

Supplementary Information

Epitopes

QQFPQQQ (IEDB ID 52028)

SMILES:

N[C@H](C(=O)N[C@H](C(=O)N[C@H](C(=O)N1[C@H](C(=O)N[C@H](C(=O)N[C@H](C(=O)N[C@H](C(=O)O)CCC(=O)N)CCC(=O)N)CCC(=O)N)CCC1)Cc1cccc1)CCC(=O)N)CCC(=O)N

InChI=1S/C39H58N12O13/c40-21(8-13-28(41)52)33(57)46-22(9-14-29(42)53)36(60)50-26(19-20-5-2-1-3-6-20)38(62)51-18-4-7-27(51)37(61)48-24(11-16-31(44)55)34(58)47-23(10-15-30(43)54)35(59)49-25(39(63)64)12-17-32(45)56/h1-3,5-6,21-27H,4,7-19,40H2,(H2,41,52)(H2,42,53)(H2,43,54)(H2,44,55)(H2,45,56)(H,46,57)(H,47,58)(H,48,61)(H,49,59)(H,50,60)(H,63,64)/t21-,22-,23-,24-,25-,26-,27-/m0/s1

InChIKey: NYDPXIRXHABUPK-DUJSLOSMSA-N

QQIPQQQ (IEDB ID 52043)

SMILES:

N[C@H](C(=O)N[C@H](C(=O)N[C@H](C(=O)N1[C@H](C(=O)N[C@H](C(=O)N[C@H](C(=O)N[C@H](C(=O)O)CCC(=O)N)CCC(=O)N)CCC(=O)N)CCC1)[C@H](CC)C)CCC(=O)N)CCC(=O)N

InChI=1S/C36H60N12O13/c1-3-17(2)29(47-33(57)21(9-14-27(41)52)43-30(54)18(37)6-11-24(38)49)35(59)48-16-4-5-23(48)34(58)45-20(8-13-26(40)51)31(55)44-19(7-12-25(39)50)32(56)46-22(36(60)61)10-15-28(42)53/h17-23,29H,3-16,37H2,1-2H3,(H2,38,49)(H2,39,50)(H2,40,51)(H2,41,52)(H2,42,53)(H,43,54)(H,44,55)(H,45,58)(H,46,56)(H,47,57)(H,60,61)/t17-,18-,19-,20-,21-,22-,23-,29-/m0/s1

InChIKey: OOICIMLPRJAEGU-GGAYEWCCSA-N

QQLPQQQ (IEDB ID 52066)

SMILES:

N[C@H](C(=O)N[C@H](C(=O)N[C@H](C(=O)N1[C@H](C(=O)N[C@H](C(=O)N[C@H](C(=O)O)CCC(=O)N)CCC(=O)N)CCC(=O)N)CCC1)CC(C)C)CCC(=O)N)CCC(=O)N

InChI=1S/C36H60N12O13/c1-17(2)16-23(47-33(57)19(6-11-26(39)50)43-30(54)18(37)5-10-25(38)49)35(59)48-15-3-4-24(48)34(58)45-21(8-13-28(41)52)31(55)44-20(7-12-27(40)51)32(56)46-22(36(60)61)9-14-29(42)53/h17-24H,3-16,37H2,1-2H3,(H2,38,49)(H2,39,50)(H2,40,51)(H2,41,52)(H2,42,53)(H,43,54)(H,44,55)(H,45,58)(H,46,56)(H,47,57)(H,60,61)/t18-,19-,20-,21-,22-,23-,24-/m0/s1

InChIKey: HBTIKQRSQNKVSN-LQDRYOBXSA-N

QQYPQQQ (IEDB ID 52180)

SMILES:

N[C@H](C(=O)N[C@H](C(=O)N[C@H](C(=O)N1[C@H](C(=O)N[C@H](C(=O)N[C@H](C(=O)O)CCC(=O)N)CCC(=O)N)CCC(=O)N)CCC1)Cc1ccc(cc1)O)CCC(=O)N)CCC(=O)N

InChI=1S/C39H58N12O14/c40-21(7-12-28(41)53)33(58)46-22(8-13-29(42)54)36(61)50-26(18-19-3-5-20(52)6-4-19)38(63)51-17-1-2-27(51)37(62)48-24(10-15-31(44)56)34(59)47-23(9-14-30(43)55)35(60)49-25(39(64)65)11-16-32(45)57/h3-6,21-27,52H,1-2,7-18,40H2,(H2,41,53)(H2,42,54)(H2,43,55)(H2,44,56)(H2,45,57)(H,46,58)(H,47,59)(H,48,62)(H,49,60)(H,50,61)(H,64,65)/t21-,22-,23-,24-,25-,26-,27-/m0/s1

InChIKey: XXLBCMJCIBJTLE-DUJSLOSMSA-N

Table S1. List oproteins containing epitopes from wheat ω -gliadin.

Domain names	Domain signatures in InterPro	Number of proteins containing domain	Number of proteins containing query sequence or sequences	Species	NCBI Taxonomy Identifiers (according to UniProt)	Proteins (entry names in UniProt)
Bromodomain, conserved site	IPR018359	3547	7	<i>Danio rerio</i>	7955	TR:Q1MT59_DANRE
						TR:F1R0I4_DANRE
						TR:A3KQN2_DANRE
				<i>Takifugu rubripes</i>	31033	TR:H2U5B7_TAKRU
						TR:H2U5B6_TAKRU
				<i>Oreochromis niloticus</i>	8128	TR:I3KHG7_ORENI
						TR:I3KHG6_ORENI
STAT transcription factor, DNA-binding	IPR013801	716	6	<i>Branchiostoma floridae</i>	7739	TR:C3ZUG6_BRAFL
				<i>Debaryomyces hansenii</i>	284592	TR:Q6BJE1_DEBHA
				<i>Vanderwaltozyma polyspora</i>	436907	TR:A7TQI4_VANPO
				<i>Caenorhabditis elegans</i>	6239	SP:P34545-3
						SP:P34545-2
						SP:CBP1_CAEEL
Domain of unknown function DUF902, CREBbp	IPR010303	215	7	<i>Danio rerio</i>	7955	TR:Q1MT59_DANRE
						TR:F1R0I4_DANRE
						TR:A3KQN2_DANRE
				<i>Takifugu rubripes</i>	31033	TR:H2U5B7_TAKRU
						TR:H2U5B6_TAKRU
				<i>Oreochromis niloticus</i>	8128	TR:I3KHG7_ORENI
						TR:I3KHG6_ORENI
Histone H3-K56 acetyltransferase, RTT109	IPR013178	576	7	<i>Danio rerio</i>	7955	TR:Q1MT59_DANRE
						TR:F1R0I4_DANRE
						TR:A3KQN2_DANRE
				<i>Takifugu rubripes</i>	31033	TR:H2U5B7_TAKRU
						TR:H2U5B6_TAKRU
				<i>Oreochromis niloticus</i>	8128	TR:I3KHG7_ORENI
						TR:I3KHG6_ORENI
Coactivator CBP, KIX domain	IPR003101	407	9	<i>Danio rerio</i>	7955	TR:Q1MT59_DANRE
						TR:F1R0I4_DANRE
						TR:A3KQN2_DANRE
				<i>Takifugu rubripes</i>	31033	TR:H2U5B7_TAKRU
						TR:H2U5B6_TAKRU
				<i>Oreochromis niloticus</i>	8128	TR:I3KHG7_ORENI

						TR:I3KHG6 ORENI TR:I3KHG7 ORENI TR:I3KHG6 ORENI
Nuclear receptor coactivator, interlocking	IPR009110	423	7	<i>Danio rerio</i> <i>Takifugu rubripes</i> <i>Oreochromis niloticus</i>	7955 31033 8128	TR:Q1MT59 DANRE TR:F1R0I4 DANRE TR:A3KQN2 DANRE TR:H2U5B7 TAKRU TR:H2U5B6 TAKRU TR:I3KHG7 ORENI TR:I3KHG6 ORENI
Nuclear receptor coactivator, CREB-bp-like, interlocking	IPR014744	162	7	<i>Danio rerio</i> <i>Takifugu rubripes</i> <i>Oreochromis niloticus</i>	7955 31033 8128	TR:Q1MT59 DANRE TR:F1R0I4 DANRE TR:A3KQN2 DANRE TR:H2U5B7 TAKRU TR:H2U5B6 TAKRU TR:I3KHG7 ORENI TR:I3KHG6 ORENI
Zinc finger, TAZ-type	IPR000197	598	10	<i>Danio rerio</i> <i>Takifugu rubripes</i> <i>Oreochromis niloticus</i> <i>Caenorhabditis elegans</i>	7955 31033 8128 6239	TR:Q1MT59 DANRE TR:F1R0I4 DANRE TR:A3KQN2 DANRE TR:H2U5B7 TAKRU TR:H2U5B6 TAKRU TR:I3KHG7 ORENI TR:I3KHG6 ORENI SP:P34545-3 SP:P34545-2 SP:CBP1 CAEEL
Zinc finger, ZZ-type	IPR000433	3365	7	<i>Danio rerio</i> <i>Takifugu rubripes</i> <i>Oreochromis niloticus</i>	7955 31033 8128	TR:Q1MT59 DANRE TR:A3KQN2 DANRE TR:F1R0I4 DANRE TR:H2U5B7 TAKRU TR:H2U5B6 TAKRU TR:I3KHG7 ORENI TR:I3KHG6 ORENI
Extracellular ligand-binding receptor	IPR001828	7136	2	<i>Danio rerio</i>	7955	TR:I3NI77 DANRE TR:Q1LUC8 DANRE
Glutamate receptor, L-glutamate/glycine-binding	IPR019594	2097	2	<i>Danio rerio</i>	7955	TR:I3NI77 DANRE TR:Q1LUC8 DANRE

Ionotropic glutamate receptor	IPR001320	3520	2	<i>Danio rerio</i>	7955	TR:I3NI77 DANRE
						TR:Q1LUC8 DANRE
N-Methyl-D-aspartate (NMDA)	IPR001508	1899	2	<i>Danio rerio</i>	7955	TR:I3NI77 DANRE
						TR:Q1LUC8 DANRE
Extracellular solute-binding protein, family 3	IPR001638	45324	2	<i>Danio rerio</i>	7955	TR:I3NI77 DANRE
						TR:Q1LUC8 DANRE
Shisa family	IPR026910	478	6	<i>Takifugu rubripes</i>	31033	TR:H2T9N9 TAKRU
						TR:H2T9N8 TAKRU
						TR:H2T9N4 TAKRU
						TR:H2T9N5 TAKRU
						TR:H2T9N6 TAKRU
						TR:H2T9N7 TAKRU
Bromodomain	IPR001487	7322	10	<i>Takifugu rubripes</i>	31033	TR:H2U5B7 TAKRU
				<i>Oreochromis niloticus</i>	8128	TR:H2U5B6 TAKRU
				<i>Branchiostoma floridae</i>	7739	TR:I3KHG7 ORENI
				<i>Debaryomyces hansenii</i>	284592	TR:I3KHG6 ORENI
				<i>Vanderwaltozyma polyspora</i>	436907	TR:C3ZUG6 BRAFL
				<i>Caenorhabditis elegans</i>	6239	TR:Q6BJE1 DEBHA
						TR:A7TQI4 VANPO
						SP:P34545-3
D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain	IPR006139	23105	3	<i>Takifugu rubripes</i>	31033	SP:P34545-2
				<i>Tetraodon nigroviridis</i>	99883	SP:CBP1 CAEEL
D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding	IPR006140	30438	3	<i>Takifugu rubripes</i>		TR:H2RUN0 TAKRU
				<i>Tetraodon nigroviridis</i>	99883	TR:H3C4K1 TETNG
						TR:H3C2Q1 TETNG
NAD(P)-binding domain	IPR016040	665366	3	<i>Takifugu rubripes</i>	31033	TR:H2RUN0 TAKRU
				<i>Tetraodon nigroviridis</i>	99883	TR:H3C4K1 TETNG
						TR:H3C2Q1 TETNG
Glycine-tyrosine-phenylalanine (GYF)	IPR003169	1085	8	<i>Homo sapiens</i>	9606	TR:I1E4Y6 HUMAN
						TR:B9EG55 HUMAN
						TR:E9PBB0 HUMAN
						SP:PERQ2 HUMAN
						SP:Q6Y7W6-3
				<i>Gorilla gorilla gorilla</i>	9595	TR:G3S2D3 GORGO

				<i>Pan troglodytes</i>	<u>9598</u>	TR:H2R5Z9 PANTR
				<i>Drosophila grimshawi</i>	<u>7222</u>	TR:B4JZU4 DROGR
CUB (complement C1r/C1s, Uegf, Bmp1)	<u>IPR000859</u>	6617	1	<i>Heterocephalus glaber</i>	<u>10181</u>	TR:G5BHP6 HETGA
frizzled (fz) domain	<u>IPR020067</u>	2130	1	<i>Heterocephalus glaber</i>	<u>10181</u>	TR:G5BHP6 HETGA
Low-density lipoprotein (LDL) receptors class A	<u>IPR023415</u>	4529	3	<i>Heterocephalus glaber</i>	<u>10181</u>	TR:G5BHP6 HETGA
				<i>Drosophila sechellia</i>	<u>7238</u>	TR:B4HWV4 DROSE
				<i>Drosophila melanogaster</i>	<u>7227</u>	TR:Q9Y110 DROME
Low-density lipoprotein (LDL) receptors class A	<u>IPR002172</u>	6374	3	<i>Heterocephalus glaber</i>	<u>10181</u>	TR:G5BHP6 HETGA
				<i>Drosophila sechellia</i>	<u>7238</u>	TR:B4HWV4 DROSE
				<i>Drosophila melanogaster</i>	<u>7227</u>	TR:Q9Y110 DROME
Zinc finger, B-box	<u>IPR000315</u>	9283	2	<i>Loxodonta africana</i>	<u>9785</u>	TR:G3TB61 LOXAF
				<i>Oxytricha trifallax</i>	<u>1172189</u>	TR:J9IX07 9SPIT
Zinc finger, RING-type	<u>IPR001841</u>	59461	10	<i>Loxodonta africana</i>	<u>9785</u>	TR:G3TB61 LOXAF
				<i>Drosophila virilis</i>	<u>7244</u>	SP:NEUR DROVI
						TR:B4M452 DROVI
				<i>Drosophila mojavensis</i>	<u>7230</u>	TR:B4KBUE DROMO
				<i>Drosophila persimilis</i>	<u>7234</u>	TR:B4GI37 DROPE
				<i>Drosophila pseudoobscura pseudoobscura</i>	<u>46245</u>	TR:Q28Z87 DROPS
				<i>Naumovozya dairenensis</i>	<u>1071378</u>	TR:G0WAM9 NAUDC
				<i>Dictyostelium discoideum</i>	<u>44689</u>	TR:Q75JM9 DICDI
				<i>Paramecium tetraurelia</i>	<u>5888</u>	TR:A0C100 PARTE
Zinc finger, RING/FYVE/PHD-type	<u>IPR013083</u>	86396	19	<i>Loxodonta africana</i>	<u>9785</u>	TR:G3TB61 LOXAF
				<i>Drosophila mojavensis</i>	<u>7230</u>	TR:B4KBUE DROMO
				<i>Drosophila virilis</i>	<u>7244</u>	TR:B4LC34 DROVI
						SP:NEUR DROVI
						TR:B4M452 DROVI
				<i>Drosophila simulans</i>	<u>7240</u>	TR:B4QJJ2 DROSI
				<i>Anopheles gambiae</i>	<u>7165</u>	TR:Q7QET6 ANOGA
						TR:A0ND10 ANOGA
				<i>Drosophila persimilis</i>	<u>7234</u>	TR:B4GI37 DROPE
				<i>Drosophila pseudoobscura pseudoobscura</i>	<u>46245</u>	TR:Q28Z87 DROPS
				<i>Drosophila erecta</i>	<u>7220</u>	TR:B3P3P0 DROER
						TR:B3ND01 DROER
				<i>Drosophila melanogaster</i>	<u>7227</u>	TR:Q9VUB5 DROME
				<i>Candida dubliniensis</i>	<u>573826</u>	TR:B9WA30 CANDC
				<i>Gaeumannomyces graminis var. tritici</i>	<u>644352</u>	TR:J3P975 GAGT3
				<i>Naumovozya dairenensis</i>	<u>1071378</u>	TR:G0WAM9 NAUDC

				<i>Dictyostelium discoideum</i>	44689	TR:Q75JM9 DICDI
				<i>Oxytricha trifallax</i>	1172189	TR:J9IX07 9SPIT
				<i>Tetrahymena thermophila</i>	312017	TR:I7LXF1 TETTS
Zinc finger, RING-type, conserved site	IPR017907	26140	1	<i>Loxodonta africana</i>	9785	TR:G3TB61 LOXAF
Mediator complex, subunit Med15, metazoa	IPR019087	209	3	<i>Gallus gallus</i>	9031	TR:F1P1D8 CHICK
				<i>Taeniopygia guttata</i>	59729	TR:H0ZIR6 TAEGU
				<i>Drosophila grimshawi</i>	7222	TR:B4JL62 DROGR
Band 4.1 domain	IPR019749	4803	1	<i>Xenopus tropicalis</i>	8364	TR:F6THY5 XENTR
Band 4.1 family	IPR019750	2356	1	<i>Xenopus tropicalis</i>	8364	TR:F6THY5 XENTR
Ezrin/radixin/moesin like	IPR000798	1508	1	<i>Xenopus tropicalis</i>	8364	TR:F6THY5 XENTR
FERM adjacent (FA)	IPR014847	1219	1	<i>Xenopus tropicalis</i>	8364	TR:F6THY5 XENTR
FERM/acyl-CoA-binding protein, 3-helical bundle	IPR014352	6107	1	<i>Xenopus tropicalis</i>	8364	TR:F6THY5 XENTR
FERM central domain	IPR019748	4904	1	<i>Xenopus tropicalis</i>	8364	TR:F6THY5 XENTR
FERM conserved site	IPR019747	2213	1	<i>Xenopus tropicalis</i>	8364	TR:F6THY5 XENTR
FERM domain	IPR000299	5158	1	<i>Xenopus tropicalis</i>	8364	TR:F6THY5 XENTR
FERM, N-terminal	IPR018979	3230	1	<i>Xenopus tropicalis</i>	8364	TR:F6THY5 XENTR
FERM, C-terminal PH-like domain	IPR018980	2555	1	<i>Xenopus tropicalis</i>	8364	TR:F6THY5 XENTR
Pleckstrin homology-like domain	IPR011993	42524	4	<i>Xenopus tropicalis</i>	8364	TR:F6THY5 XENTR
				<i>Trichosporon asahii</i> var. <i>asahii</i>	1186058	TR:J4UAX5 TRIAS
				<i>Trichinella spiralis</i>	6334	TR:E5S526 TRISP
Terminal deoxynucleotidyltransferase-interacting factor 1	PR026064	78	1	<i>Crotalus adamanteus</i>	8729	TR:J3SC40 CROAD
Insect cuticle protein	IPR000618	3690	1	<i>Antheraea yamamai</i>	7121	TR:G8FVQ1 ANTYA
NOPS	IPR012975	304	3	<i>Bombyx mori</i>	7091	TR:Q0ZAL3 BOMMO
						TR:Q2F5M7 BOMMO
						TR:H9J6N5 BOMMO

Nucleotide-binding, alpha-beta plait	IPR012677	61810	12	<i>Bombyx mori</i>	7091	TR:Q0ZAL3 BOMMO
						TR:Q2F5M7 BOMMO
						TR:H9J6N5 BOMMO
				<i>Drosophila persimilis</i>	7234	TR:B4G5G9 DROPE
				<i>Drosophila pseudoobscura pseudoobscura</i>	46245	TR:Q299N5 DROPS
				<i>Picea sitchensis</i>	3332	TR:B8LMP2 PICSJ
				<i>Yarrowia lipolytica</i>	284591	TR:Q6CDX5 YARLI
				<i>Nectria haematococca</i>	660122	TR:C7YQJ8 NECH7
				<i>Naumovozyma dairenensis</i>	1071378	TR:G0WAM9 NAUDC
				<i>Torulaspora delbrueckii</i>	1076872	TR:G8ZRC4 TORDC
RNA	IPR000504	48359	12	<i>Bombyx mori</i>	7091	TR:Q0ZAL3 BOMMO
						TR:Q2F5M7 BOMMO
						TR:H9J6N5 BOMMO
				<i>Drosophila persimilis</i>	7234	TR:B4G5G9 DROPE
				<i>Drosophila pseudoobscura pseudoobscura</i>	46245	TR:Q299N5 DROPS
				<i>Picea sitchensis</i>	3332	TR:B8LMP2 PICSJ
				<i>Yarrowia lipolytica</i>	284591	TR:Q6CDX5 YARLI
				<i>Nectria haematococca</i>	660122	TR:C7YQJ8 NECH7
				<i>Naumovozyma dairenensis</i>	1071378	TR:G0WAM9 NAUDC
				<i>Torulaspora delbrueckii</i>	1076872	TR:G8ZRC4 TORDC
TSC-22 / Dip / Bun	IPR000580	498	1	<i>Capsaspora owczarzaki</i>	595528	TR:E9C1R9 CAPO3
				<i>Tetrahymena thermophila</i>	312017	TR:I7MB64 TETTS
Putative 5-3 exonuclease	IPR004859	947	2	<i>Acyrtosiphon pisum</i>	7029	TR:J9K207 ACYPI
				<i>Drosophila mojavensis</i>	7230	TR:B4L6X0 DROMO
Domain of unknown function DUF243	IPR004145	416	1	<i>Acyrtosiphon pisum</i>	7029	TR:J9K207 ACYPI
Transcription factor IIA, helical	IPR009083	789	2	<i>Acyrtosiphon pisum</i>	7029	TR:J9K8X1 ACYPI
				<i>Phaeosphaeria nodorum</i>	321614	TR:Q0U9N8 PHANO
Transcription factor IIA, alpha/beta subunit	IPR004855	488	2	<i>Acyrtosiphon pisum</i>	7029	TR:J9K8X1 ACYPI
				<i>Phaeosphaeria nodorum</i>	321614	TR:Q0U9N8 PHANO
Transcription factor IIA, alpha subunit, N-terminal	IPR013028	1210	2	<i>Acyrtosiphon pisum</i>	7029	TR:J9K8X1 ACYPI
				<i>Phaeosphaeria nodorum</i>	321614	TR:Q0U9N8 PHANO
Transcription factor IIA, beta-barrel	IPR009088	861	2	<i>Acyrtosiphon pisum</i>	7029	TR:J9K8X1 ACYPI
				<i>Phaeosphaeria nodorum</i>	321614	TR:Q0U9N8 PHANO

BRK domain	IPR006576	518	1	<i>Acyrtosiphon pisum</i>	7029	TR:J9JZG8 ACYPI
Chromo domain	IPR023780	5455	1	<i>Acyrtosiphon pisum</i>	7029	TR:J9JZG8 ACYPI
Chromo domain/shadow	IPR000953	6667	2	<i>Acyrtosiphon pisum</i>	7029	TR:J9JZG8 ACYPI
				<i>Drosophila mojavensis</i>	7230	TR:B4L5I5 DROMO
Chromo domain-like	IPR016197	7064	2	<i>Acyrtosiphon pisum</i>	7029	TR:J9JZG8 ACYPI
				<i>Drosophila mojavensis</i>	7230	TR:B4L5I5 DROMO
Helicase, superfamily 1/2, ATP-binding domain	IPR014001	137284	12	<i>Acyrtosiphon pisum</i>	7029	TR:J9JZG8 ACYPI
				<i>Drosophila willistoni</i>	7260	TR:B4NDR4 DROWI
				<i>Arabidopsis thaliana</i>	3702	SP:RH40 ARATH
				<i>Arabidopsis lyrata subsp. lyrata</i>	81972	TR:D7L5I4 ARALL
				<i>Volvox carteri</i>	3067	TR:D8TLQ2 VOLCA
				<i>Debaryomyces hansenii</i>	284592	TR:Q6BJE1 DEBHA
				<i>Ferrimonas balearica</i>	550540	TR:E1SVZ1 FERBD
				<i>Caenorhabditis brenneri</i>	135651	TR:G0M812 CAEBE
				<i>Dictyostelium purpureum</i>	5786	TR:F1A5J1 DICPU
				<i>Dictyostelium discoideum</i>	44689	TR:Q55GK2 DICDI
				<i>Paramecium tetraurelia</i>	5888	TR:A0BWN9 PARTE
				<i>Oxytricha trifallax</i>	1172189	TR:J9HL00 9SPIT
Helicase, C-terminal	IPR001650	130072	10	<i>Acyrtosiphon pisum</i>	7029	TR:J9JZG8 ACYPI
				<i>Arabidopsis thaliana</i>	3702	SP:RH40 ARATH
				<i>Arabidopsis lyrata subsp. lyrata</i>	81972	TR:D7L5I4 ARALL
				<i>Volvox carteri</i>	3067	TR:D8TLQ2 VOLCA
				<i>Ferrimonas balearica</i>	550540	TR:E1SVZ1 FERBD
				<i>Caenorhabditis brenneri</i>	135651	TR:G0M812 CAEBE
				<i>Dictyostelium purpureum</i>	5786	TR:F1A5J1 DICPU
				<i>Dictyostelium discoideum</i>	44689	TR:Q55GK2 DICDI
				<i>Paramecium tetraurelia</i>	5888	TR:A0BWN9 PARTE
				<i>Oxytricha trifallax</i>	1172189	TR:J9HL00 9SPIT
SANT/Myb domain	IPR001005	20475	8	<i>Acyrtosiphon pisum</i>	7029	TR:J9JZG8 ACYPI
				<i>Vitis vinifera</i>	29760	TR:F6I025 VITVI
				<i>Candida parapsilosis</i>	578454	TR:G8BH70 CANPC
				<i>Cordyceps militaris</i>	983644	TR:G3JEU7 CORMM
				<i>Dictyostelium purpureum</i>	5786	TR:F1A5J1 DICPU
				<i>Dictyostelium discoideum</i>	44689	TR:Q55GK2 DICDI
						SP:MYBU DICDI
SNF2-related	IPR000330	18770	7	<i>Acyrtosiphon pisum</i>	7029	TR:J9JZG8 ACYPI
				<i>Volvox carteri</i>	3067	TR:D8TLQ2 VOLCA
				<i>Debaryomyces hansenii</i>	284592	TR:Q6BJE1 DEBHA

