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(54) **MOLECULAR DIFFERENCES BETWEEN SPECIES OF THE *M. TUBERCULOSIS* COMPLEX**

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(58) **Field of Search** 435/7.1, 6, 4; 424/190.1, 424/9, 184.1; 436/501, 517, 518, 536; 530/300, 350; 536/23.1

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(57) **ABSTRACT**

Specific genetic deletions are identified in mycobacteria isolates, including variations in the *M. tuberculosis* genome sequence between isolates, and numerous deletion present in BCG as compared to *M. tb*. These deletions are used as markers to distinguish between pathogenic and avirulent strains, and as a marker for particular *M. tb* isolates. Deletions specific to vaccine strains of BCG are useful in determining whether a positive tuberculin skin test is indicative of actual tuberculosis infection. The deleted sequences may be re-introduced into BCG to improve the efficacy of vaccination. Alternatively, the genetic sequence that corresponds to the deletion(s) are deleted from *M. bovis* or *M. tuberculosis* to attenuate the pathogenic bacteria.

8 Claims, No Drawings

MOLECULAR DIFFERENCES BETWEEN SPECIES OF THE *M. TUBERCULOSIS* COMPLEX

This invention was made with Government support and you should include the following language in the application: "This invention was made with Governement support under contract AI01137, AI35969 awarded by the National Institutes of Health. The Government has certain rights in this invention."

Tuberculosis is an ancient human scourge that continues to be an important public health problem worldwide. It is an ongoing epidemic of staggering proportions. Approximately one in every three people in the world is infected with *Mycobacterium tuberculosis*, and has a 10% lifetime risk of progressing from infection to clinical disease. Although tuberculosis can be treated, an estimated 2.9 million people died from the disease last year.

There are significant problems with a reliance on drug treatment to control active *M. tuberculosis* infections. Most of the regions having high infection rates are less developed countries, which suffer from a lack of easily accessible health services, diagnostic facilities and suitable antibiotics against *M. tuberculosis*. Even where these are available, patient compliance is often poor because of the lengthy regimen required for complete treatment, and multidrug-resistant strains are increasingly common.

Prevention of infection would circumvent the problems of treatment, and so vaccination against tuberculosis is widely performed in endemic regions. Around 100 million people a year are vaccinated with live bacillus Calmette-Guerin (BCG) vaccine. BCG has the great advantage of being inexpensive and easily administered under less than optimal circumstances, with few adverse reactions. Unfortunately, the vaccine is widely variable in its efficacy, providing anywhere from 0 to 80% protection against infection with *M. tuberculosis*.

BCG has an interesting history. It is an attenuated strain of *M. bovis*, a very close relative of *M. tuberculosis*. The *M. bovis* strain that became BCG was isolated from a cow in the late 1800's by a bacteriologist named Nocard, hence it was called Nocard's bacillus. The attenuation of Nocard's bacillus took place from 1908 to 1921, over the course of 230 in vitro passages. Thereafter, it was widely grown throughout the world, resulting in additional hundreds and sometime thousands of in vitro passages. Throughout its many years in the laboratory, there has been selection for cross-reaction with the tuberculin skin test, and for decreased side effects. The net results have been a substantially weakened pathogen, which may be ineffective in raising an adequate immune response.

New antituberculosis vaccines are urgently needed for the general population in endemic regions, for HIV-infected individuals, as well as health care professionals likely to be exposed to tubercle bacilli. Recombinant DNA vaccines bearing protective genes from virulent *M. tuberculosis* are being developed using shuttle plasmids to transfer genetic material from one mycobacterial species to another, for example see U.S. Pat. No. 5,776,465. Tuberculosis vaccine development should be given a high priority in current medical research goals.

Relevant Literature

Mahairas et al. (1996) *J Bacteriol* 178(5):1274–1282 provides a molecular analysis of genetic differences between *Mycobacterium bovis* BCG and virulent *M. bovis*. Subtractive genomic hybridization was used to identify genetic differences between virulent *M. bovis* and *M. tuberculosis* and avirulent BCG. U.S. Pat. No. 5,700,683 is directed to these genetic differences.

Cole et al. (1998) *Nature* 393:537–544 have described the complete genome of *M. tuberculosis*. To obtain the contiguous genome sequence, a combined approach was used that involved the systematic sequence analysis of selected large-insert clones as well as random small-insert clones from a whole-genome shotgun library. This culminated in a composite sequence of U.S. Pat. No. 4,411,529 base pairs, with a G+C content of 65.6%. 3,924 open reading frames were identified in the genome, accounting for ~91% of the potential coding capacity.

Mycobacterium tuberculosis (*M. tb.*) genomic sequence is available at several internet sites.

SUMMARY OF THE INVENTION

Genetic markers are provided that distinguish between strains of the *Mycobacterium tuberculosis* complex, particularly between avirulent and virulent strains. Strains of interest include *M. bovis, M. bovis* BCG strains, *M. tuberculosis* (*M. tb.*) isolates, and bacteriophages that infect mycobacteria. The genetic markers are used for assays, e.g. immunoassays, that distinguish between strains, such as to differentiate between BCG immunization and *M. tb.* infection. The protein products may be produced and used as an immunogen, in drug screening, etc. The markers are useful in constructing genetically modified *M. tb.* or *M. bovis* cells having improved vaccine characteristics.

DETAILED DESCRIPTION OF THE EMBODIMENTS

Specific genetic deletions are identified that serve as markers to distinguish between avirulent and virulent mycobacteria strains, including *M. bovis, M. bovis* BCG strains, *M. tuberculosis* (*M. tb.*) isolates, and bacteriophages that infect mycobacteria. These deletions are used as genetic markers to distinguish between the different mycobacteria. The deletions may be introduced into *M. tb.* or *M. bovis* by recombinant methods in order to render a pathogenic strain avirulent. Alternatively, the deleted genes are identified in the *M. tb.* genome sequence, and are then reintroduced by recombinant methods into BCG or other vaccine strains, in order to improve the efficacy of vaccination.

The deletions of the invention are identified by comparative DNA hybridizations from genomic sequence of mycobacterium to a DNA microarray comprising representative sequences of the *M. tb.* coding sequences. The deletions are then mapped to the known *M. tb.* genome sequence in order to specifically identify the deleted gene(s), and to characterize nucleotide sequence of the deleted region.

Nucleic acids comprising the provided deletions and junctions are used in a variety of applications. Hybridization probes may be obtained from the known *M. tb.* sequence which correspond to the deleted sequences. Such probes are useful in distinguishing between mycobacteria. For example, there is a 10% probability that an *M. tb.* infected person will progress to clinical disease, but that probability may vary depending of the particular infecting strain. Analysis for the presence or absence of the deletions provided below as "*M. tb.* variable" is used to distinguish between different *M. tb.* strains. The deletions are also useful in identifying whether a patient that is positive for a tuberculin skin test has been infected with *M. tb.* or with BCG.

In another embodiment of the invention, mycobacteria are genetically altered to delete sequences identified herein as absent in attenuated strains, but present in pathogenic strains, e.g. deletions found in BCG but present in *M. tb.* H37Rv. Such genetically engineered strains may provide superior vaccines to the present BCG isolates in use. Alternatively, BCG strains may be "reconstructed" to more closely resemble wild-type *M. tb.* by inserting certain of the deleted sequences back into the genome. Since the protein products of the deleted sequences are expressed in virulent mycobacterial species, the encoded proteins are useful as immunogens for vaccination.

The attenuation (loss of virulence) in BCG is attributed to the loss of genetic material at a number of places throughout the genome. The selection over time for fewer side-effects resulting from BCG immunization, while retaining cross-reactivity with the tuberculin skin test, has provided an excellent screen for those sequences that engender side effects. The identification of deletions that vary between BCG isolates identifies such sequences, which may be used in drug screening and biological analysis for the role of the deleted genes in causing untoward side effects and pathogenicity.

Identification of *M. Tuberculosis* Complex Deletion Markers

The present invention provides nucleic acid sequences that are markers for specific mycobacteria, including *M. tb., M. bovis*, BCG and bacteriophage. The deletions are listed in Table 1. The absence or presence of these marker sequences is characteristic of the indicated isolate, or strain. As such, they provide a unique characteristic for the identification of the indicated mycobacteria. The deletions are identified by their *M. tb.* open reading frame ("Rv" nomenclature), which corresponds to a known genetic sequence, and may be accessed as previously cited. The junctions of the deletions are provided by the designation of position in the publicly available *M. tb.* sequence.

TABLE I

SEQ ID	rd	rv_num	orf_Id	breakpoint
SEQ ID NO:1	RD01	Rv3871	MTV027.06	"H37Rv, segment 160: 7534, 16989"
SEQ ID NO:2	RD01	Rv3872	MTV027.07	"H37Rv, segment 160: 7534, 16989"
SEQ ID NO 3	RD01	Rv3873	MTV027.08	"H37Rv, segment 160: 7534, 16989"
SEQ ID NO:4	RD01	Rv3874	MTV027.09	"H37Rv, segment 160: 7534, 16989"
SEQ ID NO:5	RD01	Rv3875	MTV027.10	"H37Rv, segment 160: 7534, 16989"
SEQ ID NO:6	RD01	Rv3876	MTV027.11	"H37Rv, segment 160: 7534, 16989"
SEQ ID NO:7	RD01	Rv3877	MTV027.12	"H37Rv, segment 160: 7534, 16989"
SEQ ID NO:8	RD01	Rv3878	MTV027.13	"H37Rv, segment 160: 7534,16989"
SEQ ID NO:9	RD01	Rv3879c	MTV027.14c	"H37Rv, segment 160: 7534,16989"
SEQ ID NO:10	RD02	Rv1988	MTCY39.31c	"H37Rv segment 88: 14211, segment 89: 8598"
SEQ ID NO:11	RD02	Rv1987	MTCY39.32c	"H37Rv segment 88: 14211, segment 89: 8598"
SEQ ID NO:12	RD02	Rv1986	MTCY39.33c	"H37Rv segment 88: 14211, segment 89: 8598"
SEQ ID NO:13	RD02	Rv1985c	MTCY39.34	"H37Rv segment 88: 14211, segment 89: 8598"
SEQ ID NO:14	RD02	Rv1984c	MTCY39.35	"H37Rv segment 88: 14211, segment 89: 8598"
SEQ ID NO:15	RD02	Rv1983	MTCY39.36c	"H37Rv segment 88: 14211, segment 89: 8598"
SEQ ID NO:16	RD02	Rv1982c	MTCY39.37	"H37Rv segment 88: 14211, segment 89: 8598"
SEQ ID NO:17	RD02	Rv1981c	MTCY39.38	"H37Rv segment 88: 14211, segment 89: 8598"
SEQ ID NO:18	RD02	Rv1980c	MTCY39.39	"H37Rv segment 88: 14211, segment 89: 8598"
SEQ ID NO:19	RD02	Rv1979c	MTCY39.40	"H37Rv segment 88: 14211, segment 89: 8598"
SEQ ID NO:20	RD02	Rv1978	MTV051.16	"H37Rv segment 88: 14211, segment 89: 8598"
SEQ ID NO:21	RD03	Rv1586c	MTCY336.18	"H37Rv, segment 70: 7677, 16923"
SEQ ID NO:22	RD03	Rvl585c	MTCY336.19	"H37Rv, segment 70: 7677, 16923"
SEQ ID NO:23	RD03	Rv1584c	MTCY336.20	"H37Rv, segment 70: 7677, 16923"
SEQ ID NO 24	RD03	Rv1583c	MTCY336.21	"H37Rv, segment 70: 7677, 16923"
SEQ ID NO:25	RD03	Rv1582c	MTCY336.22	"H37Rv, segment 70: 7677, 16923"
SEQ ID NO:26	RD03	Rv1581c	MTCY336.23	"H37Rv, segment 70: 7677, 16923"
SEQ ID NO:27	RD03	Rvl580c	MTCY336.24	"H37Rv, segment 70: 7677, 16923"
SEQ ID NO:28	RD03	Rv1579c	MTCY336.25	"H37Rv, segment 70: 7677, 16923"
SEQ ID NO:29	RD03	Rv1578c	MTCY336.26	"H37Rv, segment 70: 7677, 16923"
SEQ ID NO:30	RD03	Rv1577c	MTCY336.27	"H37Rv, segment 70: 7677, 16923"
SEQ ID NO:31	RD03	Rv1576c	MTCY336.28	"H37Rv, segment 70: 7677, 16923"
SEQ ID NO:32	RD03	Rv1575	MTCY336.29c	"H37Rv, segment 70: 7677, 16923"
SEQ ID NO:33	RD03	Rv1574	MTCY336.30c	"H37Rv, segment 70: 7677, 16923"
SEQ ID NO:34	RD03	Rv1573	MTCY336.31c	"H37Rv, segment 70: 7677, 16923"
SEQ ID NO:35	RD04	Rv0221	MTCY08D5.16	"H37Rv, segment 12: 17432, 19335"
SEQ ID NO:36	RD04	Rv0222	MTCY08D5.17	"H37Rv, segment 12: 17432, 19335"
SEQ ID NO:37	RD04	Rv0223c	MTCY08D5.18	"H37Rv, segment 12: 17432, 19335"
SEQ ID NO:38	RD05	Rv3117	MTCY164.27	"H37Rv, segment 135: 27437, 30212"
SEQ ID NO:39	RD05	Rv3118	MTCY164.28	"H37Rv, segment 135: 27437, 30212"
SEQ ID NO:40	RD05	Rv3119	MTCY164.29	"H37Rv, segment 135: 27437, 30212"
SEQ ID NO:41	RD05	Rv3120	MTCY164.30	"H37Rv, segment 135: 27437, 30212"
SEQ ID NO:42	RD05	Rv3121	MTCY164.31	"H37Rv, segment 135: 27437, 30212"
SEQ ID NO:43	RD06	Rv1506c	MTCY277.28c	"H37Rv, segment 65: 23614, 36347"
SEQ ID NO:44	RD06	Rv1507c	MTCY277.29c	"H37Rv, segment 65: 23614, 36347"
SEQ ID NO:45	RD06	Rv1508c	MTCY277.30c	"H37Rv, segment 65: 23614, 36347"
SEQ ID NO:46	RD06	Rv1509	MTCY277.31	"H37Rv, segment 65: 23614, 36347"
SEQ ID NO:47	RD06	Rv1510	MTCY277.32	"H37Rv, segment 65: 23614, 36347"
SEQ ID NO:48	RD06	Rv1511	MTCY277.33	"H37Rv, segment 65: 23614, 36347"
SEQ ID NO:49	RD06	Rv1512	MTCY277.34	"H37Rv, segment 65: 23614, 36347"
SEQ ID NO:50	RD06	Rv1513	MTCY277.35	"H37Rv, segment 65: 23614, 36347"
SEQ ID NO:51	RD06	Rv1514c	MTCY277.36c	"H37Rv, segment 65: 23614, 36347"
SEQ ID NO:52	RD06	Rv1515c	MTCY277.37c	"H37Rv, segment 65: 23614, 36347"
SEQ ID NO:53	RD06	Rv1516c	MTCY277.38c	"H37Rv, segment 65: 23614, 36347"

TABLE I-continued

SEQ ID	rd	rv_num	orf_Id	breakpoint
SEQ ID NO:54	RD07	Rv2346c	MTCY98.15c	"H37Rv, segment 103: 17622, 26584"
SEQ ID NO:55	RD07	Rv2347c	MTCY98.16c	"H37Rv, segment 103: 17622, 26584"
SEQ ID NO:56	RD07	Rv2348c	MTCY98.17c	"H37Rv, segment 103: 17622, 26584"
SEQ ID NO:57	RD07	Rv2349c	MTCY98.18c	"H37Rv, segment 103: 17622, 26584"
SEQ ID NO:58	RD07	Rv2350c	MTCY98.19c	"H37Rv, segment 103: 17622, 26584"
SEQ ID NO:59	RD07	Rv2351c	MTCY98.20c	"H37Rv, segment 103: 17622, 26584"
SEQ ID NO:60	RD07	Rv2352c	MTCY98.21c	"H37Rv, segment 103: 17622, 26584"
SEQ ID NO:61	RD07	Rv2353c	MTCY98.22c	"H37Rv, segment 103: 17622, 26584"
SEQ ID NO:62	RD08	Rv0309	MTCY63.14	"H37Rv, segment 16: 17018, 20446"
SEQ ID NO:63	RD08	Rv0310c	MTCY63.15c	"H37Rv, segment 16: 17018, 20446"
SEQ ID NO:64	RD08	Rv0311	MTCY63.16	"H37Rv, segment 16: 17018, 20446"
SEQ ID NO:65	RD08	Rv0312	MTCY63.17	"H37Rv, segment 16: 17018, 20446"
SEQ ID NO:66	RD09	Rv3623	MTCY15C10.29c	"H37Rv, segment 153: 21131, segment 154: 2832"
SEQ ID NO:67	RD09	Rv3622c	MTCY15C10.30	"H37Rv, segment 153: 21131, segment 154: 2832"
SEQ ID NO:68	RD09	Rv3621c	MTCY15C10.31	"H37Rv, segment 153: 21131, segment 154: 2832"
SEQ ID NO:69	RD09	Rv3620c	MTCY15C10.32	"H37Rv, segment 153: 21131, segment 154: 2832"
SEQ ID NO:70	RD09	Rv3619c	MTCY15C10.33	"H37Rv, segment 153: 21131, segment 154: 2832"
SEQ ID NO:71	RD09	Rv3618	MTCY15C10.34c	"H37Rv, segment 153: 21131, segment 154: 2832"
SEQ ID NO:72	RD09	Rv3617	MTCY15010.35c	"H37Rv, segment 153: 21131, segment 154: 2832"
SEQ ID NO:73	RD10	Rv1257c	MTCY50.25	"H37Rv segment 55: 3689, 6696"
SEQ ID NO:74	RD10	Rv1256c	MTCY50.26	"H37Rv segment 55: 3689, 6696"
SEQ ID NO:75	RD10	Rv1255c	MTCY50.27	"H37Rv segment 55: 3689, 6696"
SEQ ID NO:76	RD11	Rv3429	MTCY77.01	"H37Rv, segment 145: 30303 to segment 146: 1475"
SEQ ID NO:77	RD11	Rv3428c	MTCY78.01	"H37Rv, segment 145: 30303 to segment 146: 1475"
SEQ ID NO:78	RD11	Rv3427c	MTCY78.02	"H37Rv, segment 145: 30303 to segment 146: 1475"
SEQ ID NO:79	RD11	Rv3426	MTCY78.03c	"H37Rv, segment 145: 30303 to segment 146: 1475"
SEQ ID NO:80	RD11	Rv3425	MTCY78.04c	"H37Rv, segment 145: 30303 to segment 146: 1475"
SEQ ID NO:81	RD12	Rv2072c	MTCY49.11c	"H37Rv segment 93: 9301, 11331"
SEQ ID NO:82	RD12	Rv2073c	MTCY49.12c	"H37Rv segment 93: 9301, 11331"
SEQ ID NO:83	RD12	Rv2074	MTCY49.13	"H37Rv segment 93: 9301, 11331"
SEQ ID NO:84	RD12	Rv2075c	MTCY49.14c	"H37Rv segment 93: 9301, 11331"
SEQ ID NO:85	RD13bis	Rv2645	MTCY441.15	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:86	RD13bis	Rv2646	MTCY441.16	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:87	RD13bis	Rv2647	MTCY441.17	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:88	RD13bis	Rv2648	MTCY441.17A	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:89	RD13bis	Rv2649	MTCY441.18	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:90	RD13bis	Rv2650c	MTCY441.19	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:91	RD13bis	Rv2651c	MTCY441.20c	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:92	RD13bis	Rv2652c	MTCY441.21c	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:93	RD13bis	Rv2653c	MTCY441.22c	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:94	RD13bis	Rv2654c	MTCY441.23c	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:95	RD13bis	Rv2655c	MTCY441.24c	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:96	RD13bis	Rv2656c	MTCY441.25c	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:97	RD13bis	Rv2657c	MTCY441.26c	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:98	RD13bis	Rv2658c	MTCY441.27c	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:99	RD13bis	Rv2659c	MTCY441.28c	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:100	RD13bis	Rv2660c	MTCY441.29c	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:101	RD14	Rv1766	MTCY28.32	"H37Rv segment 79: 30573, 39642"
SEQ ID NO:102	RD14	Rv1767	MTCY28.33	"H37Rv segment 79: 30573, 39642"
SEQ ID NO:103	RD14	Rv1768	MTCY28.34	"H37Rv segment 79: 30573, 39642"
SEQ ID NO:104	RD14	Rv1769	MTCY28.35	"H37Rv segment 79: 30573, 39642"
SEQ ID NO:105	RD14	Rv1770	MTCY28.36	"H37Rv segment 79: 30573, 39642"
SEQ ID NO:106	RD14	Rv1771	MTCY28.37	"H37Rv segment 79: 30573, 39642"
SEQ ID NO:107	RD14	Rv1772	MTCY28.38	"H37Rv segment 79: 30573, 39642"
SEQ ID NO:108	RD14	Rv1773c	MTCY28.39	"H37Rv segment 79: 30573, 39642"
SEQ ID NO:109	RD15	Rv1963c	MTV051.01c	"H37Rv segment 88: 1153, 13873"
SEQ ID NO:110	RD15	Rv1964	MTV051.02	"H37Rv segment 88: 1153, 13873"
SEQ ID NO:111	RD15	Rv1965	MTV051.03	"H37Rv segment 88: 1153, 13873"
SEQ ID NO:112	RD15	Rv1966	MTV051.04	"H37Rv segment 88: 1153, 13873"
SEQ ID NO:113	RD15	Rv1967	MTV0S1.05	"H37Rv segment 88:1153, 13873"
SEQ ID NO:114	RD15	Rv1968	MTV051.06	"H37Rv segment 88: 1153, 13873"
SEQ ID NO:115	RD15	Rv1969	MTV051.07	"H37Rv segment 88: 1153, 13873"
SEQ ID NO:116	RD15	Rv1970	MTV051.08	"H37Rv segment 88: 1153, 13873"
SEQ ID NO:117	RD15	Rv1971	MTV051.09	"H37Rv segment 88: 1153, 13873"
SEQ ID NO:118	RD15	Rv1972	MTV051.10	"H37Rv segment 88: 1153, 13873"
SEQ ID NO:119	RD15	Rv1973	MTV051.11	"H37Rv segment 88: 1153, 13873"
SEQ ID NO:120	RD15	Rv1974	MTV051.12	"H37Rv segment 88: 1153, 13873"
SEQ ID NO:121	RD15	Rv1975	MTV051.13	"H37Rv segment 88: 1153, 13873"
SEQ ID NO:122	RD15	Rv1976c	MTV051.14	"H37Rv segment 88: 1153, 13873"
SEQ ID NO:123	RD15	Rv1977	MTV051.15	"H37Rv segment 88: 1153, 13873"
SEQ ID NO:124	RD16	Rv3405c	MTCY78.23	"H37Rv, segment 145: 5012, 12621"
SEQ ID NO:125	RD16	Rv3404c	MTCY78.24	"H37Rv, segment 145: 5012, 12621"
SEQ ID NO:126	RD16	Rv3403c	MTCY78.25	"H37Rv, segment 145: 5012, 12621"
SEQ ID NO:127	RD16	Rv3402c	MTCY78.26	"H37Rv, segment 145: 5012, 12621"
SEQ ID NO:128	RD16	Rv3401	MTCY78.27c	"H37Rv, segment 145: 5012, 12621"
SEQ ID NO:129	RD16	Rv3400	MTCY78.28c	"H37Rv, segment 145: 5012, 12621"

The "Rv" column indicates public *M. tb.* sequence, open reading frame. The BCG strains were obtained as follows:

TABLE 2

Strains employed in study of BCG phylogeny

Name of strain	Synonym	Source	Descriptors
BCG-Russia	Moscow	ATCC	#35740
BCG-Moreau	Brazil	ATCC	#35736
BCG-Moreau	Brazil	IAF	dated 1958
BCG-Moreau	Brazil	IAF	dated 1961
BCG-Japan	Tokyo	ATCC	#35737
BCG-Japan	Tokyo	IAF	dated 1961
BCG-Japan	Tokyo	JATA	vaccine strain
BCG-Japan	Tokyo	JATA	bladder cancer strain
BCG-Japan	Tokyo	JATA	clinical isolate - adenitis
BCG-Sweden	Gothenburg	ATCC	#35732
BCG-Sweden	Gothenburg	IAF	dated 1958
BCG-Sweden	Gothenburg	SSI	production lot, Copenhagen
BCG-Phipps	Philadelphia	ATCC	#35744
BCG-Denmark	Danish 1331	ATCC	#35733
BCG-Copenhagen		ATCC	#27290
BCG-Copenhagen		IAF	dated 1961
BCG-Tice	Chicago	vaccine	dated 1973
BCG-Tice	Chicago	ATCC	#35743
BCG-Frappier	Montreal	IAF	primary lot, 1973
BCG-Frappier, INH-resistant	Montreal-R	IAF	primary lot, 1973
BCG-Frappier	Montreal	IAF	passage 946
BCG-Connaught	Toronto	CL	bladder cancer treatment
BCG-Birkhaug		ATCC	#35731
BCG-Prague	Czech	SSI	lyophilized 1968
BCG-Glaxo		vaccine	dated 1973
BCG-Glaxo		ATCC	#35741
BCG-Pasteur		IAF	passage 888
BCG-Pasteur		IAF	dated 1961
BCG-Pasteur		IP	1173P2-B
BCG-Pasteur		IP	1173P2-C
BCG-Pasteur		IP	clinical isolate #1
BCG-Pasteur		IP	clinical isolate #2
BCG-Pasteur		ATCC	#35734

Abbreviations: IP = Institut Pasteur, Paris, France; IAF = Institut Armand Frappier, Laval, Canada; ATCC = American Type Culture Collection, Rockville, Md, USA; SSI = Statens Serum Institute, Copenhagen, Denmark; CL = Connaught Laboratories, Willowdale, Canada, JATA = Japanese Anti-Tuberculosis Association; INH = isoniazid. Canadian BCG's refers to BCG-Montreal and BCG-Toronto, the latter being derived from the former.

In performing the initial screening method, genomic DNA is isolated from two mycobacteria microbial cell cultures. The two DNA preparations are labeled, where a different label is used for the first and second microbial cultures, typically using nucleotides conjugated to a fluorochrome that emits at a wavelength substantially different from that of the fluorochrome tagged nucleotides used to label the selected probe. The strains used were the reference strain of *Mycobacterium tuberculosis* (H37Rv), other *M. tb.* laboratory strains, such as H37Ra, the O strain, *M. tb.* clinical isolates, the reference strain of *Mycobacterium bovis*, and different strains of *Mycobacterium bovis* BCG.

The two DNA preparations are mixed, and competitive hybridization is carried out to a microarray representing all of the open reading frames in the genome of the test microbe, usually H37Rv. Hybridization of the labeled sequences is accomplished according to methods well known in the art. In a preferred embodiment, the two probes are combined to provide for a competitive hybridization to a single microarray. Hybridization can be carried out under conditions varying in stringency, preferably under conditions of high stringency (e.g., 4×SSC, 10% SDS, 65° C.) to allow for hybridization of complementary sequences having extensive homology (e.g., having at least 85% sequence identity, preferably at least 90% sequence identity, more preferably having at least 95% sequence identity). Where the target sequences are native sequences the hybridization is preferably carried out under conditions that allow hybridization of only highly homologous sequences (e.g., at least 95% to 100% sequence identity).

Two color fluorescent hybridization is utilized to assay the representation of the unselected library in relation to the selected library (i.e., to detect hybridization of the unselected probe relative to the selected probe). From the ratio of one color to the other, for any particular array element, the relative abundance of that sequence in the unselected and selected libraries can be determined. In addition, comparison of the hybridization of the selected and unselected probes provides an internal control for the assay. An absence of signal from the reference strain, as compared to H37Rv, is indicative that the open reading frame is deleted in the test strain. The deletion may be further mapped by Southern blot analysis, and by sequencing the regions flanking the deletion.

Microarrays can be scanned to detect hybridization of the selected and the unselected sequences using a custom built scanning laser microscope as described in Shalon et al., *Genome Res.* 6:639 (1996). A separate scan, using the appropriate excitation line, is performed for each of the two fluorophores used. The digital images generated from the scan are then combined for subsequent analysis. For any particular array element, the ratio of the fluorescent signal from the amplified selected cell population DNA is compared to the fluorescent signal from the unselected cell population DNA, and the relative abundance of that sequence in the selected and unselected library determined.

Nucleic Acid Compositions

As used herein, the term "deletion marker", or "marker" is used to refer to those sequences of *M. tuberculosis* complex genomes that are deleted in one or more of the strains or species, as indicated in Table 1. The bacteria of the *M. tuberculosis* complex include *M. tuberculosis, M. bovis*, and BCG, inclusive of varied isolates and strains within each species. Nucleic acids of interest include all or a portion of the deleted region, particularly complete open reading frames, hybridization primers, promoter regions, etc.

The term "junction" or "deletion junction" is used to refer to nucleic acids that comprise the regions on both the 3' and the 5' sequence immediately flanking the deletion. Such junction sequences are preferably used as short primers, e.g. from about 15 nt to about 30 nt, that specifically hybridize to the junction, but not to a nucleic acid comprising the undeleted genomic sequence. For example, the deletion found in *M. bovis*, at Rv0221, corresponds to the nucleotide sequence of the *M. tuberculosis* H37Rv genome, segment 12: 17432,19335. The junction comprises the regions upstream of position 17342, and downstream of 19335, e.g. a nucleic acid of 20 nucleotides comprising the sequence from H37Rv 17332–17342 joined to 19335–19345.

Typically, such nucleic acids comprising a junction will include at least about 7 nucleotides from each flanking region, i.e. from the 3' and from the 5' sequences adjacent to the deletion, and may be about 10 nucleotides from each flanking region, up to about 15 nucleotides, or more. Amplification primers that hybridize to the junction sequence, to the deleted sequence, and to the flanking non-deleted regions have a variety of uses, as detailed below.

The nucleic acid compositions of the subject invention encode all or a part of the deletion markers. Fragments may be obtained of the DNA sequence by chemically synthesizing oligonucleotides in accordance with conventional methods, by restriction enzyme digestion, by PCR amplification, etc. For the most part, DNA fragments will be at least about 25 nt in length, usually at least about 30 nt, more usually at least about 50 nt. For use in amplification reactions, such as PCR, a pair of primers will be used. The exact composition of the primer sequences is not critical to the invention, but for most applications the primers will hybridize to the subject sequence under stringent conditions, as known in the art. It is preferable to chose a pair of primers that will generate an amplification product of at least about 50 nt, preferably at least about 100 nt. Algorithms for the selection of primer sequences are generally known, and are available in commercial software packages. Amplification primers hybridize to complementary strands of DNA, and will prime towards each other.

Usually, the DNA will be obtained substantially free of other nucleic acid sequences that do not include a deletion marker sequence or fragment thereof, generally being at least about 50%, usually at least about 90% pure and are typically "recombinant", i.e. flanked by one or more nucleotides with which it is not normally associated on a naturally occurring chromosome.

For screening purposes, hybridization probes of one or more of the deletion sequences may be used in separate reactions or spatially separated on a solid phase matrix, or labeled such that they can be distinguished from each other. Assays may utilize nucleic acids that hybridize to one or more of the described deletions.

An array may include all or a subset of the deletion markers listed in Table 1. Usually such an array will include at least 2 different deletion marker sequences, i.e. deletions located at unique positions within the locus, and may include all of the provided deletion markers. Arrays of interest may further comprise other genetic sequences, particularly other sequences of interest for tuberculosis screening. The oligonucleotide sequence on the array will usually be at least about 12 nt in length, may be the length of the provided deletion marker sequences, or may extend into the flanking regions to generate fragments of 100 to 200 nt in length. For examples of arrays, see Ramsay (1998) *Nat. Biotech.* 16:40–44; Hacia et al. (1996) *Nature Genetics* 14:441–447; Lockhart et al. (1996) *Nature Biotechnol.* 14:1675–1680; and De Risi et al. (1996) *Nature Genetics* 14:457–460.

Nucleic acids may be naturally occurring, e.g. DNA or RNA, or may be synthetic analogs, as known in the art. Such analogs may be preferred for use as probes because of superior stability under assay conditions. Modifications in the native structure, including alterations in the backbone, sugars or heterocyclic bases, have been shown to increase intracellular stability and binding affinity. Among useful changes in the backbone chemistry are phosphorothioates; phosphorodithioates, where both of the non-bridging oxygens are substituted with sulfur; phosphoroamidites; alkyl phosphotriesters and boranophosphates. Achiral phosphate derivatives include 3'-O'-5'-S-phosphorothioate, 3'-S-5'-O-phosphorothioate, 3'-CH_2-5'-O-phosphonate and 3'-NH-5'-O-phosphoroamidate. Peptide nucleic acids replace the entire ribose phosphodiester backbone with a peptide linkage.

Sugar modifications are also used to enhance stability and affinity. The α-anomer of deoxyribose may be used, where the base is inverted with respect to the natural b-anomer. The 2'-OH of the ribose sugar may be altered to form 2'-O-methyl or 2'-O-allyl sugars, which provide resistance to degradation without comprising affinity.

Modification of the heterocyclic bases must maintain proper base pairing. Some useful substitutions include deoxyuridine for deoxythymidine; 5-methyl-2'-deoxycytidine and 5-bromo-2'-deoxycytidine for deoxycytidine. 5-propynyl-2'-deoxyuridine and 5-propynyl-2'-deoxycytidine have been shown to increase affinity and biological activity when substituted for deoxythymidine and deoxycytidine, respectively.

Polypeptide Compositions

The specific deletion markers in Table 1 correspond to open reading frames of the *M. tb.* genome, and therefore encode a polypeptide. The subject markers may be employed for synthesis of a complete protein, or polypeptide fragments thereof, particularly fragments corresponding to functional domains; binding sites; etc.; and including fusions of the subject polypeptides to other proteins or parts thereof. For expression, an expression cassette may be employed, providing for a transcriptional and translational initiation region, which may be inducible or constitutive, where the coding region is operably linked under the transcriptional control of the transcriptional initiation region, and a transcriptional and translational termination region. Various transcriptional initiation regions may be employed that are functional in the expression host.

The polypeptides may be expressed in prokaryotes or eukaryotes in accordance with conventional ways, depending upon the purpose for expression. For large scale production of the protein, a unicellular organism, such as *E. coli, B. subtilis, S. cerevisiae*, or cells of a higher organism such as vertebrates, particularly mammals, e.g. COS 7 cells, may be used as the expression host cells. Small peptides can also be synthesized in the laboratory.

With the availability of the polypeptides in large amounts, by employing an expression host, the polypeptides may be isolated and purified in accordance with conventional ways. A lysate may be prepared of the expression host and the lysate purified using HPLC, exclusion chromatography, gel electrophoresis, affinity chromatography, or other purification technique. The purified polypeptide will generally be at least about 80% pure, preferably at least about 90% pure, and may be up to and including 100% pure. Pure is intended to mean free of other proteins, as well as cellular debris.

The polypeptide is used for the production of antibodies, where short fragments provide for antibodies specific for the particular polypeptide, and larger fragments or the entire protein allow for the production of antibodies over the surface of the polypeptide. Antibodies may be raised to isolated peptides corresponding to particular domains, or to the native protein.

Antibodies are prepared in accordance with conventional ways, where the expressed polypeptide or protein is used as an immunogen, by itself or conjugated to known immunogenic carriers, e.g. KLH, pre-S HBsAg, other viral or eukaryotic proteins, or the like. Various adjuvants may be employed, with a series of injections, as appropriate. For monoclonal antibodies, after one or more booster injections, the spleen is isolated, the lymphocytes immortalized by cell fusion, and then screened for high affinity antibody binding. The immortalized cells, i.e. hybridomas, producing the desired antibodies may then be expanded. For further description, see *Monoclonal Antibodies: A Laboratory Manual*, Harlow and Lane eds., Cold Spring Harbor Laboratories, Cold Spring Harbor, N.Y., 1988. If desired, the mRNA encoding the heavy and light chains may be isolated and mutagenized by cloning in *E. coli*, and the heavy and light chains mixed to further enhance the affinity of the antibody. Alternatives to in vivo immunization as a method of raising antibodies include binding to phage "display" libraries, usually in conjunction with in vitro affinity maturation.

