | PF02469 | 8 |
| FAT domain | PF02259 | 1 |
| FATC domain | PF02260 | 1 |
| Fatty acid desaturase | PF00487 | 2 |
| Fatty acid hydroxylase superfamily | PF04116 | 1 |
| F-box domain | PF00646 | 3 |
| F-box-like | PF12937 | 2 |
| Ferric reductase like transmembrane component | PF01794 | 1 |
| Ferric reductase NAD binding domain | PF08030 | 2 |
| Ferritin-like domain | PF13668 | 3 |
| Fes/CIP4, and EFC/F-BAR homology domain | PF00611 | 1 |
| FG-GAP repeat | PF01839 | 4 |
| FGGY family of carbohydrate kinases, C-terminal domain | PF02782 | 1 |
| FGGY family of carbohydrate kinases, N-terminal domain | PF00370 | 1 |
| FHA domain | PF00498 | 1 |

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| Fibronectin type III-like domain | PF14310 | 9 |
| Fic/DOC family | PF02661 | 1 |
| Fip1 motif | PF05182 | 1 |
| Fis1 C-terminal tetratricopeptide repeat | PF14853 | 1 |
| Flavin containing amine oxidoreductase | PF01593 | 8 |
| Flavin-binding monooxygenase-like | PF00743 | 6 |
| Flavodoxin | PF00258 | 1 |
| Flavoprotein | PF02441 | 1 |
| FMN-dependent dehydrogenase | PF01070 | 4 |
| Fn3-like domain | PF06280 | 7 |
| Forkhead domain | PF00250 | 1 |
| Formamidopyrimidine-DNA glycosylase H2TH domain | PF06831 | 1 |
| Formamidopyrimidine-DNA glycosylase N-terminal domain | PF01149 | 1 |
| FR47-like protein | PF08445 | 1 |
| Fringe-like | PF02434 | 3 |
| Fructose-bisphosphate aldolase class-II | PF01116 | 1 |
| FtsJ-like methyltransferase | PF01728 | 1 |
| Fumarylacetoacetate N-terminal | PF09298 | 1 |
| Fumarylacetoacetate (FAA) hydrolase family | PF01557 | 3 |
| Fungal cellulose binding domain | PF00734 | 34 |
| Fungal chitosanase of glycosyl hydrolase group 75 | PF07335 | 1 |
| Fungal hydrophobin | PF06766 | 4 |
| Fungal specific transcription factor domain | PF04082 | 16 |
| Fungal specific transcription factor domain | PF11951 | 9 |
| Fungal trichothecene efflux pump (TRI12) | PF06609 | 6 |
| Fungal Zn(2)-Cys(6) binuclear cluster domain | PF00172 | 15 |
| Fungalysin metallopeptidase (M36) | PF02128 | 2 |
| Fungalysin/Thermolysin Propeptide Motif | PF07504 | 2 |
| FYVE zinc finger | PF01363 | 1 |
| GAG-pre-integrase domain | PF13976 | 1 |
| Galactose mutarotase-like | PF13802 | 1 |
| Galactose oxidase, central domain | PF13415 | 4 |
| Galactose oxidase, central domain | PF13418 | 5 |

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| Gamma-glutamyl cyclotransferase, AIG2-like | PF06094 | 1 |
| Gamma-glutamyltranspeptidase | PF01019 | 1 |
| GATA zinc finger | PF00320 | 1 |
| Gcd10p family | PF04189 | 1 |
| GC-rich sequence DNA-binding factor-like protein | PF07842 | 1 |
| GDA1/CD39 (nucleoside phosphatase) family | PF01150 | 1 |
| GDSL-like Lipase/Acylhydrolase | PF00657 | 16 |
| GDSL-like Lipase/Acylhydrolase family | PF13472 | 13 |
| Gelsolin repeat | PF00626 | 1 |
| GHMP kinases N terminal domain | PF00288 | 1 |
| GINS complex protein | PF05916 | 2 |
| GLEYA domain | PF10528 | 2 |
| Globin | PF00042 | 1 |
| Glucanosyltransferase | PF03198 | 4 |
| Glucosamine-6-phosphate isomerasases/6-phosphogluconolactonase | PF01182 | 2 |
| Glucose / Sorbosone dehydrogenase | PF07995 | 1 |
| Glucose inhibited division protein A | PF01134 | 3 |
| Glucosidase II beta subunit-like | PF12999 | 0 |
| Glucosidase II beta subunit-like protein | PF07915 | 2 |
| Glucosidase II beta subunit-like protein | PF13015 | 0 |
| Glutaminase | PF04960 | 1 |
| Glutamine amidotransferase class-I | PF00117 | 3 |
| Glutamine amidotransferase domain | PF13522 | 1 |
| Glutamine amidotransferase domain | PF13537 | 1 |
| Glutamine amidotransferases class-II | PF00310 | 1 |
| Glutamine amidotransferases class-II | PF13230 | 1 |
| Glutaredoxin | PF00462 | 1 |
| Glutaredoxin-like domain (DUF836) | PF05768 | 1 |
| Glutathione S-transferase, C-terminal domain | PF13410 | 1 |
| Glutathione S-transferase, C-terminal domain | PF00043 | 1 |
| Glutathione S-transferase, N-terminal domain | PF13417 | 2 |
| Glutathione S-transferase, N-terminal domain | PF13409 | 2 |
| Glutathione S-transferase, N-terminal domain | PF02798 | 2 |

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| Glutathione-dependent formaldehyde-activating enzyme | PF04828 | 2 |
| Glycerophosphoryl diester phosphodiesterase family | PF03009 | 1 |
| Glycine-rich protein domain (DUF2403) | PF10290 | 3 |
| Glycolipid 2-alpha-mannosyltransferase | PF01793 | 1 |
| Glycoside-hydrolase family GH114 | PF03537 | 2 |
| Glycosyl hydrolase catalytic core | PF11790 | 3 |
| Glycosyl hydrolase family 1 | PF00232 | 1 |
| Glycosyl hydrolase family 10 | PF00331 | 6 |
| Glycosyl hydrolase family 12 | PF01670 | 5 |
| Glycosyl hydrolase family 20, catalytic domain | PF00728 | 2 |
| Glycosyl hydrolase family 20, domain 2 | PF02838 | 1 |
| Glycosyl hydrolase family 26 | PF02156 | 1 |
| Glycosyl hydrolase family 3 C-terminal domain | PF01915 | 9 |
| Glycosyl hydrolase family 3 N terminal domain | PF00933 | 9 |
| Glycosyl hydrolase family 30 TIM-barrel domain | PF02055 | 1 |
| Glycosyl hydrolase family 45 | PF02015 | 3 |
| Glycosyl hydrolase family 47 | PF01532 | 4 |
| Glycosyl hydrolase family 49 | PF03718 | 1 |
| Glycosyl hydrolase family 53 | PF07745 | 1 |
| Glycosyl hydrolase family 57 | PF03065 | 1 |
| Glycosyl hydrolase family 61 | PF03443 | 22 |
| Glycosyl hydrolase family 63 C-terminal domain | PF03200 | 0 |
| Glycosyl hydrolase family 67 C-terminus | PF07477 | 1 |
| Glycosyl hydrolase family 67 middle domain | PF07488 | 1 |
| Glycosyl hydrolase family 67 N-terminus | PF03648 | 1 |
| Glycosyl hydrolase family 7 | PF00840 | 6 |
| Glycosyl hydrolase family 71 | PF03659 | 1 |
| Glycosyl hydrolase family 76 | PF03663 | 7 |
| Glycosyl hydrolase family 81 | PF03639 | 1 |
| Glycosyl Hydrolase Family 88 | PF07470 | 5 |
| Glycosyl hydrolase family 92 | PF07971 | 1 |
| Glycosyl hydrolases family 11 | PF00457 | 3 |
| Glycosyl hydrolases family 15 | PF00723 | 2 |

