SHEET 1

Non-redundant list of proteins found in Biyamina secretome

Accession number	Protein names	Functional categories	Number of matched peptides	Highest score
TB927.8.1440	maoC-like dehydratase	11.8 lipid metabolism	4	85
TB927.2.4930	esterase	11.9.2 lipid metabolism	1	46
TB927.8.6170	transketolase	11.1.31 lipid metabolism	13	113
TB09.211.3540	glycerol kinase glycosomal	11.5 lipid metabolism	5	91
TB09.211.3550	glycerol kinase glycosomal	11.5 lipid metabolism	11	119
TB927.8.6390	lysophospholipase	11.9.3 lipid metabolism	5	66
TB11.01.1820	biotin--acetyl-CoA-carboxylase ligase	11.1.1 lipid metabolism	5	88
TB11.01.8200	enoyl-CoA hydratase	11.9.4.3 lipid metabolism	1	102
TB927.8.3530	glycerol-3-phosphate dehydrogenase [NAD+],	11.5.2 lipid metabolism	8	81
TB927.3.3900	carnitine O-palmitoyltransferase II	11 lipid metabolism	12	80
TB927.6.2740	pyridoxal kinase	18.20* vitamine metabolism	10	92
TB927.4.4070	mevalonate kinase	16.1.2.4 secondary metabolism	1	45
TB10.05.0010	diphosphomevalonate decarboxylase	lipid metabolism	3	90
TB10.61.0980	glycosomal malate dehydrogenase	6.3 gluconeogenesis	7	91
TB927.2.4210	glycosomal phosphoenolpyruvate carboxykinase	6.4 gluconeogenese	26	122
TB11.01.3040	cytosolic malate dehydrogenase	6.3 gluconeogenesis	10	116
TB11.02.3130	malic enzyme	6.3 gluconeogenesis.	8	100
TB927.7.7500	iron/ascorbate oxidoreductase	6.4 gluconeogenese	3	43
TB10.70.5110	mitochondrial malate dehydrogenase	6.3 gluconeogenesis.	3	98
TB11.02.3120	malic enzyme	6.3 gluconeogenesis.	5	62
TB927.6.1570	2-hydroxy-3-oxopropionate reductase	6 gluconeogenese	7	94
TB927.8.7510	p-nitrophenylphosphatase	clohexane degradation	1	47
TB927.1.710	phosphoglycerate kinase	4 glycolysis	2	83
TB927.1.3830	glucose-6-phosphate isomerase, glycosomal	4 glycolysis	1	105
TB10.6K15.3850	glyceraldehyde 3-phosphate dehydrogenase cytosolic	4 glycolysis	12	95
TB927.1.700	phosphoglycerate kinase	4 glycolysis	3	48
TB10.70.1370	fructose-bisphosphate aldolase glycosomal	4 glycolysis	10	93

TB11.02.4150	pyruvate phosphate dikinase	4 glycolysis	3	69
TB927.6.4280	glyceraldehyde 3-phosphate dehydrogenase	4 glycolysis	8	81
TB10.70.5800	hexokinase	4 glycolysis	1	84
TB09.211.1370	glyceraldehyde-3-phosphate dehydrogenase	4 glycolysis	4	72
TB10.70.5820	hexokinase	4 glycolysis	15	104
TB927.3.1790	pyruvate dehydrogenase E1 beta subunit	4 glycolysis	2	71
TB10.70.4740	enolase	4.12 glycolysis	23	136
TB11.02.3210	triosephosphate isomerase	4.8 glycolysis	11	119
TB927.5.3580	phosphoglycerate mutase protein	4.4.11 glycolysis	3	75
TB10.6K15.2620	phosphoglycerate mutase	4.4.11 glycolysis	13	102
TB11.01.6410	phosphomannose isomerase	3 CHO metabolism	5	59
TB927.8.980	phosphoacetylglucosamine mutase	3 CHO metabolism	4	104
TB11.03.0090	ribokinase	3.5 CHO metabolism	1	79
TB10.6K15.3600	myo-inositol-1-phosphate synthase	3.4.3 CHO metabolism	4	68
TB10.05.0080	glucosidase	2.2.2.1CHO metabolism	3	53
TB11.01.8520	glucosamine-6-phosphate isomerase	7.1.2 OPP.oxidative PP	4	77
TB09.211.3180	6-phosphogluconate dehydrogenase	7.1.3 OPP.oxidative PP	1	80
TB927.8.5600	transaldolase	7.2.2 OPP.non-reductive PP	11	105
TB11.01.0700	ribose 5-phosphate isomerase	7.2.4 OPP.non-reductive PP	2	71
TB11.01.3550	2-oxoglutarate dehydrogenase E2 component	8.1.5 TCA / org. Transformation	8	68
TB927.3.2230	succinyl-CoA synthetase alpha subunit	8.1.6 TCA / org. Transformation	7	70
TB10.61.2880	ACO aconitase	8.1.3 TCA / org. Transformation	14	104
TB11.02.2700	fumarate hydratase class I	8.1.8 TCA / org. Transformation	6	136
TB10.6K15.3250	succinyl-CoA ligase	8.1.6 TCA / org. Transformation	1	45
TB927.3.4500	fumarate hydratase	8.1.8 TCA / org. Transformation	25	107
TB927.8.3690	isocitrate dehydrogenase	8.1.4 TCA / org. Transformation	3	54
TB11.01.8470	dihydrolipoyl dehydrogenase	8.1.1.3 TCA / org. Transformation	13	140
TB11.02.0290	succinyl-coA:3-ketoacid-coenzyme A transferase	8.1.6 TCA / org. Transformation	11	96
TB11.01.1740	2-oxoglutarate dehydrogenase E1 component	8.1.5 TCA / org. Transformation	1	23
TB11.01.0290	carbonic anhydrase-like protein	8.3 TCA / org. Transformation	1	22
TB11.03.0230	isocitrate dehydrogenase	8.1.4 TCA / org. Transformation	1	34
TB927.5.930	NADH-dependent fumarate reductase	8.1.7 TCA / org. Transformation	4	78
TB10.389.1530	ribulose-5-phosphate 3-epimerase	1.3.11 PS.calvin cyle.RPE	1	64
TB10.70.0370	phosphomannomutase	10.1.21 cell wall.precursor synthesis	4	62
TB09.211.1380	glycine cleavage system H protein	13.2.5.2 amino acid metabolism	2	52

TB927.1.3950	alanine aminotransferase	13.1.1.3 amino acid metabolism	4	94
TB09.160.4570	arginine kinase	13.1.1 amino acid metabolism	14	84
TB09.160.4560	arginine kinase	13.1.1 amino acid metabolism	5	84
TB927.2.4610	branched-chain amino acid aminotransferase	13.1.1.2 amino acid metabolism	10	81
TB11.01.1350	S-adenosylhomocysteine hydrolase	13.2.3.4 amino acid metabolism	18	91
TB927.6.1080	hydroxyacylglutathione hydrolase	13.2.3.2 amino acid metabolism	9	69
TB927.7.1110	asparagine synthetase a	13.1.1 amino acid metabolism	8	79
TB927.6.2790	L-threonine 3-dehydrogenase	13.2 amino acid metabolism	17	102
TB11.02.5400	cystathionine beta-synthase	13.1.2.3.11 amino acid metabolism	15	77
TB10.70.4280	delta-1-pyrroline-5-carboxylate dehydrogenase	13.2.2.2 amino acid metabolism	16	77
TB09.160.4590	arginine kinase	13.1.1 amino acid metabolism	18	97
TB09.211.3330	cystathione gamma lyase	13.1.2.3.11 amino acid metabolism	9	102
TB927.7.2440	pyrroline-5-carboxylate reductase	13.2.2.2 amino acid metabolism	3	60
TB927.8.2540	3-ketoacyl-CoA thiolase	13.2 amino acid metabolism	7	91
TB11.02.2740	aspartate aminotransferase mitochondrial	13.1.1.2 amino acid metabolism	6	77
TB927.8.6060	2-amino-3-ketobutyrate coenzyme A ligase	13.1.1.2 amino acid metabolism	15	97
TB10.70.3710	aspartate aminotransferase	13.1.1.2 amino acid metabolism	4	79
TB927.5.3820	aspartate carbamoyltransferase	13.1.1.2 amino acid metabolism	12	92
TB10.70.1320	N-acetyltransferase subunit Nat1	13.1.3.4.3 amino acid metabolism	1	59
TB927.2.4590	branched-chain amino acid aminotransferase	13.1.1.2 amino acid metabolism	3	70
TB927.6.4840	S-adenosylmethionine synthetase	13.1.3.4 amino acid metabolism	10	93
TB10.389.1810	kynurenine aminotransferase	13.1.1.2 amino acid metabolism	6	79
TB09.160.0770	nitrilase	22.1.5 polyamine metabolism	9	84
TB09.V1.0380	spermidine synthase	22.1.7 polyamine metabolism	10	87
TB927.7.4970	glutamine synthetase	12.2.2 N-metabolism.ammonia metabolism	5	109
TB09.160.4310	glutamate dehydrogenase	12.3.1 N-metabolism	1	48
TB927.6.950	cysteinyl-tRNA synthetase	29.1 protein.aa activation	3	38
TB927.3.5580	tryptophanyl-tRNA synthetase	29.1 protein.aa activation	4	69
TB927.7.3620	tyrosyl-tRNA synthetase	29.1 protein.aa activation	4	50
TB11.46.0008	arginyl-tRNA synthetase	29.1 protein.aa activation	18	71
TB927.5.1090	threonyl-tRNA synthetase	29.1 protein.aa activation	10	84
TB11.02.5020	seryl-tRNA synthetase	29.1 protein.aa activation	9	109
TB927.4.2310	asparaginyl-tRNA synthetase	29.1 protein.aa activation	3	75
TB927.7.2400	tyrosyl-tRNA synthetase	29.1 protein.aa activation	3	58
TB927.8.5330	tyrosyl/methionyl-tRNA synthetase	29.1 protein.aa activation	2	63

TB927.6.1880	aspartyl-tRNA synthetase	29.1 protein.aa activation	3	82
TB11.02.1210	leucyl-tRNA synthetase	29.1 protein.aa activation	18	138
TB927.6.4590	glutamyl-tRNA synthetase	29.1 protein.aa activation	2	92
TB09.160.3730	glutaminyl-tRNA synthetase	29.1 protein.aa activation	2	54
TB927.6.4480	valyl-tRNA synthetase	29.1 protein.aa activation	1	24
TB10.70.6470	methionyl-tRNA synthetase	29.1 protein.aa activation	5	57
TB927.8.550	peptide methionine sulfoxide reductase	29.11* sulfoxide reductases	2	31
TB927.3.3610	peroxisomal targeting signal type 2 receptor	29.3 protein.targeting	3	59
TB10.70.1190	valosin-containing protein homolog	29.3 protein.targeting	3	67
TB11.02.4170	40S ribosomal protein S5	29.2.4 protein.synthesis.elongation	1	66
TB11.03.0410	eukaryotic translation initiation factor 5a	29.2 protein.synthesis	4	90
TB10.61.1960	40S ribosomal protein S2	29.2.4 protein.synthesis.elongation	1	47
TB10.70.1730	40S ribosomal protein S18	29.2.4 protein.synthesis.elongation	1	59
TB09.211.0110	60S ribosomal protein L10	29.2.4 protein.synthesis.elongation	1	87
TB10.26.0560	60S ribosomal protein L6	29.2.4 protein.synthesis.elongation	2	107
TB10.70.4880	eukaryotic translation initiation factor 5	29.2 protein.synthesis	1	49
TB11.02.3595	protein translation factor SUI1-like protein	29.2 protein.synthesis	1	49
TB11.01.4830	eukaryotic translation initiation factor 2 gamma	29.2 protein.synthesis	1	53
TB10.70.1770	eukaryotic translation initiation factor 6	29.2 protein.synthesis	2	79
TB10.70.2650	elongation factor 2	29.2.4 protein.synthesis.elongation	23	95
TB11.01.2560	40S ribosomal protein SA	29.2.4 protein.synthesis.elongation	3	76
TB09.160.3270	eukaryotic initiation factor 4a	29.2 protein.synthesis	12	105
TB09.211.4550	60S ribosomal protein L12	29.2.4 protein.synthesis.elongation	2	62
TB927.4.3570	translation elongation factor 1-beta	29.2.4 protein.synthesis.elongation	8	73
TB10.70.5680	elongation factor 1-alpha	29.2.4 protein.synthesis.elongation	3	83
TB10.6K15.0410	60S ribosomal protein L18	29.2.4 protein.synthesis.elongation	1	33
TB09.244.2730	60S ribosomal protein L5	29.2.4 protein.synthesis.elongation	7	67
TB11.01.4660	elongation factor 1 gamma	29.2.4 protein.synthesis.elongation	6	82
TB10.70.1100	translation elongation factor 1-beta	29.2.4 protein.synthesis.elongation	5	85
TB10.05.0220	60S ribosomal protein L10a	29.2.4 protein.synthesis.elongation	2	59
TB927.4.3590	translation elongation factor 1-beta	29.2.4 protein.synthesis.elongation	8	68
TB927.4.3550	60S ribosomal protein L13a	29.2.4 protein.synthesis.elongation	3	55
TB10.70.5650	TEF1 elongation factor 1-alpha	29.2.4 protein.synthesis.elongation	8	140
TB10.70.3510	60S ribosomal protein L18a	29.2.4 protein.synthesis.elongation	2	76
TB927.3.5050	60S ribosomal protein L4	29.2.4 protein.synthesis.elongation	4	66