				Caenorhabditis brenneri	135651	TR:G0M812 CAEBE
				Dictyostelium purpureum	5786	TR:F1A5J1 DICPU
				Dictyostelium discoideum	44689	TR:Q55GK2 DICDI
				Oxytricha trifallax	1172189	TR:J9HL00 9SPIT
Protein of unknown function DUF745	IPR007999	193	2	Drosophila virilis	7244	TR:B4LE38 DROVI
				Drosophila grimshawi	7222	TR:B4IYI3 DROGR
Endonuclease/exonuclease/phosphatase	IPR005135	31253	2	Drosophila virilis	7244	TR:B4MF58 DROVI
				Oxytricha trifallax	1172189	TR:J9ETF9 9SPIT
FAS1 domain	IPR000782	3777	3	Drosophila virilis	7244	TR:B4M8R3 DROVI
				Drosophila mojavensis	7230	TR:B4KEJ8 DROMO
				Drosophila grimshawi	7222	TR:B4JD81 DROGR
Ankyrin repeat	IPR002110	54268	6	Drosophila virilis	7244	TR:B4M5Q9 DROVI
				Drosophila mojavensis	7230	TR:B4K7G3 DROMO
				Drosophila grimshawi	7222	TR:B4JVH5 DROGR
				Volvox carteri	3067	TR:D8U185 VOLCA
				Polysphondylium pallidum	13642	TR:D3AZ77 POLPA
Tetrahymena thermophila	312017	TR:Q23QL4 TETTS				
Ankyrin repeat-containing domain	IPR020683	57304	6	Drosophila virilis	7244	TR:B4M5Q9 DROVI
				Drosophila mojavensis	7230	TR:B4K7G3 DROMO
				Drosophila grimshawi	7222	TR:B4JVH5 DROGR
				Volvox carteri	3067	TR:D8U185 VOLCA
				Polysphondylium pallidum	13642	TR:D3AZ77 POLPA
Tetrahymena thermophila	312017	TR:Q23QL4 TETTS				
K Homology domain	IPR004087	32528	3	Drosophila virilis	7244	TR:B4M5Q9 DROVI
				Drosophila mojavensis	7230	TR:B4K7G3 DROMO
				Volvox carteri	3067	TR:D8TYC9 VOLCA
K Homology domain, type 1	IPR004088	23967	3	Drosophila virilis	7244	TR:B4M5Q9 DROVI
				Drosophila mojavensis	7230	TR:B4K7G3 DROMO
				Volvox carteri	3067	TR:D8TYC9 VOLCA
C2 calcium-dependent membrane targeting	IPR000008	18264	9	Drosophila virilis	7244	TR:B4M6Q2 DROVI
				Drosophila erecta	7220	TR:B3P3P0 DROER
				Volvox carteri	3067	TR:D8U185 VOLCA
				Gaeumannomyces graminis var. tritici	644352	TR:J3P6H6 GAGT3
				Polysphondylium pallidum	13642	TR:D3BU61 POLPA
				Dictyostelium fasciculatum	1054147	TR:F4PU20 DICFS
				Oxytricha trifallax	1172189	TR:J9EJ94 9SPIT
				Naegleria gruberi	5762	TR:D2VCR4 NAEGR

				<i>Trichomonas vaginalis</i>	5722	TR:A2EUT8 TRIVA
C2 calcium/lipid-binding domain, CaLB	IPR008973	20201	9	<i>Drosophila virilis</i> <i>Drosophila erecta</i> <i>Volvox carteri</i> <i>Gaeumannomyces graminis</i> var. <i>tritici</i> <i>Polysphondylium pallidum</i> <i>Dictyostelium fasciculatum</i> <i>Oxytricha trifallax</i> <i>Naegleria gruberi</i> <i>Trichomonas vaginalis</i>	7244 7220 3067 644352 13642 1054147 1172189 5762 5722	TR:B4M6Q2 DROVI TR:B3P3P0 DROER TR:D8U185 VOLCA TR:J3P6H6 GAGT3 TR:D3BU61 POLPA TR:F4PU20 DICFS TR:J9EJ94 9SPIT TR:D2VCR4 NAEGR TR:A2EUT8 TRIVA
Protein of unknown function DUF3498	IPR021887	276	1	<i>Drosophila virilis</i>	7244	TR:B4M6Q2 DROVI
Pleckstrin homology domain	IPR001849	29818	4	<i>Drosophila virilis</i> <i>Trichosporon asahii</i> var. <i>asahii</i> <i>Trichosporon asahii</i> var. <i>asahii</i> <i>Trichinella spiralis</i>	7244 1186058 1220162 6334	TR:B4M6Q2 DROVI TR:J4UAX5 TRIAS TR:K1WQD6 TRIAC TR:E5S526 TRISP
Ras GTPase-activating protein	IPR001936	2102	1	<i>Drosophila virilis</i>	7244	TR:B4M6Q2 DROVI
Ras GTPase-activating protein, conserved site	IPR023152	1305	1	<i>Drosophila virilis</i>	7244	TR:B4M6Q2 DROVI
Rho GTPase activation protein	IPR008936	11228	1	<i>Drosophila virilis</i>	7244	TR:B4M6Q2 DROVI
Galactose mutarotase-like domain	IPR011013	31578	1	<i>Drosophila virilis</i>	7244	TR:B4M4C9 DROVI
Glycoside hydrolase/deacetylase, beta/alpha-barrel	IPR011330	30252	1	<i>Drosophila virilis</i>	7244	TR:B4M4C9 DROVI
Glycosyl hydrolase, family 13, all-beta	IPR013780	27561	1	<i>Drosophila virilis</i>	7244	TR:B4M4C9 DROVI
Glycosyl hydrolase family 38, C-terminal	IPR011682	3048	1	<i>Drosophila virilis</i>	7244	TR:B4M4C9 DROVI
Glycoside hydrolase, family 38, central domain	IPR015341	3239	1	<i>Drosophila virilis</i>	7244	TR:B4M4C9 DROVI
Glycoside hydrolase family 38, N-terminal domain	IPR000602	3430	1	<i>Drosophila virilis</i>	7244	TR:B4M4C9 DROVI
Cysteine-rich flanking region, C-terminal	IPR000483	7421	12	<i>Drosophila virilis</i> <i>Drosophila mojavensis</i> <i>Drosophila ananassae</i> <i>Drosophila sechellia</i> <i>Drosophila simulans</i>	7244 7230 7217 7238 7240	TR:B4LQ18 DROVI TR:B4KT45 DROMO TR:B3MJR7 DROAN TR:B3MEY9 DROAN TR:B4HSK9 DROSE TR:B4QHG3 DROSI

				<i>Drosophila yakuba</i>	<u>7245</u>	TR:B4P6Q2 DROYA
				<i>Drosophila erecta</i>	<u>7220</u>	TR:B3NPW3 DROER
				<i>Drosophila melanogaster</i>	<u>7227</u>	TR:A1ZAB1 DROME
						TR:C4IXX4 DROME
						TR:C4IXX5 DROME
				<i>Drosophila grimshawi</i>	<u>7222</u>	TR:B4JWA4 DROGR
Immunoglobulin-like domain	<u>IPR007110</u>	63124	13	<i>Drosophila virilis</i>	<u>7244</u>	TR:B4LQ18 DROVI
				<i>Drosophila mojavensis</i>	<u>7230</u>	TR:B4KT45 DROMO
				<i>Drosophila ananassae</i>	<u>7217</u>	TR:B3MJR7 DROAN
						TR:B3MEY9 DROAN
				<i>Drosophila sechellia</i>	<u>7238</u>	TR:B4HSK9 DROSE
				<i>Drosophila simulans</i>	<u>7240</u>	TR:B4QHG3 DROSI
				<i>Drosophila yakuba</i>	<u>7245</u>	TR:B4P6Q2 DROYA
				<i>Drosophila erecta</i>	<u>7220</u>	TR:B3NPW3 DROER
				<i>Drosophila melanogaster</i>	<u>7227</u>	TR:A1ZAB1 DROME
						TR:C4IXX4 DROME
				<i>Drosophila grimshawi</i>	<u>7222</u>	TR:B4JWA4 DROGR
				<i>Pristionchus pacificus</i>	<u>54126</u>	TR:H3FTN9 PRIPA
				<i>Ascaris suum</i>	<u>6253</u>	TR:F1KQG0 ASCSU
Immunoglobulin-like fold	<u>IPR013783</u>	128338	16	<i>Drosophila virilis</i>	<u>7244</u>	TR:B4LQ18 DROVI
				<i>Drosophila mojavensis</i>	<u>7230</u>	TR:B4KT45 DROMO
				<i>Drosophila ananassae</i>	<u>7217</u>	TR:B3MJR7 DROAN
						TR:B3MEY9 DROAN
				<i>Drosophila sechellia</i>	<u>7238</u>	TR:B4HSK9 DROSE
				<i>Drosophila simulans</i>	<u>7240</u>	TR:B4QHG3 DROSI
				<i>Drosophila yakuba</i>	<u>7245</u>	TR:B4P6Q2 DROYA
				<i>Drosophila erecta</i>	<u>7220</u>	TR:B3NPW3 DROER
				<i>Drosophila melanogaster</i>	<u>7227</u>	TR:A1ZAB1 DROME
						TR:C4IXX4 DROME
				<i>Drosophila grimshawi</i>	<u>7222</u>	TR:B4JWA4 DROGR
						TR:B4JD22 DROGR
				<i>Pristionchus pacificus</i>	<u>54126</u>	TR:H3FTN9 PRIPA
				<i>Ascaris suum</i>	<u>6253</u>	TR:F1KQG0 ASCSU
				<i>Kitasatospora setae</i>	<u>452652</u>	TR:E4N1V7 KITSK
				<i>Dictyostelium purpureum</i>	<u>5786</u>	TR:F0ZYQ8 DICPU
Immunoglobulin I-set	<u>IPR013098</u>	19132	13	<i>Drosophila virilis</i>	<u>7244</u>	TR:B4LQ18 DROVI
				<i>Drosophila mojavensis</i>	<u>7230</u>	TR:B4KT45 DROMO
				<i>Drosophila ananassae</i>	<u>7217</u>	TR:B3MJR7 DROAN
						TR:B3MEY9 DROAN
				<i>Drosophila sechellia</i>	<u>7238</u>	TR:B4HSK9 DROSE
				<i>Drosophila simulans</i>	<u>7240</u>	TR:B4QHG3 DROSI
				<i>Drosophila yakuba</i>	<u>7245</u>	TR:B4P6Q2 DROYA

				<i>Drosophila erecta</i>	<u>7220</u>	TR:B3NPW3 DROER
				<i>Drosophila melanogaster</i>	<u>7227</u>	TR:A1ZAB1 DROME
						TR:C4IXX4 DROME
				<i>Drosophila grimshawi</i>	<u>7222</u>	TR:B4JWA4 DROGR
				<i>Pristionchus pacificus</i>	<u>54126</u>	TR:H3FTN9 PRIPA
				<i>Ascaris suum</i>	<u>6253</u>	TR:F1KQG0 ASCSU
Immunoglobulin subtype	<u>IPR003599</u>	28488	12	<i>Drosophila virilis</i>	<u>7244</u>	TR:B4LQ18 DROVI
				<i>Drosophila mojavensis</i>	<u>7230</u>	TR:B4KT45 DROMO
				<i>Drosophila ananassae</i>	<u>7217</u>	TR:B3MEY9 DROAN
				<i>Drosophila sechellia</i>	<u>7238</u>	TR:B4HSK9 DROSE
				<i>Drosophila simulans</i>	<u>7240</u>	TR:B4QHG3 DROSI
				<i>Drosophila yakuba</i>	<u>7245</u>	TR:B4P6Q2 DROYA
				<i>Drosophila erecta</i>	<u>7220</u>	TR:B3NPW3 DROER
				<i>Drosophila melanogaster</i>	<u>7227</u>	TR:A1ZAB1 DROME
						TR:C4IXX4 DROME
				<i>Drosophila grimshawi</i>	<u>7222</u>	TR:B4JWA4 DROGR
				<i>Pristionchus pacificus</i>	<u>54126</u>	TR:H3FTN9 PRIPA
				<i>Ascaris suum</i>	<u>6253</u>	TR:F1KQG0 ASCSU
Immunoglobulin subtype 2	<u>IPR003598</u>	19241	12	<i>Drosophila virilis</i>	<u>7244</u>	TR:B4LQ18 DROVI
				<i>Drosophila mojavensis</i>	<u>7230</u>	TR:B4KT45 DROMO
				<i>Drosophila ananassae</i>	<u>7217</u>	TR:B3MJR7 DROAN
						TR:B3MEY9 DROAN
				<i>Drosophila sechellia</i>	<u>7238</u>	TR:B4HSK9 DROSE
				<i>Drosophila simulans</i>	<u>7240</u>	TR:B4QHG3 DROSI
				<i>Drosophila yakuba</i>	<u>7245</u>	TR:B4P6Q2 DROYA
				<i>Drosophila melanogaster</i>	<u>7227</u>	TR:A1ZAB1 DROME
						TR:C4IXX4 DROME
				<i>Drosophila grimshawi</i>	<u>7222</u>	TR:B4JWA4 DROGR
				<i>Pristionchus pacificus</i>	<u>54126</u>	TR:H3FTN9 PRIPA
				<i>Ascaris suum</i>	<u>6253</u>	TR:F1KQG0 ASCSU
Leucine	<u>IPR001611</u>	42876	16	<i>Drosophila virilis</i>	<u>7244</u>	TR:B4LQ18 DROVI
				<i>Drosophila mojavensis</i>	<u>7230</u>	TR:B4KT45 DROMO
				<i>Drosophila ananassae</i>	<u>7217</u>	TR:B3MJR7 DROAN
						TR:B3MEY9 DROAN
				<i>Drosophila sechellia</i>	<u>7238</u>	TR:B4HSK9 DROSE
						TR:B4HTZ7 DROSE
				<i>Drosophila simulans</i>	<u>7240</u>	TR:B4QHG3 DROSI
				<i>Drosophila yakuba</i>	<u>7245</u>	TR:B4PHP3 DROYA
						TR:B4P6Q2 DROYA
				<i>Drosophila erecta</i>	<u>7220</u>	TR:B3NG33 DROER
						TR:B3NPW3 DROER
				<i>Drosophila melanogaster</i>	<u>7227</u>	TR:A1ZAB1 DROME

						TR:C4IXX4 DROME
						TR:C4IXX5 DROME
				<i>Drosophila grimshawi</i>	7222	TR:B4JWA4 DROGR
				<i>Yarrowia lipolytica</i>	284591	TR:Q6C1M0 YARLI
Leucine-rich repeat, typical subtype	IPR003591	16374	12	<i>Drosophila virilis</i>	7244	TR:B4LQ18 DROVI
				<i>Drosophila mojavensis</i>	7230	TR:B4KT45 DROMO
				<i>Drosophila ananassae</i>	7217	TR:B3MJR7 DROAN
						TR:B3MJR7 DROAN
						TR:B3MEY9 DROAN
				<i>Drosophila sechellia</i>	7238	TR:B4HSK9 DROSE
				<i>Drosophila simulans</i>	7240	TR:B4QHG3 DROSI
				<i>Drosophila erecta</i>	7220	TR:B3NPW3 DROER
				<i>Drosophila melanogaster</i>	7227	TR:A1ZAB1 DROME
						TR:C4IXX4 DROME
						TR:C4IXX5 DROME
				<i>Drosophila grimshawi</i>	7222	TR:B4JWA4 DROGR
Leucine-rich repeat-containing N-terminal	IPR000372	8238	11	<i>Drosophila virilis</i>	7244	TR:B4LQ18 DROVI
				<i>Drosophila mojavensis</i>	7230	TR:B4KT45 DROMO
				<i>Drosophila ananassae</i>	7217	TR:B3MEY9 DROAN
				<i>Drosophila sechellia</i>	7238	TR:B4HSK9 DROSE
				<i>Drosophila simulans</i>	7240	TR:B4QHG3 DROSI
				<i>Drosophila yakuba</i>	7245	TR:B4P6Q2 DROYA
				<i>Drosophila erecta</i>	7220	TR:B3NPW3 DROER
				<i>Drosophila melanogaster</i>	7227	TR:A1ZAB1 DROME
						TR:C4IXX4 DROME
						TR:C4IXX5 DROME
				<i>Drosophila grimshawi</i>	7222	TR:B4JWA4 DROGR
BRCT domain	IPR001357	13569	7	<i>Drosophila virilis</i>	7244	TR:B4LC32 DROVI
				<i>Drosophila mojavensis</i>	7230	TR:B4L165 DROMO
				<i>Drosophila sechellia</i>	7238	TR:B4HHB0 DROSE
				<i>Drosophila simulans</i>	7240	TR:B4QJ4 DROSI
				<i>Drosophila willistoni</i>	7260	TR:B4MLV6 DROWI
				<i>Drosophila melanogaster</i>	7227	TR:Q9VUB7 DROME
				<i>Drosophila grimshawi</i>	7222	TR:B4IXZ0 DROGR
NEUZ is a domain of unknown function found in neuralized proteins	IPR006573	500	3	<i>Drosophila virilis</i>	7244	SP:NEUR DROVI
				<i>Drosophila mojavensis</i>	7230	TR:B4KBU2 DROMO
				<i>Drosophila virilis</i>	7244	TR:B4M452 DROVI
Zinc finger, C2H2	IPR007087	72394	19	<i>Drosophila virilis</i>	7244	SP:NEUR DROVI
						TR:B4M452 DROVI

				<i>Drosophila mojavensis</i>	<u>7230</u>	TR:B4KUQ6 DROMO
						TR:B4L1S9 DROMO
						TR:B4KIA8 DROMO
				<i>Drosophila willistoni</i>	<u>7260</u>	TR:B4N1N6 DROWI
						TR:B4MIRO DROWI
				<i>Anopheles gambiae</i>	<u>7165</u>	TR:Q7QET6 ANOGA
						TR:A0ND10 ANOGA
				<i>Tetraodon nigroviridis</i>	<u>99883</u>	TR:Q4RUC4 TETNG
				<i>Yarrowia lipolytica</i>	<u>284591</u>	TR:Q6CGR7 YARLI
				<i>Candida dubliniensis</i>	<u>573826</u>	TR:B9WEZ3 CANDC
				<i>Spathaspora passalidarum</i>	<u>619300</u>	TR:G3AT45 SPAPN
				<i>Macrophomina phaseolina</i>	<u>1126212</u>	TR:K2S7S7 MACPH
				<i>Vanderwaltozyma polyspora</i>	<u>436907</u>	TR:A7TRZ6 VANPO
				<i>Caenorhabditis remanei</i>	<u>31234</u>	TR:E3LN59 CAERE
Zinc finger, C2H2-like	<u>IPR015880</u>	82683	21	<i>Drosophila virilis</i>	<u>7244</u>	SP:NEUR DROVI
						TR:B4M452 DROVI
				<i>Culex quinquefasciatus</i>	<u>7176</u>	TR:B0W767 CULQU
				<i>Drosophila mojavensis</i>	<u>7230</u>	TR:B4KUQ6 DROMO
						TR:B4L1S9 DROMO
						TR:B4KIA8 DROMO
				<i>Drosophila willistoni</i>	<u>7260</u>	TR:B4N1N6 DROWI
				<i>Anopheles gambiae</i>	<u>7165</u>	TR:Q7QET6 ANOGA
						TR:A0ND10 ANOGA
				<i>Tetraodon nigroviridis</i>	<u>99883</u>	TR:Q4RUC4 TETNG
				<i>Yarrowia lipolytica</i>	<u>284591</u>	TR:Q6CGR7 YARLI
				<i>Candida dubliniensis</i>	<u>573826</u>	TR:B9WEZ3 CANDC
				<i>Spathaspora passalidarum</i>	<u>619300</u>	TR:G3AT45 SPAPN
				<i>Macrophomina phaseolina</i>	<u>1126212</u>	TR:K2S5I6 MACPH
Zinc finger C2H2-type/integrase DNA-binding domain	<u>IPR013087</u>	63783	13			TR:K2S7S7 MACPH
				<i>Vanderwaltozyma polyspora</i>	<u>436907</u>	TR:A7TRZ6 VANPO
				<i>Caenorhabditis remanei</i>	<u>31234</u>	TR:E3LN59 CAERE
				<i>Dictyostelium discoideum</i>	<u>44689</u>	TR:Q556F5 DICDI
				<i>Tetrahymena thermophila</i>	<u>312017</u>	TR:I7MB64 TETTS
				<i>Monosiga brevicollis</i>	<u>81824</u>	TR:A9V3U7 MONBE
				<i>Salpingoeca rosetta</i>	<u>946362</u>	TR:F2TZX2 SALS5
				<i>Drosophila virilis</i>	<u>7244</u>	TR:B4LV56 DROVI
				<i>Drosophila mojavensis</i>	<u>7230</u>	TR:B4KUQ6 DROMO
						TR:B4L1S9 DROMO
				<i>Drosophila willistoni</i>	<u>7260</u>	TR:B4N1N6 DROWI
				<i>Anopheles gambiae</i>	<u>7165</u>	TR:Q7QET6 ANOGA

						TR:A0ND10 ANOGA
				<i>Yarrowia lipolytica</i>	<u>284591</u>	TR:Q6CGR7 YARLI
				<i>Candida dubliniensis</i>	<u>573826</u>	TR:B9WEZ3 CANDC
				<i>Spathaspora passalidarum</i>	<u>619300</u>	TR:G3AT45 SPAPN
				<i>Vanderwaltozyma polyspora</i>	<u>436907</u>	TR:A7TRZ6 VANPO
				<i>Caenorhabditis remanei</i>	<u>31234</u>	TR:E3LN59 CAERE
				<i>Monosiga brevicollis</i>	<u>81824</u>	TR:A9V3U7 MONBE
				<i>Salpingoeca rosetta</i>	<u>946362</u>	TR:F2TZX2 SALS5
Nuclear hormone receptor, ligand-binding	<u>IPR008946</u>	8956	4	<i>Drosophila virilis</i>	<u>7244</u>	TR:B4LHV8 DROVI
				<i>Drosophila grimshawi</i>	<u>7222</u>	TR:B4JON8 DROGR
				<i>Drosophila mojavensis</i>	<u>7230</u>	TR:B4L034 DROMO
				<i>Aedes aegypti</i>	<u>7159</u>	TR:Q0IE91 AEDAE
Zinc finger, nuclear hormone receptor-type	<u>IPR001628</u>	7972	4	<i>Drosophila virilis</i>	<u>7244</u>	TR:B4LHV8 DROVI
				<i>Drosophila mojavensis</i>	<u>7230</u>	TR:B4L034 DROMO
				<i>Drosophila grimshawi</i>	<u>7222</u>	TR:B4JON8 DROGR
				<i>Aedes aegypti</i>	<u>7159</u>	TR:Q0IE91 AEDAE
Homeobox protein, antennapedia type, conserved site	<u>IPR001827</u>	1969	13	<i>Drosophila virilis</i>	<u>7244</u>	TR:Q8I195 DROVI
				<i>Drosophila mojavensis</i>	<u>7230</u>	TR:B4K6G4 DROMO
				<i>Drosophila sechellia</i>	<u>7238</u>	TR:B4I4J9 DROSE
				<i>Drosophila simulans</i>	<u>7240</u>	TR:B4QYW7 DROSI
				<i>Drosophila persimilis</i>	<u>7234</u>	TR:B4GEM5 DROPE
				<i>Drosophila pseudoobscura pseudoobscura</i>	<u>46245</u>	TR:Q296U8 DROPS
				<i>Drosophila yakuba</i>	<u>7245</u>	TR:B4PSJ0 DROYA
				<i>Drosophila erecta</i>	<u>7220</u>	TR:B3P2P9 DROER
				<i>Drosophila melanogaster</i>	<u>7227</u>	SP:HMPB DROME
				<i>Drosophila grimshawi</i>	<u>7222</u>	TR:B4JGM0 DROGR
				<i>Drosophila melanogaster</i>	<u>7227</u>	SP:P31264-2
						SP:P31264-3
		SP:P31264-4				
UBA-like	<u>IPR009060</u>	16268	5	<i>Drosophila virilis</i>	<u>7244</u>	TR:B4M1G9 DROVI
				<i>Rhizopus deleamar</i>	<u>246409</u>	TR:I1BLN6 RHIO9
						TR:I1BI10 RHIO9
				<i>Phaeosphaeria nodorum</i>	<u>321614</u>	TR:Q0UXI8 PHANO
			<i>Ichthyophthirius multifiliis</i>	<u>857967</u>	TR:G0R1R9 ICHMG	
Armadillo-like helical	<u>IPR011989</u>	58193	11	<i>Drosophila virilis</i>	<u>7244</u>	TR:B4LHR0 DROVI
				<i>Drosophila grimshawi</i>	<u>7222</u>	TR:B4JNB2 DROGR
				<i>Anopheles gambiae</i>	<u>7165</u>	TR:A7UVK4 ANOGA
						TR:Q7PNN3 ANOGA
				<i>Arthroderma benhamiae</i>	<u>663331</u>	TR:D4AIT9 ARTBC
				<i>Trichophyton verrucosum</i>	<u>663202</u>	TR:D4DFR8 TRIVH

				<i>Nectria haematococca</i>	<u>660122</u>	<u>TR:C7YQJ8 NECH7</u>
				<i>Loa loa</i>	<u>7209</u>	<u>TR:J0DW06 LOALO</u>
				<i>Dictyostelium purpureum</i>	<u>5786</u>	<u>TR:F0ZS77 DICPU</u>
				<i>Paramecium tetraurelia</i>	<u>5888</u>	<u>TR:A0CBT3 PARTE</u>
				<i>Oxytricha trifallax</i>	<u>1172189</u>	<u>TR:J9I6T8 9SPIT</u>
Armadillo -type fold	<u>IPR016024</u>	77988	7	<i>Drosophila virilis</i>	<u>7244</u>	<u>TR:B4LHR0 DROVI</u>
				<i>Drosophila persimilis</i>	<u>7234</u>	<u>TR:B4G502 DROPE</u>
				<i>Drosophila pseudoobscura pseudoobscura</i>	<u>46245</u>	<u>TR:B5DYF9 DROPS</u>
				<i>Rhizopus delemar</i>	<u>246409</u>	<u>TR:I1CEW0 RHIO9</u>
				<i>Dictyostelium purpureum</i>	<u>5786</u>	<u>TR:F0ZS77 DICPU</u>
				<i>Paramecium tetraurelia</i>	<u>5888</u>	<u>TR:A0CBT3 PARTE</u>
				<i>Oxytricha trifallax</i>	<u>1172189</u>	<u>TR:J9I6T8 9SPIT</u>
Cell morphogenesis protein N-terminal	<u>IPR025614</u>	418	1	<i>Drosophila virilis</i>	<u>7244</u>	<u>TR:B4LHR0 DROVI</u>
Cell morphogenesis protein C-terminal	<u>IPR025481</u>	410	1	<i>Drosophila virilis</i>	<u>7244</u>	<u>TR:B4LHR0 DROVI</u>
SET domain	<u>IPR001214</u>	11343	5	<i>Drosophila virilis</i>	<u>7244</u>	<u>TR:B4LC34 DROVI</u>
				<i>Drosophila simulans</i>	<u>7240</u>	<u>TR:B4QJJ2 DROSI</u>
				<i>Drosophila erecta</i>	<u>7220</u>	<u>TR:B3ND01 DROER</u>
				<i>Drosophila melanogaster</i>	<u>7227</u>	<u>TR:Q9VUB5 DROME</u>
				<i>Candida dubliniensis</i>	<u>573826</u>	<u>TR:B9WA30 CANDC</u>
Zinc finger, PHD-type, conserved site	<u>IPR019786</u>	10490	6	<i>Drosophila virilis</i>	<u>7244</u>	<u>TR:B4LC34 DROVI</u>
				<i>Drosophila simulans</i>	<u>7240</u>	<u>TR:B4QJJ2 DROSI</u>
				<i>Drosophila erecta</i>	<u>7220</u>	<u>TR:B3ND01 DROER</u>
				<i>Drosophila melanogaster</i>	<u>7227</u>	<u>TR:Q9VUB5 DROME</u>
				<i>Candida dubliniensis</i>	<u>573826</u>	<u>TR:B9WA30 CANDC</u>
				<i>Gaeumannomyces graminis var. tritici</i>	<u>644352</u>	<u>TR:J3P975 GAGT3</u>
Zinc finger, FYVE/PHD-type	<u>IPR011011</u>	20769	9	<i>Drosophila virilis</i>	<u>7244</u>	<u>TR:B4LC34 DROVI</u>
				<i>Drosophila simulans</i>	<u>7240</u>	<u>TR:B4QJJ2 DROSI</u>
				<i>Drosophila erecta</i>	<u>7220</u>	<u>TR:B3P3P0 DROER</u>
						<u>TR:B3ND01 DROER</u>
				<i>Drosophila melanogaster</i>	<u>7227</u>	<u>TR:Q9VUB5 DROME</u>
				<i>Anopheles gambiae</i>	<u>7165</u>	<u>TR:Q7QET6 ANOGA</u>
						<u>TR:A0ND10 ANOGA</u>
				<i>Candida dubliniensis</i>	<u>573826</u>	<u>TR:B9WA30 CANDC</u>
Zinc finger, PHD-type	<u>IPR001965</u>	14838	7	<i>Drosophila virilis</i>	<u>7244</u>	<u>TR:B4LC34 DROVI</u>
				<i>Drosophila simulans</i>	<u>7240</u>	<u>TR:B4QJJ2 DROSI</u>
				<i>Drosophila erecta</i>	<u>7220</u>	<u>TR:B3ND01 DROER</u>
				<i>Anopheles gambiae</i>	<u>7165</u>	<u>TR:Q7QET6 ANOGA</u>