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| Glycosyl hydrolases family 16 | PF00722 | 8 |
| Glycosyl hydrolases family 17 | PF00332 | 2 |
| Glycosyl hydrolases family 18 | PF00704 | 10 |
| Glycosyl hydrolases family 2 | PF00703 | 2 |
| Glycosyl hydrolases family 2, sugar binding domain | PF02837 | 2 |
| Glycosyl hydrolases family 2, TIM barrel domain | PF02836 | 2 |
| Glycosyl hydrolases family 28 | PF00295 | 11 |
| Glycosyl hydrolases family 31 | PF01055 | 1 |
| Glycosyl hydrolases family 32 C terminal | PF08244 | 3 |
| Glycosyl hydrolases family 32 N-terminal domain | PF00251 | 6 |
| Glycosyl hydrolases family 35 | PF01301 | 2 |
| Glycosyl hydrolases family 39 | PF01229 | 1 |
| Glycosyl hydrolases family 43 | PF04616 | 19 |
| Glycosyl hydrolases family 6 | PF01341 | 4 |
| Glycosyl transferase family 64 domain | PF09258 | 1 |
| Glycosyl transferase family 8 | PF01501 | 1 |
| Glycosyl transferase family 90 | PF05686 | 2 |
| Glycosyl transferase family group 2 | PF13632 | 2 |
| Glycosyl transferases group 1 | PF00534 | 1 |
| Glycosyltransferase family 28 N-terminal domain | PF03033 | 1 |
| Glycosyltransferase like family 2 | PF13641 | 1 |
| Glycosyltransferase sugar-binding region containing DXD motif | PF04488 | 2 |
| Glyoxal oxidase N-terminus | PF07250 | 2 |
| GMC oxidoreductase | PF00732 | 16 |
| GMC oxidoreductase | PF05199 | 16 |
| GMP synthase C terminal domain | PF00958 | 1 |
| Golgi CORVET complex core vacuolar protein 8 | PF12816 | 1 |
| Golgi phosphoprotein 3 (GPP34) | PF05719 | 1 |
| Golgi-body localisation protein domain | PF10351 | 1 |
| Got1/Sft2-like family | PF04178 | 1 |
| G-patch domain | PF01585 | 1 |
| Gpi16 subunit, GPI transamidase component | PF04113 | 1 |
| GPI-GlcNAc transferase complex, PIG-H component | PF10181 | 2 |

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| GPR1/FUN34/yaaH family | PF01184 | 1 |
| GrpE | PF01025 | 1 |
| GTPase-activator protein for Ras-like GTPase | PF00616 | 1 |
| Gtr1/RagA G protein conserved region | PF04670 | 3 |
| Guanine nucleotide exchange factor in Golgi transport N-terminal | PF12783 | 1 |
| Guanylate kinase | PF00625 | 1 |
| GYF domain | PF02213 | 1 |
| HAD-hyrolase-like | PF13242 | 2 |
| Haem-containing dehydratase | PF13816 | 1 |
| haloacid dehalogenase-like hydrolase | PF12710 | 5 |
| haloacid dehalogenase-like hydrolase | PF00702 | 4 |
| Haloacid dehalogenase-like hydrolase | PF13344 | 2 |
| Haloacid dehalogenase-like hydrolase | PF13419 | 1 |
| haloacid dehalogenase-like hydrolase | PF08282 | 1 |
| HAT (Half-A-TPR) repeat | PF02184 | 1 |
| HEAT repeat | PF02985 | 5 |
| HEAT repeats | PF13646 | 4 |
| HEAT-like repeat | PF13513 | 4 |
| HECT-domain (ubiquitin-transferase) | PF00632 | 2 |
| HeH/LEM domain | PF12949 | 1 |
| Helicase associated domain (HA2) | PF04408 | 2 |
| Helicase conserved C-terminal domain | PF00271 | 5 |
| Helix-loop-helix DNA-binding domain | PF00010 | 3 |
| Hemerythrin HHE cation binding domain | PF01814 | 1 |
| Hepatocellular carcinoma-associated antigen 59 | PF07052 | 1 |
| Heterokaryon incompatibility protein (HET) | PF06985 | 4 |
| Heterokaryon incompatibility protein Het-C | PF07217 | 3 |
| Hexokinase | PF03727 | 1 |
| Hexokinase | PF00349 | 1 |
| HhH-GPD superfamily base excision DNA repair protein | PF00730 | 1 |
| HI0933-like protein | PF03486 | 6 |
| His Kinase A (phospho-acceptor) domain | PF00512 | 1 |
| Histidine biosynthesis protein | PF00977 | 1 |

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| Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase | PF13589 | 1 |
| Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase | PF02518 | 3 |
| Histidine phosphatase superfamily (branch 1) | PF00300 | 4 |
| Histidine phosphatase superfamily (branch 2) | PF00328 | 5 |
| Histidinol dehydrogenase | PF00815 | 1 |
| Histone acetyltransferases subunit 3 | PF10198 | 1 |
| Histone chaperone Rtp106-like | PF08512 | 1 |
| Histone deacetylase domain | PF00850 | 2 |
| Histone-like transcription factor (CBF/NF-Y) and archaeal histone | PF00808 | 2 |
| HIT zinc finger | PF04438 | 1 |
| HMG (high mobility group) box | PF00505 | 4 |
| HMG-box domain | PF09011 | 3 |
| HMGL-like | PF00682 | 1 |
| HNH endonuclease | PF01844 | 1 |
| Holliday junction DNA helicase ruvB N-terminus | PF05496 | 3 |
| homogentisate 1,2-dioxygenase | PF04209 | 2 |
| HOOK protein | PF05622 | 1 |
| HPC2 and ubinuclein domain | PF08729 | 1 |
| HpcH/HpaI aldolase/citrate lyase family | PF03328 | 2 |
| Hpt domain | PF01627 | 1 |
| Hsp70 protein | PF00012 | 3 |
| HxxPF-repeated domain | PF13745 | 2 |
| Hydrogenase-1 expression protein HydE | PF07449 | 1 |
| Hydrophobic surface binding protein A | PF12296 | 4 |
| IBR domain, a half RING-finger domain | PF01485 | 1 |
| ICE2 | PF08426 | 1 |
| IKI3 family | PF04762 | 1 |
| Immune inhibitor A peptidase M6 | PF05547 | 1 |
| IMP dehydrogenase / GMP reductase domain | PF00478 | 2 |
| Importin-beta N-terminal domain | PF03810 | 1 |
| Indoleamine 2,3-dioxygenase | PF01231 | 1 |
| Inhibitor of Apoptosis domain | PF00653 | 1 |
| Inhibitor of growth proteins N-terminal histone-binding | PF12998 | 1 |