TB11.01.3020	40S ribosomal protein L14	29.2.4 protein.synthesis.elongation	2	46
TB10.70.7695	40S ribosomal protein S11	29.2.4 protein.synthesis.elongation	2	65
TB927.3.3310	60S ribosomal protein L13	29.2.4 protein.synthesis.elongation	1	35
TB10.70.1380	40S ribosomal protein S9	29.2.4 protein.synthesis.elongation	3	38
TB927.5.2570	translation initiation factor	29.2 protein.synthesis	1	73
TB927.8.5880	eukaryotic translation initiation factor 1A	29.2 protein.synthesis	1	59
TB09.160.4450	40S ribosomal protein S3	29.2.4 protein.synthesis.elongation	5	101
TB09.160.2550	ribosomal protein S7	29.2.4 protein.synthesis.elongation	3	56
TB11.02.1085	40s ribosomal protein S4	29.2.4 protein.synthesis.elongation	4	74
TB11.46.0001	60S acidic ribosomal subunit protein	29.2.4 protein.synthesis.elongation	4	93
TB10.6K15.2050	40S ribosomal protein S12	29.2.4 protein.synthesis.elongation	3	70
TB09.211.0120	nascent polypeptide associated complex subunit	29.2.4 protein.synthesis.elongation r	2	59
TB927.8.1330	60S ribosomal protein L7a	29.2.4 protein.synthesis.elongation	1	54
TB10.70.7020	40S ribosomal protein S23	29.2.4 protein.synthesis.elongation	1	24
TB927.7.1730	60S ribosomal protein L7	29.2.4 protein.synthesis.elongation	1	36
TB10.6K15.0510	60S ribosomal protein L22	29.2.4 protein.synthesis.elongation	1	53
TB09.160.4200	60S acidic ribosomal protein	29.2.4 protein.synthesis.elongation	2	71
TB927.6.4980	40S ribosomal protein S14	29.2.4 protein.synthesis.elongation	2	52
TB11.50.0005	60S ribosomal protein L21E	29.2.4 protein.synthesis.elongation	1	62
TB11.02.4030	eukaryotic release factor 3	29.2 protein.synthesis	1	34
TB11.01.7960	60S ribosomal protein L2	29.2.4 protein.synthesis.elongation	1	52
TB927.7.230	40S ribosomal protein S33	29.2.4 protein.synthesis.elongation	1	32
TB09.160.3670	ribosomal protein S6	29.2.4 protein.synthesis.elongation	1	30
TB10.70.3360	40S ribosomal protein S3a	29.2.4 protein.synthesis.elongation	3	57
TB09.211.4850	60S ribosomal protein L26	29.2.4 protein.synthesis.elongation	1	20
TB927.7.1040	40S ribosomal protein S16	29.2.4 protein.synthesis.elongation	3	58
TB927.5.1660	protein phosphatase 2C	29.4 protein.postranslational modification	4	58
TB10.389.1730	protein kinase	29.4 protein.postranslational modification	3	91
TB10.61.2550	N-myristoyl transferase	29.4 protein.postranslational modification	1	44
TB11.01.8740	protein phosphatase 2A catalytic subunit	29.4 protein.postranslational modification	1	72
TB11.01.0450	serine/threonine protein phosphatase catalytic	29.4 protein.postranslational modification	2	69
TB927.1.3200	phosphatase-like protein	29.4 protein.postranslational modification	3	37
TB11.03.0390	protein phosphatase 2C	29.4 protein.postranslational modification	5	96
TB10.05.0110	serine/threonine protein phosphatase type 5	29.4 protein.postranslational modification	1	42
TB11.02.4830	protein kinase	29.4 protein.postranslational modification	1	27

TB11.46.0003	protein kinase	29.4 protein.postranslational modification	1	26
TB927.8.7350	trans-sialidase	29.5 protein.degradation	1	72
TB927.5.1880	ecotin	29.5 protein.degradation	3	55
TB927.7.4070	calpain-like cysteine peptidase	29.5 protein.degradation	6	53
TB927.7.6270	peptidase T	29.5 protein.degradation	1	75
TB10.70.6620	methionine aminopeptidase 2	29.5 protein.degradation	6	76
TB10.70.7090	serine carboxypeptidase III precursor	29.5 protein.degradation	1	110
TB927.7.190	thimet oligopeptidase A	29.5 protein.degradation	12	78
TB927.3.4750	aminopeptidase, Family M1	29.5 protein.degradation	11	104
TB11.52.0003	oligopeptidase b	29.5 protein.degradation	8	110
TB927.8.1610	major surface protease gp63	29.5 protein.degradation	1	35
TB10.6K15.2520	prolyl oligopeptidase	29.5 protein.degradation	27	110
TB10.61.1870	aminopeptidase, Family M24	29.5 protein.degradation	3	72
TB11.47.0036	calpain, family C2	29.5 protein.degradation	2	39
TB927.1.2100	calpain-like cysteine peptidase, family C2	29.5 protein.degradation	27	107
TB11.02.1070	aminopeptidase, Family M1	29.5 protein.degradation	22	90
TB927.6.1000	cysteine peptidase, family C1	29.5 protein.degradation	1	66
TB927.3.3410	aspartyl aminopeptidase	29.5 protein.degradation	2	67
TB11.02.0100	carboxypeptidase, Family M32	29.5 protein.degradation	12	93
TB10.61.1210	methionine aminopeptidase, Family M24	29.5 protein.degradation	1	59
TB927.6.400	peptidase M20/M25/M40	29.5 protein.degradation	1	70
TB927.7.4060	calpain-like cysteine peptidase	29.5 protein.degradation	1	31
TB11.02.4440	aminopeptidase, Family M17	29.5 protein.degradation	14	120
TB927.6.1030	cysteine peptidase, family C1	29.5 protein.degradation	1	29
TB927.3.2090	aminopeptidase P1	29.5 protein.degradation	2	81
TB10.389.1480	cytosolic dipeptidase, M20/M25/M40 family	29.5 protein.degradation	9	129
TB927.1.2260	calpain-like protein fragment	29.5.3 protein.degradation	1	43
TB10.70.0850	proteasome subunit alpha 1	29.5.11.20 protein.degradation	10	94
TB11.02.0815	ubiquitin-conjugating enzyme	29.5.11 protein.degradation	3	63
TB10.100.0170	proteasome subunit alpha 2	29.5.11.20 protein.degradation	5	117
TB09.211.0050	ubiquitin-conjugating enzyme E2	29.5.11 protein.degradation	3	74
TB09.211.2590	proteasome subunit beta 2	29.5.11.20 protein.degradation	4	50
TB11.01.1680	polyubiquitin	29.5.11 protein.degradation	1	44
TB927.5.1000	ubiquitin-conjugating enzyme E2	29.5.11 protein.degradation	1	48
TB927.7.4790	proteasome beta 6 subunit	29.5.11.20 protein.degradation	4	80

TB10.100.0120	proteasome subunit alpha 5	29.5.11.20 protein.degradation	6	101
TB10.70.3660	proteasome activator protein PA26	29.5.11.20 protein.degradation	7	84
TB10.70.2490	proteasome subunit beta 2	29.5.11.20 protein.degradation	4	62
TB09.211.1250	proteasome subunit alpha 1	29.5.11.20 protein.degradation	3	72
TB11.02.4870	proteasome subunit alpha 7	29.5.11.20 protein.degradation	10	99
TB927.7.4420	proteasome alpha 3 subunit	29.5.11.20 protein.degradation	4	107
TB927.3.780	proteasome alpha 7 subunit	29.5.11.20 protein.degradation	4	91
TB927.6.1260	proteasome beta-1 subunit	29.5.11.20 protein.degradation	3	91
TB11.02.5170	proteasome subunit beta 3	29.5.11.20 protein.degradation	1	55
TB927.4.430	proteasome beta 7 subunit	29.5.11.20 protein.degradation	1	50
TB10.70.0790	proteasome subunit beta 5	29.5.11.20 protein.degradation	6	76
TB927.3.5340	Hsc70-interacting protein (Hip)	29.5.11.4.2 protein.degradation	5	74
TB11.01.2000	HslVU complex proteolytic subunit	29.5 protein.degradation	2	63
TB927.3.2600	ATP-dependent DEAD/H RNA helicase	27.5* RNA.DEAD/DEAH BOX helicase	17	73
TB10.70.3290	ATP-dependent DEAD-box RNA helicase	27.5* RNA.DEAD/DEAH BOX helicase	1	78
TB10.70.7730	ATP-dependent DEAD/H RNA helicase	27.5* RNA.DEAD/DEAH BOX helicase	2	83
TB09.211.2150	poly(A)-binding protein 1	27.3 RNA.regulation of transcription	4	69
TB09.211.0560	DRBD3 RNA-binding protein	27.4 RNA.RNA binding	2	70
TB927.8.2740	mitochondrial RNA binding protein	27.4 RNA.RNA binding	7	75
TB927.8.740	nucleolar RNA-binding protein	27.4 RNA.RNA binding	2	42
TB11.01.4860	guide RNA-binding protein	27.4 RNA.RNA binding	4	58
TB11.55.0009	mitochondrial RNA-binding protein 1	27.4 RNA.RNA binding	3	68
TB11.02.5770	mitochondrial RNA-binding protein	27.4 RNA.RNA binding	3	46
TB10.70.5360	La protein	27.4 RNA.RNA binding	9	78
TB10.6K15.3160	fibrillarin	27.1 RNA.processing	1	50
TB927.5.1710	ribonucleoprotein p18, mitochondrial precursor	27.1 RNA.processing	2	37
TB927.6.2700	small nuclear ribonucleoprotein Sm-E	27.1 RNA.processing	1	43
TB11.02.0490	RNA editing complex protein MP46	27.1 RNA.processing	1	30
TB10.61.1920	fibrillarin	27.1 RNA.processing	2	35
TB927.4.890	small nuclear ribonucleoprotein SmD3	27.1 RNA.processing	1	30
TB927.2.5850	small nuclear ribonucleoprotein	27.1 RNA.processing	1	38
TB09.211.1695	small nuclear ribonucleoprotein Sm-F	27.1 RNA.processing	1	25
TB927.8.3380	electron transfer protein	34 transport	1	30
TB927.8.5030	trafficking protein particle complex subunit 3	34 transport	1	43
TB10.100.0070	ATP synthase F1 subunit gamma	34.1 transport.p- and v-ATPases	7	59

TB927.7.7420	ATP synthase alpha chain	34.1 transport.p- and v-ATPases	12	83
TB927.3.1380	ATP synthase beta chain	34.1 transport.p- and v-ATPases	8	109
TB927.6.4990	ATP synthase, epsilon chain	34.1 transport.p- and v-ATPases	2	98
TB927.5.3400	calcium-translocating P-type ATPase	34.1 transport.p- and v-ATPases	1	20
TB10.389.1170	P-type H+-ATPase	34.1.1 transport.p- and v-ATPases	1	23
TB927.8.5120	cytochrome c	9.7 mitochondrial electron transport	4	67
TB10.70.0830	CHC clathrin heavy chain	31.4 cell. vesicle transport	1	28
TB927.3.4680	RAB GDP dissociation inhibitor alpha	31.4 cell. vesicle transport	8	98
TB10.6K15.3970	developmentally regulated GTP-binding protein	31.4 cell. vesicle transport	1	56
TB927.3.1120	GTP-binding nuclear protein rtb2	31.4 cell. vesicle transport	1	42
TB927.8.890	small GTP-binding protein Rab1	31.4 cell. vesicle transport	3	70
TB927.8.4330	small GTP-binding protein Rab11	31.4 cell. vesicle transport	2	50
TB11.01.5320	RAB4 small GTPase	31.4 cell. vesicle transport	1	66
TB10.389.1370	hypothetical protein	35.1 not assigned.no ontology	1	38
TB10.6K15.0480	hypothetical protein	35.1 not assigned.no ontology	1	40
TB927.8.6760	IgE-dependent histamine-releasing factor	35.2 not assigned.unknown	4	66
TB927.7.4520	hypothetical protein	35.1 not assigned.no ontology	7	87
TB09.211.1690	hypothetical protein	35.1 not assigned.no ontology	5	75
TB927.7.6890	hypothetical protein	35.1 not assigned.no ontology	1	81
TB927.6.2280	hypothetical protein	35.1 not assigned.no ontology	3	72
TB927.4.1380	hypothetical protein	35.1 not assigned.no ontology	1	46
TB11.02.2030	hypothetical protein	35.1 not assigned.no ontology	3	92
TB10.70.5050	hypothetical protein	35.1 not assigned.no ontology	1	59
TB927.7.5210	hypothetical protein	35.1 not assigned.no ontology	1	71
TB11.01.7740	hypothetical protein	35.1 not assigned.no ontology	2	61
TB11.02.2840	hypothetical protein	35.1 not assigned.no ontology	7	74
TB927.7.2650	hypothetical protein	35.1 not assigned.no ontology	1	42
TB927.1.180	retrotransposon hot spot (RHS) protein	35.1 not assigned.no ontology	14	75
TB927.5.1460	hypothetical protein	35.1 not assigned.no ontology	2	67
TB927.8.4780	hypothetical protein	35.1 not assigned.no ontology	3	63
TB11.02.2520	hypothetical protein	35.1 not assigned.no ontology	7	71
TB927.4.2030	hypothetical protein	35.1 not assigned.no ontology	3	74
TB927.2.340	retrotransposon hot spot (RHS) protein	35.1 not assigned.no ontology	5	64
TB10.70.2770	stress-inducible protein STI1-like	35.2 not assigned.unknown	9	103
TB927.2.470	retrotransposon hot spot (RHS) protein	35.1 not assigned.no ontology	11	98

TB927.1.3170	hypothetical protein	35.1 not assigned.no ontology	3	38
TB927.4.3740	hypothetical protein	35.1 not assigned.no ontology	6	59
TB927.3.2100	hypothetical protein	35.1 not assigned.no ontology	9	98
TB927.7.3330	hypothetical protein	35.1 not assigned.no ontology	1	30
TB11.01.7120	hypothetical protein	35.1 not assigned.no ontology	1	56
TB11.01.5590	hypothetical protein	35.1 not assigned.no ontology	1	60
TB10.61.0620	hypothetical protein	35.1 not assigned.no ontology	1	74
TB10.70.4930	hypothetical protein	35.1 not assigned.no ontology	5	68
TB927.1.220	retrotransposon hot spot (RHS) protein	35.1 not assigned.no ontology	8	65
TB927.6.2090	hypothetical protein	35.1 not assigned.no ontology	1	31
TB927.2.280	retrotransposon hot spot (RHS) protein	35.1 not assigned.no ontology	7	68
TB11.01.5680	hypothetical protein	35.1 not assigned.no ontology	2	71
TB927.5.2640	hypothetical protein	35.1 not assigned.no ontology	1	75
TB927.4.380	hypothetical protein	35.1 not assigned.no ontology	2	46
TB927.4.2240	hypothetical protein	35.1 not assigned.no ontology	4	57
TB10.61.0540	hypothetical protein	35.1 not assigned.no ontology	3	59
TB09.160.5100	hypothetical protein	35.1 not assigned.no ontology	3	55
TB927.3.1030	hypothetical protein	35.1 not assigned.no ontology	1	28
TB927.3.4040	hypothetical protein	35.1 not assigned.no ontology	2	65
TB11.55.0024	hypothetical protein	35.1 not assigned.no ontology	11	85
TB10.70.1490	hypothetical protein	35.1 not assigned.no ontology	6	80
TB09.160.5530	hypothetical protein	35.1 not assigned.no ontology	6	77
TB927.7.2990	hypothetical protein	35.1 not assigned.no ontology	1	29
TB10.70.4130	hypothetical protein	35.1 not assigned.no ontology	1	30
TB927.7.2980	hypothetical protein	35.1 not assigned.no ontology	10	67
TB927.2.100	retrotransposon hot spot (RHS) protein	35.1 not assigned.no ontology	2	61
TB11.02.0140	hypothetical protein	35.1 not assigned.no ontology	1	45
TB927.8.1140	hypothetical protein	35.1 not assigned.no ontology	1	31
TB927.7.7460	hypothetical protein	35.1 not assigned.no ontology	4	51
TB11.02.0210	hypothetical protein	35.1 not assigned.no ontology	5	62
TB927.4.1300	hypothetical protein	35.1 not assigned.no ontology	17	97
TB09.211.4630	hypothetical protein	35.1 not assigned.no ontology	1	58
TB927.6.4000	hypothetical protein	35.1 not assigned.no ontology	5	64
TB927.3.5310	hypothetical protein	35.1 not assigned.no ontology	1	79
TB09.211.3300	hypothetical protein	35.1 not assigned.no ontology	1	34

