Lister 427 *VSG* summary

MITat[1]	Preferred name[1]	Lab of origin[2]	Local Names[3]	Copies[4]	BES[5]	GenBank Number	Comments[6]
1.1	Lister 427-1	Cross	060	?		X56761	Genbank sequence by Carrington Lab
1.2	Lister 427-2	Cross	221	1	1	X56762	Genbank sequence by Carrington Lab
1.3	Lister 427-3	Cross	224 (Luisa 17.9)	2	6 & 7	AY935575	Genbank sequence by Cross Lab
1.4	Lister 427-4	Cross	117	>5		V01387	Genbank sequence by Cross Lab
1.5	Lister 427-5	Cross	118	2		X56763	Genbank sequence by Carrington Lab
1.6	Lister 427-6	Cross	121	4–5	3	X56764	Genbank sequence by Carrington Lab
1.7	Lister 427-7	Cross	055	?		AJ937311	Genbank sequence by Carrington Lab
1.8	Lister 427-8	Borst/Cross	1.8 (Dreesen OD1)	?	12 & 14??	AY935574	Genbank sequence by Cross Lab
1.9	Lister 427-9	Borst/Cross	Luisa 17. 23 (Borst VO2)	2	**2**	AY935573	Genbank sequence by Cross Lab
1.10	Lister 427-10	Cross	VSG K (Navarro)	?		no sequence	
1.11	Lister 427-11	Cross	bR2 (Davies)	2–3	15	AY935571	Genbank sequence by Cross Lab
1.12	Lister 427-12	Cross	Oliver 501c2 (Navarro B)	?		AY935577	Genbank sequence by Cross Lab
1.13	Lister 427-13	Cross	Luisa 17.13	2	**17**	AY935576	Genbank sequence by Cross Lab
1.14	Lister 427-14	Rudenko	TAR64		8	FM162575	Sanger sequencing
1.15	Lister 427-15	Rudenko	TAR134		**10**	FM162576	Sanger sequencing
1.16	Lister 427-16	Rudenko	TAR122		11	FM162577	Sanger sequencing
1.17	Lister 427-17	Cross	Luisa 17.7 (Rudenko JS1)	1	**13**	DQ826504	Genbank sequence by Cross Lab
1.18	Lister 427-18	Cross/Hajduk	Luisa 17.22 (Hajduk 800)	?	5	DQ826505	Genbank sequence by Cross Lab
1.19	Lister 427-19	Rudenko	TAR10		14	FM162580	Sanger sequencing
1.20	Lister 427-20						To be assigned
1.21	Lister 427-21	Cross	Luisa 17.21 (Horn T3)	2/3	**4**	AY935572	Genbank sequence by Cross Lab

1.22	Lister 427-22	Borst/Clayton	222	?		AJ007019	Genbank sequence by Clayton Lab
1.23	Lister 427-23	Papavasiliou	28	1	MC	FJ798214	Papavasiliou Lab
1.24	Lister 427-24	Papavasiliou	31	1	MC	FJ798212	Papavasiliou Lab
1.25	Lister 427-25	Papavasiliou	42	1	MC	FJ798213	Papavasiliou Lab
1.26	Lister 427-26						To be assigned
1.27	Lister 427-27						To be assigned
1.28	Lister 427-28						To be assigned
1.29	Lister 427-29						To be assigned
1.30	Lister 427-30	Gull	S8	1		AF294806	Genbank sequence by Gull Lab. Absent from our cells.
1.31	Lister 427-31	Gull	G4	?		AF294807	Genbank sequence by Gull Lab. MC multi-copy
		Rudenko	NA1	?			identified in 2005 Mol Micro paper

Comments omitted from edited GenBank files of our newly submitted sequences

New entries from our lab, unless otherwise annotated , were amplified by RT-PCR using primers corresponding to the 5′ spliced leader and the VSG 3′ UTR conserved 14-mer (for protocol see our web site), both of which are excluded from the sequence shown, which starts at the first nt following the spliced leader and ends before the first nt of the conserved 3′ UTR sequence.