						TR:A0ND10 ANOGA
				<i>Drosophila melanogaster</i>	7227	TR:Q9VUB5 DROME
				<i>Gaeumannomyces graminis var. tritici</i>	644352	TR:J3P975 GAGT3
Zinc finger, PHD-finger	<u>IPR019787</u>	11882	8	<i>Drosophila virilis</i>	7244	TR:B4LC34 DROVI
				<i>Drosophila simulans</i>	7240	TR:B4QJJ2 DROSI
				<i>Drosophila erecta</i>	7220	TR:B3ND01 DROER
				<i>Anopheles gambiae</i>	7165	TR:Q7QET6 ANOGA
						TR:A0ND10 ANOGA
				<i>Drosophila melanogaster</i>	7227	TR:Q9VUB5 DROME
				<i>Candida dubliniensis</i>	573826	TR:B9WA30 CANDC
				<i>Gaeumannomyces graminis var. tritici</i>	644352	TR:J3P975 GAGT3
Sec23/Sec24, helical domain	<u>IPR006900</u>	1663	7	<i>Drosophila virilis</i>	7244	TR:B4LL65 DROVI
				<i>Drosophila mojavensis</i>	7230	TR:B4KQA1 DROMO
				<i>Drosophila sechellia</i>	7238	TR:B4I2G8 DROSE
				<i>Drosophila yakuba</i>	7245	TR:B4NW71 DROYA
				<i>Drosophila erecta</i>	7220	TR:B3N9H8 DROER
				<i>Drosophila melanogaster</i>	7227	TR:Q9VQ94 DROME
				<i>Paramecium tetraurelia</i>	5888	TR:A0DPT5 PARTE
Sec23/Sec24, trunk domain	<u>IPR006896</u>	1755	7	<i>Drosophila virilis</i>	7244	TR:B4LL65 DROVI
				<i>Drosophila mojavensis</i>	7230	TR:B4KQA1 DROMO
				<i>Drosophila sechellia</i>	7238	TR:B4I2G8 DROSE
				<i>Drosophila yakuba</i>	7245	TR:B4NW71 DROYA
				<i>Drosophila erecta</i>	7220	TR:B3N9H8 DROER
				<i>Drosophila melanogaster</i>	7227	TR:Q9VQ94 DROME
				<i>Paramecium tetraurelia</i>	5888	TR:A0DPT5 PARTE
Sec23/Sec24 beta-sandwich	<u>IPR012990</u>	1658	7	<i>Drosophila virilis</i>	7244	TR:B4LL65 DROVI
				<i>Drosophila mojavensis</i>	7230	TR:B4KQA1 DROMO
				<i>Drosophila sechellia</i>	7238	TR:B4I2G8 DROSE
				<i>Drosophila yakuba</i>	7245	TR:B4NW71 DROYA
				<i>Drosophila erecta</i>	7220	TR:B3N9H8 DROER
				<i>Drosophila melanogaster</i>	7227	TR:Q9VQ94 DROME
				<i>Paramecium tetraurelia</i>	5888	TR:A0DPT5 PARTE
Zinc finger, Sec23/Sec24-type	<u>IPR006895</u>	1711	7	<i>Drosophila virilis</i>	7244	TR:B4LL65 DROVI
				<i>Drosophila mojavensis</i>	7230	TR:B4KQA1 DROMO
				<i>Drosophila sechellia</i>	7238	TR:B4I2G8 DROSE
				<i>Drosophila yakuba</i>	7245	TR:B4NW71 DROYA
				<i>Drosophila erecta</i>	7220	TR:B3N9H8 DROER
				<i>Drosophila melanogaster</i>	7227	TR:Q9VQ94 DROME
				<i>Paramecium tetraurelia</i>	5888	TR:A0DPT5 PARTE

Gelsolin domain	IPR007123	2644	6	<i>Drosophila mojavensis</i>	7230	TR:B4KQA1 DROMO
				<i>Drosophila sechellia</i>	7238	TR:B4I2G8 DROSE
				<i>Drosophila yakuba</i>	7245	TR:B4NW71 DROYA
				<i>Drosophila erecta</i>	7220	TR:B3N9H8 DROER
				<i>Drosophila melanogaster</i>	7227	TR:Q9VQ94 DROME
				<i>Paramecium tetraurelia</i>	5888	TR:A0DPT5 PARTE
Zinc finger, C2CH-type	IPR006612	1885	1	<i>Drosophila mojavensis</i>	7230	TR:B4KIA8 DROMO
Zinc finger, double-stranded RNA binding	IPR022755	2427	2	<i>Drosophila mojavensis</i>	7230	TR:B4L1S9 DROMO
				<i>Drosophila willistoni</i>	7260	TR:B4N1N6 DROWI
Nuclear hormone receptor, ligand-binding, core	IPR000536	7988	3	<i>Drosophila mojavensis</i>	7230	TR:B4L034 DROMO
				<i>Drosophila grimshawi</i>	7222	TR:B4J0N8 DROGR
				<i>Aedes aegypti</i>	7159	TR:Q0IE91 AEDAE
Steroid hormone receptor	IPR001723	6406	3	<i>Drosophila mojavensis</i>	7230	TR:B4L034 DROMO
				<i>Drosophila grimshawi</i>	7222	TR:B4J0N8 DROGR
				<i>Aedes aegypti</i>	7159	TR:Q0IE91 AEDAE
Zinc finger, NHR/GATA-type	IPR013088	13177	6	<i>Drosophila mojavensis</i>	7230	TR:B4L034 DROMO
				<i>Drosophila grimshawi</i>	7222	TR:B4J0N8 DROGR
				<i>Aedes aegypti</i>	7159	TR:Q0IE91 AEDAE
				<i>Rhizopus delemar</i>	246409	TR:I1CHV5 RHIO9
				<i>Dictyostelium discoideum</i>	44689	SP:GTAG DICDI
				<i>Salpingoeca rosetta</i>	946362	TR:F2TY54 SALS5
Leucine rich repeat 5	IPR026906	5070	1	<i>Drosophila mojavensis</i>	7230	TR:B4KT45 DROMO
Polyadenylate-binding protein/Hyperplastic disc protein	IPR002004	1618	2	<i>Drosophila mojavensis</i>	7230	TR:B4L3F3 DROMO
				<i>Capsaspora owczarzaki</i>	595528	TR:E9C1R9 CAPO3
Chitin binding domain	IPR002557	3833	3	<i>Drosophila mojavensis</i>	7230	TR:B4KNT1 DROMO
				<i>Anopheles gambiae</i>	7165	TR:A7UVK4 ANOGA
						TR:Q7PNN3 ANOGA
High mobility group (HMG) box domain	IPR009071	10524	3	<i>Drosophila mojavensis</i>	7230	TR:B4KRC4 DROMO
				<i>Drosophila ananassae</i>	7217	TR:B3MM06 DROAN
				<i>Komagataella pastoris</i>	981350	TR:F2QM85 PICP7
Homeobox, conserved site	IPR017970	20442	20	<i>Drosophila mojavensis</i>	7230	TR:B4K845 DROMO
						TR:B4K6G4 DROMO
				<i>Drosophila ananassae</i>	7217	TR:B3M2C6 DROAN
				<i>Drosophila sechellia</i>	7238	TR:B4I4J9 DROSE
						TR:B4IBQ1 DROSE

				<i>Drosophila simulans</i>	<u>7240</u>	TR:B4QYW7 DROSI TR:B4QWE8 DROSI
				<i>Drosophila persimilis</i>	<u>7234</u>	TR:B4GEM5 DROPE
				<i>Drosophila pseudoobscura pseudoobscura</i>	<u>46245</u>	TR:Q296U8 DROPS
				<i>Drosophila yakuba</i>	<u>7245</u>	TR:B4PSJ0 DROYA TR:B4PMW0 DROYA
				<i>Drosophila erecta</i>	<u>7220</u>	TR:B3P2P9 DROER TR:B3NZB3 DROER
				<i>Drosophila grimshawi</i>	<u>7222</u>	TR:B4JGM0 DROGR TR:B4JX14 DROGR
				<i>Drosophila melanogaster</i>	<u>7227</u>	SP:ABDB DROME SP:HMPB DROME SP:P31264-2 SP:P31264-3 SP:P31264-4
Homeodomain, metazoa	<u>IPR020479</u>	9494	19	<i>Drosophila mojavensis</i>	<u>7230</u>	TR:B4K845 DROMO TR:B4K6G4 DROMO
				<i>Drosophila ananassae</i>	<u>7217</u>	TR:B3M2C6 DROAN
				<i>Drosophila sechellia</i>	<u>7238</u>	TR:B4I4J9 DROSE TR:B4IBQ1 DROSE
				<i>Drosophila simulans</i>	<u>7240</u>	TR:B4QYW7 DROSI TR:B4QWE8 DROSI
				<i>Drosophila persimilis</i>	<u>7234</u>	TR:B4GEM5 DROPE
				<i>Drosophila pseudoobscura pseudoobscura</i>	<u>46245</u>	TR:Q296U8 DROPS
				<i>Drosophila yakuba</i>	<u>7245</u>	TR:B4PSJ0 DROYA TR:B4PMW0 DROYA
				<i>Drosophila erecta</i>	<u>7220</u>	TR:B3P2P9 DROER TR:B3NZB3 DROER
				<i>Drosophila grimshawi</i>	<u>7222</u>	TR:B4JGM0 DROGR
				<i>Drosophila melanogaster</i>	<u>7227</u>	SP:ABDB DROME SP:HMPB DROME SP:P31264-2 SP:P31264-3 SP:P31264-4
Homeodomain	<u>IPR001356</u>	30961	20	<i>Drosophila mojavensis</i>	<u>7230</u>	TR:B4K845 DROMO TR:B4K6G4 DROMO
				<i>Drosophila ananassae</i>	<u>7217</u>	TR:B3M2C6 DROAN
				<i>Drosophila sechellia</i>	<u>7238</u>	TR:B4I4J9 DROSE TR:B4IBQ1 DROSE
				<i>Drosophila simulans</i>	<u>7240</u>	TR:B4QYW7 DROSI TR:B4QWE8 DROSI
				<i>Drosophila persimilis</i>	<u>7234</u>	TR:B4GEM5 DROPE
				<i>Drosophila pseudoobscura pseudoobscura</i>	<u>46245</u>	TR:Q296U8 DROPS

				<i>Drosophila yakuba</i>	<u>7245</u>	TR:B4PSJ0_DROYA TR:B4PMW0_DROYA
				<i>Drosophila erecta</i>	<u>7220</u>	TR:B3P2P9_DROER TR:B3NZB3_DROER
				<i>Drosophila grimshawi</i>	<u>7222</u>	TR:B4JGM0_DROGR TR:B4JX14_DROGR
				<i>Drosophila melanogaster</i>	<u>7227</u>	SP:ABDB_DROME SP:HMPB_DROME SP:P31264-2 SP:P31264-3 SP:P31264-4
Homeodomain-like	<u>IPR009057</u>	322630	26	<i>Drosophila mojavensis</i>	<u>7230</u>	TR:B4K845_DROMO TR:B4K6G4_DROMO
				<i>Drosophila ananassae</i>	<u>7217</u>	TR:B3M2C6_DROAN
				<i>Drosophila sechellia</i>	<u>7238</u>	TR:B4I4J9_DROSE TR:B4IBQ1_DROSE
				<i>Drosophila simulans</i>	<u>7240</u>	TR:B4QYW7_DROSI TR:B4QWE8_DROSI
				<i>Drosophila persimilis</i>	<u>7234</u>	TR:B4GEM5_DROPE
				<i>Drosophila yakuba</i>	<u>7245</u>	TR:B4PSJ0_DROYA TR:B4PMW0_DROYA
				<i>Drosophila erecta</i>	<u>7220</u>	TR:B3P2P9_DROER TR:B3NZB3_DROER
				<i>Drosophila grimshawi</i>	<u>7222</u>	TR:B4JGM0_DROGR TR:B4JX14_DROGR
				<i>Drosophila melanogaster</i>	<u>7227</u>	SP:ABDB_DROME SP:HMPB_DROME SP:P31264-2 SP:P31264-3 SP:P31264-4
				<i>Dictyostelium discoideum</i>	<u>44689</u>	SP:MYBU_DICDI
				<i>Lodderomyces elongisporus</i>	<u>379508</u>	TR:A5E1L5_LODEL
				<i>Candida parapsilosis</i>	<u>578454</u>	TR:G8BH70_CANPC
				<i>Cordyceps militaris</i>	<u>983644</u>	TR:G3JEU7_CORMM
				<i>Vitis vinifera</i>	<u>29760</u>	TR:F6I025_VITVI
				<i>Dictyostelium purpureum</i>	<u>5786</u>	TR:F1A5J1_DICPU
				<i>Dictyostelium discoideum</i>	<u>44689</u>	TR:Q55GK2_DICDI
Nebulin 35 residue motif	<u>IPR000900</u>	520	3	<i>Drosophila mojavensis</i>	<u>7230</u>	TR:B4KXK5_DROMO
				<i>Drosophila pseudoobscura pseudoobscura</i>	<u>46245</u>	TR:Q29DT1_DROPS TR:Q296U8_DROPS
Src homology-3 domain	<u>IPR001452</u>	24640	11	<i>Drosophila mojavensis</i>	<u>7230</u>	TR:B4KXK5_DROMO
				<i>Drosophila sechellia</i>	<u>7238</u>	TR:B4ID22_DROSE

				<i>Drosophila simulans</i>	7240	TR:B4Q6K2 DROSI
				<i>Drosophila pseudoobscura pseudoobscura</i>	46245	TR:Q29DT1 DROPS
				<i>Drosophila willistoni</i>	7260	TR:B4NBV6 DROWI
				<i>Drosophila erecta</i>	7220	TR:B3N892 DROER
				<i>Drosophila melanogaster</i>	7227	TR:Q9VPU1 DROME
				<i>Drosophila grimshawi</i>	7222	TR:B4JVH5 DROGR
				<i>Lachancea thermotolerans</i>	559295	TR:C5DLP2 LACTC
				<i>Colletotrichum graminicola</i>	645133	TR:E3QDI8 COLGM
				<i>Kluyveromyces lactis</i>	284590	TR:Q6CPM1 KLULA
Zinc finger, LIM-type	IPR001781	8426	3	<i>Drosophila mojavensis</i>	7230	TR:B4KXK5 DROMO
				<i>Drosophila pseudoobscura pseudoobscura</i>	46245	TR:Q29DT1 DROPS
				<i>Scheffersomyces stipitis</i>	322104	TR:A3LYJ2 PICST
RNA binding activity-knot of a chromodomain	IPR025995	1322	1	<i>Drosophila mojavensis</i>	7230	TR:B4LSI5 DROMO
MADF domain	IPR006578	1553	2	<i>Drosophila mojavensis</i>	7230	TR:B4KR77 DROMO
				<i>Drosophila willistoni</i>	7260	TR:B4MYB5 DROWI
Homeobox protein, antennapedia type	IPR017995	1086	4	<i>Drosophila mojavensis</i>	7230	TR:B4K6G4 DROMO
				<i>Drosophila persimilis</i>	7234	TR:B4GEM5 DROPE
				<i>Drosophila pseudoobscura pseudoobscura</i>	46245	TR:Q296U8 DROPS
				<i>Drosophila grimshawi</i>	7222	TR:B4JGM0 DROGR
Myc-type, basic helix-loop-helix (bHLH) domain	IPR011598	17829	2	<i>Drosophila mojavensis</i>	7230	TR:B4K809 DROMO
				<i>Drosophila sechellia</i>	7238	TR:B4IFN2 DROSE
Translation Initiation factor eIF- 4e-like domain	IPR023398	1969	1	<i>Drosophila mojavensis</i>	7230	TR:B4KW75 DROMO
Translation Initiation factor eIF- 4e	IPR001040	1780	1	<i>Drosophila mojavensis</i>	7230	TR:B4KW75 DROMO
Eukaryotic translation initiation factor 4E (eIF-4E), conserved site	IPR019770	976	1	<i>Drosophila mojavensis</i>	7230	TR:B4KW75 DROMO
GRASP55/65 PDZ-like domain (Golgi reassembly stacking protein of 55/65 kDa)	IPR024958	473	1	<i>Culex quinquefasciatus</i>	7176	TR:B0XBV1 CULQU
GRASP55 (Golgi reassembly stacking protein of 55 kDa) and GRASP65 (a 65 kDa)	IPR007583	444	1	<i>Culex quinquefasciatus</i>	7176	TR:B0XBV1 CULQU
PDZ domain	IPR001478	48125	5	<i>Culex quinquefasciatus</i>	7176	TR:B0XBV1 CULQU
				<i>Drosophila simulans</i>	7240	TR:B4QFM5 DROSI
				<i>Drosophila willistoni</i>	7260	TR:B4NBV6 DROWI
				<i>Drosophila grimshawi</i>	7222	TR:B4JVH5 DROGR

ALIX V-shaped domain	IPR025304	680	4	<i>Culex quinquefasciatus</i>	7176	TR:B0WWP0_CULQU
				<i>Paramecium tetraurelia</i>	5888	TR:A0CDE8_PARTE
						TR:A0DFK8_PARTE
				<i>Leishmania braziliensis</i>	5660	TR:A4HFU0_LEIBR
BRO1 domain	IPR004328	1272	4	<i>Culex quinquefasciatus</i>	7176	TR:B0WWP0_CULQU
				<i>Paramecium tetraurelia</i>	5888	TR:A0CDE8_PARTE
						TR:A0DFK8_PARTE
				<i>Leishmania braziliensis</i>	5660	TR:A4HFU0_LEIBR
Protein-tyrosine phosphatase, receptor/non-receptor type	IPR000242	6714	1	<i>Culex quinquefasciatus</i>	7176	TR:B0WWP0_CULQU
Peptidase C48, SUMO/Sentrin/ Ubl1	IPR003653	3905	2	<i>Anopheles gambiae</i>	7165	TR:A7UVK4_ANOGA
						TR:Q7PNN3_ANOGA
Acyl-CoA N-acyltransferase	IPR016181	182379	2	<i>Anopheles gambiae</i>	7165	TR:A0ND10_ANOGA
						TR:Q7QET6_ANOGA
Histone H1/H5	IPR005818	2159	2	<i>Anopheles gambiae</i>	7165	TR:A0ND10_ANOGA
						TR:Q7QET6_ANOGA
MOZ/SAS-like protein	IPR002717	1432	2	<i>Anopheles gambiae</i>	7165	TR:A0ND10_ANOGA
						TR:Q7QET6_ANOGA
Mediator complex, subunit Med21	IPR021384	320	1	<i>Anopheles gambiae</i>	7165	SP:MED21_ANOGA
DnaJ domain	IPR001623	38316	1	<i>Aedes aegypti</i>	7159	TR:Q17E65_AEDAE
	IPR003095		1	<i>Aedes aegypti</i>	7159	TR:Q17E65_AEDAE
EF-hand-like domain	IPR011992	45075	7	<i>Volvox carteri</i>	3067	TR:D8U185_VOLCA
				<i>Apis mellifera</i>	7460	TR:H9K2L4_APIME
				<i>Branchiostoma floridae</i>	7739	TR:C3ZBA3_BRAFL
				<i>Emericella nidulans</i>	227321	TR:Q5B077_EMENI
				<i>Dictyostelium fasciculatum</i>	1054147	TR:F4Q4C0_DICFS
				<i>Paramecium tetraurelia</i>	5888	TR:A0BWN9_PARTE
				<i>Phaeodactylum tricornutum</i>	556484	TR:B7FRA9_PHATC
EF-Hand 1, calcium-binding site	IPR018247	73783	4	<i>Volvox carteri</i>	3067	TR:D8U185_VOLCA
				<i>Apis mellifera</i>	7460	TR:H9K2L4_APIME
				<i>Emericella nidulans</i>	227321	TR:Q5B077_EMENI
				<i>Paramecium tetraurelia</i>	5888	TR:A0BWN9_PARTE

Ribosomal protein L14 domain	IPR023571	7979	1	<i>Drosophila ananassae</i>	7217	TR:B3MYV1 DROAN
Ribosomal protein L14b/L23e	IPR000218	7984	1	<i>Drosophila ananassae</i>	7217	TR:B3MYV1 DROAN
Genetic suppressor element-like	IPR022207	123	12	<i>Drosophila ananassae</i>	7217	TR:B3M3P4 DROAN
				<i>Drosophila sechellia</i>	7238	TR:B4HUG6 DROSE
				<i>Drosophila simulans</i>	7240	TR:B4QRL6 DROSI
				<i>Drosophila persimilis</i>	7234	TR:B4H3D3 DROPE
				<i>Drosophila pseudoobscura pseudoobscura</i>	46245	TR:Q2LZM8 DROPS
				<i>Drosophila yakuba</i>	7245	TR:B4PIU8 DROYA
				<i>Drosophila erecta</i>	7220	TR:B3NGC4 DROER
				<i>Drosophila melanogaster</i>	7227	TR:F0JAN7 DROME
						TR:Q26459 DROME
						TR:Q8IGD4 DROME
						TR:Q9VRM5 DROME
						TR:Q8IQ63 DROME
Peptidase C2, calpain family	IPR022684	2050	1	<i>Drosophila ananassae</i>	7217	TR:B3MXY5 DROAN
Cysteine peptidase, cysteine active site	IPR000169	7906	1	<i>Drosophila ananassae</i>	7217	TR:B3MXY5 DROAN
Peptidase C2, calpain, catalytic domain	IPR001300	2584	1	<i>Drosophila ananassae</i>	7217	TR:B3MXY5 DROAN
Zinc finger, RanBP2-type	IPR001876	5271	3	<i>Drosophila ananassae</i>	7217	TR:B3MXY5 DROAN
				<i>Tetrahymena thermophila</i>	312017	TR:I7MB64 TETTS
				<i>Sulfolobus acidocaldarius</i>	330779	TR:Q4J9H4 SULAC
COPII coat assembly protein, Sec16	IPR024880	475	2	<i>Drosophila ananassae</i>	7217	TR:B3MRZ5 DROAN
				<i>Drosophila grimshawi</i>	7222	TR:B4JNJ2 DROGR
Single-stranded nucleic acid binding R3H	IPR001374	4026	3	<i>Drosophila ananassae</i>	7217	TR:B3M803 DROAN
				<i>Drosophila persimilis</i>	7234	TR:B4GS08 DROPE
				<i>Drosophila grimshawi</i>	7222	TR:B4IZW4 DROGR
SUZ domain	IPR024771	586	3	<i>Drosophila ananassae</i>	7217	TR:B3M803 DROAN
				<i>Drosophila persimilis</i>	7234	TR:B4GS08 DROPE
				<i>Drosophila grimshawi</i>	7222	TR:B4IZW4 DROGR
SH2 domain	IPR000980	10236	6	<i>Drosophila sechellia</i>	7238	TR:B4ID22 DROSE
				<i>Drosophila simulans</i>	7240	TR:B4Q6K2 DROSI
				<i>Drosophila erecta</i>	7220	TR:B3N892 DROER
				<i>Drosophila melanogaster</i>	7227	TR:Q9VPU1 DROME
				<i>Drosophila grimshawi</i>	7222	TR:B4JNB2 DROGR
				<i>Branchiostoma floridae</i>	7739	TR:C3ZBA3 BRAFL

BTB/POZ-like	IPR000210	20275	4	<i>Drosophila sechellia</i>	7238	TR:B4IGL8 DROSE
				<i>Drosophila simulans</i>	7240	TR:B4R414 DROSI
				<i>Drosophila yakuba</i>	7245	TR:B4Q201 DROYA
				<i>Drosophila melanogaster</i>	7227	TR:Q9I7S4 DROME
BTB/POZ fold	IPR011333	24169	4	<i>Drosophila sechellia</i>	7238	TR:B4IGL8 DROSE
				<i>Drosophila simulans</i>	7240	TR:B4R414 DROSI
				<i>Drosophila yakuba</i>	7245	TR:B4Q201 DROYA
				<i>Drosophila melanogaster</i>	7227	TR:Q9I7S4 DROME
BTB/POZ	IPR013069	16378	4	<i>Drosophila sechellia</i>	7238	TR:B4IGL8 DROSE
				<i>Drosophila simulans</i>	7240	TR:B4R414 DROSI
				<i>Drosophila yakuba</i>	7245	TR:B4Q201 DROYA
				<i>Drosophila melanogaster</i>	7227	TR:Q9I7S4 DROME
Rap GTPase activating proteins domain	IPR000331	1449	4	<i>Drosophila sechellia</i>	7238	TR:B4IGL8 DROSE
				<i>Drosophila simulans</i>	7240	TR:B4R414 DROSI
				<i>Drosophila yakuba</i>	7245	TR:B4Q201 DROYA
				<i>Drosophila melanogaster</i>	7227	TR:Q9I7S4 DROME
Inositol polyphosphate kinase	IPR005522	1250	5	<i>Drosophila sechellia</i>	7238	TR:B4I7T1 DROSE
				<i>Drosophila simulans</i>	7240	TR:B4QG10 DROSI
				<i>Drosophila yakuba</i>	7245	TR:B4P8W1 DROYA
				<i>Drosophila erecta</i>	7220	TR:B3NMY7 DROER
				<i>Drosophila melanogaster</i>	7227	TR:Q9W2E9 DROME
Seven cysteines	IPR013980	333	2	<i>Drosophila sechellia</i>	7238	TR:B4HWV4 DROSE
				<i>Drosophila melanogaster</i>	7227	TR:Q9Y110 DROME
Seven cysteines, N-terminal	IPR011106	292	2	<i>Drosophila sechellia</i>	7238	TR:B4HWV4 DROSE
				<i>Drosophila melanogaster</i>	7227	TR:Q9Y110 DROME
Wnt	IPR005817	11699	2	<i>Drosophila sechellia</i>	7238	TR:B4HY51 DROSE
				<i>Drosophila simulans</i>	7240	TR:B4Q5E7 DROSI
Wnt-10 protein	IPR013302	188	2	<i>Drosophila sechellia</i>	7238	TR:B4HY51 DROSE
				<i>Drosophila simulans</i>	7240	TR:B4Q5E7 DROSI
Wnt protein, conserved site	IPR018161	2610	2	<i>Drosophila sechellia</i>	7238	TR:B4HY51 DROSE
				<i>Drosophila simulans</i>	7240	TR:B4Q5E7 DROSI
Leucine rich repeat 4	IPR025875	15629	5	<i>Drosophila sechellia</i>	7238	TR:B4HTZ7 DROSE
				<i>Drosophila yakuba</i>	7245	TR:B4PHP3 DROYA
				<i>Drosophila yakuba</i>	7245	TR:B4PHP3 DROYA
				<i>Drosophila erecta</i>	7220	TR:B3NG33 DROER