The antibody may be produced as a single chain, instead of the normal multimeric structure. Single chain antibodies are described in Jost et al. (1994) *J.B.C.* 269:26267–73, and others. DNA sequences encoding the variable region of the heavy chain and the variable region of the light chain are ligated to a spacer encoding at least about 4 amino acids of small neutral amino acids, including glycine and/or serine. The protein encoded by this fusion allows assembly of a functional variable region that retains the specificity and affinity of the original antibody.

Use of Deletion Markers in Identification of Mycobacteria

The deletions provided in Table 1 are useful for the identification of a mycobacterium as (a) variants of *M. tb.* (b) isolates of BCG (c) *M. bovis* strains or (d) carrying the identified mycobacterial bacteriophage, depending on the specific marker that is chosen. Such screening is particularly useful in determining whether a particular infection or isolate is pathogenic. The term mycobacteria may refer to any member of the family Mycobacteriacaeae, including *M. tuberculosis, M. avium* complex, *M. kansasii, M. scrofulaceum, M. bovis* and *M. leprae.*

Means of detecting deletions are known in the art. Deletions may be identified through the absence or presence of the sequences in mRNA or genomic DNA, through analysis of junctional regions that flank the deletion, or detection of the gene product, or, particularly relating to the tuberculin skin test, by identification of antibodies that react with the encoded gene product.

While deletions can be easily determined by the absence of hybridization, in many cases it is desirable to have a positive signal, in order to minimize artifactual negative readings. In such cases the deletions may be detected by designing a primer that flanks the junction formed by the deletion. Where the deletion is present, a novel sequence is formed between the flanking regions, which can be detected by hybridization. Preferably such a primer will be sufficiently short that it will only hybridize to the junction, and will fail to form stable hybrids with either of the separate parts of the junction.

Diagnosis is performed by protein, DNA or RNA sequence and/or hybridization analysis of any convenient sample, e.g. cultured mycobacteria, biopsy material, blood sample, etc. Screening may also be based on the functional or antigenic characteristics of the protein. Immunoassays designed to detect the encoded proteins from deleted sequences may be used in screening.

A number of methods are available for analyzing nucleic acids for the presence of a specific sequence. Where large amounts of DNA are available, genomic DNA is used directly. Alternatively, the region of interest is cloned into a suitable vector and grown in sufficient quantity for analysis. The nucleic acid may be amplified by conventional techniques, such as the polymerase chain reaction (PCR), to provide sufficient amounts for analysis. The use of the polymerase chain reaction is described in Saiki, et al. (1985) *Science* 239:487, and a review of current techniques may be found in Sambrook, et al. *Molecular Cloning: A Laboratory Manual*, CSH Press 1989, pp.14.2–14.33. Amplification may also be used to determine whether a polymorphism is present, by using a primer that is specific for the polymorphism. Alternatively, various methods are known in the art that utilize oligonucleotide ligation, for examples see Riley et al. (1990) *N.A.R.* 18:2887–2890; and Delahunty et al. (1996) *Am. J. Hum. Genet.* 58:1239–1246.

A detectable label may be included in an amplification reaction. Suitable labels include fluorochromes, e.g. fluorescein isothiocyanate (FITC), rhodamine, Texas Red, phycoerythrin, allophycocyanin, 6-carboxyfluorescein (6-FAM), 2',7'-dimethoxy-4',5'-dichloro-6-carboxyfluorescein (JOE), 6-carboxy-X-rhodamine (ROX), 6-carboxy-2',4',7',4,7-hexachlorofluorescein (HEX), 5-carboxyfluorescein (5-FAM) or N,N,N',N'-tetramethyl-6-carboxyrhodamine (TAMRA), radioactive labels, e.g. ^{32}P, ^{35}S, ^{3}H; etc. The label may be a two stage system, where the amplified DNA is conjugated to biotin, haptens, etc. having a high affinity binding partner, e.g. avidin, specific antibodies, etc., where the binding partner is conjugated to a detectable label. The label may be conjugated to one or both of the primers. Alternatively, the pool of nucleotides used in the amplification is labeled, so as to incorporate the label into the amplification product.

The sample nucleic acid, e.g. amplified or cloned fragment, is analyzed by one of a number of methods known in the art. The nucleic acid may be sequenced by dideoxy or other methods, and the sequence of bases compared to the deleted sequence. Hybridization with the variant sequence may also be used to determine its presence, by Southern blots, dot blots, etc. The hybridization pattern of a control and variant sequence to an array of oligonucleotide probes immobilized on a solid support, as described in U.S. Pat. No. 5,445,934, or in WO95/35505, may also be used as a means of detecting the presence of variable sequences. Single strand conformational polymorphism (SSCP) analysis, denaturing gradient gel electrophoresis (DGGE), mismatch cleavage detection, and heteroduplex analysis in gel matrices are used to detect conformational changes created by DNA sequence variation as alterations in electrophoretic mobility. Alternatively, where a polymorphism creates or destroys a recognition site for a restriction endonuclease (restriction fragment length polymorphism, RFLP), the sample is digested with that endonuclease, and the products size fractionated to determine whether the fragment was digested. Fractionation is performed by gel or capillary electrophoresis, particularly acrylamide or agarose gels.

The hybridization pattern of a control and variant sequence to an array of oligonucleotide probes immobilized on a solid support, as described in U.S. Pat. No. 5,445,934, or in WO95/35505, may be used as a means of detecting the presence or absence of deleted sequences. In one embodiment of the invention, an array of oligonucleotides is provided, where discrete positions on the array are complementary to at least a portion of *M. tb.* genomic DNA, usually comprising at least a portion from the identified open reading frames. Such an array may comprise a series of oligonucleotides, each of which can specifically hybridize to a nucleic acid, e.g. mRNA, cDNA, genomic DNA, etc.

Deletions may also be detected by amplification. In an embodiment of the invention, sequences are amplified that include a deletion junction, i.e. where the amplification primers hybridize to a junction sequence. In a nucleic acid sample where the marker sequence is deleted, a junction will be formed, and the primer will hybridize, thereby allowing amplification of a detectable sequence. In a nucleic acid sample where the marker sequence is present, the primer will not hybridize, and no amplification will take place. Alternatively, amplification primers may be chosen such that amplification of the target sequence will only take place where the marker sequence is present. The amplification products may be separated by size using any convenient method, as known in the art, including gel electrophoresis, chromatography, capillary electrophoresis, density gradient fractionation, etc.

In addition to the detection of deletions by the detection of junctions sequences, or detection of the marker sequences themselves, one may determine the presence or absence of the encoded protein product. The specific deletions in Table 1 correspond to open reading frames of the *M. tb.* genome, and therefore encode polypeptides. Polypeptides are detected by means known in the art, including determining the presence of the specific polypeptide in a sample through biochemical, functional or immunological characterization. The detection of antibodies in patient serum that react with a polypeptide is of particular interest.

Immunization with BCG typically leads to a positive response against tuberculin antigens in a skin test. In people who have been immunized, which includes a significant proportion of the world population, it is therefore difficult to determine whether a positive test is the result of an immune reaction to the BCG vaccine, or to an ongoing *M. tb.* infection. The subject invention has provided a number of open reading frame sequences that are present in *M. tb.* isolates, but are absent in BCG. As a primary or a secondary screening method, one may test for immunoreactivity of the patient with the polypeptides encoded by such deletion markers. Diagnosis may be performed by a number of methods. The different methods all determine the presence of an immune response to the polypeptide in a patient, where a positive response is indicative of an *M. tb.* infection. The immune response may be determined by determination of antibody binding, or by the presence of a response to intradermal challenge with the polypeptide.

In one method, a dose of the deletion marker polypeptide, formulated as a cocktail of proteins or as individual protein species, in a suitable medium is injected subcutaneously into the patient. The dose will usually be at least about 0.05 μg of protein, and usually not more than about 5 μg of protein. A control comprising medium alone, or an unrelated protein will be injected nearby at the same time. The site of injection is examined after a period of time for the presence of a wheal. The wheal at the site of polypeptide injection is compared to that at the site of the control injection, usually by measuring the size of the wheal. The skin test readings may be assessed by a variety of objective grading systems. A positive result for the presence of an allergic condition will show an increased diameter at the site of polypeptide injection as compared to the control, usually at least about 50% increase in size, more usually at least 100% increase in size.

An alternative method for diagnosis depends on the in vitro detection of binding between antibodies in a patient sample and the subject polypeptides, either as a cocktail or as individual protein species, where the presence of specific binding is indicative of an infection. Measuring the concentration of polypeptide specific antibodies in a sample or fraction thereof may be accomplished by a variety of specific assays. In general, the assay will measure the reactivity between a patient sample, usually blood derived, generally in the form of plasma or serum. The patient sample may be used directly, or diluted as appropriate, usually about 1:10 and usually not more than about 1:10,000. Immunoassays may be performed in any physiological buffer, e.g. PBS, normal saline, HBSS, dPBS, etc.

In a preferred embodiment, a conventional sandwich type assay is used. A sandwich assay is performed by first attaching the polypeptide to an insoluble surface or support. The polypeptide may be bound to the surface by any convenient means, depending upon the nature of the surface, either directly or through specific antibodies. The particular manner of binding is not crucial so long as it is compatible with the reagents and overall methods of the invention. They may be bound to the plates covalently or non-covalently, preferably non-covalently. Samples, fractions or aliquots thereof are then added to separately assayable supports (for example, separate wells of a microtiter plate) containing support-bound polypeptide. Preferably, a series of standards, containing known concentrations of antibodies is assayed in parallel with the samples or aliquots thereof to serve as controls.

Immune specific receptors may be labeled to facilitate direct, or indirect quantification of binding. Examples of labels which permit direct measurement of second receptor binding include radiolabels, such as ^{3}H or ^{125}I, fluorescers, dyes, beads, chemilumninescers, colloidal particles, and the like. Examples of labels which permit indirect measurement of binding include enzymes where the substrate may provide for a colored or fluorescent product. In a preferred embodiment, the second receptors are antibodies labeled with a covalently bound enzyme capable of providing a detectable product signal after addition of suitable substrate. Examples of suitable enzymes for use in conjugates include horseradish peroxidase, alkaline phosphatase, malate dehydrogenase and the like. Where not commercially available, such antibody-enzyme conjugates are readily produced by techniques known to those skilled in the art.

In some cases, a competitive assay will be used. In addition to the patient sample, a competitor to the antibody is added to the reaction mix. The competitor and the antibody compete for binding to the polypeptide. Usually, the competitor molecule will be labeled and detected as previously described, where the amount of competitor binding will be proportional to the amount of Immune present. The concentration of competitor molecule will be from about 10 times the maximum anticipated Immune concentration to about equal concentration in order to make the most sensitive and linear range of detection.

Alternatively, antibodies may be used for direct determination of the presence of the deletion marker polypeptide. Antibodies specific for the subject deletion markers as previously described may be used in screening immunoassays. Samples, as used herein, include microbial cultures, biological fluids such as tracheal lavage, blood, etc. Also included in the term are derivatives and fractions of such fluids. Diagnosis may be performed by a number of methods. The different methods all determine the absence or presence of polypeptides encoded by the subject deletion markers. For example, detection may utilize staining of mycobacterial cells or histological sections, performed in accordance with conventional methods. The antibodies of interest are added to the cell sample, and incubated for a period of time sufficient to allow binding to the epitope, usually at least about 10 minutes. The antibody may be labeled with radioisotopes, enzymes, fluorescers, chemiluminescers, or other labels for direct detection. Alternatively, a second stage antibody or reagent is used to amplify the signal. Such reagents are well known in the art. For example, the primary antibody may be conjugated to biotin, with horseradish peroxidase-conjugated avidin added as a second stage reagent. Final detection uses a substrate that undergoes a color change in the presence of the peroxidase. The absence or presence of antibody binding may be determined by various methods, including microscopy, radiography, scintillation counting, etc.

An alternative method for diagnosis depends on the in vitro detection of binding between antibodies and the subject polypeptides in solution, e.g. a cell lysate. Measuring the concentration of binding in a sample or fraction thereof may be accomplished by a variety of specific assays. A conventional sandwich type assay may be used. For example, a sandwich assay may first attach specific antibodies to an insoluble surface or support. The particular manner of binding is not crucial so long as it is compatible with the reagents and overall methods of the invention. They may be bound to the plates covalently or non-covalently, preferably non-covalently. The insoluble supports may be any compositions to which polypeptides can be bound, which is readily separated from soluble material, and which is otherwise compatible with the overall method. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports to which the receptor is bound include beads, e.g. magnetic beads, membranes and microtiter plates. These are typically made of glass, plastic (e.g. polystyrene), polysaccharides, nylon or nitrocellulose. Microtiter plates are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples.

Samples are then added to separately assayable supports (for example, separate wells of a microtiter plate) containing antibodies. Preferably, a series of standards, containing known concentrations of the polypeptides is assayed in parallel with the samples or aliquots thereof to serve as controls. Preferably, each sample and standard will be added to multiple wells so that mean values can be obtained for each. The incubation time should be sufficient for binding, generally, from about 0.1 to 3 hr is sufficient. After incubation, the insoluble support is generally washed of non-bound components. Generally, a dilute non-ionic detergent medium at an appropriate pH, generally 7–8, is used as a wash medium. From one to six washes may be employed, with sufficient volume to thoroughly wash non-specifically bound proteins present in the sample.

After washing, a solution containing a second antibody is applied. The antibody will bind with sufficient specificity such that it can be distinguished from other components present. The second antibodies may be labeled to facilitate direct, or indirect quantification of binding. Examples of labels that permit direct measurement of second receptor binding include radiolabels, such as ^{3}H or ^{125}I, fluorescers, dyes, beads, chemilumninescers, colloidal particles, and the like. Examples of labels which permit indirect measurement of binding include enzymes where the substrate may provide for a colored or fluorescent product. In a preferred embodiment, the antibodies are labeled with a covalently bound enzyme capable of providing a detectable product signal after addition of suitable substrate. Examples of suitable enzymes for use in conjugates include horseradish peroxidase, alkaline phosphatase, malate dehydrogenase and the like. Where not commercially available, such antibody-enzyme conjugates are readily produced by techniques known to those skilled in the art. The incubation time should be sufficient for the labeled ligand to bind available molecules. Generally, from about 0.1 to 3 hr is sufficient, usually 1 hr sufficing.

After the second binding step, the insoluble support is again washed free of non-specifically bound material. The signal produced by the bound conjugate is detected by conventional means. Where an enzyme conjugate is used, an appropriate enzyme substrate is provided so a detectable product is formed.

Other immunoassays are known in the art and may find use as diagnostics. Ouchterlony plates provide a simple determination of antibody binding. Western blots may be performed on protein gels or protein spots on filters, using a detection system specific for the polypeptide, conveniently using a labeling method as described for the sandwich assay.

Recombinant Mycobacterium

Mycobacterium, particularly those of the *M. tuberculosis* complex, are genetically engineered to contain specific deletions or insertions corresponding to the identified genetic markers. In particular, attenuated BCG strains are modified to introduce deleted genes encoding sequences important in the establishment of effective immunity. Alternatively, *M. bovis* or *M. tuberculosis* are modified by homologous recombination to create specific deletions in sequences that determine virulence, i.e. the bacteria are attenuated through recombinant techniques.

In order to stably introduce sequences into BCG, the *M. tb.* open reading frame corresponding to one of the deletions in Table 1 is inserted into a vector that is maintained in *M. bovis* strains. Preferably, the native 5' and 3' flanking sequences are included, in order to provide for suitable regulation of transcription and translation. However, in special circumstances, exogenous promoters and other regulatory regions may be included. Vectors and methods of transfection for BCG are known in the art. For example, U.S. Pat. No. 5,776,465, herein incorporated by reference, describes the introduction of exogenous genes into BCG.

In one embodiment of the invention, the complete deleted region is replaced in BCG. The junctions of the deletion are determined as compared to a wild type *M. tb.* or *M. bovis* sequence, for example as set forth in the experimental section. The deleted region is cloned by any convenient method, as known in the art, e.g. PCR amplification of the region, restriction endonuclease digestion, chemical synthesis, etc. Preferably the cloned region will further comprise flanking sequences of a length sufficient to induce homologous recombination, usually at least about 25 nt, more usually at least about 100 nt, or greater. Suitable vectors and methods are known in the art, for an example, see Norman et al. (1995) *Mol. Microbiol.* 16:755–760.

In an alternative embodiment, one or more of the deletions provided in Table 1 are introduced into a strain of *M. tuberculosis* or *M. bovis*. Preferably such a strain is reduced in virulence, e.g. H37Ra, etc. Methods of homologous recombination in order to effect deletions in mycobacteria are known in the art, for example, see Norman et al., supra.; Ganjam et al. (1991) *P.N.A.S.* 88:5433–5437; and Aldovini et al. (1993) *J. Bacteriol.* 175:7282–7289. Deletions may comprise an open reading frame identified in Table 1, or may extend to the full deletion, i.e. extending into flanking regions, and may include multiple open reading frames.

The ability of the genetically altered mycobacterium to cause disease may be tested in one or more experimental models. For example, *M. tb.* is known to infect a variety of animals, and cells in culture. In one assay, mammalian macrophages, preferably human macrophages, are infected. In a comparison of virulent, avirulent and attenuated strains of the *M. tuberculosis* complex, alveolar or peripheral blood monocytes are infected at a 1:1 ratio (Silver et al. (1998) *Infect Immun* 66(3):1190–1199; Paul et al. (1996) *J Infect Dis* 174(1):105–112.) The percentages of cells infected by the strains and the initial numbers of intracellular organisms are equivalent, as were levels of monocyte viability up to 7 days following infection. However, intracellular growth reflects virulence, over a period of one or more weeks. Mycobacterial growth may be evaluated by acid-fast staining, electron microscopy, and colony-forming units (cfu) assays. Monocyte production of tumor necrosis factor alpha may also be monitored as a marker for virulence.

Other assays for virulence utilize animal models. The *M. tb.* complex bacteria are able to infect a wide variety of animal hosts. One model of particular interest is cavitary tuberculosis produced in rabbits by aerosolized virulent tubercle bacilli (Converse et al. (1996) *Infect Immun* 64(11) :4776–4787). In liquefied caseum, the tubercle bacilli grow extracellularly for the first time since the onset of the disease and can reach such large numbers that mutants with antimicrobial resistance may develop. From a cavity, the bacilli enter the bronchial tree and spread to other parts of the lung and also to other people. Of the commonly used laboratory animals, the rabbit is the only one in which cavitary tuberculosis can be readily produced.

Vaccines may be formulated according to methods known in the art. Vaccines of the modified bacteria are administered to a host which may be exposed to virulent tuberculosis. In many countries where tuberculosis is endemic, vaccination may be performed at birth, with additional vaccinations as necessary. The compounds of the present invention are administered at a dosage that provides effective immunity while minimizing any side-effects. It is contemplated that the composition will be obtained and used under the guidance of a physician.

Conventional vaccine strains of BCG may be formulated in a combination vaccine with polypeptides identified in the present invention and produced as previously described, in order to improve the efficacy of the vaccine.

Various methods for administration may be employed. The formulation may be injected intramuscularly, intravascularly, subcutaneously, etc. The dosage will be conventional. The bacteria can be formulated into pharmaceutical compositions by combination with appropriate, pharmaceutically acceptable carriers or diluents, and may be formulated into preparations in semi-solid or liquid forms, such as solutions, injections, etc. The following methods and excipients are merely exemplary and are in no way limiting.

The modified bacteria can be formulated into preparations for injections by dissolving, suspending or emulsifying them in an aqueous or nonaqueous solvent, such as vegetable or other similar oils, synthetic aliphatic acid glycerides, esters of higher aliphatic acids or propylene glycol; and if desired, with conventional additives such as solubilizers, isotonic agents, suspending agents, emulsifying agents, stabilizers and preservatives. Unit dosage forms for injection or intravenous administration may comprise the bacteria of the present invention in a composition as a solution in sterile water, normal saline or another pharmaceutically acceptable carrier.

The term "unit dosage form," as used herein, refers to physically discrete units suitable as unitary dosages for human and animal subjects, each unit containing a predetermined quantity of vaccine, calculated in an amount sufficient to produce the desired effect in association with a pharmaceutically acceptable diluent, carrier or vehicle. The specifications for the unit dosage forms of the present invention depend on the particular bacteria employed and the effect to be achieved, and the pharmacodynamics associated with each complex in the host.

The pharmaceutically acceptable excipients, such as vehicles, adjuvants, carriers or diluents, are readily available to the public. Moreover, pharmaceutically acceptable auxiliary substances, such as pH adjusting and buffering agents, tonicity adjusting agents, stabilizers, wetting agents and the like, are readily available to the public.

The following examples are put forth so as to provide those of ordinary skill in the art with a complete disclosure and description of how to make and use the subject invention, and are not intended to limit the scope of what is regarded as the invention. Efforts have been made to ensure accuracy with respect to the numbers used (e.g. amounts, temperature, concentrations, etc.) but some experimental errors and deviations should be allowed for. Unless otherwise indicated, parts are parts by weight, molecular weight is average molecular weight, temperature is in degrees centigrade; and pressure is at or near atmospheric.

Experimental

Methods:

The technical methods used begin with extraction of whole genomic DNA from bacteria grown in culture.

Day 1

Inoculate culture medium of choice (LJ/7H9) and incubate at 35° C. until abundant growth. Dispense 500 μl 1× TE into each tube. (If DNA is in liquid medium, no TE needed.) Transfer loopful (sediment) of cells into microcentrifuge tube containing 500 μl of 1*TE. If taking DNA from liquid medium, let cells collect in bottom of flask. Pipette cells (about 1 ml) into tube. Heat 20 min at 80° C. to kill cells, centrifuge, resuspend in 500 μl of 1*TE. Add 50 μl of 10 mg/ml lysozyme, vortex, incubate overnight at 37° C.

Day2

Add 70 μl of 10% SDS and 10 μl proteinase K, vortex and incubate 20 min. at 65° C. Add 100 μl of 5M NaCl. Add 100 μl of CTAB/NaCl solution, prewarmed at 65° C. Vortex until liquid content white ("milky"). Incubate 10 min at 65° C. Outside of hood, prepare new microcentrifuge tubes labeled with culture # on top, and culture #, tube #, date on side. Add 550 μl isopropanol to each and cap. Back in the hood, add 750 μl of chloroform/isoamyl alcohol, vortex for 10 sec. Centrifuge at room temp for 5 min. at 12,000 g. Transfer aqueous supernatant in 180 μl amounts to new tube using pipetter, being careful to leave behind solids and non-aqueous liquid. Place 30 min at −20 C. Spin 15 min at room temp in a microcentrifuge at 12,000 g. Discard supernatant; leave about 20 μl above pellet. Add 1 ml cold 70% ethanol and turn tube a few times upside down. Spin 5 min at room temp in a microcentrifuge. Discard supernatant; leave about 20 μl above the pellet. Spin 1 min in a microcentrifuge and discard cautiously the last 20 μl supernatant just above the pellet using a pipetter (P-20). Be sure that all traces of ethanol are removed. Allow pellet to dry at room temp for 10 min or speed vac 2–3 min. (Place open tubes in speed vac, close lid, start rotor, turn on vacuum. After 3 min. push red button, turn off vacuum, turn off rotor. Check if pellets are dry by flicking tube to see if pellet comes away from side of tube.) Redissolve the pellet in 20–50 μl of ddH2O. Small pellets get 20, regular sized get 30 and very large get 50. DNA can be stored at 4° C. for further use.

DNA array: was made by spotting DNA fragments onto glass microscope slides which were pretreated with poly-L-lysine. Spotting onto the array was accomplished by a robotic arrayer. The DNA was cross-linked to the glass by ultraviolet irradiation, and the free poly-L-lysine groups were blocked by treatment with 0.05% succinic anhydride, 50% 1-methyl-2-pyrrolidinone and 50% borate buffer.

The majority of spots on the array were PCR-derived products, produced by selecting over 9000 primer pairs designed to amplify the predicted open reading frames of the sequences strain H37Rv (ftp.sanger.ac.uk/pub/TB.seq). Some internal standards and negative control spots including plasmid vectors and non-*M. tb.* DNA were also on the array.

Therefore, with the preparation for an array that contained the whole genome of *Mycobacterium tuberculosis*, we compared BCG-Connaught to *Mycobacterium tuberculosis*, using the array for competitive hybridization. The protocol follows:

DNA labeling protocol. Add 4 µg DNA in 20 µl H_2O, 2 ml dN10N6 and 36 µl H_2O. 2 ml DNA spike for each DNA sample, for total of 60 µl. Boil 3 minutes to denature DNA, then snap cool on ice water bath. Add 1 µl dNTP (5 mM ACG), 10 µl 10 buffer, 4 µl Klenow, 22 µl H_2O to each tube. Add 3 µl of Cy3 or Cy5 dUTP, for total of 100 µl. Incubate 3 hours at 37 C. Add 11 µl 3M NaAc, 250 µl 100% EtOH to precipitate, store O/N at −20 C. Centrifuge genomic samples 30 minutes at 13K to pellet precipitate. Discard supernatant, add 70% EtOH, spin 15 minutes, discard sup and speed-vac to dry. This provides DNA for two experiments.

DNA hybridization to microarray, protocol. Resuspend the labeled DNA in 11 µl dH_2O (for 2 arrays). Run out 1 µl DNA on a 1.5% agarose gel to document sample to be hybridized. Of the remaining 10 µl of solution, half will be used for this hyb, and half will be left for later date. Take 5 µl of solution Cy3 and add to same amount of Cy5 solution, for total volume 10 µl mixed labeled DNA. Add 1 µl tRNA, 2.75 µl 20×SSC, 0.4 µl SDS, for total volume 14.1 µl. Place on slide at array site, cover with 22 mm coverslip, put slide glass over and squeeze onto rubber devices, then hybridize 4 hours at 65 C. After 4 hours, remove array slides from devices, leave coverslip on, and dip in slide tray into wash buffer consisting of 1×SSC with 0.05% SDS for about 2 minutes. Cover slip should fall off into bath. After 2 minutes in wash buffer, dip once into a bath with 0.06×SSC, then rinse again in 0.06×SSC in separate bath. Dry slides in centrifuge about 600 rpm. They are now ready for scanning.

Fluorescence scanning and data acquisition. Fluorescence scanning was set for 20 microns/pixel and two readings were taken per pixel. Data for channel 1 was set to collect fluorescence from Cy3 with excitation at 520 nm and emission at 550–600 nm. Channel 2 collected signals excited at 647 nm and emitted at 660–705 nm, appropriate for Cy5. No neutral density filters were applied to the signal from either channel, and the photomultiplier tube gain was set to 5. Fine adjustments were then made to the photomultiplier gain so that signals collected from the two spots containing genomic DNA were equivalent.

To analyze the signal from each spot on the array, a 14×14 grid of boxes was applied to the data collected from the array such that signals from within each box were integrated and a value was assigned to the corresponding spot. A background value was obtained for each spot by integrating the signals measured 2 pixels outside the perimeter of the corresponding box. The signal and background values for each spot were imported into a spreadsheet program for further analysis. The background values were subtracted from the signals and a factor of 1.025 was applied to each value in channel 2 to normalize the data with respect to the signals from the genomic DNA spots.

Because the two samples are labeled with different fluorescent dyes, it is possible to determine that a spot of DNA on the array has hybridized to *Mycobacterium tuberculosis* (green dye) and not to BCG (red dye), thus demonstrating a likely deletion from the BCG genome.

However, because the array now contains spots representing 4000 spots, one may expect up to 100 spots with hybridization two standard deviations above or below the mean. Consequently, we have devised a screening protocol, where we look for mismatched hybridization in two consecutive genes on the genome. Therefore, we are essentially looking only for deletions of multiple genes at this point.

To confirm that a gene or group of genes is deleted, we perform Southern hybridization, employing a separate probe from the DNA on the array. Digestions of different mycobacterium DNAs are run on an agarose gel, and transferred to membranes. The membranes can be repeatedly used for probing for different DNA sequences. For the purposes of this project, we include DNA from the reference strain of *Mycobacterium tuberculosis* (H37Rv), from other laboratory strains, such as H37Ra, the O strain, from clinical isolates, from the reference strain of *Mycobacterium bovis*, and from different strains of *Mycobacterium bovis* BCG.

Once a deletion is confirmed by Southern hybridization, we then set out to characterize the exact genomic location. This is done by using polymerase chain reaction, with primers designed to be close to the edges of the deletion, see Talbot (1997) *J Clin Micro.* 35: 566–9

Primers have been chosen to amplify across the deleted region. Only in the absence of this region does one obtain an amplicon. PCR products were examined by electrophoresis (1.5% agarose) and ethidium bromide staining.

Once a short amplicon is obtained, this amplicon is then sequenced. A search of the genome database is performed to determine whether the sequence is exactly identical to one part of the *Mycobacterium tuberculosis* genome, and that the next part of the amplicon is exactly identical to another part of the *Mycobacterium tuberculosis* genome. This permits precise identification of the site of deletion.

Below follows an example of the kind of report obtained:

rd6 bridging PCR, blast search of sequence

emb|Z79701|MTCY277 *Mycobacterium tuberculosis* cosmid Y277

Length=38,908

Plus Strand HSPs:

Score=643 (177.7 bits), Expect=1.6e−54, Sum P(2)=1.6e−54

Identities=129/131 (98%), Positives=129/131 (98%), Strand=Plus/Plus

```
Query:     12  ANTAGTAATGTGCGAGCTGAGCGATGTCGCCGCTCCCAAAAATTACCAATGGTTNGGTCA     71  (SEQ ID NO:130)
               | |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct:  24874  AGTAGTAATGTGCGAGCTGAGCGATGTCGCCGCTCCCAAAAATTACCAATGGTTTGGTCA         (SEQ ID NO:131)

Query:     72  TGACGCCTTCCTAACCAGAATTGTGAATTCATACAAGCCGTAGTCGTGCAGAAGCGCAAC
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  24844  TGACGCCTTCCTAACCAGAATTGTGAATTCATACAAGCCGTAGTCGTGCAGAAGCGCAAC

Query:    132  ACTCTTGGAGT                                                  142
               |||||||||||
Sbjct:  24904  ACTCTTGGAGT                                                24914
```

Score=224 (61.9 bits), Expect=1.6e−54, Sum P(2)=1.6e−54
Identities=46/49 (93%), Positives=46/49 (93%), Strand=
Plus/Plus

```
Query:    141 GTGGCCTACAACGGNGCTCTCCGNGGCGCGGGCGTACCGGATATCTTAG    189 (SEQ ID NO:132)
              | |||||||||||| |||||||| |||||||||||||||||||||||||
Sbjct:  37645 GCGGCCTACAACGGCGCTCTCCGCGGCGCGGGCGTACCGGATATCTTAG  37693 (SEQ ID NO:133)
```

This process is repeated with each suggested deletion, beginning with the three previously described deletions to serve as controls. Sixteen deletions have been identified by these methods, and are listed in Table 1.

It is to be understood that this invention is not limited to the particular methodology, protocols, formulations and reagents described, as such may, of course, vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention which will be limited only by the appended claims.

It must be noted that as used herein and in the appended claims, the singular forms “a”, “and”, and “the” include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to “a complex” includes a plurality of such complexes and reference to “the formulation” includes reference to one or more formulations and equivalents thereof known to those skilled in the art, and so forth.

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention belongs. Although any methods, devices and material similar or equivalent to those described herein can be used in the practice or testing of the invention, the preferred methods, devices and material are now described.

All publications mentioned herein are incorporated herein by reference to the purpose of describing and disclosing, for example, the cell line, constructs, and methodologies that are described in the publications which might be used in connection with the presently described invention. The publications discussed above and throughout the text are provided solely for their disclosure prior to the filing date of the present application. Nothing herein is to be construed as an admission that the inventor are not entitled to antedate such disclosure by virtue of prior invention.