MITat 1.3: Originally identified as clone 224, isolated in 1978 by E.N. Miller and M.J. Turner (unpublished) as a relapse from clone 221 (MITat 1.2). VSG purified and characterized by G.A.M. Cross (1979, unpublished).

MITat 1.8: Short 3' end sequence previously reported (Accession X00625). Michels, P.A.M., van der Ploeg, L.H.T., Liu, A.Y.C. and Borst, P. (1984) The inactivation and reactivation of an expression-linked gene copy for a variant surface glycoprotein in Trypanosoma brucei. EMBO J., 3, 1345-1351.

MITat 1.9: VSG MITat 1.9 sequence previously unpublished and referred to as VSG VO2, but its expression and chromosomal location have been described in several papers, the most relevant of which are the two following.~~Rudenko, G., Chaves, I., Dirks-Mulder, A. and Borst, P. (1998) Selection for activation of a new variant surface glycoprotein gene expression site in Trypanosoma brucei can result in deletion of the old one. Mol. Biochem. Parasitol., 95, 97-109.~~Berriman, M., Hall, N., Sheader, K., Bringaud, F., Tiwari, B., Isobe, T., Bowman, S., Corton, C., Clark, L., Cross, G.A.M., Hoek, M., Zanders, T., Berberof, M., Borst, P. and Rudenko, G. (2002) The architecture of variant surface glycoprotein gene expression sites in Trypanosoma brucei. Mol. Biochem. Parasitol., 122, 131-140.

MITat 1.11: Originally identified as VSG bR2 (Liu, A.Y., Michels, P.A., Bernards, A. and Borst, P. (1985) Trypanosome variant surface glycoprotein genes expressed early in infection. J. Mol. Biol., 175, 383-386).~~Further characterized by Davies, K.P., Carruthers, V.B. and Cross, G.A.M. (1997) Manipulation of the VSG co-transposed region increases expression-site switching in Trypanosoma brucei. Mol. Biochem. Parasitol., 86, 163-177.~~Horn, D. and Cross, G.A.M. (1997) Analysis of Trypanosoma brucei vsg expression

site switching in vitro. Mol. Biochem. Parasitol., 84, 189-201.~~Partly sequenced previously (Davies, K. and Cross, G.A.M. unpublished).

MITat 1.12: Corresponds to vsgB (Navarro and Cross, unpublished partial sequence) in Navarro, M. and Cross, G.A.M. (1996) DNA rearrangements associated with multiple consecutive directed antigenic switches in Trypanosoma brucei. Mol. Cell. Biol., 16, 3615-3625.

MITat 1.21: Previous partial sequence D. Horn and G.A.M. Cross, unpublished.

Footnotes:

1 Although only the original 8 MITat numbers strictly fit the definition for this 'at'-based nomenclature, in being characterized at the Molteno Institute, 'ghost' MITat numbers have been assigned to all Lister 427 VSGs. I would much prefer to adopt a strain-designated number. The ancient 'at' system was never satisfactory and is currently totally inappropriate and inadequate as it tags the variant types to particular labs, and it is based on polyvalent phenotyping reagents (antibodies) that do not necessarily resolve genotypes. It is not linked to the genotype! An alternative system would refer to the expressed genotype: Lister 427-13.2, for example, for the variant 13 family gene 2. The gene number only has to be used if it is really necessary to distinguish a particular member of the family and the number can be omitted from the prototype.

2 The lab in which this variant was first characterized plus, if different, the lab from which the complete gene sequence was determined.

3 Lab's 'pet' name, usually corresponding to or based upon a clone number.

4 The number of copies is likely to vary depending on propagation history among different labs.

5 ES numbers in red indicate Intermediate Chromosome

6 Unless a TAR clone is mentioned, the GenBank sequences are for cDNA. TAR clones are cloned expression sites sequenced by the Sanger Institute.