				<i>Yarrowia lipolytica</i>	284591	TR:Q6C1M0_YARLI
U2A'/phosphoprotein 32 family A, C-terminal	IPR003603	1754	3	<i>Drosophila sechellia</i>	7238	TR:B4HTZ7_DROSE
				<i>Drosophila simulans</i>	7240	TR:B4QQ40_DROSI
				<i>Drosophila erecta</i>	7220	TR:B3NG33_DROER
WW domain	IPR001202	8029	14	<i>Drosophila simulans</i>	7240	TR:B4QFM5_DROSI
				<i>Drosophila willistoni</i>	7260	TR:B4MKD0_DROWI
				<i>Arabidopsis thaliana</i>	3702	SP:RH40_ARATH
				<i>Arabidopsis lyrata subsp. lyrata</i>	81972	TR:D7LSI4_ARALL
				<i>Lodderomyces elongisporus</i>	379508	TR:A5DRZ7_LODEL
				<i>Cryptococcus neoformans</i> var. <i>neoformans</i>	283643	TR:F5HHK8_CRYNB
						TR:Q5KNA4_CRYNJ
				<i>Tetrapisispora phaffii</i>	1071381	TR:G8BS80_TETPH
				<i>Lachancea thermotolerans</i>	559295	TR:C5DBI0_LACTC
				<i>Mixia osmundae</i>	764103	TR:G7EAV5_MIXOS
				<i>Cryptococcus neoformans</i> var. <i>grubii</i>	235443	TR:J9VX35_CRYNV
				<i>Glarea lozoyensis</i>	1104152	TR:H0EF05_GLAL7
				<i>Polysphondylium pallidum</i>	13642	TR:D3BU61_POLPA
				<i>Dictyostelium fasciculatum</i>	1054147	TR:F4PU20_DICFS
2OGFeDO domain, nucleic acid-modifying type	IPR024779	347	4	<i>Drosophila simulans</i>	7240	TR:B4QNM4_DROSI
				<i>Drosophila melanogaster</i>	7227	TR:Q9VZX4_DROME
						TR:Q8T0I1_DROME
						TR:Q8T9G4_DROME
Cleavage stimulation factor subunit 2, hinge domain	IPR025742	495	2	<i>Drosophila persimilis</i>	7234	TR:B4G5G9_DROPE
				<i>Drosophila pseudoobscura pseudoobscura</i>	46245	TR:Q299N5_DROPS
Transcription termination and cleavage factor C-terminal domain	IPR026896	381	2	<i>Drosophila persimilis</i>	7234	TR:B4G5G9_DROPE
				<i>Drosophila pseudoobscura pseudoobscura</i>	46245	TR:Q299N5_DROPS
E2F Family	IPR015633	962	2	<i>Drosophila persimilis</i>	7234	TR:B4GDR3_DROPE
				<i>Drosophila pseudoobscura pseudoobscura</i>	46245	TR:Q295K4_DROPS
Transcription factor E2F/ dimerisation partner	IPR003316	1350	2	<i>Drosophila persimilis</i>	7234	TR:B4GDR3_DROPE
				<i>Drosophila pseudoobscura pseudoobscura</i>	46245	TR:Q295K4_DROPS
Winged helix-turn-helix transcription repressor DNA-binding domain	IPR011991	772973	4	<i>Drosophila persimilis</i>	7234	TR:B4GDR3_DROPE
				<i>Drosophila pseudoobscura pseudoobscura</i>	46245	TR:Q295K4_DROPS
				<i>Candida dubliniensis</i>	573826	TR:B9WKI8_CANDC
				<i>Thalassiosira pseudonana</i>	35128	TR:B8LD72_THAPS
Protease-associated domain, PA	IPR003137	6308	2	<i>Drosophila persimilis</i>	7234	TR:B4GI37_DROPE
				<i>Drosophila pseudoobscura pseudoobscura</i>	46245	TR:Q28Z87_DROPS

Initiation factor eIF-4 gamma, MA3	IPR003891	1618	3	<i>Drosophila persimilis</i>	7234	TR:B4G502 DROPE
				<i>Drosophila pseudoobscura pseudoobscura</i>	46245	TR:B5DYF9 DROPS
				<i>Rhizopus deleamar</i>	246409	TR:I1CEW0 RHIO9
MIF4-like, type 1/2/3	IPR016021	4469	3	<i>Drosophila persimilis</i>	7234	TR:B4G502 DROPE
				<i>Drosophila pseudoobscura pseudoobscura</i>	46245	TR:B5DYF9 DROPS
				<i>Rhizopus deleamar</i>	246409	TR:I1CEW0 RHIO9
MIF4G-like, type 3	IPR003890	2636	3	<i>Drosophila persimilis</i>	7234	TR:B4G502 DROPE
				<i>Drosophila pseudoobscura pseudoobscura</i>	46245	TR:B5DYF9 DROPS
				<i>Rhizopus deleamar</i>	246409	TR:I1CEW0 RHIO9
Protein kinase-like domain	IPR011009	205404	23	<i>Drosophila persimilis</i>	7234	TR:B4G6Q5 DROPE
				<i>Drosophila pseudoobscura pseudoobscura</i>	46245	TR:I5ANW1 DROPS
				<i>Drosophila willistoni</i>	7260	TR:B4NEN2 DROWI
				<i>Volvox carteri</i>	3067	TR:D8UGB6 VOLCA
				<i>Clavispora lusitaniae</i>	306902	TR:C4Y9B9 CLAL4
				<i>Gaeumannomyces graminis var. tritici</i>	644352	TR:J3P6H6 GAGT3
				<i>Candida dubliniensis</i>	573826	TR:B9WBA1 CANDC
				<i>Candida parapsilosis</i>	578454	TR:G8B5E8 CANPC
				<i>Podospira anserina</i>	515849	TR:B2AX04 PODAN
				<i>Beauveria bassiana</i>	655819	TR:J5IXA4 BEAB2
				<i>Candida albicans</i>	294748	TR:C4YSR4 CANAW
				<i>Wuchereria bancrofti</i>	6293	TR:J9EPD0 WUCBA
				<i>Trichinella spiralis</i>	6334	TR:E5S526 TRISP
				<i>Polysphondylium pallidum</i>	13642	TR:D3B3V6 POLPA
				<i>Dictyostelium discoideum</i>	44689	SP:FRAY2 DICDI
						SP:Y9844 DICDI
						SP:PKD1 DICDI
						SP:PLK DICDI
				<i>Paramecium tetraurelia</i>	5888	TR:A0D439 PARTE
						TR:A0BWN9 PARTE
				<i>Oxytricha trifallax</i>	1172189	TR:J9I6Z1 9SPIT
						TR:J9FQG1 9SPIT
						TR:J9HUE1 9SPIT
Mad3/BUB1 homology region 1	IPR013212	511	2	<i>Drosophila persimilis</i>	7234	TR:B4G6Q5 DROPE
				<i>Drosophila pseudoobscura pseudoobscura</i>	46245	TR:B5DVC6 DROPS
Protein kinase, catalytic domain	IPR000719	155751	23	<i>Drosophila persimilis</i>	7234	TR:B4G6Q5 DROPE
				<i>Drosophila pseudoobscura pseudoobscura</i>	46245	TR:I5ANW1 DROPS
				<i>Drosophila willistoni</i>	7260	TR:B4NEN2 DROWI
				<i>Volvox carteri</i>	3067	TR:D8UGB6 VOLCA
				<i>Candida parapsilosis</i>	578454	TR:G8B5E8 CANPC

				<i>Podospora anserina</i>	<u>515849</u>	TR:B2AX04 PODAN
				<i>Candida dubliniensis</i>	<u>573826</u>	TR:B9WBA1 CANDC
				<i>Gaeumannomyces graminis</i> var. <i>tritici</i>	<u>644352</u>	TR:J3P6H6 GAGT3
				<i>Clavispora lusitaniae</i>	<u>306902</u>	TR:C4Y9B9 CLAL4
				<i>Beauveria bassiana</i>	<u>655819</u>	TR:J5JXA4 BEAB2
				<i>Candida albicans</i>	<u>294748</u>	TR:C4YSR4 CANAW
				<i>Wuchereria bancrofti</i>	<u>6293</u>	TR:J9EPD0 WUCBA
				<i>Trichinella spiralis</i>	<u>6334</u>	TR:E5S526 TRISP
				<i>Polysphondylium pallidum</i>	<u>13642</u>	TR:D3B3V6 POLPA
				<i>Dictyostelium discoideum</i>	<u>44689</u>	SP:FRAY2 DICDI
						SP:Y9844 DICDI
						SP:PKD1 DICDI
						SP:PLK DICDI
				<i>Paramecium tetraurelia</i>	<u>5888</u>	TR:A0D439 PARTE
<i>Oxytricha trifallax</i>	<u>1172189</u>	TR:A0BWN9 PARTE				
		TR:J9I6Z1 9SPIT				
		TR:J9FQG1 9SPIT				
		TR:J9HUE1 9SPIT				
Protein kinase, ATP binding site	<u>IPR017441</u>	88650	17	<i>Drosophila persimilis</i>	<u>7234</u>	TR:B4G6Q5 DROPE
				<i>Drosophila pseudoobscura pseudoobscura</i>	<u>46245</u>	TR:I5ANW1 DROPS
				<i>Drosophila willistoni</i>	<u>7260</u>	TR:B4NEN2 DROWI
				<i>Gaeumannomyces graminis</i> var. <i>tritici</i>	<u>644352</u>	TR:J3P6H6 GAGT3
				<i>Clavispora lusitaniae</i>	<u>306902</u>	TR:C4Y9B9 CLAL4
				<i>Candida parapsilosis</i>	<u>578454</u>	TR:G8B5E8 CANPC
				<i>Podospora anserina</i>	<u>515849</u>	TR:B2AX04 PODAN
				<i>Candida albicans</i>	<u>294748</u>	TR:C4YSR4 CANAW
				<i>Trichinella spiralis</i>	<u>6334</u>	TR:E5S526 TRISP
				<i>Polysphondylium pallidum</i>	<u>13642</u>	TR:D3B3V6 POLPA
				<i>Dictyostelium discoideum</i>	<u>44689</u>	SP:FRAY2 DICDI
						SP:Y9844 DICDI
						SP:PLK DICDI
						SP:PLK DICDI
<i>Paramecium tetraurelia</i>	<u>5888</u>	TR:A0D439 PARTE				
<i>Oxytricha trifallax</i>	<u>1172189</u>	TR:A0BWN9 PARTE				
		TR:J9I6Z1 9SPIT				
		TR:J9FQG1 9SPIT				
		TR:J9HUE1 9SPIT				
Serine/threonine-protein kinase, active site	<u>IPR008271</u>	101014	19	<i>Drosophila persimilis</i>	<u>7234</u>	TR:B4G6Q5 DROPE
				<i>Drosophila pseudoobscura pseudoobscura</i>	<u>46245</u>	TR:I5ANW1 DROPS
				<i>Drosophila willistoni</i>	<u>7260</u>	TR:B4NEN2 DROWI
				<i>Candida dubliniensis</i>	<u>573826</u>	TR:B9WBA1 CANDC
				<i>Gaeumannomyces graminis</i> var. <i>tritici</i>	<u>644352</u>	TR:J3P6H6 GAGT3
				<i>Clavispora lusitaniae</i>	<u>306902</u>	TR:C4Y9B9 CLAL4
				<i>Candida parapsilosis</i>	<u>578454</u>	TR:G8B5E8 CANPC
				<i>Candida albicans</i>	<u>294748</u>	TR:C4YSR4 CANAW

				<i>Wuchereria bancrofti</i>	<u>6293</u>	TR:J9EPD0_WUCBA
				<i>Trichinella spiralis</i>	<u>6334</u>	TR:E5S526_TRISP
				<i>Polysphondylium pallidum</i>	<u>13642</u>	TR:D3B3V6_POLPA
				<i>Dictyostelium discoideum</i>	<u>44689</u>	SP:Y9844_DICDI
						SP:PKD1_DICDI
						SP:PLK_DICDI
				<i>Paramecium tetraurelia</i>	<u>5888</u>	TR:A0D439_PARTE
<i>Oxytricha trifallax</i>	<u>1172189</u>	TR:J9I6Z1_9SPIT				
		TR:J9FQG1_9SPIT				
		TR:J9HUE1_9SPIT				
Mitotic checkpoint serine/threonine protein kinase Bub1/Mitotic spindle checkpoint component Mad3	<u>IPR015661</u>	555	2	<i>Drosophila persimilis</i>	<u>7234</u>	TR:B4G6Q5_DROPE
				<i>Drosophila pseudoobscura pseudoobscura</i>	<u>46245</u>	TR:B5DVC6_DROPS
B30.2/SPRY domain	<u>IPR001870</u>	8684	1	<i>Drosophila pseudoobscura pseudoobscura</i>	<u>46245</u>	TR:Q28Z53_DROPS
Concanavalin A-like lectin/glucanases superfamily	<u>IPR008985</u>	59437	1	<i>Drosophila pseudoobscura pseudoobscura</i>	<u>46245</u>	TR:Q28Z53_DROPS
SAP domain	<u>IPR003034</u>	5302	2	<i>Drosophila pseudoobscura pseudoobscura</i>	<u>46245</u>	TR:Q28Z53_DROPS
				<i>Candida albicans</i>	<u>237561</u>	TR:Q5A8Y9_CANAL
SPLa/RYanodine receptor SPRY	<u>IPR003877</u>	8592	1	<i>Drosophila pseudoobscura pseudoobscura</i>	<u>46245</u>	TR:Q28Z53_DROPS
Peptidase C19, ubiquitin carboxyl-terminal hydrolase 2, conserved site	<u>IPR018200</u>	8328	1	<i>Drosophila pseudoobscura pseudoobscura</i>	<u>46245</u>	TR:Q2LZV0_DROPS
Peptidase C19, ubiquitin carboxyl-terminal hydrolase 2	<u>IPR001394</u>	10281	1	<i>Drosophila pseudoobscura pseudoobscura</i>	<u>46245</u>	TR:Q2LZV0_DROPS
Serine/threonine- / dual specificity protein kinase, catalytic domain	<u>IPR002290</u>	46148	9	<i>Drosophila pseudoobscura pseudoobscura</i>	<u>46245</u>	TR:I5ANW1_DROPS
				<i>Candida dubliniensis</i>	<u>573826</u>	TR:B9WBA1_CANDC
				<i>Gaeumannomyces graminis</i> var. <i>tritici</i>	<u>644352</u>	TR:J3P6H6_GAGT3
				<i>Clavispora lusitaniae</i>	<u>306902</u>	TR:C4Y9B9_CLAL4
				<i>Trichinella spiralis</i>	<u>6334</u>	TR:E5S526_TRISP
				<i>Dictyostelium discoideum</i>	<u>44689</u>	SP:FRAY2_DICDI
						SP:PKD1_DICDI
						SP:PLK_DICDI
<i>Paramecium tetraurelia</i>	<u>5888</u>	TR:A0D439_PARTE				
Basic-leucine zipper domain	<u>IPR004827</u>	11371	4	<i>Drosophila willistoni</i>	<u>7260</u>	TR:B4MYE3_DROWI
				<i>Oryza brachyantha</i>	<u>4533</u>	TR:J3NC10_ORYBR
				<i>Wickerhamomyces ciferrii</i>	<u>1206466</u>	TR:K0KJU9_9ASCO

				<i>Candida tropicalis</i>	<u>294747</u>	TR:C5ME60 CANTT
Guanylate kinase	<u>IPR008144</u>	10579	1	<i>Drosophila willistoni</i>	<u>7260</u>	TR:B4NBV6 DROWI
Guanylate kinase/L-type calcium channel	<u>IPR008145</u>	10614	1	<i>Drosophila willistoni</i>	<u>7260</u>	TR:B4NBV6 DROWI
Guanylate kinase, conserved site	<u>IPR020590</u>	7776	1	<i>Drosophila willistoni</i>	<u>7260</u>	TR:B4NBV6 DROWI
L27	<u>IPR004172</u>	1263	1	<i>Drosophila willistoni</i>	<u>7260</u>	TR:B4NBV6 DROWI
L27, C-terminal	<u>IPR014775</u>	904	1	<i>Drosophila willistoni</i>	<u>7260</u>	TR:B4NBV6 DROWI
Variant SH3	<u>IPR011511</u>	6612	2	<i>Drosophila willistoni</i>	<u>7260</u>	TR:B4NBV6 DROWI
				<i>Drosophila grimshawi</i>	<u>7222</u>	TR:B4JVH5 DROGR
Coronin	<u>IPR015505</u>	1011	1	<i>Drosophila willistoni</i>	<u>7260</u>	TR:B4MJ97 DROWI
Domain of unknown function DUF1899	<u>IPR015048</u>	761	1	<i>Drosophila willistoni</i>	<u>7260</u>	TR:B4MJ97 DROWI
Domain of unknown function DUF1900	<u>IPR015049</u>	922	1	<i>Drosophila willistoni</i>	<u>7260</u>	TR:B4MJ97 DROWI
WD40/YVTN repeat-like-containing domain	<u>IPR015943</u>	109781	20	<i>Drosophila willistoni</i>	<u>7260</u>	TR:B4MJ97 DROWI
				<i>Zea mays</i>	<u>4577</u>	TR:B6SPQ9 MAIZE
						TR:COP3D9 MAIZE
				<i>Saccharomyces cerevisiae</i>	<u>764102</u>	TR:E7Q1H5 YEASB
						SP:TUP1 YEAST
						TR:A6ZTQ6 YEAS7
						TR:B3LUD8 YEAS1
						TR:B5VF12 YEAS6
						TR:C7GUW4 YEAS2
						TR:C8Z4H1 YEAS8
						TR:E7NFE6 YEASO
						TR:E7QC78 YEASZ
						TR:H0GD95 9SACH
						TR:G2WA92 YEASK
						TR:E7KA75 YEASA
				<i>Saccharomyces arboricola</i>	<u>1160507</u>	TR:J8Q781 SACAR
WD40 repeat	<u>IPR001680</u>	70208	19	<i>Drosophila willistoni</i>	<u>7260</u>	TR:B4MJ97 DROWI
				<i>Zea mays</i>	<u>4577</u>	TR:B6SPQ9 MAIZE
						TR:COP3D9 MAIZE

				<i>Saccharomyces cerevisiae</i>	<u>764102</u>	TR:E7Q1H5 YEASB SP:TUP1 YEAST TR:A6ZTQ6 YEAS7 TR:B3LUD8 YEAS1 TR:B5VF12 YEAS6 TR:C7GUW4 YEAS2 TR:C8Z4H1 YEAS8 TR:E7NFE6 YEASO TR:E7QC78 YEASZ TR:H0GD95 9SACH TR:G2WA92 YEASK TR:E7KA75 YEASA
				<i>Saccharomyces arboricola</i>	<u>1160507</u>	TR:J8Q781 SACAR
				<i>Paramecium tetraurelia</i>	<u>5888</u>	TR:A0CXK4 PARTE TR:A0CYP9 PARTE TR:A0E4C1 PARTE
WD40 repeat, conserved site	<u>IPR019775</u>	39072	19	<i>Drosophila willistoni</i>	<u>7260</u>	TR:B4MJ97 DROWI
				<i>Zea mays</i>	<u>4577</u>	TR:B6SPQ9 MAIZE TR:C0P3D9 MAIZE
				<i>Saccharomyces cerevisiae</i>	<u>764102</u>	TR:E7Q1H5 YEASB SP:TUP1 YEAST TR:A6ZTQ6 YEAS7 TR:B3LUD8 YEAS1 TR:B5VF12 YEAS6 TR:C7GUW4 YEAS2 TR:C8Z4H1 YEAS8 TR:E7NFE6 YEASO TR:E7QC78 YEASZ TR:H0GD95 9SACH TR:G2WA92 YEASK TR:E7KA75 YEASA
				<i>Saccharomyces arboricola</i>	<u>1160507</u>	TR:J8Q781 SACAR
				<i>Paramecium tetraurelia</i>	<u>5888</u>	TR:A0CXK4 PARTE TR:A0CYP9 PARTE TR:A0E4C1 PARTE
WD40-repeat-containing domain	<u>IPR017986</u>	74523	19	<i>Drosophila willistoni</i>	<u>7260</u>	TR:B4MJ97 DROWI
				<i>Zea mays</i>	<u>4577</u>	TR:B6SPQ9 MAIZE TR:C0P3D9 MAIZE
				<i>Saccharomyces cerevisiae</i>	<u>764102</u>	TR:E7Q1H5 YEASB SP:TUP1 YEAST TR:A6ZTQ6 YEAS7 TR:B3LUD8 YEAS1 TR:B5VF12 YEAS6

						TR:C7GUW4 YEAS2
						TR:C8Z4H1 YEAS8
						TR:E7NFE6 YEASO
						TR:E7QC78 YEASZ
						TR:H0GD95 9SACH
						TR:G2WA92 YEASK
						TR:E7KA75 YEASA
				<i>Saccharomyces arboricola</i>	1160507	TR:J8Q781 SACAR
				<i>Paramecium tetraurelia</i>	5888	TR:A0CXK4 PARTE
						TR:A0CYP9 PARTE
						TR:A0E4C1 PARTE
RNA helicase UPF1, UPF2-interacting domain	IPR018999	364	1	<i>Drosophila willistoni</i>	7260	TR:B4NDR4 DROWI
GRAM	IPR004182	2817	1	<i>Drosophila willistoni</i>	7260	TR:B4NLS4 DROWI
mRNA decapping protein 2, Box A	IPR007722	359	1	<i>Drosophila willistoni</i>	7260	TR:B4MXW4 DROWI
NUDIX hydrolase, conserved site	IPR020084	36499	1	<i>Drosophila willistoni</i>	7260	TR:B4MXW4 DROWI
NUDIX hydrolase domain	IPR000086	60977	2	<i>Drosophila willistoni</i>	7260	TR:B4MXW4 DROWI
				<i>Dictyostelium fasciculatum</i>	1054147	TR:F4Q5V6 DICFS
NUDIX hydrolase domain-like	IPR015797	67351	2	<i>Drosophila willistoni</i>	7260	TR:B4MXW4 DROWI
				<i>Dictyostelium fasciculatum</i>	1054147	TR:F4Q5V6 DICFS
Peptidase A22, presenilin signal peptide	IPR006639	1285	1	<i>Drosophila willistoni</i>	7260	TR:B4N6M7 DROWI
Peptidase A22A, presenilin	IPR001108	404	1	<i>Drosophila willistoni</i>	7260	TR:B4N6M7 DROWI
Paramecium bursaria Chlorella virus 1, A79R	IPR009820	55	1	<i>Drosophila willistoni</i>	7260	TR:B4MIR0 DROWI
C2 membrane targeting protein	IPR018029	13871	6	<i>Drosophila erecta</i>	7220	TR:B3P3P0 DROER
				<i>Polysphondylium pallidum</i>	13642	TR:D3BU61 POLPA
				<i>Dictyostelium fasciculatum</i>	1054147	TR:F4PU20 DICFS
				<i>Oxytricha trifallax</i>	1172189	TR:J9EJ94 9SPIT
				<i>Naegleria gruberi</i>	5762	TR:D2VCR4 NAAGR
				<i>Trichomonas vaginalis</i>	5722	TR:A2EUT8 TRIVA
Synaptotagmin	IPR001565	1408	1	<i>Drosophila erecta</i>	7220	TR:B3P3P0 DROER
Transcription factor CBF/NF-Y/archaeal histone	IPR003958	3170	1	<i>Drosophila affinis</i>	7246	TR:D9MUS3 DROAI
Histone-fold	IPR009072	27659	4	<i>Drosophila affinis</i>	7246	TR:D9MUS3 DROAI
				<i>Chaetomium thermophilum</i>	759272	TR:G0S2A1 CHATD

				<i>Grosmannia clavigera</i>	655863	TR:FOXN84 GROCL
				<i>Dictyostelium discoideum</i>	44689	SP:TAF12 DICDI
Histone acetyltransferases subunit 3	IPR019340	280	1	<i>Drosophila grimshawi</i>	7222	TR:B4JJ95 DROGR
Thyroid hormone receptor	IPR001728	734	1	<i>Drosophila grimshawi</i>	7222	TR:B4J0N8 DROGR
SOCS protein, C-terminal	IPR001496	2535	1	<i>Drosophila grimshawi</i>	7222	TR:B4JNB2 DROGR
Dorsal protein	IPR011363	39	1	<i>Drosophila grimshawi</i>	7222	TR:B4JD22 DROGR
Immunoglobulin E-set	IPR014756	54860	2	<i>Drosophila grimshawi</i>	7222	TR:B4JD22 DROGR
				<i>Dictyostelium purpureum</i>	5786	TR:F0ZYQ8 DICPU
Cell surface receptor IPT/TIG	IPR002909	4608	2	<i>Drosophila grimshawi</i>	7222	TR:B4JD22 DROGR
				<i>Dictyostelium purpureum</i>	5786	TR:F0ZYQ8 DICPU
NF-kappa-B/Rel/Dorsal	IPR000451	622	1	<i>Drosophila grimshawi</i>	7222	TR:B4JD22 DROGR
p53-like transcription factor, DNA- binding	IPR008967	5876	4	<i>Drosophila grimshawi</i>	7222	TR:B4JD22 DROGR
				<i>Branchiostoma floridae</i>	7739	TR:C3ZBA3 BRAFL
				<i>Lodderomyces elongisporus</i>	379508	TR:A5H2N9 LODEL
				<i>Spathaspora passalidarum</i>	619300	TR:G3AKA5 SPAPN
Rel homology domain	IPR011539	1184	1	<i>Drosophila grimshawi</i>	7222	TR:B4JD22 DROGR
Sec16, central conserved domain	IPR024340	391	3	<i>Drosophila grimshawi</i>	7222	TR:B4JNJ2 DROGR
				<i>Komagataella pastoris</i>	981350	TR:F2R092 PICP7
				<i>Komagataella pastoris</i>	4922	TR:Q45TY0 PICPA
Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain	IPR016140	7058	197	<i>Triticum aestivum</i>	4565	TR:Q0ZCA8 WHEAT
						TR:Q0ZCB0 WHEAT
						TR:Q5TLY8 WHEAT
						TR:B3EY90 WHEAT
						TR:Q5MFP7 WHEAT
						TR:Q41551 WHEAT
						TR:Q5MFP8 WHEAT
						TR:D0EVP6 WHEAT
						TR:G3F3Z1 WHEAT
						TR:G3F3Z3 WHEAT
						TR:I3RTU0 WHEAT
						TR:Q5MFQ5 WHEAT
						TR:I1XB56 WHEAT
						TR:D3UAL6 WHEAT
						TR:F8SGN9 WHEAT