SEQUENCE LISTING

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gagctcatcg cccgtgatcg gcgacaaccc ctgcgatttg ccctggggat catggatgaa    180

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gacaaggtca accgggtggt cgcagagatg caagccgtca tgcggcaacg ggaaaccacc    480

ttcaaggaac accgagtggg ctcgatcggg atgtaccggc agctgcgtga cgatccaagt    540

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gcgttcggcg tccacgtcat catctccacg ccacgctgga cagagctgaa gtcgcgtgtt    720

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```

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gagtccgact accgcactcg ctgggagatt ccgatcggct tgcgcgagac ggacctgacg 1080

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gcgggggccg atgaggtctc cgcccaagcg gcgacggcgt tcacatcgga gggcatccaa 180

ttgctggctt ccaatgcatc ggcccaagac cagctccacc gtgcgggcga agcggtccag 240

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agcacgacga acccgatctt cggaatgccc tcccctggca gctcaacacc ggttggccag 600

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<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 7

ttgagcgcac ctgctgttgc tgctggtcct accgccgcgg gggcaaccgc tgcgcggcct   60

gccaccaccc gggtgacgat cctgaccggc agacggatga ccgatttggt actgccagcg   120

gcggtgccga tggaaactta tattgacgac accgtcgcgg tgctttccga ggtgttggaa   180

gacacgccgg ctgatgtact cggcggcttc gactttaccg cgcaaggcgt gtgggcgttc   240

gctcgtcccg gatcgccgcc gctgaagctc gaccagtcac tcgatgacgc cggggtggtc   300

gacgggtcac tgctgactct ggtgtcagtc agtcgcaccg agcgctaccg accgttggtc   360

gaggatgtca tcgacgcgat cgccgtgctt gacgagtcac ctgagttcga ccgcacggca   420

ttgaatcgct ttgtgggggc ggcgatcccg cttttgaccg cgcccgtcat cgggatggcg   480

atgcgggcgt ggtgggaaac tgggcgtagc ttgtggtggc cgttggcgat tggcatcctg   540

gggatcgctg tgctggtagg cagcttcgtc gcgaacaggt tctaccagag cggccacctg   600

gccgagtgcc tactggtcac gacgtatctg ctgatcgcaa ccgccgcagc gctggccgtg   660

ccgttgccgc gcggggtcaa ctcgttgggg gcgccacaag ttgccggcgc cgctacggcc   720

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gtgctgtttt tgaccttgat gacgcggggc ggccctcgga agcgtcatga gttggcgtcg 780

tttgccgtga tcaccgctat cgcggtcatc gcggccgccg ctgccttcgg ctatggatac 840

caggactggg tccccgcggg ggggatcgca ttcgggctgt tcattgtgac gaatgcggcc 900

aagctgaccg tcgcggtcgc gcggatcgcg ctgccgccga ttccggtacc cggcgaaacc 960

gtggacaacg aggagttgct cgatcccgtc gcgaccccgg aggctaccag cgaagaaacc 1020

ccgacctggc aggccatcat cgcgtcggtg cccgcgtccg cggtccggct caccgagcgc 1080

agcaaactgg ccaagcaact tctgatcgga tacgtcacgt cgggcaccct gattctggct 1140

gccggtgcca tcgcggtcgt ggtgcgcggg cacttctttg tacacagcct ggtggtcgcg 1200

ggtttgatca cgaccgtctg cggatttcgc tcgcggcttt acgccgagcg ctggtgtgcg 1260

tgggcgttgc tggcggcgac ggtcgcgatt ccgacgggtc tgacggccaa actcatcatc 1320

tggtacccgc actatgcctg gctgttgttg agcgtctacc tcacggtagc cctggttgcg 1380

ctcgtggtgg tcgggtcgat ggctcacgtc cggcgcgttt caccggtcgt aaaacgaact 1440

ctggaattga tcgacggcgc catgatcgct gccatcattc ccatgctgct gtggatcacc 1500

ggggtgtacg acacggtccg caatatccgg ttc 1533

<210> SEQ ID NO 8
<211> LENGTH: 840
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 8

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ggcctcgttt ttccgcagcc tccggcgccg atcgcggtca gcggaacgga ttcggtggta 120

gcagcaatca acgagaccat gccaagcatc gaatcgctgg tcagtgacgg gctgcccggc 180

gtgaaagccg ccctgactcg aacagcatcc aacatgaacg cggcggcgga cgtctatgcg 240

aagaccgatc agtcactggg aaccagtttg agccagtatg cattcggctc gtcgggcgaa 300

ggcctggctg gcgtcgcctc ggtcggtggt cagccaagtc aggctaccca gctgctgagc 360

acacccgtgt cacaggtcac gacccagctc ggcgagacgg ccgctgagct ggcaccccgt 420

gttgttgcga cggtgccgca actcgttcag ctggctccgc acgccgttca gatgtcgcaa 480

aacgcatccc ccatcgctca gacgatcagt caaaccgccc aacaggccgc ccagagcgcg 540

cagggcggca gcggcccaat gcccgcacag cttgccagcg ctgaaaaacc ggccaccgag 600

caagcggagc cggtccacga agtgacaaac gacgatcagg gcgaccaggg cgacgtgcag 660

ccggccgagg tcgttgccgc ggcacgtgac gaaggcgccg gcgcatcacc gggccagcag 720

cccggcgggg gcgttcccgc gcaagccatg gataccggag ccggtgcccg cccagcggcg 780

agtccgctgg cggcccccgt cgatccgtcg actccggcac cctcaacaac cacaacgttg 840

<210> SEQ ID NO 9
<211> LENGTH: 2187
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 9

atgagtatta ccaggccgac gggcagctat gccagacaga tgctggatcc gggcggctgg 60

gtggaagccg atgaagacac tttctatgac cgggcccagg aatatagcca ggttttgcaa 120

agggtcaccg atgtattgga cacctgccgc cagcagaaag gccacgtctt cgaaggcggc 180

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ctatggtccg gcggcgccgc caatgctgcc aacggcgccc tgggtgcaaa catcaatcaa 240

ttgatgacgc tgcaggatta tctcgccacg gtgattacct ggcacaggca tattgccggg 300

ttgattgagc aagctaaatc cgatatcggc aataatgtgg atggcgctca acgggagatc 360

gatatcctgg agaatgaccc tagcctggat gctgatgagc gccataccgc catcaattca 420

ttggtcacgg cgacgcatgg ggccaatgtc agtctggtcg ccgagaccgc tgagcgggtg 480

ctggaatcca agaattggaa acctccgaag aacgcactcg aggatttgct tcagcagaag 540

tcgccgccac ccccagacgt gcctaccctg gtcgtgccat ccccgggcac accgggcaca 600

ccgggaaccc cgatcacccc gggaaccccg atcaccccgg gaaccccaat cacacccatc 660

ccgggagcgc cggtaactcc gatcacacca acgcccggca ctcccgtcac gccggtgacc 720

ccgggcaagc cggtcacccc ggtgaccccg gtcaaaccgg gcacaccagg cgagccaacc 780

ccgatcacgc cggtcacccc cccggtcgcc ccggccacac cggcaacccc ggccacgccc 840

gttaccccag ctcccgctcc acacccgcag ccggctccgg caccggcgcc atcgcctggg 900

ccccagccgg ttacaccggc cactcccggt ccgtctggtc cagcaacacc gggcacccca 960

gggggcgagc cggcgccgca cgtcaaaccc gcggcgttgg cggagcaacc tggtgtgccg 1020

ggccagcatg cgggcggggg gacgcagtcg gggcctgccc atgcggacga atccgccgcg 1080

tcggtgacgc cggctgcggc gtccggtgtc ccgggcgcac gggcggcggc cgccgcgccg 1140

agcggtaccg ccgtgggagc gggcgcgcgt tcgagcgtgg gtacggccgc ggcctcgggc 1200

gcggggtcgc atgctgccac tgggcgggcg ccggtggcta cctcggacaa ggcggcggca 1260

ccgagcacgc gggcggcctc ggcgcggacg gcacctcctg cccgcccgcc gtcgaccgat 1320

cacatcgaca aacccgatcg cagcgagtct gcagatgacg gtacgccggt gtcgatgatc 1380

ccggtgtcgg cggctcgggc ggcacgcgac gccgccactg cagctgccag cgcccgccag 1440

cgtggccgcg gtgatgcgct gcggttggcg cgacgcatcg cggcggcgct caacgcgtcc 1500

gacaacaacg cgggcgacta cgggttcttc tggatcaccg cggtgaccac cgacggttcc 1560

atcgtcgtgg ccaacagcta tgggctggcc tacatacccg acgggatgga attgccgaat 1620

aaggtgtact tggccagcgc ggatcacgca atcccggttg acgaaattgc acgctgtgcc 1680

acctacccgg ttttggccgt gcaagcctgg gcggctttcc acgacatgac gctgcgggcg 1740

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gagccagatg acattccgga gagcggcaaa atgacgggcc ggtcgcggct ggaggtcgtc 1860

gacccctcgg cggcggctca gctggccgac actaccgatc agcgtttgct cgacttgttg 1920

ccgccggcgc cggtggatgt caatccaccg ggcgatgagc ggcacatgct gtggttcgag 1980

ctgatgaagc ccatgaccag caccgctacc ggccgcgagg ccgctcatct gcgggcgttc 2040

cgggcctacg ctgcccactc acaggagatt gccctgcacc aagcgcacac tgcgactgac 2100

gcggccgtcc agcgtgtggc cgtcgcggac tggctgtact ggcaatacgt caccgggttg 2160

ctcgaccggg ccctggccgc cgcatgc 2187

<210> SEQ ID NO 10
<211> LENGTH: 426
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 10

atggccggac tgaacattta cgtgaggcgc tggcggacag cgcttcacgc aaccgtgtcg 60

gcattgatag ttgccatcct cggactcgcc atcaccccgg tcgctagtgc ggcgacggcc 120

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agggcgacgt tgtcggtgac atcgacgtgg cagaccggtt tcatcgcccg cttcaccatc 180

acaaactcga gcacggcgcc gctaaccgat tggaagcttg aattcgactt gccggcagga 240

gaatccgtct tgcacacatg gaatagcacc gttgcacgat ctggcacgca ctacgttctc 300

agcccagcga attggaatcg catcattgcc cccggtggtt cagccacggg cggcctaaga 360

ggcgggctga ccggttctta ctcgccgccg tcgagttgtc tgctcaacgg gcaatatcct 420

tgcacc 426

<210> SEQ ID NO 11
<211> LENGTH: 597
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 11

gtgaactcac cactggtcgt cggcttcctg gcctgcttca cgctgatcgc cgcgattggc 60

gcgcagaacg cattcgtgct gcggcaggga atccagcgtg agcacgtgct gccggtggtg 120

gcgctgtgca cggtgtccga catcgtgctg atcgccgccg gtatcgcggg gttcggcgca 180

ttgatcggcg cacatccgcg tgcgctcaat gtcgtcaagt ttggcggcgc cgccttccta 240

atcggctacg ggctacttgc ggcccggcgg gcgtggcgac ctgttgcgct gatcccatct 300

ggcgccacgc cggttcgctt agccgaggtc ctggtgacct gtgcggcatt cacgttcctc 360

aacccacacg tctacctcga caccgtcgtg ttgctaggcg cgctggccaa cgagcacagc 420

gaccagcgct ggctgttcgg cctcggcgcg gtcacagcca gtgcggtatg gttcgccacc 480

ctcgggttcg gagccggccg gttgcgcggg ctgttcacca accccggctc gtggagaatc 540

ctcgacggcc tgatcgcggt catgatggtt gcgctgggaa tctcgctgac cgtgacc 597

<210> SEQ ID NO 12
<211> LENGTH: 909
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 12

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ggcagcttcg atgcggccgc ggagcgccta catgtcaccc cgtcggctgt cagtcagcgc 120

atcaagtcgt tggagcagca ggtcggccag gtgctggtgg tcagggaaaa gccatgtcgg 180

gcgacgaccg caggtatccc gctgttgcgg ttggccgcgc aaacagcgtt gctcgagtcc 240

gaggcgctcg ctgaaatggg tggcaacgcg tcgctgaaac gcacgcggat caccattgcg 300

gtaaacgccg attccatggc gacatggttt tcggccgtgt tcgacggtct cggcgacgtc 360

ctgctcgacg ttcggatcga ggaccaggac cattccgcgc ggctgctacg ggagggtgtg 420

gcgatgggcg cggtgaccac cgagcggaac ccggtgccgg gctgccgggt gcacccgctg 480

ggtgaaatgc gctacctacc agtggccagc aggccattcg tccagcgcca tctatccgac 540

gggttcactg ccgccgcggc ggctaaagct ccgtcactgg cgtggaatcg tgacgatggg 600

ctgcaggaca tgttggtgcg taaggccttt cgtcgcgcca tcaccagacc gacgcacttt 660

gtcccgacca cagagggctt caccgccgca gcgcgcgccg ggctgggatg gggcatgttc 720

cccgagaagc tggcagcatc tccgcttgcc gatggatcgt tcgtacgggt ctgcgacata 780

cacctcgacg tccctctcta ttggcaatgc tggaaactgg acagtccgat catcgcgcga 840

attaccgaca cggtgagggc ggcggcaagc ggtctgtacc ggggccagca acgccgccgc 900

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cgaccgggt                                                            909


<210> SEQ ID NO 13
<211> LENGTH: 651
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 13

atgactccac gcagccttgt tcgcatcgtt ggtgtcgtgg ttgcgacgac cttggcgctg     60

gtgagcgcac ccgccggcgg tcgtgccgcg catgcggatc cgtgttcgga catcgcggtc    120

gttttcgctc gcggcacgca tcaggcttct ggtcttggcg acgtcggtga ggcgttcgtc    180

gactcgctta cctcgcaagt tggcgggcgg tcgattgggg tctacgcggt gaactaccca    240

gcaagcgacg actaccgcgc gagcgcgtca aacggttccg atgatgcgag cgcccacatc    300

cagcgcaccg tcgccagctg cccgaacacc aggattgtgc ttggtggcta ttcgcagggt    360

gcgacggtca tcgatttgtc cacctcggcg atgccgcccg cggtggcaga tcatgtcgcc    420

gctgtcgccc ttttcggcga gccatccagt ggtttctcca gcatgttgtg gggcggcggg    480

tcgttgccga caatcggtcc gctgtatagc tctaagacca taaacttgtg tgctcccgac    540

gatccaatat gcaccggagg cggcaatatt atggcgcatg tttcgtatgt tcagtcgggg    600

atgacaagcc aggcggcgac attcgcggcg aacaggctcg atcacgccgg a             651


<210> SEQ ID NO 14
<211> LENGTH: 1674
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 14

gtgtcatttc tggtcgtggt tcccgagttc ttgacgtccg cggcagcgga tgtggagaac     60

ataggttcca cactgcgcgc ggcgaatgcc gcggctgccg cctcgaccac cgcgcttgcg    120

gccgctggcg ctgatgaggt atcggcggcg gtggcagcgc tgtttgccag gttcggtcag    180

gaatatcaag cggtcagcgc gcaggcgagc gctttccatc aacagttcgt gcagacgctg    240

aactcggcgt caggatcgta tgcggccgcg gaggccacca tcgcgtcaca gttgcagacc    300

gcgcagcacg atctgctggg cgcggtcaat gcaccaaccg aaacgttgtt ggggcgtccg    360

ctaatcggcg acggagcacc cgggacggca acgagtccga atggcggggc gggtgggctg    420

ctgtacggca acggcggcaa cggttattcc gcgacggcgt cgggggtcgg cggcggggcc    480

ggcggttccg cggggttgat cggcaatggc ggcgccgggg gagccggcgg acccaacgcc    540

cccgggggag ccggcggcaa cggtggctgg ctgctcggca acggcgggat cggcgggccc    600

gggggcgcgt cgagcatccc cggcatgagt ggtggagccg gcggaaccgg cggtgccgca    660

ggacttttgg gctggggagc gaacggcgga gccggcggcc tcggtgatgg agtcggtgtc    720

gatcgtggca cgggcggcgc cggaggccgc ggcggcctgt tgtatggcgg atacggcgtc    780

agtgggccag gcggcgacgg cagaaccgtc ccgctggaga taattcatgt cacagagccg    840

acggtacatg ccaacgtcaa cggcggaccg acgtcaacca ttctggtcga caccggatcc    900

gctggtcttg ttgtctcgcc tgaggatgtc gggggaatcc tgggagtgct tcacatgggc    960

ctcccaaccg gattgagcat cagcggttac agcgggggc tgtactacat cttcgccacg    1020

tataccacga cggtggactt cgggaatggc atcgtcaccg cgccgaccgc cgttaatgtc   1080

gtcctcttgt ccatcccaac gtccccttc gccatttcga cctacttcag cgccttgctg    1140

gccgatccga caacaactcc gttcgaagcc tatttcggtg ccgtcggcgt ggacggcgtt   1200
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ctgggagttg ggcccaatgc ggtgggacca ggccccagca ttccgacgat ggcgttaccg 1260

ggtgacctca accagggagt gctcatcgac gcacccgcag gtgagctcgt gttcggtccc 1320

aacccgctac ctgcgcccaa cgtcgaggtc gtcggatcgc cgatcaccac cctgtacgta 1380

aagatcgatg gtgggactcc catacccgtc ccctcgatca tcgattccgg tggggtaacg 1440

ggaaccatcc cgtcatatgt catcggatcc ggaaccctgc cggcgaacac aaacattgag 1500

gtctacacca gccccggcgg tgatcggctc tacgcgttca acacaaacga ttaccgcccg 1560

accgtcattt catccggcct gatgaatacc gggttcttgc ccttcagatt ccagccggtg 1620

tacatcgact acagccccag cggtataggg acaacagtct ttgatcatcc ggcg 1674

<210> SEQ ID NO 15
<211> LENGTH: 1674
<212> TYPE: DNA
<213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 15

gtgtcatttc tggtcgtggt tcccgagttc ttgacgtccg cggcagcgga tgtggagaac 60

ataggttcca cactgcgcgc ggcgaatgcc gcggctgccg cctcgaccac cgcgcttgcg 120

gccgctggcg ctgatgaggt atcggcggcg gtggcagcgc tgtttgccag gttcggtcag 180

gaatatcaag cggtcagcgc gcaggcgagc gctttccatc aacagttcgt gcagacgctg 240

aactcggcgt caggatcgta tgcggccgcg gaggccacca tcgcgtcaca gttgcagacc 300

gcgcagcacg atctgctggg cgcggtcaat gcaccaaccg aaacgttgtt ggggcgtccg 360

ctaatcggcg acggagcacc cgggacggca acgagtccga atggcggggc gggtgggctg 420

ctgtacggca acggcggcaa cggttattcc gcgacggcgt cgggggtcgg cggcggggcc 480

ggcggttccg cggggttgat cggcaatggc ggcgccgggg gagccggcgg acccaacgcc 540

cccgggggag ccggcggcaa cggtggctgg ctgctcggca acggcgggat cggcgggccc 600

gggggcgcgt cgagcatccc cggcatgagt ggtggagccg gcggaaccgg cggtgccgca 660

ggacttttgg gctggggagc gaacggcgga gccggcggcc tcggtgatgg agtcggtgtc 720

gatcgtggca cgggcggcgc cggaggccgc ggcggcctgt tgtatggcgg atacggcgtc 780

agtgggccag gcggcgacgg cagaaccgtc ccgctggaga taattcatgt cacagagccg 840

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gtcctcttgt ccatcccaac gtccccttc gccatttcga cctacttcag cgccttgctg 1140

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ctgggagttg ggcccaatgc ggtgggacca ggccccagca ttccgacgat ggcgttaccg 1260

ggtgacctca accagggagt gctcatcgac gcacccgcag gtgagctcgt gttcggtccc 1320

aacccgctac ctgcgcccaa cgtcgaggtc gtcggatcgc cgatcaccac cctgtacgta 1380

aagatcgatg gtgggactcc catacccgtc ccctcgatca tcgattccgg tggggtaacg 1440

ggaaccatcc cgtcatatgt catcggatcc ggaaccctgc cggcgaacac aaacattgag 1500

gtctacacca gccccggcgg tgatcggctc tacgcgttca acacaaacga ttaccgcccg 1560

accgtcattt catccggcct gatgaatacc gggttcttgc ccttcagatt ccagccggtg 1620

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tacatcgact acagccccag cggtataggg acaacagtct ttgatcatcc ggcg 1674

<210> SEQ ID NO 16
<211> LENGTH: 417
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 16

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ctggtcgcgg ccgccctggc cggcgcccat agccccgtca tgtctgcacc caccgtcgcc 120

gaatgcctga ttgtcttgac cgcccgtcac ggccccgttg cgcgcacgat cttcgaacga 180

cttcgcagcg aaatcggctt gagcgtgtca tctttcaccg ccgagcatgc cgctgccacg 240

caacgagcct ttctgcgata cggcaagggg cgccaccgcg cggctctcaa cttcggagac 300

tgtatgacgt acgcgaccgc ccagctgggc caccaaccac tgctggccgt cggcaacgac 360

ttcccgcaaa ccgaccttga gttccgcggc gtcgtcggct actggccagg cgtcgcg 417

<210> SEQ ID NO 17
<211> LENGTH: 684
<212> TYPE: DNA
<213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 17

gtgcgcatca agatcttcat gctggtcacg gctgtcgttt tgctctgttg ttcgggtgtg 60

gccacggccg cgcccaagac ctactgcgag gagttgaaag gcaccgatac cggccaggcg 120

tgccagattc aaatgtccga cccggcctac aacatcaaca tcagcctgcc cagttactac 180

cccgaccaga agtcgctgga aaattacatc gcccagacgc gcgacaagtt cctcagcgcg 240

gccacatcgt ccactccacg cgaagccccc tacgaattga atatcacctc ggccacatac 300

cagtccgcga taccgccgcg tggtacgcag gccgtggtgc tcaaggtcta ccagaacgcc 360

ggcggcacgc acccaacgac cacgtacaag gccttcgatt gggaccaggc ctatcgcaag 420

ccaatcacct atgacacgct gtggcaggct gacaccgatc cgctgccagt cgtcttcccc 480

attgtgcaag gtgaactgag caagcagacc ggacaacagg tatcgatagc gccgaatgcc 540

ggcttggacc cggtgaatta tcagaacttc gcagtcacga acgacggggt gattttcttc 600

ttcaacccgg gggagttgct gcccgaagca gccggcccaa cccaggtatt ggtcccacgt 660

tccgcgatcg actcgatgct ggcc 684

<210> SEQ ID NO 18
<211> LENGTH: 684
<212> TYPE: DNA
<213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 18

gtgcgcatca agatcttcat gctggtcacg gctgtcgttt tgctctgttg ttcgggtgtg 60

gccacggccg cgcccaagac ctactgcgag gagttgaaag gcaccgatac cggccaggcg 120

tgccagattc aaatgtccga cccggcctac aacatcaaca tcagcctgcc cagttactac 180

cccgaccaga agtcgctgga aaattacatc gcccagacgc gcgacaagtt cctcagcgcg 240

gccacatcgt ccactccacg cgaagccccc tacgaattga atatcacctc ggccacatac 300

cagtccgcga taccgccgcg tggtacgcag gccgtggtgc tcaaggtcta ccagaacgcc 360

ggcggcacgc acccaacgac cacgtacaag gccttcgatt gggaccaggc ctatcgcaag 420

ccaatcacct atgacacgct gtggcaggct gacaccgatc cgctgccagt cgtcttcccc 480

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ggcttggacc cggtgaatta tcagaacttc gcagtcacga acgacggggt gattttcttc 600

ttcaacccgg gggagttgct gcccgaagca gccggcccaa cccaggtatt ggtcccacgt 660

tccgcgatcg actcgatgct ggcc 684

<210> SEQ ID NO 19
<211> LENGTH: 1443
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 19

gtggtcggcc cgcggacgag aggatatgcg atccacaagc tgggtttctg cagcgtcgtc 60

atgctcggga tcaactcgat aatcggcgcc ggtatcttcc taactccagg tgaggtgatc 120

gggctcgcag gacccttcgc gccgatggcc tatgttttag ctggcatttt cgcgggtgtc 180

gtggcgatcg tcttcgcgac ggcggcaagg tacgtcagaa caaacggtgc ctcctacgcc 240

tacacaacgg ccgcatttgg gcgccggatc ggcatctatg tcggtgtcac ccacgccatt 300

accgcgtcca tcgcttgggg ggtgttggct tctttttttcg tctcgacgct gttgcgagtg 360

gccttccccg acaaggcctg ggccgacgcc gagcaactgt tcagtgtgaa gacgctgacg 420

tttctcggct ttatcggcgt gctgttggcc atcaacctct tcggcaaccg ggcgatcaag 480

tgggccaacg gaacgtcaac ggtaggcaag gcattcgcgc tctcggcatt cattgtcggc 540

gggctgtgga tcatcaccac ccagcacgtg aacaactacg caacggcgtg gtcggcatac 600

agcgcgaccc cgtactcgtt gcttggcgtc gccgaaattg gcaagggcac gttctcgagt 660

atggcgctgg ccacgattgt cgcgttgtac gcattcaccg gtttcgaatc gatcgcgaac 720

gccgccgaag aaatggacgc gccggaccgg aacctgccga gagctatacc gatcgcgatc 780

ttctcggttg gcgcgatcta cttgctcacc ctaacggtag cgatgctgct cggatcgaac 840

aagatcgccg cgtcggacga caccgtgaaa ctggccgcgg ccatcggaaa cgctaccttc 900

cgaacgatca tcgtcgtcgg agccctgata tcgatgttcg gcatcaatgt cgcggcctcg 960

ttcggtgcac cgcggctttg gaccgcgtta gcggacagcg ggttctgcc gacacgcttg 1020

tcacgcaaga accaatacga cgtgccgatg gtctccttcg caattacggc gtcgttggcg 1080

ctcgcattcc cgttggcgct gcggttcgac aacctgcacc tgaccggcct ggcggtgatc 1140

gcccgattcg tccagttcat catcgtgccg atcgctctca tcgcattggc gaggtctcag 1200

gcagtagaac atgctgctgt gcggcgaaat gcgttcaccg acaaggtgtt accgcttgtt 1260

gcgatcgtgg tctcggttgg gctggcagtg tcctacgact accgctgcat ctttctagtg 1320

cggggtggtc cgaactactt ctcgattgct ttgatcgtga tcacgttcgt cgtggtaccg 1380

gcgatggctt atctgcacta ctaccgaatc attcgccggg ttggcgatcg gccgagcact 1440

cgc 1443

<210> SEQ ID NO 20
<211> LENGTH: 846
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 20

atgggtgagg cgaacatccg cgagcaggcg atcgccacga tgccacgggg tggccccgac 60

gcgtcttggc tggatcgtcg attccagacc gacgcactgg agtacctcga ccgcgacgat 120

-continued

gtgcccgatg aggtcaaaca gaagatcatc ggggtgctcg accgggtggg caccctgacc 180

aacctgcacg agaagtacgc ccggatagcc ctgaaacttg tttctgacat tcccaacccg 240

cgaatcctgg aacttggtgc gggccatggc aagctctcag cgaaaatcct cgagctacac 300

ccgacagcga cggtgacgat cagcgatcta gatcccacct cggtggccaa catcgccgcg 360

ggagagctgg gaacacatcc gcgagcacgc acccaagtga tcgacgccac cgcaatcgac 420

ggccacgacc acagctatga cctggcggtc ttcgcgctgg catttcacca cctgccgcct 480

acggtcgcct gcaaagcgat cgccgaggcc acccgggtgg ggaagcgctt tctgatcatc 540

gacctcaaac ggcagaaacc gctgtcgttc acgctctctt cggtgctgct actgccgctc 600

cacctactgc tgctgccatg gtcgtcgatg cgctcgagca tgcacgacgg ctttatcagc 660

gcactacgtg cctacagtcc ctcggcgttg cagacgcttg cccgcgccgc cgatccggga 720

atgcaggttg aaatcttgcc cgcaccgacc aggctattcc cgccatcgct cgccgttgtg 780

ttctcccgtt cgagctcagc gccaacggaa tctagcgagt gctcggccga tcgccaaccc 840

ggcgaa 846

<210> SEQ ID NO 21
<211> LENGTH: 1407
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 21

gtgagataca ctacacctgt gcgtgctgct gtctacctcc gaatctcaga agaccgctcc 60

ggcgaacagc tcggcgtggc ccgccaacgc gaggactgcc taaagctgtg cgggcagcga 120

aaatgggtgc ccgtcgagta cctcgacaac gacgtcagcg catcaaccgg caagcgccgc 180

cccgcctacg agcagatgtt ggccgacatc accgccggca agatcgccgc cgtggtggcc 240

tgggacctgg accggctcca tcgccgtccc atcgagctgg aagccttcat gtcattagcc 300

gacgagaagc ggctggccct ggccaccgtc gccggcgacg ttgacctggc gacaccccag 360

ggccggctag tcgcccgcct gaaggggtcg gtggccgctc acgaaaccga gcacaagaag 420

gcacgacagc gccgcgccgc ccgccagaaa gctgaacgcg gccaccccaa ctggtcgaaa 480

gccttcggct acctgcccgg ccccaacggt cccgaacccg acccccggac agcgccgctg 540

gtcaaacagg cctacgccga catcctcgcc ggggcgtccc tgggcgacgt gtgccgccag 600

tggaacgacg ccggggcgtt caccatcacc ggccgcccgt ggacgactac aacgctgtcg 660

aaattcttgc gcaaaccccg caacgccgga ctacgcgcat ataagggtgc ccgctacggc 720

ccggtggacc gcgacgcgat tgtcggcaag gcccagtggt cgccgctggt ggacgaggcg 780

acgttctggg ccgcccaggc cgtgctggac gcccccggcc gcgcccccgg ccgcaaaagc 840

gtgcgccgcc acctgctgac cgggctggca ggctgcggca aatgcggcaa ccacctggcc 900

ggcagctacc gcaccgacgg ccaggtcgtc tacgtgtgca aggcgtgcca cggggtggcc 960

atcctggccg acaacatcga accgatcctg tatcacatcg tggccgagcg gctggccatg 1020

cccgacgccg ttgacttgtt gcgccgggag attcacgacg ccgccgaagc cgaaaccatc 1080

cgcctggaac tggaaaccct ctacggggag ctggacaggc tcgccgtcga acgcgccgaa 1140

gggctactga ccgcgcgcca ggtgaagatc agcaccgaca tcgtcaacgc caagataacg 1200

aaacttcagg cccgccaaca ggatcaggaa cggctccgag tgttcgacgg gataccgttg 1260

ggaacaccgc aagtcgccgg gatgatagcc gagctgtcgc cggaccggtt ccgcgccgtc 1320

ctcgacgtcc tcgctgaagt cgttgtccag ccggtcggca agagcggcag gatattcaat 1380

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cccgaacggg tgcaggtgaa ttggcga 1407

<210> SEQ ID NO 22
<211> LENGTH: 513
<212> TYPE: DNA
<213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 22

atgagccggc accacaacat cgtgatcgtc tgtgaccacg gccgcaaagg cgatggccgc 60

atcgaacacg agcgctgcga tcttgtcgcg ccgatcattt gggtcgacga gacccagggc 120

tggttaccgc aggcgccagc ggtggcaaca ttactcgacg acgacaacca gccgcgagcc 180

gttattggct tgccgcccaa cgagtctcgc ctacgacctg aaatgcgccg cgacgggtgg 240

gtgcggctgc actgggaatt cgcctgcctg aggtacggcg ccgccggcgt gcgcacgtgc 300

gagcagcggc ccgtgcgggt tcgcaacggc gacctgcaaa cactgtgcga gaacgttccg 360

cggctactga ccggactggc cggcaacccc gactacgcac cgggttttgc ggtgcagtcg 420

gacgcggtgg tcgtcgccat gtggctgtgg cgcacgctct gcgaaagcga cacgccgaac 480

aaactacgcg ccaccccaac gcgtggtagc tgc 513

<210> SEQ ID NO 23
<211> LENGTH: 219
<212> TYPE: DNA
<213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 23

gtgtcgacca tctaccatca tcgcggccgc gtagccgcac tgtctcgttc ccgcgcatcc 60

gacgatcccg agttcatcgc cgcgaaaacc gatctcgttg ccgcgaacat cgcggactac 120

ctcatccgca ccctcgccgc agcgccgccc ctgactgacg agcagcgcac ccggctggcc 180

gagctgctgc gccccgtgcg gcggtcaggc ggtgcccga 219

<210> SEQ ID NO 24
<211> LENGTH: 396
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 24

atgaccgccg gcgccggcgg gtcgccgccg acgcgacgat gcccggccac ggaggaccgg 60

gcacccgcga cagtcgccac accgtctagc gccgatccta ccgcgtcacg cgccgtgtcg 120

tggtggtcgg tgcacgagca tgtcgcgccg gtcctggatg ctgccgggtc gtggccgatg 180

gccggcacac cggcctggcg tcagctcgac gacgccgatc ctcgcaaatg ggccgcgatc 240

tgcgacgcag cccggcactg ggctctgagg gtagagacgt gccaggaggc gatggcgcag 300

gcgtcacgtg acgtatctgc ggccgccgac tggcccggca tcgcccgcga gatcgtccga 360

cggcgcggcg tgtacatccc gcgggcgggg gtggcg 396

<210> SEQ ID NO 25
<211> LENGTH: 1413
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 25

atggccgaca tcccctacgg caccgactat cccgacgccc cctggatcga ccgggacggg 60

cacgtgctca tcgacgacgg tggcaaaccg acgcaagttc atcgcggcca agcccgaatc 120

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gcctaccggc tagccgaacg ttaccaggac aagctgctgc acgtggccgg gatcggctgg 180

cactcctggg acggcagacg ctgggcagcc gacgaccgcg gcgaagccaa acgtgcagtg 240

ctggcagagc tgcgccaagc gctctcagac agcctcaacg acaaggaatt acgcgccgac 300

gtccgaaaat gcgaatcggc gtccggcgtg gccggcgtgc tcgacctggc cgccgcactg 360

gtaccattcg ccgcgacggt agccgacctc gacagcgacc cgcacttgct caacgtcgcg 420

aatgggacgc tggacctgca cacgctcaaa ttgcggcccc acgcgcccgc tgaccgcatc 480

acaaagatat gccgcggtgc ctaccagtcc gacaccgaat cgcctctctg gcaagcgttc 540

ttgacccgcg ttctgcccga tgaaggtgtg cgcgggttcg tgcaacgcct ggccggcgtc 600

ggcctactag gcaccgtccg cgaacatgtc ctggcgattc ttatcggtgt aggtgccaac 660

ggaaaatctg tgttcgacaa ggcgattcgc tatgcccttg gcgattatgc ctgcaccgct 720

gagcctgacc ttttcatgca ccgggaaaac gctcacccaa caggcgaaat ggacctccgc 780

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gaattcacgc cgtcacatac cccactgctc atcaccaacc acctaccgag agtgcccggc 960

gatgatacgg ccatctggcg gcgaattcga gtggtgccgt ttgaagtagt gattcctgcc 1020

gacgagcagg accgggaact ggacgcacgg ttgcagttgg aggccgacag catcctgtcc 1080

tgggcggtgg ccggatggag cgactatcag cgaatcggac tatcccagcc ggacgcggtg 1140

ctcgcggcaa cgtcgaatta ccgcgaggac tccgacacga taaagaggtt catcgacgac 1200

gaatgcgtca ccagctcgcc ggtgctgaaa gccactacta cgcatctgtt cgaggcgtgg 1260

caaaggtggc gggtgcaaga aggcgtaccc gaaatctcgc gcaaagcgtt cggccagtcg 1320

ctcgacaccc acggataccc ggtcactgac aaggcccgtg atggtcgttg gcgggccgga 1380

atagcggtga gaggggccga tgatttcgat gat 1413

<210> SEQ ID NO 26
<211> LENGTH: 393
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 26

atgaccgctg tcgcgatcac cccggcatcc ggcggtcggc acagcgtccg attcgcctac 60

gactctgcga tcgtgtcgtt gatcaagtcc acgatccccg cctatgcccg ctcctggtcc 120

gcgcacaccc gctgctggtt catcgacgct gactggaccc cactgctggc cgccgagctg 180

cgctaccacg gccacaccgt caccggaccc gccgacccgg cgcaacagca gtgcaccgac 240

tgggccaaag cgttgttccg ggcggtcgga ccccagcgga cacccgccgt gtacagggct 300

ttatccaaag tgctgcaccc cgacgcccca accggatgcc cgatactgca acagcagctc 360

aatgccgcca gaaccgcact taccaaccct gct 393

<210> SEQ ID NO 27
<211> LENGTH: 270
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 27

atggctgaaa cccccgacca cgccgaactg cggcgacgaa tcgccgacat ggctttcaac 60

gccgatgtcg gtatggcgac ctgcaaacgc tgtggtgacg ccgtgccgta catcatcctg 120

ccgaacctgc agaccggcga acccgtcatg ggtgtcgccg acaacaaatg gaagcgcgcg 180

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aactgtcccg tcgacgtcgg taagccgtgc ccgttcctaa tcgccgaggg tgtcgccgac 240

agcaccgacg acaccataga ggtcgaccag 270

<210> SEQ ID NO 28
<211> LENGTH: 312
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 28

gtgaccccga tcaaccggcc cctgaccaac gacgaacgac aactgatgca cgagctggca 60

gtccaggttg tctgctcgca gacgggttgc tcacccgatg cggcggtcga agcactcgaa 120

tccttcgcga aagacggaac acttatcctc cgcggcgaca ccgagaacgc ctacctcgaa 180

gccggaggca atgttcttgt ccatgccgat cgtgactggc ttgccttcca cgcgtcgtat 240

cccggcaacg acccgctgcg agacgcccga cctatcgagc aggacgacga ccaggggcg 300

gggtcgccat cg 312

<210> SEQ ID NO 29
<211> LENGTH: 468
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 29

atgccaagac caccgaaacc ggcccggctc aaactggttg agggccgctc ccccggccgc 60

gattccggcg gccggaaagt ccccgagtcg ccgaagttta tccgtcaggc accggatgcc 120

ccggactggc tcgacgccga ggcgctggcc gaatggcggc gcgtcgcacc gactttggag 180

cggcttgacc tgctcaaacc tgaggatcgg gcgctcctgt ccgcgtactg cgagacctgg 240

tccgtctacg tcgcggcggt tcagcgggtc cgcgccgaag gcctcacaat tacctcaccg 300

aaatccggtg tcgtgcaccg gaacccggcg gtgacggttg cggagacggc gcgcatgcat 360

ctgctgcgct tggcctccga gtttggcctg accccggccg ccgagcagcg actggcggtg 420

gcgccgggcg acgacggcga cgggctcaac ccgtttgccc cggaccgg 468

<210> SEQ ID NO 30
<211> LENGTH: 510
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 30

atggccgagc tgcggtctgg cgaaggccga accgtgcacg gcaccatcgt gccctacaac 60

gaggcgacca ccgtccgcga cttcgacggc gagttccagg aaatgttcgc tcctggcgct 120

tttcggcgct ccatcgccga gcgcggccac aaattgaagc tgctggtctc tcacgacgct 180

cgaacccgct acccggtggg ccgggccgtt gagttgcggg aggagcctca cggcttgttc 240

ggggcgttcg agattgcgga caccccggac ggcgacgagg ctttggcgaa cgtaaaagct 300

ggtgtcgtcg actcgttttc ggtgggtttc cgaccgatcc gggaccgtcg cgaaggggat 360

gtgctggtgc gcgtcgaagc ggcgctgtta gaggtttccc taaccggcgt tccggcctat 420

tcgggggcac aaatcgccgg ggtgcgcgcg gaatcgctta cagtcgtttc ccgttcgaca 480

gccgaagcct ggctgtccct actcgattgg 510

<210> SEQ ID NO 31
<211> LENGTH: 1419
<212> TYPE: DNA

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<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 31

atgaccgaat tcgacgacat caaaaacctc tctttacctg aaacccgtga cgcggcgaag 60

cagctcctcg acagtgtcgc cggcgacctg accggtgagg cggcgcagcg ttttcaggcg 120

ctgacgcgcc acgccgagga actgcgggcg gagcagcgcc gccgcggccg cgaagccgag 180

gaggcgctgc gccgctaccg ggccggtgag ctgagggtgg tgcccggcgc tcccaccggc 240

ggcgacgacg gcgacgcgcc gccgggcaac tcgttgcggg acaccgcgtt tcgcacactg 300

gattcttgtg tgcgagacgg cctgatgtcg tcgcgggcgg cggagaccgc ggaaaccttg 360

tgccgcaccg ggccgccgca gtccacctcg tgggcgcagc gctggctggc ggccaccggc 420

agccgcgact atttgggcgc gttcgtcaag cgggtttcca atcctgttgc ggggcacacg 480

gtttggaccg accgggaagc ggccgcgtgg cgtgaggctg ccgcggtggc cgccgagcag 540

cgagcgatgg gcctggtgga cacccaaggc gggtttctga tcccggcggc gctggacccg 600

gcgatcctgc tgtcgggtga tgggtcgacg aacccgattc ggcaggtggc gagggtggtg 660

caaacgacct ccgagatttg gcggggcgtg acttccgaag gcgccgaagc tcgttggtac 720

tccgaagccc aggaggtgtc cgacgattcg ccagcgttgg cccagccggc ggtgccgaac 780

taccgtggaa gctgctggat tccgttctcc atcgagctgg agggtgacgc ggcgagcttc 840

gttggcgaga tcggcaagat tctcgcggac agcgttgagc aactgcaggc cgcggcgttc 900

gtcaacggct ccggcaacgg cgagcccacc gggttcgtca gcgcgctaac cggcacctcc 960

gatcaggtgg tcgtcggcgc ggggtcagaa gcgattgtgg cggcggatgt ttacgcgttg 1020

cagtcggcgc tgccgccaag gttccaggcc agcgccgcgt tcgcggcgaa cttgtccacc 1080

atcaacacgt tgcggcaggc ggaaacttcg aatggcgcgc tgaaattccc atcgctgcac 1140

gacagtccgc cgatgctagc cgggaagtct gtcctggaag tctcccacat ggacaccgtt 1200

gattcggcgg tgacagcgac gaatcatcca ctggtgcttg gcgactggaa gcaattcctc 1260

atcggcgaca gagttgggtc catggtggag ttggtgcctc acctgttcgg gccgaatcgc 1320

cggccgaccg ggcagcgcgg attcttcgcc tggttcaggg tcggatcaga tgtgctggtg 1380

cgcaacgcgt ttcgagttct gaaggtggag actaccgcg 1419

<210> SEQ ID NO 32
<211> LENGTH: 351
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 32

atggcgccgc tggccgccgg atcgccgagc tggaacggcc gaaagccaag cagcggcaac 60

aggaaggcgg cgaccatggc cgccaggctc gatattctgg cttggggccc atgggcccca 120

agccagaatc ggagcgtcgt tcgacgaaaa cagacactgc tatcggcgca gccctcggca 180

tctccgccgg cacctaccgg cggctcaaac gaatcgacaa cgcaacccgc agcgagttgg 240

cgcgtgggcg gcccggcacc cctaagcaga ggccgcccac gcctggccct atcctaccta 300

cgcggtagtc tccaccttca gaactcgaaa cgcgttgcgc accagcacat c 351

<210> SEQ ID NO 33
<211> LENGTH: 309
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis

<400> SEQUENCE: 33

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atgggctaca aaccagaatc agagcgtcat tcgacgaaaa cagacactgc tatcggcgca 60

gccctcggca tctccgccgg cacctaccgg cggctcaaac gaatcgacaa cgcaacccac 120

agcgacgaca aagaaatccg ccggttcgcg gagaaacaaa tggcgccgct ggtcgccgga 180

tcgccgagct ggaacgcccg aaagccaagg agcgccaacg cgagggtggt cgcctcggtg 240

catcgatcac caatgccggc tttggtccca tggaaccaaa gccgtctcag cgccacactg 300

acaaggagg 309

<210> SEQ ID NO 34
<211> LENGTH: 408
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis

<400> SEQUENCE: 34

atgaccacca caccagcacg tttcaaccac ttggtgacgg taaccgacct ggaaacgggt 60

gaccgcgccg tctgcgaccg cgaccaggtg gccgagacga tccgggcgtg gttcccggac 120

gcgcccttgg aggtgaggga agcgctcgtt cggctgcagg ccgcgttgaa tcggcacgag 180

cacaccggcg agctcgaagc gttcctgcgg atcagcgtcg agcacgccga cgccgccggc 240

ggcgacgagt gcggcccggc gatcctggcc ggccgctccg ggccggaaca agccgccatc 300

aaccggcaac tcggactcgc cggcgacgac gagcccgacg gcgacgacac cccgccgtgg 360

agccggatga tcgggcttgg cggcggaagc ccagcggaag acgagcgc 408

<210> SEQ ID NO 35
<211> LENGTH: 1407
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis

<400> SEQUENCE: 35

gtgaaacggc tcagcggctg ggacgcggta ctgctttaca gcgagacccc gaatgtgcac 60

atgcacacac tcaaggtcgc cgtgatcgaa ttggattcgg acagacagga attcggtgtc 120

gacgcgtttc gcgaggtgat cgctggccgg ctgcataagc ttgagccatt gggctatcag 180

ctggttgatg tcccgttgaa gttccatcac ccgatgtggc gggagcactg ccaggtcgat 240

ctcaactacc acatccggcc gtggcggttg cgcgccccgg ggggtcggcg cgaactcgac 300

gaggcggtcg gagaaatcgc cagcaccccg ctgaaccgcg accacccgct gtgggagatg 360

tacttcgttg aggggcttgc caaccaccgg atcgcggtgg ttgccaaaat tcaccatgcg 420

ttggctgacg gtgttgcctc ggcaaacatg atggcacggg ggatggatct gctgccggga 480

ccggaggtcg gccgctatgt gcctgacccc gctcctacca agcggcagtt gctgtccgcg 540

gcgttcatcg accacttgcg ccacctcggc cggattcctg caaccatccg gtacaccacg 600

cagggtctag gccgggtgcg acgtagctcg cgcaagctct cacccgcact gaccatgcca 660

tttaccccgc caccgacgtt catgaatcac cggctcaccc cggagcgcag gttcgccacc 720

gccaccctgg cgctgattga cgtgaaggcg acggccaagt tgctgggggc gacgatcaac 780

gacatggtgc tggccatgtc gaccggcgct ctgcgtaccc tgctattgcg ctatgacggc 840

aaggccgaac cgctgctggc gtcggtcccg gtgagttacg acttctcacc ggagcggatc 900

tccggtaacc gcttcaccgg aatgctggtg gcgctgcctg ccgactccga cgacccgttg 960

cagcgggtgc gcgtctgtca cgaaaacgcg gtctccgcca aggagagcca ccagcttttg 1020

ggaccggagt tgatcagccg ctgggcggct tactggccac ctgccggtgc ggaagccttg 1080

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ttccggtggt tgtctgagcg cgacgggcag aacaaggtac tcaacttgaa tatctcgaat 1140

gttcccggtc cgcgcgaacg cggccgcgtg ggggccgcgc tggtcaccga gatctattcg 1200

gtgggcccgt tgaccgccgg tagcggattg aatatcacgg tgtggagtta tgtcgatcag 1260

ctcaatatct cggtgttaac cgatggttcc accgtgcagg acccgcatga agtaaccgcg 1320

ggaatgatcg cggacttcat cgaaatacgc cgcgccgctg gtctttccgt ggagttgaca 1380

gtcgtcgagt ccgcgatggc gcaggca 1407

<210> SEQ ID NO 36
<211> LENGTH: 786
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis

<400> SEQUENCE: 36

atgagcagcg aaagcgacgc agccaacacc gaacctgagg ttctggtaga acagcgggat 60

cggattttga tcatcacgat caaccgcccg aaagccaaga acgcggtcaa cgccgcagtc 120

agccggggct tggccgatgc gatggatcag cttgacggcg atgccggcct gtcggtggca 180

atcctgaccg gtgggggcgg ttcgttctgc gcgggcatgg acctcaaggc gttcgcccgg 240

ggcgagaatg tcgtcgtcga aggtcgcggc cttggcttta ccgaacgtcc gccgaccaag 300

ccgctcattg ctgcggtgga aggctacgcg ttggcgggtg gcaccgagct ggcgcttgct 360

gccgacctga tcgtggcggc cagggattcg gcgttcggga ttcctgaagt caagcggggt 420

ctggttgccg gcggcggggg attgctgcgg ttgccggagc gcatcccgta tgcgatagcc 480

atggagttgg cgctgaccgg tgacaaccta ccggccgaac gcgcgcacga gctggggctc 540

gtcaacgttt tggccgagcc ggggaccgcc ctcgatgctg cgatcgcgtt ggcggagaag 600

atcaccgcca atgggccgct ggcggtggtg gccaccaagc ggattatcac cgagtcgcgt 660

gggtggagtc ccgacactat gttcgctgag cagatgaaga tcctggtgcc ggtgttcacc 720

tccaacgacg cgaaggaagg tgcgatcgcg ttcgccgaga ggcgccggcc ccgttggacg 780

ggcacc 786

<210> SEQ ID NO 37
<211> LENGTH: 1461
<212> TYPE: DNA
<213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 37

atgtctgaca gtgccacgga atacgacaag cttttcatcg gcggcaagtg gaccaaaccg 60

tcgacctccg atgttatcga ggtacgctgc ccagccactg gggaatatgt cggcaaggtg 120

ccgatggcgg ccgccgccga cgtcgacgcc gcggtcgccg cagcacgtgc ggcgttcgac 180

aacggcccct ggccctcgac cccgccgcac gagcgtgcgg cggtgatcgc tgcggcggtc 240

aagatgctgg ctgagcgcaa ggacctgttc accaagctgc tcgcagccga aaccggccag 300

ccgccgacca tcatcgagac gatgcactgg atgggttcga tgggggcgat gaactacttt 360

gccggtgcag cggacaaggt cacctggacc gaaacccgca ccggctccta tggacagagc 420

attgtcagcc gtgagccggt cggtgtggtg ggcgcgatcg tggcctggaa cgtcccgctg 480

tttctggccg tcaacaagat tgcgccggcg ctgctggccg gctgcaccat cgtgctcaag 540

cccgccgccg aaacaccgct gaccgcaaac gctttggcgg aggtgttcgc cgaggtgggc 600

ctgcccgagg gggtgttgtc ggtagtgccg ggagggattg agaccggtca ggcgctgacg 660

tctaacccgg acatcgacat gtttaccttc accggcagct cggccgtcgg ccgagaggtc 720

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ggcaggcgtg ccgctgagat gctcaagccg tgcaccttag aactcggcgg caagtcggcg 780

gccatcattc tcgaggacgt cgacctggcc gcagctattc cgatgatggt gttctccggc 840

gtcatgaacg ccggacaggg ctgcgtcaac cagacccgca ttctggctcc gcgctcccgg 900

tacgacgaaa tcgtggctgc ggtaactaat ttcgtaacgg ctctcccggt gggcccgccg 960

tcggacccgg cagctcagat cgggccgctg atctcggaga agcagcggac tcgcgttgaa 1020

ggctacatcg ccaagggcat cgaggagggc gctcggttgg tgtgcggcgg cggccgtccc 1080

gagggcttgg acaacggctt ctttatccaa cccaccgtat tcgccgatgt cgacaacaag 1140

atgaccatcg cacaggagga gatcttcggg ccggtgctgg ccatcattcc ttatgacacc 1200

gaggaggacg cgatcgcgat cgccaacgat tcagtgtatg ggctggcggg cagcgtgtgg 1260

accaccgacg tgcccaaagg catcaagatc tcgcagcaga tccgcaccgg gacatacgga 1320

atcaactggt acgccttcga tcccggctca cccttcggcg gctacaagaa ctccggaatc 1380

ggccgcgaga acgggcccga gggtgtcgaa cacttcaccc agcaaaagag tgtcctgctg 1440

ccgatgggct acaccgtcgc g 1461

<210> SEQ ID NO 38
<211> LENGTH: 831
<212> TYPE: DNA
<213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 38

atggcacgct gcgatgtcct ggtctccgcc gactgggctg agagcaatct gcacgcgccg 60

aaggtcgttt tcgtcgaagt ggacgaggac accagtgcat atgaccgtga ccatattgcc 120

ggcgcgatca agttggactg gcgcaccgac ctgcaggatc cggtcaaacg tgacttcgtc 180

gacgcccagc aattctccaa gctgctgtcc gagcgtggca tcgccaacga ggacacggtg 240

atcctgtacg gcggcaacaa caattggttc gccgcctacg cgtactggta tttcaagctc 300

tacggccatg agaaggtcaa gttgctcgac ggcggccgca agaagtggga gctcgacgga 360

cgcccgctgt ccagcgaccc ggtcagccgg ccggtgacct cctacaccgc ctccccgccg 420

gataacacga ttcgggcatt ccgcgacgag gtcctggcgg ccatcaacgt caagaacctc 480

atcgacgtgc gctctcccga cgagttctcc ggcaagatcc tggcccccgc gcacctgccg 540

caggaacaaa gccagcggcc cggacacatt cctggtgcca tcaacgtgcc gtggagcagg 600

gccgccaacg aggacggcac cttcaagtcc gatgaggagt tggccaagct ttacgccgac 660

gccggcctag acaacagcaa ggaaacgatt gcctactgcc gaatcgggga acggtcctcg 720

cacacctggt tcgtgttgcg ggaattactc ggacaccaaa acgtcaagaa ctacgacggc 780

agttggacag aatacggctc cctggtgggc gccccgatcg agttgggaag c 831

<210> SEQ ID NO 39
<211> LENGTH: 300
<212> TYPE: DNA
<213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 39

atgtgctctg gacccaagca aggactgaca ttgccggcca gcgtcgacct ggaaaaagaa 60

acggtgatca ccggccgcgt agtggacggt gacggccagg ccgtgggcgg cgcgttcgtg 120

cggctgctgg actcctccga cgagttcacc gcggaggtcg tcgcgtcggc caccggcgat 180

ttccggttct tcgccgcgcc cggatcctgg acgctgcgcg cgctgtcggc ggccggcaac 240

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ggcgacgcgg tggtgcagcc ctcgggcgcg ggcatccacg aggtagacgt caagatcacc 300

<210> SEQ ID NO 40
<211> LENGTH: 441
<212> TYPE: DNA
<213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 40

atggccaatg tggtagctga aggtgcctac ccttactgtc ggctcactga tcagccgctg 60

agtgtggacg aagtgctagc cgccgtctcg ggccccgaac aaggcggcat tgtcatattt 120

gtgggaaacg tgcgtgacca caatgccggg catgatgtca cgcggttgtt ctacgaggcg 180

tatccgccga tggtgattcg gacattgatg tcgatcatcg gacggtgtga agacaaggcc 240

gagggtgtcc gcgttgctgt cgcgcaccgg accggtgaat tgcaaatcgg tgatgccgcg 300

gtcgttattg gcgcgtcagc tccccaccgt gcggaggcat ttgacgccgc gcgtatgtgt 360

atcgagttgc ttaagcagga agtgccgatt tggaagaagg aattcagctc gaccggtgct 420

gaatgggtcg gcgatagacc a 441

<210> SEQ ID NO 41
<211> LENGTH: 600
<212> TYPE: DNA
<213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 41

atgagtccgt ctccatcggc cctgctcgcc gaccacccgg accgcattcg ttggaacgcg 60

aaatacgagt gcgctgaccc cacggaggcg gtatttgcgc ccatatcctg gctcggcgac 120

gtgctgcagt tcggggtgcc agaagggccg gttctggaac tggcgtgcgg tcggtccggc 180

accgcgctgg ggctagccgc ggcgggccgc tgcgtgactg cgatcgacgt ttccgatacc 240

gcgttggttc agctcgagct cgaagcgacc cgacgggaat tggccgatcg cctcacactg 300

gtgcacgccg atctctgctc ctggcagtcg ggggatggac gctttgctct ggtactttgc 360

cgactattct ggcatccgcc cacttttcgc caggcttgcg aggctgtggc gccgggcggt 420

gtagtggcgt gggaggcatg gcggcggccc atcgatgtcg ctcgggatac ccgtcgagcc 480

gaatggtgct tgaagccagg ccagcccgag tctgaacttc ccgccggctt cacggtgatt 540

cgggtggtcg acaccgatgg ttcagagccg tcgcggcgca tcatcgccca acggtcactg 600

<210> SEQ ID NO 42
<211> LENGTH: 1200
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis

<400> SEQUENCE: 42

atgacaagca cctcgattcc gacgttcccg ttcgaccggc cggtcccgac ggagccgtcc 60

ccaatgctgt cggaactgag aaacagctgt ccggtagccc cgatagagtt gccctcgggg 120

cacacagcat ggctcgtcac tcgctttgac gatgtaaagg gagtgctgtc cgacaagcgt 180

ttcagctgca gggcggcagc gcacccgtcg tcgcccccgt tcgtgccgtt cgtgcagctt 240

tgccccagct tgttgagcat cgatgggccc caacacaccg cggcccgccg tctgctcgcg 300

cagggcctaa atcccggctt catcgcacgc atgcggcccg ttgtccaaca gatcgtcgac 360

aatgcgctcg acgatctggc agccgcggaa ccaccggtgg acttccagga aatagtaagt 420

gtccctatcg gagaacagct catggccaag ctactcgggg tcgagcccaa aaccgtgcac 480

gagctcgcgg cgcacgtgga tgcggcgatg tccgtgtgtg agatcggcga cgaggaggtg 540

-continued

agccggcggt ggtcagcact gtgcacgatg gtcatcgaca tactgcaccg caagctcgcc 600

gaaccgggtg atgacctact tagcacgatc gcccaggcga accggcaaca gtccaccatg 660

accgacgagc aggttgtcgg catgctcctc accgtcgtga tcggaggagt cgacacaccg 720

atcgccgtga tcacaaacgg gctggcgagc ctgctgcacc accgcgatca atatgaacgg 780

ctcgttgaag acccaggccg tgtcgctcgt gcggttgaag aaatagtccg gtttaatccg 840

gcaactgaaa ttgagcactt gcgagttgtc accgaggatg tcgtcattgc cggaaccgcg 900

ctatcggcgg ggagcccagc atttacctct atcacttcgg ctaaccgcga ctccgaccaa 960

ttcctggacc ccgatgagtt tgatgtcgaa cgtaatccga acgaacacat agcatttgga 1020

tatggtccac atgcttgccc ggcctcagcg tattcacgca tgtgcttgac gacgttcttc 1080

acctcgctta cccagcgatt tccgcaactt caactcgcaa gaccgtttga ggatttggaa 1140

cgacggggta agggcctaca ttcggtgggg atcaaggaac tccttgttac ctggccgacg 1200

<210> SEQ ID NO 43
<211> LENGTH: 498
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis

<400> SEQUENCE: 43

gtgcgcattg tcaatgcggc ggacccattt tcgatcaacg atctaggctg tggctatggg 60

gctctactgg actacctaga tgcgcgtggc ttcaaaactg attacaccgg catcgacgtc 120

tcccccgaaa tggtgcgcgc ggccgcacta cgtttcgaag gtcgggcgaa cgcagacttc 180

atctgcgcgg cgcgcataga tcgggaggcg gactatagcg tcgcgagtgg aatattcaat 240

gttcgtctga aatcgttgga cacggaatgg tgcgctcaca tcgaagcgac gctcgacatg 300

ctgaatgccg cgagtcgccg tggcttctct tttaattgcc tgacatctta ttccgatgca 360

tcaaagatgc gcgacgacct gtactatgct gacccatgcg ccctatttga tctctgcaag 420

cgcaggtact ccaagagtgt tgcgcttctg cacgactacg gcttgtatga attcacaatt 480

ctggttagga aggcgtca 498

<210> SEQ ID NO 44
<211> LENGTH: 693
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis

<400> SEQUENCE: 44

ttgaagaaag tcgcgattgt tcaatcaaat tacatacctt ggcgaggata ttttgacctg 60

attgcattcg tcgatgaatt catcatctat gatgacatgc aatataccaa gcgtgattgg 120

cgaaacagaa atcggatcaa aacgagccag gggttacagt ggataactgt tcccgtccag 180

gtgaagggac gtttccatca aaagatacgt gagacgctga tcgacggcac cgattgggcg 240

aaagcgcact ggcgggcact agaattcaac tacagcgcgg ccgctcattt tgcggagatc 300

gctgactggc tcgcgccgat ttacctcgaa gaacagcaca cgaatctttc cttactcaac 360

aggcgtctat tgaatgcgat ttgcagttat ctcggtatca gcacgcgact ggcaaattcg 420

tgggactacg aattagccga cggcaagacc gagagactgg ccaacctctg ccaacaggcc 480

gcagcgaccg aatatgtctc tggcccctca gcccgttcgt atgtcgatga gcgcgtgttc 540

gacgaactta gcatccgggt aacttggttc gattatgacg gctaccgcga ttataagcaa 600

ttgtggggag ggttcgagcc cgccgtgtcg attctggatc tgctctttaa cgtcggagcc 660 gaggctccgg actatttgag gtactgtcgc cag 693

<210> SEQ ID NO 45
<211> LENGTH: 395
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)...(395)
<223> OTHER INFORMATION: n = A,T,C or G
<221> NAME/KEY: misc_feature
<222> LOCATION: 27, 44, 104, 119, 180, 224, 237, 245, 254, 301, 327,
370, 385, 393
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 45

vvmsartgva rhgtsgrgcg dvgargndvs vatrkrsrgd rvgnhgarar rmkrvrgavt 60

asrrwagssr tmgtasvsaa tayaswyavd vstvvgdcwd wgmngrhcsd yamvaaagna 120

dysadytava awaaryagsh wgargcyvat mavsawaarg argrvvvtga aaawgvdrgn 180

stgvvaayva srrwgattva vvkvvgvvaa rwrwaggtgv vvsnaawrgg tashgknssg 240

grdrnvsgka dsknysgkgt grtgavvvvv avagrrvmvg vatatsadva yyvvaavard 300

nggagdaahg drrravgvcv savasvnvav gyvyggakgv vgttvttvtw awvtcvvvsy 360

arkarhdshn gtrsddtaas ttscnvssrg gcnyt 395

<210> SEQ ID NO 46
<211> LENGTH: 879
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis

<400> SEQUENCE: 46

gtgtttgcgt tgagtaataa tctgaaccgt gtgaacgcat gcatggatgg attccttgcc 60

cgtatccgct cacatgttga tgcgcacgcg ccagaattgc gttcactgtt cgatacgatg 120

gcggccgagg cccgatttgc acgcgactgg ctgtccgagg acctcgcgcg gttgcctgtc 180

ggtgcagcat tgctggaagt gggcgggggg gtacttctgc tcagctgtca actggcggcg 240

gagggatttg acatcaccgc catcgagccg acgggtgaag gttttggcaa gttcagacag 300

cttggcgaca tcgtgctgga attggctgca gcacgaccca ccatcgcgcc atgcaaggcg 360

gaagacttta tttccgagaa gcggttcgac ttcgccttct cgctgaatgt gatggagcac 420

atcgaccttc cggatgaggc agtcaggcgg gtatcggaag tgctgaaacc gggggccagt 480

taccacttcc tgtgcccgaa ttacgtattc ccgtacgaac cgcatttcaa tatcccaaca 540

ttcttcacca aagagctgac atgccgggtg atgcgacatc gcatcgaggg caatacgggc 600

atggatgacc cgaagggagt ctggcgttcg ctcaactgga ttacggttcc caaggtgaaa 660

cgctttgcgg cgaaggatgc gacgctgacc ttgcgcttcc accgtgcaat gttggtatgg 720

atgctggaac gcgcgctgac ggataaggaa ttcgctggtc gccgggcaca atggatggtc 780

gctgctattc gctcggcggt gaaattgcgt gtgcatcatc tggcaggcta tgttcccgct 840

acgctgcagc ccatcatgga tgtgcggcta acgaagagg 879

<210> SEQ ID NO 47
<211> LENGTH: 1296
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis

<400> SEQUENCE: 47

atgtacgaga gacggcatga gcgcggaatg tgcgaccgtg ccgtcgagat gaccgacgtc 60

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ggcgctacgg cagcccccac cggacctatc gcgcggggca gcgtcgctcg ggtcggcgcg 120

gcgaccgcgt tggccgttgc ctgcgtctac acggtcatct atctggcggc ccgcgaccta 180

cccccggctt gtttttcgat attcgcggtg ttttgggggg cgctcggcat tgccaccggc 240

gccacccacg gcctcctgca agaaacgacc cgcgaggtcc gctgggtgcg ctccacccaa 300

atagttgcgg gccatcgtac ccatccgctg cgggtggccg ggatgattgg caccgtcgcg 360

gccgtcgtaa ttgcgggtag ctcaccgctg tggagccgac agctattcgt cgaggggcgc 420

tggctgtccg tggggctact cagcgttggg gtggccgggt tctgcgcgca ggcgaccctg 480

ctgggcgcgc tggccggcgt cgaccggtgg acacagtacg ggtcactgat ggtgaccgac 540

gcggtcatcc ggttggcggt cgccgcggca gcggttgtga tcggatgggg tctggccggg 600

tacttgtggg ccgccaccgc gggagcggtg gcgtggctgc tcatgctgat ggcctcgccc 660

accgcgcgca gcgcggccag cctgctgacg cccgggggaa tcgccacgtt cgtgcgcggt 720

gccgctcatt cgataaccgc cgcgggtgcc agcgcgattc tggtaatggg tttcccagtg 780

ttgctcaaag tgacctccga ccagttaggg gcaaagggcg gagcggtcat cctggctgtg 840

accttgacgc gtgcgccgct tctggtccca ctgagcgcga tgcaaggcaa cctgatcgcg 900

catttcgtcg accggcgcac ccaacggctt cgggcgctga tcgcaccggc gctggtcgtc 960

ggcggcatcg gtgcggtcgg gatgttggcc gcagggctta ccggtccctg gttgctgcgt 1020

gttggattcg gccccgacta ccaaactggc ggggcgttgc tggcctggtt gacggcagcg 1080

gcggtagcta tcgccatgct gacgctgacc ggcgccgccg cggtcgcggc cgcactgcac 1140

cgggcgtatt tgctgggctg ggtcagcgcg acggtggcgt cgacgctgtt gctgctgctg 1200

ccgatgccgc tggagacgcg caccgtgatc gcgctgttgt tcggtccaac ggtgggaatc 1260

gccatccatg tggccgcgtt ggcgcggcga cccgac 1296

<210> SEQ ID NO 48
<211> LENGTH: 1020
<212> TYPE: DNA
<213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 48

gtgaagcgag cgctcatcac cggaatcacc ggccaggacg gctcgtatct cgccgaactg 60

ctgctggcca aggggtatga ggttcacggg ctcatccggc gcgcttcgac gttcaacacc 120

tcgcggatcg atcacctcta cgtcgacccg caccaaccgg gcgcgcggct gtttctgcac 180

tatggtgacc tgatcgacgg aacccggttg gtgaccctgc tgagcaccat cgaacccgac 240

gaggtgtaca acctggcggc gcagtcacac gtgcgggtga gcttcgacga acccgtgcac 300

accggtgaca ccaccggcat gggatccatg cgactgctgg aagccgttcg gctctctcgg 360

gtgcactgcc gcttctatca ggcgtcctcg tcggagatgt tcggcgcctc gccgccaccg 420

cagaacgagc tgacgccgtt ctacccgcgg tcaccgtatg gcgccgccaa ggtctattcg 480

tactgggcga cccgcaatta tcgcgaagcg tacggattgt tcgccgttaa cggcatcttg 540

ttcaatcacg aatcaccgcg gcgcggtgag acgttcgtga cccgaaagat caccagggcc 600

gtggcacgca tcaaggccgg tatccagtcc gaggtctata tgggcaatct ggatgcggtc 660

cgcgactggg ggtacgcgcc cgaatacgtc gaaggcatgt ggcggatgct gcagaccgac 720

gagcccgacg acttcgtttt ggcgaccggg cgcggtttca ccgtgcgtga gttcgcgcgg 780

gccgcgttcg agcatgccgg tttggactgg cagcagtacg tgaaattcga ccaacgctat 840

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ctgcggccca ccgaggtgga ttcgctgatc ggcgacgcga ccaaggctgc cgaattgctg 900

ggctggaggg cttcggtgca cactgacgag ttggctcgga tcatggtcga cgcggacatg 960

gcggcgctgg agtgcgaagg caagccgtgg atcgacaagc cgatgatcgc cggccggaca 1020

<210> SEQ ID NO 49
<211> LENGTH: 966
<212> TYPE: DNA
<213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 49

atgaacgcgc acacctcggt cggcccgctt gaccgcgcgg cccgggtcta catcgccggg 60

catcgcggcc tggtcgggtc cgcgctgcta cgcacgtttg cgggcgcggg gttcaccaac 120

ctgctggtgc ggtcacgcgc cgagcttgat ctgacggatc gggccgcgac gttcgacttc 180

gttctcgagt cgaggccgca ggtcgtcatc gacgcggcgg cccgggtcgg cggcatcctg 240

gccaacgaca cctacccggc cgatttcctg tcggaaaacc tccagatcca ggtcaacctg 300

ctggatgccg ccgtggcggc gcgggtgccg cggctgctgt tcctgggctc gtcgtgcatc 360

tacccgaaac tcgccccgca gccgatcccg gagagcgcgc tgctcaccgg tccgttggag 420

ccgaccaacg acgcgtacgc gatcgccaaa atcgccggca tccttgcggt ccaggcggtg 480

cgccgccaac atggcctgcc gtggatctcg gcgatgccca ccaacctgta cgggccaggc 540

gacaactttt cgccgtccgg ctcgcatctg ctgccggcac tcatccgccg ctatgacgag 600

gccaaagcca gtggcgcgcc caacgtgacc aactggggca ccggcacgcc ccgacgggag 660

ttgctgcacg tcgacgacct ggcgagcgca tgcctgtatc tgctggaaca tttcgacggg 720

ccgacccatg tcaacgtggg aaccggcatc gaccacacca tcggcgagat cgccgagatg 780

gtcgcctcgg cggtaggcta tagcggcgaa acccgctggg atccaagcaa accggacgga 840

acaccacgca aactgctgga tgtttcggtg ctacgggagg cgggatggcg gccttcgatc 900

gcgctgcgcg acggcatcga ggcgacggtg gcgtggtatc gcgagcacgc gggaacggtt 960

cggcaa 966

<210> SEQ ID NO 50
<211> LENGTH: 729
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 50

atgaggctgg cccgtcgcgc tcggaacatc ttgcgtcgca acggcatcga ggtgtcgcgc 60

tactttgccg aactggactg ggaacgcaat ttcttgcgcc aactgcaatc gcatcgggtc 120

agtgccgtgc tcgatgtcgg ggccaattcg gggcagtacg ccaggggtct gcgcggcgcg 180

ggcttcgcgg gccgcatcgt ctcgttcgag ccgctgcccg ggccctttgc cgtcttgcag 240

cgcagcgcct ccacggaccc gttgtgggaa tgccggcgct gtgcgctggg cgatgtcgat 300

ggaaccatct cgatcaacgt cgccggcaac gagggcgcca gcagttccgt cttgccgatg 360

ttgaaacgac atcaggacgc ctttccacca gccaactacg tgggcgccca acgggtgccg 420

atacatcgac tcgattccgt ggctgcagac gttctgcggc ccaacgatat tgcgttcttg 480

aagatcgacg ttcaaggatt cgagaagcag gtgatcgcgg gtggcgattc aacggtgcac 540

gaccgatgcg tcggcatgca gctcgagctg tctttccagc cgttgtacga gggtggcatg 600

ctcatccgcg aggcgctcga tctcgtggat tcgttgggct ttacgctctc gggattgcaa 660

cccggtttca ccgacccccg caacggtcga atgctgcagg ccgatggcat cttcttccgg 720

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ggcagcgat 729

<210> SEQ ID NO 51
<211> LENGTH: 786
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis

<400> SEQUENCE: 51

gtgacgtctg ctccgaccgt ctcggtgata acgatctcgt tcaacgacct cgacgggttg 60

cagcgcacgg tgaaaagtgt gcgggcgcaa cgctaccggg gacgcatcga gcacatcgta 120

atcgacggtg gcagcggcga cgacgtggtg gcatacctgt ccgggtgtga accaggcttc 180

gcgtattggc agtccgagcc cgacggcggg cggtacgacg cgatgaacca gggcatcgcg 240

cacgcatcgg gtgatctgtt gtggttcttg cactccgccg atcgtttttc cgggcccgac 300

gtggtagccc aggccgtgga ggcgctatcc ggcaagggac cggtgtccga attgtggggc 360

ttcgggatgg atcgtctcgt cgggctcgat cgggtgcgcg gcccgatacc tttcagcctg 420

cgcaaattcc tggccggcaa gcaggttgtt ccgcatcaag catcgttctt cggatcatcg 480

ctggtggcca agatcggtgg ctacgacctt gatttcggga tcgccgccga ccaggaattc 540

atattgcggg ccgcgctggt atgcgagccg gtcacgattc ggtgtgtgct gtgcgagttc 600

gacaccacgg gcgtcggctc gcaccgggaa ccaagcgcgg tcttcggtga tctgcgccgc 660

atgggcgacc ttcatcgccg ctacccgttc gggggaaggc gaatatcaca tgcctaccta 720

cgcggccggg agttctacgc ctacaacagt cgattctggg aaaacgtctt cacgcgaatg 780

tcgaaa 786

<210> SEQ ID NO 52
<211> LENGTH: 894
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis

<400> SEQUENCE: 52

atgtcgacaa acccaggacc agccgaaggg gctaaccaag tgatggcaca ggaacattcg 60

gccggcgcgg tacaattcac cgcccacaac gttcgcctcg acgacggaac cttgacgata 120

ccggagtcct cgcgcacgtt agacgaatcg tcctggttca tctcggcgcg cgggattctg 180

gaaaccgtct ttcccgggga caagagccac ctacgcctgg ccgatgtcgg ctgcttggaa 240

ggcgggtacg cggtcgggtt cgcgcgcatg ggatttcagg tcctcgggat cgaggttcgc 300

gagctgaaca tggcggcctg caactacatc aaatcgaaga ccaacctgcc gaatctccgg 360

ttcgtccacg acaacgccct caacatcgcc aaccacgggc tcttcgatac cgtcttctgc 420

tgcggcctct tctaccacct ggagaatccg aagcaatacc tggaaaccct ctcgtcggta 480

acgaacaagc tgctgattct ccagacgcac ttctcgatca tcaaccggag cgataaatgg 540

ctccggttgc ccacgacggc acgacaattg accgatcggt tgctgcggcg gccggcgccg 600

gtgaagttca tgctctcggc gcccaccgaa catgagggac ttcccggtag gtggtttacc 660

gagttttccg acgaccgctc gtttggccag cgcgacaccg caaaatgggc gtcctgggac 720

aatcgccggt cattctggat tcaacgcgag cacctacttc aggccatcaa agacgtcggc 780

gtcgacctgg tgatggagga gtacgacaac ttggaaccaa gcatcgccga gtcgttgctc 840

ggaggttcct atgcggcgaa tcttcgaggc accttcatcg gtatcaagac ccgg 894

<210> SEQ ID NO 53

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<211> LENGTH: 1119
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis

<400> SEQUENCE: 53

gtgccgtacg tccgccgacc accaggccac gacggccgac ggccggcggg cacaggcgat 60

tcacgttcgc catcgcaata cccttgcggc cgcgcaggaa aagggccgac ggtgagtccc 120

cagctttgcc ccaaggtgag catcgtctcg accactcaca accaggcggg ctacgcccgt 180

caggccttcg acagctttct cgaccagcaa accgacttcc cggtggagat catcgtcgcc 240

gacgacgcgt cgaccgatgc caccccggcg atcatccgtg agtacgccga gcggtacccg 300

cacgtgttcc ggccgatctt caggaccgaa aacctcggcc tcaatgggaa cctgaccggc 360

gccctgtcgg ccgctcgcgg cgagtacgtc gcgttgtgcg aggcggacga ctactggatc 420

gatccgctga agctaagcaa acaggtcgca ttcctcgacc ggcaccccaa gacgacggtg 480

tgcttccatc ccgtccgagt gatatgggag gacggccatg ccaaggactc gaagttcccc 540

ccggttcggg tgcggggcaa cttgagcctg gatgcgttga tcttgatgaa cttcatccag 600

accaactcgg ccgtgtaccg tcgcctcgag cgctacgacg acattcctgc cgacgtcatg 660

cccctggact ggtatctgca cgtccggcac gcggtgcatg gcgacatcgc catgttgccc 720

gacaccatgg ccgtgtatcg ccgccacgcc caaggcatgt ggcacaacca ggtggtggac 780

ccgccaaagt tctggttgac gcagggtccg gggcatgcgg cgacgtttga cgcgatgctc 840

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cttcgccaga tcgccaacgt tccaggcccg gaggggcgcg ccgcgctgca ggaaaccatc 960

gcgcgccatc cccggatcgc catgctggcg ctgcagcacc gcggggcgac acccgcgcgg 1020

cggctcaaga cccagtggcg caagctcgcc gccgcgacgc cgagccgcag gggctcgtg 1080

gatgtgtggc cctcccggct ccgacgcggc tgtcgagcc 1119

<210> SEQ ID NO 54
<211> LENGTH: 282
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis

<400> SEQUENCE: 54

atgaccatca actatcagtt cggtgatgtc gacgctcatg gcgccatgat ccgcgctcag 60

gccgggttgc tggaggcgga gcatcaggcc atcgttcgtg atgtgttggc cgcgggtgac 120

ttttggggcg gcgccggttc ggtggcttgc caggagttca tcacccagct gggccgtaac 180

ttccaggtga tctacgagca ggccaacgcc cacgggcaga aggtgcaggc tgccggcaac 240

aacatggcac aaaccgacag cgccgtcggc tccagctggg cc 282

<210> SEQ ID NO 55
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis

<400> SEQUENCE: 55

atggcaacac gttttatgac ggatccgcac gcgatgcggg acatggcggg ccgttttgag 60

gtgcacgccc agacggtgga ggacgaggct cgccggatgt gggcgtccgc gcaaaacatc 120

tcgggcgcgg gctggagtgg catggccgag gcgacctcgc tagacaccat ggcccagatg 180

aatcaggcgt ttcgcaacat cgtgaacatg ctgcacgggg tgcgtgacgg gctggttcgc 240

gacgccaaca actacgagca gcaagagcag gcctcccagc agatcctcag cagc 294

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<210> SEQ ID NO 56
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis

<400> SEQUENCE: 56

gtgcttttgc ctcttggtcc gcctttgccg cccgacgcgg tggtggcgaa acgggctgag 60

tcgggaatgc tcggcgggtt gtcggttccg ctcagctggg gagtggctgt gccacccgat 120

gattatgacc actgggcgcc tgcgccggag gacggcgccg atgtcgatgt ccaggcggcc 180

gaaggggcgg acgcagaggc cgcggccatg gacgagtggg atgagtggca ggcgtggaac 240

gagtgggtgg cggagaacgc tgaacccccgc tttgaggtgc cacggagtag cagcagcgtg 300

attccgcatt ctccggcggc cggc 324

<210> SEQ ID NO 57
<211> LENGTH: 1524
<212> TYPE: DNA
<213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 57

atgtcacgcc gagcattcct ggctaaggcg gctggagccg gggcagcggc ggttttgacg 60

gactgggccg caccggtgat cgaaaaggcc tatggtgccg gtccctgctc gggtcatttg 120

accgatatcg agcacatcgt gctgtgccta caggagaaca ggtcgttcga tcactatttc 180

ggcacgcttt ctgccgtcga cgggttcgac actccgacgc cgctgtttca acaaaagggc 240

tggaacccgg agacgcaggc gctggacccc accggcatta cgctgcccta ccgcatcaat 300

accaccgggg gtcccaacgg ggttggcgag tgcgtcaacg acccagacca ccagtggatt 360

gccgcgcact tgtcatggaa cggcggcgcc aatgacggct ggctgccggc gcaggcgcgg 420

acccggtcgg tggccaacac gcccgtggtg atgggctatt acgcacgtcc tgacataccg 480

atccactact tgttggccga taccttcacg atctgcgacc agtacttctc gtcgcttctt 540

ggcgggacga tgcctaaccg gctctattgg atcagcgcca ccgtcaatcc cgacggggat 600

caaggtgggc cgcagatcgt cgaacccgcc atccagccga agttgacctt cacctggcgc 660

atcatgccgc agaacctcag tgacgccggc atcagttgga aggtgtacaa cagcaagctg 720

ctcggcgggc tcaacgacac ttccttgagc cgtaacgggt atgtgggcag tttcaaacag 780

gccgcagatc cgaggtcgga cctggcccgt tatggcatcg ccccggccta cccgtgggat 840

ttcatccgcg acgtcatcaa caacacgctg ccccaggtgt cctgggtcgt tccgttgacc 900

gtcgagtccg aacatccgtc attcccggtg gcagtcggtg cggtgacgat cgtgaacttg 960

ataagggtgt tgctgcgcaa tccggcggtg tgggagaaaa ccgcgttgat catcgcctat 1020

gacgaacatg gcggcttctt cgaccacgtc acaccgctca ccgcgccgga gggcacaccc 1080

ggcgaatgga ttcccaacag tgttgacatc gacaaggtcg acggctccgg cggaatacgt 1140

ggacccatcg gcttgggctt tcgcgtgccc tgcttcgtca tttcgcctta cagtcgcggc 1200

gggctgatgg tccatgatcg gttcgaccac acatcgcagc tgcaattgat cggcaagcgt 1260

ttcggggtgc cggttcccaa cttgacaccc tggcgtgcca gtgtcaccgg cgatatgacg 1320

tcggcattca atttcgcggc cccgccggac ccgtcgccac ccaatctgga ccacccggtc 1380

cgtcaattgc cgaaggtcgc caagtgcgtg cccaatgtgg tgctgggttt cttgaacgaa 1440

ggcctgccgt atcgggtgcc ctaccccaa acaacgccag tccaggaatc cggtcccgcg 1500

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cggccgattc ccagcggcat ctgc 1524

<210> SEQ ID NO 58
<211> LENGTH: 1536
<212> TYPE: DNA
<213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 58

atgtcacgtc gagagttttt gacaaagctc actggcgcag gcgcagcggc attcctgatg 60

gactgggctg caccggtgat tgaaaaggcc tacggcgccg ggccttgtcc cggacatttg 120

accgacatcg agcatatcgt gttgctgatg caggagaacc ggtcattcga ccactatttc 180

ggaacgcttt ccagcaccaa tgggttcaac gccgcgtcgc cggcattcca acaaatgggt 240

tggaacccca tgacgcaggc gttggacccc gccggggtca ccattccgtt ccgcttggac 300

accacccgag gccccttcct ggacggcgag tgcgtcaacg accccgagca ccagtgggtg 360

gggatgcacc tggcctggaa cggtggtgcc aacgacaact ggctgccggc gcaggcgacc 420

acccgcgcag gaccatatgt ccctttgacc atgggttact acacgcgcca agacatcccg 480

atccactatc tgctggccga cacgttcacc atctgcgacg gctaccattg ctcgctgctg 540

acgggcaccc tgcccaaccg gctctactgg ttgagcgcca acatcgaccc cgccggcacc 600

gacgggggac cccaattggt agagccgggc ttcctgccgc tgcagcaatt cagttggcgc 660

atcatgccgg aaaacctcga agatgccggg gtcagctgga aggtgtacca gaacaagggc 720

ctcgggcgat tcatcaacac gcccatcagc aataacgggc tggtgcaggc cttccgccag 780

gcagctgatc cgaggtcgaa cttggcccgc tacggtatcg ccccgaccta ccctggggac 840

ttcgctgccg acgtcagggc caaccggcta cccaaggtct cctggttagt tcccaacatc 900

ctgcagtccg aacaccccgc cctgccggta gcgcttggcg cggtgtccat ggtgaccgcg 960

ctgcggatct tgctgtccaa tcccgcggtg tgggaaaaga ccgcacttat cgtcagctat 1020

gacgagaacg gcggcttctt cgaccacgtc acgcccccca cggcaccgcc cgggacaccc 1080

ggcgaattcg tcacggtgcc caacatcgac gcagtacccg ggtccggtgg cattcgtggt 1140

ccgctcggtc tgggttttcg cgttccctgc attgtcattt cgccgtacag ccgcggcccg 1200

ctgatggtct ccgacacgtt cgaccacacc tcgcaattga agttgattcg cgcccggttc 1260

ggcgtgccgg ttcccaacat gaccgcctgg cgcgacggcg tggttggcga catgacctca 1320

gcgttcaact ttgcgactcc accgaattcg accagaccca acttgagcca cccgttgctg 1380

ggagcgctgc cgaagctgcc gcagtgcatc cctaacgtgg tgttgggaac caccgacggc 1440

gcgttgccga gcattcccta tcgggtgccc tatccgcagg tgatgccaac tcaggaaacc 1500

acacccgtcc gcgggactcc cagcgggctg tgcagc 1536

<210> SEQ ID NO 59
<211> LENGTH: 1536
<212> TYPE: DNA
<213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 59

atgtcacgtc gagagttttt gacaaagctc actggcgcag gcgcagcggc attcctgatg 60

gactgggctg caccggtgat tgaaaaggcc tacggcgccg ggccttgtcc cggacatttg 120

accgacatcg agcatatcgt gttgctgatg caggagaacc ggtcattcga ccactatttc 180

ggaacgcttt ccagcaccaa tgggttcaac gccgcgtcgc cggcattcca acaaatgggt 240

tggaacccca tgacgcaggc gttggacccc gccggggtca ccattccgtt ccgcttggac 300

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accacccgag gccccttcct ggacggcgag tgcgtcaacg accccgagca ccagtgggtg 360

gggatgcacc tggcctggaa cggtggtgcc aacgacaact ggctgccggc gcaggcgacc 420

acccgcgcag gaccatatgt ccctttgacc atgggttact acacgcgcca agacatcccg 480

atccactatc tgctggccga cacgttcacc atctgcgacg gctaccattg ctcgctgctg 540

acgggcaccc tgcccaaccg gctctactgg ttgagcgcca acatcgaccc cgccggcacc 600

gacgggggac cccaattggt agagccgggc ttcctgccgc tgcagcaatt cagttggcgc 660

atcatgccgg aaaacctcga agatgccggg gtcagctgga aggtgtacca gaacaagggc 720

ctcgggcgat tcatcaacac gcccatcagc aataacgggc tggtgcaggc cttccgccag 780

gcagctgatc cgaggtcgaa cttggcccgc tacggtatcg ccccgaccta ccctggggac 840

ttcgctgccg acgtcagggc caaccggcta cccaaggtct cctggttagt tcccaacatc 900

ctgcagtccg aacaccccgc cctgccggta gcgcttggcg cggtgtccat ggtgaccgcg 960

ctgcggatct tgctgtccaa tcccgcggtg tgggaaaaga ccgcacttat cgtcagctat 1020

gacgagaacg gcggcttctt cgaccacgtc acgcccccca cggcaccgcc cgggacaccc 1080

ggcgaattcg tcacggtgcc caacatcgac gcagtacccg ggtccggtgg cattcgtggt 1140

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gcgttcaact ttgcgactcc accgaattcg accagaccca acttgagcca cccgttgctg 1380

ggagcgctgc cgaagctgcc gcagtgcatc cctaacgtgg tgttgggaac caccgacggc 1440

gcgttgccga gcattcccta tcgggtgccc tatccgcagg tgatgccaac tcaggaaacc 1500

acacccgtcc gcgggactcc cagcgggctg tgcagc 1536

<210> SEQ ID NO 60
<211> LENGTH: 1173
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis

<400> SEQUENCE: 60

atgattttgg atttttcgtg gttgccgccg gagatcaact cggcgcggat ctatgccggt 60

gcggggtcgg ggccgttgtt tatggcggcg gcggcgtggg aggggttggc tgcggatttg 120

cgggcctcgg cgtcctcgtt tgatgcggtg atcgccgggt tggcggctgg gccgtggtcg 180

ggtccggcgt cggtggcgat ggcgggggcg gcggcgccgt atgtggggtg gttgagtgcg 240

gcggccgggc aggcggagtt gtcggctggt caggctaccg cggcggcgac ggcgtttgag 300

gcggcgttgg cggccacggt gcatccggcg gcggtgacgg cgaatcgggt gttgttgggg 360

gcgttggtgg cgacgaacat tttgggtcag aacacgccgg cgattgcggc cactgagttc 420

gattatgtgg agatgtgggc tcaggacgtg ggtgcgatgg tggggtatca cgcgggggcg 480

gcggcggtgg ctgagacgtt gacgccgttt agtgtgccgc cgctggattt ggcggggttg 540

gcttcccagg ccggtgcgca gttgaccggg atggcgacgt cggtttcggc tgcgttgtct 600

ccgatcgcgg agggtgcggt ggagggggtg ccggctgtgg tggctgcggc gcagtcggtg 660

gcggcggggt tgccggtgga tgcggcgctg caggtggggc aggccgcggc gtatccggcc 720

agtatgttga ttgggccgat gatgcagttg gcgcagatgg ggactacggc caacacggct 780

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gagttgggta aggcgcggtt ggtgggggcg atgtcggtgc ctccgacctg ggaggggtcg 960

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ccggcggcag gcgggcccat ggggatgatg ccgatgccga tgggtatggg gggtgctggg 1080

gcgggtatgc cggccgggat gatgggccgc ggtggcgcaa atccgcatgt ggtgcaggct 1140

cggcccagtg tggtgccgcg ggtcgggatc gga 1173

<210> SEQ ID NO 61
<211> LENGTH: 1062
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis

<400> SEQUENCE: 61

atgccggggc ggttcagaaa cttcggtagc caaaacctgg gtagcggcaa catcggcagc 60

accaacgtgg gcagcggcaa catcggcagc accaacgtgg gcagcggcaa catcggcgac 120

acgaacttcg gtaacggaaa caacggcaac ttcaactttg gtagcggcaa taccggcagt 180

aacaacatcg gcttcggaaa caccggcagc gggaatttcg gtttcggaaa cacgggcaac 240

aacaacatcg gtatcgggct caccggcgat ggtcagatcg gcatcggcgg actgaactcg 300

ggcagcggaa acatcggttt cgggaactcc ggcaccggaa acgtcggttt gttcaactcc 360

ggcaccggca acgtaggctt cgggaactcc ggtactgcga acactggatt cgggaacgcg 420

ggcaacgtca acaccggatt ttggaacggc ggcagcacaa acactggcct cgctaacgcc 480

ggcgccggca acacaggctt tttcgacgct ggcaactaca acttcggcag tcttaacgcc 540

ggaaacataa actcgagttt tgggaattcg ggtgacggca acagtggttt cctcaatgct 600

ggcgacgtca actccggtgt gggcaatgcg ggtgatgtca acactggctt agggaactcg 660

ggcaacatca atactggtgg gtttaatccg ggcacgctca acacgggctt cttcagcgcg 720

atgacccaag ctggtccgaa ttcgggcttc ttcaacgccg gtaccggtaa ctctggtttc 780

gggcacaacg acccggctgg cagtggcaac tcgggcattc agaactcggg cttcggcaac 840

tcgggctatg tcaataccag caccacaagc atgttcggcg gtaactcagg ggtgctcaac 900

acgggctacg gcaactcagg tttctataac gcggccgtca acaacaccgg gatttttgtg 960

accggcgtga tgagttcggg atttttcaat tttgggacgg gcaactcggg cctgctggtc 1020

agcggcaatg ggctttcggg tttcttcaag aacttgttcg ga 1062

<210> SEQ ID NO 62
<211> LENGTH: 654
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis

<400> SEQUENCE: 62

atgagccgac tcctagcttt gctgtgcgct gcggtatgca cgggctgcgt tgctgtggtt 60

ctcgcgccag tgagcctggc cgtcgtcaac ccgtggttcg cgaactcggt cggcaatgcc 120

actcaggtgg tttcggtggt gggaaccggc ggttcgacgg ccaagatgga tgtctaccaa 180

cgcaccgccg ccggctggca gccgctcaag accggtatca ccacccatat cggttcggcg 240

ggcatggcgc cggaagccaa gagcggatat ccggccactc cgatgggggt ttacagcctg 300

gactccgctt ttggcaccgc gccgaatccc ggtggcgggt tgccgtatac ccaagtcgga 360

cccaatcact ggtggagtgg cgacgacaat agccccacct ttaactccat gcaggtctgt 420

cagaagtccc agtgcccgtt cagcacggcc gacagcgaga acctgcaaat cccgcagtac 480

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aagcattcgg tcgtgatggg cgtcaacaag gccaaggtcc caggcaaagg ctccgcgttc    540

ttctttcaca ccaccgacgg cgggcccacc gcgggttgtg tggcgatcga cgatgccacg    600

ctggtgcaga tcatccgttg gctgcggcct ggtgcggtga tcgcgatcgc caag          654


<210> SEQ ID NO 63
<211> LENGTH: 489
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis

<400> SEQUENCE: 63

gtgtgctgca atggcgtggt gactccgggt gatccagccg acattgcagc gatcaaacag     60

ctcaaatacc ggtatctgcg ggcattggac accaagcatt gggacgactt caccgacacc    120

ctggccgagg atgtcaccgg cgattacggg tcatcggtcg gtacggagct gcacttcacc    180

aaccgcgccg acctggtcga ctacctgcgc caggcactcg gcccgggtgt catcaccgaa    240

caccgggtca cccatccgga aatcaccgtg accggcgata ccgcaaccgg catctggtac    300

ctgcaagacc gggtcatcgt cgccgagttc aatttcatgc tcatcggcgc cgcgttctac    360

cacgaccagt accgacgaac caccgacggc tggcggatca gcgccaccgg ctacgaccga    420

acctacgagg cgaccatgtc gttggcgggc cttaacttca acatcaggcc gggccgcgcg    480

ctggccgat                                                            489


<210> SEQ ID NO 64
<211> LENGTH: 1227
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis

<400> SEQUENCE: 64

atgagccaat cccggtacgc ggggttgtcc cgcagcgagc tggcagttct gttacccgag     60

ctgttgttga tcggccagct gatcgaccga tcgggcatgg cctggtgtat acaggcattc    120

ggccgccagg agatgctgca gatcgccatc gaggagtggg cgggcgccag cccgatctac    180

accaagcgca tgcaaaaggc gctgaacttc gagggcgacg acgtgcccac catcttcaag    240

gggctacagc tcgacatcgg cgcgccgccg caattcatgg acttccgttt caccctgcac    300

gaccgctggc acggcgagtt tcacctcgac cactgcggtg cgctgctcga cgtggagccg    360

atgggcgacg actacgtcgt cggcatgtgc cacaccatcg aagatccgac gttcgacgcc    420

accgcgatcg cgaccaaccc gcgcgcgcag gtgcgcccca tccaccggcc gccccgcaag    480

ccggccgacc ggcatccgca ctgtgcgtgg accgtcatca tcgacgagtc ctatcccgag    540

gctgagggta ttccggcgct ggacgcggtc cgtgaaacca aagctgccac ctgggaatta    600

gacaacgtcg atgcgtctga cgacgggctg gtggactatt cgggtccgct ggtgtccgac    660

ctggacttcg gggcgttctc gcattccgca ctggtgcgga tggccgatga ggtctgcctg    720

caaatgcacc tgctgaatct gtcgttcgcc attgccgtgc ggaaacgggc caaagccgat    780

gctcaactgg ccatttcggt gaacacccgc cagttgatcg gagtggccgg gctgggcgca    840

gaacgcattc accgtgcgat ggctttaccc ggcggaatcg aaggcgcgtt aggtgtgctg    900

gagctacacc cgctgctcaa cccggccggt tacgtgctgg ccgaaacgtc gccggaccgt    960

ctggtggtgc acaactcgcc agcccacgcc gacggcgcct ggatttcgtt gtgcacaccg   1020

gcatccgtgc agccgttgca ggccatcgcc accgctgtag acccgcatct gaaggttcgg   1080

atcagcggga cggacaccga ctggaccgcg gaactcatcg aggccgatgc cccagcgagc   1140
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gaactgccgg aggtgttggt agccaaggtc agtcgcggat cggtcttcca gttcgagccg   1200

aggcgctcac tgccgttgac cgtgaaa   1227

<210> SEQ ID NO 65
<211> LENGTH: 1860
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis

<400> SEQUENCE: 65

atgtacgacc cgctggggtt gtcgatcggg accacaaacc tggtcgcggc gggtaacgga   60

ggtccgccgg ttactcgtcg cgccgtgctg accctgtacc cgcattgcgc accgaaaatc   120

ggtgtgccta gccagaaccc gaacttgatc gagccgggcg ccctaatgag cggctttgtt   180

gagcgcattg gagatgcggt ggcgctggtg tctcccgacg gatccgtgca cgatccagac   240

ctcttgctgg tcgaggcgct ggatgcgatg gtgctgaccg ccggtgcgga cgcgagttcc   300

tcggagatcg ccattgccgt tcccgcgcat tggaagcccg gagctgtaca cgcactgcgt   360

aacggtttgc ggacgcacgt cggcttcgtc cgcagcggca tggcgccgcg cctggtttcc   420

gatgcgatcg cggcgttgac cgcggtgaac tcggaattgg gcctgcccca cggcagtgtg   480

gtggggttgc ttgatttcgg tggctccgcg acttacgtca ccttggtgga gaccaagtcg   540

gattccagga cgtcggattt ccagcccgtt agtgccacgg cacggtacca ggacttttcc   600

ggtagtcaga tcgaccaggc tttgctgctt cgggtcatcg accaattcgg gtacggcgat   660

gacgtcgatc cggccagtac cgccgcggtc gggcaactcg gccaactcag ggagcagtgc   720

cgtgcggcaa aggaacgact gtccaccgac gttgccacgg aattgttcgc tgagcttgcc   780

gggtgcagct cgagcatcga gatgactcgg gaacagctcg aagacctgat ccaggatcca   840

ttgaccggct tcatctacgc gttcgacgac atgctggcgc gccacaacgc gagctgggcg   900

gatctcgcgg cggtggtcac cgtcggcggt ggtgccaata ttccccttgt gactcaacgt   960

ctttcgttcc acactcgtcg acctgtgctg accgcgtcgc aacccgggtg cgcggcggcg   1020

atgggtgcgt tgctgctcgc caaccgtggg ggagagcgcg attcgcgaac gcggacgtcc   1080

atcggcctcg ccacggccgc agccgccggc accagtgtca tcgagctgcc ggccggcgac   1140

gtcatggtca tcgaccatga ggccttgacc gatcgcgagt tggcctggtc gcagaccgac   1200

ttcccaagcg aagctccggc gcgtttcgag ggcgactcgt ataacgaagg cggcccctgc   1260

tggtcgatgc gtctgaacgc ggtcgagccc cccaaaggac cagcgtggcg gcgaatccgg   1320

gtgtcgcagt tgctcatcgg ggtgtcggcg gtagtggcca tgaccgcgat cgggggcgtg   1380

gcattgacgt tgacagccat cgagagacgc ccaagcccgc taccaacccc aattgtgccc   1440

ggcctggccc cgatgccgcc cggatccgtc gtgcctagct cgcgcgcacc gaccccgccg   1500

ccaccgccgt cgaccgttgc gccgcttccc agtgcggcac cggccccgac gacggtcgcg   1560

ccggcaccgc cgccgcccac acaggtggtg acgaccacga cagcgccacc cgtcaccacg   1620

acgccgaggc cgtcgccgac caccacaacg accaccgcgc caccgtcgac aacgacgaca   1680

accgagccgc cggtgacgac cacttcgacg attccaacga ttccgacgac tacgacgacg   1740

gtgaagatga ccacggagtg gttgcacgtc ccgtttttgc ccgttccgat cccggtcccg   1800

attccgcaaa atccgggtgc cggcgaaccg cagaacccgt tcggaagcct tggctctggg   1860

<210> SEQ ID NO 66
<211> LENGTH: 720
<212> TYPE: DNA
<213> ORGANISM: M. tuberculosis

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<400> SEQUENCE: 66

atgatccgat tggtccgtca ttcgatcgcc ctggtggccg ccggccttgc cgccgcattg 60

tcggggtgcg attcccacaa ctcgggatcg ctcggtgccg atccgcggca ggtgaccgtg 120

ttcggatccg ggcaagtgca gggtgtgccg gacacgttga tcgctgacgt cggcattcag 180

gtcaccgcgg ccgacgtcac cagcgcgatg aaccagacca atgatcgcca gcaagcggtg 240

atcgatgcac tggtgggtgc cggcctggac cgcaaggaca tccgcaccac cagggtcacc 300

gtggcaccgc agtacagcaa tccggagccg gccggaaccg ccaccatcac cgggtatcgg 360

gcagacaacg acatcgaggt gaagatccac ccgaccgacg ccgcgtcgcg gctgctggcc 420

ctcgtcgtca gcaccggcgg tgacgccacc cggatcagct cggtcagcta ctcgattggc 480

gacgactcgc agctggtgaa ggatgcccgg gcgcgcgcct tccaagacgc caagaaccgt 540

gcggaccagt acgcacaact gtcggggctg cggctaggca aggtgatctc gatctccgag 600

gcatctggcg ccgcgcccac gcacgaggcg ccggcgccgc cgcgcggcct atccgcggtg 660

ccgctggaac ccggccagca gacggtgggc ttctcggtca cggtggtctg ggaactgacc 720

<210> SEQ ID NO 67
<211> LENGTH: 297
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis

<400> SEQUENCE: 67

atgtcgatca tgcacgccga gccagagatg ctggctgcga ccgcggggga actgcagtcg 60

atcaacgccg ttgcgcgggc cggaaatgca gcggtggcgg gcccgacgac gggtgtggtt 120

ccggccgccg ctgatttggt gtccctgcta accgcctccc agtttgccgc gcatgcacag 180

ctgtaccagg cgattagtgc cgaggcgatg gcggtccagg agcagttggc gaccacgctg 240

ggcatcagcg ccggttcata tgcggccacc gaggctgcca acgccgccac gatcgct 297

<210> SEQ ID NO 68
<211> LENGTH: 1239
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis

<400> SEQUENCE: 68

atgctggact ttgctcagtt accgccggag gtcaactccg cgctgatgta cgccggaccc 60

ggttcgggac cgatgctggc tgccgcggcg gcctgggagg cgctggccgc cgagttgcaa 120

accacggcgt ccacctacga cgctctgatc actggcctgg ccgacgggcc atggcagggg 180

tcctccgcgg cgtccatggt ggctgccgcc acgccccagg tggcgtggtt gaggagcacc 240

gccgggcagg ccgagcaagc cggcagccaa gcggtggcag cggcgagtgc ttatgaggcg 300

gcgtttttcg cgaccgtgcc gcccccggag atcgcggcca acagggcgtt gttgatggcg 360

ttgctggcga cgaacttcct tggccagaac acggcggcga tcgcggccac cgaggcgcaa 420

tacgccgaga tgtgggccca ggatgcggcc gcgatgtacg gctatgctgg cgcgtcggcg 480

gcggcgacgc agttgtcgcc attcaatccg gcggcgcaga ccatcaaccc ggccgggctg 540

gccagccagg ccgcatctgt cggacaagct gtcagcgggg ccgcaaatgc gcaagcactc 600

accgacattc ctaaagcgtt gtttgggctt agcggaatct tcaccaatga accgccttgg 660

ctcaccgacc ttggcaaggc gctcggtttg accgggcaca cctggtcctc ggacggtagc 720

gggctcatcg tgggcggagt gcttggcgac tttgtgcagg gtgtgaccgg gtcggccgaa 780

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gtcacccaat tcaaggacta ctttggcctg gcgcacgacc tgccgaagtg ggcgagtgaa 900

ggcgccaaag ccgccggtga ggccgccaag gcgttgccgg ccgccgttcc ggccattccg 960

agtgctggcc tgagcggcgt tgcgggcgcc gtcggtcagg cggcgtcggt cgggggattg 1020

aaggttccgg ccgtttggac cgccacgacc ccggcggcga gccccgcggt gctggcggcg 1080

tccaacggcc tcggagccgc ggccgccgct gaaggttcga cacacgcgtt tggcgggatg 1140

ccgctcatgg gtagcggtgc cggacgtgcg tttaacaact tcgctgcccc tcgatacgga 1200

ttcaagccga ccgtgatcgc ccaaccgccg gctggcgga 1239

<210> SEQ ID NO 69
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis

<400> SEQUENCE: 69

atgacctcgc gttttatgac ggatccgcac gcgatgcggg acatggcggg ccgttttgag 60

gtgcacgccc agacggtgga ggacgaggct cgccggatgt gggcgtccgc gcaaaacatt 120

tccggcgcgg gctggagtgg catggccgag gcgacctcgc tagacaccat gacccagatg 180

aatcaggcgt ttcgcaacat cgtgaacatg ctgcacgggg tgcgtgacgg gctggttcgc 240

gacgccaaca actacgaaca gcaagagcag gcctcccagc agatcctcag cagc 294

<210> SEQ ID NO 70
<211> LENGTH: 282
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis

<400> SEQUENCE: 70

atgaccatca actatcaatt cggggacgtc gacgctcacg gcgccatgat ccgcgctcag 60

gccgggtcgc tggaggccga gcatcaggcc atcatttctg atgtgttgac cgcgagtgac 120

ttttggggcg gcgccggttc ggcggcctgc caggggttca ttacccagct gggccgtaac 180

ttccaggtga tctacgagca ggccaacgcc cacgggcaga aggtgcaggc tgccggcaac 240

aacatggcac aaaccgacag cgccgtcggc tccagctggg cc 282

<210> SEQ ID NO 71
<211> LENGTH: 1185
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis

<400> SEQUENCE: 71

atgaaggcac cgttgcgttt tggcgttttc atcacgccat tccatccgac cggtcaatcc 60

ccgaccgtgg cgttgcaata cgacatggag cgcgtcgttg cgctggaccg gctcggctac 120

gacgaggcgt ggtttggcga acaccactcc ggtggctacg agctgatcgc ttgcccggag 180

gtgtttatcg cggccgcagc ggaacggacc acccacatcc ggctaggtac cggagtggtt 240

tcgctgccct accatcatcc gctaatggtg gccgaccgtt gggtgctgct ggatcacctg 300

acccgtgggc gggtcatgtt cggcaccggc cccggcgcgc tgccgtcgga cgcctacatg 360

atgggcatcg atccggtcga gcagcgacga atgatgcagg agtccctcga ggcgattctc 420

gcgctgttcc gtgccgcacc tgacgagcga atcgaccgcc actccgactg gttcaccctg 480

cgtgaagcgc aattgcacat ccgcccctac acctggccgt accccgaaat cgctaccgca 540

gccatgattt cgccatcggg tccgcgactg gccggtgcgc tgggcacgtc gctgttatca 600

-continued

ctgtcgatgt cagtgcccgg cggctacgct gcgctggaaa cagcgtgggg cgtggtgcgg 660

gagcaggccg ccaaagctgg gcggggcgag ccggatcgcg ccgattggcg ggtgttgagc 720

atcatgcact tgtcggacag ccgcgaccag gcgatcgacg actgcactta cgggttaccc 780

gacttctcga ggtacttcgg cgcggcaggg tttgtcccgt tggcgaacac cgtggaaggc 840

acccagtcgt ctcgggaatt cgtcgagcaa tacgcggcca agggaaattg ctgcatcggc 900

acgcccgatg acgcgatcgc ccacattgaa gacttgctgc accggtcggg tggcttcgga 960

acgttgctac tgctcggcca cgactgggcc ccgccaccgg caacctttca ctcctatgag 1020

ctgttcgccc gtgctgtgat tccttatttc aagggacaac tcgcggcgcc gcgggcgtcg 1080

cacgaatggg ctagaggcaa gcgcgaccaa ttgattggcc gcgccggcga agcggtcgtc 1140

aaagccatca ccgagcacgt cgccgaacaa ggggaagcgg gcagc 1185

<210> SEQ ID NO 72
<211> LENGTH: 966
<212> TYPE: DNA
<213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 72

atgggcgcac ctaccgaacg gttagttgat accaacggcg tgcgactgcg agtggtcgag 60

gccggtgagc ccggcgcacc cgtggtgata ctggcccacg gctttcccga actggcctat 120

tcatggagac accagattcc tgcgcttgcc gacgccggct accacgtgtt ggctcccgat 180

cagcgcggtt acggcggatc gtctcgccca gaggcgatcg aggcctacga cattcaccgg 240

ttgaccgctg acctagtggg cctactagat gatgtcggtg ccgagcgggc ggtctgggtt 300

ggtcatgact ggggtgccgt ggtggtgtgg aacgcgccac tgctgcacgc tgaccgagtc 360

gccgccgttg ccgcgttgag cgtccccgcg ctgccccggg cacaggtgcc gccgacgcaa 420

gcgttccgca gcaggtttgg ggagaacttc ttctacatcc tttatttcca ggagcccggc 480

atcgccgacg ccgaactcaa tggcgacccg gcccgcacga tgcgccgaat gatcggcggt 540

ctgcgccctc cgggcgatca gagcgcggca atgcgtatgc tggcgcccgg ccccgacggc 600

tttatcgatc ggcttccgga gccggccggg ttgccggcct ggattagtca ggaggaactc 660

gaccactaca tcggcgagtt cacccgcacc ggtttcaccg gcggcctgaa ctggtaccgc 720

aacttcgacc gcaactggga gaccacggcc gacctcgccg gcaagacgat ctccgtgccc 780

tcgttgttca ttgcgggcac agccgatccc gtcttgacgt tcacccgcac cgaccgcgct 840

gcggaggtga tctccggccc gtatcgcgag gtgctgatcg acggggccgg tcactggctg 900

cagcaggaac gtcccggtga ggtgaccgcg gccctgctgg agttcctgac ggggttggag 960

ttgcga 966

<210> SEQ ID NO 73
<211> LENGTH: 1365
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis

<400> SEQUENCE: 73

gtgaataccg atgtgctggc tggcctgatg gccgagctgc ccgaggggat ggtggtcacc 60

gaccccgccg tcaccgacgg ctaccggcaa gaccgggcct ttgacccttc ggccggcaaa 120

ccgctggcaa tcatccggcc acggcgcacc gaagaggtgc agacggtgct gcgttgggcc 180

agtgcgaacc aggtgcccgt ggtgacccga ggagccggta gcggcctttc gggcggggcg 240

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accgccctgg atggcgggat cgtgctgtcc accgaaaaga tgcgcgacat caccgtcgac    300

ccggtcaccc gcaccgcagt gtgccagccc ggcctgtaca acgccgaggt gaaggaggcc    360

gccgccgaac acggcctgtg gtatccccg gatccgtcgt cgttcgagat ctgcagcatc    420

ggcggcaaca tcgccaccaa cgccggcggg ctgtgctgcg tgaagtacgg cgtcacaggc    480

gactacgtac tgggcatgca ggttgtgctg gccaacggca ccgcggtccg gctgggcggc    540

ccacggctca aggacgtcgc cgggctttcc ctgaccaaac tgttcgtcgg cagcgaaggc    600

acgctgggcg tcatcacgga ggtgacgttg cgactgctgc ccgcacagaa tgcatcgagc    660

atcgtggtgg ccagcttcgg ctcggtgcag gcggcggtcg atgcggtgct cggggttacc    720

ggccgacttc gccccgcgat gctggagttc atggattcgg tggcgatcaa cgccgtcgag    780

gacaccttgc ggatggacct ggaccgcgat gcggcggcca tgctggtggc tggttctgat    840

gaacgtggcc gcgcggccac cgaagacgcc gccgtgatgg ccgccgtgtt cgccgaaaac    900

ggtgcgatag acgtgttttc gaccgacgac ccggatgagg gcgaggcgtt cattgcggcc    960

cggcggttcg ccattccggc ggtcgagagc aagggggcgt tgctgctcga ggacgtcggg   1020

gtaccgctgc ccgcactggg cgaactggtc accgggattg cgcgcatcgc cgaggagcgg   1080

aatctgatga tctcggtgat cgcccacgcc ggggacggca atacccaccc gttgctggtg   1140

tacgaccccg cagatgccgc gatgctagag cgcgcccacc tcgcgtacgg cgaaatcatg   1200

gacctggccg tcggcctggg cggcacgatc accggcgaac acggcgtggg ccggttgaaa   1260

cggccgtggt tggccggcta tctcgggccc gacgtcctgg ccctcaacca gcgcatcaag   1320

caagcgctgg acccccaggg catcctcaat cccggctcgg cgatc                   1365


<210> SEQ ID NO 74
<211> LENGTH: 1215
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis

<400> SEQUENCE: 74

atgacatcag taatgtctca cgaattccag ctcgccaccg ccgaaacctg gccgaatccg     60

tggccgatgt accgcgcgtt gcgcgaccac gacccggtgc accacgtcgt cccgccgcag    120

cgtcccgagt acgactacta cgtgctgtcc cggcacgccg acgtctggtc ggcagcgcgg    180

gaccatcaga cgttctcgtc ggcgcaaggc ttgaccgtta actacggcga gctggaaatg    240

attggactgc acgacacccc gcccatggtg atgcaggatc cgccggtcca caccgagttt    300

cgcaagctgg tgtcgcgcgg cttcacgcca cgacaggtcg aaaccgtcga gcccacggtg    360

cgcaagttcg tcgttgagcg gctcgaaaag ctgcgcgcca acggtggcgg cgacattgtc    420

accgaactat tcaaaccgct cccgtcgatg gtggtggcgc actatctcgg tgttcccgaa    480

gaggattgga cgcaattcga cgggtggacc caggccatcg tggcggcgaa cgcggttgac    540

ggcgccacca ccggcgcact ggacgcggtc ggctcgatga tggcctactt caccgggctg    600

atcgagcgac gccgcaccga gcccgccgac gacgccatct cccacctggt agccgccggg    660

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gtcaccggcg gcaacgacac cgtcaccggc atgctaggcg gttcgatgcc gttgctgcac    780

cggcggcccg accagcgccg gctgctgctg gatgacccag agggcatccc cgacgcggtc    840

gaggagctgc tgcggctcac ctcgccggtg caggggctgg cgcgcacaac cacgcgcgac    900

gtcacgatcg gtgacaccac catcccggcc ggtcgccggg tgctgctgct gtacggctcg    960

gccaaccgtg acgaacgcca atacggcccg gacgcagccg aactcgatgt cactcggtgc   1020
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ccgcgcaaca tcttgacctt cagccacggc gcccaccact gcctgggtgc ggccgcggcc 1080

cggatgcaat gccgggtggc gctgaccgaa ctgctggccc ggtgcccgga cttcgaggtg 1140

gccgagtcac gcatcgtgtg gtccggcggc agttatgtcc ggcgtccgct gtcggtgccg 1200

ttccgagtga catcc 1215

<210> SEQ ID NO 75
<211> LENGTH: 606
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis

<400> SEQUENCE: 75

atggcgggta ccgactggct gtccgcgcgt cggaccgagt tagccgcaga tcggatactc 60

gacgccgccg agcgactctt tacgcagcgt gacccggcgt cgatcggcat gaacgagatc 120

gccaaggccg caggctgttc gcgcgcaaca ctgtatcggt acttcgacag ccgcgaggcg 180

ctgcgaaccg cgtacgtgca ccgcgagacc cgccggctcg gccgcgagat catggtgaag 240

atcgccgatg tcgtcgaacc tgccgaacgg ctgctggtga gcatcaccac gacgttgcgg 300

atggtccgcg acaaccccgc gttggccgcg tggtttacca ccacccgccc accgatcggc 360

ggcgagatgg ccggacggtc cgaggtgatc gcggccctgg ccgcggcatt cctcaactca 420

ctaggtcccg acgatccgac caccgtcgaa cgccgcgccc gctgggtggt ccggatgctc 480

acatcgctgc tgatgttccc cggccgtgac gaagccgacg aacgagcgat gatcgcggag 540

ttcgtcgtcc cgatcgtgac acctgcttct gccgccgcta ggaaggccgg tcaccctgga 600

cccgag 606

<210> SEQ ID NO 76
<211> LENGTH: 534
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis

<400> SEQUENCE: 76

atgcatccaa tgataccagc ggagtatatc tccaacataa tatatgaagg tccgggtgct 60

gactcattgt ctgccgccgc cgagcaattg cgactaatgt ataactcagc taacatgacg 120

gctaagtcgc tcaccgacag gctcggcgag ctgcaggaga actggaaagg tagttcgtcg 180

gacttgatgg ccgacgcggc tgggcggtat ctcgactggc tgactaaaca ctctcgtcaa 240

attctggaaa ccgcctacgt gatcgacttc ctcgcatacg tctatgagga gacacgtcac 300

aaggtggtac ccccggcgac tatcgccaac aaccgcgagg aggtgcacag gctgatcgcg 360

agcaacgtgg ccggggtaaa cactccagca atcgcaggac tcgatgcaca atatcagcag 420

taccgggccc aaaatatcgc tgtcatgaac gactatcaaa gtaccgcccg gtttatccta 480

gcgtatctgc cccgatggca ggagccgccg cagatctacg gggcggggg cggg 534

<210> SEQ ID NO 77
<211> LENGTH: 1230
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuburculosis

<400> SEQUENCE: 77

gtggccacga tagcccaacg gctgcgtgac gaccacgggg tggcggcgtc ggagtcgtcg 60

gtgaggcgtt ggatcgcaac gcatttcgcc gaggaggtgg cccgcgagag agtcacggtg 120

ccgcgcggac cggtcgatgc gggtagtgag gcgcagatcg attacgggcg gctgggcatg 180

-continued

tggttcgacc cggccaccgc gcgccgggtc gcggtgtggg cgttcgtgat ggtgctggcg   240

ttctcccgac acctgttcgt gcgtccggtc atccggatgg accaaaccgc ttggtgtgct   300

tgccatgtcg ccgcattcga attcttcgac ggggtgccgg cgcggctagt gtgtgacaac   360

ctcaggaccg ggtggacaa gcccgacctg tacgacccgc agatcaaccg ctcctacgcc   420

gagctggcca gccactacgc cacgctggtc gacccggccc gcgccagaaa acccaaagat   480

aaaccccgcg tggagcggcc gatgacctat gtgcgggact cgttttggaa aggccgcgag   540

ttcgattcgc tggcccagat gcagcaggcg gcggtcacct ggagcaccga agtggccggg   600

cttcggtact tacgtgcctt ggagggcgcc caacccctgc ggatgttcga agctgtggag   660

caacaagcgt tgatcgcatt gccgcccagg gcatttgaac tcaccagctg gtcgatcggc   720

accgtcgggg tggacacgca cctcaaagtt ggcaaggcac tctattccgt gccgtggcgg   780

ctgatcgggc aacgcctgca cgcgcgcacc gccggtgatg tggtgcagat cttcgccggc   840

aacgatgtgg tggccaccca tgtgcgccga cccagcgggc gctccaccga cttctcccac   900

tacccaccgg agaagatcgc cttccacatg cgcaccccga cctggtgtcg acacaccgcc   960

gaactggtcg gcccagccag ccagcaagtg atcgccgaat tcatgcgcga caacgccatc   1020

caccacctac ggtcggccca aggcgtgctc gggctacgcg acaaacacgg ctgcgaccgg   1080

ctggaggccg cctgcgcccg cgccatcgag gtcggcgacc cgagctatcg caccatcaag   1140

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agcaccgctg gggcgttcc tgcgcggccc   1230

<210> SEQ ID NO 78
<211> LENGTH: 753
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberulosis

<400> SEQUENCE: 78

atgtctatct gtgatccggc gctgcgtaat gcgctacgta ccctgaaact gtccggcatg   60

ctcgacaccc tcgacgcccg cctggcccaa acccgcaacg gcgacctggg gcatctggaa   120

ttcctgcaag cgttgcgtga agacgagatc gcccgccgcg agtccgccgc cctgacacga   180

cgattacgcc gcgccaagtt cgaagcccaa gccaccttcg aagacttcga cttcactgcc   240

aacccgaaac tgcccggtgc gatgttgcgc gatctggccg cgctgcgctg gctggatgcc   300

ggcgaatcgg tcatcctcca cggcccggtc ggcgtcggaa aaacccatgt agcacaagca   360

cttgtccacg ccgtggcccg ccgcggcggc gacgtgcgct tcgccaaaac ctcccgcatg   420

ctctccgacc tcgccggcgg gcacgccgac cgatcctggg gccaacgcat ccgcgaatac   480

accaagccgc tcgtgctcat tctggacgac ttcgcgatgc gtgagcacac cgccatgcac   540

gctgatgacc tctacgagct catcagcgac cgcgccatca ctggcaaacc gctgatcttg   600

accagcaacc gcgcaccgaa taactggtac ggcctgttcc ccaaccccgt cgtcgccgaa   660

tcactcctgg atcggctcat caacaccagc caccaaatcc tcatggacgg acccagctac   720

cgaccccgca agagacccgg ccgcaccacc agc   753

<210> SEQ ID NO 79
<211> LENGTH: 696
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberulosis

<400> SEQUENCE: 79

atgcatctaa tgatacccgc ggagtatatc tccaacgtaa tatatgaagg tccgcgtgct   60

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gactcattgt atgccgccga ccagcgattg cgacaattag ctgactcagt tagaacgact 120

gccgagtcgc tcaacaccac gctcgacgag ctgcacgaga actggaaagg tagttcatcg 180

gaatggatgg ccgacgcggc tttgcggtat ctcgactggc tgtctaaaca ctcccgtcag 240

attttgcgaa ccgcccgcgt gatcgaatcc ctcgtaatgg cctatgagga gacacttctg 300

agggtggtac ccccggcgac tatcgccaac aaccgcgagg aggtgcgcag gctgatcgcg 360

agcaacgtgg ccgggggtaa acactccagc aatcgcagac ctcgaggcac aatacgagca 420

gtaccgggcc gaaaatatcc aagcaatgga ccgctatcta agttggaccc gatttgcgct 480

atcgaagctg ccccgatggc gggagccgcc gcagatccac aggagcgggt aggtccaaga 540

ggccggcgcg gtcttgcagg ccagcaacaa tgccgcggtc gaccaggccc atcgcttcgc 600

tgctcgcacg acacaccgcg gtttcagatg aatcaggcgt ttcacaccat ggtgaacatg 660

ttgctgacgt gttttgcatg tcaggagaaa ccgaga 696

<210> SEQ ID NO 80
<211> LENGTH: 528
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberulosis

<400> SEQUENCE: 80

atgcatccaa tgataccagc ggagtatatc tccaacataa tatatgaagg cccgggcgct 60

gactcattgt tttcgcctc cgggcaattg cgagaattgg cttactcagt tgaaacgacg 120

gctgagtcgc tcgaggacga gctcgacgag ctggatgaga actggaaagg tagttcgtcg 180

gacttgttgg ccgacgcggt tgagcggtat ctccaatggc tgtctaaaca ctccagtcag 240

cttaagcatg ccgcctgggt gatcaacggc ctcgcgaacg cctataacga cacacgtcgg 300

aaggtggtac ccccggagga gatcgccgcc aaccgcgagg agaggcgcag gctgatcgcg 360

agcaacgtgg ccggggtaaa cactccagca atcgcagacc tcgatgcaca atacgaccag 420

taccgggccc gcaatgtcgc tgtaatgaac gcctatgtaa gttggacccg atctgcgcta 480

tcggatctgc cccggtggcg ggaaccgccg cagatctaca ggggcggg 528

<210> SEQ ID NO 81
<211> LENGTH: 1170
<212> TYPE: DNA
<213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 81

atgatcatcg ttgtcgggat cggcgccgac ggcatgaccg gtctctccga gcattctcgc 60

tccgaattgc gcagggccac agtaatttac ggctcgaaac ggcaacttgc cctgctcgac 120

gataccgtca ccgccgagcg ctgggagtgg ccgacgccga tgctgcccgc ggtgcaaggc 180

ctgtcaccgg atggggctga cctacacgtg gttgccagcg gcgacccgtt gttgcatggt 240

atcggctcca ccctgatccg gctgttcggc cacgacaacg tgaccgtgtt gccgcacgtg 300

tccgcggtga cgttggcgtg cgcccggatg ggctggaacg tgtatgacac cgaggtgatc 360

agcctggtca ccgcgcaacc acacaccgcg gtgcgccgcg gcggccgggc catcgtgctg 420

tccggcgatc ggtccacccc gcaggcgctg gcggtgctgc tgaccgagca cggtcgcggt 480

gactccaagt tcagcgtgct cgaacagctt ggcggcccgg ccgaacgccg ccgcgacggt 540

acggcccggg catgggcctg cgacccaccc ctcgatgtcg atgagctcaa cgtgatcgcc 600

gtgcgctacc tgctcgacga gcgcacgtcg tgggcacccg acgaggcatt cgcgcacgac 660

-continued

gggcagatca ccaaacaccc gatccgcgtg ctgaccctgg ctgcgctggc gccaaggccc 720

gggcagcggt tatgggacgt cggcgcgggc tcaggcgcca tcgcggtcca gtggtgtcgg 780

agctggccgg gctgcaccgc ggtggcgttc gagcgcgacg aacggcgccg ccgcaacatt 840

gggttcaatg ccgcggcctt cggggtgagc gtcgacgtgc gcggcgacgc gcccgatgcg 900

ttcgacgacg ccgcacggcc gtcggtgatt tttcttggcg gtggtgtaac ccagccaggc 960

ctgcttgagg cctgcctgga cagcctgccc gcaggcggga acttggtcgc caacgctgtc 1020

accgtcgaat cggaagccgc tctggcgcat gcatattcgc gcctcggtgg cgagctacga 1080

cgattccagc actatctcgg cgaaccgctg ggcggcttca ccggttggcg cccacagctg 1140

ccggtcaccc agtggtcggt gaccaagcga 1170

<210> SEQ ID NO 82
<211> LENGTH: 747
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberulosis

<400> SEQUENCE: 82

gtggacgaca cgggcgctgc tccggtagta attttcggcg gccgcagcca gatcggcggc 60

gaactcgcgc gacgcctggc tgccggggcg acgatggtgc tggccgcgcg gaacgccgat 120

caactcgccg accaggccgc cgcactccgc gcagctggcg ctatagcggt gcacacccgg 180

gagttcgacg ccgacgacct ggccgcacac ggcccgttgg tcgcttcgct cgttgccgag 240

cacggcccca tcggcaccgc ggtgctggcc ttcgggatac tcggcgacca ggcccgcgcc 300

gagacagacg cggcgcacgc ggtggccatc gtgcacaccg actacgtcgc ccaggtcagc 360

ctgctgactc atctggcagc ggcgatgcgc accgccggac ggggatcgct ggtggtgttc 420

tcctcggtcg ccgggattcg ggtgcgccgc gccaactatg tctacggatc ggccaaagcc 480

ggcctggacg gcttcgccag cggcctggcc gatgcgttgc acggcaccgg ggtgcggtta 540

ctgatcgcgc ggccgggatt cgtcatcggg cgcatgaccg agggcatgac gcccgcaccc 600

ctgtcggtca ccccggagcg ggtggccgcc gcgaccgcgc gtgcgctggt caacggtaag 660

cgcgtggtgt ggattccgtg ggcgctgcgg ccaatgtttg ttgcgctgcg gttgcttccc 720

cggttcgtct ggcgcaggat gccgcga 747

<210> SEQ ID NO 83
<211> LENGTH: 411
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberulosis

<400> SEQUENCE: 83

gtggcgatgg tcaacaccac tacgcggctt agtgacgacg cgctggcgtt tctttccgaa 60

cgccatctgg ccatgctgac cacgctgcgg gcggacaact cgccgcacgt ggtggcggta 120

ggtttcacct tcgaccccaa gactcacatc gcgcgggtca tcaccaccgg cggctcccaa 180

aaggccgtca atgccgaccg cagtgggctt gccgtgctca gccaggtcga cggcgcgcgc 240

tggctctcac tggagggtag ggcggcggtg aacagcgaca tcgacgccgt gcgcgacgcc 300

gagctgcgct acgcgcagcg ctatcgcacc ccgcgtccca atccacgccg agtggtcatc 360

gaggtccaga ttgagcgcgt gctgggatcc gcggatctgc tcgaccgggc c 411

<210> SEQ ID NO 84
<211> LENGTH: 1461
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberulosis

<400> SEQUENCE: 84

atgccccgcg cccgatggct gcagagcgcg gccctcatgg gcgccttggc cgtggtgttg 60

ataaccgcgg caccggtggc cgccgatgcc taccaggtgc ccgctccgcc ctcgcccacc 120

gcatcctgtg acgtaataag cccggttgcg atcccctgcg tggcgctcgg caagttcgcc 180

gacgcggtcg ctgcggagtg tcgccgcgtc ggtgtgcccg atgcgcggtg cgtgcttccg 240

ctcgcgcacc gggtgaccca ggccgcgcgt gatgcctacc tacagtcttg ggtgcatcgc 300

accgcgcggt tccaggatgc gttgcaagac ccggtgccgc tgcgggaaac tcagtggctc 360

ggcacgcaca actcgttcaa cagcctcagc gattcgttca cggtctcgca cgcagactca 420

aaccagcagc tgtcgttggc ccaacagctc gacatcgacg tccgcgcgct cgagctagac 480

ctgcactact tgccccgcct cgagggccac ggcgccccg gcgtcaccgt gtgtcacggg 540

ctgggaccga agaacgcgaa cctaggctgc accgtcgaac ctctgctggc cacagtgctg 600

ccgcagatcg ccaactggtt gaacgcaccc gggcataccg aggaggtcat cctgctctac 660

ctggaggacc agctgaagaa cgcgtcggcg tatgagtcgg tggtggctac cctcgaccaa 720

gtgttgcggc gtgcggacgg aacaagcctt atctaccgtc ccaacccggc ccggcgtgcc 780

accaacggct gtgtcccgct tccactcgac gtgtcgcggg aggaaatccg cgcatccggc 840

gcacgagccg tgctcgtcgg gtcttgtgcg ccaggttggt cggccgccgt cttcgactgg 900

agcggcgttg agctggaaag cggctcgaac tccggctacc ggccataccc ggcctgcgat 960

gccacctatg gccgcggtgt ctacgcttgg cgactggtcc gctattacga ggactccacg 1020

ctggccacgg cgttggccaa cccgacccgt ccaccggcca atccgcaggc gcttaccccg 1080

ccgaaggtgc cggcgatgac cgattgcggg gtcaatctgt tcggcttcga tcagctgctc 1140

cccgaagacg gccgcattca ggcgtcgttg tggagctggg caccggacga accgcgtgcc 1200

ggtgccggag catgcgccct gcagggcgcg gatggccgct gggtcgccgc atcgtgcggt 1260

gacccacacc ctgcggcctg tcgggacgcg gcaggcaggt ggaccgtgac gccggcaccc 1320

gtggtcttcg ccggggctgc cctagcctgc acagccatcg gcgcggactt taccctgccc 1380

cgaacgggca atcagaacgc ccgtctgcac gccgtggccg ggcccgccgg tggcgcctgg 1440

gtgcattacc tactgccgcc a 1461

<210> SEQ ID NO 85
<211> LENGTH: 429
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberulosis

<400> SEQUENCE: 85

atgaccacca cgccccgaca accccctgttc tgcgcccacg ccgacaccaa cggcgacccg 60

ggccgctgcg cctgcggcca gcagctcgcc gacgtcggcc cggccacccc gccaccgccc 120

tggtgcgaac cgggcaccga acccatctgg gagcagctca ccgaacgata cggcggcgtc 180

acaatctgcc agtggacacg atattttccg gccggcgacc cggtggctgc cgacgtgtgg 240

atcgccgccg acgatcgtgt cgttgacggc cgggtgctgc gcacccaacc ggcgattcac 300

tacacggaac cgcccgtgtt ggggatcggc ccggcggcgg cccgccggct ggccgctgag 360

ctgctcaacg ccgccgacac cctcgacgac ggccgccggc agctagacga cctcggcgaa 420

caccggcgg 429

<210> SEQ ID NO 86

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<211> LENGTH: 996
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberulosis

<400> SEQUENCE: 86

gtgaacaccg cgacccgggt ccggctggcc cgcaaacgcg ccgaccggct caatctgaaa 60

ctaatcaaga acggccacca cttcaggttg cgtgacgccg acgagatcac gctggcggtc 120

gggcacctag ggtggtggga agccttcctg gcggcggcca agtcgcaaaa caagccgccc 180

ggtccgccgc cgagcctcca cgccccgcca tcctggcggc gcgacatcga cgactacctg 240

ctcaacctga acgccgccgg tcaacgccca gcgacgatcc ggctacgcaa gacggtgctg 300

tgcgcagccg cccacggcct cggccgccca cccgccgacg tcaccgccga acacctcctg 360

gactggctag gcaaacagca gcacctctcc ccagagggcc gcaaaaccta tcgcagcacg 420

ttgcggggct tcttcgtgtg ggcctacgaa atggaccggg tgcgcgacta tgtcgcagac 480

tccctgccta aggtgcgctg cccgaaacag ccgccccgcc cggccggcga cgacgtctgg 540

caagcggcgc tggccaaggc cgaccgtcga atcgagctga tgatccgcct agccggtgag 600

gccgggctgc gacgcgccga agccgcccag gcgcacaccg gcgacttgat ggacggcggg 660

cttctcctcg ttcacggcaa aggtggtaaa cgccgtattg tgccgatcag cgactacttg 720

gccgcgctca tccgcgacac cccgcacggc tacctgttcc ccaacggcac cggcggccac 780

ctcaccgccg aacacgtggg aaaactcgtc tcccgggcat tacccggtga cgcgaccatg 840

cacaccctgc ggcaccgata cgccacccgc gcctaccgcg gctcccacaa cttgcgagct 900

gtacaacaac ttctcggtca cgcctcgatc gtgacaacag aacgctacac agcgctgtgc 960

gacgacgagg tgcgcgccgc agcagcagcc gcatgg 996

<210> SEQ ID NO 87
<211> LENGTH: 366
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberulosis

<400> SEQUENCE: 87

gtgcacgtgt gccacacgat cgccgacgtg gtcgaccggg ccaaagccga acgctccgaa 60

aacacgcttc gcaaggattt cacccccctcg gagctgctcg ccgctggtcg ccggatcgcc 120

gagctggaac ggccgaaagc caaacagcgg caacgcgaag gcggcgacca tggccgccag 180

gctcgatatt ctggcttagg ctccatggag cctaagccag aatcagagcg cgatgcccac 240

aaagccgaca ctgccatcag cgaagccctc ggcatctccc gcggccacta ccagcggctc 300

aaacgaatcg acaacgcaac ccgcagcgaa gctggctacc gggatggttt aaacggttgg 360

agcggc 366

<210> SEQ ID NO 88
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberulosis

<400> SEQUENCE: 88

atgtcaggtg gttcatcgag gaggtacccg ccggagctgc gtgagcgggc ggtgcggatg 60

gtcgcagaga tccgcggtca gcacgattcg gagtgggcag cgatcagtga ggtcgcccgt 120

ctacttggtg ttggctgcgc ggagacggtg cgtaagtggg tgcgccaggc gcaggtcgat 180

gccggcgcac ggcccgggac cacgaccgaa gaatccgctg agctgaagcg cttgcggcgg 240

gacaacgccg aattgcgaag ggcgaacgcg attttaaaga ccgcgtcggc tttcttcgcg 300 gccgagctcg accggccagc acgc 324

<210> SEQ ID NO 89
<211> LENGTH: 984
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberulosis

<400> SEQUENCE: 89

aaagaccgcg tcggctttct tcgcggccga gctcgaccgg ccagcacgct aattacccgg 60

ttcatcgccg atcatcaggg ccaccgcgag ggccccgatg gtttgcggtg gggtgtcgag 120

tcgatctgca cacagctgac cgagctgggt gtgccgatcg ccccatcgac ctactacgac 180

cacatcaacc gggagcccag ccgccgcgag ctgcgcgatg gcgaactcaa ggagcacatc 240

agccgcgtcc acgccgccaa ctacggtgtt tacggtgccc gcaaagtgtg gctaaccctg 300

aaccgtgagg gcatcgaggt ggccagatgc accgtcgaac ggctgatgac caaactcggc 360

ctgtccggga ccacccgcgg caaagcccgc aggaccacga tcgctgatcc ggccacagcc 420

cgtcccgccg atctcgtcca gcgccgcttc ggaccaccag cacctaaccg gctgtgggta 480

gcagacctca cctatgtgtc gacctgggca gggttcgcct acgtggcctt tgtcaccgac 540

gcctacgctc gcaggatcct gggctggcgg gtcgcttcca cgatggccac ctccatggtc 600

ctcgacgcga tcgagcaagc catctggacc cgccaacaag aaggcgtact cgacctgaaa 660

gacgttatcc accatacgga taggggatct cagtacacat cgatccggtt cagcgagcgg 720

ctcgccgagg caggcatcca accgtcggtc ggagcggtcg gaagctccta tgacaatgca 780

ctagccgaga cgatcaacgg cctatacaag accgagctga tcaaacccgg caagccctgg 840

cggtccatcg aggatgtcga gttggccacc gcgcgctggg tcgactggtt caaccatcgc 900

cgcctctacc agtactgcgg cgacgtcccg ccggtcgaac tcgaggctgc ctactacgct 960

caacgccaga gaccagccgc cggc 984

<210> SEQ ID NO 90
<211> LENGTH: 1437
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberulosis

<400> SEQUENCE: 90

atgactaatg aacaacattt cgctgacgat ggcgacatca aacagctcag cctcgacgaa 60

acccgttccg cggcaaaaca gctcctcgac tccgtcgagg gcgacctgac cggtgatgtg 120

gcgcaacgtt ttcaggcgct gacacgccac gccgaggaac tgcgggcgga gcagcgccgc 180

cgcggccgcg aagccgagga ggcgctgcgc cgctgccggg ccggtgagct gagggtggtg 240

cccggtgctc ccaccggcgg cgacgacggc gacgcgccgc cgggcaactc gttgcgcgac 300

atcgcgtttc gcacactgga cgtttgtgtg cgcgatggcc tgatgtcgtc gcgggcggcg 360

gaagccgcgg aaaccttgtg ccgcaccggg ccgccgcagt cgacgtcgtg ggcgcagcgc 420

tggctggcgg ccaccggcaa ccgcgactac ctgggggcgt tcgtcaagag ggtttcgaac 480

cctgttgcgg ggcacacgac ctggaccgac cgggaagcgg ccgcgtggcg tgaggcggcc 540

gcggtggccg ccgagcagcg agcaatgggc ttggtggaca ccgccggcgg gtttttgatc 600

ccggcggcgc tggatccggc gattctgctg tcgggtgatg gttcaacgaa tccgatccgg 660

caggtggcga gggtggtgca aacgacctcc gaggtttggc ggggcgtgac ctccgaaggc 720

gccgaggctc attggtactc cgaagcccag gaggtgtccg acgattcgcc aacgctggcc 780

-continued

cagccggcgg tgccgagcta ccgtggctcc tgctggattc cgttcagtct cgagattgag 840

ggtgacgccg ccggattcgt cgcagaggtg ggccgcgtcc tagcggattc ggttgagcag 900

ctgcaggcgg cggcgttcgt cagcggctcc ggcaacggcg agcccaccgg attcgtctcc 960

gcactgaccg gcaccgcgga ctacaccgtc accggcgcgg ggacggaagc cgttgtagcc 1020

gccgacgttt acgcgctgca gtcggcgttg ccgccgcgct ttcaatccaa cagcgcgttc 1080

gcggcgaact tgtccaccat caacgtgctg cgccaggcgg aaaccgcgaa tggggcgctg 1140

aaattcccat cgctgcacgc cagcccgccg atgctggccg ggaaacacat ctgggaggtg 1200

tcgaacatgg acaccgtgga cgcggcggtg accgccacca attacccgct ggtgcttggc 1260

gactggaagc agttcatcat caccgaccgg gtcgggtcga cggtggagct ggtgccgcac 1320

gtgttcggcg gcaaccgccg accgaccgga cagcgcggat tcttctgctg gttccgagtc 1380

ggttctgatg tgctggtgga caatgcgttc cgcgtgctga aggtgcagac caccgcg 1437

<210> SEQ ID NO 91
<211> LENGTH: 531
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberulosis

<400> SEQUENCE: 91

ttgagtagca tccttttccg cacggccgag ctgcggcctg gtgagggccg caccgtgtac 60

ggcgtcatcg tgccttatgg cgaggtgacc accgtccgcg acctcgacgg cgagttccgg 120

gaaatgttcg ctcctggcgc ttttcggcgc tccatcgctg agcgcggcca caaggtgaag 180

ctgctggtct cccacgacgc tcgaacccgc tacccggttg gccgggccgt cgagctgcgt 240

gaggagcctc acggcttgtt cggggcgttc gagcttgcga acaccccgga cggcgacgag 300

gccctggcga atgtgaaagc tggtgtggtg gacgcgtttt cggtgggttt ccggccgatc 360

cgggaccgcc gggaagggga tgtgatcgtg cgggtcgagg cggcgctgtt ggaggtctcc 420

ttgaccggcg ttccggccta tctgggcgcg cagatcgccg gtgtgcgcgc ggaatcgctt 480

gcagtcgttt cccgttcgct agccgaagcc aggttagccc tgatggattg g 531

<210> SEQ ID NO 92
<211> LENGTH: 624
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 92

ttgccatcgc cagcaaccgc ccgaccggac accgccacgg tgggagagcg tgtgcgcgct 60

caagttttat ggggcgtttt ttggcatcat ggcattcgcg acccgaaacc cggaaagagg 120

agggtggtgt tgaaaatggg taggcgtggt cccgcgccgg cgccggcgca gttgaaactc 180

ctcggcggcc gctcgccggg ccgtgattct ggcggccggc gggttacacc accggcggcg 240

ttcgagcgtg ttgcgccgga atgcccggat tggttgccgc caggcgctaa agacatgtgg 300

gggcgcgtcg ttcccgagct tgcggcatta aacctgctga aggagtccga ccttggggtg 360

ctgacctcct tctgcgtcgc ctgggatcag ctcatgcagg ctgtaacagc ctaccgtgaa 420

cagggtttca tcgcgacgaa cgcccgcagc cgacgggtga cggtgcatcc tgccgtggcc 480

gcggcccggg ccgcgacgag ggacgttttg gtgctcgcgc gcgaattggg gtgcacgcca 540

agcgctgagg cgaatttggc tgctgtgctg gcggcggcgg gggaccccga cgacgacgag 600

ttcaacccgt tcgccccaga ccgg 624

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<210> SEQ ID NO 93
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 93

ttgacccaca agcgcactaa acgccagcca gccatcgccg cagggctcaa cgccccgcgt     60

cggaatcgcg ttgggcggca acatggttgg ccggccgacg ttccgtccgc cgagcagcgc    120

cgcgcccaac ggcagcgcga cctcgaggct atccgccgag cgtacgccga gatggtggcg    180

acatcacacg aaatcgacga cgacacagcc gaactggcgc tgttgtcgat gcatctcgac    240

gatgagcagc gccggcttga ggcggggatg aagctcggct ggcatccgta tcacttcccc    300

gacgaacccg acagcaaaca g                                              321


<210> SEQ ID NO 94
<211> LENGTH: 243
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 94

atgagcggcc acgcgttggc tgctcggacg ttgctggccg ccgcggacga gcttgtcggc     60

ggcccgccag tcgaggcttc ggccgccgcg ctggccggcg acgccgcggg cgcatggcgg    120

accgcggccg tcgagcttgc gcgagcgttg gtccgcgctg tggcggagtc gcacggcgtc    180

gcggccgttt tgttcgccgc gacggccgcc gcggcggcgg ccgtcgaccg gggtgatccg    240

ccg                                                                  243


<210> SEQ ID NO 95
<211> LENGTH: 1425
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 95

atggctgaca tcccctacgg ccgtgactat cccgacccga tctggtgtga cgaggacggc     60

cagccgatgc cgccggtcgg cgccgaattg ctcgacgaca ttagggcatt cttgcggcgg    120

ttcgtagtct atccaagcga ccatgaactg atcgcgcaca ccctctggat tgcgcattgc    180

tggtttatgg aggcgtggga ctcaacgccc cgaatcgctt ttttgtcacc ggaacccggc    240

tctggcaaga gccgcgcact cgaagtcacg gaaccgctag tgccccggcc ggtgcatgcc    300

atcaactgca caccggccta cctgttccgt cgggtggccg atccggtcgg gcggccgacc    360

gtcctgtacg acgagtgtga caccctgttt ggcccgaaag ctaaagaaca cgaggaaatt    420

cgcggcgtga tcaacgccgg ccaccgcaag ggagccgtcg cgggccgctg cgtcatccgc    480

ggcaagatcg ttgagaccga ggaactgcca gcgtactgtg cggtcgcctt ggccggcctc    540

gacgacctgc ccgacaccat catgtctcgg tcgatcgtgg tgaggatgcg caggagggca    600

ccaaccgaac ccgtggagcc gtggcgcccc cgcgtcaacg gccccgaggc cgagaagctg    660

cacgaccggt tggcgaactg ggcggccgcc attaacccgc tggaaagcgg ttggccggcg    720

atgccggacg gggtgaccga ccggcgcgcc gacgtctggg agtccctggt tgcggttgct    780

gacaccgcgg gcgggcactg gcccaaaacc gcccgtgcaa ccgcagaaac ggatgcaacc    840

gcaaatcgag gagccaagcc cagcataggc gtgctgctgc tgcgggatat ccgtcgagtc    900

ttcagcgacc gggaccggat gcgcaccagc gacatcctga ccggactgaa ccggatggag    960

gagggaccgt ggggctccat ccgccgcggc gacccgctcg acgcgcgcgg cctcgcgacc   1020
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cggctcggca gatacggcat cgggccgaag ttccagcaca gtggtggcga accaccctac   1080

aaagggtatt cgcggaccca gttcgaggat gcgtggtccc ggtatctctc tgccgacgac   1140

gaaacccccg aggaacgaga tttatcggtt tccgcggttt ccgcggtttc accgccggtt   1200

ggcgatcccg gtgatgcaac cggcgcaacc gatgcaaccg atctcccgga ggcgggcgac   1260

ttgccgtacg agccgccggc gcccaacggg caccccaacg gcgacgcgcc gctgtgctcc   1320

gggccgggat gccccaacaa gctcctcagt actgaggcca aggccgccgg caaatgccgg   1380

ccctgccgag gtcgagcggc ggctagcgct cgggacggcg cccga                   1425


<210> SEQ ID NO 96
<211> LENGTH: 390
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 96

atgaccgccg tcggcgggtc gccgccgacg cgacgatgcc cggccacaga ggaccgggca     60

cccgcgacag tcgccacacc gtctagcacc gatcctaccg cgtcccgcgc cgtgtcgtgg    120

tggtcggtgc acgagtatgt cgcaccgacc ctggccgccg ccgtggaatg gccgatggcc    180

ggcaccccgg cgtggtgcga cctcgacgac accgacccgg tcaaatgggc cgcgatctgc    240

gacgctgctc ggcattgggc actccgggtg gagacgtgcc aggccgcgtc ggccgaggca    300

tcacgtgacg tatccgccgc cgccgactgg ccggcggtct ctcgggagat ccagcgtcgg    360

cgtgacgcct acattcggcg ggtggtggtc                                     390


<210> SEQ ID NO 97
<211> LENGTH: 258
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 97

atgtgcgcgt tcccgtcgcc gagtctcggg tggacggtct ctcacgagac cgaaaggccc     60

ggcatggcag acgctccccc gttgtcacgg cggtacatca cgatcagtga ggccgccgaa    120

tatctagcgg tcaccgaccg cacggtccgc cagatgatcg ccgacggccg cctacgcgga    180

taccgctccg gcacccgcct cgtccgtctg cgccgcgatg aggtcgacgg cgccatgcac    240

ccgttcggtg gtgccgca                                                  258


<210> SEQ ID NO 98
<211> LENGTH: 360
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 98