TB927.2.240	retrotransposon hot spot (RHS) protein	35.1 not assigned.no ontology	11	68
TB927.1.420	retrotransposon hot spot (RHS) protein	35.1 not assigned.no ontology	2	73
TB09.211.1620	hypothetical protein	35.1 not assigned.no ontology	9	69
TB927.2.1170	retrotransposon hot spot (RHS) protein	35.1 not assigned.no ontology	1	36
TB11.02.4950	hypothetical protein	35.1 not assigned.no ontology	3	39
TB927.4.1220	leucine-rich repeat protein (LRRP)	35 not assigned	1	70
TB927.5.1160	hypothetical protein	35.1 not assigned.no ontology	1	31
TB927.2.510	retrotransposon hot spot (RHS) protein	35.1 not assigned.no ontology	1	38
TB11.03.0620	hypothetical protein	35.1 not assigned.no ontology	1	42
TB09.160.2540	alpha/beta-hydrolase-like protein	35.1 not assigned.no ontology	1	97
TB927.1.3390	hypothetical protein	35.1 not assigned.no ontology	1	60
TB927.5.1280	hypothetical protein	35.1 not assigned.no ontology	1	24
TB927.2.4580	hypothetical protein	35.1 not assigned.no ontology	2	89
TB10.70.2180	hypothetical protein	35.1 not assigned.no ontology	1	32
TB927.2.450	retrotransposon hot spot (RHS) protein	35.1 not assigned.no ontology	2	55
TB11.01.7325	hypothetical protein	35.1 not assigned.no ontology	2	65
TB927.7.6770	hypothetical protein	35.1 not assigned.no ontology	1	44
TB11.02.2040	hypothetical protein	35.1 not assigned.no ontology	4	51
TB927.8.6110	hypothetical protein	35.1 not assigned.no ontology	1	58
TB10.389.1890	hypothetical protein	35.1 not assigned.no ontology	1	20
TB09.211.2400	hypothetical protein	35.1 not assigned.no ontology	1	33
TB927.4.5340	hypothetical protein	35.1 not assigned.no ontology	1	31
TB927.1.120	retrotransposon hot spot (RHS) protein	35.1 not assigned.no ontology	3	57
TB927.4.2740	hypothetical protein	35.1 not assigned.no ontology	4	90
TB10.70.7950	hypothetical protein	35.1 not assigned.no ontology	1	39
TB11.02.3330	hypothetical protein	35.1 not assigned.no ontology	1	27
TB927.8.4210	hypothetical protein	35.1 not assigned.no ontology	2	37
TB10.389.1260	hypothetical protein	35.1 not assigned.no ontology	1	22
TB11.01.8610	hypothetical protein	35.1 not assigned.no ontology	1	27
TB927.7.3170	hypothetical protein	35.1 not assigned.no ontology	1	28
TB927.5.700	hypothetical protein	35.1 not assigned.no ontology	1	20
TB927.5.2260	hypothetical protein	35.1 not assigned.no ontology	4	62
TB11.02.0690	hypothetical protein	35.1 not assigned.no ontology	1	20
TB11.02.2670	hypothetical protein	35.1 not assigned.no ontology	1	27
TB11.03.0335	hypothetical protein	35.1 not assigned.no ontology	1	37

TB927.4.4660	hypothetical protein	35.1 not assigned.no ontology	3	77
TB11.47.0016	hypothetical protein	35.1 not assigned.no ontology	2	48
TB10.6K15.1900	hypothetical protein	35.1 not assigned.no ontology	2	75
TB927.5.2160	hypothetical protein	35.1 not assigned.no ontology	1	53
TB11.01.5570	hypothetical protein	35.1 not assigned.no ontology	1	73
TB927.4.360	hypothetical protein	35.1 not assigned.no ontology	1	68
TB927.6.2200	hypothetical protein	35.1 not assigned.no ontology	3	50
TB10.70.1130	hypothetical protein	35.1 not assigned.no ontology	5	101
TB11.01.5440	hypothetical protein	35.1 not assigned.no ontology	1	52
TB11.02.0660	hypothetical protein	35.1 not assigned.no ontology	1	75
TB09.211.3050	hypothetical protein	35.1 not assigned.no ontology	1	50
TB11.01.8770	hypothetical protein	35.1 not assigned.no ontology	7	62
TB09.160.4480	hypothetical protein	35.1 not assigned.no ontology	2	29
TB10.6K15.0290	hypothetical protein	35.1 not assigned.no ontology	1	53
TB927.5.4470	hypothetical protein	35.1 not assigned.no ontology	1	21
TB11.01.8390	hypothetical protein	35.1 not assigned.no ontology	1	27
TB10.6K15.0080	hypothetical protein	35.1 not assigned.no ontology	1	20
TB11.02.0870	hypothetical protein	35.1 not assigned.no ontology	5	70
TB09.211.1950	hypothetical protein	35.1 not assigned.no ontology	1	60
TB927.2.1080	retrotransposon hot spot (RHS) protein	35.1 not assigned.no ontology	9	57
TB09.160.0465	hypothetical protein	35.1 not assigned.no ontology	1	62
TB927.5.2940	stress-induced protein sti1	35.2 not assigned.unknown	3	80
TB10.26.0680	hypothetical protein	35.1 not assigned.no ontology	3	44
TB927.3.4880	hypothetical protein	35.1 not assigned.no ontology	2	64
TB927.4.2040	hypothetical protein	35.1 not assigned.no ontology	8	75
TB11.01.2120	hypothetical protein	35.1 not assigned.no ontology	1	25
TB927.3.1010	hypothetical protein	35.1 not assigned.no ontology	2	54
TB927.5.1360	hypothetical protein	35.1 not assigned.no ontology	3	46
TB09.142.0100	variant surface glycoprotein	31.99 cell.unspecified	1	25
TB927.8.4970	69 kDa paraflagellar rod protein	31.6* cell organization	1	27
TB927.4.2070	antigenic protein	31.6* cell organization	2	77
TB09.160.1200	mitotubule-associated protein Gb4	31.1 cell.organisation	2	28
TB11.01.3805	microtubule-associated protein	31.1 cell.organisation	1	53
TB09.211.4511	kinetoplastid membrane protein KMP-11	31.1 cell.organisation	2	40
TB927.4.3950	cytoskeleton-associated protein CAP5.5	31.1 cell.organisation	2	42

TB11.02.3390	dynein light chain	31.1 cell.organisation	1	69
TB10.6K15.1160	G-actin binding protein	31.6* cell organization	3	103
TB11.01.2530	kinesin-like protein	31.1 cell.organisation	3	64
TB927.1.2340	alpha tubulin	31.1 cell.organisation	10	133
TB927.3.4290	73 kDa paraflagellar rod protein	31.1 cell.organisation	5	54
TB10.406.0560	microtubule-associated protein	31.1 cell.organisation	5	50
TB927.1.2330	beta tubulin	31.1 cell.organisation	9	77
TB10.406.0650	microtubule-associated protein	31.1 cell.organisation	3	74
TB927.6.2420	p22 protein precursor	31.1 cell.organisation	3	42
TB927.7.3440	I/6 autoantigen	31.1 cell.organisation	1	70
TB09.211.0620	actin A	31.1 cell.organisation	1	36
TB927.3.5180	cofilin/actin depolymerizing factor	31.1 cell.organisation	2	59
TB09.211.0740	p21 antigen protein	31.6* cell organization	2	65
TB927.6.3740	heat shock 70 kDa protein	29.6 protein.(un)folding	10	110
TB927.7.710	heat shock 70 kDa protein	29.6 protein.(un)folding	6	61
TB10.6K15.2290	protein disulfide isomerase	29.6 protein.(un)folding	3	72
TB09.211.1350	peptidyl-prolyl cis-trans isomerase (cyclophilin- 40)	29.6 protein.(un)folding	7	90
TB11.01.8510	t-complex protein 1 subunit alpha	29.6 protein.(un)folding	4	70
TB11.02.0750	t-complex protein 1 subunit zeta	29.6 protein.(un)folding	2	80
TB10.70.0280	chaperonin Hsp60	29.6 protein.(un)folding	9	112
TB10.70.7050	t-complex protein 1 subunit delta	29.6 protein.(un)folding	5	55
TB927.2.1560	cyclophilin type peptidyl-prolyl cis-trans isomerase	29.6 protein.(un)folding	1	59
TB927.7.280	cyclophilin-type peptidyl-prolyl cis-trans isomerase	29.6 protein.(un)folding	1	27
TB927.6.2170	co-chaperone GrpE, putative	29.6 protein.(un)folding	4	67
TB10.389.0880	heat shock protein	29.6 protein.(un)folding	16	92
TB11.01.3110	heat shock protein 70	29.6 protein.(un)folding	33	106
TB10.26.1080	heat shock protein 83	29.6 protein.(un)folding	27	93
TB927.8.2000	cyclophilin type peptidyl-prolyl cis-trans isomerase	29.6 protein.(un)folding	1	36
TB927.3.3330	heat shock protein 20	29.6 protein.(un)folding	3	95
TB927.7.2590	prefoldin	29.6 protein.(un)folding	2	79
TB927.7.4770	cyclophilin-type peptidyl-prolyl cis-trans isomerase	29.6 protein.(un)folding	2	60
TB927.7.1320	10 kDa heat shock protein	29.6 protein.(un)folding	1	37
TB11.02.5450	glucose-regulated protein 78	29.6 protein.(un)folding	15	113
TB927.7.1300	protein disulfide isomerase	29.6 protein.(un)folding	6	81
TB927.7.570	prefoldin	29.6 protein.(un)folding	5	58

TB927.7.5790	protein disulfide isomerase	29.6 protein.(un)folding	1	43
TB09.211.2850	cyclophilin type peptidyl-prolyl cis-trans isomerase	29.6 protein.(un)folding	1	42
TB11.03.0250	cyclophilin A	29.6 protein.(un)folding	6	98
TB10.6K15.2330	t-complex protein 1 subunit theta	29.6 protein.(un)folding	2	74
TB10.61.0180	peptidylprolyl isomerase-like protein	29.6 protein.(un)folding	3	74
TB11.01.3080	heat shock protein 70	29.6 protein.(un)folding	2	87
TB927.7.4480	adenosine 5'-monophosphoramidase	23 nucleotide metabolism	4	63
TB927.8.5630	dihydroorotase	23.2 nucleotide metabolism.	2	54
TB10.70.5150	adenylate kinase	23.1.2 nucleotide metabolism.	2	52
TB927.7.1780	adenine phosphoribosyltransferase	23 nucleotide metabolism	1	82
TB09.211.0350	adenylate kinase	23.1.2 nucleotide metabolism.	5	57
TB927.8.4430	nucleoside phosphorylase	23 nucleotide metabolism	5	86
TB927.6.2360	adenosine kinase	23 nucleotide metabolism	7	87
TB11.01.7800	nucleoside diphosphate kinase	23 nucleotide metabolism	5	89
TB10.26.0200	guanylate kinase	23.1.2 nucleotide metabolism.	7	70
TB927.4.3320	uracil phosphoribosyltransferase	23.3.1.3 nucleotide metabolism	4	80
TB09.160.4620	inositol-1(or 4)-monophosphatase	23.2 nucleotide metabolism	1	61
TB927.5.3830	dihydroorotate dehydrogenase	23.2 nucleotide metabolism.	3	88
TB10.6K15.0970	phosphoribosylpyrophosphate synthetase	23 nucleotide metabolism	1	47
TB10.70.6660	hypoxanthine-guanine phosphoribosyltransferase	23.1.2 nucleotide metabolism.	4	84
TB11.V4.0004	ribonucleoside-diphosphate reductase small chain	23 nucleotide metabolism	6	83
TB927.7.4570	nucleoside hydrolase	23 nucleotide metabolism	11	78
TB927.6.3650	ADP-ribosylation factor	23 nucleotide metabolism	3	78
TB927.3.2960	inosine-adenosine-guanosine-nucleoside hydrolase	23 nucleotide metabolism	8	78
TB927.7.5160	deoxyuridine triphosphatase	23 nucleotide metabolism	1	84
TB927.5.4560	guanine deaminase	23.2 nucleotide metabolism.	1	83
TB10.70.6540	hypoxanthine-guanine phosphoribosyltransferase	23.1.2 nucleotide metabolism.	4	51
TB09.211.4460	ADP-ribosylation factor	23 nucleotide metabolism	5	72
TB927.7.2100	GMP synthase	23.1.2.31 nucleotide metabolism.	9	90
TB927.3.3450	ADP-ribosylation factor-like protein 3A	23 nucleotide metabolism	4	92
TB11.02.1120	adenylosuccinate synthetase	23.1.2 nucleotide metabolism.	8	77
TB09.160.3710	proliferative cell nuclear antigen	31.3 cell.cycle	4	99
TB11.02.3990	S-phase kinase-associated protein	31.3 cell.cycle	1	33
TB927.8.6750	translationally controlled tumor protein	31.3 cell.cycle	4	72
TB11.02.2310	prostaglandin f synthase	30.99 signalling.unspecified	14	125

TB09.211.2360	protein kinase A catalytic subunit isoform 2	30 signalling	4	71
TB927.2.2130	small GTP-binding protein	30.5 signalling.G-proteins	1	47
TB927.2.5060	GTP binding protein	30.5 signalling.G-proteins	1	34
TB09.211.2330	small GTPase	30.5 signalling.G-proteins	3	44
TB11.01.3170	guanine nucleotide-binding protein subunit beta	30.5 signalling.G-proteins	14	100
TB927.3.5550	small GTP-binding protein	30.5 signalling.G-proteins	1	62
TB927.8.7410	calreticulin	30.3 signaling.calcium	9	96
TB09.160.4520	calmodulin	30.3 signalling.calcium	1	39
TB927.8.5440	flagellar calcium-binding protein TB-24	30.3 signalling.calcium	1	61
TB10.61.3180	calcium-dependent lipid binding protein	30.3 signalling.calcium	1	38
TB11.01.4621	calmodulin	30.3 signalling.calcium	2	57
TB09.211.2540	calmodulin-like protein	30.3 signalling.calcium	2	34
TB927.4.5010	calreticulin	30.3 signaling.calcium	3	86
TB11.01.1290	14-3-3-like protein	30.7 signalling.14-3-3 proteins	10	82
TB11.02.4700	14-3-3-like protein	30.7 signalling.14-3-3 proteins	6	70
TB927.5.950	thioredoxin-like protein	21.5 redox.peroxiredoxins	1	76
TB927.7.1140	trypanothione/tryparedoxin dependent peroxidase 3	21.5 redox.peroxiredoxins	1	20
TB927.7.1130	trypanothione/tryparedoxin dependent peroxidase 2	21.5 redox.peroxiredoxins	5	83
TB927.3.3760	tryparedoxin	21.5 redox.peroxiredoxins	4	72
TB10.406.0520	trypanothione reductase	21.2 redox.ascorbate and glutathione	12	117
TB11.47.0012	glutaredoxin	21.4 redox.glutaredoxins	1	38
TB927.2.4370	trypanothione synthetase	21.2 redox.ascorbate and glutathione	13	76
TB09.160.4250	tryparedoxin peroxidase	21.5 redox.peroxiredoxins	7	72
TB11.01.7550	iron superoxide dismutase	21.6 redox.dismutases and catalases	5	79
TB927.5.3350	iron superoxide dismutase	21.6 redox.dismutases and catalases	4	64
TB11.01.6660	iron superoxide dismutase	21.6 redox.dismutases and catalases	3	42
TB927.8.1990	tryparedoxin peroxidase	21.5 redox.peroxiredoxins	10	86
TB927.7.2700	NADH-cytochrome b5 reductase	21.99 redox.misc	5	60
TB927.7.2710	NADH-cytochrome b5 reductase	21.99 redox.misc	5	69
TB927.5.1470	NADH-cytochrome b5 reductase	21.99 redox.misc	7	74
TB927.8.2210	pteridine reductase	21 redox	2	58
TB10.406.0330	histone H2B	28.1 DNA.synthesis/chromatin structure	2	81
TB10.70.0800	universal minicircle sequence binding protein (UMSBP)	28.1 DNA.synthesis/chromatin structure	2	91
TB927.7.7040	methylthioadenosine phosphorylase	28.1 DNA.synthesis/chromatin structure	8	64
TB927.5.1700	replication Factor A 28 kDa subunit	28.1 DNA.synthesis/chromatin structure	3	64