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| Initiation factor eIF2 gamma, C terminal | PF09173 | 1 |
| Inorganic pyrophosphatase | PF00719 | 1 |
| Inosine-uridine preferring nucleoside hydrolase | PF01156 | 1 |
| Inositol phosphatase | PF12456 | 1 |
| Inositol-pentakisphosphate 2-kinase | PF06090 | 1 |
| Inositolphosphorylceramide synthase subunit Kei1 | PF08552 | 1 |
| Insecticide toxin TcdB middle/N-terminal region | PF12256 | 4 |
| Insulin-induced protein (INSIG) | PF07281 | 1 |
| Integrase core domain | PF00665 | 1 |
| Ion channel regulatory protein UNC-93 | PF05978 | 1 |
| IQ calmodulin-binding motif | PF00612 | 1 |
| Iron/manganese superoxide dismutases, alpha-hairpin domain | PF00081 | 1 |
| Iron/manganese superoxide dismutases, C-terminal domain | PF02777 | 1 |
| Iron-containing alcohol dehydrogenase | PF00465 | 1 |
| Iron-containing alcohol dehydrogenase | PF13685 | 1 |
| Isochorismatase family | PF00857 | 4 |
| Isocitrate/isopropylmalate dehydrogenase | PF00180 | 1 |
| Isy1-like splicing family | PF06246 | 1 |
| JAB1/Mov34/MPN/PAD-1 ubiquitin protease | PF01398 | 1 |
| Jacalin-like lectin domain | PF01419 | 1 |
| Kelch motif | PF13854 | 7 |
| Kelch motif | PF01344 | 4 |
| Kelch motif | PF13964 | 5 |
| Kelch motif | PF07646 | 3 |
| KH domain | PF00013 | 1 |
| KilA-N domain | PF04383 | 1 |
| Kinase-like | PF14531 | 2 |
| Kinesin motor domain | PF00225 | 1 |
| Kinetochore complex Sim4 subunit Fta1 | PF13092 | 1 |
| KR domain | PF08659 | 13 |
| Ku C terminal domain like | PF08785 | 1 |
| Ku70/Ku80 beta-barrel domain | PF02735 | 1 |
| Ku70/Ku80 N-terminal alpha/beta domain | PF03731 | 1 |

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| La domain | PF05383 | 1 |
| Lactonase, 7-bladed beta-propeller | PF10282 | 3 |
| Legume-like lectin family | PF03388 | 1 |
| LETM1-like protein | PF07766 | 1 |
| LeuA allosteric (dimerisation) domain | PF08502 | 1 |
| Leucine rich repeat | PF13855 | 2 |
| Leucine Rich Repeat | PF00560 | 2 |
| Leucine Rich repeat | PF13516 | 2 |
| Leucine Rich repeats (2 copies) | PF12799 | 1 |
| Leucine-rich repeat | PF14580 | 1 |
| LicD family | PF04991 | 2 |
| Life-span regulatory factor | PF12855 | 1 |
| LIM domain | PF00412 | 1 |
| Lipase (class 3) | PF01764 | 5 |
| Lipase 3 N-terminal region | PF03893 | 1 |
| Lipocalin-like domain | PF08212 | 1 |
| Lipocalin-like domain | PF13924 | 1 |
| LisH | PF08513 | 1 |
| LITAF-like zinc ribbon domain | PF10601 | 1 |
| L-lysine 6-monoxygenase (NADPH-requiring) | PF13434 | 8 |
| LMBR1-like membrane protein | PF04791 | 1 |
| LRR_7,Leucine rich repeat | PF13504 | 1 |
| LSM domain | PF01423 | 4 |
| Lung seven transmembrane receptor | PF06814 | 1 |
| Lyase | PF00206 | 1 |
| Lycopene cyclase protein | PF05834 | 3 |
| Lysine-specific metallo-endopeptidase | PF14521 | 1 |
| LysM domain | PF01476 | 9 |
| Lysophospholipase catalytic domain | PF01735 | 1 |
| Lytic polysaccharide mono-oxygenase, cellulose-degrading | PF03067 | 3 |
| Lytic transglycolase | PF03330 | 3 |
| M42 glutamyl aminopeptidase | PF05343 | 1 |
| Mad3/BUB1 homology region 1 | PF08311 | 2 |

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| Maintenance of mitochondrial morphology protein 1 | PF10296 | 1 |
| Maintenance of mitochondrial structure and function | PF13012 | 1 |
| Major Facilitator Superfamily | PF07690 | 17 |
| Major intrinsic protein | PF00230 | 1 |
| Male sterility protein | PF07993 | 6 |
| Mandelate racemase / muconate lactonizing enzyme, C-terminal domain | PF01188 | 1 |
| Mandelate racemase / muconate lactonizing enzyme, N-terminal domain | PF02746 | 1 |
| MBOAT, membrane-bound O-acyltransferase family | PF03062 | 2 |
| Mechanosensitive ion channel | PF00924 | 2 |
| Meiosis protein SPO22/ZIP4 like | PF08631 | 1 |
| Melibiase | PF02065 | 1 |
| Membrane magnesium transporter | PF10270 | 1 |
| Metallo-beta-lactamase superfamily | PF00753 | 2 |
| Metallo-peptidase family M12 | PF13688 | 2 |
| Metallo-peptidase family M12B Reprolysin-like | PF13583 | 2 |
| Metallo-peptidase family M12B Reprolysin-like | PF13582 | 4 |
| Metallo-peptidase family M12B Reprolysin-like | PF13574 | 1 |
| Metallopeptidase family M24 | PF00557 | 1 |
| Methyltransf_26 | PF13659 | 6 |
| Methyltransferase domain | PF13383 | 1 |
| Methyltransferase domain | PF13489 | 9 |
| Methyltransferase domain | PF08241 | 11 |
| Methyltransferase domain | PF12847 | 9 |
| Methyltransferase domain | PF08242 | 8 |
| Methyltransferase domain | PF13847 | 9 |
| Methyltransferase domain | PF13649 | 5 |
| Methyltransferase FkbM domain | PF05050 | 1 |
| Methyltransferase small domain | PF05175 | 3 |
| MGS-like domain | PF02142 | 1 |
| Microtubule-associated protein CRIP | PF10235 | 2 |
| Mid2 like cell wall stress sensor | PF04478 | 2 |
| MIF4G domain | PF02854 | 2 |
| Misato Segment II tubulin-like domain | PF10644 | 1 |

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| Mitochondrial ATPase inhibitor, IATP | PF04568 | 1 |
| Mitochondrial biogenesis AIM24 | PF01987 | 1 |
| Mitochondrial branched-chain alpha-ketoacid dehydrogenase kinase | PF10436 | 2 |
| Mitochondrial carrier protein | PF00153 | 7 |
| Mitochondrial F1-F0 ATP synthase subunit F of fungi | PF10791 | 1 |
| Mitochondrial function, CLU-N-term | PF15044 | 1 |
| Mitochondrial import protein Pam17 | PF08566 | 1 |
| Mitochondrial protein from FMP27 | PF10344 | 1 |
| Mitochondrial ribosomal protein L28 | PF09812 | 1 |
| Mitochondrial ribosomal protein L37 | PF08561 | 1 |
| Mitochondrial ribosomal subunit S27 | PF08293 | 1 |
| ML domain | PF02221 | 1 |
| ML-like domain | PF14558 | 3 |
| Mo-co oxidoreductase dimerisation domain | PF03404 | 1 |
| MoeZ/MoeB domain | PF05237 | 1 |
| Molybdopterin oxidoreductase | PF00384 | 1 |
| Molybdopterin-binding domain of aldehyde dehydrogenase | PF02738 | 1 |
| Mono-functional DNA-alkylating methyl methanesulfonate N-term | PF10433 | 1 |
| MOSC domain | PF03473 | 1 |
| MOSC N-terminal beta barrel domain | PF03476 | 1 |
| MreB/Mbl protein | PF06723 | 2 |
| MSP (Major sperm protein) domain | PF00635 | 1 |
| Multicopper oxidase | PF07732 | 5 |
| Multicopper oxidase | PF07731 | 5 |
| Multicopper oxidase | PF00394 | 5 |
| Mycolic acid cyclopropane synthetase | PF02353 | 3 |
| MYND finger | PF01753 | 2 |
| N terminal extension of bacteriophage endosialidase | PF12218 | 3 |
| N2227-like protein | PF07942 | 1 |
| Na ⁺ dependent nucleoside transporter C-terminus | PF07662 | 1 |
| Na ⁺ dependent nucleoside transporter N-terminus | PF01773 | 1 |
| NACHT domain | PF05729 | 6 |
| NAD dependent epimerase/dehydratase family | PF01370 | 8 |