						TR:Q8W3W0 WHEAT
						TR:D0EVP1 WHEAT
						TR:C5IXL3 WHEAT
						TR:F8SGL6 WHEAT
						TR:F8SGL8 WHEAT
						TR:F8SGL9 WHEAT
						TR:Q571Q5 WHEAT
						TR:F8SGL7 WHEAT
						TR:Q18NR2 WHEAT
						TR:Q68AN2 WHEAT
						TR:Q75ZV8 WHEAT
						TR:D3UAL8 WHEAT
						TR:Q8W3W1 WHEAT
						TR:B3EY89 WHEAT
						TR:B5TWK5 WHEAT
						TR:Q5MFQ4 WHEAT
						TR:Q5MFQ6 WHEAT
						TR:B2BZC4 WHEAT
						TR:B2BZD2 WHEAT
						TR:B2Y2S1 WHEAT
						TR:B2Y2S6 WHEAT
						TR:B3EY88 WHEAT
						TR:B5TWK4 WHEAT
						TR:C3VN79 WHEAT
						TR:C3VN80 WHEAT
						TR:D3U318 WHEAT
						TR:F8SGL2 WHEAT
						TR:F8SGL3 WHEAT
						TR:F8SGL4 WHEAT
						TR:F8SGM0 WHEAT
						TR:F8SGM5 WHEAT
						TR:F8SGM7 WHEAT
						TR:F8SGM8 WHEAT
						TR:F8SGM9 WHEAT
						TR:F8SGN0 WHEAT
						TR:F8SGP6 WHEAT
						TR:F8SGP8 WHEAT
						TR:F8SGQ1 WHEAT
						TR:F8SGQ2 WHEAT
						TR:I3RTU2 WHEAT
						TR:Q00M61 WHEAT
						TR:Q84U20 WHEAT
						TR:Q8W3W2 WHEAT
						TR:D0EVP0 WHEAT
						TR:D0EVP2 WHEAT

						TR:D0EVP4 WHEAT
						TR:Q5MFQ1 WHEAT
						TR:Q5MFQ2 WHEAT
						TR:B2Y2Q1 WHEAT
						TR:B2Y2Q4 WHEAT
						TR:B2Y2Q3 WHEAT
						TR:Q8W3V6 WHEAT
						TR:B2Y2R5 WHEAT
						TR:B2Y2Q2 WHEAT
						TR:Q9ZNY0 WHEAT
						TR:Q8H0J4 WHEAT
						TR:O22108 WHEAT
						TR:F6M7E1 WHEAT
						TR:H9XH02 WHEAT
						TR:D2DII8 WHEAT
						TR:A4KZ73 WHEAT
						TR:H9XGZ8 WHEAT
						TR:Q52NZ4 WHEAT
						TR:Q8W3V8 WHEAT
						TR:Q8W3V9 WHEAT
						TR:D2DII5 WHEAT
						TR:D3U315 WHEAT
						TR:D2DII6 WHEAT
						TR:Q8GU18 WHEAT
						TR:Q41550 WHEAT
						TR:B5ANT3 WHEAT
				<i>Triticum aestivum subsp. yunnanense</i>	<u>425487</u>	TR:A8CA05 WHEAT
						TR:A9YSH4 WHEAT
				<i>Triticum aestivum subsp. tibeticum</i>	<u>231718</u>	TR:Q7Y075 WHEAT
				<i>Triticum turgidum subsp. dicoccon</i>	<u>49225</u>	TR:D5FPE5 TRITU
				<i>Triticum turgidum</i>	<u>4571</u>	TR:Q0Q2J0 TRITU
						TR:Q0Q2J1 TRITU
						TR:A7XDG0 TRITU
						TR:A7X9X7 TRITU
				<i>Triticum turgidum subsp. durum</i>	<u>4567</u>	TR:D5FPE4 TRIDB
						TR:Q49958 TRIDB
						TR:Q9XGE9 TRIDB
						TR:Q9FEQ1 TRIDB
						TR:Q41603 TRIDB
				<i>Triticum monococcum</i>	<u>4568</u>	TR:B8XU58 TRIMO
						TR:B8XU59 TRIMO
						TR:I7G262 TRIMO
						TR:B8XU60 TRIMO
				<i>Triticum dicoccoides</i>	<u>85692</u>	TR:B8YOL5 TRIDC
						TR:D5FPE0 TRIDC

						TR:B6UKK3 TRIDC
						TR:B6UKJ8 TRIDC
						TR:B6UKK0 TRIDC
						TR:B6UKK1 TRIDC
						TR:B6UKK4 TRIDC
						TR:B6UKK6 TRIDC
						TR:B6UKK9 TRIDC
						TR:B6UKL0 TRIDC
						TR:A2IBJ9 TRIDC
						TR:D5FPE7 TRIDC
				<i>Triticum zhukovskyi</i>	<u>77602</u>	TR:A2IBK1 9POAL
						TR:A2IBK1 9POAL
						TR:Q84U13 9POAL
				<i>Leymus mollis</i>	<u>183794</u>	TR:C6K8R5 9POAL
						TR:F5A7G7 9POAL
						TR:F5A7G8 9POAL
						TR:F5A7G6 9POAL
				<i>Secale sylvestre</i>	<u>4552</u>	TR:Q5MGR3 9POAL
						TR:Q5MGR4 9POAL
				<i>Triticum polonicum</i>	<u>77606</u>	TR:A2TN60 9POAL
				<i>Thinopyrum intermedium</i>	<u>85679</u>	TR:E5FEZ7 9POAL
						TR:Q84U17 9POAL
				<i>Dasypyrum villosum</i>	<u>40247</u>	TR:A9Z0K7 9POAL
						TR:F6KHQ1 9POAL
						TR:J9QGN7 9POAL
						TR:F8S8T4 9POAL
						TR:F8S8T7 9POAL
						TR:F8S8U3 9POAL
						TR:F8S8U4 9POAL
						TR:F8S8U6 9POAL
						TR:J9QFU9 9POAL
						TR:J9QGY5 9POAL
						TR:F6KHQ0 9POAL
						TR:F8S8T5 9POAL
						TR:F8S8T6 9POAL
						TR:F8S8T8 9POAL
						TR:F8S8T9 9POAL
						TR:F8S8U0 9POAL
						TR:F8S8U1 9POAL
						TR:F8S8U2 9POAL
						TR:F8S8U5 9POAL
						TR:F8S8U7 9POAL
						TR:J9QFV1 9POAL
						TR:J9QEK9 9POAL
						TR:J9QFG0 9POAL

						TR:A9Z0J9 9POAL
						TR:A9Z0K1 9POAL
						TR:A9Z0K4 9POAL
						TR:A9Z0K2 9POAL
						TR:A9Z0K5 9POAL
						TR:A9Z0K6 9POAL
						TR:A9Z0K8 9POAL
						TR:A9Z0K3 9POAL
				<i>Dasypyrum hordeaceum</i>	49449	TR:A8VZH1 9POAL
						TR:A8VZI4 9POAL
						TR:A9Z0L4 9POAL
						TR:A8VZF6 9POAL
						TR:D1MI66 9POAL
				<i>Thinopyrum elongatum</i>	4588	TR:A7LHA8 LOPEL
						TR:Q5XY00 LOPEL
				<i>Hordeum vulgare</i>	4513	SP:HOG3 HORVU
						TR:I6TEV2 HORVU
				<i>Aegilops longissima</i>	4486	TR:A9YWM3 AEGLO
						TR:D5FPF2 AEGLO
						TR:D5FPF0 AEGLO
						TR:C8CCM4 AEGLO
						TR:A2IBJ8 AEGLO
						TR:A9YWM2 AEGLO
						TR:A9YWM7 AEGLO
				<i>Aegilops tauschii</i>	37682	TR:Q5MB98 AEGTA
						TR:D3U335 AEGTA
						TR:Q6J6U9 AEGTA
						TR:B6UKJ3 AEGTA
						TR:B6UKJ4 AEGTA
						TR:B6UKI7 AEGTA
						TR:B6UKI9 AEGTA
						TR:B6UKJ1 AEGTA
						TR:B6UKJ5 AEGTA
						TR:D3U330 AEGTA
						TR:Q5MB99 AEGTA
				<i>Aegilops tauschii</i> x <i>Triticum turgidum</i>	285950	TR:Q6B780 9POAL
				<i>Thinopyrum ponticum</i> x <i>Triticum aestivum</i>	222994	TR:A8IEA6 9POAL
				<i>Aegilops markgrafii</i>	4494	TR:C8CCM6 9POAL
				<i>Psathyrostachys huashanica</i>	37730	TR:B8Y444 9POAL
						TR:E3UMZ0 9POAL
						TR:E3UMZ1 9POAL
				<i>Psathyrostachys juncea</i>	4586	TR:G0YLZ5 PSAJU
						TR:G0YLZ4 PSAJU
						TR:G0YLZ0 PSAJU
						TR:G0YLZ1 PSAJU

				<i>Aegilops speltoides</i>	4573	TR:C8CCM8 AEGSP
				<i>Aegilops triuncialis</i>	39391	TR:Q5MB97 AEGTR
Gliadin /Low molecular weight glutenin	<u>IPR001954</u>	2080	199	<i>Triticum aestivum</i>	4565	TR:Q0ZCA8 WHEAT TR:Q0ZCB0 WHEAT TR:Q5TLY8 WHEAT TR:B3EY90 WHEAT TR:Q5MFP7 WHEAT TR:Q41551 WHEAT TR:Q5MFP8 WHEAT TR:D0EVP6 WHEAT TR:G3F3Z1 WHEAT TR:G3F3Z3 WHEAT TR:I3RTU0 WHEAT TR:Q5MFQ5 WHEAT TR:I1XB56 WHEAT TR:D3UAL6 WHEAT TR:F8SGN9 WHEAT TR:Q8W3W0 WHEAT TR:D0EVP1 WHEAT TR:C5IXL3 WHEAT TR:F8SGL6 WHEAT TR:F8SGL8 WHEAT TR:F8SGL9 WHEAT TR:Q571Q5 WHEAT TR:F8SGL7 WHEAT TR:Q18NR2 WHEAT TR:Q68AN2 WHEAT TR:Q75ZV8 WHEAT TR:D3UAL8 WHEAT TR:Q8W3W1 WHEAT TR:B3EY89 WHEAT TR:B5TWK5 WHEAT TR:Q5MFQ4 WHEAT TR:Q5MFQ6 WHEAT TR:B2BZC4 WHEAT TR:B2BZD2 WHEAT TR:B2Y2S1 WHEAT TR:B2Y2S6 WHEAT TR:B3EY88 WHEAT TR:B5TWK4 WHEAT TR:C3VN79 WHEAT TR:C3VN80 WHEAT TR:D3U318 WHEAT TR:F8SGL2 WHEAT

						TR:F8SGL3 WHEAT
						TR:F8SGL4 WHEAT
						TR:F8SGM0 WHEAT
						TR:F8SGM5 WHEAT
						TR:F8SGM7 WHEAT
						TR:F8SGM8 WHEAT
						TR:F8SGM9 WHEAT
						TR:F8SGN0 WHEAT
						TR:F8SGP6 WHEAT
						TR:F8SGP8 WHEAT
						TR:F8SGQ1 WHEAT
						TR:F8SGQ2 WHEAT
						TR:I3RTU2 WHEAT
						TR:Q00M61 WHEAT
						TR:Q84U20 WHEAT
						TR:Q8W3W2 WHEAT
						TR:D0EVP0 WHEAT
						TR:D0EVP2 WHEAT
						TR:D0EVP4 WHEAT
						TR:Q5MFQ1 WHEAT
						TR:Q5MFQ2 WHEAT
						TR:B2Y2Q1 WHEAT
						TR:B2Y2Q4 WHEAT
						TR:B2Y2Q3 WHEAT
						TR:Q8W3V6 WHEAT
						TR:B2Y2R5 WHEAT
						TR:B2Y2Q2 WHEAT
						TR:Q9ZNY0 WHEAT
						TR:Q8H0J4 WHEAT
						TR:O22108 WHEAT
						TR:F6M7E1 WHEAT
						TR:H9XH02 WHEAT
						TR:D2DII8 WHEAT
						TR:A4KZ73 WHEAT
						TR:H9XGZ8 WHEAT
						TR:Q52NZ4 WHEAT
						TR:Q8W3V8 WHEAT
						TR:Q8W3V9 WHEAT
						TR:D2DII5 WHEAT
						TR:D3U315 WHEAT
						TR:D2DII6 WHEAT
						TR:Q8GU18 WHEAT
						TR:Q41550 WHEAT
						TR:B5ANT3 WHEAT
				<i>Triticum aestivum subsp. yunnanense</i>	425487	TR:A8CA05 WHEAT

						TR:A9YSH4 WHEAT
				<i>Triticum aestivum subsp. tibeticum</i>	<u>231718</u>	TR:Q7Y075 WHEAT
				<i>Triticum turgidum subsp. dicoccon</i>	<u>49225</u>	TR:D5FPE5 TRITU
				<i>Triticum turgidum</i>	<u>4571</u>	TR:QOQ2J0 TRITU
						TR:QOQ2J1 TRITU
						TR:A7XDG0 TRITU
						TR:A7X9X7 TRITU
				<i>Triticum turgidum subsp. durum</i>	<u>4567</u>	TR:D5FPE4 TRIDB
						TR:O49958 TRIDB
						TR:Q9XGE9 TRIDB
						TR:Q9FEQ1 TRIDB
						TR:Q41603 TRIDB
				<i>Triticum monococcum</i>	<u>4568</u>	TR:B8XU58 TRIMO
						TR:B8XU59 TRIMO
						TR:I7G262 TRIMO
						TR:B8XU60 TRIMO
				<i>Triticum dicoccoides</i>	<u>85692</u>	TR:B8Y0L5 TRIDC
						TR:D5FPE0 TRIDC
						TR:B6UKK3 TRIDC
						TR:B6UKJ8 TRIDC
						TR:B6UKK0 TRIDC
						TR:B6UKK1 TRIDC
						TR:B6UKK4 TRIDC
						TR:B6UKK6 TRIDC
						TR:B6UKK9 TRIDC
						TR:B6UKL0 TRIDC
						TR:A2IBJ9 TRIDC
						TR:D5FPE7 TRIDC
				<i>Triticum zhukovskyi</i>	<u>77602</u>	TR:A2IBK1 9POAL
						TR:A2IBK1 9POAL
				<i>Triticum aestivum/Thinopyrum intermedium</i>	<u>218488</u>	TR:Q84U13 9POAL
				<i>Secale sylvestre</i>	<u>4552</u>	TR:C6K8R5 9POAL
						TR:F5A7G7 9POAL
						TR:F5A7G8 9POAL
						TR:F5A7G6 9POAL
						TR:Q5MGR3 9POAL
						TR:Q5MGR4 9POAL
				<i>Triticum polonicum</i>	<u>77606</u>	TR:A2TN60 9POAL
				<i>Thinopyrum intermedium</i>	<u>85679</u>	TR:E5FEZ7 9POAL
						TR:Q84U17 9POAL
				<i>Dasypyrum villosum</i>	<u>40247</u>	TR:A9Z0K7 9POAL
						TR:F6KHQ1 9POAL
						TR:J9QGN7 9POAL
						TR:F8S8T4 9POAL
						TR:F8S8T7 9POAL

						TR:F8S8U3 9POAL
						TR:F8S8U4 9POAL
						TR:F8S8U6 9POAL
						TR:J9QFU9 9POAL
						TR:J9QGY5 9POAL
						TR:F6KHQ0 9POAL
						TR:F8S8T5 9POAL
						TR:F8S8T6 9POAL
						TR:F8S8T8 9POAL
						TR:F8S8T9 9POAL
						TR:F8S8U0 9POAL
						TR:F8S8U1 9POAL
						TR:F8S8U2 9POAL
						TR:F8S8U5 9POAL
						TR:F8S8U7 9POAL
						TR:J9QFV1 9POAL
						TR:J9QEK9 9POAL
						TR:J9QFG0 9POAL
						TR:A9Z0J9 9POAL
						TR:A9Z0K1 9POAL
						TR:A9Z0K4 9POAL
						TR:A9Z0K2 9POAL
						TR:A9Z0K5 9POAL
						TR:A9Z0K6 9POAL
						TR:A9Z0K8 9POAL
						TR:A9Z0K3 9POAL
				<i>Dasypyrum hordeaceum</i>	49449	TR:A8VZH1 9POAL
						TR:A8VZI4 9POAL
						TR:A9Z0L4 9POAL
						TR:A8VZF6 9POAL
						TR:D1MI66 9POAL
				<i>Thinopyrum elongatum</i>	4588	TR:A7LHA8 LOPEL
						TR:Q5XY00 LOPEL
				<i>Hordeum vulgare</i>	4513	SP:HOG3 HORVU
						TR:I6TEV2 HORVU
				<i>Aegilops longissima</i>	4486	TR:A9YWM3 AEGLO
						TR:D5FPF2 AEGLO
						TR:D5FPF0 AEGLO
						TR:C8CCM4 AEGLO
						TR:A2IBJ8 AEGLO
						TR:A9YWM2 AEGLO
						TR:A9YWM7 AEGLO
				<i>Aegilops tauschii</i>	37682	TR:Q5MB98 AEGTA
						TR:D3U335 AEGTA
						TR:Q6J6U9 AEGTA

						TR:B6UKJ3 AEGTA TR:B6UKJ4 AEGTA TR:B6UKI7 AEGTA TR:B6UKI9 AEGTA TR:B6UKJ1 AEGTA TR:B6UKJ5 AEGTA TR:D3U330 AEGTA TR:Q5MB99 AEGTA
				<i>Aegilops tauschii</i> x <i>Triticum turgidum</i>	285950	TR:Q6B780 9POAL
				<i>Thinopyrum ponticum</i> x <i>Triticum aestivum</i>	222994	TR:A8IEA6 9POAL
				<i>Aegilops markgrafii</i>	4494	TR:C8CCM6 9POAL
				<i>Psathyrostachys huashanica</i>	37730	TR:B8Y444 9POAL TR:E3UMZ0 9POAL TR:E3UMZ1 9POAL
				<i>Psathyrostachys juncea</i>	4586	TR:G0YLZ5 PSAJU TR:G0YLZ4 PSAJU TR:G0YLZ0 PSAJU TR:G0YLZ1 PSAJU
				<i>Aegilops speltoides</i>	4573	TR:C8CCM8 AEGSP
				<i>Aegilops triuncialis</i>	39391	TR:Q5MB97 AEGTR
Gliadin, alpha/beta	IPR001376	1965	208	<i>Triticum aestivum</i>	4565	TR:Q0ZCA8 WHEAT
						TR:Q0ZCB0 WHEAT
						TR:Q5TLY8 WHEAT
						TR:B3EY90 WHEAT
						TR:Q5MFP7 WHEAT
						TR:Q41551 WHEAT
						TR:Q5MFP8 WHEAT
						TR:B6ETS0 WHEAT
						TR:D0EVP6 WHEAT
						TR:G3F3Z1 WHEAT
						TR:G3F3Z3 WHEAT
						TR:I3RTU0 WHEAT
						TR:Q5MFQ5 WHEAT
						TR:I1XB56 WHEAT
						TR:D3UAL6 WHEAT
						TR:F8SGN9 WHEAT
						TR:Q8W3W0 WHEAT
						TR:D0EVP1 WHEAT
						TR:C5IXL3 WHEAT
						TR:F8SGL6 WHEAT
						TR:F8SGL8 WHEAT
						TR:F8SGL9 WHEAT
						TR:Q571Q5 WHEAT
						TR:F8SGL7 WHEAT

					TR:Q18NR2 WHEAT
					TR:Q68AN2 WHEAT
					TR:Q75ZV8 WHEAT
					TR:D3UAL8 WHEAT
					TR:B6ETS1 WHEAT
					TR:Q8W3W1 WHEAT
					TR:B3EY89 WHEAT
					TR:B5TWK5 WHEAT
					TR:Q5MFQ4 WHEAT
					TR:Q5MFQ6 WHEAT
					TR:B2BZC4 WHEAT
					TR:B2BZD2 WHEAT
					TR:B2Y2S1 WHEAT
					TR:B2Y2S6 WHEAT
					TR:B3EY88 WHEAT
					TR:B5TWK4 WHEAT
					TR:C3VN79 WHEAT
					TR:C3VN80 WHEAT
					TR:D3U318 WHEAT
					TR:F8SGL2 WHEAT
					TR:F8SGL3 WHEAT
					TR:F8SGL4 WHEAT
					TR:F8SGM0 WHEAT
					TR:F8SGM5 WHEAT
					TR:F8SGM7 WHEAT
					TR:F8SGM8 WHEAT
					TR:F8SGM9 WHEAT
					TR:F8SGN0 WHEAT
					TR:F8SGP6 WHEAT
					TR:F8SGP8 WHEAT
					TR:F8SGQ1 WHEAT
					TR:F8SGQ2 WHEAT
					TR:I3RTU2 WHEAT
					TR:Q00M61 WHEAT
					TR:Q84U20 WHEAT
					TR:Q8W3W2 WHEAT
					TR:D0EVP0 WHEAT
					TR:D0EVP2 WHEAT
					TR:D0EVP4 WHEAT
					TR:Q5MFQ1 WHEAT
					TR:Q5MFQ2 WHEAT
					TR:B2Y2Q1 WHEAT
					TR:B2Y2Q4 WHEAT
					TR:B2Y2Q3 WHEAT
					TR:Q402I5 WHEAT

						TR:Q8W3V6 WHEAT
						TR:B2Y2R5 WHEAT
						TR:B2Y2Q2 WHEAT
						TR:Q9ZNY0 WHEAT
						TR:Q8H0J4 WHEAT
						TR:Q22108 WHEAT
						TR:F6M7E1 WHEAT
						TR:H9XH02 WHEAT
						TR:D2DII8 WHEAT
						TR:A4KZ73 WHEAT
						TR:H9XGZ8 WHEAT
						TR:Q52NZ4 WHEAT
						TR:Q8W3V8 WHEAT
						TR:Q8W3V9 WHEAT
						TR:D2DII5 WHEAT
						TR:D3U315 WHEAT
						TR:D2DII6 WHEAT
						TR:Q8GU18 WHEAT
						TR:Q41550 WHEAT
						TR:B5ANT3 WHEAT
				<i>Triticum aestivum subsp. yunnanense</i>	<u>425487</u>	TR:A8CA05 WHEAT
						TR:A9YSH4 WHEAT
				<i>Triticum aestivum subsp. tibeticum</i>	<u>231718</u>	TR:Q7Y075 WHEAT
				<i>Triticum turgidum subsp. dicoccon</i>	<u>49225</u>	TR:D5FPE5 TRITU
				<i>Triticum turgidum</i>	<u>4571</u>	TR:Q0Q2J0 TRITU
						TR:Q0Q2J1 TRITU
						TR:A7XDG0 TRITU
						TR:A7X9X7 TRITU
				<i>Triticum turgidum subsp. durum</i>	<u>4567</u>	TR:D5FPE4 TRIDB
						TR:O49958 TRIDB
						TR:Q9XGE9 TRIDB
						TR:Q9FEQ1 TRIDB
						TR:Q41603 TRIDB
				<i>Triticum monococcum</i>	<u>4568</u>	TR:B8XU58 TRIMO
						TR:B8XU59 TRIMO
						TR:I7G262 TRIMO
						TR:B8XU60 TRIMO
				<i>Triticum dicoccoides</i>	<u>85692</u>	TR:B8Y0L5 TRIDC
						TR:D5FPE0 TRIDC
						TR:B6UKK3 TRIDC
						TR:B6UKJ8 TRIDC
						TR:B6UKK0 TRIDC
						TR:B6UKK1 TRIDC
						TR:B6UKK4 TRIDC
						TR:B6UKK6 TRIDC

						TR:B6UUK9 TRIDC
						TR:B6UKL0 TRIDC
						TR:A2IBJ9 TRIDC
						TR:D5FPE7 TRIDC
				<i>Triticum zhukovskyi</i>	<u>77602</u>	TR:A2IBK1 9POAL
						TR:A2IBK1 9POAL
						TR:Q84U13 9POAL
				<i>Leymus mollis</i>	<u>183794</u>	TR:C6K8R5 9POAL
						TR:F5A7G7 9POAL
						TR:F5A7G8 9POAL
						TR:F5A7G6 9POAL
				<i>Secale sylvestre</i>	<u>4552</u>	TR:Q5MGR3 9POAL
						TR:Q5MGR4 9POAL
				<i>Triticum polonicum</i>	<u>77606</u>	TR:A2TN60 9POAL
				<i>Thinopyrum intermedium</i>	<u>85679</u>	TR:E5FEZ7 9POAL
						TR:Q84U17 9POAL
				<i>Dasypyrum villosum</i>	<u>40247</u>	TR:A9Z0K7 9POAL
						TR:F6KHQ1 9POAL
						TR:J9QGN7 9POAL
						TR:F8S8T4 9POAL
						TR:F8S8T7 9POAL
						TR:F8S8U3 9POAL
						TR:F8S8U4 9POAL
						TR:F8S8U6 9POAL
						TR:J9QFU9 9POAL
						TR:J9QGY5 9POAL
						TR:F6KHQ0 9POAL
						TR:F8S8T5 9POAL
						TR:F8S8T6 9POAL
						TR:F8S8T8 9POAL
						TR:F8S8T9 9POAL
						TR:F8S8U0 9POAL
						TR:F8S8U1 9POAL
						TR:F8S8U2 9POAL
						TR:F8S8U5 9POAL
						TR:F8S8U7 9POAL
						TR:J9QFV1 9POAL
						TR:J9QEK9 9POAL
						TR:J9QFG0 9POAL
						TR:A9Z0J9 9POAL
						TR:A9Z0K1 9POAL
						TR:A9Z0K4 9POAL
						TR:A9Z0K2 9POAL
						TR:A9Z0K5 9POAL
						TR:A9Z0K6 9POAL

						TR:A9ZOK8 9POAL
						TR:A9ZOK3 9POAL
				<i>Dasypyrum hordeaceum</i>	<u>49449</u>	TR:A8VZH1 9POAL
						TR:A8VZI4 9POAL
						TR:A9ZOL4 9POAL
						TR:A8VZF6 9POAL
						TR:D1MI66 9POAL
				<i>Thinopyrum elongatum</i>	<u>4588</u>	TR:G8G230 LOPEL
						TR:G8G227 LOPEL
						TR:G8G225 LOPEL
						TR:G8G229 LOPEL
						TR:G8G226 LOPEL
						TR:G8G231 LOPEL
						TR:G8G228 LOPEL
						TR:A7LHA8 LOPEL
						TR:Q5XY00 LOPEL
				<i>Hordeum vulgare</i>	<u>4513</u>	SP:HOG3 HORVU
						TR:I6TEV2 HORVU
				<i>Aegilops longissima</i>	<u>4486</u>	TR:A9YWM3 AEGLO
						TR:D5FPF2 AEGLO
						TR:D5FPF0 AEGLO
						TR:C8CCM4 AEGLO
						TR:A2IBJ8 AEGLO
						TR:A9YWM2 AEGLO
						TR:A9YWM7 AEGLO
				<i>Aegilops tauschii</i>	<u>37682</u>	TR:Q5MB98 AEGTA
						TR:D3U335 AEGTA
						TR:Q6J6U9 AEGTA
						TR:B6UKJ3 AEGTA
						TR:B6UKJ4 AEGTA
						TR:B6UKI7 AEGTA
						TR:B6UKI9 AEGTA
						TR:B6UKJ1 AEGTA
						TR:B6UKJ5 AEGTA
						TR:D3U330 AEGTA
						TR:Q5MB99 AEGTA
				<i>Aegilops tauschii</i> x <i>Triticum turgidum</i>	<u>285950</u>	TR:Q6B780 9POAL
				<i>Thinopyrum ponticum</i> x <i>Triticum aestivum</i>	<u>222994</u>	TR:A8IEA6 9POAL
				<i>Aegilops markgrafii</i>	<u>4494</u>	TR:C8CCM6 9POAL
				<i>Psathyrostachys huashanica</i>	<u>37730</u>	TR:B9VSH9 9POAL
						TR:B8Y444 9POAL
						TR:E3UMZ0 9POAL
						TR:E3UMZ1 9POAL
				<i>Psathyrostachys juncea</i>	<u>4586</u>	TR:G0YLZ5 PSAJU
						TR:G0YLZ4 PSAJU