TB10.70.0820	universal minicircle sequence binding protein (UMSBP)	28.1 DNA.synthesis/chromatin structure	2	107

SHEET 2

Non-redundant list of proteins found in Stib 215 secretome

Accession number	Protein names	Functional categories	Number of matched peptides	Highest score
TB927.6.2740	pyridoxal kinase	18.20* vitamine metabolism	12	87
TB11.01.1820	biotin--acetyl-CoA-carboxylase ligase	18 vitamine metabolism	6	77
TB927.6.1080	hydroxyacylglutathione hydrolase	24.1 Biodegradation of Xenobiotics	3	59
TB927.3.3900	carnitine O-palmitoyltransferase II	11 lipid metabolism	14	75
TB09.211.3550	glycerol kinase glycosomal	11.5 lipid metabolism	9	89
TB927.8.3530	glycerol-3-phosphate dehydrogenase [NAD+], glycosomal	11.5.2 lipid metabolism	12	105
TB927.8.6170	transketolase	11.1.31 lipid metabolism	14	112
TB927.1.4830	phospholipase A1	11.9.3 lipid metabolism	1	85
TB927.8.1440	maoC-like dehydratase	11.8 lipid metabolism	5	79
TB927.8.7100	acetyl-CoA carboxylase	11.1.1 lipid metabolism	3	78
TB927.8.6390	lysophospholipase	11.9.3 lipid metabolism	2	56
TB927.8.2540	3-ketoacyl-CoA thiolase	11.9.4.5 lipid metabolism	2	62
TB11.01.8470	dihydrolipoyl dehydrogenase	11.1.31 lipid metabolism	5	69
TB09.160.2780	fatty acyl CoA synthetase 2	11 lipid metabolism	1	30
TB927.2.4930	esterase	11.9.2 lipid metabolism	4	43
TB927.7.7420	ATP synthase alpha chain	34.1 transport.p- and v-ATPases	14	66
TB10.389.1170	P-type H+-ATPase	34.1.1 transport.p- and v-ATPases	1	64
TB09.244.2570	calcium motive p-type ATPase	34.1 transport.p- and v-ATPases	3	60
TB927.4.1080	V-type ATPase, A subunit	34.1 transport.p- and v-ATPases	1	48
TB10.389.1180	P-type H+-ATPase	34.1.1 transport.p- and v-ATPases	7	81
TB927.3.1380	ATP synthase beta chain	34.1 transport.p- and v-ATPases	8	88
TB10.70.0830	clathrin heavy chain	31.4 cell. vesicle transport	5	86
TB09.160.4680	Rab geranylgeranyl transferase component A	31.4 cell. vesicle transport	1	105
TB927.8.890	small GTP-binding protein Rab1	31.4 cell. vesicle transport	3	61
TB10.6K15.3970	developmentally regulated GTP-binding protein	31.4 cell. vesicle transport	1	58
TB927.2.5060	GTP binding protein	31.4 cell. vesicle transport	4	70
TB11.02.5380	exosome complex exonuclease RRP44p-like protein	31.4 cell. vesicle transport	1	70

TB927.8.4330	small GTP-binding protein Rab11	31.4 cell. vesicle transport	1	32
TB10.70.4720	importin subunit beta-1	34 transport	4	102
TB10.6K15.2840	protein transport protein Sec23A	34 transport	1	52
TB10.6K15.2020	glucose transporter 2A	34.2 transporter.sugars	4	70
TB927.6.1520	aquaporin 3	34.19.1 transport	1	33
TB09.160.4560	arginine kinase	13.1.1 amino acid metabolism	17	80
TB11.01.1350	S-adenosylhomocysteine hydrolase	13.2.3.4 amino acid metabolism	3	74
TB927.7.1110	asparagine synthetase a	13.1.1 amino acid metabolism	7	66
TB927.5.3820	aspartate carbamoyltransferase	13.1.1.2 amino acid metabolism	11	92
TB927.7.4390	threonine synthase	13.2 amino acid metabolism	1	50
TB927.6.2790	L-threonine 3-dehydrogenase	13.2 amino acid metabolism	14	107
TB11.02.5400	cystathionine beta-synthase	13.1.2.3.11 amino acid metabolism	13	73
TB09.160.4590	arginine kinase	13.1.1 amino acid metabolism	5	56
TB09.160.4310	glutamate dehydrogenase	13 amino acid metabolism	10	93
TB09.211.3330	cystathione gamma lyase	13.1.1 amino acid metabolism	8	100
TB927.5.3800	carbomoyl phosphate synthase	13.1.2.3.11 amino acid metabolism	27	74
TB927.6.4840	S-adenosylmethionine synthetase	13.1.3.4 amino acid metabolism	16	85
TB10.389.1810	kynurenine aminotransferase	13.1.1.2 amino acid metabolism	12	90
TB09.160.4570	arginine kinase	13.1.1 amino acid metabolism	14	82
TB09.160.1950	acidocalcisomal exopolyphosphatase	13.1.5.1.3 amino acid metabolism	4	71
TB09.160.0810	kynureninase	13.1.1 amino acid metabolism	2	49
TB11.02.2740	aspartate aminotransferase mitochondrial	13.1.1.2 amino acid metabolism	1	49
TB927.7.5920	mercaptopyruvate sulfurtransferase	13.2.5.3 amino acid metabolism	1	52
TB10.70.4280	delta-1-pyrroline-5-carboxylate dehydrogenase	13.2.2.2 amino acid metabolism	4	42
TB927.2.4590	branched-chain amino acid aminotransferase	13 amino acid metabolism	2	60
TB927.7.2440	pyrroline-5-carboxylate reductase	13.2.2.2 amino acid metabolism	1	36
TB11.01.0420	protein transport protein Sec13	29.3.4.4 protein.targeting.secretory pathway.plasma membrane	1	79
TB10.70.1190	valosin-containing protein homolog	29.3 protein.targeting	2	79
TB927.8.1600	lysyl-tRNA synthetase	29.1 protein.aa activation	3	92
TB10.6K15.1220	isoleucyl-tRNA synthetase	29.1 protein.aa activation	39	85
TB11.02.1210	leucyl-tRNA synthetase	29.1 protein.aa activation	35	126
TB927.7.2400	tyrosyl-tRNA synthetase	29.1 protein.aa activation	6	102
TB927.6.700	alanyl-tRNA synthetase	29.1 protein.aa activation	23	94
TB11.01.1400	glycyl-tRNA synthetase	29.1 protein.aa activation	2	84
TB10.389.0630	prolyl-tRNA synthetase	29.1 protein.aa activation	10	88

TB11.46.0008	arginyl-tRNA synthetase	29.1 protein.aa activation	32	83
TB927.8.5330	tyrosyl/methionyl-tRNA synthetase	29.1 protein.aa activation	4	86
TB927.5.1090	threonyl-tRNA synthetase	29.1 protein.aa activation	1	70
TB09.160.3730	glutaminyl-tRNA synthetase	29.1 protein.aa activation	8	70
TB10.70.6470	methionyl-tRNA synthetase	29.1 protein.aa activation	16	85
TB927.4.2310	asparaginyl-tRNA synthetase	29.1 protein.aa activation	17	90
TB11.22.0005	phenylalanyl-tRNA synthetase	29.1 protein.aa activation	1	48
TB927.6.1880	aspartyl-tRNA synthetase	29.1 protein.aa activation	1	63
TB927.7.3620	tyrosyl-tRNA synthetase	29.1 protein.aa activation	4	65
TB927.6.4590	glutamyl-tRNA synthetase	29.1 protein.aa activation	7	111
TB927.6.4480	valyl-tRNA synthetase	29.1 protein.aa activation	29	79
TB927.7.4970	glutamine synthetase	12.2.2 N-metabolism.ammonia metabolism.glutamine synthase	6	73
TB09.V1.0380	spermidine synthase	22.1.7 polyamine metabolism.synthesis.spermine synthase	13	76
TB09.160.0770	nitrilase	22.1.5 polyamine metabolism	14	68
TB11.02.1085	40s ribosomal protein S4	29.2.4 protein.synthesis.elongation	10	97
TB10.70.2650	elongation factor 2	29.2.4 protein.synthesis.elongation	37	122
TB11.01.2560	40S ribosomal protein SA	29.2.4 protein.synthesis.elongation	3	92
TB09.160.3270	eukaryotic initiation factor 4a	29.2 protein.synthesis	11	72
TB09.211.4550	60S ribosomal protein L12	29.2.4 protein.synthesis.elongation	3	49
TB10.70.5680	elongation factor 1-alpha	29.2.4 protein.synthesis.elongation	4	68
TB09.211.0110	60S ribosomal protein L10	29.2.4 protein.synthesis.elongation	5	75
TB927.6.5120	60S acidic ribosomal protein P2	29.2.4 protein.synthesis.elongation	3	60
TB09.244.2730	60S ribosomal protein L5	29.2.4 protein.synthesis.elongation	7	73
TB11.01.4660	elongation factor 1 gamma	29.2.4 protein.synthesis.elongation	5	73
TB09.244.2630	40S ribosomal protein S6	29.2.4 protein.synthesis.elongation	1	65
TB10.70.1100	translation elongation factor 1-beta	29.2.4 protein.synthesis.elongation	1	77
TB09.160.3670	ribosomal protein S6	29.2.4 protein.synthesis.elongation	2	50
TB11.02.4000	40S ribosomal protein S15a	29.2.4 protein.synthesis.elongation	1	47
TB10.05.0220	60S ribosomal protein L10a	29.2.4 protein.synthesis.elongation	4	82
TB09.160.4200	60S acidic ribosomal protein	29.2.4 protein.synthesis.elongation	2	77
TB10.70.3360	40S ribosomal protein S3a	29.2.4 protein.synthesis.elongation	8	102
TB10.61.1960	40S ribosomal protein S2	29.2.4 protein.synthesis.elongation	3	49
TB11.02.4030	eukaryotic release factor 3	29.2 protein.synthesis	3	73
TB927.4.3550	60S ribosomal protein L13a	29.2.4 protein.synthesis.elongation	3	55
TB11.03.0410	eukaryotic translation initiation factor 5a	29.2 protein.synthesis	4	71

TB10.70.5650	elongation factor 1-alpha	29.2.4 protein.synthesis.elongation	1	69
TB927.8.550	peptide methionine sulfoxide reductase	29.11* protein.methione sulfoxide reductases	2	56
TB09.211.0120	nascent polypeptide associated complex subunit	29.2.4 protein.synthesis.elongation	2	47
TB09.160.5580	60S ribosomal protein L11	29.2.4 protein.synthesis.elongation	1	81
TB10.70.7695	40S ribosomal protein S11	29.2.4 protein.synthesis.elongation	1	54
TB927.6.4980	40S ribosomal protein S14	29.2.4 protein.synthesis.elongation	2	63
TB11.50.0005	60S ribosomal protein L21E	29.2.4 protein.synthesis.elongation	1	30
TB927.4.3570	translation elongation factor 1-beta	29.2.4 protein.synthesis.elongation	3	69
TB10.70.1770	eukaryotic translation initiation factor 6	29.2 protein.synthesis	6	87
TB11.01.7535	60S ribosomal protein L27	29.2.4 protein.synthesis.elongation	2	31
TB10.70.1730	40S ribosomal protein S18	29.2.4 protein.synthesis.elongation	4	54
TB11.01.7960	60S ribosomal protein L2	29.2.4 protein.synthesis.elongation	2	68
TB927.5.1820	60S acidic ribosomal protein	29.2.4 protein.synthesis.elongation	1	86
TB09.211.4850	60S ribosomal protein L26	29.2.4 protein.synthesis.elongation	1	43
TB09.160.4450	40S ribosomal protein S3	29.2.4 protein.synthesis.elongation	4	102
TB10.26.0560	60S ribosomal protein L6	29.2.4 protein.synthesis.elongation	4	100
TB927.7.1040	40S ribosomal protein S16	29.2.4 protein.synthesis.elongation	2	64
TB11.46.0001	60S acidic ribosomal subunit	29.2.4 protein.synthesis.elongation	5	81
TB10.6K15.2050	40S ribosomal protein S12	29.2.4 protein.synthesis.elongation	6	56
TB927.7.190	thimet oligopeptidase A, Family M3	29.5 protein.degradation	15	82
TB11.52.0003	oligopeptidase b; family S9A-like protein	29.5 protein.degradation	18	92
TB927.3.2090	aminopeptidase P1	29.5 protein.degradation	19	95
TB927.7.4070	calpain-like cysteine peptidase	29.5 protein.degradation	6	59
TB10.6K15.2520	prolyl oligopeptidase, family S9A	29.5 protein.degradation	18	95
TB11.02.0070	aminopeptidase, Family M17	29.5 protein.degradation	10	97
TB927.6.400	peptidase M20/M25/M40	29.5 protein.degradation	8	87
TB927.7.6270	peptidase T	29.5 protein.degradation	6	84
TB10.61.1870	aminopeptidase, Family M24	29.5 protein.degradation	10	59
TB927.8.7020	metallo-peptidase, Family M16	29.5 protein.degradation	19	77
TB927.8.8330	calpain	29.5 protein.degradation	1	83
TB927.1.2100	calpain-like cysteine peptidase, family C2	29.5 protein.degradation	23	82
TB927.8.1860	pitrilysin-like metalloprotease; Family M16C	29.5 protein.degradation	2	82
TB11.02.1070	aminopeptidase, Family M1	29.5 protein.degradation	30	131
TB927.3.4750	aminopeptidase, Family M1	29.5 protein.degradation	12	101