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| NAD synthase | PF02540 | 1 |
| NAD(P)-binding Rossmann-like domain | PF13450 | 21 |
| NAD(P)H-binding | PF13460 | 9 |
| NADH:flavin oxidoreductase / NADH oxidase family | PF00724 | 1 |
| NADH-ubiquinone oxidoreductase subunit G, C-terminal | PF09326 | 1 |
| NADH-ubiquinone oxidoreductase-G iron-sulfur binding region | PF10588 | 1 |
| NADP oxidoreductase coenzyme F420-dependent | PF03807 | 1 |
| NAT, N-acetyltransferase, of N-acetylglutamate synthase | PF04768 | 1 |
| Nbl1 / Borealin N terminal | PF10444 | 1 |
| Ndr family | PF03096 | 1 |
| Necrosis inducing protein (NPP1) | PF05630 | 6 |
| Neutral/alkaline non-lysosomal ceramidase, N-terminal | PF04734 | 1 |
| NHL repeat | PF01436 | 1 |
| Nitrite and sulphite reductase 4Fe-4S domain | PF01077 | 1 |
| Nitrite/Sulfite reductase ferredoxin-like half domain | PF03460 | 1 |
| Nitrogen Permease regulator of amino acid transport activity 3 | PF03666 | 1 |
| Nitronate monooxygenase | PF03060 | 2 |
| NLI interacting factor-like phosphatase | PF03031 | 1 |
| NmrA-like family | PF05368 | 6 |
| NMT1/THI5 like | PF09084 | 1 |
| NMT1-like family | PF13379 | 1 |
| Noc2p family | PF03715 | 1 |
| non-haem dioxygenase in morphine synthesis N-terminal | PF14226 | 4 |
| Non-repetitive/WGA-negative nucleoporin C-terminal | PF03177 | 1 |
| non-SMC mitotic condensation complex subunit 1 | PF12717 | 2 |
| Nop53 (60S ribosomal biogenesis) | PF07767 | 1 |
| NOSIC | PF08060 | 1 |
| Nrap protein | PF03813 | 1 |
| Nsp1-like C-terminal region | PF05064 | 1 |
| N-terminal domain of ribose phosphate pyrophosphokinase | PF13793 | 1 |
| N-terminal region of Chorein or VPS13 | PF12624 | 1 |
| N-terminus of kinetochore NMS complex subunit Spc7 | PF15402 | 1 |
| NUBPL iron-transfer P-loop NTPase | PF10609 | 1 |

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| NUC153 domain | PF08159 | 1 |
| Nucleoporin FG repeat region | PF13634 | 1 |
| Nucleoporin Nup120/160 | PF11715 | 6 |
| Nucleoside transporter | PF01733 | 2 |
| Nucleosome assembly protein (NAP) | PF00956 | 1 |
| Nucleotide exchange factor Fes1 | PF08609 | 1 |
| Nucleotide-sugar transporter | PF04142 | 1 |
| Nucleotidyltransferase | PF06042 | 1 |
| Nucleotidyltransferase domain | PF01909 | 2 |
| NUDIX domain | PF00293 | 3 |
| Nuf2 family | PF03800 | 1 |
| Nup133 N terminal like | PF08801 | 1 |
| Nup53/35/40-type RNA recognition motif | PF14605 | 2 |
| O-Glycosyl hydrolase family 30 | PF14587 | 1 |
| Oligonucleotide/oligosaccharide-binding (OB)-fold | PF07717 | 2 |
| Oligosaccharyltransferase subunit Ribophorin II | PF05817 | 1 |
| O-methyltransferase | PF00891 | 1 |
| OST3 / OST6 family, transporter family | PF04756 | 1 |
| Oxidoreductase FAD-binding domain | PF00970 | 3 |
| Oxidoreductase family, C-terminal alpha/beta domain | PF02894 | 1 |
| Oxidoreductase family, NAD-binding Rossmann fold | PF01408 | 1 |
| Oxidoreductase molybdopterin binding domain | PF00174 | 1 |
| Oxidoreductase NAD-binding domain | PF00175 | 3 |
| PA domain | PF02225 | 11 |
| PA14 domain | PF07691 | 1 |
| Paf1 | PF03985 | 1 |
| Paired amphipathic helix repeat | PF02671 | 1 |
| PalH/RIM21 | PF08733 | 1 |
| Palmitoyl protein thioesterase | PF02089 | 0 |
| Pam16 | PF03656 | 1 |
| PAN domain | PF00024 | 1 |
| PAP2 superfamily | PF01569 | 1 |
| Parkin co-regulated protein | PF10274 | 1 |

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| Part of AAA domain | PF13245 | 2 |
| Patatin-like phospholipase | PF01734 | 1 |
| Pathogen effector | PF14856 | 5 |
| PB1 domain | PF00564 | 1 |
| PCI domain | PF01399 | 1 |
| PCRF domain | PF03462 | 1 |
| Pectate lyase | PF00544 | 15 |
| Pectate lyase | PF03211 | 16 |
| Pectate lyase superfamily protein | PF12708 | 3 |
| Pectinesterase | PF01095 | 5 |
| Pentatricopeptide repeat domain | PF13812 | 1 |
| PE-PPE domain | PF08237 | 5 |
| Peptidase C13 family | PF01650 | 1 |
| Peptidase C26 | PF07722 | 3 |
| Peptidase dimerisation domain | PF07687 | 3 |
| Peptidase family M1 | PF01433 | 1 |
| Peptidase family M20/M25/M40 | PF01546 | 7 |
| Peptidase family M28 | PF04389 | 12 |
| Peptidase family M3 | PF01432 | 1 |
| Peptidase family M49 | PF03571 | 1 |
| Peptidase family S41 | PF03572 | 3 |
| Peptidase inhibitor I78 family | PF11720 | 1 |
| Peptidase inhibitor I9 | PF05922 | 6 |
| Pericentrin-AKAP-450 domain of centrosomal targeting protein | PF10495 | 1 |
| Periplasmic copper-binding protein (NosD) | PF05048 | 1 |
| Permease family | PF00860 | 1 |
| Permease for cytosine/purines, uracil, thiamine, allantoin | PF02133 | 1 |
| Peroxidase | PF00141 | 6 |
| Peroxidase, family 2 | PF01328 | 1 |
| Peroxin 13, N-terminal region | PF04088 | 2 |
| PH domain | PF00169 | 3 |
| Phage lysozyme | PF00959 | 1 |
| PHD-finger | PF00628 | 3 |

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| PHD-finger | PF13831 | 1 |
| PHD-like zinc-binding domain | PF13771 | 1 |
| PHD-zinc-finger like domain | PF13832 | 1 |
| Phenazine biosynthesis-like protein | PF02567 | 1 |
| PHF5-like protein | PF03660 | 1 |
| PhoD-like phosphatase | PF09423 | 2 |
| Phorbol esters/diacylglycerol binding domain (C1 domain) | PF00130 | 1 |
| Phosphate transporter family | PF01384 | 2 |
| Phosphatidylethanolamine-binding protein | PF01161 | 2 |
| Phosphatidylinositol 3- and 4-kinase | PF00454 | 2 |
| Phosphatidylinositol-4-phosphate 5-Kinase | PF01504 | 1 |
| Phosphoesterase family | PF04185 | 1 |
| Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain I | PF02878 | 1 |
| Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain II | PF02879 | 1 |
| Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain III | PF02880 | 1 |
| Phosphoglucomutase/phosphomannomutase, C-terminal domain | PF00408 | 1 |
| Phosphoinositide 3-kinase C2 | PF00792 | 1 |
| Phosphoinositide 3-kinase family, accessory domain (PIK domain) | PF00613 | 1 |
| Phospholipase/Carboxylesterase | PF02230 | 1 |
| Phosphopantetheine attachment site | PF00550 | 5 |
| Phosphoribosyl synthetase-associated domain | PF14572 | 1 |
| Phosphoribosyl transferase domain | PF00156 | 1 |
| Phosphoribulokinase / Uridine kinase family | PF00485 | 1 |
| Phosphorylase superfamily | PF01048 | 3 |
| Phosphotransferase enzyme family | PF01636 | 3 |
| PHP domain | PF02811 | 1 |
| Phytanoyl-CoA dioxygenase (PhyH) | PF05721 | 1 |
| Phytase | PF02333 | 1 |
| pinin/SDK/memA/ protein conserved region | PF04696 | 2 |
| Pirin | PF02678 | 1 |
| Plant protein of unknown function (DUF946) | PF06101 | 1 |
| Platelet-activating factor acetylhydrolase, isoform II | PF03403 | 2 |
| Pleckstrin homology domain | PF15411 | 1 |