						TR:G0YLZ0_PSAJU TR:G0YLZ1_PSAJU Aegilops speltoides 4573 TR:C8CCM8_AEGSP Aegilops triuncialis 39391 TR:Q5MB97_AEGTR
Bifunctional trypsin/alpha-amylase inhibitor helical domain	IPR013771	3533	199	<i>Triticum aestivum</i>	4565	TR:Q0ZCA8_WHEAT TR:Q0ZCB0_WHEAT TR:Q5TLY8_WHEAT TR:B3EY90_WHEAT TR:Q5MFP7_WHEAT TR:Q41551_WHEAT TR:Q5MFP8_WHEAT TR:D0EVP6_WHEAT TR:G3F3Z1_WHEAT TR:G3F3Z3_WHEAT TR:I3RTU0_WHEAT TR:Q5MFQ5_WHEAT TR:I1XB56_WHEAT TR:D3UAL6_WHEAT TR:F8SGN9_WHEAT TR:Q8W3W0_WHEAT TR:D0EVP1_WHEAT TR:C5IXL3_WHEAT TR:F8SGL6_WHEAT TR:F8SGL8_WHEAT TR:F8SGL9_WHEAT TR:Q571Q5_WHEAT TR:F8SGL7_WHEAT TR:Q18NR2_WHEAT TR:Q68AN2_WHEAT TR:Q75ZV8_WHEAT TR:D3UAL8_WHEAT TR:Q8W3W1_WHEAT TR:B3EY89_WHEAT TR:B5TWK5_WHEAT TR:Q5MFQ4_WHEAT TR:Q5MFQ6_WHEAT TR:B2BZC4_WHEAT TR:B2BZD2_WHEAT TR:B2Y2S1_WHEAT TR:B2Y2S6_WHEAT TR:B3EY88_WHEAT TR:B5TWK4_WHEAT TR:C3VN79_WHEAT TR:C3VN80_WHEAT

						TR:D3U318 WHEAT
						TR:F8SGL2 WHEAT
						TR:F8SGL3 WHEAT
						TR:F8SGL4 WHEAT
						TR:F8SGM0 WHEAT
						TR:F8SGM5 WHEAT
						TR:F8SGM7 WHEAT
						TR:F8SGM8 WHEAT
						TR:F8SGM9 WHEAT
						TR:F8SGN0 WHEAT
						TR:F8SGP6 WHEAT
						TR:F8SGP8 WHEAT
						TR:F8SGQ1 WHEAT
						TR:F8SGQ2 WHEAT
						TR:I3RTU2 WHEAT
						TR:Q00M61 WHEAT
						TR:Q84U20 WHEAT
						TR:Q8W3W2 WHEAT
						TR:D0EVP0 WHEAT
						TR:D0EVP2 WHEAT
						TR:D0EVP4 WHEAT
						TR:Q5MFAQ1 WHEAT
						TR:Q5MFAQ2 WHEAT
						TR:B2Y2Q1 WHEAT
						TR:B2Y2Q4 WHEAT
						TR:B2Y2Q3 WHEAT
						TR:Q8W3V6 WHEAT
						TR:B2Y2R5 WHEAT
						TR:B2Y2Q2 WHEAT
						TR:Q9ZNY0 WHEAT
						TR:Q8H0J4 WHEAT
						TR:Q22108 WHEAT
						TR:F6M7E1 WHEAT
						TR:H9XH02 WHEAT
						TR:D2DII8 WHEAT
						TR:A4KZ73 WHEAT
						TR:H9XGZ8 WHEAT
						TR:Q52NZ4 WHEAT
						TR:Q8W3V8 WHEAT
						TR:Q8W3V9 WHEAT
						TR:D2DII5 WHEAT
						TR:D3U315 WHEAT
						TR:D2DII6 WHEAT
						TR:Q8GU18 WHEAT
						TR:Q41550 WHEAT

						TR:B5ANT3 WHEAT
				<i>Triticum aestivum subsp. yunnanense</i>	<u>425487</u>	TR:A8CA05 WHEAT
						TR:A9YSH4 WHEAT
				<i>Triticum aestivum subsp. tibeticum</i>	<u>231718</u>	TR:Q7Y075 WHEAT
				<i>Triticum turgidum subsp. dicoccon</i>	<u>49225</u>	TR:D5FPE5 TRITU
				<i>Triticum turgidum</i>	<u>4571</u>	TR:Q0Q2J0 TRITU
						TR:Q0Q2J1 TRITU
						TR:A7XDG0 TRITU
						TR:A7X9X7 TRITU
				<i>Triticum turgidum subsp. durum</i>	<u>4567</u>	TR:D5FPE4 TRIDB
						TR:O49958 TRIDB
						TR:Q9XGE9 TRIDB
						TR:Q9FEQ1 TRIDB
						TR:Q41603 TRIDB
				<i>Triticum monococcum</i>	<u>4568</u>	TR:B8XU58 TRIMO
						TR:B8XU59 TRIMO
						TR:I7G262 TRIMO
						TR:B8XU60 TRIMO
				<i>Triticum dicoccoides</i>	<u>85692</u>	TR:B8YOL5 TRIDC
						TR:D5FPE0 TRIDC
						TR:B6UKK3 TRIDC
						TR:B6UKJ8 TRIDC
						TR:B6UKK0 TRIDC
						TR:B6UKK1 TRIDC
						TR:B6UKK4 TRIDC
						TR:B6UKK6 TRIDC
						TR:B6UKK9 TRIDC
						TR:B6UKL0 TRIDC
						TR:A2IBJ9 TRIDC
						TR:D5FPE7 TRIDC
				<i>Triticum zhukovskyi</i>	<u>77602</u>	TR:A2IBK1 9POAL
						TR:A2IBK1 9POAL
				<i>Triticum aestivum/Thinopyrum intermedium</i>	<u>218488</u>	TR:Q84U13 9POAL
				<i>Leymus mollis</i>	<u>183794</u>	TR:C6K8R5 9POAL
						TR:F5A7G7 9POAL
						TR:F5A7G8 9POAL
						TR:F5A7G6 9POAL
				<i>Secale sylvestre</i>	<u>4552</u>	TR:Q5MGR3 9POAL
						TR:Q5MGR4 9POAL
				<i>Triticum polonicum</i>	<u>77606</u>	TR:A2TN60 9POAL
				<i>Thinopyrum intermedium</i>	<u>85679</u>	TR:E5FEZ7 9POAL
						TR:Q84U17 9POAL
				<i>Dasypyrum villosum</i>	<u>40247</u>	TR:A9ZOK7 9POAL
						TR:F6KHQ1 9POAL
						TR:J9QGN7 9POAL

						TR:F8S8T4 9POAL
						TR:F8S8T7 9POAL
						TR:F8S8U3 9POAL
						TR:F8S8U4 9POAL
						TR:F8S8U6 9POAL
						TR:J9QFU9 9POAL
						TR:J9QGY5 9POAL
						TR:F6KHQ0 9POAL
						TR:F8S8T5 9POAL
						TR:F8S8T6 9POAL
						TR:F8S8T8 9POAL
						TR:F8S8T9 9POAL
						TR:F8S8U0 9POAL
						TR:F8S8U1 9POAL
						TR:F8S8U2 9POAL
						TR:F8S8U5 9POAL
						TR:F8S8U7 9POAL
						TR:J9QFV1 9POAL
						TR:J9QEK9 9POAL
						TR:J9QFG0 9POAL
						TR:A9Z0J9 9POAL
						TR:A9Z0K1 9POAL
						TR:A9Z0K4 9POAL
						TR:A9Z0K2 9POAL
						TR:A9Z0K5 9POAL
						TR:A9Z0K6 9POAL
						TR:A9Z0K8 9POAL
						TR:A9Z0K3 9POAL
				<i>Dasypyrum hordeaceum</i>	<u>49449</u>	TR:A8VZH1 9POAL
						TR:A8VZI4 9POAL
						TR:A9Z0L4 9POAL
						TR:A8VZF6 9POAL
						TR:D1MI66 9POAL
				<i>Thinopyrum elongatum</i>	<u>4588</u>	TR:A7LHA8 LOPEL
						TR:Q5XY00 LOPEL
				<i>Hordeum vulgare</i>	<u>4513</u>	SP:HOG3 HORVU
						TR:I6TEV2 HORVU
				<i>Aegilops longissima</i>	<u>4486</u>	TR:A9YWM3 AEGLO
						TR:D5FPF2 AEGLO
						TR:D5FPF0 AEGLO
						TR:C8CCM4 AEGLO
						TR:A2IBJ8 AEGLO
						TR:A9YWM2 AEGLO
						TR:A9YWM7 AEGLO
				<i>Aegilops tauschii</i>	<u>37682</u>	TR:Q5MB98 AEGTA

						TR:D3U335 AEGTA TR:Q6J6U9 AEGTA TR:B6UKJ3 AEGTA TR:B6UKJ4 AEGTA TR:B6UKI7 AEGTA TR:B6UKI9 AEGTA TR:B6UKJ1 AEGTA TR:B6UKJ5 AEGTA TR:D3U330 AEGTA TR:Q5MB99 AEGTA
				<i>Aegilops tauschii</i> x <i>Triticum turgidum</i>	285950	TR:Q6B780 9POAL
				<i>Thinopyrum ponticum</i> x <i>Triticum aestivum</i>	222994	TR:A8IEA6 9POAL
				<i>Aegilops markgrafii</i>	4494	TR:C8CCM6 9POAL
				<i>Psathyrostachys huashanica</i>	37730	TR:B8Y444 9POAL TR:E3UMZ0 9POAL TR:E3UMZ1 9POAL
				<i>Psathyrostachys juncea</i>	4586	TR:G0YLZ5 PSAJU TR:G0YLZ4 PSAJU TR:G0YLZ0 PSAJU TR:G0YLZ1 PSAJU
				<i>Aegilops speltoides</i>	4573	TR:C8CCM8 AEGSP
				<i>Aegilops triuncialis</i>	39391	TR:Q5MB97 AEGTR
F-box associated interaction domain	IPR017451	6512	1	<i>Sorghum bicolor</i>	4558	TR:C5WR35 SORBI
ATP-dependent RNA helicase DEAD-box, conserved site	IPR000629	63977	2	<i>Arabidopsis thaliana</i> <i>Arabidopsis lyrata</i> subsp. <i>lyrata</i>	3702 81972	SP:RH40 ARATH TR:D7L5I4 ARALL
DWNN domain	IPR014891	794	1	<i>Coccomyxa subellipsoidea</i> C-169	574566	TR:I0Z6X5 9CHLO
Zinc knuckle CX2CX3GHX4C	IPR025829	382	1	<i>Coccomyxa subellipsoidea</i> C-169	574566	TR:I0Z6X5 9CHLO
Protein of unknown function DUF3250	IPR021656	259	1	<i>Volvox carteri</i>	3067	TR:D8U185 VOLCA
DNA helicase, UvrD-like, C-terminal	IPR014017	74617	1	<i>Volvox carteri</i>	3067	TR:D8U185 VOLCA
Calcium/calmodulin-dependent/calcium-dependent protein kinase	IPR020636	10583	1	<i>Volvox carteri</i>	3067	TR:D8UGB6 VOLCA
HARP domain	IPR010003		1	<i>Volvox carteri</i>	3067	TR:D8TLQ2 VOLCA
CHCH	IPR010625	1095	3	<i>Tetraodon nigroviridis</i>	99883	TR:Q4TG53 TETNG TR:Q4REM5 TETNG TR:H3C8B8 TETNG

DZF	IPR006561	578	1	<i>Tetraodon nigroviridis</i>	99883	TR:Q4RUC4 TETNG
Zinc finger, U1-type	IPR003604	3080	1	<i>Tetraodon nigroviridis</i>	99883	TR:Q4RUC4 TETNG
Helicase/SANT-associated, DNA binding	IPR014012	1065	5	<i>Vitis vinifera</i>	29760	TR:F6I025 VITVI
				<i>Debaryomyces hansenii</i>	284592	TR:Q6BJE1 DEBHA
				<i>Caenorhabditis brenneri</i>	135651	TR:G0M812 CAEBE
				<i>Dictyostelium purpureum</i>	5786	TR:F1A5J1 DICPU
				<i>Dictyostelium discoideum</i>	44689	TR:Q55GK2 DICDI
HSA	IPR006562	943	3	<i>Vitis vinifera</i>	29760	TR:F6I025 VITVI
				<i>Candida parapsilosis</i>	578454	TR:G8BH70 CANPC
				<i>Dictyostelium purpureum</i>	5786	TR:F1A5J1 DICPU
Myb-like domain	IPR017877	4255	4	<i>Vitis vinifera</i>	29760	TR:F6I025 VITVI
				<i>Candida parapsilosis</i>	578454	TR:G8BH70 CANPC
				<i>Dictyostelium purpureum</i>	5786	TR:F1A5J1 DICPU
				<i>Dictyostelium discoideum</i>	44689	TR:Q55GK2 DICDI
AUX/IAA protein	IPR003311	1935	1	<i>Cucumis sativus</i>	3659	TR:Q6L8U3 CUCSA
Aux/IAA-ARF-dimerisation	IPR011525	1942	1	<i>Cucumis sativus</i>	3659	TR:Q6L8U3 CUCSA
Auxin response factor	IPR010525	804	1	<i>Cucumis sativus</i>	3659	TR:Q6L8U3 CUCSA
B3 DNA binding domain	IPR003340	2168	1	<i>Cucumis sativus</i>	3659	TR:Q6L8U3 CUCSA
DNA-binding pseudobarrel domain	IPR015300	2609	1	<i>Cucumis sativus</i>	3659	TR:Q6L8U3 CUCSA
PWI domain	IPR002483	1166	1	<i>Yarrowia lipolytica</i>	284591	TR:Q6CDX5 YARLI
Transcription factor	IPR007219	12952	5	<i>Yarrowia lipolytica</i>	284591	TR:Q6CHB0 YARLI
				<i>Spathaspora passalidarum</i>	619300	TR:G3ATH7 SPAPN
				<i>Hypocrea atroviridis</i>	452589	TR:G9NL19 HYPAL
				<i>Podospora anserina</i>	515849	TR:B2ACE3 PODAN
				<i>Verticillium alfalfae</i>	526221	TR:C9SN42 VERA1
Zn(2)-C6 fungal-type DNA-binding domain	IPR001138	17917	17	<i>Yarrowia lipolytica</i>	284591	TR:Q6CHB0 YARLI
				<i>Spathaspora passalidarum</i>	619300	TR:G3APH2 SPAPN
				<i>Hypocrea atroviridis</i>	452589	TR:G9NL19 HYPAL
				<i>Podospora anserina</i>	515849	TR:B2ACE3 PODAN
				<i>Verticillium alfalfae</i>	526221	TR:C9SN42 VERA1
				<i>Saccharomyces cerevisiae</i>	764102	TR:E7Q716 YEASB
						SP:ECM22 YEAST
						TR:A7A1B5 YEAS7

						TR:B5VNE5 YEAS6 TR:C7GT26 YEAS2 TR:C8ZDJ2 YEAS8 TR:E7LXR7 YEASV TR:E7NKS4 YEASO TR:E7QI59 YEASZ TR:H0GKF3 9SACH TR:G2WJ57 YEASK TR:E7KRV5 YEASL
RAM signalling pathway, SOG2	IPR019487	158	1	<i>Yarrowia lipolytica</i>	284591	TR:Q6C1M0 YARLI
Transcription factor, STE-like	IPR003120	210	1	<i>Yarrowia lipolytica</i>	284591	TR:Q6C5Q0 YARLI
Cyclin-like	IPR013763	11051	5	<i>Lodderomyces elongisporus</i> <i>Arthroderma benhamiae</i> <i>Trichophyton verrucosum</i> <i>Trichophyton tonsurans</i> <i>Trichophyton equinum</i>	379508 663331 663202 647933 559882	TR:A5DUV2 LODEL TR:D4AIT9 ARTBC TR:D4DFR8 TRIVH TR:F2RYA1 TRIT1 TR:F2PRJ7 TRIEC
Cyclin, C-terminal domain	IPR004367	3414	1	<i>Lodderomyces elongisporus</i>	379508	TR:A5DUV2 LODEL
NDT80 DNA-binding domain	IPR024061	463	2	<i>Lodderomyces elongisporus</i> <i>Spathaspora passalidarum</i>	379508 619300	TR:A5H2N9 LODEL TR:G3AKA5 SPAPN
DDE superfamily endonuclease, CENP-B-like	IPR004875	3316	3	<i>Lodderomyces elongisporus</i> <i>Candida albicans</i>	379508 294748	TR:A5E1L5 LODEL TR:C4YMY3 CANAW TR:Q59NK7 CANAL
HTH CenpB-type DNA-binding domain	IPR006600	2593	2	<i>Lodderomyces elongisporus</i> <i>Komagataella pastoris</i>	379508 981350	TR:A5E1L5 LODEL TR:F2QM85 PICP7
Ubiquitin system component Cue	IPR003892	2120	2	<i>Komagataella pastoris</i> <i>Saccharomyces cerevisiae</i>	644223 764097	TR:C4QW10 PICPG TR:E7KEY3 YEASA
PSP1, C-terminal	IPR007557	2263	1	<i>Candida dubliniensis</i>	573826	TR:B9WJJ2 CANDC
RNA- binding protein Lupus La	IPR006630	1617	1	<i>Candida dubliniensis</i>	573826	TR:B9WKI8 CANDC
6-phosphogluconate dehydrogenase, C-terminal-like	IPR008927	78846	1	<i>Scheffersomyces stipitis</i>	322104	TR:A3GHQ4 PICST
Ketopantoate reductase ApbA/PanE, C-terminal	IPR013752	6448	1	<i>Scheffersomyces stipitis</i>	322104	TR:A3GHQ4 PICST
Dehydrogenase, multihelical	IPR013328	58539	1	<i>Scheffersomyces stipitis</i>	322104	TR:A3GHQ4 PICST

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Activator of mitotic machinery Cdc14 phosphatase activation C-terminal	IPR013941	165	1	<i>Scheffersomyces stipitis</i>	322104	TR:A3LS86 PICST
ARID/BRIGHT DNA-binding domain	IPR001606	2042	5	<i>Naumovozyma castellii</i>	1064592	TR:G0VCN5 NAUCC
				<i>Meyerozyma guilliermondii</i>	294746	TR:A5DE07 PICGU
				<i>Candida parapsilosis</i>	578454	TR:G8BIK7 CANPC
				<i>Trichosporon asahii</i> var. <i>asahii</i>	1186058	TR:J6EXZ0 TRIAS
				<i>Trichosporon asahii</i> var. <i>asahii</i>	1220162	TR:K1WJ31 TRIAC
Transcription factor, MADS-box	IPR002100	6778	4	<i>Tetrapisispora blattae</i>	1071380	TR:I2GZF5 TETBL
				<i>Kazachstania africana</i>	1071382	TR:H2AN55 KAZAF
				<i>Rhizopus delemar</i>	246409	TR:I1BLN6 RHIO9
				<i>Rhizopus delemar</i>	246409	TR:I1BI10 RHIO9
LsmAD domain	IPR009604	472	4	<i>Hypocrea jecorina</i>	431241	TR:G0RDB0 HYPJQ
				<i>Nectria haematococca</i>	660122	TR:C7YH26 NECH7
				<i>Tetrahymena thermophila</i>	312017	TR:Q23QL4 TETTS
				<i>Salpingoeca rosetta</i>	946362	TR:F2UB05 SALS5
AAA+ ATPase domain	IPR003593	657571	2	<i>Hypocrea jecorina</i>	431241	TR:G0RGX3 HYPJQ
				<i>Saccharomonospora viridis</i>	471857	TR:C7MXV2 SACVD
ATPase, AAA-type, core	IPR003959	62855	1	<i>Hypocrea jecorina</i>	431241	TR:G0RGX3 HYPJQ
Mediator complex, subunit Med15, fungi	IPR008626	99	1	<i>Rhizopus delemar</i>	246409	TR:I1BJ65 RHIO9
Protein of unknown function DUF1752, fungi	IPR013860	541	1	<i>Rhizopus delemar</i>	246409	TR:I1CHV5 RHIO9
Zinc finger, GATA-type	IPR000679	3775	3	<i>Rhizopus delemar</i>	246409	TR:I1CHV5 RHIO9
				<i>Dictyostelium discoideum</i>	44689	SP:GTAG DICI
				<i>Salpingoeca rosetta</i>	946362	TR:F2TY54 SALS5
Fungal chitin synthase	IPR004835	1505	1	<i>Fibroporia radiculosa</i>	1078123	TR:J4G782 9APHY
SNF5/SMARCB1/INI1	IPR006939	546	3	<i>Cryptococcus neoformans</i> var. <i>neoformans</i>	283643	TR:F5HD71 CRYNB
				<i>Cryptococcus gattii</i>	367775	TR:Q5KNA4 CRYNJ
						TR:E6QYJ3 CRYGW
Chitin synthesis regulation, Congo red resistance, RCR protein	IPR020999	333	4	<i>Arthroderma otae</i>	554155	TR:C5G0Y8 ARTOC
				<i>Trichophyton tonsurans</i>	647933	TR:F2S4E4 TRIT1
				<i>Trichophyton equinum</i>	559882	TR:F2PUE2 TRIEC
				<i>Trichophyton rubrum</i>	559305	TR:F2SKR7 TRIRC
C4-dicarboxylate transporter/malic acid	IPR004695	3750	1	<i>Magnaporthe oryzae</i>	242507	TR:G4MY83 MAGO7

transport protein						
Arf GTPase activating protein	IPR001164	3825	2	<i>Phaeosphaeria nodorum</i> <i>Eimeria tenella</i>	321614 5802	TR:QOUX18 PHANO TR:C8TDR1 EIMTE
Ubiquitin-associated/translation elongation factor EF1B, N-terminal, eukaryote	IPR015940	6732	2	<i>Phaeosphaeria nodorum</i> <i>Ichthyophthirius multifiliis</i>	321614 857967	TR:QOUX18 PHANO TR:GQR1R9 ICHMG
Uncharacterised protein family Cys-rich	IPR006461	1339	1	<i>Pyrenophora teres f. teres</i>	861557	TR:E3SA10 PYRTT
Nuclear abundant poly(A) RNA-binding protein 2, Nab2	IPR021083	31	1	<i>Kazachstania naganishii</i>	1071383	TR:I7S062 KAZNA
Zinc finger, BED-type predicted	IPR003656	1939	1	<i>Macrophomina phaseolina</i>	1126212	TR:K2S7S7 MACPH
Transcription factor Aft1, osmotic stress domain	IPR020956	144	2	<i>Wickerhamomyces ciferrii</i> <i>Candida tropicalis</i>	1206466 294747	TR:K0KJU9 9ASCO TR:C5ME60 CANTT
Sel1-like	IPR006597	15768	2	<i>Wickerhamomyces ciferrii</i> <i>Botryotinia fuckeliana</i>	1206466 999810	TR:K0KUU0 9ASCO TR:G2XW17 BOTF4
Tetratricopeptide-like helical	IPR011990	180074	4	<i>Wickerhamomyces ciferrii</i> <i>Botryotinia fuckeliana</i> <i>Burkholderia phytofirmans</i> <i>Dictyostelium purpureum</i>	1206466 999810 398527 5786	TR:K0KUU0 9ASCO TR:G2XW17 BOTF4 TR:B2TFR9 BURPP TR:F0ZYQ8 DICPU
Subunit of cleavage factor IA Pcf11	IPR021605	59	1	<i>Wickerhamomyces ciferrii</i>	1206466	TR:K0KL65 9ASCO
ENTH/VHS	IPR008942	6361	7	<i>Wickerhamomyces ciferrii</i> <i>Meyerozyma guilliermondii</i> <i>Zygosaccharomyces rouxii</i> <i>Verticillium dahliae</i> <i>Verticillium alfalfae</i> <i>Entamoeba dispar</i> <i>Oxytricha trifallax</i>	1206466 294746 559307 498257 526221 370354 1172189	TR:K0KL65 9ASCO TR:A5DGW4 PICGU TR:C5DYJ4 ZYGRC TR:G2X9K9 VERDV TR:C9SQG8 VERA1 TR:B0EU18 ENTDS TR:J918U5 9SPIT
CID domain	IPR006569	2116	2	<i>Wickerhamomyces ciferrii</i> <i>Entamoeba dispar</i>	1206466 370354	TR:K0KL65 9ASCO TR:B0EU18 ENTDS
LisH dimerisation motif, subgroup	IPR013720	1567	2	<i>Pichia sorbitophila</i> <i>Lachancea thermotolerans</i>	559304 559295	TR:G8YRJ1 PICSO TR:C5DE52 LACTC
LisH dimerisation motif	IPR006594	4924	3	<i>Pichia sorbitophila</i> <i>Lachancea thermotolerans</i> <i>Tetrahymena thermophila</i>	559304 559295 312017	TR:G8YRJ1 PICSO TR:C5DE52 LACTC TR:Q231Q2 TETTS

Transcription initiation factor TFIID	IPR003228	420	3	<i>Chaetomium thermophilum</i>	759272	TR:G0S2A1_CHATD
				<i>Grosmannia clavigera</i>	655863	TR:FOXN84_GROCL
				<i>Dictyostelium discoideum</i>	44689	SP:TAF12_DICDI
Heat shock protein 70 family	IPR013126	24709	1	<i>Gaeumannomyces graminis var. tritici</i>	644352	TR:J3PE17_GAGT3
Glycoside hydrolase, catalytic domain	IPR013781	118272	1	<i>Gaeumannomyces graminis var. tritici</i>	644352	TR:J3NUQ4_GAGT3
Glycoside hydrolase, superfamily	IPR017853	148383	1	<i>Gaeumannomyces graminis var. tritici</i>	644352	TR:J3NUQ4_GAGT3
Rab-GTPase-TBC domain	IPR000195	8059	1	<i>Gaeumannomyces graminis var. tritici</i>	644352	TR:J3NNY7_GAGT3
AGC-kinase, C-terminal	IPR000961	8598	2	<i>Gaeumannomyces graminis var. tritici</i>	644352	TR:J3P6H6_GAGT3
				<i>Trichinella spiralis</i>	6334	TR:E5S526_TRISP
HR1 rho-binding repeat	IPR011072	986	1	<i>Gaeumannomyces graminis var. tritici</i>	644352	TR:J3P6H6_GAGT3
Protein kinase, C-terminal	IPR017892	4478	2	<i>Gaeumannomyces graminis var. tritici</i>	644352	TR:J3P6H6_GAGT3
				<i>Trichinella spiralis</i>	6334	TR:E5S526_TRISP
Protein kinase C-like, phorbol ester/diacylglycerol binding	IPR002219	6999	2	<i>Gaeumannomyces graminis var. tritici</i>	644352	TR:J3P6H6_GAGT3
				<i>Trichinella spiralis</i>	6334	TR:E5S526_TRISP
Transcription factor Spt20	IPR021950	359	6	<i>Clavispora lusitaniae</i>	306902	TR:C4Y1X6_CLAL4
				<i>Ajellomyces dermatitidis</i>	559298	TR:C5JYC6_AJEDS
						TR:C5GM52_AJEDR
				<i>Paracoccidioides brasiliensis</i>	502780	TR:C1GH85_PARBD
				<i>Paracoccidioides lutzii</i>	502779	TR:C1H3C8_PARBA
				<i>Paracoccidioides brasiliensis</i>	482561	TR:C0SEI1_PARBP
Ubiquitin-associated domain	IPR013896	157	1	<i>Clavispora lusitaniae</i>	306902	TR:C4Y9B9_CLAL4
AP180 N-terminal homology (ANTH) domain	IPR011417	1306	4	<i>Meyerozyma guilliermondii</i>	294746	TR:A5DGW4_PICGU
				<i>Zygosaccharomyces rouxii</i>	559307	TR:C5DYJ4_ZYGRC
				<i>Verticillium dahliae</i>	498257	TR:G2X9K9_VERDV
						TR:C9SQG8_VERA1
Clathrin adaptor, phosphoinositide-binding, GAT-like	IPR014712	821	4	<i>Meyerozyma guilliermondii</i>	294746	TR:A5DGW4_PICGU
				<i>Zygosaccharomyces rouxii</i>	559307	TR:C5DYJ4_ZYGRC
				<i>Verticillium dahliae</i>	498257	TR:G2X9K9_VERDV
						TR:C9SQG8_VERA1
Epsin-like, N-terminal	IPR013809	2434	5	<i>Meyerozyma guilliermondii</i>	294746	TR:A5DGW4_PICGU
				<i>Zygosaccharomyces rouxii</i>	559307	TR:C5DYJ4_ZYGRC