TB10.389.1480	cytosolic nonspecific dipeptidase, M20/M25/M40 family	29.5 protein.degradation	11	123
TB927.7.4060	calpain-like cysteine peptidase	29.5 protein.degradation	2	31
TB10.70.6620	methionine aminopeptidase 2, Family M24	29.5 protein.degradation	3	63
TB09.160.5550	calpain-like cysteine peptidase, family C2	29.5 protein.degradation	2	34
TB09.211.4330	aminopeptidase P, Family M24	29.5 protein.degradation	1	96
TB10.61.1210	methionine aminopeptidase, Family M24	29.5 protein.degradation	3	78
TB11.57.0008	calpain-like protein	29.5 protein.degradation	5	54
TB927.5.1730	ecotin	29.5 protein.degradation	1	37
TB09.211.3610	ubiquitin-activating enzyme E1	29.5.11 protein.degradation	17	112
TB11.02.0815	ubiquitin-conjugating enzyme	29.5.11 protein.degradation	7	65
TB10.70.3660	proteasome activator protein PA26	29.5.11.20 protein.degradation	1	80
TB09.211.0050	ubiquitin-conjugating enzyme E2	29.5.11 protein.degradation	3	51
TB11.02.4870	proteasome subunit alpha 7	29.5.11.20 protein.degradation	9	94
TB927.3.4840	ubiquitin hydrolase, putative	29.5.11 protein.degradation	9	73
TB10.100.0170	proteasome subunit alpha 2	29.5.11.20 protein.degradation	6	81
TB10.70.0850	proteasome subunit alpha 1	29.5.11.20 protein.degradation	5	82
TB927.8.2640	ubiquitin-activating enzyme E1	29.5.11 protein.degradation	18	83
TB927.3.780	proteasome alpha 7 subunit	29.5.11.20 protein.degradation	5	79
TB11.01.1680	polyubiquitin	29.5.11 protein.degradation	1	32
TB09.211.1250	proteasome subunit alpha 1	29.5.11.20 protein.degradation	3	70
TB927.7.4790	proteasome beta 6 subunit	29.5.11.20 protein.degradation	2	69
TB927.5.3210	small ubiquitin protein	29.5.11 protein.degradation	2	73
TB927.8.5210	cullin	29.5.11.4.3.3 protein.degradation	1	23
TB09.211.2590	proteasome subunit beta 2	29.5.11.20 protein.degradation	4	58
TB927.4.2710	ubiquitin-conjugating enzyme E2	29.5.11 protein.degradation	1	41
TB927.5.1000	ubiquitin-conjugating enzyme E2	29.5.11 protein.degradation	3	71
TB10.100.0120	proteasome subunit alpha 5	29.5.11.20 protein.degradation	4	66
TB11.01.5790	ubiquitin-conjugating enzyme E2	29.5.11 protein.degradation	1	41
TB927.7.4420	proteasome alpha 3 subunit	29.5.11.20 protein.degradation	8	72
TB927.6.1260	proteasome beta-1 subunit	29.5.11.20 protein.degradation	2	56
TB927.4.3620	serine/threonine-protein phosphatase PP1	29.4 protein.postranslational modification	3	58
TB11.01.8740	protein phosphatase 2A catalytic subunit	29.4 protein.postranslational modification	6	85
TB11.01.0450	serine/threonine protein phosphatase catalytic subunit	29.4 protein.postranslational modification	2	73
TB927.4.2110	protein phosphatase 2C	29.4 protein.postranslational modification	3	57
TB927.7.2080	methyltransferase	29.4 protein.postranslational modification	2	56

TB10.61.1880	protein kinase	29.4 protein.postranslational modification	3	42
TB927.8.5780	protein tyrosine phosphatase	29.4 protein.postranslational modification	1	41
TB927.5.1660	protein phosphatase 2C	29.4 protein.postranslational modification	1	23
TB927.5.3960	arginine N-methyltransferase	26.6 misc.O- methyl transferases	1	72
TB927.8.7340	trans-sialidase	29.5.11 protein.degradation	2	38
TB927.4.4650	diphthine synthase	26.6 misc.O- methyl transferases	5	93
TB11.01.2140	glycosyl hydrolase-like protein	26.3 misc.gluco-, galacto- and mannosidases	1	37
TB927.7.1300	protein disulfide isomerase	29.6 protein.(un)folding	1	80
TB09.211.1350	peptidyl-prolyl cis-trans isomerase (cyclophilin- 40)	29.6 protein.(un)folding	2	60
TB10.70.0280	chaperonin Hsp60	29.6 protein.(un)folding	13	109
TB11.02.5450	glucose-regulated protein 78	29.6 protein.(un)folding	8	114
TB10.389.0880	heat shock protein	29.6 protein.(un)folding	25	104
TB10.6K15.2330	t-complex protein 1 subunit theta	29.6 protein.(un)folding	11	86
TB11.01.4520	prefoldin subunit 2	29.6 protein.(un)folding	1	45
TB10.6K15.2000	chaperone protein DnaJ	29.6 protein.(un)folding	4	92
TB11.01.3080	heat shock protein 70	29.6 protein.(un)folding	1	51
TB11.01.3110	heat shock protein 70	29.6 protein.(un)folding	25	114
TB927.7.5790	protein disulfide isomerase	29.6 protein.(un)folding	3	53
TB10.26.1080	heat shock protein 83	29.6 protein.(un)folding	17	103
TB11.03.0250	cyclophilin A	29.6 protein.(un)folding	7	96
TB09.211.2570	t-complex protein 1 subunit eta	29.6 protein.(un)folding	2	75
TB927.8.3150	t-complex protein 1 gamma subunit	29.6 protein.(un)folding	3	82
TB11.01.5860	t-complex protein 1 subunit epsilon	29.6 protein.(un)folding	1	38
TB927.7.2590	prefoldin	29.6 protein.(un)folding	2	68
TB11.02.0250	heat shock protein mitochondrial precursor	29.6 protein.(un)folding	3	77
TB927.6.3740	heat shock 70 kDa protein	29.6 protein.(un)folding	23	121
TB927.7.710	heat shock 70 kDa protein	29.6 protein.(un)folding	11	97
TB927.7.570	prefoldin	29.6 protein.(un)folding	7	71
TB10.6K15.2290	protein disulfide isomerase	29.6 protein.(un)folding	8	57
TB11.02.2310	prostaglandin f synthase	30.99 signalling.unspecified	8	104
TB09.160.4520	calmodulin	30.3 signalling.calcium	1	43
TB11.01.4621	calmodulin	30.3 signalling.calcium	1	74
TB927.8.5440	flagellar calcium-binding protein TB-24	30.3 signalling.calcium	1	54
TB11.01.3170	guanine nucleotide-binding protein subunit beta	30.5 signalling.G-proteins	12	85
TB11.01.1290	14-3-3-like protein	30.7 signalling.14-3-3 proteins	10	100

TB11.02.4700	14-3-3-like protein	30.7 signalling.14-3-3 proteins	10	92
TB09.160.3710	proliferative cell nuclear antigen	31.3 cell.cycle	8	82
TB927.8.6750	translationally controlled tumor protein (TCTP)	31.3 cell.cycle	4	93
TB10.70.7040	cell division protein kinase 2 homolog 1	31.3 cell.cycle	1	67
TB11.01.8520	glucosamine-6-phosphate isomerase	7.1.2 OPP.oxidative PP	9	88
TB11.02.4200	6-phosphogluconolactonase	7.1.2 OPP.oxidative PP	4	72
TB927.8.5600	transaldolase	7.2.2 OPP.non-reductive PP	14	78
TB11.01.0700	ribose 5-phosphate isomerase	7.2.4 OPP.non-reductive PP	5	83
TB11.02.3040	aldo/keto reductase	3.5 minor CHO metabolism	1	43
TB927.8.980	phosphoacetylglucosamine mutase	3 minor CHO metabolism	14	101
TB11.03.0090	ribokinase	3.5 minor CHO metabolism.others	2	68
TB10.61.2880	aconitase	8.1.3 TCA / org. Transformation	12	108
TB927.3.2230	succinyl-CoA synthetase alpha subunit	8.1.6 TCA / org. Transformation	5	52
TB11.02.0290	succinyl-coA:3-ketoacid-coenzyme A transferase	8.1.6 TCA / org. Transformation	3	51
TB11.47.0004	2-oxoglutarate dehydrogenase subunit	8.1.5 TCA / org. Transformation	4	54
TB10.6K15.3250	succinyl-CoA ligase [GDP-forming] beta-chain	8.1.6 TCA / org. Transformation	5	68
TB11.01.1740	2-oxoglutarate dehydrogenase E1 component	8.1.5 TCA / org. Transformation	9	87
TB927.5.930	NADH-dependent fumarate reductase	8.1.7 TCA / org. Transformation	4	74
TB927.3.4500	fumarate hydratase	8.1.8 TCA / org. Transformation	28	107
TB10.389.1530	ribulose-5-phosphate 3-epimerase	1.3.11 PS.calvin cyle.RPE	3	64
TB11.01.3040	cytosolic malate dehydrogenase	6.3 gluconeogenesis	11	111
TB10.70.5110	mitochondrial malate dehydrogenase	6.3 gluconeogenesis	2	73
TB927.6.1570	2-hydroxy-3-oxopropionate reductase	6 gluconeogenese	7	64
TB11.02.3120	malic enzyme	6.3 gluconeogenesis.	11	103
TB10.61.0980	glycosomal malate dehydrogenase	6.3 gluconeogenesis	6	80
TB927.2.4210	glycosomal phosphoenolpyruvate carboxykinase	6.4 gluconeogenese	12	82
TB10.6K15.3850	glyceraldehyde 3-phosphate dehydrogenase cytosolic	4 glycolysis	9	102
TB10.6K15.2620	phosphoglycerate mutase	4.4.11 glycolysis	15	116
TB10.70.1370	fructose-bisphosphate aldolase glycosomal	4 glycolysis	8	104
TB11.02.3210	triosephosphate isomerase	4 glycolysis	8	82
TB11.02.4150	pyruvate phosphate dikinase	4 glycolysis	10	108
TB927.6.4280	glyceraldehyde 3-phosphate dehydrogenase, glycosomal	4 glycolysis	18	61
TB10.70.4740	enolase	4.12 glycolysis	22	129
TB927.1.3830	glucose-6-phosphate isomerase, glycosomal	4 glycolysis	1	73
TB927.3.1790	pyruvate dehydrogenase E1 beta subunit	4 glycolysis	2	64

TB927.1.710	phosphoglycerate kinase	4 glycolysis	8	91
TB10.70.5200	glucose-6-phosphate 1-dehydrogenase	4 glycolysis	1	39
TB10.70.0370	phosphomannomutase	3 CHO metabolism	7	78
TB11.01.6410	phosphomannose isomerase	3 CHO metabolism	1	60
TB927.1.2340	alpha tubulin	31.1 cell.organisation	18	133
TB09.211.0740	p21 antigen protein	31.6* cell organization	1	56
TB11.01.5100	paraflagellar rod component	31.1 cell.organisation	6	90
TB09.211.4511	kinetoplastid membrane protein KMP-11	31.1 cell.organisation	4	46
TB927.3.4290	73 kDa paraflagellar rod protein	31.1 cell.organisation	12	73
TB927.8.4970	69 kDa paraflagellar rod protein	31.1 cell.organisation	23	92
TB10.406.0560	microtubule-associated protein	31.1 cell.organisation	4	56
TB927.3.5180	cofilin/actin depolymerizing factor	31.1 cell.organisation	3	71
TB927.7.3440	I/6 autoantigen	31.1 cell.organisation	2	61
TB927.4.3950	cytoskeleton-associated protein CAP5.5	31.1 cell.organisation	11	86
TB927.4.2070	antigenic protein	31.6* cell organization	4	77
TB927.8.6200	tubulin folding cofactor D	31.1 cell.organisation	8	64
TB927.1.2330	beta tubulin	31.1 cell.organisation	15	91
TB11.01.5350	profilin	31.1 cell.organisation	2	79
TB10.406.0650	microtubule-associated protein	31.1 cell.organisation	3	75
TB11.02.3390	dynein light chain	31.1 cell.organisation	2	65
TB09.211.0620	actin A	31.1 cell.organisation	2	50
TB927.7.3160	dynein heavy chain, cytosolic	31.1 cell.organisation	1	29
TB09.160.1200	mitotubule-associated protein Gb4	31.1 cell.organisation	1	29
TB11.02.1120	adenylosuccinate synthetase	23.1.2 nucleotide metabolism	20	89
TB927.3.3450	ADP-ribosylation factor-like protein 3A	23 nucleotide metabolism	7	75
TB927.7.2100	GMP synthase	23.1.2.31 nucleotide metabolism	13	90
TB927.8.2050	mannose-1-phosphate guanyltransferase	23 nucleotide metabolism	2	87
TB11.V4.0004	ribonucleoside-diphosphate reductase small chain	23 nucleotide metabolism	6	66
TB09.211.4460	ADP-ribosylation factor	23 nucleotide metabolism	5	81
TB927.7.7530	receptor-type adenylate cyclase GRESAG 4	23 nucleotide metabolism	1	26
TB927.7.1780	adenine phosphoribosyltransferase	23 nucleotide metabolism	4	81
TB927.7.4570	nucleoside hydrolase	23 nucleotide metabolism	10	79
TB927.7.5160	deoxyuridine triphosphatase	23 nucleotide metabolism	6	91
TB927.3.2960	inosine-adenosine-guanosine-nucleoside hydrolase	23 nucleotide metabolism	5	81
TB927.2.5660	adenylate kinase	23.1.2 nucleotide metabolism	4	56