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| Pleckstrin homology domain | PF15410 | 2 |
| Pleckstrin homology domain | PF15413 | 2 |
| P-loop containing region of AAA domain | PF13555 | 2 |
| Poly A polymerase head domain | PF01743 | 1 |
| Poly(A) polymerase central domain | PF04928 | 1 |
| Poly(A) polymerase predicted RNA binding domain | PF04926 | 1 |
| Poly(ADP-ribose) polymerase catalytic domain | PF00644 | 1 |
| Polyketide synthase dehydratase | PF14765 | 2 |
| Polysaccharide biosynthesis protein | PF02719 | 1 |
| Polysaccharide deacetylase | PF01522 | 5 |
| Polysaccharide lyase family 4, domain II | PF14686 | 3 |
| Polysaccharide lyase family 4, domain III | PF14683 | 3 |
| PPIC-type PPIASE domain | PF13616 | 1 |
| PPIC-type PPIASE domain | PF00639 | 1 |
| PPR repeat | PF12854 | 1 |
| PPR repeat | PF01535 | 1 |
| PPR repeat family | PF13041 | 1 |
| PQQ-like domain | PF13360 | 2 |
| PQQ-like domain | PF13570 | 1 |
| Predicted ATPase of the ABC class | PF09818 | 1 |
| Prefoldin subunit | PF01920 | 1 |
| Pregnancy-associated plasma protein-A | PF05572 | 6 |
| PRELI-like family | PF04707 | 1 |
| Pre-mRNA 3'-end-processing endonuclease polyadenylation factor C-term | PF11718 | 1 |
| pre-mRNA processing factor 4 (PRP4) like | PF08799 | 2 |
| Prenylcysteine lyase | PF07156 | 0 |
| Prion-inhibition and propagation | PF14479 | 3 |
| Probable RNA and SrmB- binding site of polymerase A | PF12627 | 1 |
| Prokaryotic phospholipase A2 | PF09056 | 2 |
| Pro-kumamolisin, activation domain | PF09286 | 1 |
| Prolyl oligopeptidase family | PF00326 | 8 |
| Proprotein convertase P-domain | PF01483 | 2 |
| Proteasome complex subunit Rpn13 ubiquitin receptor | PF04683 | 1 |

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| Proteasome maturation factor UMP1 | PF05348 | 1 |
| Proteasome subunit | PF00227 | 1 |
| Protein kinase C terminal domain | PF00433 | 1 |
| Protein kinase domain | PF00069 | 16 |
| Protein of unknown function (DUF1077) | PF06417 | 1 |
| Protein of unknown function (DUF1237) | PF06824 | 1 |
| Protein of unknown function (DUF1295) | PF06966 | 1 |
| Protein of unknown function (DUF1399) | PF07173 | 1 |
| Protein of unknown function (DUF1446) | PF07287 | 1 |
| Protein of unknown function (DUF1479) | PF07350 | 2 |
| Protein of unknown function (DUF1513) | PF07433 | 1 |
| Protein of unknown function (DUF1524) | PF07510 | 2 |
| Protein of unknown function (DUF1565) | PF07602 | 1 |
| Protein of unknown function (DUF1620) | PF07774 | 2 |
| Protein of unknown function (DUF1640) | PF07798 | 1 |
| Protein of unknown function (DUF1682) | PF07946 | 1 |
| Protein of unknown function (DUF1688) | PF07958 | 1 |
| Protein of unknown function (DUF1749) | PF08538 | 1 |
| Protein of unknown function (DUF1762) | PF08574 | 1 |
| Protein of unknown function (DUF1765) | PF08578 | 1 |
| Protein of unknown function (DUF2456) | PF10445 | 1 |
| Protein of unknown function (DUF2638) | PF10937 | 1 |
| Protein of unknown function (DUF2823) | PF11034 | 1 |
| Protein of unknown function (DUF3074) | PF11274 | 1 |
| Protein of unknown function (DUF3128) | PF11326 | 2 |
| Protein of unknown function (DUF3129) | PF11327 | 4 |
| Protein of unknown function (DUF3405) | PF11885 | 3 |
| Protein of unknown function (DUF3419) | PF11899 | 1 |
| Protein of unknown function (DUF3429) | PF11911 | 1 |
| Protein of unknown function (DUF3433) | PF11915 | 2 |
| Protein of unknown function (DUF3435) | PF11917 | 1 |
| Protein of unknown function (DUF3455) | PF11937 | 2 |
| Protein of unknown function (DUF3602) | PF12223 | 1 |

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| Protein of unknown function (DUF3659) | PF12396 | 1 |
| Protein of unknown function (DUF3723) | PF12520 | 2 |
| Protein of unknown function (DUF3752) | PF12572 | 1 |
| Protein of unknown function (DUF3759) | PF12585 | 1 |
| Protein of unknown function (DUF3807) | PF12720 | 1 |
| Protein of unknown function (DUF3984) | PF13136 | 1 |
| Protein of unknown function (DUF410) | PF04190 | 1 |
| Protein of unknown function (DUF4243) | PF14027 | 1 |
| Protein of unknown function (DUF4448) | PF14610 | 3 |
| Protein of unknown function (DUF726) | PF05277 | 1 |
| Protein of unknown function (DUF815) | PF05673 | 1 |
| Protein of unknown function (DUF861) | PF05899 | 1 |
| Protein of unknown function (DUF962) | PF06127 | 1 |
| Protein of unknown function DUF45 | PF01863 | 1 |
| Protein of unknown function, DUF258 | PF03193 | 4 |
| Protein phosphatase 2C | PF13672 | 2 |
| Protein phosphatase 2C | PF00481 | 3 |
| Protein prenyltransferase alpha subunit repeat | PF01239 | 1 |
| Protein tyrosine kinase | PF07714 | 13 |
| Protein-arginine deiminase (PAD) | PF03068 | 2 |
| Prp31 C terminal domain | PF09785 | 1 |
| PUA domain | PF01472 | 1 |
| Pumilio-family RNA binding repeat | PF00806 | 1 |
| Putative carbohydrate metabolism domain | PF13201 | 2 |
| Putative cyclase | PF04199 | 1 |
| Putative diphthamide synthesis protein | PF01866 | 1 |
| Putative exonuclease SbcCD, C subunit | PF13558 | 1 |
| Putative Ig domain | PF05345 | 1 |
| Putative NAD(P)-binding | PF13241 | 1 |
| Putative peptidase family | PF13933 | 1 |
| Putative S-adenosyl-L-methionine-dependent methyltransferase | PF02636 | 1 |
| Putative SAM-dependent methyltransferase | PF11312 | 1 |
| Putative serine dehydratase domain | PF14031 | 2 |