				<i>Verticillium dahliae</i>	<u>498257</u>	<u>TR:G2X9K9 VERDV</u> <u>TR:C9SQG8 VERA1</u>
				<i>Oxytricha trifallax</i>	<u>1172189</u>	<u>TR:J9I8U5 9SPIT</u>
Glutamine-Leucine-Glutamine	<u>IPR014978</u>	673	1	<i>Debaryomyces hansenii</i>	<u>284592</u>	<u>TR:Q6BJE1 DEBHA</u>
Like-Sm (LSM) domain	<u>IPR010920</u>	29772	1	<i>Emericella nidulans</i>	<u>227321</u>	<u>TR:Q5B077 EMENI</u>
Mechanosensitive ion channel MscS-like, plants/fungi	<u>IPR016688</u>	181	1	<i>Emericella nidulans</i>	<u>227321</u>	<u>TR:Q5B077 EMENI</u>
Mechanosensitive ion channel MscS	<u>IPR006685</u>	19061	1	<i>Emericella nidulans</i>	<u>227321</u>	<u>TR:Q5B077 EMENI</u>
Domain of unknown function DUF1720	<u>IPR013182</u>	117	1	<i>Colletotrichum graminicola</i>	<u>645133</u>	<u>TR:E3QDI8 COLGM</u>
SLA1 homology domain 1, SHD1	<u>IPR007131</u>	197	1	<i>Colletotrichum graminicola</i>	<u>645133</u>	<u>TR:E3QDI8 COLGM</u>
AT hook, DNA-binding motif	<u>IPR017956</u>	7441	2	<i>Neurospora crassa</i>	<u>367110</u>	<u>TR:Q7S0G6 NEUCR</u>
				<i>Dictyostelium purpureum</i>	<u>5786</u>	<u>TR:F0ZB68 DICPU</u>
Zinc finger, MIZ-type	<u>IPR004181</u>	1329	2	<i>Neurospora crassa</i>	<u>367110</u>	<u>TR:Q7S0G6 NEUCR</u>
				<i>Candida albicans</i>	<u>237561</u>	<u>TR:Q5A8Y9 CANAL</u>
Cyclin PHO80-like	<u>IPR013922</u>	1585	5	<i>Arthroderma benhamiae</i>	<u>663331</u>	<u>TR:D4AIT9 ARTBC</u>
				<i>Trichophyton verrucosum</i>	<u>663202</u>	<u>TR:D4DFR8 TRIVH</u>
				<i>Trichophyton tonsurans</i>	<u>647933</u>	<u>TR:F2RYA1 TRIT1</u>
				<i>Trichophyton equinum</i>	<u>559882</u>	<u>TR:F2PRJ7 TRIEC</u>
				<i>Lachancea thermotolerans</i>	<u>559295</u>	<u>TR:C5DLP2 LACTC</u>
Neutrophil cytosol factor 2 p67phox	<u>IPR000108</u>	2328	1	<i>Kluyveromyces lactis</i>	<u>284590</u>	<u>TR:Q6CPM1 KLULA</u>
Domain of unknown function DUF1771	<u>IPR013899</u>	579	2	<i>Penicillium marneffei</i>	<u>441960</u>	<u>TR:B6QCM0 PENMQ</u>
				<i>Aspergillus kawachii</i>	<u>1033177</u>	<u>TR:G7XNI2 ASPKW</u>
Smr protein/MutS2 C-terminal	<u>IPR002625</u>	7475	2	<i>Penicillium marneffei</i>	<u>441960</u>	<u>TR:B6QCM0 PENMQ</u>
				<i>Aspergillus kawachii</i>	<u>1033177</u>	<u>TR:G7XNI2 ASPKW</u>
Steadiness box	<u>IPR017916</u>	411	1	<i>Pyrenophora tritici-repentis</i>	<u>426418</u>	<u>TR:B2WIB9 PYRTR</u>
Ubiquitin-conjugating enzyme/RWD-like	<u>IPR016135</u>	13589	1	<i>Pyrenophora tritici-repentis</i>	<u>426418</u>	<u>TR:B2WIB9 PYRTR</u>
Ubiquitin E2 variant, N-terminal	<u>IPR008883</u>	525	1	<i>Pyrenophora tritici-repentis</i>	<u>426418</u>	<u>TR:B2WIB9 PYRTR</u>
5-AMP-activated protein kinase, beta subunit, interaction domain	<u>IPR006828</u>	591	1	<i>Naumovozyma dairenensis</i>	<u>1071378</u>	<u>TR:G0W772 NAUDC</u>

Zinc finger, CCCH-type	IPR000571	12071	2	<i>Naumovozya dairenensis</i>	1071378	TR:G0WAM9 NAUDC
				<i>Ajellomyces dermatitidis</i>	559298	TR:C5JW14 AJEDS
Bromo adjacent homology (BAH) domain	IPR001025	2315	1	<i>Vanderwaltozyma polyspora</i>	436907	TR:A7TQI4 VANPO
von Willebrand factor, type A	IPR002035	31980	4	<i>Ajellomyces capsulatus</i>	544712	TR:C6HR06 AJECH
				<i>Ajellomyces dermatitidis</i>	559297	TR:C5GNZ8 AJEDR
				<i>Ajellomyces dermatitidis</i>	653446	TR:F2TDT9 AJEDA
				<i>Naegleria gruberi</i>	5762	TR:D2VCR4 NAEGR
Anp1	IPR005109	473	1	<i>Zygosaccharomyces rouxii</i>	559307	TR:C5DXH7 ZYGR
Glycosyl transferase, family 8	IPR002495	7788	1	<i>Chaetomium globosum</i>	306901	TR:Q2GW94 CHAGB
Cohesin loading factor	IPR019440	262	1	<i>Fusarium pseudograminearum</i>	1028729	TR:K3W1C3 FUSPC
CYTH-like domain	IPR023577	5948	2	<i>Verticillium dahliae</i>	498257	TR:G2X9B0 VERDV
				<i>Hypocrea virens</i>	413071	TR:G9N2J5 HYPVG
mRNA capping enzyme, beta subunit, structural domain	IPR004206	309	2	<i>Verticillium dahliae</i>	498257	TR:G2X9B0 VERDV
				<i>Hypocrea virens</i>	413071	TR:G9N2J5 HYPVG
DNA/RNA non-specific endonuclease, active site	IPR018524	1398	2	<i>Aspergillus niger</i>	425011	TR:A2QZ96 ASPNC
						TR:G3XVE5 ASPNA
DNA/RNA non-specific endonuclease	IPR001604	3452	2	<i>Aspergillus niger</i>	425011	TR:A2QZ96 ASPNC
						TR:G3XVE5 ASPNA
Extracellular Endonuclease, subunit A	IPR020821	2700	2	<i>Aspergillus niger</i>	425011	TR:A2QZ96 ASPNC
						TR:G3XVE5 ASPNA
PINIT domain	IPR023321	542	1	<i>Candida albicans</i>	237561	TR:Q5A8Y9 CANAL
CCR4-Not complex component, Not1, C-terminal	IPR007196	471	1	<i>Candida tropicalis</i>	294747	TR:C5M8N8 CANTT
CCR4-Not complex, Not1 subunit, domain of unknown function DUF3819	IPR024557	437	1	<i>Candida tropicalis</i>	294747	TR:C5M8N8 CANTT
TORC1 complex, subunit TCO89	IPR018857	61	1	<i>Candida tropicalis</i>	294747	TR:C5MEJ3 CANTT
Ovarian tumour, otubain	IPR003323	3211	2	<i>Arthroderma gypseum</i>	535722	TR:E4UWP5 ARTGP
				<i>Paramecium tetraurelia</i>	5888	TR:A0BX13 PARTE
Peptidase C65, otubain	IPR019400	512	2	<i>Arthroderma gypseum</i>	535722	TR:E4UWP5 ARTGP

				<i>Paramecium tetraurelia</i>	5888	TR:A0BX13 PARTE
Dcp1-like decapping	IPR010334	478	1	<i>Puccinia triticina</i>	630390	TR:I3QDM0 PUCT1
Myb domain	IPR017930	11779	1	<i>Cordyceps militaris</i>	983644	TR:G3JEU7 CORMM
Telomere repeat-binding factor, dimerisation domain	IPR013867	298	1	<i>Cordyceps militaris</i>	983644	TR:G3JEU7 CORMM
Kelch-type beta propeller	IPR015915	16973	2	<i>Eremothecium cymbalariae</i>	931890	TR:G8JP18 ERECY
				<i>Chlorella variabilis</i>	554065	TR:E1ZPR5 CHLVA
Kelch repeat type 1	IPR006652	9098	1	<i>Eremothecium cymbalariae</i>	931890	TR:G8JP18 ERECY
Protein of unknown function DUF3468	IPR021858	4243	12	<i>Saccharomyces cerevisiae</i>	764102	TR:E7Q716 YEASB
					559292	SP:ECM22 YEAST
					307796	TR:A7A1B5 YEAS7
					545124	TR:B5VNE5 YEAS6
					574961	TR:C7GT26 YEAS2
					643680	TR:C8ZDJ2 YEAS8
					764099	TR:E7LXR7 YEASV
					764101	TR:E7NKS4 YEASO
					764100	TR:E7QI59 YEASZ
					1095631	TR:H0GKF3 9SACH
					721032	TR:G2WJ57 YEASK
					764098	TR:E7KRV5 YEASL
G-protein beta WD-40 repeat	IPR020472	21634	15	<i>Saccharomyces cerevisiae</i>	764102	TR:E7Q1H5 YEASB
					559292	SP:TUP1 YEAST
					307796	TR:A6ZTQ6 YEAS7
					285006	TR:B3LUD8 YEAS1
					545124	TR:B5VF12 YEAS6
					574961	TR:C7GUW4 YEAS2
					643680	TR:C8Z4H1 YEAS8
					764101	TR:E7NFE6 YEASO
					764100	TR:E7QC78 YEASZ
					1095631	TR:H0GD95 9SACH
					721032	TR:G2WA92 YEASK
					764097	TR:E7KA75 YEASA
				<i>Saccharomyces arboricola</i>	1160507	TR:I8Q781 SACAR
				<i>Paramecium tetraurelia</i>	5888	TR:A0CCK4 PARTE
				<i>Paramecium tetraurelia</i>	5888	TR:A0CYP9 PARTE
Transcriptional repressor Tup1, N-terminal	IPR013890	204	13	<i>Saccharomyces cerevisiae</i>	764102	TR:E7Q1H5 YEASB
					559292	SP:TUP1 YEAST

					307796	TR:A6ZTQ6 YEAS7
					285006	TR:B3LUD8 YEAS1
					545124	TR:B5VF12 YEAS6
					574961	TR:C7GUW4 YEAS2
					643680	TR:C8Z4H1 YEAS8
					764101	TR:E7NFE6 YEASO
					764100	TR:E7QC78 YEASZ
					1095631	TR:H0GD95 9SACH
					721032	TR:G2WA92 YEASK
					764097	TR:E7KA75 YEASA
				<i>Saccharomyces arboricola</i>	1160507	TR:J8Q781 SACAR
Quinonprotein alcohol dehydrogenase-like-superfamily	IPR011047	15130	1	<i>Kitasatospora setae</i>	452652	TR:E4N3L6 KITSK
Collagen-binding surface protein Cna-like, B-type domain	IPR008454	6667	1	<i>Kitasatospora setae</i>	452652	TR:E4N1V7 KITSK
LPXTG-motif cell wall anchor	IPR019931	22958	1	<i>Kitasatospora setae</i>	452652	TR:E4N1V7 KITSK
Twin-arginine translocation pathway, signal sequence	IPR006311	73771	3	<i>Kitasatospora setae</i>	452652	TR:E4N1V7 KITSK
				<i>Pseudomonas chlororaphis</i>	1037915	TR:I4XT35 9PSED
						TR:J2YIM7 9PSED
Uncharacterised protein family UPF0755, YceG-like	IPR003770	5547	4	<i>Kitasatospora setae</i>	452652	TR:E4N7R6 KITSK
				<i>Streptomyces sp. W007</i>	1055352	TR:H0BMT4 9ACTO
				<i>Streptomyces griseus</i>	649189	TR:G0Q9Q0 STRGR
				<i>Streptomyces griseus subsp. griseus</i>	455632	TR:B1W448 STRGG
Polyadenylate binding protein, human types 1, 2, 3, 4	IPR006515	711	1	<i>Capsaspora owczarzaki</i>	595528	TR:E9C1R9 CAPO3
Sterile alpha motif domain	IPR001660	8644	1	<i>Capsaspora owczarzaki</i>	595528	TR:E9BWQ2 CAPO3
Sterile alpha motif/pointed domain	IPR013761	11290	1	<i>Capsaspora owczarzaki</i>	595528	TR:E9BWQ2 CAPO3
Sterile alpha motif, type 2	IPR011510	3760	1	<i>Capsaspora owczarzaki</i>	595528	TR:E9BWQ2 CAPO3
DNA/RNA helicase, DEAD/DEAH box type, N-terminal	IPR011545	80893	4	<i>Arabidopsis thaliana</i>	3702	SP:RH40 ARATH
				<i>Arabidopsis lyrata subsp. lyrata</i>	81972	TR:D7L5I4 ARALL
				<i>Ferrimonas balearica</i>	550540	TR:E1SVZ1 FERBD
				<i>Paramecium tetraurelia</i>	5888	TR:A0BWN9 PARTE
Domain of unknown function DUF3854	IPR024385	289	1	<i>Nostoc sp.</i>	103690	TR:Q8YKS6 NOSS1

Domain of unknown function DUF4149	IPR025423	1238	1	<i>Neisseria shayeganii</i>	1032488	TR:G4CEQ1_9NEIS
Fimbrial assembly PilN	IPR007813	2315	1	<i>Idiomarina xiamenensis</i>	740709	TR:K2JPH4_9GAMM
Lactobacillus phage LBR48, DUF805	IPR008523	4961	1	<i>Arthrobacter globiformis</i>	1077972	TR:H0QLI2_ARTGO
ATPase, AAA-3	IPR011703	5429	1	<i>Nocardia brasiliensis</i>	1133849	TR:K0F1A7_9NOCA
Domain of unknown function DUF4333	IPR025637	396	1	<i>Mycobacterium colombiense</i>	1041522	TR:J5EM93_9MYCO
Integrating conjugative element protein, PFL4697-type	IPR022266	549	3	<i>Erwinia amylovora</i>	1027397	TR:G8LQK2_ERWAM
				<i>Erwinia amylovora</i>	1027397	TR:I1VYP7_ERWAM
				<i>Erwinia billingiae</i>	634500	TR:D8MJF0_ERWBE
Bax inhibitor-1	IPR010539	957	2	<i>Micromonospora aurantiaca</i>	644283	TR:D9TB19_MICAI
				<i>Micromonospora sp.</i>	648999	TR:E8S0K6_MICSL
Outer membrane protein, bacterial	IPR006664	14910	1	<i>Methylobacterium methanica</i>	857087	TR:G0A7E8_METMM
Outer membrane protein, conserved site	IPR006690	6247	1	<i>Methylobacterium methanica</i>	857087	TR:G0A7E8_METMM
Outer membrane protein, C-terminal	IPR006665	25722	1	<i>Methylobacterium methanica</i>	857087	TR:G0A7E8_METMM
SNARE associated Golgi protein	IPR015414	22314	1	<i>Streptomyces hygroscopicus subsp. jinggangensis</i>	1133850	TR:H2JM60_STRHJ
ABC transporter-like	IPR003439	422549	1	<i>Saccharomonospora viridis</i>	471857	TR:C7MXV2_SACVD
ABC transporter, conserved site	IPR017871	348002	1	<i>Saccharomonospora viridis</i>	471857	TR:C7MXV2_SACVD
CheC-like protein	IPR007597	1466	1	<i>Clostridium clariflavum</i>	720554	TR:G8LVG6_CLOCD
Flagellar motor switch FliN	IPR012826	3186	1	<i>Clostridium clariflavum</i>	720554	TR:G8LVG6_CLOCD
Flagellar motor switch FliN/Type III secretion HrcQb	IPR001172	4473	1	<i>Clostridium clariflavum</i>	720554	TR:G8LVG6_CLOCD
Surface presentation of antigen (SpoA)	IPR001543	8751	1	<i>Clostridium clariflavum</i>	720554	TR:G8LVG6_CLOCD
Beta-lactamase /transpeptidase-like	IPR012338	79727	1	<i>Saccharophagus degradans</i>	203122	TR:Q21N62_SACD2
Glycosyl transferase, family 51	IPR001264	17316	1	<i>Saccharophagus degradans</i>	203122	TR:Q21N62_SACD2
Penicillin-binding protein 1C	IPR011815	1648	1	<i>Saccharophagus degradans</i>	203122	TR:Q21N62_SACD2

Penicillin-binding, C-terminal	IPR009647	1745	1	<i>Saccharophagus degradans</i>	203122	TR:Q21N62_SACD2
Penicillin-binding protein, transpeptidase	IPR001460	33574	1	<i>Saccharophagus degradans</i>	203122	TR:Q21N62_SACD2
Cellulose synthase operon C, C-terminal	IPR008410	1093	1	<i>Burkholderia phytofirmans</i>	398527	TR:B2TFR9_BURPP
Cellulose synthase, subunit C	IPR003921	269	1	<i>Burkholderia phytofirmans</i>	398527	TR:B2TFR9_BURPP
Tetratricopeptide repeat-containing domain	IPR013026	88871	2	<i>Burkholderia phytofirmans</i>	398527	TR:B2TFR9_BURPP
				<i>Dictyostelium purpureum</i>	5786	TR:F0ZYQ8_DICPU
Tetratricopeptide repeat	IPR019734	81297	2	<i>Burkholderia phytofirmans</i>	398527	TR:B2TFR9_BURPP
				<i>Dictyostelium purpureum</i>	5786	TR:F0ZYQ8_DICPU
LemA	IPR007156	3765	1	<i>Xanthomonas vesicatoria</i>	925775	TR:F0BH19_9XANT
LemA-like domain	IPR023353	3912	1	<i>Xanthomonas vesicatoria</i>	925775	TR:F0BH19_9XANT
NYN domain, limkain-b1-type	IPR021139	3904	1	<i>Hyphomicrobium denitrificans</i>	582899	TR:D8JU17_HYPDA
Mycobacterial pentapeptide repeat	IPR002989	1059	1	<i>Nocardia farcinica</i>	247156	TR:Q5Z1N9_NOCFA
Phosphoesterase	IPR007312	2531	3	<i>Pseudomonas chlororaphis</i>	1037915	TR:J2MZD3_9PSED
						TR:I4XT35_9PSED
						TR:J2YIM7_9PSED
Phospholipase C, bacterial, C-terminal	IPR008475	772	3	<i>Pseudomonas chlororaphis</i>	1037915	TR:J2MZD3_9PSED
						TR:I4XT35_9PSED
						TR:J2YIM7_9PSED
Phospholipase C, phosphocholine-specific	IPR017767	719	3	<i>Pseudomonas chlororaphis</i>	1037915	TR:J2MZD3_9PSED
						TR:I4XT35_9PSED
						TR:J2YIM7_9PSED
Flagellar hook-length control protein-like, C-terminal	IPR021136	3875	1	<i>Idiomarina loihiensis</i>	283942	TR:Q5QZP6_IDILO
Protein of unknown function DUF459	IPR007407	216	1	<i>Xanthobacter autotrophicus</i>	78245	TR:A7IGS6_XANP2
SGNH hydrolase-type esterase domain	IPR013830	95206	1	<i>Xanthobacter autotrophicus</i>	78245	TR:A7IGS6_XANP2
SGNH hydrolase-type esterase domain	IPR013831	25619	1	<i>Xanthobacter autotrophicus</i>	78245	TR:A7IGS6_XANP2
Metallopeptidase, catalytic domain	IPR024079	30369	1	<i>Moumouvirus Monve</i>	1128131	TR:H2EF10_9VIRU

Peptidase M43, pregnancy-associated plasma-A	IPR008754	707	1	<i>Moumouvirus Monve</i>	1128131	TR:H2EF10_9VIRU
Oxoglutarate / iron-dependent dioxygenase	IPR005123	18771	1	<i>Pristionchus pacificus</i>	54126	TR:H3F7D7_PRIPA
Prolyl 4-hydroxylase, alpha subunit	IPR006620	6062	1	<i>Pristionchus pacificus</i>	54126	TR:H3F7D7_PRIPA
Domain of unknown function DB	IPR002602	276	1	<i>Pristionchus pacificus</i>	54126	TR:H3DZM1_PRIPA
Potential DNA-binding domain	IPR025927	307	3	<i>Wuchereria bancrofti</i>	6293	TR:J9F0P6_WUCBA
				<i>Brugia malayi</i>	6279	TR:A8QG91_BRUMA
				<i>Dictyostelium purpureum</i>	5786	TR:F1A3Z1_DICPU
Serine/threonine-protein kinase OSR1/WNK, CCT domain	IPR024678	494	1	<i>Wuchereria bancrofti</i>	6293	TR:J9EPD0_WUCBA
Protein of unknown function DUF1136	IPR010939	129	1	<i>Ascaris suum</i>	6253	TR:F1KQG0_ASCSU
CTF transcription factor/nuclear factor 1	IPR000647	562	1	<i>Caenorhabditis remanei</i>	31234	TR:E3LQ82_CAERE
CTF transcription factor/nuclear factor 1, DNA-binding domain	IPR020604	494	1	<i>Caenorhabditis remanei</i>	31234	TR:E3LQ82_CAERE
CTF transcription factor/nuclear factor 1, N-terminal	IPR019548	456	1	<i>Caenorhabditis remanei</i>	31234	TR:E3LQ82_CAERE
	IPR003619		1	<i>Caenorhabditis remanei</i>	31234	TR:E3LQ82_CAERE
C-5 cytosine methyltransferase	IPR001525	8738	1	<i>Caenorhabditis remanei</i>	31234	TR:E3MFU8_CAERE
Zinc finger, CXXC-type	IPR002857	953	1	<i>Caenorhabditis remanei</i>	31234	TR:E3MFU8_CAERE
Domain of unknown function DUF148	IPR003677	266	1	<i>Caenorhabditis briggsae</i>	6238	TR:A8X193_CAEBR
Citron -like	IPR001180	2260	1	<i>Trichinella spiralis</i>	6334	TR:E5S526_TRISP
Myotonic dystrophy protein kinase, coiled coil	IPR014930	320	1	<i>Trichinella spiralis</i>	6334	TR:E5S526_TRISP
Serine/threonine-protein kinase MRCK	IPR026611	351	1	<i>Trichinella spiralis</i>	6334	TR:E5S526_TRISP
CCR4-NOT complex, subunit 3/ 5	IPR012270	334	1	<i>Loa loa</i>	7209	TR:J0DW06_LOALO
NOT2/NOT3/NOT5	IPR007282	926	1	<i>Loa loa</i>	7209	TR:J0DW06_LOALO
Not CCR4-Not complex component, N-terminal	IPR007207	441	1	<i>Loa loa</i>	7209	TR:J0DW06_LOALO

VHS	IPR002014	2099	1	<i>Entamoeba dispar</i>	370354	TR:B0EU18 ENTDS
Dbl homology (DH) domain	IPR000219	8248	2	<i>Entamoeba dispar</i>	370354	TR:B0EAI1 ENTDS TR:B0EP22 ENTDS
Serine-threonine/tyrosine-protein kinase catalytic domain	IPR001245	27727	1	<i>Polysphondylium pallidum</i>	13642	TR:D3B3V6 POLPA
Kinesin, motor region, conserved site	IPR019821	7503	1	<i>Polysphondylium pallidum</i>	13642	TR:D3BBQ6 POLPA
Kinesin, motor domain	IPR001752	10590	1	<i>Polysphondylium pallidum</i>	13642	TR:D3BBQ6 POLPA
Adenylyl cyclase class-3/4/guanylyl cyclase	IPR001054	71551	1	<i>Polysphondylium pallidum</i>	13642	TR:D3BFN2 POLPA
Adenylyl cyclase class-3/4/guanylyl cyclase, conserved site	IPR018297	3012	1		13642	TR:D3BFN2 POLPA
CHASE	IPR006189	1636	1	<i>Polysphondylium pallidum</i>	13642	TR:D3BFN2 POLPA
EPS15 homology (EH)	IPR000261	2081	1	<i>Dictyostelium fasciculatum</i>	1054147	TR:F4Q4C0 DICFS
			1	<i>Phaeodactylum tricornutum</i>	556484	TR:B7FRA9 PHATC
DNA repair protein Sae2/CtIP	IPR013882	244	1	<i>Dictyostelium fasciculatum</i>	1054147	TR:F4Q497 DICFS
Vacuolar protein sorting-associated	IPR007143	436	1	<i>Dictyostelium fasciculatum</i>	1054147	TR:F4PUM6 DICFS
Vacuolar protein sorting-associated, VPS28, C-terminal	IPR017899	368	1	<i>Dictyostelium fasciculatum</i>	1054147	TR:F4PUM6 DICFS
Vacuolar protein sorting-associated, VPS28, N-terminal	IPR017898	370	1	<i>Dictyostelium fasciculatum</i>	1054147	TR:F4PUM6 DICFS
Cell division protein FtsZ	IPR000158	7980	1	<i>Dictyostelium fasciculatum</i>	1054147	TR:F4QDY7 DICFS
Cell division protein FtsZ, conserved site	IPR020805	7056	1	<i>Dictyostelium fasciculatum</i>	1054147	TR:F4QDY7 DICFS
Cell division protein FtsZ, C-terminal	IPR024757	7353	1	<i>Dictyostelium fasciculatum</i>	1054147	TR:F4QDY7 DICFS
Tubulin/FtsZ, C-terminal	IPR008280	18645	1	<i>Dictyostelium fasciculatum</i>	1054147	TR:F4QDY7 DICFS
Tubulin/FtsZ, 2-layer sandwich domain	IPR018316	18326	1	<i>Dictyostelium fasciculatum</i>	1054147	TR:F4QDY7 DICFS
Tubulin/FtsZ, GTPase domain	IPR003008	25809	1	<i>Dictyostelium fasciculatum</i>	1054147	TR:F4QDY7 DICFS