TB11.02.4140	inositol-1,4,5-trisphosphate 5-phosphatase	23.1.2 nucleotide metabolism	1	54
TB10.70.7330	adenylate kinase	23.1.2 nucleotide metabolism	2	58
TB927.4.3320	uracil phosphoribosyltransferase	23.3.1.3 nucleotide metabolism	5	49
TB10.70.6540	hypoxanthine-guanine phosphoribosyltransferase	23.1.2 nucleotide metabolism	1	46
TB11.01.7800	nucleoside diphosphate kinase	23 nucleotide metabolism	9	92
TB927.7.4480	adenosine 5'-monophosphoramidase	23 nucleotide metabolism	5	66
TB09.160.4250	tryparedoxin peroxidase	21.5 redox.peroxiredoxins	9	67
TB10.406.0520	trypanothione reductase	21.2 redox.ascorbate and glutathione	11	82
TB927.3.3760	tryparedoxin	21.5 redox.peroxiredoxins	5	61
TB927.7.1120	trypanothione/tryparedoxin dependent peroxidase 1	21.5 redox.peroxiredoxins	1	50
TB927.7.1140	trypanothione/tryparedoxin dependent peroxidase 3	21.5 redox.peroxiredoxins	1	25
TB927.7.1130	trypanothione/tryparedoxin dependent peroxidase 2	21.5 redox.peroxiredoxins	5	60
TB927.2.4370	trypanothione synthetase	21.2.2 redox.ascorbate and glutathione.glutathione	11	86
TB11.47.0012	glutaredoxin	21.4 redox.glutaredoxins	2	42
TB11.02.0490	RNA editing complex protein MP46	27.1 RNA.processing	1	28
TB09.211.2150	poly(A)-binding protein 1	27.3 RNA.regulation of transcription	5	61
TB927.2.5850	small nuclear ribonucleoprotein	27.1 RNA.processing	2	75
TB927.8.740	nucleolar RNA-binding protein, truncated	27.4 RNA.RNA binding	1	24
TB10.70.5360	La protein	27.4 RNA.RNA binding	8	87
TB11.55.0009	mitochondrial RNA-binding protein 1	27.4 RNA.RNA binding	1	42
TB927.8.6440	RNA-binding protein	27.4 RNA.RNA binding	1	24
TB10.61.2130	ATP-dependent DEAD/H RNA helicase	27.5* RNA.DEAD/DEAH BOX helicase	5	85
TB927.3.2600	ATP-dependent DEAD/H RNA helicase, putative	27.5* RNA.DEAD/DEAH BOX helicase	31	90
TB10.70.3290	ATP-dependent DEAD-box RNA helicase	27.5* RNA.DEAD/DEAH BOX helicase	5	93
TB927.7.4900	5'-3' exonuclease XRNA	28.1 DNA.synthesis/chromatin structure	1	24
TB10.70.0800	universal minicircle sequence binding protein (UMSBP)	28.1 DNA.synthesis/chromatin structure	3	85
TB10.406.0330	histone H2B	28.1 DNA.synthesis/chromatin structure	4	83
TB11.01.0870	replication factor A 51kDa subunit	28.1 DNA.synthesis/chromatin structure	1	48
TB927.7.2820	histone H2A	28.1 DNA.synthesis/chromatin structure	2	67
TB927.5.4170	histone H4	28.1 DNA.synthesis/chromatin structure	2	99
TB927.7.7040	methylthioadenosine phosphorylase, putative	28.1 DNA.synthesis/chromatin structure	5	47
TB927.2.2670	histone H4	28.1 DNA.synthesis/chromatin structure	1	25
TB927.5.1700	replication Factor A 28 kDa subunit, putative	28.1 DNA.synthesis/chromatin structure	1	52
TB09.160.4090	DNA topoisomerase II	28.1 DNA.synthesis/chromatin structure	1	28
TB09.160.1240	hypothetical protein	35.1 not assigned.no ontology	1	55

TB927.5.1460	hypothetical protein	35.1 not assigned.no ontology	6	70
TB09.211.0900	hypothetical protein	35.1 not assigned.no ontology	1	61
TB10.406.0280	hypothetical protein	35.1 not assigned.no ontology	3	73
TB927.5.2930	hypothetical protein	35.1 not assigned.no ontology	6	64
TB11.01.7010	hypothetical protein	35.1 not assigned.no ontology	23	114
TB927.4.2030	hypothetical protein	35.1 not assigned.no ontology	3	74
TB927.2.340	retrotransposon hot spot (RHS)	35.1 not assigned.no ontology	7	67
TB927.7.6090	hypothetical protein	35.1 not assigned.no ontology	2	74
TB10.70.2770	stress-inducible protein STI1-like	35.2 not assigned.unknown	8	86
TB927.5.2940	stress-induced protein sti1	35.2 not assigned.unknown	8	79
TB927.2.470	retrotransposon hot spot (RHS)	35.1 not assigned.no ontology	4	88
TB11.42.0004	hypothetical protein	35.1 not assigned.no ontology	3	67
TB927.4.3740	hypothetical protein	35.1 not assigned.no ontology	6	93
TB09.160.4480	hypothetical protein	35.1 not assigned.no ontology	1	29
TB927.3.2100	hypothetical protein	35.1 not assigned.no ontology	11	81
TB927.6.2200	hypothetical protein	35.1 not assigned.no ontology	4	85
TB11.01.0120	haloacid dehalogenase-like hydrolase	35.1 not assigned.no ontology	2	63
TB10.6K15.1900	hypothetical protein	35.1 not assigned.no ontology	7	89
TB927.4.4660	hypothetical protein	35.1 not assigned.no ontology	6	75
TB927.5.1280	hypothetical protein	35.1 not assigned.no ontology	5	93
TB11.01.5780	hypothetical protein	35.1 not assigned.no ontology	3	63
TB09.211.0560	hypothetical protein	35.1 not assigned.no ontology	5	66
TB927.4.360	hypothetical protein	35.1 not assigned.no ontology	3	91
TB927.8.3790	hypothetical protein	35.1 not assigned.no ontology	1	60
TB10.70.4930	hypothetical protein	35.1 not assigned.no ontology	7	67
TB927.1.220	retrotransposon hot spot (RHS)	35.1 not assigned.no ontology	6	57
TB09.211.3140	hypothetical protein	35.1 not assigned.no ontology	1	54
TB927.6.2280	hypothetical protein	35.1 not assigned.no ontology	4	55
TB927.2.280	retrotransposon hot spot (RHS)	35.1 not assigned.no ontology	4	59
TB11.01.5680	hypothetical protein	35.1 not assigned.no ontology	3	70
TB927.5.1360	hypothetical protein	35.1 not assigned.no ontology	4	50
TB09.160.1160	hypothetical protein	35.1 not assigned.no ontology	4	76
TB11.01.5570	hypothetical protein	35.1 not assigned.no ontology	2	72
TB10.61.0540	hypothetical protein	35.1 not assigned.no ontology	4	72
TB09.160.5100	hypothetical protein	35.1 not assigned.no ontology	10	68

TB927.3.4040	hypothetical protein	35.1 not assigned.no ontology	5	80
TB927.7.5950	hypothetical protein	35.1 not assigned.no ontology	1	50
TB927.6.4140	hypothetical protein	35.1 not assigned.no ontology	1	56
TB09.211.4360	hypothetical protein	35.1 not assigned.no ontology	4	75
TB09.160.4460	hypothetical protein	35.1 not assigned.no ontology	9	50
TB09.160.2350	hypothetical protein	35.1 not assigned.no ontology	2	78
TB927.3.4880	hypothetical protein	35.1 not assigned.no ontology	3	47
TB11.02.0870	hypothetical protein	35.1 not assigned.no ontology	7	63
TB927.5.2160	hypothetical protein	35.1 not assigned.no ontology	3	97
TB927.7.2980	hypothetical protein	35.1 not assigned.no ontology	3	65
TB10.26.0960	hypothetical protein	35.1 not assigned.no ontology	2	66
TB11.01.8770	hypothetical protein	35.1 not assigned.no ontology	12	88
TB11.02.4250	hypothetical protein	35.1 not assigned.no ontology	3	75
TB11.01.6740	hypothetical protein	35.1 not assigned.no ontology	3	60
TB927.8.6660	hypothetical protein	35.1 not assigned.no ontology	2	41
TB927.4.1300	hypothetical protein	35.1 not assigned.no ontology	11	73
TB11.02.1690	hypothetical protein	35.1 not assigned.no ontology	9	112
TB927.6.4770	hypothetical protein	35.1 not assigned.no ontology	5	75
TB11.01.4740	hypothetical protein	35.1 not assigned.no ontology	2	86
TB927.4.2740	hypothetical protein	35.1 not assigned.no ontology	5	61
TB11.02.2030	hypothetical protein	35.1 not assigned.no ontology	4	85
TB927.3.5310	hypothetical protein	35.1 not assigned.no ontology	4	54
TB927.2.450	retrotransposon hot spot (RHS) protein	35.1 not assigned.no ontology	14	77
TB09.211.3300	hypothetical protein	35.1 not assigned.no ontology	2	56
TB927.2.240	retrotransposon hot spot (RHS) protein	35.1 not assigned.no ontology	2	46
TB927.1.420	retrotransposon hot spot (RHS) protein	35.1 not assigned.no ontology	1	26
TB927.7.4520	hypothetical protein	35.1 not assigned.no ontology	7	81
TB09.211.1620	hypothetical protein	35.1 not assigned.no ontology	20	65
TB927.1.1670	hypothetical protein	35.1 not assigned.no ontology	3	57
TB927.2.1170	retrotransposon hot spot (RHS) protein	35.1 not assigned.no ontology	5	73
TB11.01.5440	hypothetical protein	35.1 not assigned.no ontology	1	69
TB927.2.5150	hypothetical protein	35.1 not assigned.no ontology	1	21
TB927.3.1010	hypothetical protein	35.1 not assigned.no ontology	2	73
TB10.70.6610	hypothetical protein	35.1 not assigned.no ontology	2	74
TB11.47.0011	hypothetical protein	35.1 not assigned.no ontology	1	34

TB10.70.0860	hypothetical protein	35.1 not assigned.no ontology	1	29
TB10.70.1130	hypothetical protein	35.1 not assigned.no ontology	2	104
TB927.5.440	hypothetical protein	35.1 not assigned.no ontology	1	53
TB11.01.8610	hypothetical protein	35.1 not assigned.no ontology	1	27
TB927.5.2260	hypothetical protein	35.1 not assigned.no ontology	2	48
TB927.6.1530	hypothetical protein	35.1 not assigned.no ontology	3	46
TB11.02.4760	hypothetical protein	35.1 not assigned.no ontology	1	23
TB927.3.3510	hypothetical protein	35.1 not assigned.no ontology	1	23
TB927.7.4290	hypothetical protein	35.1 not assigned.no ontology	3	53
TB10.6K15.1910	hypothetical protein	35.1 not assigned.no ontology	1	27
TB09.211.1050	hypothetical protein	35.1 not assigned.no ontology	1	22
TB10.26.0385	hypothetical protein	35.1 not assigned.no ontology	1	49
TB09.211.1950	hypothetical protein	35.1 not assigned.no ontology	1	75
TB09.160.0465	hypothetical protein	35.1 not assigned.no ontology	1	44
TB927.4.1890	hypothetical protein	35.1 not assigned.no ontology	3	67
TB927.7.4270	hypothetical protein	35.1 not assigned.no ontology	2	47
TB10.6K15.3240	hypothetical protein	35.1 not assigned.no ontology	1	65
TB11.02.3760	hypothetical protein	35.1 not assigned.no ontology	1	55
TB11.02.0660	hypothetical protein	35.1 not assigned.no ontology	1	36
TB927.2.1180	retrotransposon hot spot (RHS) protein	35.1 not assigned.no ontology	1	25
TB927.6.2120	hypothetical protein	35.1 not assigned.no ontology	1	22
TB927.6.1950	hypothetical protein	35.1 not assigned.no ontology	2	70
TB11.01.2790	hypothetical protein	35.1 not assigned.no ontology	1	22
TB927.8.2080	hypothetical protein	35.1 not assigned.no ontology	1	73
TB927.2.100	retrotransposon hot spot (RHS) protein	35.1 not assigned.no ontology	3	49
TB11.01.4880	hypothetical protein	35.1 not assigned.no ontology	1	52
TB927.2.2770	hypothetical protein	35.1 not assigned.no ontology	1	51
TB10.61.3130	hypothetical protein	35.1 not assigned.no ontology	2	65
TB11.02.0210	hypothetical protein	35.1 not assigned.no ontology	2	60
TB927.6.3840	reticulon domain protein	31.99 cell.unspecified	1	52
TB927.5.3030	hypothetical protein	35.1 not assigned.no ontology	1	22
TB927.7.3550	hypothetical protein	35.1 not assigned.no ontology	1	24
TB927.3.3000	hypothetical protein	35.1 not assigned.no ontology	1	30
TB11.02.2040	hypothetical protein	35.1 not assigned.no ontology	3	50
TB10.70.5050	hypothetical protein	35.1 not assigned.no ontology	2	96

TB927.2.4580	hypothetical protein	35.1 not assigned.no ontology	2	49
TB927.3.4940	hypothetical protein	35.1 not assigned.no ontology	2	57
TB11.01.8590	hypothetical protein	35.1 not assigned.no ontology	1	85
TB927.8.1170	hypothetical protein	35.1 not assigned.no ontology	1	32
TB11.01.8030	hypothetical protein	35.1 not assigned.no ontology	1	67
TB927.7.4500	hypothetical protein	35.1 not assigned.no ontology	1	43
TB09.211.1690	hypothetical protein	35.1 not assigned.no ontology	1	75
TB10.389.1370	hypothetical protein	35.1 not assigned.no ontology	1	34
TB927.8.5890	hypothetical protein	35.1 not assigned.no ontology	3	27
TB927.4.380	hypothetical protein	35.1 not assigned.no ontology	1	34
TB10.61.3210	hypothetical protein	35.1 not assigned.no ontology	2	92
TB927.7.1010	hypothetical protein	35.1 not assigned.no ontology	1	24
TB11.02.5000	NGG1 interacting factor 3-like	35.1 not assigned.no ontology	1	37
TB927.6.5370	variant surface glycoprotein (VSG)	31.99 cell.unspecified	1	28
TB09.142.0230	variant surface glycoprotein	31.99 cell.unspecified	1	25
TB927.5.2700	otubain	35.2 not assigned.unknown	1	39

SHEET 3

Comparison between secretome of two procyclic strains (Biyamina and Stib 215)