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| Putative Sin3 binding protein | PF10330 | 1 |
| Putative stress-responsive nuclear envelope protein | PF10281 | 1 |
| Putative threonine-serine exporter | PF06738 | 1 |
| Putative TOS1-like glycosyl hydrolase (DUF2401) | PF10287 | 3 |
| Putative zinc finger in N-recognin (UBR box) | PF02207 | 1 |
| Putative zinc-finger of transcription factor IIIC complex | PF12660 | 1 |
| PX domain | PF00787 | 1 |
| Pyoverdine/dityrosine biosynthesis protein | PF05141 | 1 |
| Pyridine nucleotide-disulphide oxidoreductase | PF07992 | 15 |
| Pyridine nucleotide-disulphide oxidoreductase | PF13738 | 10 |
| Pyridine nucleotide-disulphide oxidoreductase | PF00070 | 8 |
| Pyridoxal-phosphate dependent enzyme | PF00291 | 1 |
| Pyridoxamine 5'-phosphate oxidase | PF13883 | 1 |
| Pyridoxamine 5'-phosphate oxidase | PF01243 | 1 |
| Pyrroline-5-carboxylate reductase dimerisation | PF14748 | 1 |
| Pyruvate flavodoxin/ferredoxin oxidoreductase, thiamine diP-bdg | PF01855 | 1 |
| Rad17 cell cycle checkpoint protein | PF03215 | 3 |
| RanBP1 domain | PF00638 | 1 |
| Ras family | PF00071 | 4 |
| Ras of Complex, Roc, domain of DAPkinase | PF08477 | 4 |
| RasGAP C-terminus | PF03836 | 1 |
| RasGEF domain | PF00617 | 1 |
| RasGEF N-terminal motif | PF00618 | 1 |
| Receptor L domain | PF01030 | 1 |
| RecF/RecN/SMC N terminal domain | PF02463 | 4 |
| Redoxin | PF08534 | 1 |
| Region in Clathrin and VPS | PF00637 | 1 |
| Regulator of chromosome condensation (RCC1) repeat | PF00415 | 1 |
| Regulator of chromosome condensation (RCC1) repeat | PF13540 | 1 |
| Regulator of volume decrease after cellular swelling | PF03517 | 1 |
| Repair protein Rad1/Rec1/Rad17 | PF02144 | 1 |
| Repeat domain in Vibrio, Colwellia, Bradyrhizobium and Shewanella | PF13517 | 4 |
| Replication factor C C-terminal domain | PF08542 | 2 |

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| Replication factor RFC1 C terminal domain | PF08519 | 1 |
| Reprolysin (M12B) family zinc metalloprotease | PF01421 | 1 |
| Rer1 family | PF03248 | 1 |
| Retinal pigment epithelial membrane protein | PF03055 | 1 |
| Reverse transcriptase (RNA-dependent DNA polymerase) | PF07727 | 1 |
| Reverse transcriptase (RNA-dependent DNA polymerase) | PF00078 | 1 |
| RF-1 domain | PF00472 | 2 |
| Rhamnogalacturonan lyase B, N-terminal | PF09284 | 1 |
| Rhodanese-like domain | PF00581 | 1 |
| RhoGAP domain | PF00620 | 1 |
| RhoGEF domain | PF00621 | 1 |
| ribonuclease | PF00545 | 2 |
| Ribonuclease III domain | PF00636 | 1 |
| Ribonuclease T2 family | PF00445 | 2 |
| Ribonuclease-III-like | PF14622 | 1 |
| Ribonucleotide reductase, small chain | PF00268 | 2 |
| Ribophorin I | PF04597 | 1 |
| Ribosomal L29 protein | PF00831 | 1 |
| Ribosomal L29e protein family | PF01779 | 1 |
| Ribosomal L37ae protein family | PF01780 | 1 |
| ribosomal L5P family C-terminus | PF00673 | 1 |
| Ribosomal protein L16p/L10e | PF00252 | 1 |
| Ribosomal protein L19e | PF01280 | 1 |
| Ribosomal protein L22p/L17e | PF00237 | 1 |
| Ribosomal protein L24e | PF01246 | 1 |
| Ribosomal protein L3 | PF00297 | 1 |
| Ribosomal protein L44 | PF00935 | 1 |
| Ribosomal protein L6e | PF01159 | 1 |
| Ribosomal protein L7Ae/L30e/S12e/Gadd45 family | PF01248 | 2 |
| Ribosomal protein S17 | PF00366 | 1 |
| Ribosomal protein S19 | PF00203 | 1 |
| Ribosomal protein S21e | PF01249 | 1 |
| Ribosomal protein S5, C-terminal domain | PF03719 | 1 |

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| Ribosomal protein S5, N-terminal domain | PF00333 | 1 |
| Ribosomal protein S6e | PF01092 | 2 |
| Ribosomal protein S8 | PF00410 | 1 |
| Ribosomal protein S8e | PF01201 | 1 |
| Ribosomal proteins 50S-L15, 50S-L18e, 60S-L27A | PF00828 | 1 |
| Ribosome biogenesis protein SLX9 | PF15341 | 1 |
| RIC1 | PF07064 | 1 |
| Ricin-type beta-trefoil lectin domain | PF00652 | 2 |
| Right handed beta helix region | PF13229 | 8 |
| Ring finger domain | PF13639 | 7 |
| RING-H2 zinc finger domain | PF12678 | 3 |
| RING-type zinc-finger | PF13445 | 1 |
| RING-variant domain | PF12906 | 2 |
| Rix1 complex component involved in 60S ribosome maturation | PF12333 | 1 |
| RmlD substrate binding domain | PF04321 | 1 |
| RNA binding motif | PF08777 | 1 |
| RNA cap guanine-N2 methyltransferase | PF09445 | 2 |
| RNA dependent RNA polymerase | PF05183 | 1 |
| RNA pol II promoter Fmp27 protein domain | PF10359 | 1 |
| RNA pol II promoter Fmp27 protein domain | PF10347 | 1 |
| RNA pol II promoter Fmp27 protein domain | PF10305 | 1 |
| RNA polymerase I specific transcription initiation factor RRN3 | PF05327 | 1 |
| RNA polymerase Rpb1, domain 1 | PF04997 | 1 |
| RNA polymerase Rpb1, domain 2 | PF00623 | 1 |
| RNA polymerase Rpb1, domain 3 | PF04983 | 1 |
| RNA polymerase Rpb1, domain 4 | PF05000 | 1 |
| RNA polymerase Rpb1, domain 5 | PF04998 | 1 |
| RNA polymerase Rpb3/Rpb11 dimerisation domain | PF01193 | 1 |
| RNA polymerase Rpb3/RpoA insert domain | PF01000 | 1 |
| RNA polymerase Rpb4 | PF03874 | 2 |
| RNA polymerase Rpb8 | PF03870 | 1 |
| RNA polymerases N / 8 kDa subunit | PF01194 | 1 |
| RNA recognition motif 2 | PF04059 | 1 |

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| RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) | PF00076 | 9 |
| RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) | PF13893 | 8 |
| RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) | PF14259 | 7 |
| RNA12 protein | PF10443 | 2 |
| RNase P subunit Pop3 | PF08228 | 1 |
| RNB domain | PF00773 | 1 |
| RPAP1-like, C-terminal | PF08620 | 1 |
| RPAP1-like, N-terminal | PF08621 | 1 |
| rRNA processing/ribosome biogenesis | PF08167 | 1 |
| RTA1 like protein | PF04479 | 2 |
| RTC4-like domain | PF14474 | 1 |
| RWD domain | PF05773 | 1 |
| S1 RNA binding domain | PF00575 | 1 |
| S1/P1 Nuclease | PF02265 | 3 |
| SAC3/GANP family | PF03399 | 1 |
| Saccharopine dehydrogenase NADP binding domain | PF03435 | 1 |
| SacI homology domain | PF02383 | 2 |
| SAD/SRA domain | PF02182 | 1 |
| Sad1 / UNC-like C-terminal | PF07738 | 1 |
| SAM domain (Sterile alpha motif) | PF07647 | 1 |
| SAM domain (Sterile alpha motif) | PF00536 | 1 |
| SAP domain | PF02037 | 1 |
| Sas10/Utp3/C1D family | PF04000 | 1 |
| SCA7, zinc-binding domain | PF08313 | 1 |
| Scytalone dehydratase | PF02982 | 1 |
| Sds3-like | PF08598 | 2 |
| Sec61beta family | PF03911 | 1 |
| Sec7 domain | PF01369 | 1 |
| Secretory lipase | PF03583 | 1 |
| Secretory pathway protein Sec39 | PF08314 | 1 |
| Sedlin, N-terminal conserved region | PF04628 | 2 |
| Sell repeat | PF08238 | 1 |
| Semialdehyde dehydrogenase, NAD binding domain | PF01118 | 2 |