atggccgatg cggttaagta cgtagttatg tgcaactgcg acgacgaacc gggagcgctc     60

atcatcgcct ggatcgacga cgaacgaccc gccggcgggc acatacagat gcggtcgaac    120

acccgcttca ccgaaacaca gtggggccgc catatcgagt ggaaactcga atgccgggca    180

tgccgaaagt atgcgccgat atccgagatg accgccgcgg cgatcctcga cggtttcggg    240

gcgaagcttc acgagctgag aacgtcgacc atccccgacg ctgacgatcc atcaatagca    300

gaggcgcgac acgtaattcc gttcagcgca ttatgcttgc gcttgagcca gctaggcggg    360


<210> SEQ ID NO 99
<211> LENGTH: 1125
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis
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<400> SEQUENCE: 99

gtgacgcaaa ccggcaagcg tcagagacgc aaattcggtc gcatccgaca gttcaactcc     60

ggccgctggc aagccagcta caccggcccc gacggccgcg tgtacatcgc ccccaaaacc    120

ttcaacgcca agatcgacgc cgaagcatgg ctcaccgacc gccgccgcga aatcgaccga    180

caactatggt ccccggcatc gggtcaggaa gaccgccccg gagccccatt cggtgagtac    240

gccgaaggat ggctgaagca gcgtggaatc aaggaccgca cccgcgccca ctatcgcaaa    300

ctgctggaca accacatcct ggccaccttc gctgacaccg acctacgcga catcaccccg    360

gccgccgtgc gccgctggta cgccaccacc gccgtgggca caccgaccat gcgggcacac    420

tcctacagct tgctgcgcgc aatcatgcag accgccttgg ccgacgacct gatcgactcc    480

aacccctgcc gcatctcagg cgcgtccacc gcccgccgcg tccacaagat caggcccgcc    540

accctcgacg agctggaaac catcaccaaa gccatgcccg acccctacca ggcgttcgtg    600

ctgatggcgg catggctggc catgcgctac ggcgagctga ccgaattacg ccgcaaagac    660

atcgacctgc acggcgaggt tgcgcgggtg cggcgggctg tcgttcgggt gggcgaaggc    720

ttcaaggtga cgacaccgaa aagcgatgcg ggagtgcgcg acataagtat cccgccacat    780

ctgatacccg ccatcgaaga ccaccttcac aaacacgtca accccggccg ggagtccctg    840

ctgttcccat cggtcaacga ccccaaccgt cacctagcac cctcggcgct gtaccgcatg    900

ttctacaagg cccgaaaagc cgccggccga ccagacttac gggtgcacga ccttcgacac    960

tccggcgccg tgttggctgc atccaccggc gccacactgg ccgaactgat gcagcggcta   1020

ggacacagca cagccggcgc cgcactccgc taccagcacg ccgccaaggg ccgggaccgc   1080

gaaatcgccg cactgttaag caaactggcc gagaaccagg agatg                   1125


<210> SEQ ID NO 100
<211> LENGTH: 225
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 100

gtgatagcgg gcgtcgacca ggcgcttgca gcaacaggcc aggctagcca gcgggcggca     60

ggcgcatctg gtggggtcac cgtcggtgtc ggcgtgggca cggaacagag gaacctttcg    120

gtggttgcac cgagtcagtt cacatttagt tcacgcagcc cagattttgt ggatgaaacc    180

gcaggtcaat cgtggtgcgc gatactggga ttgaaccagt ttcac                    225


<210> SEQ ID NO 101
<211> LENGTH: 186
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 101

atgatcgagc agggccgcga ctgccgggac gtggtcaccc agctcgccgc ggtatcgcgc     60

gcactcgacc gcgccggatt caagatcgtt gcggcagggt tgaaggaatg cgtgtccggg    120

gccacggcca gcggcgcggc accgctgagt gcagctgagc tagaaaagct gttcctggcg    180

ctcgct                                                               186


<210> SEQ ID NO 102
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis
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<400> SEQUENCE: 102

atgtcggacc agccacgtca tcaccaggtc ctcgacgacc tgctgcccca acaccgcgct   60

ctacgtcacc agattcccca ggtgtaccag cgatttgtag ccctgggcga cgccgcgctt   120

accgacggcg ctctcagccg caaggtcaag gagcttgtgg cgctggcgat cgcggttgtg   180

caggggtgcg atggctgcgt cgcatcacac gcccaagccg cggtacgggc cggcgctaca   240

gcgcaagaag ccgctgaggc catcggggtc accatcttga tgcacggtgg accggccacc   300

atccacggtg ctcgtgccta cgcggcattt tgcgaattcg ctgacacaac gccgtcc   357

<210> SEQ ID NO 103
<211> LENGTH: 1854
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 103

atgtcctatc tcgtcgtggt gccggagttg gtcgcagcgg cggcaacaga tttggcgaac   60

atcggttcgt cgattagtgc agccaacgcg gccgcggcgg caccgaccac ggcactggtc   120

gcagccggcg gcgacgaggt atcggcggcc atagccgcgt tgttcggagc gcatgctcgg   180

gcatatcaag cgttgagtgc ccaggcggcg atgtttcatg aacagtttgt ccgggccctc   240

gccgccggcg gtaactccta cgccgtcgct gaggcggcaa ccgcgcaatc ggttcagcaa   300

gatctgctca acctgatcaa tgcgcccacc caggcgctgt tggggcgtcc gctgatcggc   360

aacggcgcca acgggctgcc gggtacgggc cagaacggcg gcgacggcgg gattctgtac   420

ggcaacggcg gcaacggtgg gtccggcggg gtcaaccagg ccggtggcaa tggcgggaat   480

gctgggctgt ggggcaatgg cggatccggc ggagccggcg ggaacgccac cactgccggc   540

cgcaacggct tcaacggggg cgccgggggga agcggcggtt tgctgtgggg caatggcggt   600

gccggcgggg ccggtgggaa cggcggtccg gctccgctcg tgggcggggt gggcaccacc   660

ggtggcgccg gcgggaacgg cggcggcgcc gggttgttct acggtttcgg cggcgccggt   720

gggaacggcg ggatgggcgg ggtggcaccg agcaccggcc cctcgatggg catcctcccg   780

gccggcggtg tcggcgggcc tggtggctcc ggcggggcga gcgcgcttgc cttcggctcc   840

ggcggcgtcg gcggtgccgg tggcttgggc gggccgaccg atggcaccgt ccagggggtg   900

ggcggcttcg gcggtcaggg cggcaacggc gggcagagcg gcttgttgtt tggcaacgcg   960

ggagccggcg gggcaggcgc tgccggcgga gccggcaccg gcgacaccga gagcttcggc   1020

ggccacggcg gggccggcgg tgatggcggc gctgttggct tgatcggtaa cggcggggcc   1080

ggcggcaccg gatctcccgg cgctgtggtg ggtggtaacg gcggcgtcgg tggtctgggt   1140

ggcgccggca gtcccggggg tctgttgtac ggcaccgggg gggccggcgg caatggcgga   1200

ccgggtggtg acggtggtac tggcgcgacg gtgggctttg ccggctccgg cggtttcggc   1260

ggtgcggggg gcatcgccca gctgtttggc acgggtggca tgggtggtag cggcggtggt   1320

ataggcgctg gcaccacgac cgtggtgccg cccgacgtcg ccccggtggg tggcacaggc   1380

ggcaatggcg gtcgcgccgg gctgctgttg ggtgtgggtg gcatgggcgg taatggcggt   1440

gccaccagcg tcggcgggac gctctacgcc gccggtggaa acggcggcga cggcgggttg   1500

gtgtggggca acggtggcac cggcgggagc ggtggcgccg gcggggcggg cagcgtcggc   1560

aacggcggtg cgggtggcaa cgcggcactg ctgttcggca acggcggggc gggcggggcc   1620

ggcggcgccg gcggcatcgg tgccggcgga gccggcggct tcggcgcggt tctgtttggc   1680

aacggcgggg ctggcgggag cggtgccccc ggtggcatcg gcgccggtgg caatggcgga   1740

-continued

aacgcgctgc tggtcggcaa cggcggcaac ggtggggcag gtaccggtgg ggctgctggc 1800

ggtgccggtg gctcgggcgg gttgctattc ggccaaaatg ggatgcccgg gccg 1854

<210> SEQ ID NO 104
<211> LENGTH: 1242
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 104

gtgcatgagg tggctgctcg tgagcaacgt tcggacgggc cgatgaggct ggatgcgcag 60

ggccgactgc agcgttacga ggaggcgttc gctgactacg atgcaccgtt tgcgttcgta 120

gatctcgacg cgatgtgggg caatgccgat caactgcttg cgcgcgccgg cgacaagccg 180

atccgggtgg cgtcgaagtc gctgcgttgc cgaccactgc aacgcgaaat ccttgatgcc 240

agtgagcgat tcgacgggct attgacgttc acgcttaccg agacgctgtg gcttgccggc 300

caaggtttct cgaacctgtt gttggcctac ccgccgaccg accgggcggc attgcgtgcg 360

cttggcgagc tgacggccaa ggacccggac ggggcgccga tcgtgatggt ggacagcgtg 420

gagcaccttg acctgatcga gcgcacgacc gacaagccgg tacggctgtg tctggatttc 480

gatgccggct attggcgcgc cggcgggcgg ataaaaattg gttccaagcg ctcgccgctg 540

cacaccccgg agcaggctcg cgcactcgcg gtggagatcg cgcggcggcc ggcgctaacg 600

ttggcggcgt tgatgtgcta cgaggcccac attgcgggcc tcggtgacaa cgtcgccggc 660

aagcgggtcc acaacgcgat catccgtcgg atgcagcgca tgtcgttcga agagctgcgc 720

gagcgtcgtg cccgggccgt cgagctggtg cgcgaggtcg ccgacatcaa gatcgtcaac 780

gccggtggca ccggcgactt gcagctggtt gcgcaggagc cgttgattac cgaagcgacc 840

gccggctcgg gtttttacgc gccgacactg ttcgactcgt attcgacgtt cacgctgcag 900

cccgcggcga tgttcgcgct gccggtatgc cgtcgtcccg gtgcaaagac cgtgaccgcg 960

ctcgggggtg gctatttagc cagcggggtc ggggcgaagg accgcatgcc gactccctac 1020

ctgccggtcg ggctgaagct caatgcgctg gagggaacgg gcgaagttca gacaccgcta 1080

tccggtgatg cagcccgacg gctgaagctt ggcgacaagg tctacttccg ccacaccaag 1140

gccggtgagc tgtgtgagcg gttcgaccat ctgcatctgg tccgtggcgc tgaagtagtc 1200

gacaccgtcc ccacctaccg ggtgaaggg cgcaccttcc tc 1242

<210> SEQ ID NO 105
<211> LENGTH: 1284
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 105

atggacgagg cccacccggc tcacccggca gatgcggggc ggcccggtgg cccaattcaa 60

ggcgcgcgaa gaggagctgc catgacaccg atcaccgccc tgccgaccga gttggcggcc 120

atgcgcgagg tagtcgagac gctcgcaccc attgagcgtg ccgcgggcga gccgggtgag 180

cacaaggcgg ccgagtggat cgtcgagcgc ctgcgcacgg cgggcgcgca ggacgcgcgc 240

atcgaggagg agcagtacct cgacggctac ccgaggctgc acctcaagct gtcggtgatc 300

ggggtggcgg ccggcgtcgc gggcctgctc agcagacgtt tgcgcatccc cgccgcgctg 360

gccggggtgg gtgcggggct ggcaatcgcc gacgattgcg ccaacgggcc gcgcattgtg 420

cgcaaacgaa cggagacgcc ccggacgaca tggaacgcgg tagccgaggc cggtgatcct 480

-continued

gctggtcagc taacagttgt tgtgtgcgct caccacgacg ccgcgcacag cggcaagttt 540

ttcgaggctc atattgagga ggtaatggtc gagctgtttc ccgggattgt ggagcgcatc 600

gacacgcagc tgccgaactg gtgggggccg atcctcgcgc ccgcactcgc cggtgtcggc 660

gccctgcgcg gcagccggcc gatgatgatc gccggaacgg tgggtagcgc cctggccgcc 720

gctttgttcg ccgacatcgc gcgcagtccg gtcgtccccg gtgccaacga caatctctcc 780

gcggttgcgc tgctggtcgc gctggccgag cggctgcgcg agcggccggt gaagggcgtg 840

cgagtgttgc tcgtgtccct gggggccgag gaaacgttgc agggcgggat ctacgggttc 900

ctggcgcgac acaaacccga gctggaccgc gaccgcacat acttcctgaa cttcgacacc 960

atcggctcac ccgagctcat catgctcgag ggcgagggcc cgacggtcat ggaggactac 1020

ttctatcggc cattccggga tctggtcatc cgggcggccg agcgcgccga cgcgccgctg 1080

cggcgcggca tccggtcgcg caacagtacc gacgcggtgt tgatgagccg cgccggctac 1140

ccgaccgcgt gctttgtgtc gatcaaccgg cacaagtcgg tggccaatta ccacctgatg 1200

tccgatacac ctgagaatct ctgctatgag acggtgtccc acgccgtcac cgtcgccgaa 1260

tccgtgatca gggagctggc ccga 1284

<210> SEQ ID NO 106
<211> LENGTH: 1284
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 106

atgagcccga tatggagtaa ttggcctggt gagcaagtct gcgcgccgtc ggcgatcgta 60

cggccgacct cggaggctga gctggccgac gtgatcgcgc aggcggcgaa aagaggcgag 120

cgggtacgcg cggttggcag cgggcattcg tttaccgaca tcgcctgcac ggacggggtc 180

atgatcgaca tgaccggcct gcagcgggtc ctcgacgtgg accagccgac tggcctggtg 240

acggtcgagg ggggcgcaaa gctacgtgcg ctgggacccc aattggcgca acgacggctc 300

ggcctggaga accagggtga cgtggatccc caatccatca ccggcgcgac cgcgaccgcg 360

acgcacggaa ccggggtgcg tttccagaat ctgtcggcgc ggatcgtttc gctgcggctg 420

gtcaccgcgg gcggggaagt gctcagtctg tccgaaggtg acgattacct ggcggcacgg 480

gtttccctcg gcgcgctagg agtgatctca caggtcaccc tgcagacggt tccgctattc 540

acgttgcatc gccatgatca gcgacgctcg ctggcgcaga cgctggagcg cctcgacgag 600

ttcgtggacg gtaatgacca tttcgagttt ttcgtattcc cttacgcaga taaggcgttg 660

acgcgcacca tgcatcgcag tgacgagcag cccaaaccca cgcccgggtg gcagcgcatg 720

gtcggcgaga acttcgagaa cgggggattg agcctgatct gccagaccgg ccgtcgtttt 780

cctagtgtgg cgccgcgact gaaccgcctg atgacgaaca tgatgtcgtc ctccaccgtg 840

caagaccgcg cctacaaggt ctttgcgacc caacgcaagg tcaggttcac cgagatggag 900

tacgcgatcc cgcgtgaaaa cgggcgcgag gcgctccagc gtgtcatcga ccttgtgcgc 960

cgtcgcagct tgccgatcat gtttccgatt gaggtgcgat tctccgcccc cgacgattcc 1020

ttcctgtcga ccgcatatgg gcgcgacact tgctacatcg cggttcatca atacgccggt 1080

atggagttcg aaagctactt ccgcgccgtc gaggagatca tggacgacta cgccggtcgg 1140

ccacactggg gtaaacgtca ctatcagacc gccgccacgc ttcgtgagcg ctatccgcag 1200

tgggatcggt tcgccgcggt tcgcgatcgc ctcgatccgg accgggtgtt tctcaacgac 1260

tacacccggc gcgttctcgg tccc 1284

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<210> SEQ ID NO 107
<211> LENGTH: 309
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 107

ttgggttcaa caggaggtag ccaacccatg acggcgaatc gagggcccgc tgcaatctcg      60

agcggctcga actctggccg cgttctcgac accgcccggg gtatcctcat cgctcttcgg     120

cggtgccccg cagagaccgc gttcgacgag ttgcacaacg ccgctcaacg gcacagattg     180

ccggtcttcg aaatagcttg ggcactagtg catttggcgg tcgagggaag cacgccatgc     240

cggagcttcg tcgatgccca gtcggcggct cggcgggagt ggggtcagct ttttgcgcat     300

gcggcggcg                                                             309


<210> SEQ ID NO 108
<211> LENGTH: 744
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 108

gtgccgccta cggaaggaaa gtcgacaacg aatcgcgacg aaggcatcca ggtgctccgt      60

cgcgccgtcg ccgcgctgga cgaaatagct gccgaaccgg gacacctgcg cctagtcgat     120

ctctgcgagc ggctggggct ggccaaatcg acgactcgac gcttgctggt cggcctggtc     180

gaggtggggc tggttagtgt cgattcgcac ggccgcttcg cactgggcga gcgtttgctg     240

ggattcggaa gtgtcaccgg agcccacata gccgcggcgt tccggccgac cgtcgagcga     300

gttgcccgcg cgaccgacgg cgaaacggtc gacctgtcgg tactgcgcgg ccagcgaatg     360

tggtttgtcg accagatcga atcgtcttac cggctgcgtg cggtctcagc cgtcgggctc     420

cgcttcccgt tgaacggaac cgcgaatgga aaagcggcgc tggctgctct cgacgacgcc     480

gacgccgagg ccgcgctctg ccgtctggat cccatggtgg ccgaaggtct acggcgcgag     540

atcgtcgaga tccggcgcac cggtatcgct ttcgaccgca acgagcacac cccagggata     600

tccgcggctg cgatcgcacg acgcgccctg ggcgacaacg tgatcgcgat ctcggtgccg     660

gcgcccaccg cacgatttct ggaaaaagag cagcgcataa tcgccgcgtt gcgcgccgcc     720

gcggactcgc cggactggac tcgc                                            744


<210> SEQ ID NO 109
<211> LENGTH: 1218
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 109

atggcatccg tcgcccaacc cgttaggcgc cgcccaaagg accggaagaa gcagattttg      60

gatcaggccg ttggactgtt catcgaacgt ggcttccatt cggtcaaatt ggaggacatt     120

gccgaggcgg ccggggtgac cgcgcgcgcg ttgtatcgcc actacgacaa caagcaggcg     180

ttgctcgccg aagcgatccg aaccggccag gatcagtacc agagcgcgcg tcgtctcacc     240

gagggcgaga cggagccgac gccgcggccg ttgaacgccg atctggaaga cctgatcgcc     300

gcggcggtcg cctctcgggc gttgacggtg ctgtggcagc gcgaggcccg ctacctcaac     360

gaggacgacc gcacggcggt ccggcgccgc atcaacgcga tcgtcgccgg catgcgtgac     420

agcgtgctgc tggaggtgcc cgatctgagt ccacagcatt cggagttgcg ggcgtgggcg     480
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gtgtccagca ctttgaccag cctgggccgg cacagcctaa gcctgccggg cgaggaactg 540

aaaaagcttc tctaccaggc gtgtatggcc gcggcaagga cgcctcccgt ctgcgaattg 600

ccgccactgc cggccggtga tgccgcacgc gacgaggccg acgtgctgtt ctcccgctac 660

gagaccctgc tggccgcggg cgcgcggctg ttccgtgcgc agggctatcc ggccgtcaac 720

accagcgaaa tcggcaaggg agccggcatc gcgggcccgg ggctgtaccg ttcgttttct 780

tccaaacagg ccatcctgga cgcgctcatc cgccgcctcg acgagtggcg ctgcctggag 840

tgcatccgag cgctacgagc gaatcagcaa gcggcacaac ggttgcgcgg ccttgtccaa 900

gggcacgttc ggatcagctt ggacgctccg gatctggtgg cagtgtcggt caccgaactg 960

tcgcacgcct ctgtcgaagt acgcgacggc tacctgcgaa atcagggcga ccgcgaggcc 1020

gtgtggatcg acctcatcgg caagctggta cccgcgacca gtgtcgccca ggggcgactg 1080

ctggtcgcgg cggcgattag cttcatcgaa gacgtcgctc gcacctggca tctcacgcgc 1140

tacgccggag tcgccgacga gatcagtggc ctggcgctgg cgatcctgac cagcggggca 1200

ggtaacctct tgcgcgca 1218

<210> SEQ ID NO 110
<211> LENGTH: 795
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 110

atggtaatcg tggccgacaa ggcggccggt cgggtcgctg atccggtctt gcggccggtg 60

ggcgcgctgg gcgatttctt cgcgatgacg ctcgacacgt ccgtgtgcat gttcaagccg 120

cctttcgcgt ggcgtgaata cctacttcag tgctggttcg tggcgcgggt gtcgacgctg 180

cctggggtgt tgatgacgat cccatgggcg gtgatctcgg ggtttctctt caacgtcttg 240

ctgaccgaca tcggtgccgc ggacttttcc ggcaccggct gtgcgatctt caccgtgaac 300

caaagcgccc cgatcgtcac ggtcttggtg gtcgcgggcg cgggcgccac cgccatgtgc 360

gccgatctgg gtgcgcgcac catccgtgag gaactcgacg cactgcgggt gatgggcatc 420

aacccgatcc aagcgctagc ggctccgcgc gtgctggcgg ccaccacggt gtcgttggcg 480

ctgaattcgg tggtgaccgc gacggggctg atcggcgcgt tcttttgctc ggtgtttctc 540

atgcacgtct cggcgggggc atgggtgacc gggcttacca cgctgaccca caccgtggac 600

gtcgtcattt cgatgatcaa ggcgacgttg ttcgggctga tggccggact gatcgcctgc 660

tataagggca tgtcggtcgg tggcggcccg gccggagtcg gccgggcggt gaacgaaacc 720

gtggtgtttg ccttcatcgt cttgttcgtg atcaacatcg tcgtcaccgc ggtcggcatc 780

ccattcatgg tgtcc 795

<210> SEQ ID NO 111
<211> LENGTH: 813
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 111

atgacggcag cgaaagccct tgtaagcgaa tggaatcgga tgggatcgca gatgcggttc 60

ttcgtcggca cgctggccgg gattcccgac gccctcatgc actaccgcgg cgagctgctg 120

cgggtgatcg cgcaaatggg gttggggacc ggggttcttg cggtgatcgg tggaacggtc 180

gcgatcgtcg ggttcttggc gatgaccacc ggcgcgatcg tggccgtgca gggctacaac 240

cagttcgctt cggtgggtgt ggaggcgctg accggcttcg cgtcggcctt cttcaacacc 300

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cgcgagattc agcccggaac cgtgatggtc gcgctagcgg ccaccgtcgg tgccggtacc 360

accgctgcgc tgggggcgat gcggataaac gaggagatcg acgcgctcga ggtgatcggc 420

atccgcagca tcagctacct ggcgagcacc cgggtgctgg ccggagtggt cgtggccgtc 480

cctctgttct gtgtgggact gatgacggcc tacctggccg cgcgcgtcgg caccaccgcc 540

atctatggcc aggggtcggg cgtgtacgac cactacttca acacgttcct gcgcccgacc 600

gacgtgctct ggtcgtcggt tgaagtcgtc gtggtcgctc tgatgatcat gctggtgtgc 660

acctattacg gctacgccgc acatggcggg ccggccgggg ttggcgaggc ggtcggccgg 720

gccgtgcgtg cctcgatggt cgtcgcgtcg atcgcaatcc ttgtcatgac gctggccatc 780

tacggccagt cgcccaactt tcacctggcg acc 813

<210> SEQ ID NO 112
<211> LENGTH: 1275
<212> TYPE: DNA
<213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 112

atgagacgcg ggccgggtcg acaccgtttg cacgacgcgt ggtggacgct gatcctgttc 60

gcggtgatcg gggtggctgt cctggtgacg gcggtgtcct tcacgggcag cttgcggtcg 120

actgtgccgg tgacgctggc ggccgaccgc tccgggctgg tgatggactc cggcgccaag 180

gtcatgatgc gcggtgtgca ggtcggccgg gtcgcccaga tcggtcggat cgagtgggcc 240

cagaacgggg cgagcctcag actggagatc gaccccgacc agatccggta catcccggcc 300

aatgtcgagg cacagatcag cgccaccacc gcattcggtg ccaagttcgt cgacctggtg 360

atgccgcaaa acccaagtcg tgcacggctg tccgctgggg cggtactgca ttcgaagaac 420

gtcagcacgg aaatcaacac cgtcttcgaa aacgtcgtcg acctgctcaa catgatcgac 480

ccgctgaaac tgaacgccgt gctgaccgcg gtcgccgacg ccgttcgcgg gcaaggtgaa 540

cggataggcc aggccaccac cgacctcaac gaggtgctgg aggcactcaa cgcacgcggc 600

gacaccatcg gcggcaactg gcgatcgctc aagaacttca ccgacaccta tgacgcggcc 660

gcccaagaca tcctgacgat cctgaacgcc gccagcacca ccagtgcgac cgtcgtgaat 720

cattcgacgc agctggatgc cttgctactc aacgccatcg gactatccaa cgctggcacc 780

aacctgcttg gcagcagccg agacaatctc gtcggcgcgg ccgacatcct ggcgccgacc 840

acgagcctgc tgttcaagta caaccccgaa tacacctgct tcctgcaggg cgccaagtgg 900

tatctcgaca acggcggcta tgcggcctgg ggcggggccg acgggcgcac gctacaactc 960

gatgtggcgc tactgttcgg caacgacccc tatgtctatc cggacaacct gccggttgtc 1020

gcggccaagg ggggtcccgg cggaaggccg ggatgcgggc cattgccgga tgccacccac 1080

aacttcccgg tgcgccagct ggtcaccaac accggatggg gaaccgggct ggacatccgg 1140

cccaaccccg gcatcgggca tccctgctgg gccaactact tcccggtgac ccgcgcggtg 1200

cccgagccgc cgtcgatccg tcagtgcatc cccgggccgg cgatcgggcc caaccccgcg 1260

gcgggggagc agcca 1275

<210> SEQ ID NO 113
<211> LENGTH: 1026
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 113

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atgagggaga acctgggggg cgtcgtggtg cgcctcggcg tcttcctggc ggtatgcctg 60

ctgacggcgt tcctgctgat tgccgtcttc ggggaggtgc gcttcggcga cggcaagacc 120

tactacgccg agttcgccaa cgtgtccaat ctgcgaacgg gcaagctggt gcgcatcgcc 180

ggcgtcgagg tcggcaaggt caccaggatc tccatcaacc ccgacgcgac ggtgcgggtg 240

cagttcaccg ccgacaactc ggtcaccctc acgcggggca cccgggcggt gatccgctac 300

gacaacctgt tcggtgaccg ctatttggcg ctggaggaag ggccggcgg actcgccgtt 360

cttcgtcccg gtcacacgat tccgttggcg cgcacccaac cggcgttgga tctggatgcc 420

ctgatcggtg gattcaagcc gctgtttcgt gcgctgaacc ccgagcaggt caacgcgctg 480

agcgaacagt tgctgcacgc gtttgccgga caggggccca cgatcgggtc attgctggcc 540

cagtccgcgg ccgtgaccaa caccctggcc gaccgtgatc ggctgatcgg gcaggtgatc 600

accaacctca acgtggtgct gggctcgctg ggcgctcaca ccgatcggtt ggaccaggcg 660

gtgacgtcgc tatcagcgtt gattcaccgg ctcgcgcaac gcaagaccga catctccaac 720

gccgtggcct acaccaacgc cgccgccggc tcggtcgccg atctgctgtc gcaggctcgc 780

gcgccgttgg cgaaggtggt tcgcgagacc gatcgggtgg ccggcatcgc ggccgccgac 840

cacgactacc tcgacaatct gctcaacacg ctgccggaca aataccaggc gctggtccgc 900

cagggtatgt acggcgactt cttcgccttc tacctgtgcg acgtcgtgct caaggtcaac 960

ggcaagggcg gccagccggt gtacatcaag ctggccggtc aggacagcgg gcggtgcgcg 1020

ccgaaa 1026

<210> SEQ ID NO 114
<211> LENGTH: 1230
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 114

atgaaatcct tcgccgaacg caaccgtctg gccatcggca cagtcggcat cgtcgtcgtc 60

gccgccgttg cgctggccgc gctgcaatac cagcggctgc cgtttttcaa ccagggcacc 120

agggtctccg cctatttcgc cgacgccggc gggctgcgca ccggcaacac cgtcgaggtc 180

tccggctatc cggtgggaaa agtgtccagc atctcgctcg acggaccggg cgtgctggtg 240

gagttcaagg tcgacaccga cgtccgactc ggaaaccgca ccgaagtggc aatcaaaacc 300

aagggcttgt tgggcagcaa gttcctcgac gtcacccccc gcggggacgg ccgactcgat 360

tctccgatcc cgatcgagcg gaccacgtcg ccctaccaac tgcccgacgc ccttggcgat 420

ttggccgcca cgatcagcgg gttgcacacc gagcggctgt ccgaatcgct ggccaccctg 480

gcgcagacct ttgccgatac gccggcgcac ttccgcaacg ccatacacgg ggtggcccgg 540

ctcgcccaaa ccctcgatga gcgcgacaac caactgcgca gcctgctggc caacgcggcc 600

aaagccaccg gggtgctggc caaccgcacc gaccagatcg tcggcctggt gcgcgacacg 660

aatgtggtct tggcgcagct gcgcacccaa agcgccgccc tggaccggat ctgggcgaac 720

atctcggcgg tggccgaaca actgcggggc ttcatcgctg agaaccgcca gcagctgcgc 780

ccggcgctgg acaagctcaa cggggtgctg gctatcgtcg aaaaccgcaa agagcgtgtg 840

cggcaggcca tcccgctgat caacacctat gtcatgtcgc tgggtgagtc gctgtcgtcg 900

ggcccgttct tcaaggcata cgtggtgaac ctgctgccgg gtcagttcgt gcaaccgttc 960

atcagcgccg cgttctccga cctggggctc gacccggcca cgttgctgcc gtcgcagctg 1020

accgacccac cgaccggtca acccggaacc ccgccgttgc cgatgcccta cccgcgcacg 1080

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ggccagggcg gtgagccgcg gctgacgctg cccgacgcga tcaccggcaa tcccggcgat 1140

ccgcgctatc cgtaccggcc ggagccgccc gcgccgccgc ccggcgggcc gccgcccggc 1200

ccgcccgcgc agcagccggg agaccaaccg 1230

<210> SEQ ID NO 115
<211> LENGTH: 1269
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 115

gtgacaacga aactcagacg tgcccgctcg gtgttggcga ccgccctggt gctggtcgcg 60

ggcgtgatcc tggccatgcg caccgccgac gccgccgccc gcacgaccgt ggtcgcctac 120

ttcgacaaca gcaacggtgt gttcgccggt gacgacgtgc tcattcgggg cgtgccggtg 180

ggcaagatcg tcaagatcga accgcaaccg ctgcgcgcca agatttcgtt ctggttcgac 240

cgcaaatacc gagtccccgc cgatgccgcc gcggcgatcc tgtcgccgca actggtgacc 300

ggccgggcca tccagctgac accgccgtat gccggcgggc cgaccatggc cgacggcaca 360

gtaatcccgc aagagcgcac cgtggtgccg gtggagtggg acgacttgcg ggcgcaactt 420

cagcggctga ccgcattgct gcagcccacc cggccgggcg gcgtcagcac gctgggtgcg 480

ctcatcaata ctgccgccga caacctgcgc gggcaaggcg ccaccatccg cgacaccatc 540

atcaaactgt cacaagcgat ttcggctctc ggtgaccaca gcaaagacat cttctccacc 600

gtgacgaacc tgtcgacgct ggtcacggcg ctgcatgaca gcgctgacct gctcgaacgg 660

ctcaaccaca acctggccgc ggtgacctcg ctgctggccg atggcccgga caagatcggt 720

caggcagccg aggacctcaa cgcggtcgta gccgacgtcg gcagcttcgc cgccgagcac 780

cgcgaggcga tcggcaccgc atcagacaag ctcgcgtcaa tcaccaccgc gctggtcgac 840

agcctcgacg acatcaagca gacgctgcat atcagcccga cggtgttgca gaacttcaac 900

aacatcttcg aaccggccaa cggcgcgctg accggcgcgc tggcgggcaa caacatggcc 960

aacccaatcg ccttcctgtg cggcgcgatc caggctgcct cccggctggg cggcgagcaa 1020

gcggccaaat tgtgcgtgca atacctggcg ccgatcgtga agaaccgcca gtacaactac 1080

ccgccgctgg gggcgaacct gttcgtcggg gcgcaggcca ggcctaacga ggtcacctac 1140

agcgaggact ggctgcggcc cgattacgtt gcaccagttg cggacacgcc gccagatccg 1200

gccgcggccg tgaccgtcga tcccgcgacc ggcctgcgcg gcatgatgat gccgccgggg 1260

ggtggctcg 1269

<210> SEQ ID NO 116
<211> LENGTH: 1131
<212> TYPE: DNA
<213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 116

gtgaggatcg gcctgaccct ggtgatgatc gcggccgtgg tagcgagctg cggctggcgc 60

gggctgaatt cgctgccgct gcccggcacg cagggcaacg gcccggggtc cttcgcggtc 120

caggcgcagc tgccggatgt caacaacatc cagccgaact cgcgggtgcg ggttgccgac 180

gtgacggtcg gccacgtcac gaaaatcgag cgccaaggct ggcacgcgtt ggtgaccatg 240

cggctggatg gcgacgtcga tttgcccgcc aacgcaacgg ccaagatcgg caccaccagc 300

ctgctgggtt cctaccacat cgagctggcg ccaccgaaag gcgaagcgcg gcaaggcaag 360

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ctgcgcgacg gttcactcat tgcgctgtca cacggtagcg cctacccaag caccgagcag 420

acgctggcag cgctgtcgct ggtgctcaac ggcggcggac tgggccaggt tcaagacatc 480

accgaggcgt tgagcaccgc gtttgccggc cgtgagcacg atctgcgcgg gctgattggg 540

cagctggaca ccttcaccgc atacctcaac aaccagtccg gtgacatcat cgcggccacc 600

gacagcctca accgcctcgt cggcaagttc gccgaccagc aacccgtctt cgatcgggcc 660

ctggccacca tccccgacgc gctcgcggtg ctggccgatg agcgggacac gctcgtcgag 720

gctgccgagc agctgagcaa gttcagcgcc ctgaccgtcg actcggtcaa caagaccacc 780

gcgaacctgg tcaccgaact gcggcaactc ggaccggtgt tggagtcgct ggccaattcc 840

ggtccggcgc tgacccgatc gctgtccctg ctggccacgt tcccgttccc gaacgagacg 900

ttccaaaatt tccagcgcgg cgaatacgcc aacctgaccg cgatcgtcga cctcacgctc 960

agccgcatcg accagggcct gttgaccggc acccgctggg agtgtcatct gacccagctc 1020

gagctgcagt ggggtcgcac cattgggcag ttccccagcc cgtgtaccgc gggctatcgg 1080

ggtaccccgg gcaatccgct gacgatcgcc taccgctggg atcaggggcc c 1131

<210> SEQ ID NO 117
<211> LENGTH: 1311
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 117

atgctgcatc taccgcgccg agtgatcgtt cagctggccg tctttaccgt gatcgcggtg 60

ggcgtgctgg ccatcacgtt cctgcatttc gtgaggctgc cggcgatgct tttcggcgtc 120

ggccgctaca cggtgacgat ggagctggtc gaagccggtg ggctgtatcg caccggcaat 180

gtcacctacc gcggctttga ggtgggccgg gtggcagcgg tgcggctcac cgacaccggg 240

gtgcaagcgg tgctggccct gaaatcgggc atcgatatcc cgtcggacct caaggccgag 300

gtgcacagcc acaccgcgat cggcgaaacc tacgtcgagt tgttgccgcg caacgccgcc 360

tcgccgccac tgaagaacgg cgatgtcatt gcgctggccg acacctcggt gccgcccgac 420

atcaacgacc tgctcagcgc ggccaacacc gcattggagg caatacctca cgagaacctg 480

cagaccgtca tcgacgagtc gtacaccgcg gtggccgggt tagggctcga actttcccgg 540

ctgatcaagg gctcggcgga actggcgatc gatgctcgcg cgaatctcga tccgctggtg 600

gcgctgatcg accgggcagg accggtgctg gattcgcaga cccacacctc ggatgcgatc 660

gcggcctggg cggcacagct ggccgcagtc accggccaat tgcagacaca cgactcggcg 720

gtcggcgatc tcatcgaccg ggcggtccg gcgttggggg agacgcgcca actgctcgag 780

cggctacaac ccaccgtgcc catcctgctg gccaacctgg tcagcgtcgg ccaggtcgca 840

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gaacaggccg gcatcctggc caacctcaac accaagcagg cctaccgggg ccagtatctg 960