Specific to procyclic Biyamina		Specific to procyclic Stib 215		common to Biyamina and Stib 215	
accession number	**protein names**	**accession number**	**protein names**	**accession number**	**protein names**
TB09.211.0350	adenylate kinase	TB927.7.1120	peroxidase 1, cytosolic	TB927.6.3740	heat shock 70 kDa protein
TB927.8.4430	nucleoside phosphorylase	TB09.160.1160	hypothetical protein	TB927.8.980	phosphoacetylglucosamine mutase
TB11.01.3020	40S ribosomal protein L14	TB927.1.4830	phospholipase A1	TB09.160.4560	arginine kinase
TB11.01.2530	kinesin-like protein	TB09.160.1240	hypothetical protein	TB927.8.6390	lysophospholipase
TB10.6K15.1160	G-actin binding protein	TB09.160.5580	60S ribosomal protein L11	TB927.7.710	heat shock 70 kDa protein
TB927.8.1330	60S ribosomal protein L7a	TB09.211.2570	t-complex protein 1	TB09.211.0120	nascent polypeptide associated complex subunit
TB927.6.2360	adenosine kinase	TB10.389.1180	P-type H+-ATPase	TB927.6.2740	pyridoxal kinase
TB11.01.4860	guide RNA-binding protein	TB927.8.8330	calpain	TB927.3.3900	carnitine O-palmitoyltransferase II
TB927.7.5210	hypothetical protein	TB927.6.1520	aquaporin 3	TB927.3.1380	ATP synthase beta chain
TB11.01.7740	hypothetical protein	TB927.4.4650	diphthine synthase	TB11.01.5440	hypothetical protein
TB11.02.2840	hypothetical protein	TB927.2.5150	hypothetical protein	TB927.6.4480	valyl-tRNA synthetase
TB927.7.2650	hypothetical protein	TB10.70.4720	importin subunit beta-1	TB11.02.4700	hypothetical protein
TB10.70.7090	serine carboxypeptidase	TB11.02.4000	40S ribosomal protein S15a	TB10.61.0980	glycosomal malate dehydrogenase
TB09.211.2360	protein kinase A	TB10.70.7040	cell division protein kinase	TB927.7.1040	40S ribosomal protein S16
TB927.1.180	retrotransposon hot spot protein	TB11.02.5000	interacting factor 3-like	TB10.70.7695	40S ribosomal protein S11
TB927.2.4610	amino acid aminotransferase	TB927.5.4170	histone H4	TB927.3.4500	fumarate hydratase
TB927.4.4070	mevalonate kinase	TB10.61.1880	protein kinase	TB11.46.0001	60S acidic ribosomal subunit protein
TB927.5.1160	hypothetical protein	TB927.8.3150	t-complex protein 1	TB10.6K15.2050	40S ribosomal protein S12
TB927.3.3310	60S ribosomal protein L13	TB10.70.6610	hypothetical protein	TB10.70.6620	methionine aminopeptidase 2
TB927.5.3580	phosphoglycerate mutase	TB09.160.5550	calpain	TB927.1.2340	alpha tubulin
TB927.2.510	retrotransposon hot spot protein	TB11.47.0011	hypothetical protein	TB11.01.7800	nucleoside diphosphate kinase
TB10.70.1380	40S ribosomal protein S9	TB927.7.5950	hypothetical protein	TB927.2.5060	GTP binding protein
TB927.7.280	cyclophilin	TB11.47.0004	2-oxoglutarate dehydrogenase	TB10.389.1530	ribulose-5-phosphate 3-epimerase

TB10.389.1260	hypothetical protein
TB927.7.3170	hypothetical protein
TB11.02.0690	hypothetical protein
TB927.5.700	hypothetical protein
TB927.8.4780	hypothetical protein
TB11.02.2520	hypothetical protein
TB09.142.0100	variant surface glycoprotein
TB927.8.5120	cytochrome c
TB10.26.0200	guanylate kinase
TB09.211.2540	calmodulin-like protein
TB927.2.2130	rab6 small GTP-binding protein
TB927.7.1730	60S ribosomal protein L7
TB11.01.3550	2-oxoglutarate dehydrogenase
TB11.02.4170	40S ribosomal protein S5
TB10.6K15.0080	hypothetical protein
TB11.01.3805	microtubule-associated protein
TB927.1.3170	hypothetical protein
TB927.3.5550	small GTP-binding protein
TB927.5.1710	ribonucleoprotein p18
TB11.01.8200	enoyl-CoA hydratase
TB10.6K15.0290	hypothetical protein
TB927.3.3610	targeting signal type 2 receptor
TB927.4.5010	calreticulin
TB11.01.8390	hypothetical protein
TB927.7.3330	hypothetical protein
TB10.6K15.3160	fibrillarin
TB10.389.1730	protein kinase
TB927.6.950	cysteinyl-tRNA synthetase
TB10.61.2550	N-myristoyl transferase
TB11.01.7550	iron superoxide dismutase
TB927.5.950	thioredoxin-like protein
TB09.211.3180	6-phosphogluconate dehydrogenase
TB11.03.0335	hypothetical protein
TB11.47.0016	hypothetical protein
TB927.3.5340	Hsc70-interacting protein (Hip)
TB927.7.7530	GRESAG 4
TB927.8.6440	RNA-binding protein
TB10.70.0860	hypothetical protein
TB927.7.4900	5'-3' exonuclease XRNA
TB09.211.0900	hypothetical protein
TB927.5.440	hypothetical protein
TB10.406.0280	hypothetical protein
TB09.160.1950	exopolyphosphatase
TB927.5.2930	hypothetical protein
TB927.8.1860	pitrilysin-like metalloprotease
TB927.5.3210	small ubiquitin protein
TB11.01.2140	glycosyl hydrolase-like protein
TB927.6.4140	hypothetical protein
TB09.160.0810	kynureninase
TB09.211.4360	hypothetical protein
TB09.211.4330	aminopeptidase P
TB09.160.4460	hypothetical protein
TB927.6.5370	variant surface glycoprotein
TB927.6.1530	hypothetical protein
TB11.02.4760	hypothetical protein
TB09.160.2350	hypothetical protein
TB11.01.7010	hypothetical protein
TB927.3.3510	hypothetical protein
TB927.7.4290	hypothetical protein
TB927.4.1080	V-type ATPase, A subunit
TB10.6K15.1910	hypothetical protein
TB09.211.3610	ubiquitin-activating enzyme E1
TB927.8.7340	trans-sialidase
TB927.5.2700	otubain
TB927.7.6090	hypothetical protein
TB09.211.1050	hypothetical protein
TB10.26.0385	hypothetical protein
TB927.3.4840	ubiquitin hydrolase
TB927.8.5210	cullin
TB11.42.0004	hypothetical protein
TB927.7.4790	proteasome beta 6 subunit
TB10.6K15.2290	protein disulfide isomerase
TB11.02.3390	dynein light chain
TB11.47.0012	glutaredoxin
TB927.7.7040	methylthioadenosine phosphorylase
TB927.6.4590	glutamyl-tRNA synthetase
TB927.5.1460	hypothetical protein
TB927.7.570	prefoldin
TB927.2.4210	glycosomal phosphoenolpyruvate carboxykinase
TB927.7.190	thimet oligopeptidase A, putative
TB10.70.1130	hypothetical protein
TB09.160.4520	calmodulin
TB11.55.0009	mitochondrial RNA-binding protein 1
TB09.211.0620	actin A
TB11.02.1085	40s ribosomal protein S4
TB09.211.3550	glycerol kinase glycosomal
TB11.52.0003	oligopeptidase b
TB11.01.3040	cytosolic malate dehydrogenase
TB11.01.1350	S-adenosylhomocysteine hydrolase
TB927.5.2260	hypothetical protein
TB09.211.0740	p21 antigen protein
TB10.70.2650	elongation factor 2
TB927.3.2090	aminopeptidase P1
TB927.6.4980	40S ribosomal protein S14
TB927.7.4070	calpain-like cysteine peptidase
TB927.4.2030	hypothetical protein
TB927.2.340	retrotransposon hot spot (RHS) protein
TB10.70.2770	stress-inducible protein STI1-like
TB927.5.2940	stress-induced protein sti1
TB11.01.2560	40S ribosomal protein SA
TB09.160.3270	eukaryotic initiation factor 4a
TB09.211.1950	hypothetical protein
TB927.2.470	retrotransposon hot spot protein
TB927.8.3530	glycerol-3-phosphate dehydrogenase
TB927.6.1080	hydroxyacylglutathione hydrolase

TB11.01.7120	hypothetical protein
TB10.6K15.0410	60S ribosomal protein L18
TB11.01.8510	t-complex protein 1 subunit alpha
TB11.01.2000	HslVU complex proteolytic subunit
TB927.8.1610	major surface protease gp63
TB11.02.3330	hypothetical protein
TB11.01.5590	hypothetical protein
TB10.389.1890	hypothetical protein
TB10.61.0620	hypothetical protein
TB927.4.5340	hypothetical protein
TB927.1.3200	phosphatase-like protein
TB927.4.430	proteasome beta 7 subunit
TB10.70.7020	40S ribosomal protein S23
TB927.4.890	small nuclear ribonucleoprotein
TB09.211.3540	glycerol kinase glycosomal
TB927.6.1030	cysteine peptidase precursor
TB927.5.1470	NADH-cytochrome b5 reductase
TB10.70.0790	proteasome subunit beta 5
TB09.160.4620	inositol-1(or 4)-monophosphatase
TB927.1.700	phosphoglycerate kinase
TB11.03.0390	protein phosphatase 2C
TB927.7.4770	cyclophilin
TB10.05.0010	diphosphomevalonate decarboxylase
TB927.3.5580	tryptophanyl-tRNA synthetase
TB927.5.3830	dihydroorotate dehydrogenase
TB11.01.7325	hypothetical protein
TB927.7.2710	NADH-cytochrome b5 reductase
TB11.02.4440	aminopeptidase
TB927.6.2090	hypothetical protein
TB927.7.6890	hypothetical protein
TB927.3.1120	GTP-binding nuclear protein rtb2
TB927.5.2640	hypothetical protein
TB927.8.5630	dihydroorotase
TB11.02.4830	protein kinase
TB927.3.4680	RAB GDP dissociation inhibitor alpha
TB927.4.1890	hypothetical protein
TB927.4.3620	serine/threonine-phosphatase
TB11.02.5380	exosome complex exonuclease
TB927.2.2670	histone H4
TB11.01.5100	paraflagellar rod component
TB927.7.4270	hypothetical protein
TB927.6.700	alanyl-tRNA synthetase
TB09.142.0230	variant surface glycoprotein
TB11.01.4520	prefoldin subunit 2
TB10.6K15.3240	hypothetical protein
TB11.02.4140	inositol-1,4,5-trip 5-phosphatase
TB10.6K15.2000	chaperone protein DnaJ
TB927.8.5780	protein tyrosine phosphatase
TB10.70.7330	adenylate kinase
TB11.02.3760	hypothetical protein
TB927.8.1600	lysyl-tRNA synthetase
TB11.02.3040	aldo/keto reductase
TB10.6K15.2840	protein transport protein Sec23A
TB10.61.2130	DEAD/H RNA helicase
TB11.01.0120	hydrolase
TB927.2.1180	retrotransposon hot spot protein
TB11.01.1400	glycyl-tRNA synthetase
TB927.6.2120	hypothetical protein
TB927.6.1950	hypothetical protein
TB927.7.5920	sulfurtransferase
TB927.4.2710	ubiquitin-conjugating enzyme E2
TB11.01.2790	hypothetical protein
TB927.8.2080	hypothetical protein
TB10.26.0960	hypothetical protein
TB11.22.0005	phenylalanyl-tRNA synthetase
TB927.4.2110	protein phosphatase 2C
TB11.01.7535	60S ribosomal protein L27
TB10.70.5200	glucose-6-phos1-dehydrogenase
TB11.01.5780	hypothetical protein
TB927.2.2770	hypothetical protein
TB927.4.3740	hypothetical protein
TB09.160.4480	hypothetical protein
TB09.211.2590	proteasome subunit beta 2
TB09.211.4550	60S ribosomal protein L12
TB11.01.6410	phosphomannose isomerase
TB927.3.2100	hypothetical protein
TB11.01.8520	glucosamine-6-phosphate isomerase
TB11.03.0090	ribokinase
TB927.5.1660	protein phosphatase 2C
TB09.160.4250	tryparedoxin peroxidase
TB927.7.1110	asparagine synthetase a
TB927.6.2200	hypothetical protein
TB927.6.2790	L-threonine 3-dehydrogenase
TB11.02.0660	hypothetical protein
TB11.02.1120	adenylosuccinate synthetase
TB11.02.5400	cystathionine beta-synthase
TB10.6K15.1900	hypothetical protein
TB927.7.1300	protein disulfide isomerase
TB10.70.4280	delta-1-pyrroline-5-carboxylate dehydrogenase
TB927.4.3570	translation elongation factor 1-beta
TB09.160.4590	arginine kinase
TB927.4.4660	hypothetical protein
TB11.01.8740	protein phosphatase 2A catalytic subunit
TB11.01.0450	serine/threonine protein phosphatase
TB10.70.5680	elongation factor 1-alpha
TB09.211.1350	cyclophilin- 40
TB927.5.1000	ubiquitin-conjugating enzyme E2
TB10.70.1770	eukaryotic translation initiation factor 6
TB927.4.3320	uracil phosphoribosyltransferase
TB09.160.4310	glutamate dehydrogenase
TB927.5.1280	hypothetical protein
TB10.6K15.2520	prolyl oligopeptidase
TB09.211.4511	kinetoplastid membrane protein KMP-11
TB09.211.0110	60S ribosomal protein L10
TB09.211.3330	cystathione gamma lyase

TB10.70.2180	hypothetical protein
TB11.02.3595	SUI1-like protein
TB11.02.0750	t-complex protein 1 subunit zeta
TB10.6K15.0970	phosphoribosylpyrophosphate synthetase
TB11.47.0036	calpain
TB927.6.4990	ATP synthase, epsilon chain
TB10.70.6660	hypox-guanine phosphoribosyltransferase
TB09.211.1380	glycine cleavage system H protein
TB10.70.2490	proteasome subunit beta 2
TB10.70.4880	eukaryotic translation initiation factor 5
TB927.4.2240	hypothetical protein
TB927.3.1030	hypothetical protein
TB11.02.4950	hypothetical protein
TB927.6.2420	p22 protein precursor
TB10.26.0680	hypothetical protein
TB11.55.0024	hypothetical protein
TB10.6K15.3600	myo-inositol-1-phosphate synthase
TB11.02.3130	malic enzyme
TB10.70.7050	t-complex protein 1 subunit delta
TB927.4.1220	leucine-rich repeat protein (LRRP)
TB10.70.1490	hypothetical protein
TB927.8.2740	mitochondrial RNA binding protein
TB11.01.4830	translation initiation factor 2 gamma
TB11.01.6660	iron superoxide dismutase
TB11.01.2120	hypothetical protein
TB11.02.3990	S-phase kinase-associated protein
TB09.160.5530	hypothetical protein
TB09.211.2330	small GTPase
TB11.02.5770	mitochondrial RNA-binding protein
TB927.7.2990	hypothetical protein
TB10.70.5150	adenylate kinase
TB11.03.0230	isocitrate dehydrogenase
TB927.5.4470	hypothetical protein
TB11.03.0620	hypothetical protein
TB10.70.7730	ATP-dependent DEAD/H RNA helicase
TB11.01.4880	hypothetical protein
TB11.02.4250	hypothetical protein
TB927.7.3160	dynein heavy chain, cytosolic
TB927.6.5120	60S acidic ribosomal protein P2
TB11.01.6740	hypothetical protein
TB10.389.0630	prolyl-tRNA synthetase
TB10.61.3130	hypothetical protein
TB927.8.6200	tubulin folding cofactor D
TB10.6K15.2020	glucose transporter
TB11.02.0070	aminopeptidase
TB927.5.3960	arginine N-methyltransferase
TB927.8.6660	hypothetical protein
TB11.01.5860	t-complex protein 1 subunit epsilon
TB927.6.3840	reticulon domain protein
TB927.5.3030	hypothetical protein
TB927.8.2640	ubiquitin-activating enzyme E1
TB927.7.3550	hypothetical protein
TB09.160.4680	geranylgeranyl transferase
TB11.01.5790	ubiquitin-conjugating enzyme E2
TB11.57.0008	calpain-like protein
TB09.244.2570	calcium motive p-type ATPase
TB927.3.3000	hypothetical protein
TB10.6K15.1220	isoleucyl-tRNA synthetase
TB09.160.2780	fatty acyl CoA synthetase 2
TB11.02.1690	hypothetical protein
TB927.5.1820	60S acidic ribosomal protein
TB927.8.3790	hypothetical protein
TB927.6.4770	hypothetical protein
TB927.5.3800	carbomoyl phosphate synthase
TB11.01.4740	hypothetical protein
TB927.5.1730	ecotin
TB11.02.4200	6-phosphogluconolactonase
TB927.8.7020	peptidase
TB09.211.3140	hypothetical protein
TB927.3.4940	hypothetical protein
TB11.02.0490	RNA editing complex protein MP46
TB10.70.1730	40S ribosomal protein S18
TB09.211.0560	hypothetical protein
TB09.160.0770	nitrilase
TB10.100.0120	proteasome subunit alpha 5
TB927.7.7420	ATP synthase alpha chain
TB927.3.2230	succinyl-CoA synthetase alpha subunit
TB927.7.6270	peptidase T, putative
TB10.61.1870	aminopeptidase
TB09.244.2730	60S ribosomal protein L5
TB10.406.0520	trypanothione reductase
TB927.7.4970	glutamine synthetase
TB10.6K15.3850	glyceraldehyde 3-phosphate dehydrogenase
TB927.4.360	hypothetical protein
TB11.01.4660	elongation factor 1 gamma
TB10.70.4930	hypothetical protein
TB11.01.1820	biotin--acetyl-CoA-carboxylase ligase
TB11.02.0815	ubiquitin-conjugating enzyme
TB11.02.2040	hypothetical protein
TB927.1.220	retrotransposon hot spot protein
TB927.3.4290	73 kDa paraflagellar rod protein
TB927.3.3450	ADP-ribosylation factor-like protein 3A
TB927.6.2280	hypothetical protein
TB10.6K15.2620	phosphoglycerate mutase
TB927.2.280	retrotransposon hot spot protein
TB927.7.2100	GMP synthase
TB10.70.1370	fructose-bisphosphate aldolase glycosomal
TB10.70.3660	proteasome activator protein PA26
TB11.01.5680	hypothetical protein
TB10.70.0370	phosphomannomutase
TB09.V1.0380	spermidine synthase
TB10.389.1370	hypothetical protein
TB10.70.0830	clathrin heavy chain
TB927.8.4970	69 kDa paraflagellar rod protein
TB927.6.4840	S-adenosylmethionine synthetase