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| Septin | PF00735 | 2 |
| Serine aminopeptidase, S33 | PF12146 | 2 |
| Serine carboxypeptidase | PF00450 | 7 |
| Serine carboxypeptidase S28 | PF05577 | 2 |
| Serine hydrolase (FSH1) | PF03959 | 1 |
| Serine hydroxymethyltransferase | PF00464 | 1 |
| Serine-threonine protein kinase 19 | PF10494 | 1 |
| Ser-Thr-rich glycosyl-phosphatidyl-inositol-anchored membrane family | PF10342 | 4 |
| SET domain | PF00856 | 6 |
| SH3 domain | PF00018 | 5 |
| Shikimate kinase | PF01202 | 2 |
| short chain dehydrogenase | PF00106 | 14 |
| SHR-binding domain of vacuolar-sorting associated protein 13 | PF06650 | 1 |
| SHS2 domain found in N terminus of Rpb7p/Rpc25p/MJ0397 | PF03876 | 1 |
| Sigma-54 interaction domain | PF00158 | 1 |
| Signal recognition particle 9 kDa protein (SRP9) | PF05486 | 2 |
| Signal recognition particle receptor beta subunit | PF09439 | 2 |
| Sin3 family co-repressor | PF08295 | 1 |
| Sirohaem biosynthesis protein central | PF14824 | 1 |
| Sirohaem biosynthesis protein C-terminal | PF14823 | 1 |
| SIS domain | PF01380 | 1 |
| SIT4 phosphatase-associated protein | PF04499 | 1 |
| Slx4 endonuclease | PF09494 | 1 |
| SMC proteins Flexible Hinge Domain | PF06470 | 1 |
| SMP-30/Gluconolaconase/LRE-like region | PF08450 | 1 |
| Snare region anchored in the vesicle membrane C-terminus | PF12352 | 1 |
| SNF2 family N-terminal domain | PF00176 | 3 |
| Snf7 | PF03357 | 2 |
| SnoaL-like domain | PF13577 | 2 |
| snoRNA binding domain, fibrillarin | PF01798 | 1 |
| Sodium Bile acid symporter family | PF01758 | 1 |
| Sodium:dicarboxylate symporter family | PF00375 | 1 |
| Something about silencing, SAS, complex subunit 4 | PF15460 | 1 |

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| SOS response associated peptidase (SRAP) | PF02586 | 1 |
| Spa2 homology domain (SHD) of GIT | PF08518 | 1 |
| Spc7 kinetochore protein | PF08317 | 1 |
| Spc7_C2 | PF15577 | 1 |
| SPFH domain / Band 7 family | PF01145 | 1 |
| Spherulation-specific family 4 | PF12138 | 1 |
| Sphingolipid Delta4-desaturase (DES) | PF08557 | 1 |
| Splicing factor 3B subunit 1 | PF08920 | 1 |
| SPX domain | PF03105 | 1 |
| SRF-type transcription factor (DNA-binding and dimerisation domain) | PF00319 | 1 |
| SRI (Set2 Rpb1 interacting) domain | PF08236 | 1 |
| Ssl1-like | PF04056 | 1 |
| Ssu72-like protein | PF04722 | 1 |
| Stage II sporulation protein E (SpoIIE) | PF07228 | 2 |
| Starch binding domain | PF00686 | 3 |
| STAS domain | PF01740 | 1 |
| Stc1 domain | PF12898 | 1 |
| STE like transcription factor | PF02200 | 1 |
| Sterol methyltransferase C-terminal | PF08498 | 2 |
| Stigma-specific protein, Stig1 | PF04885 | 3 |
| Stress responsive A/B Barrel Domain | PF07876 | 1 |
| Stretch-activated Ca2+-permeable channel component | PF12929 | 1 |
| Subtilase family | PF00082 | 18 |
| Sugar (and other) transporter | PF00083 | 8 |
| Sugar-binding cellulase-like | PF12876 | 7 |
| Sugar-transporters, 12 TM | PF05631 | 1 |
| Sulfatase | PF00884 | 2 |
| Sulfate permease family | PF00916 | 1 |
| Suppressor of forked protein (Suf) | PF05843 | 2 |
| SUR7/PalI family | PF06687 | 1 |
| Surfeit locus protein 6 | PF04935 | 1 |
| Survival protein SurE | PF01975 | 1 |
| Sybindin-like family | PF04099 | 1 |

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| SYF2 splicing factor | PF08231 | 1 |
| Synaptobrevin | PF00957 | 1 |
| TAFII55 protein conserved region | PF04658 | 1 |
| Tannase and feruloyl esterase | PF07519 | 4 |
| Taurine catabolism dioxygenase TauD, TfdA family | PF02668 | 2 |
| TCP-1/cpn60 chaperonin family | PF00118 | 3 |
| TEA/ATTS domain family | PF01285 | 1 |
| Tetratricopeptide repeat | PF13428 | 7 |
| Tetratricopeptide repeat | PF00515 | 5 |
| Tetratricopeptide repeat | PF14559 | 3 |
| Tetratricopeptide repeat | PF13432 | 4 |
| Tetratricopeptide repeat | PF07719 | 6 |
| Tetratricopeptide repeat | PF13181 | 3 |
| Tetratricopeptide repeat | PF13431 | 4 |
| Tetratricopeptide repeat | PF13371 | 3 |
| Tetratricopeptide repeat | PF13176 | 3 |
| Tetratricopeptide repeat | PF13429 | 3 |
| Tetratricopeptide repeat | PF13174 | 2 |
| Tetratricopeptide repeat | PF13424 | 4 |
| Tetratricopeptide repeat | PF14561 | 1 |
| Tetratricopeptide repeat | PF13374 | 1 |
| TFIIS helical bundle-like domain | PF08711 | 1 |
| Thi4 family | PF01946 | 4 |
| Thiamine-binding protein | PF01910 | 1 |
| ThiF family | PF00899 | 1 |
| Thioesterase domain | PF00975 | 1 |
| Thioesterase superfamily | PF03061 | 1 |
| Thioesterase-like superfamily | PF13622 | 1 |
| Thioesterase-like superfamily | PF13279 | 1 |
| Thiolase, C-terminal domain | PF02803 | 1 |
| Thiolase, N-terminal domain | PF00108 | 3 |
| Thioredoxin | PF00085 | 4 |
| Thioredoxin | PF14595 | 0 |