Argonaute / Dicer protein, PAZ	IPR003100	2705	1	<i>Dictyostelium fasciculatum</i>	1054147	TR:F4PME8 DICFS
Stem cell self - renewal protein Piwi	IPR003165	2451	1	<i>Dictyostelium fasciculatum</i>	1054147	TR:F4PME8 DICFS
Ribonuclease H-like domain	IPR012337	174851	1	<i>Dictyostelium fasciculatum</i>	1054147	TR:F4PME8 DICFS
AT hook -like	IPR020478	957	1	<i>Dictyostelium purpureum</i>	5786	TR:F0ZB68 DICPU
High mobility group	IPR000116	299	1	<i>Dictyostelium purpureum</i>	5786	TR:F0ZB68 DICPU
Domain of unknown function DUF4062	IPR025139	510	1	<i>Dictyostelium purpureum</i>	5786	TR:F0ZYQ8 DICPU
SAC3/GANP/Nin1/mts3/eIF-3 p25	IPR005062	1273	1	<i>Dictyostelium purpureum</i>	5786	TR:F0ZXV1 DICPU
Adaptor protein complex AP-2, alpha subunit	IPR017104	411	1	<i>Dictyostelium purpureum</i>	5786	TR:F0ZS77 DICPU
Clathrin / coatomer adaptor, adaptin-like, N-terminal	IPR002553	4234	2	<i>Dictyostelium purpureum</i>	5786	TR:F0ZS77 DICPU
				<i>Paramecium tetraurelia</i>	5888	TR:A0CBT3 PARTE
Clathrin adaptor, alpha-adaptin, appendage, Ig-like subdomain	IPR013038	494	1	<i>Dictyostelium purpureum</i>	5786	TR:F0ZS77 DICPU
Clathrin adaptor, alpha-adaptin, appendage, C-terminal subdomain	IPR003164	401	1	<i>Dictyostelium purpureum</i>	5786	TR:F0ZS77 DICPU
Clathrin adaptor, alpha/beta/gamma-adaptin, appendage, Ig-like subdomain	IPR008152	1617	1	<i>Dictyostelium purpureum</i>	5786	TR:F0ZS77 DICPU
Clathrin alpha-adaptin/coatomer adaptor, appendage, C-terminal subdomain	IPR015873	913	1	<i>Dictyostelium purpureum</i>	5786	TR:F0ZS77 DICPU
Coatomer/clathrin adaptor appendage, C-terminal subdomain	IPR009028	1154	1	<i>Dictyostelium purpureum</i>	5786	TR:F0ZS77 DICPU
Coatomer/clathrin adaptor appendage, Ig-like subdomain	IPR013041	2331	2	<i>Dictyostelium purpureum</i>	5786	TR:F0ZS77 DICPU
				<i>Paramecium tetraurelia</i>	5888	TR:A0CBT3 PARTE
Zinc finger, N- recognin	IPR003126	1363	1	<i>Dictyostelium discoideum</i>	44689	TR:Q75JM9 DICDI
PWWP	IPR000313	2721	1	<i>Dictyostelium discoideum</i>	44689	TR:Q75JG1 DICDI
Mediator complex, subunit Med12	IPR019035	329	1	<i>Dictyostelium discoideum</i>	44689	SP:MED12 DICDI
POLO box duplicated domain	IPR000959	655	1	<i>Dictyostelium discoideum</i>	44689	SP:PLK DICDI

Peptidase C1A, papain C-terminal	IPR000668	7839	1	<i>Plasmodium vivax</i>	126793	TR:A5KBM4 PLAVS
Peptidase C1A, papain	IPR013128	7674	1	<i>Plasmodium vivax</i>	126793	TR:A5KBM4 PLAVS
Exoribonuclease, phosphorolytic domain 1	IPR001247	12219	1	<i>Eimeria tenella</i>	5802	TR:H9B9T6 EIMTE
Ribosomal protein S5 domain 2-type fold	IPR020568	136229	1	<i>Eimeria tenella</i>	5802	TR:H9B9T6 EIMTE
Calcium-binding EF-hand	IPR002048	40446	2	<i>Volvox carteri</i>	3067	TR:D8U185 VOLCA
				<i>Paramecium tetraurelia</i>	5888	TR:A0BWN9 PARTE
RNA helicase, DEAD-box type, Q motif	IPR014014	29092	4	<i>Arabidopsis thaliana</i>	3702	SP:RH40 ARATH
				<i>Arabidopsis lyrata subsp. lyrata</i>	81972	TR:D7L5I4 ARALL
				<i>Paramecium tetraurelia</i>	5888	TR:A0BWN9 PARTE
				<i>Paramecium tetraurelia</i>	5888	TR:A0CI00 PARTE
Katanin p80 subunit B1	IPR026962	300	2	<i>Paramecium tetraurelia</i>	5888	TR:A0CXK4 PARTE
						TR:A0CYP9 PARTE
Mannose-binding lectin	IPR001229	1224	1	<i>Paramecium tetraurelia</i>	5888	TR:A0C353 PARTE
LPS-induced tumor necrosis factor alpha factor	IPR006629	860	4	<i>Paramecium tetraurelia</i>	5888	TR:A0DA79 PARTE
						TR:A0CFW6 PARTE
						TR:A0D0N7 PARTE
				<i>Ichthyophthirius multifiliis</i>	857967	TR:G0R2G1 ICHMG
Ubiquitin	IPR000626	10610	1	<i>Paramecium tetraurelia</i>	5888	TR:A0CBH5 PARTE
Ubiquitin supergroup	IPR019955	11848	1	<i>Paramecium tetraurelia</i>	5888	TR:A0CBH5 PARTE
Arfaptin homology (AH) domain	IPR010504	570	1	<i>Paramecium tetraurelia</i>	5888	TR:A0EC99 PARTE
Protein of unknown function DUF2816	IPR021258	73	1	<i>Paramecium tetraurelia</i>	5888	TR:Q3SDH1 PARTE
HECT	IPR000569	5084	1	<i>Paramecium tetraurelia</i>	5888	TR:A0CYJ5 PARTE
AP complex subunit beta	IPR026739	1443	1	<i>Paramecium tetraurelia</i>	5888	TR:A0CBT3 PARTE
Beta-adaptin appendage, C-terminal subdomain	IPR015151	447	1	<i>Paramecium tetraurelia</i>	5888	TR:A0CBT3 PARTE
Clathrin adaptor, beta-adaptin, appendage, Ig-like subdomain	IPR013037	343	1	<i>Paramecium tetraurelia</i>	5888	TR:A0CBT3 PARTE
MORN motif	IPR003409	4670	2	<i>Paramecium tetraurelia</i>	5888	TR:A0CR71 PARTE

						TR:A0CJB5 PARTE
Cyclic nucleotide-binding-like	IPR018490	32809	1	<i>Paramecium tetraurelia</i>	5888	TR:A0D372 PARTE
Cyclic nucleotide-binding domain	IPR000595	32468	1	<i>Paramecium tetraurelia</i>	5888	TR:A0D372 PARTE
Ion transport 2	IPR013099	9320	1	<i>Paramecium tetraurelia</i>	5888	TR:A0D372 PARTE
RmlC-like jelly roll fold	IPR014710	114755	1	<i>Paramecium tetraurelia</i>	5888	TR:A0D372 PARTE
Zinc finger, CCHC-type	IPR001878	48430	2	<i>Paramecium tetraurelia</i>	5888	TR:A0D372 PARTE
				<i>Coccomyxa subellipsoidea C-169</i>	574566	TR:I0Z6X5 9CHLO
Oxysterol-binding protein	IPR000648	2803	1	<i>Paramecium tetraurelia</i>	5888	TR:A0DIZ9 PARTE
Oxysterol-binding protein, conserved site	IPR018494	1938	1	<i>Paramecium tetraurelia</i>	5888	TR:A0DIZ9 PARTE
START-like domain	IPR023393	24503	1	<i>Paramecium tetraurelia</i>	5888	TR:A0DIZ9 PARTE
START domain	IPR002913	3166	1	<i>Paramecium tetraurelia</i>	5888	TR:A0DIZ9 PARTE
Nucleic acid-binding, OB-fold	IPR012340	237689	1	<i>Oxytricha trifallax</i>	1172189	TR:J9F316 9SPIT
	IPR016027	?	1	<i>Oxytricha trifallax</i>	1172189	TR:J9F316 9SPIT
IQ motif, EF-hand binding site	IPR000048	13024	1	<i>Oxytricha trifallax</i>	1172189	TR:J9ISV1 9SPIT
Zinc finger C2HC domain-containing protein	IPR026319	410	1	<i>Oxytricha trifallax</i>	1172189	TR:J9IYU2 9SPIT
Pumilio RNA-binding repeat	IPR001313	2344	1	<i>Oxytricha trifallax</i>	1172189	TR:J9I6T8 9SPIT
Epsin domain, N-terminal	IPR001026	1289	1	<i>Oxytricha trifallax</i>	1172189	TR:J9I8U5 9SPIT
Inositol polyphosphate-related phosphatase	IPR000300	2292	1	<i>Oxytricha trifallax</i>	1172189	TR:J9ETF9 9SPIT
Synaptojanin, N-terminal	IPR002013	1824	1	<i>Oxytricha trifallax</i>	1172189	TR:J9ETF9 9SPIT
Peptidase A2A, retrovirus, catalytic	IPR001995	136363	1	<i>Ichthyophthirius multifiliis</i>	857967	TR:G0R1R9 ICHMG
Aspartic peptidase	IPR021109	150638	1	<i>Ichthyophthirius multifiliis</i>	857967	TR:G0R1R9 ICHMG
	IPR009007	?	1	<i>Ichthyophthirius multifiliis</i>	857967	TR:G0R1R9 ICHMG
Aspartic peptidase, DDI1-type	IPR019103	499	1	<i>Ichthyophthirius multifiliis</i>	857967	TR:G0R1R9 ICHMG

Ubiquitin- associated/translation elongation factor EF1B, N-terminal	IPR000449	10774	1	<i>Ichthyophthirius multifiliis</i>	857967	TR:G0R1R9 ICHMG
GCN5-like 1	IPR009395	270	1	<i>Tetrahymena thermophila</i>	312017	TR:I7LT28 TETTS
Nucleotidyl transferase domain	IPR002934	11708	1	<i>Tetrahymena thermophila</i>	312017	TR:I7LWD5 TETTS
Nucleotidyltransferase, class I, C-terminal-like	IPR011068	913	1	<i>Tetrahymena thermophila</i>	312017	TR:I7LWD5 TETTS
Poly(A) polymerase, central domain	IPR007012	841	1	<i>Tetrahymena thermophila</i>	312017	TR:I7LWD5 TETTS
Poly(A) polymerase, RNA-binding domain	IPR007010	731	1	<i>Tetrahymena thermophila</i>	312017	TR:I7LWD5 TETTS
SIT4 phosphatase-associated protein family	IPR007587	715	1	<i>Tetrahymena thermophila</i>	312017	TR:Q22CQ3 TETTS
Domain of unknown function DUF221	IPR003864	1564	1	<i>Tetrahymena thermophila</i>	312017	TR:I7LUC5 TETTS
SM domain found in ataxin-2	IPR025852	451	1	<i>Salpingoeca rosetta</i>	946362	TR:F2UB05 SALS5
Autophagy- related protein 13	IPR018731	380	1	<i>Salpingoeca rosetta</i>	946362	TR:F2UPL9 SALS5
Aspartyl/Asparaginyl beta-hydroxylase	IPR007803	1500	1	<i>Salpingoeca rosetta</i>	946362	TR:F2TYA9 SALS5
Galactose-binding domain-like	IPR008979	40946	1	<i>Naegleria gruberi</i>	5762	TR:D2VQJ6 NAEGR
Major facilitator superfamily	IPR011701	206718	1	<i>Naegleria gruberi</i>	5762	TR:D2VQJ6 NAEGR
Major facilitator superfamily domain, general substrate transporter	IPR016196	288356	1	<i>Naegleria gruberi</i>	5762	TR:D2VQJ6 NAEGR
Peptidase S8/S53 domain	IPR000209	18527	1	<i>Naegleria gruberi</i>	5762	TR:D2VQJ6 NAEGR
Peptidase S8, subtilisin, His-active site	IPR022398	8940	1	<i>Naegleria gruberi</i>	5762	TR:D2VQJ6 NAEGR
Peptidase S8, subtilisin-related	IPR015500	16364	1	<i>Naegleria gruberi</i>	5762	TR:D2VQJ6 NAEGR
Copine	IPR010734	1260	1	<i>Naegleria gruberi</i>	5762	TR:D2VCR4 NAEGR
Annexin	IPR001464	2369	2	<i>Trichomonas vaginalis</i>	5722	TR:A2EUT8 TRIVA
				<i>Daphnia pulex</i>	6669	TR:E9GWX4 DAPPU
Forkhead-associated (FHA) domain	IPR000253	14600	1	<i>Sulfolobus acidocaldarius</i>	330779	TR:Q4J9H4 SULAC
SMAD/FHA domain	IPR008984	16138	1	<i>Sulfolobus acidocaldarius</i>	330779	TR:Q4J9H4 SULAC

Heat shock factor (HSF)-type, DNA-binding	IPR000232	2344	1	<i>Thalassiosira pseudonana</i>	35128	TR:B8LD72 THAPS
STAT transcription factor, all-alpha	IPR013801	712	1	<i>Branchiostoma floridae</i>	7739	TR:C3ZBA3 BRAFL
STAT transcription factor, coiled coil	IPR015988	691	1	<i>Branchiostoma floridae</i>	7739	TR:C3ZBA3 BRAFL
STAT transcription factor, core	IPR001217	915	1	<i>Branchiostoma floridae</i>	7739	TR:C3ZBA3 BRAFL
STAT transcription factor, DNA-binding, subdomain	IPR012345	676	1	<i>Branchiostoma floridae</i>	7739	TR:C3ZBA3 BRAFL
STAT transcription factor, protein interaction	IPR013799	652	1	<i>Branchiostoma floridae</i>	7739	TR:C3ZBA3 BRAFL
Domain of unknown function DUF4587	IPR027904	111	1	<i>Danio rerio</i>	7955	TR:Q566X1 DANRE
Not attributed				<i>Danio rerio</i>	7955	TR:F1QT44 DANRE
						TR:Q5BLC6 DANRE
						TR:F1QT44 DANRE
				<i>Takifugu rubripes</i>	31033	TR:Q5BU16 TAKRU
				<i>Latimeria chalumnae</i>	7897	TR:H3AUV9 LATCH
				<i>Oncorhynchus mykiss</i>	8022	TR:D3X7I3 ONCMY
				<i>Mus musculus</i>	10090	TR:E9Q7R5 MOUSE
						TR:Q3TT67 MOUSE
						TR:Q80X27 MOUSE
						TR:Q9D0B9 MOUSE
						TR:G5E8K1 MOUSE
				<i>Monodelphis domestica</i>	13616	TR:F6YC76 MONDO
				<i>Harpegnathos saltator</i>	610380	TR:E2B4P5 HARSA
				<i>Solenopsis invicta</i>	13686	TR:E9IBS4 SOLIN
				<i>Acyrtosiphon pisum</i>	7029	TR:J9LYX7 ACYPI
						TR:J9K6H4 ACYPI
				<i>Drosophila virilis</i>	7244	TR:B4LG92 DROVI
						TR:B4LT47 DROVI
						TR:B4LP27 DROVI
				<i>Drosophila mojavensis</i>	7230	TR:B4L247 DROMO
						TR:B4KYR0 DROMO
						TR:B4L855 DROMO
						TR:B4L698 DROMO
				<i>Culex quinquefasciatus</i>	7176	TR:B0XIY3 CULQU
						TR:B0X335 CULQU
				<i>Drosophila ananassae</i>	7217	TR:B3MYT4 DROAN
				<i>Drosophila sechellia</i>	7238	TR:B4IAK4 DROSE
						TR:B4HHA9 DROSE
						TR:B4HS46 DROSE
				<i>Drosophila simulans</i>	7240	TR:B4QGV2 DROSI

						TR:B4QJN8 DROSI
						TR:Q8ITK5 DROSI
						TR:B4Q806 DROSI
						TR:B4Q807 DROSI
				<i>Drosophila persimilis</i>	<u>7234</u>	TR:B4G4N1 DROPE
						TR:B4GID5 DROPE
				<i>Drosophila pseudoobscura pseudoobscura</i>	<u>46245</u>	TR:Q298T3 DROPS
						TR:Q28Z24 DROPS
						TR:Q29GM3 DROPS
				<i>Drosophila yakuba</i>	<u>7245</u>	TR:B4PXM1 DROYA
						TR:B4P7D2 DROYA
				<i>Drosophila erecta</i>	<u>7220</u>	TR:B3NQC8 DROER
				<i>Drosophila melanogaster</i>	<u>7227</u>	TR:J7KEC1 DROME
						TR:J7KG79 DROME
						TR:J7KH78 DROME
						TR:J7KH84 DROME
						TR:J7KEB3 DROME
						TR:J7KG95 DROME
						TR:J7KH93 DROME
						TR:J7KHA7 DROME
						TR:Q8IO53 DROME
						TR:Q8IO54 DROME
						TR:Q8ITL0 DROME
						TR:Q8IOJ7 DROME
						TR:Q8ITK6 DROME
						TR:Q8ITK8 DROME
						TR:Q8ITK9 DROME
						TR:Q8ITK7 DROME
						TR:Q29QW0 DROME
						TR:Q9VP73 DROME
				<i>Drosophila grimshawi</i>	<u>7222</u>	TR:B4JIE8 DROGR
						TR:B4J2G2 DROGR
						TR:B4K3U5 DROGR
						TR:B4JNG4 DROGR
						TR:B4JL13 DROGR
						TR:B4JZQ4 DROGR
				<i>Daphnia pulex</i>	<u>6669</u>	TR:E9HPD0 DAPPU
				<i>Crassostrea gigas</i>	<u>29159</u>	TR:K1Q341 CRAGI
				<i>Triticum turgidum</i>	<u>4571</u>	TR:A7X9X5 TRITU
						TR:A7X9X4 TRITU
				<i>Triticum turgidum subsp. turgidum</i>	<u>357456</u>	TR:A7X9X3 TRITU
				<i>Selaginella moellendorffii</i>	<u>88036</u>	TR:D8QZB0 SELML
						TR:D8RWJ4 SELML
				<i>Physcomitrella patens</i>	<u>3218</u>	TR:A9SPD2 PHYPA
				<i>Medicago truncatula</i>	<u>3880</u>	TR:G7JYQ3 MEDTR

			<i>Vitis vinifera</i>	<u>29760</u>	TR:F6H085 VITVI
			<i>Coccomyxa subellipsoidea</i> C-169	<u>574566</u>	TR:I027H7 9CHLO
			<i>Volvox carteri</i>	<u>3067</u>	TR:D8UH55 VOLCA
					TR:D8TIG8 VOLCA
			<i>Coprinopsis cinerea</i>	<u>240176</u>	TR:A8NSW4 COPC7
			<i>Rhizopus delemar</i>	<u>246409</u>	TR:I1BU39 RHIO9
			<i>Ustilago hordei</i>	<u>1128400</u>	TR:I2FNA1 USTHO
					TR:I2FX35 USTHO
			<i>Arthroderma otae</i>	<u>554155</u>	TR:C5FMN6 ARTOC
			<i>Lodderomyces elongisporus</i>	<u>379508</u>	TR:A5DX59 LODEL
			<i>Komagataella pastoris</i>	<u>981350</u>	TR:F2QZ34 PICP7
					TR:C4R811 PICPG
			<i>Candida dubliniensis</i>	<u>573826</u>	TR:B9WK29 CANDC
			<i>Spathaspora passalidarum</i>	<u>619300</u>	TR:G3AT38 SPAPN
			<i>Pyrenophora teres</i> f. <i>teres</i>	<u>861557</u>	TR:E3SA50 PYRTT
			<i>Macrophomina phaseolina</i>	<u>1126212</u>	TR:K2QZ41 MACPH
			<i>Wickerhamomyces ciferrii</i>	<u>1206466</u>	TR:K0KRY0 9ASCO
			<i>Metarhizium anisopliae</i>	<u>655844</u>	TR:E9EYN1 METAR
			<i>Metarhizium acridum</i>	<u>655827</u>	TR:E9E5K2 METAQ
			<i>Gaeumannomyces graminis</i> var. <i>tritici</i>	<u>644352</u>	TR:J3PGZ9 GAGT3
			<i>Emericella nidulans</i>	<u>227321</u>	TR:C8VHT4 EMENI
			<i>Marssonina brunnea</i>	<u>1072389</u>	TR:K1WK26 MARBU
			<i>Mycosphaerella graminicola</i>	<u>336722</u>	TR:F9XKR1 MYCGM
			<i>Arthroderma benhamiae</i>	<u>663331</u>	TR:D4AUL2 ARTBC
					TR:D4AQZ3 ARTBC
			<i>Trichophyton verrucosum</i>	<u>663202</u>	TR:D4DAF9 TRIVH
					TR:D4DE92 TRIVH
			<i>Kluyveromyces lactis</i>	<u>284590</u>	TR:Q6CV84 KLULA
			<i>Thielavia heterothallica</i>	<u>573729</u>	TR:G2QL79 THIHA
					TR:G2Q6L9 THIHA
			<i>Ajellomyces capsulatus</i>	<u>447093</u>	TR:C0NY22 AJECG
			<i>Zygosaccharomyces rouxii</i>	<u>559307</u>	TR:C5DZG0 ZYGRC
					TR:C5DPG9 ZYGRC
			<i>Candida orthopsilosis</i>	<u>1136231</u>	TR:H8XAW0 CANO9
			<i>Chaetomium globosum</i>	<u>306901</u>	TR:Q2GSW4 CHAGB
			<i>Batrachochytrium dendrobatidis</i>	<u>684364</u>	TR:F4POI6 BATDJ
			<i>Tuber melanosporum</i>	<u>656061</u>	TR:D5GLS3 TUBMM
			<i>Beauveria bassiana</i>	<u>655819</u>	TR:J4UW00 BEAB2
			<i>Ashbya gossypii</i>	<u>284811</u>	SP:DEF1 ASHGO
			<i>Thielavia terrestris</i>	<u>578455</u>	TR:G2RF30 THITE
			<i>Puccinia graminis</i> f. <i>sp. tritici</i>	<u>418459</u>	TR:E3KED1 PUCGT
			<i>Sporisorium reilianum</i>	<u>999809</u>	TR:E6ZQ89 SPORE
			<i>Capsaspora owczarzaki</i>	<u>595528</u>	TR:E9CJ30 CAPO3
					TR:E9CF31 CAPO3
			<i>Nocardia brasiliensis</i>	<u>1133849</u>	TR:K0F7I8 9NOCA

				<i>Nocardiopsis alba</i>	<u>1205910</u>	TR:J7KZ35 NOCAA
				<i>Streptomyces sp. W007</i>	<u>1055352</u>	TR:D6K5N2 9ACTO
				<i>Fischerella sp. JSC-11</i>	<u>741277</u>	TR:G6FWH2 9CYAN
				<i>Pristionchus pacificus</i>	<u>54126</u>	TR:H3FY38 PRIPA
						TR:H3EBC9 PRIPA
						TR:H3DTB9 PRIPA
				<i>Wuchereria bancrofti</i>	<u>6293</u>	TR:J9EL61 WUCBA
				<i>Caenorhabditis remanei</i>	<u>31234</u>	TR:E3LNM4 CAERE
				<i>Caenorhabditis brenneri</i>	<u>135651</u>	TR:G0NPV9 CAEBE
						TR:G0NPR5 CAEBE
				<i>Caenorhabditis briggsae</i>	<u>6238</u>	TR:A8XR05 CAEBR
						TR:A8XK30 CAEBR
				<i>Litomosoides sigmodontis</i>	<u>42156</u>	TR:Q25256 LITS!
				<i>Schistosoma mansoni</i>	<u>6183</u>	TR:G4VJV4 SCHMA
				<i>Entamoeba histolytica</i>	<u>5759</u>	TR:C4M3M4 ENTHI
						TR:C4M689 ENTHI
				<i>Entamoeba nuttalli</i>	<u>1076696</u>	TR:K2GGH5 ENTNP
						TR:K2H758 ENTNP
				<i>Entamoeba dispar</i>	<u>370354</u>	TR:B0EIL3 ENTDS
						TR:B0ESJ3 ENTDS
				<i>Polysphondylium pallidum</i>	<u>13642</u>	TR:D3BG46 POLPA
						TR:D3BNS0 POLPA
						TR:D3BNM9 POLPA
						TR:D3AYF3 POLPA
				<i>Dictyostelium fasciculatum</i>	<u>1054147</u>	TR:F4PUM8 DICFS
						TR:F4QDD3 DICFS
				<i>Dictyostelium purpureum</i>	<u>5786</u>	TR:F0ZCL9 DICPU
						TR:F0ZMS5 DICPU
				<i>Dictyostelium discoideum</i>	<u>44689</u>	TR:Q86K61 DICDI
						TR:Q54PL8 DICDI
						SP:Y6864 DICDI
						SP:MED29 DICDI
				<i>Theileria annulata</i>	<u>5874</u>	TR:Q4UA28 THEAN
				<i>Perkinsus marinus</i>	<u>423536</u>	TR:C5LYD3 PERM5
				<i>Plasmodium vivax</i>	<u>5855</u>	TR:Q0PCK3 PLAVI
						TR:Q0PCK4 PLAVI
						TR:Q0PCK5 PLAVI
						TR:Q0PCK7 PLAVI
						TR:Q0PCK8 PLAVI
				<i>Eimeria tenella</i>	<u>5802</u>	TR:C8TDR1 EIMTE
				<i>Paramecium tetraurelia</i>	<u>5888</u>	TR:A0DYU8 PARTE
						TR:A0DZK0 PARTE
						TR:A0BYF9 PARTE
						TR:A0CG64 PARTE
						TR:A0C835 PARTE

						TR:A0CDZ1 PARTE
						TR:A0DHH5 PARTE
						TR:A0BJH2 PARTE
				<i>Oxytricha trifallax</i>	<u>1172189</u>	TR:J9IRJ0 9SPIT
						TR:J9IEL1 9SPIT
						TR:J9IQ3 9SPIT
						TR:J9FAN6 9SPIT
						TR:J9HYX8 9SPIT
						TR:J9IXJ9 9SPIT
						TR:J9HXG0 9SPIT
						TR:J9J1X5 9SPIT
						TR:J9J4Z1 9SPIT
						TR:J9IPS8 9SPIT
						TR:J9FLL3 9SPIT
						TR:J9I670 9SPIT
				<i>Tetrahymena thermophila</i>	<u>312017</u>	TR:Q23314 TETTS
						TR:I7M4F5 TETTS
						TR:I7M7L9 TETTS
						TR:I7MJC7 TETTS
						TR:Q22B69 TETTS
						TR:Q23AJ1 TETTS
						TR:Q248F6 TETTS
						TR:I7MFV7 TETTS
						TR:I7MMJ5 TETTS
				<i>Salpingoeca rosetta</i>	<u>946362</u>	TR:F2TZS0 SALS5
						TR:F2U3D3 SALS5
						TR:F2UN53 SALS5
						TR:F2UG92 SALS5
						TR:F2U7C0 SALS5
						TR:F2U792 SALS5
						TR:F2TVN4 SALS5
				<i>Naegleria gruberi</i>	<u>5762</u>	TR:D2W3F9 NAEGR
				<i>Giardia intestinalis</i>	<u>598745</u>	TR:C6M0F7 GIAIB
				<i>Trichomonas vaginalis</i>	<u>5722</u>	TR:A2FXN1 TRIVA
						TR:A2G269 TRIVA
						TR:A2FUX5 TRIVA
				<i>Trypanosoma brucei gambiense</i>	<u>679716</u>	TR:C9ZUC7 TRYB9
				<i>Trypanosoma brucei brucei</i>	<u>185431</u>	TR:Q57TW9 TRYB2
				<i>Ectocarpus siliculosus</i>	<u>2880</u>	TR:D8LSY3 ECTSI
				<i>Thalassiosira pseudonana</i>	<u>35128</u>	TR:B5YUJ3 THAPS