TB927.2.1080	retrotransposon hot spot (RHS) protein	TB11.01.8590	hypothetical protein	TB09.211.0050	ubiquitin-conjugating enzyme E2
TB11.01.5320	small GTPase	TB927.8.1170	hypothetical protein	TB927.4.380	hypothetical protein
TB10.70.5800	hexokinase	TB927.7.4390	threonine synthase	TB10.70.1100	translation elongation factor 1-beta
TB10.70.4130	hypothetical protein	TB11.01.0870	replication factor A 51kDa subunit	TB11.01.3170	guanine nucleotide-binding protein -like protein
TB09.160.2540	alpha/beta-hydrolase-like protein	TB11.02.0250	heat shock protein	TB927.7.2440	pyrroline-5-carboxylate reductase
TB927.7.7500	iron/ascorbate oxidoreductase	TB11.01.8030	hypothetical protein	TB11.02.1210	leucyl-tRNA synthetase
TB927.5.3350	iron superoxide dismutase	TB927.7.45000	hypothetical protein	TB11.02.0290	3-ketoacid-coenzyme A transferase
TB11.02.2700	fumarate hydratase class I	TB09.244.2630	40S ribosomal protein S6	TB10.26.0560	60S ribosomal protein L6
TB927.8.3690	isocitrate dehydrogenase	TB927.7.2820	histone H2A	TB927.7.3620	tyrosyl-tRNA synthetase
TB09.211.2850	cyclophilin	TB927.8.7100	acetyl-CoA carboxylase	TB10.70.0280	chaperonin Hsp60
TB11.02.5170	proteasome subunit beta 3	TB11.01.0420	protein transport protein Sec13	TB09.160.3670	ribosomal protein S6
TB09.211.1370	glyceraldehyde-3-phosphate dehydrogenase	TB927.8.5890	hypothetical protein	TB927.3.3760	tryparedoxin
TB927.8.7510	p-nitrophenylphosphatase	TB11.01.5350	profilin	TB927.8.6170	transketolase, putative
TB10.05.0080	glucosidase	TB927.2.5660	adenylate kinase	TB10.389.1810	kynurenine aminotransferase
TB927.8.3380	electron transfer protein	TB10.61.3210	hypothetical protein	TB11.02.5450	glucose-regulated protein 78
TB927.6.3650	ADP-ribosylation factor	TB927.1.1670	hypothetical protein	TB11.02.3210	triosephosphate isomerase
TB927.5.2570	translation initiation factor	TB927.7.2080	methyltransferase	TB927.5.1360	hypothetical protein
TB11.02.2670	hypothetical protein	TB09.160.4090	DNA topoisomerase II	TB10.61.2880	aconitase
TB927.1.3390	hypothetical protein	TB927.8.2050	mannose-1-phosguanyltransferase	TB11.V4.0004	ribonucleoside-diphosphate reductase
TB927.6.2700	small nuclear ribonucleoprotein Sm-E	TB927.7.1010	hypothetical protein	TB927.8.2540	3-ketoacyl-CoA thiolase
TB10.05.0110	serine/threonine protein phosphatase type 5			TB10.6K15.3970	developmentally regulated GTP-binding protein
TB11.02.0140	hypothetical protein			TB11.02.4150	pyruvate phosphate dikinase
TB927.6.1000	cysteine peptidase precursor			TB927.7.4060	calpain-like cysteine peptidase
TB927.8.5030	trafficking protein particle complex subunit 3			TB11.01.5570	hypothetical protein
TB10.70.5820	hexokinase			TB10.61.0540	hypothetical protein
TB927.8.4210	hypothetical protein			TB10.406.0560	microtubule-associated protein
TB927.8.1140	hypothetical protein			TB09.160.4570	arginine kinase
TB09.211.3050	hypothetical protein			TB927.6.4280	glyceraldehyde 3-phosphate dehydrogenase
TB09.211.1695	small nuclear ribonucleoprotein Sm-F			TB09.160.5100	hypothetical protein
TB10.70.7950	hypothetical protein			TB927.6.400	peptidase M20/M25/M40
TB10.70.1320	N-acetyltransferase subunit Nat1			TB927.3.1010	hypothetical protein
TB927.8.7410	calreticulin			TB11.01.1680	polyubiquitin
TB09.211.2400	hypothetical protein			TB11.01.8470	dihydrolipoyl dehydrogenase
TB927.7.7460	hypothetical protein			TB927.3.4040	hypothetical protein
TB927.8.2000	cyclophilin			TB927.3.2600	ATP-dependent DEAD/H RNA helicase

TB11.02.0100	carboxypeptidase
TB927.8.6060	2-amino-3-ketobutyrate coenzyme A ligase
TB10.100.0070	ATP synthase F1 subunit gamma
TB10.61.0180	peptidylprolyl isomerase-like protein
TB927.4.3590	translation elongation factor 1-beta
TB927.8.6110	hypothetical protein
TB09.211.1510	small nuclear RNA gene activation protein 50
TB927.3.3410	aspartyl aminopeptidase
TB10.6K15.0510	60S ribosomal protein L22
TB09.211.4630	hypothetical protein
TB11.46.0003	protein kinase
TB927.8.7350	trans-sialidase
TB10.61.3180	calcium-dependent lipid binding protein
TB927.5.4560	guanine deaminase
TB927.6.2170	co-chaperone GrpE
TB927.7.1320	10 kDa heat shock protein
TB11.02.5020	seryl-tRNA synthetase
TB927.7.6770	hypothetical protein
TB927.8.5880	eukaryotic translation initiation factor 1A
TB927.1.120	retrotransposon hot spot (RHS) protein
TB927.6.4000	hypothetical protein
TB927.4.2040	hypothetical protein
TB10.70.3710	aspartate aminotransferase
TB927.4.1380	hypothetical protein
TB927.5.1880	ecotin
TB927.7.2700	NADH-cytochrome b5 reductase
TB10.6K15.0480	hypothetical protein
TB927.1.2260	calpain-like protein fragment
TB927.3.3330	heat shock protein 20
TB927.8.6760	IgE-dependent histamine-releasing factor
TB927.2.1560	cyclophilin
TB10.70.3510	60S ribosomal protein L18a
TB927.5.3400	calcium-translocating P-type ATPase
TB11.01.0290	carbonic anhydrase-like protein
TB927.3.5050	60S ribosomal protein L4
TB09.211.4460	ADP-ribosylation factor
TB09.211.1250	proteasome subunit alpha 1
TB10.05.0220	60S ribosomal protein L10a
TB927.3.5180	cofilin/actin depolymerizing factor
TB927.7.1140	peroxidase 3
TB927.7.2400	tyrosyl-tRNA synthetase
TB927.7.1780	adenine phosphoribosyltransferase
TB11.02.2310	prostaglandin f synthase
TB927.1.2100	calpain-like cysteine peptidase, family C2
TB11.01.8610	hypothetical protein
TB927.7.3440	I/6 autoantigen
TB10.70.4740	enolase
TB11.02.1070	aminopeptidase
TB11.02.4870	proteasome subunit alpha 7
TB927.3.4880	hypothetical protein
TB927.8.740	nucleolar RNA-binding protein, truncated
TB10.389.0880	heat shock protein
TB09.160.0465	hypothetical protein
TB927.2.5850	small nuclear ribonucleoprotein
TB10.6K15.2330	t-complex protein 1 subunit theta
TB10.100.0170	proteasome subunit alpha 2
TB11.01.4621	calmodulin
TB927.7.4570	nucleoside hydrolase
TB11.02.0870	hypothetical protein
TB10.70.3290	ATP-dependent DEAD-box RNA helicase
TB11.01.3080	heat shock protein 70
TB927.1.3830	glucose-6-phosphate isomerase, glycosomal
TB927.7.5160	deoxyuridine triphosphatase
TB10.70.5110	mitochondrial malate dehydrogenase
TB10.70.0800	universal minicircle sequence binding protein
TB09.160.4200	60S acidic ribosomalprotein
TB11.01.3110	heat shock protein 70
TB927.7.4480	adenosine 5'-monophosphoramidase
TB927.8.4330	small GTP-binding protein Rab11
TB927.4.3950	cytoskeleton-associated protein CAP5.5

TB927.7.230	40S ribosomal protein S33
TB10.70.0820	universal minicircle sequence binding protein
TB927.1.3950	alanine aminotransferase
TB09.160.2550	ribosomal protein S7
TB10.61.1920	fibrillarin
TB927.8.1990	tryparedoxin peroxidase
TB927.8.2210	pteridine reductase

TB10.406.0330	histone H2B
TB09.160.3710	proliferative cell nuclear antigen
TB11.02.2740	aspartate aminotransferase mitochondrial
TB927.5.2160	hypothetical protein
TB11.50.0005	60S ribosomal protein L21E
TB927.7.5790	protein disulfide isomerase
TB10.70.0850	proteasome subunit alpha 1
TB927.3.2960	I-A-G-nucleoside hydrolase
TB10.70.3360	40S ribosomal protein S3a
TB927.7.2980	hypothetical protein
TB10.61.1210	methionine aminopeptidase
TB11.01.0700	ribose 5-phosphate isomerase
TB927.4.2070	antigenic protein
TB10.26.1080	heat shock protein 83
TB927.2.100	retrotransposon hot spot protein
TB927.7.1130	peroxidase 2
TB927.6.1880	aspartyl-tRNA synthetase
TB09.211.2150	poly(A)-binding protein 1
TB927.5.1700	replication Factor A 28 kDa subunit
TB10.389.1170	P-type H+-ATPase
TB11.01.8770	hypothetical protein
TB10.61.1960	40S ribosomal protein S2
TB927.6.1570	2-hydroxy-3-oxopropionate reductase
TB11.46.0008	arginyl-tRNA synthetase
TB927.8.5330	tyrosyl/methionyl-tRNA synthetase
TB11.02.0210	hypothetical protein
TB927.4.1300	hypothetical protein
TB927.5.1090	threonyl-tRNA synthetase
TB11.02.4030	eukaryotic release factor 3
TB927.3.1790	pyruvate dehydrogenase E1 beta subunit
TB11.01.7960	60S ribosomal protein L2
TB927.4.3550	60S ribosomal protein L13a
TB11.03.0410	eukaryotic translation initiation factor 5a
TB927.1.710	phosphoglycerate kinase
TB927.8.5440	flagellar calcium-binding protein TB-24

TB10.70.6540	hypoxanthine-guanin phosphoribosyltransferase
TB11.01.1290	hypothetical protein
TB927.7.4420	proteasome alpha 3 subunit
TB927.4.2740	hypothetical protein
TB11.02.2030	hypothetical protein
TB927.2.4930	esterase
TB10.70.5050	hypothetical protein
TB927.8.6750	translationally controlled tumor protein
TB927.2.4580	hypothetical protein
TB927.8.1440	maoC-like dehydratase
TB927.7.2590	prefoldin
TB927.3.5310	hypothetical protein
TB10.70.5650	elongation factor 1-alpha
TB09.160.3730	glutaminyl-tRNA synthetase
TB927.2.450	retrotransposon hot spot protein
TB10.70.1190	valosin-containing protein homolog
TB10.6K15.3250	succinyl-CoA ligase [GDP-forming] beta-chain
TB09.211.3300	hypothetical protein
TB09.211.1690	hypothetical protein
TB927.3.4750	aminopeptidase
TB927.5.3820	aspartate carbamoyltransferase
TB10.389.1480	cytosolic nonspecific dipeptidase
TB927.8.890	small GTP-binding protein Rab1
TB09.211.4850	60S ribosomal protein L26
TB11.02.3120	malic enzyme
TB927.2.4370	trypanothione synthetase
TB927.2.240	retrotransposon hot spot protein
TB927.1.420	retrotransposon hot spot protein
TB927.7.4520	hypothetical protein
TB927.1.2330	beta tubulin
TB09.211.1620	hypothetical protein
TB927.2.4590	branched-chain amino acid aminotransferase
TB09.160.1200	mitotubule-associated protein Gb4
TB10.406.0650	microtubule-associated protein
TB11.01.1740	2-oxoglutarate dehydrogenase E1 component

TB927.2.1170	retrotransposon hot spot protein
TB927.3.780	proteasome alpha 7 subunit
TB09.160.4450	40S ribosomal protein S3
TB927.8.5600	transaldolase
TB10.70.6470	methionyl-tRNA synthetase
TB927.5.930	NADH-dependent fumarate reductase
TB927.6.1260	proteasome beta-1 subunit
TB11.03.0250	cyclophilin A
TB927.4.2310	asparaginyl-tRNA synthetase
TB927.8.550	peptide methionine sulfoxide reductase
TB10.70.5360	La protein