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| Thioredoxin-like | PF13905 | 4 |
| Thioredoxin-like | PF13899 | 1 |
| Thioredoxin-like domain | PF13848 | 3 |
| Thioredoxin-like domain | PF13098 | 2 |
| THO complex subunit 1 transcription elongation factor | PF11957 | 1 |
| Threonine/Serine exporter, ThrE | PF12821 | 1 |
| Tim17/Tim22/Tim23/Pmp24 family | PF02466 | 1 |
| TIP49 C-terminus | PF06068 | 1 |
| TLC domain | PF03798 | 1 |
| Toprim domain | PF01751 | 1 |
| TPR repeat | PF13414 | 8 |
| TRAF-type zinc finger | PF02176 | 1 |
| TRAM1-like protein | PF08390 | 1 |
| Transcription factor IIIC subunit delta N-term | PF12657 | 1 |
| Transcription factor S-II (TFIIS) | PF01096 | 1 |
| Transcription factor S-II (TFIIS), central domain | PF07500 | 1 |
| Transcription factor TFIID complex subunit 8 C-term | PF10406 | 1 |
| Transcription factor TFIIH complex subunit Tfb5 | PF06331 | 1 |
| Transferase family | PF02458 | 1 |
| Transferrin receptor-like dimerisation domain | PF04253 | 2 |
| Transglutaminase-like superfamily | PF13369 | 1 |
| Transient receptor potential (TRP) ion channel | PF06011 | 3 |
| Transketolase, C-terminal domain | PF02780 | 1 |
| Transketolase, pyrimidine binding domain | PF02779 | 1 |
| Transketolase, thiamine diphosphate binding domain | PF00456 | 1 |
| Translation initiation factor eIF3 subunit | PF08597 | 1 |
| Translation initiation factor eIF3 subunit 135 | PF12807 | 1 |
| Translation initiation factor SUI1 | PF01253 | 2 |
| Translation-initiation factor 2 | PF11987 | 1 |
| Translin family | PF01997 | 1 |
| Translocon-associated protein (TRAP), alpha subunit | PF03896 | 1 |
| Transmembrane amino acid transporter protein | PF01490 | 2 |
| Trehalase | PF01204 | 2 |

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| Trimerisation motif | PF08954 | 1 |
| tRNA pseudouridine synthase | PF01416 | 2 |
| tRNA synthetases class I (W and Y) | PF00579 | 2 |
| Trypsin | PF00089 | 2 |
| Tryptophan halogenase | PF04820 | 2 |
| Tubulin C-terminal domain | PF03953 | 1 |
| Tubulin domain | PF14881 | 1 |
| Tubulin/FtsZ family, GTPase domain | PF00091 | 2 |
| Tuftelin interacting protein N terminal | PF12457 | 1 |
| twin BRCT domain | PF12738 | 1 |
| Type I phosphodiesterase / nucleotide pyrophosphatase | PF01663 | 1 |
| Type II/IV secretion system protein | PF00437 | 1 |
| Type III restriction enzyme, res subunit | PF04851 | 3 |
| U3 small nucleolar RNA-associated protein 6 | PF08640 | 1 |
| U3 snoRNA associated | PF08297 | 1 |
| UAA transporter family | PF08449 | 1 |
| UBA/TS-N domain | PF00627 | 2 |
| ubiE/COQ5 methyltransferase family | PF01209 | 7 |
| Ubiquitin 3 binding protein But2 C-terminal domain | PF09792 | 1 |
| Ubiquitin carboxyl-terminal hydrolase | PF13423 | 3 |
| Ubiquitin carboxyl-terminal hydrolase | PF00443 | 3 |
| Ubiquitin carboxyl-terminal hydrolase, family 1 | PF01088 | 1 |
| Ubiquitin elongating factor core | PF10408 | 1 |
| Ubiquitin family | PF00240 | 4 |
| Ubiquitin fusion degradation protein UFD1 | PF03152 | 1 |
| Ubiquitin-2 like Rad60 SUMO-like | PF11976 | 1 |
| Ubiquitin-2 like Rad60 SUMO-like | PF13881 | 1 |
| Ubiquitin-conjugating enzyme | PF00179 | 3 |
| Ubiquitin-like autophagy protein Apg12 | PF04110 | 1 |
| U-box domain | PF04564 | 2 |
| UBX domain | PF00789 | 1 |
| UDP-glucuronosyl and UDP-glucosyl transferase | PF00201 | 1 |
| UDP-glucose 4-epimerase C-term subunit | PF13950 | 1 |

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| UDP-glucose:Glycoprotein Glucosyltransferase | PF06427 | 0 |
| Ulp1 protease family, C-terminal catalytic domain | PF02902 | 1 |
| Uncharacterised ACR, YagE family COG1723 | PF02582 | 1 |
| Uncharacterised protein family UPF0052 | PF01933 | 1 |
| Uncharacterized ACR, YdiU/UPF0061 family | PF02696 | 1 |
| Uncharacterized alpha/beta hydrolase domain (DUF2235) | PF09994 | 1 |
| Uncharacterized protein conserved in bacteria (DUF2264) | PF10022 | 1 |
| Up-frameshift suppressor 2 | PF04050 | 1 |
| Uracil phosphoribosyltransferase | PF14681 | 1 |
| Urease alpha-subunit, N-terminal domain | PF00449 | 1 |
| Urease beta subunit | PF00699 | 1 |
| Urease, gamma subunit | PF00547 | 1 |
| UTP--glucose-1-phosphate uridylyltransferase | PF01704 | 1 |
| Vacuolar 14 Fab1-binding region | PF12755 | 3 |
| Vacuolar ATP synthase subunit S1 (ATP6S1) | PF05827 | 1 |
| Vacuolar protein sorting protein 11 C terminal | PF12451 | 1 |
| Vacuolar protein sorting-associated protein 35 | PF03635 | 1 |
| Vacuolar segregation subunit 7 | PF12751 | 1 |
| Vacuolar sorting 38 and autophagy-related subunit 14 | PF10186 | 1 |
| Vacuolar sorting protein 9 (VPS9) domain | PF02204 | 1 |
| Variant SH3 domain | PF14604 | 4 |
| Variant SH3 domain | PF07653 | 4 |
| VHS domain | PF00790 | 1 |
| Vitamin B6 photo-protection and homoeostasis | PF04884 | 1 |
| Vitamin-D-receptor interacting Mediator subunit 4 | PF10018 | 1 |
| Voltage gated chloride channel | PF00654 | 1 |
| Voltage-dependent anion channel | PF03595 | 1 |
| von Willebrand factor type A domain | PF13519 | 1 |
| von Willebrand factor type A domain | PF00092 | 1 |
| Vps5 C terminal like | PF09325 | 1 |
| Vta1 like | PF04652 | 1 |
| V-type ATPase 116kDa subunit family | PF01496 | 1 |
| WD domain, G-beta repeat | PF00400 | 14 |

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| WD40-like Beta Propeller Repeat | PF07676 | 1 |
| WH2 motif | PF02205 | 1 |
| WLM domain | PF08325 | 1 |
| WSC domain | PF01822 | 15 |
| WW domain | PF00397 | 1 |
| X8 domain | PF07983 | 1 |
| XFP C-terminal domain | PF09363 | 1 |
| XFP N-terminal domain | PF09364 | 1 |
| XPG I-region | PF00867 | 2 |
| XPG N-terminal domain | PF00752 | 2 |
| Xylanase inhibitor C-terminal | PF14541 | 1 |
| Xylanase inhibitor N-terminal | PF14543 | 5 |
| Xylose isomerase-like TIM barrel | PF01261 | 1 |
| Yeast cortical protein KAR9 | PF08580 | 1 |
| Yeast mitochondrial distribution and morphology (MDM) proteins | PF08118 | 1 |
| YEATS family | PF03366 | 1 |
| Yippee zinc-binding/DNA-binding /Mis18, centromere assembly | PF03226 | 1 |
| Zeta toxin | PF06414 | 1 |
| Zinc carboxypeptidase | PF00246 | 14 |
| Zinc finger C-x8-C-x5-C-x3-H type (and similar) | PF00642 | 1 |
| zinc finger of C3HC4-type, RING | PF15227 | 1 |
| Zinc finger, C2H2 type | PF00096 | 3 |
| Zinc finger, C3HC4 type (RING finger) | PF00097 | 8 |
| Zinc finger, C3HC4 type (RING finger) | PF13923 | 2 |
| Zinc finger, C3HC4 type (RING finger) | PF13920 | 2 |
| Zinc-binding | PF12907 | 2 |
| Zinc-binding dehydrogenase | PF00107 | 4 |
| Zinc-finger double domain | PF13465 | 3 |
| zinc-RING finger domain | PF14634 | 2 |
| Zn-dependent metallo-hydrolase RNA specificity domain | PF07521 | 1 |