agcttcaacc tcaacctgaa cctgccgccg ccgtgcacca ccggctttct gccggcccag 1020

cagcggcgca ttcccacgtt cgaggactac ccggatcgcc cggccggtga tctgtactgc 1080

cgggtgcccc aggattcgcc gtttaacgtg cgcggcgccc gcaacatccc ctgtgaaacc 1140

gtgccgggca agcgcgcacc caccgtgaag ttatgcgaga gcgacgcgcc atacctgccg 1200

ctgaacgacg gctacaactg gaagggcgac cccaacgcca cggtgccggg tttggggtcc 1260

ggccaggaca tcccgcagac atggcaaacg atgctgctgc cgccgggcag c 1311

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<210> SEQ ID NO 118
<211> LENGTH: 573
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 118

atgtcggtag cagtggattc cgacgccgag gatgacgccg tatcggagat cgctgaggca     60

gccggcgtgt cgccggcccc agccaaacca tccatgtcgg cgccgcggcg catgctgctg    120

ttcggcctgg tcgtcgtcgt cgctttggcg gtgctgttgt gttgctgggg atttcgcgtc    180

cagcgggcac gccatgcgca ggaccagcgt ggtcacttcc tgcaagcggc ccggcagtgc    240

gcgctgaacc taacgaccat cgactggcgc aacgccgagg cggatgtgcg ccgcattctg    300

gacggcgcca caggcgagtt ttacaacgac ttcgcccagc ggtcccagcc cttcgtcgaa    360

gtactgaggc acgcaaaggc cagcacggtc ggcacgatca ccgaggccgg gctgcagacg    420

cagaccgccg acacggccca ggcgctggtg gcggtgtccg tgcaaacgtc gaatgccggc    480

gaagccgacc cggttccacg agcgtggcga atgcgcatca ccgtgcagcg ggtcggcgac    540

cgggtcaagg tgtccgacgt cgggttcgtg ccg                                 573


<210> SEQ ID NO 119
<211> LENGTH: 480
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 119

gtgagctggt cgcgggtgat cgcctacggg ctgctgcccg ggctggcgtt ggcgctgacg     60

tgtggcgcgg gcttgctgaa atggcaggac ggcgccgtcc gcgacgccgc ggttgcccgt    120

gcggaatccg tgcgggccgc gaccgacggc accaccgcgc tgctgtctta ccggcccgac    180

accgtgcagc atgacctcga gagcgcgcga agcaggctca cgggcacgtt cctcgacgcc    240

tacacacagc tgacccacga cgtggtgatc cccggcgcac agcagaagca gatctcggcc    300

gtggccaccg tcgcggccgc ggcgtcggtg tcgacttccg ccgaccgcgc cgtcgtcctg    360

ctgttcgtaa accagaccat caccgtcggc aaggacgcgc cgaccaccgc cgcttccagc    420

gttcgggtga ccctcgacaa catcaacggg cgttggctga tctcgcaatt cgaaccgatc    480


<210> SEQ ID NO 120
<211> LENGTH: 375
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 120

gtgcagcgcc aatcattgat gccccagcag acccttgccg ccggcgtttt cgtgggtgcg     60

ctgctatgcg gtgtcgtgac ggcggcggtg ccaccacacg cacgcgccga cgtggtcgcc    120

tatctggtca acgtgacggt acgcccgggc tacaacttcg ccaacgccga cgccgcgttg    180

agttacggac atggcctctg cgagaaggtg tctcggggcc gcccttacgc acagatcatc    240

gccgacgtca aggctgattt cgacacccgc gaccaatacc aggcctcgta tctgctcagc    300

caggctgtca acgaactctg ccccgcgctg atctggcagt tgcgaaactc cgcagtcgac    360

aatcggcgct cgggc                                                     375


<210> SEQ ID NO 121
<211> LENGTH: 663
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis
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<400> SEQUENCE: 121

atgtcgcgtc gagcatcggc cacgtgtgcc ttgtccgcga ccaccgccgt cgccataatg 60

gctgctcccg ccgcacgggc cgacgacaag cggctcaacg acggcgtggt cgccaacgtc 120

tacaccgttc aacgtcaggc cggctgcacc aacgacgtca cgatcaaccc gcaactacaa 180

ttggccgccc aatggcacac cctcgatctg ctgaacaacc ggcacctcaa cgacgacacc 240

ggttctgacg gatccacacc gcaagaccgc gcgcatgccg ccggcttccg cgggaaagtc 300

gctgaaaccg tggcgatcaa tcccgccgta gcgatcagcg gcatcgagtt gataaaccag 360

tggtactaca accccgcgtt tttcgcgatc atgtccgact gcgccaacac ccagatcggg 420

gtgtggtcag aaaacagccc ggatcgcacc gtcgtggtgg ccgtttacgg acagcccgat 480

cgaccttccg cgatgccgcc caggggagcg gtaaccggac cgccgtcccc ggtggccgcg 540

caagagaacg ttcctatcga ccccagcccc gactacgacg ccagcgacga gatcgaatac 600

ggcatcaact ggctgccatg gatcctgcgc ggcgtgtacc cgccgcccgc aatgccgccg 660

cag 663

<210> SEQ ID NO 122
<211> LENGTH: 405
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 122

gtgcggtgga ttgtcgacgg tatgaacgtg atcggaagtc gtccggatgg ttggtggcgc 60

gaccgccatc gcgcgatggt gatgctggtg gaaaggctcg aggggtgggc catcaccaag 120

gctcggggcg acgacgtgac ggtggtgttc gagcggccgc cgtcgaccgc catcccgtca 180

tcggtggtcg aagtggcgca tgcgcccaag gcggccgcca actcggccga cgacgagatc 240

gtccggctgg tccgatccgg cgcccagcca caagagattc gtgtggtgac atcggacaaa 300

gcgttgaccg accgggtccg agacttgggt gcggcagtct acccggcaga acggttccgt 360

gaccttatcg acccgcgcgg gtcgaacgcg gcccgccgca cgcag 405

<210> SEQ ID NO 123
<211> LENGTH: 1044
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 123

atgtctcaga cacccgctac aacccgcaaa acgtttcccg agatcagctc aagagcgtgg 60

gagcaccccg ccgaccggac cgccctttcc gcgctgcgcc ggctcaaagg cttcgaccag 120

atcttgaagc tgatgtcggg gatgttgcgg gaacggcagc accggctgct gtacctggcc 180

agcgcggcac gggtcgggcc gcggcagttc gccgacctcg acgcgctgct ggacgaatgc 240

gtggatgtgc tggacgcgtc ggcgaaaccc gaactctacg tgatgcagtc accaatcgcg 300

gatgccttca ccatcggcat gggcaagcca ttcaccgtga tcacctcggg gctgtacgac 360

ctggtgacac acgacgagat gcggttcgtg atgggccacg agctcggcca cgcactgtcc 420

ggccacgcgg tgtaccgcac gatgatgatg catctgctgc ggttggcccg gtcattcggc 480

gtcttgccgg ttggcggctg ggcgctgcgc gcaatcgtgg ctgcgctgct ggaatggcag 540

cgcaaatcgg agctgtccgg cgatcgcgct gggttgctgt gcgcgcagga tttggacacc 600

gcgctcaggg tggagatgaa gctcgctggc ggctgccggc tggacaagct ggactcggag 660

gccttcttgg ctcaggcccg ggaatacgag acatccggcg atatgcgcga cggggtgctc 720

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aagctgctca acctggagct gcagacccat ccgttctctg tgctgcgggc tgccgccttg 780

actcactggg tggacaccgg cggctatgcc aaggtgatag ccggcgagta cccgcgtcgg 840

gccgacgacg gcaacgccaa atttgcagac gaccttggcg cggccgcccg gtactaccgg 900

gacggcttcg accagtccaa cgacccgctg atcaaaggta tccgcgacgg attcggtggc 960

atcgtcgagg gcgtgggacg ggcagcctcg aacgcggccg attcattggg ccgcaagatc 1020

accgagtggc ggcagccctc gaag 1044

<210> SEQ ID NO 124
<211> LENGTH: 564
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 124

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gccgcaatcc tgcaggccgc caccgacctg ttcgccgagc gtgggccagc cgcgacgtcg 120

attcgcgaca tcgccgctcg atccaaggtc aaccacgggc tggtgtttcg tcacttcggc 180

accaaggacc aactggttgg ggccgtgctc gatcacctgg gcacgaagct gaccagactg 240

ttgcactccg aggcgcccgc tgacatcatc gaacgggctc tcgaccgaca tgggcgggtc 300

ttagcccggg cactgctgga cggatatccc gtgggccagc tgcaacagcg atttcccaat 360

gttgcggagc tgctcgacgc ggtacggcct cgctacgaca gcgacttggg cgcgcggctg 420

gcggtcgcgc acgcccttgc gctgcaattc ggttggcggc tctttgcgcc catgctgcgc 480

tcggcgacgg gtatcgacga gctgaccggt gacgaactac ggctgtccgt gaacgatgcg 540

gtagcccgga tcctggaacc gcac 564

<210> SEQ ID NO 125
<211> LENGTH: 702
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 125

gtgacgatat tgatcctgac cgacaacgtc cacgcccatg ctctggcggt cgatctgcag 60

gccaggcatg gcgatatgga cgtctatcag tcccccatcg gccagctgcc gggtgtcccg 120

cgatgtgatg tcgcagagcg cgtcgcggaa atcgtggagc ggtatgacct cgtcctttcc 180

ttccactgta aacagaggtt tcccgccgct ttgatcgatg ggtcaggtg tgtgaatgtt 240

catccgggtt tcaaccccta caaccgcggc tggtttcccc aggtcttctc gatcatcgac 300

gggcaaaaag tcggcgtgac gatccacgag atcgacgatc agttggacca tggtccgatc 360

atcgcccagc gggaatgcgc gatcgagtcg tgggattcct cgggaagtgt ctacgcccgg 420

ctgatggaca tcgagcgtga gttggtgctg gaacatttcg acgccatccg ggacggcagc 480

tacacggcta aatcgccggc caccgagggc aacctcaacc tgaaaaagga tttcgaacaa 540

ctccggcggc tagacctgaa cgagcgcgga acgtttgggc atttcctgaa tcgcctgcgc 600

gcgttgaccc atgatgattt ccgcaacgct tggttcgtcg atgcgtcagg ccgcaaggtg 660

tttgtccgcg tcgtgctcga accggagaag cccgcggaag cc 702

<210> SEQ ID NO 126
<211> LENGTH: 1599
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 126

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atcggcagcg gggccgcgtg ctctatgact ctgctggaaa tggccgatgc cctgctgagc 120

agcccctcgg catcgcccaa gttgcgcatc gcggtggtgg agcgagacga gcagttctgg 180

tgcggaatcc cctatggcca acgctccagc atcggatcgc tggccattca gaagctcgac 240

gatttcgccg acgagccgga aaaggccgcc taccggatct ggctggagca gaacaagcag 300

cgctggctgg cgttcttcca ggcagagggc ggtgcggccg cggcccgctg gatctgcgac 360

aaccgcgacg cattggacgg caaccagtgg ggggagctct acctgccgcg gtttctcttc 420

ggtgtatttc tgtcggagca gatgattgcc gccatcgccg cgctcggcga gcgtgacctg 480

gccgaaatcg tcaccatccg cgctgaggcc atgagcgccc actccgcaga cggccactac 540

cgaatcggcc tccgcccgtc tggaaacggt ccaacggcaa ttgctgcagg caaagtggtt 600

gtggccattg gcagcccccc gaccaaagcc atccttgcga gcgattccga acccgcattc 660

acctatatca acgatttcta ctcccccggc ggggagagca acgttgcgcg actgcgcgat 720

tcgctcgacc gcgtcgagtc gtgggagaag cgcaacgtac tggtcgtggg ttccaacgcc 780

acctcgctgg aagcgctcta cctaatgcgt cacgacgcgc gcatccgcgc acgcgtccgg 840

tccatcaccg tcatctcgcg ctccggcgtg ctgccctaca tgatctgcaa tcagccgccg 900

gagtttgact tcccgcggct gcgcacgctg ctctgtacgg aagcgatcgc cgcggcggat 960

ctcatgtccg cgatccgcga cgatctcgcg acggccgaag aacgctcgtt gaacctggcc 1020

gatttgtacg acgccgttgc cgccctgttt gggcaggcgc tgcacaagat ggatctcgtg 1080

cagcaggaag agttcttctg cgtgcacggc atgaacttca ccaagttggt gcggcgtgcg 1140

ggacgcgatt gccgccaggc atccgaggag ctagccgcgg acggcacgct gagcctgctc 1200

gccggcgaag tactgcgcgt ggatgcctgc gcgtccggcc agccgttcgc caccatgacc 1260

taccgagccg cgggagccga gcatacccac cccgtcccct tcgctgcggt ggtgaattgt 1320

ggcggtttcg aggagctgga cacgtgttcc tcgccgttcc tggtcagcgc gatgcagaac 1380

gggctgtgcc gcccgaaccg caccaaccgt ggccttctgg ttaacgacga cttcgaggcc 1440

agcccaggtt tttgcgtcat cgggccccta gtcggcggca atttcactcc caagatccgt 1500

ttttggcacg tcgagagcgc accgcgcgtc cggtcgctgg cgaaatcgct ggcggccagc 1560

ctgcttgctt cgctccagcc cgtcgcactg gccccatgc 1599

<210> SEQ ID NO 127
<211> LENGTH: 1236
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 127

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ccaggcacgt ccatgttaaa actcgagccg ggtggctcga cgatccccaa gatccccttc 120

atccgcccga gctttcccgg gccagccgag ctcgccgagg acttcgtaca gatcgcccag 180

gctaactggt acacgaactt cggtccgaac gagcggcggt ttgcccgcgc cctgcgcgac 240

tatctgggac ctcatctgca cgttgctacc ctcgccaacg gcaccctggc actcctcgcg 300

gcgctccacg tcagtttcgg cgccggtacg cgggaccgct acctgctgat gccgtcgttc 360

acgttcgtcg gcgtggctca ggctgcgcta tggactgggt accgtccctg gttcatcgac 420

atcgacgcca acacatggca gccatgcgtc cactccgccc gcgccgtcat cgaacgcttc 480

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cgcgaccgga tcgccggcat cctgctggcc aatgtgttcg gcgtcggcaa tccccagatc 540

agcgtctggg aggagctcgc cgccgaatgg gagctaccga ttgtgctcga ctcggcggcc 600

ggcttcggct ccacgtacgc cgacggcgag cgcctcggtg gacgcggtgc atgcgagatc 660

ttctccttcc atgcgaccaa gccgttcgcg gttggtgagg gcggcgctct ggtttctcgc 720

gatccacggc tcgtcgagca cgcatacaag ttccagaact tcggcttggt gcaaacacgc 780

gagtccatcc agctcggaat gaacggcaag ctgtcggaga tcagcgccgc tattggccta 840

cgccaactag tcgggcttga tcgccgcctg gcaagtcgcc gcaaggtcct cgagtgctat 900

cgcaccggta tggccgacgc gggtgtgcgt ttccaggaca acgccaatgt tgcgtcgctc 960

tgtttcgcga gcgcttgctg cacgtccgcc gaccacaagg ccgcggttct gggtagcctg 1020

cgtaggcacg cgatcgaggc gcgcgactac tacaacccac cgcagcaccg acatccgtac 1080

tttgtgacga atgccgagtt agtcgagtcg accgatctag ccgtcacggc ggacatttgc 1140

tcgcgaatcg tgtcgctgcc agtccacgac cacatggccc cggatgacgt tgcccgggtc 1200

gtcgccgccg tgcaggaagc ggaggtgcgc ggtgaa 1236

<210> SEQ ID NO 128
<211> LENGTH: 2358
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 128

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ctgaacctgc tggcccagtc cgaatcccta ttcgccttgt ccaacgggca cattggatta 120

cgcggcaacc tcgacgaggg cgaacccttc ggactgccgg gcacctacct gaactctttc 180

tacgaaatcc ggccgctgcc gtacgccgag gccggttatg gatatccgga ggccggccag 240

accgttgtcg acgtcaccaa cggcaagatc tttcgcctgt tggtcggcga cgagccgttc 300

gacgtccggt atggcgaatt gatctcccac gaacggatcc tcgacctgcg cgccgggacg 360

ctgacccgcc gcgcgcactg gcgctcaccg gcgggcaagc aagtcaaagt gacgtccacc 420

cggctggtgt cgctggccca ccgcagcgtc gcggcgatcg agtacgtcgt cgaggcaatc 480

gaggaattcg ttcgcgtgac cgtgcagtcc gaactcgtca ccaacgagga cgtaccggag 540

acctcggccg acccgcgggt gtcggccatc ctggacaggc cgctacaggc cgtcgagcac 600

gaacgcaccg agcggggtgc acttctcatg caccgcaccc gagccagcgc gctgatgatg 660

gccgcaggga tggaacacga ggtcgaggtt cccgggcggg tcgagatcac caccgacgcc 720

cgcccggacc tggcccgaac caccgtgatc tgcgggctgc gcccgggaca gaagctgcgc 780

atcgtcaaat acctggccta tggctggtcc agcctgcgct cccgcccggc gctgcgcgac 840

caggccgccg gcgcgctgca cggtgcccgc tacagcggct ggcaggggct gctggacgcg 900

caacgcgcct acctcgacga cttctgggac agcgcggacg tggaggtcga gggcgacccg 960

gaatgtcagc aagcggtgcg tttcgggtta tttcacctgt tgcaggccag cgcgcgcgcc 1020

gaacgccgcg cgatccccag caaggggctc accggaaccg ggtatgacgg ccacgccttt 1080

tgggacaccg aaggtttcgt gctaccggtg ctcacctaca ccgcaccgca tgcggtcgcc 1140

gacgcgctgc ggtggcgggc gtcgacgttg gacctggcca aggagcgggc ggccgagctc 1200

ggcctggaag gtgccgcctt tccctggcgg accatccgcg gacaggagtc ctcggcctac 1260

tggccggccg gcacggcggc ctggcacatc aacgccgaca tcgcgatggc gttcgagcgg 1320

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taccgcatcg tcaccggcga cggttcgctg gaggaggaat gcggccttgc ggtgctgatc 1380

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gacggggtca ccggtcccga cgagtacacg gcggtcgtcc gcgacaacgt gttcacgaat 1500

ctgatggcgg cgcacaatct gcacaccgcc gccgatgctt gcttgcgcca ccccgaggcg 1560

gcggaggcca tgggtgtcac caccgaggag atggccgcct ggcgcgacgc ggccgacgcc 1620

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gtgcgcttgt atcccgcaca ggtgatcaag caggccgacc tggtgctggc gatgcagtgg 1800

cagagtcacg cgttcacgcc cgagcagaag gcgcgcaacg tcgactacta cgaacggcgc 1860

atggtgcgcg actcgtcgtt gtcggcctgc actcaggcgg tgatgtgcgc cgaggtcggc 1920

catctcgagt tggcccacga ctatgcctac gaagccgccc tgatcgacct gcgcgacctg 1980

caccgcaaca cccgtgacgg cctacacatg gcttcgctgg ccggagcctg gacggcgctg 2040

gtcgtaggct tcggcggcct acgcgacgac gagggcatcc tgtccatcga tccgcagctg 2100

cccgacggca tctcgcggct gcggttccgg ctgcgatggc gcggcttccg gctgatcgtc 2160

gacgccaacc acaccgacgt caccttcatc cttggcgacg gtcccggcac ccagctgacc 2220

atgcgccacg ccggccaaga tctgacgctg cacacggaca caccgtccac catcgccgtg 2280

cgcacccgta agccgctgct gccgccacca ccgcagccgc caggccgcga gccagtgcac 2340

cgccgggctt tagcccgg 2358

<210> SEQ ID NO 129
<211> LENGTH: 786
<212> TYPE: DNA
<213> ORGANISM: Mycobacteria tuberculosis

<400> SEQUENCE: 129

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gagaaggtgc gtgcttgcct gttcgacctc gacggtgtgc tcaccgatac cgcgagcctg 120

cataccaagg cgtggaaggc catgtttgac gcctacctag ccgagcgagc cgagcgcacc 180

ggcgaaaaat tcgttccctt cgaccctgcc gcggactatc acacgtatgt ggacggcaag 240

aaacgcgaag acggcgttcg atcgtttctg agcagccgcg ccatcgaaat acccgacggt 300

tccccggatg acccgggcgc cgccgagacg gtgtatggcc tgggcaaccg caagaacgac 360

atgttgcaca agctgctgcg cgacgatggg gcccaggtgt tcgacgggtc gcggcgctac 420

ctggaggcgg tcacggccgc gggtctcggt gtggccgtgg tgtcttcgag cgccaacacc 480

cgcgacgtgc tcgcgaccac cggtctggac cggttcgtcc agcagcgggt ggacggcgtg 540

acgttgcgcg aagagcacat cgccggcaag ccggcccccg actccttcct gcgcgcggca 600

gaactgttgg gggttacccc cgacgcggcg gcggtgttcg aggacgccct gtccggggtg 660

gcggccggcc gcgccggcaa cttcgccgta gtggtgggca tcaaccgaac gggccgggcg 720

gctcaggccg cccagttgcg ccgccatggc gccgacgtgg tggtaaccga tctcgccgag 780

ctgctg 786

<210> SEQ ID NO 130
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: M. tuberculosis
<220> FEATURE:
<221> NAME/KEY: misc_feature

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<222> LOCATION: (1)...(60)
<223> OTHER INFORMATION: n = A,T,C or G
<221> NAME/KEY: misc_feature
<222> LOCATION: 2, 55
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 130

antagtaatg tgcgagctga gcgatgtcgc cgctcccaaa aattaccaat ggttnggtca     60


<210> SEQ ID NO 131
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 131

agtagtaatg tgcgagctga gcgatgtcgc cgctcccaaa aattaccaat ggtttggtca     60


<210> SEQ ID NO 132
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: M. tuberbulosis

<400> SEQUENCE: 132

tgacgccttc ctaaccagaa ttgtgaattc atacaagccg tagtcgtgca gaagcgcaac     60


<210> SEQ ID NO 133
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 133

tgacgccttc ctaaccagaa ttgtgaattc atacaagccg tagtcgtgca gaagcgcaac     60


<210> SEQ ID NO 134
<211> LENGTH: 11
<212> TYPE: DNA
<213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 134

actcttggag t                                                          11


<210> SEQ ID NO 135
<211> LENGTH: 11
<212> TYPE: DNA
<213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 135

actcttggag t                                                          11


<210> SEQ ID NO 136
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<212> TYPE: DNA
<213> ORGANISM: M. tuberculosis
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)...(49)
<223> OTHER INFORMATION: n = A,T,C or G
<221> NAME/KEY: misc_feature
<222> LOCATION: 15, 24
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 136

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<210> SEQ ID NO 137
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<211> LENGTH: 49
<212> TYPE: DNA
<213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 137

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```

What is claimed is:

1. A method of distinguishing whether a patient has been exposed to a virulent strain of the *M. tuberculosis* complex, the method comprising:

contacting said patient or a sample obtained therefrom with a polypeptide encoded by a nucleotide sequence comprising the open reading frame Rv2654c (SEQ ID NO: 94) or a polypeptide encoded by a nucleotide fragment of at least 25 contiguous nucleotides of SEQ ID NO: 94; and

determining the presence of an immune reaction to said polypeptide, wherein a positive response is indicative of exposure to a virulent strain of the *M. tuberculosis* complex.

2. The method of claim **1**, wherein said contacting step comprises sub-cutaneous injection of said polypeptide.

3. The method of claim **1**, wherein said contacting step is performed in vitro and said sample comprises a blood sample or derivative thereof.

4. The method according to claim **2**, wherein said polypeptide is injected at a dose of from 0.05 μg to 5 μg.

5. The method according to claim **4**, wherein the site of injection is examined for the presence of a wheal, indicative of said positive response.

6. The method according to claim **1**, wherein said determining step comprises:

detecting binding of an antibody to said polypeptide, said binding being an indication that said subject is infected by *Mycobacterium tuberculosis* or is diseased with *Mycobacterium tuberculosis*.

7. The method of claim **1**, wherein said polypeptide is a fusion protein comprising the polypeptide sequence encoded by SEQ ID NO: 94 or comprising the polypeptide sequence encoded by a nucleotide fragment of at least 25 nucleotides of SEQ ID NO: 94.

8. A method of distinguishing whether a patient has been exposed to a virulent strain of the *M. tuberculosis* complex, the method comprising:

contacting said patient or a sample obtained therefrom with a polypeptide or polypeptide fragment encoded by a nucleotide sequence set forth in the open reading frame Rv2654c (SEQ ID NO:94); and

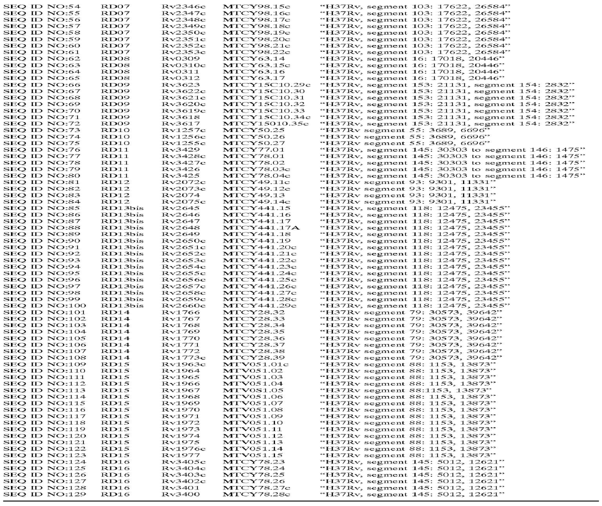
determining the presence of an immune reaction to said polypeptide, wherein a positive response is indicative of exposure to a virulent strain of the *M. tuberculosis* complex.

* * * * *

专利名称(译)	结核分枝杆菌复合体的物种之间的分子差异		
公开(公告)号	US6686166	公开(公告)日	2004-02-03
申请号	US09/894844	申请日	2001-06-27
[标]申请(专利权)人(译)	BEHR MARCEL 小PETER SCHOOLNIK GARY WILSON迈克尔		
申请(专利权)人(译)	BEHR MARCEL 小PETER SCHOOLNIK GARY WILSON MICHAEL A.		
当前申请(专利权)人(译)	THE利兰·斯坦福，齐齐哈尔大学董事会		
[标]发明人	BEHR MARCEL SMALL PETER SCHOOLNIK GARY WILSON MICHAEL A		
发明人	BEHR, MARCEL SMALL, PETER SCHOOLNIK, GARY WILSON, MICHAEL A.		
IPC分类号	C12Q1/68 C12N1/21 G01N33/53 A61K39/00 A61K39/02 C07H21/04		
CPC分类号	C12Q1/689 C12Q2600/156		
优先权	60/097936 1998-08-25 US		
其他公开文献	US20020176873A1		
外部链接	Espacenet USPTO		

摘要(译)

在分枝杆菌分离株中鉴定出特异性遗传缺失，包括分离株之间结核分枝杆菌基因组序列的变异，以及与M.tb相比BCG中存在的大量缺失。这些缺失用作区分致病菌株和无毒菌株的标记物，并用作特定M.tb分离株的标记物。对BCG疫苗株特异的缺失可用于确定结核菌素阳性皮肤试验是否指示实际的结核感染。可以将缺失的序列重新引入BCG以提高疫苗接种的功效。或者，从牛分枝杆菌或结核分枝杆菌中删除对应于缺失的遗传序列以减弱致病细菌。



SEQ ID NO:54	RD07	Rv2346c	MTCY98.15c	"H37Rv, segment 103: 17622, 26584"
SEQ ID NO:55	RD07	Rv2347c	MTCY98.16c	"H37Rv, segment 103: 17622, 26584"
SEQ ID NO:56	RD07	Rv2348c	MTCY98.17c	"H37Rv, segment 103: 17622, 26584"
SEQ ID NO:57	RD07	Rv2349c	MTCY98.18c	"H37Rv, segment 103: 17622, 26584"
SEQ ID NO:58	RD07	Rv2350c	MTCY98.19c	"H37Rv, segment 103: 17622, 26584"
SEQ ID NO:59	RD07	Rv2351c	MTCY98.20c	"H37Rv, segment 103: 17622, 26584"
SEQ ID NO:60	RD07	Rv2352c	MTCY98.21c	"H37Rv, segment 103: 17622, 26584"
SEQ ID NO:61	RD07	Rv2353c	MTCY98.22c	"H37Rv, segment 103: 17622, 26584"
SEQ ID NO:62	RD08	Rv0309	MTCY63.14	"H37Rv, segment 16: 17018, 20446"
SEQ ID NO:63	RD08	Rv0310c	MTCY63.15c	"H37Rv, segment 16: 17018, 20446"
SEQ ID NO:64	RD08	Rv0311	MTCY63.16	"H37Rv, segment 16: 17018, 20446"
SEQ ID NO:65	RD08	Rv0312	MTCY63.17	"H37Rv, segment 16: 17018, 20446"
SEQ ID NO:66	RD09	Rv3623	MTCY15C10.29c	"H37Rv, segment 153: 21131, segment 154: 2832"
SEQ ID NO:67	RD09	Rv3622c	MTCY15C10.30	"H37Rv, segment 153: 21131, segment 154: 2832"
SEQ ID NO:68	RD09	Rv3621c	MTCY15C10.31	"H37Rv, segment 153: 21131, segment 154: 2832"
SEQ ID NO:69	RD09	Rv3620c	MTCY15C10.32	"H37Rv, segment 153: 21131, segment 154: 2832"
SEQ ID NO:70	RD09	Rv3619c	MTCY15C10.33	"H37Rv, segment 153: 21131, segment 154: 2832"
SEQ ID NO:71	RD09	Rv3618	MTCY15C10.34c	"H37Rv, segment 153: 21131, segment 154: 2832"
SEQ ID NO:72	RD09	Rv3617	MTCY15010.35c	"H37Rv, segment 153: 21131, segment 154: 2832"
SEQ ID NO:73	RD10	Rv1257c	MTCY50.25	"H37Rv segment 55: 3689, 6696"
SEQ ID NO:74	RD10	Rv1256c	MTCY50.26	"H37Rv segment 55: 3689, 6696"
SEQ ID NO:75	RD10	Rv1255c	MTCY50.27	"H37Rv segment 55: 3689, 6696"
SEQ ID NO:76	RD11	Rv3429	MTCY77.01	"H37Rv, segment 145: 30303 to segment 146: 1475"
SEQ ID NO:77	RD11	Rv3428c	MTCY78.01	"H37Rv, segment 145: 30303 to segment 146: 1475"
SEQ ID NO:78	RD11	Rv3427c	MTCY78.02	"H37Rv, segment 145: 30303 to segment 146: 1475"
SEQ ID NO:79	RD11	Rv3426	MTCY78.03c	"H37Rv, segment 145: 30303 to segment 146: 1475"
SEQ ID NO:80	RD11	Rv3425	MTCY78.04c	"H37Rv, segment 145: 30303 to segment 146: 1475"
SEQ ID NO:81	RD12	Rv2072c	MTCY49.11c	"H37Rv segment 93: 9301, 11331"
SEQ ID NO:82	RD12	Rv2073c	MTCY49.12c	"H37Rv segment 93: 9301, 11331"
SEQ ID NO:83	RD12	Rv2074	MTCY49.13	"H37Rv segment 93: 9301, 11331"
SEQ ID NO:84	RD12	Rv2075c	MTCY49.14c	"H37Rv segment 93: 9301, 11331"
SEQ ID NO:85	RD13bis	Rv2645	MTCY441.15	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:86	RD13bis	Rv2646	MTCY441.16	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:87	RD13bis	Rv2647	MTCY441.17	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:88	RD13bis	Rv2648	MTCY441.17A	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:89	RD13bis	Rv2649	MTCY441.18	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:90	RD13bis	Rv2650c	MTCY441.19	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:91	RD13bis	Rv2651c	MTCY441.20c	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:92	RD13bis	Rv2652c	MTCY441.21c	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:93	RD13bis	Rv2653c	MTCY441.22c	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:94	RD13bis	Rv2654c	MTCY441.23c	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:95	RD13bis	Rv2655c	MTCY441.24c	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:96	RD13bis	Rv2656c	MTCY441.25c	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:97	RD13bis	Rv2657c	MTCY441.26c	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:98	RD13bis	Rv2658c	MTCY441.27c	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:99	RD13bis	Rv2659c	MTCY441.28c	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:100	RD13bis	Rv2660c	MTCY441.29c	"H37Rv, segment 118: 12475, 23455"
SEQ ID NO:101	RD14	Rv1766	MTCY28.32	"H37Rv segment 79: 30573, 39642"
SEQ ID NO:102	RD14	Rv1767	MTCY28.33	"H37Rv segment 79: 30573, 39642"
SEQ ID NO:103	RD14	Rv1768	MTCY28.34	"H37Rv segment 79: 30573, 39642"
SEQ ID NO:104	RD14	Rv1769	MTCY28.35	"H37Rv segment 79: 30573, 39642"
SEQ ID NO:105	RD14	Rv1770	MTCY28.36	"H37Rv segment 79: 30573, 39642"
SEQ ID NO:106	RD14	Rv1771	MTCY28.37	"H37Rv segment 79: 30573, 39642"
SEQ ID NO:107	RD14	Rv1772	MTCY28.38	"H37Rv segment 79: 30573, 39642"
SEQ ID NO:108	RD14	Rv1773c	MTCY28.39	"H37Rv segment 79: 30573, 39642"
SEQ ID NO:109	RD15	Rv1963c	MTV051.01c	"H37Rv segment 88: 1153, 13873"
SEQ ID NO:110	RD15	Rv1964	MTV051.02	"H37Rv segment 88: 1153, 13873"
SEQ ID NO:111	RD15	Rv1965	MTV051.03	"H37Rv segment 88: 1153, 13873"
SEQ ID NO:112	RD15	Rv1966	MTV051.04	"H37Rv segment 88: 1153, 13873"
SEQ ID NO:113	RD15	Rv1967	MTV0S1.05	"H37Rv segment 88:1153, 13873"
SEQ ID NO:114	RD15	Rv1968	MTV051.06	"H37Rv segment 88: 1153, 13873"
SEQ ID NO:115	RD15	Rv1969	MTV051.07	"H37Rv segment 88: 1153, 13873"
SEQ ID NO:116	RD15	Rv1970	MTV051.08	"H37Rv segment 88: 1153, 13873"
SEQ ID NO:117	RD15	Rv1971	MTV051.09	"H37Rv segment 88: 1153, 13873"
SEQ ID NO:118	RD15	Rv1972	MTV051.10	"H37Rv segment 88: 1153, 13873"
SEQ ID NO:119	RD15	Rv1973	MTV051.11	"H37Rv segment 88: 1153, 13873"
SEQ ID NO:120	RD15	Rv1974	MTV051.12	"H37Rv segment 88: 1153, 13873"
SEQ ID NO:121	RD15	Rv1975	MTV051.13	"H37Rv segment 88: 1153, 13873"
SEQ ID NO:122	RD15	Rv1976c	MTV051.14	"H37Rv segment 88: 1153, 13873"
SEQ ID NO:123	RD15	Rv1977	MTV051.15	"H37Rv segment 88: 1153, 13873"
SEQ ID NO:124	RD16	Rv3405c	MTCY78.23	"H37Rv, segment 145: 5012, 12621"
SEQ ID NO:125	RD16	Rv3404c	MTCY78.24	"H37Rv, segment 145: 5012, 12621"
SEQ ID NO:126	RD16	Rv3403c	MTCY78.25	"H37Rv, segment 145: 5012, 12621"
SEQ ID NO:127	RD16	Rv3402c	MTCY78.26	"H37Rv, segment 145: 5012, 12621"
SEQ ID NO:128	RD16	Rv3401	MTCY78.27c	"H37Rv, segment 145: 5012, 12621"
SEQ ID NO:129	RD16	Rv3400	MTCY78.28c	"H37Rv, segment 145: 5012, 12621"