

Mit1

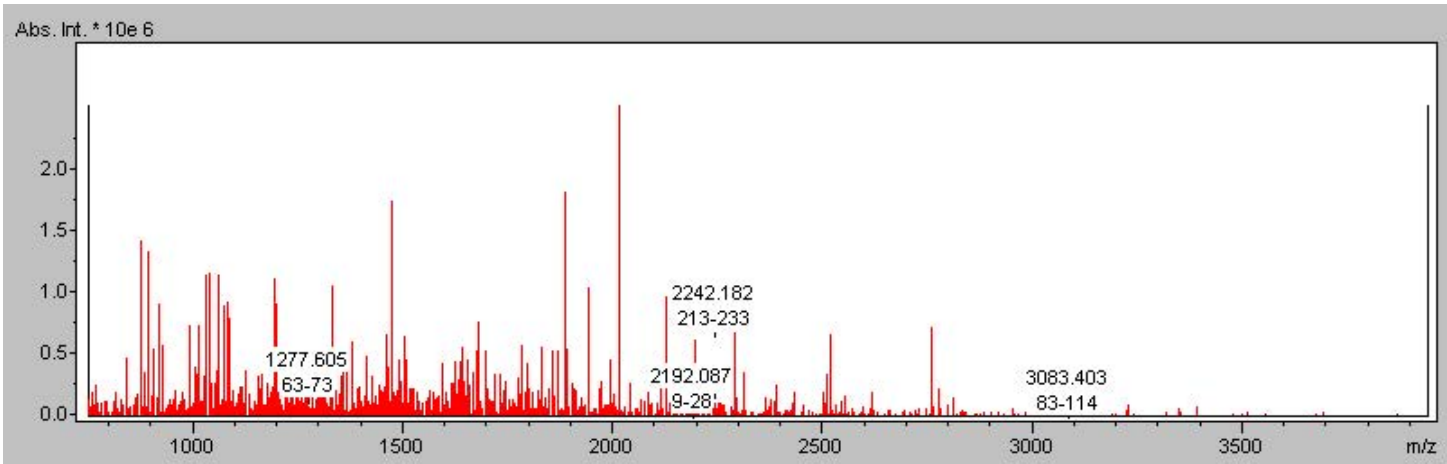
Sequence Name:Transcriptional regulator MIT1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=MIT1 PE=1 SV=1 MIT1_YEAST

MH+ (avg):1.008

MH+ (mono):1.008

Number of Peaks:1266

Tolerance (Da):0.900



Sequence data:

Intensity Coverage:0.2 % (281329 cnts)

Sequence Coverage MS/MS:12.6%

Sequence Coverage MS:pl (isoelectric point):12.6%

pl (isoelectric point):6.7

10	20	30	40	50	60	70	80	90	100	110	120
MDIEPTFKGY	IEDEDDALLI	LQATLDGKLK	HIPRRPYEIE	RPYLIVSGSI	FVFIEEISGI	KRWTDGVSW	PSRISGKFLI	YKELDKENAG	SNANATSSGS	TDSAVITDGT	SGAFNNPSSS
130	140	150	160	170	180	190	200	210	220	230	240
KIKLPPLKNH	QFDLPPTMGH	SSFESQDTS	ISPSNRSNLP	LKYTGLVKKT	ISVKLRPPF	NSIENLHIVS	YYSVKDIQON	CLVTPKASPF	LKDVRPSQEL	IVAMGNITLG	NVKNNSTTTG
250	260	270	280	290	300	310	320	330	340	350	360
NGPMNNINKS	NSSTPLNTVI	STNNNSANIN	AAGSNQFTSA	NKNYYYKND	SSGYPITQFA	PALPSTTLMY	TANPPYITQS	PDNTNATGMN	THVNNNNNS	NNSSNSNNSN	NNNNNNNNNN
370	380	390	400	410	420	430	440	450	460	470	480
NNNNNNINNI	NNVNTNAGNG	NNPNRFHNAS	FAYNTTGDFI	NPQQGQISY	PFYYTTIPIN	NPNYITTQPP	NPVTNASITNE	NQGYSTSSTQ	HPYYGHPTES	QSASAAAAGAT	GTPGTAENVL
490	500	510	520	530	540	550	560	570	580	590	600
PVSSMQPLLH	QANNNSASSA	TSTAPYPVYS	MNVNVPYYNS	SASAYKRAQE	NTTSNTNAEP	SGATSTNSGT	MLSNPAYANS	QYTPSQVYYQ	GFPQYAMASA	QNPSMYQHGH	QHPLPTVYPI
610	620	630	640	650	660	670					
ATPQQNIMSS	GHTLSTIGSD	PQHHHYQQEP	NDHKNFAMGH	ANNNILNITN	NDTMNNLNTN	TSITTTQ					