## Supplemental Materials and Methods

### *Cell isolation and in vitro stimulation*

Human monocytes and neutrophils were isolated from fresh peripheral blood using RosetteSep™ Human Monocyte Enrichment Cocktail (STEMCELL Technology) and Polymorphophrep solution (Axis-Shield), respectively. Fresh cells (1 x $10^6$) resuspended in complete RPMI 1640 medium without penicillin and streptomycin were plated into 96-well U-bottom plates, and then infected with live BPZE1 at a bacterium-to-cell ratio of 10:1. Cells and bacteria were centrifuged to facilitate contact at 2200 rpm for 2 min, followed by incubation for 2h at 37°C in a 5% $CO_2$ atmosphere. Afterwards, polymyxin B (5 µg/ml) was added to kill extracellular bacteria. Then cells were extensively washed and further incubated for 6h or 12h. Cell activation was evaluated using flow cytometric analysis. Supernatants were collected from cell culture for the measurement of cytokines.

### *Bacterial strains, growing conditions and lysates preparation*

Vaccine strain BPZE1 and a virulent clinical *B. pertussis* strain BP611-98 were obtained from the Public Health Agency of Sweden. As for the lysates preparation, both *B. pertussis* strains were grown on charcoal agar plates supplemented with 10% horse blood for 5 days at 37°C. Bacteria were then scraped gently from the plates, suspended in PBS, and then filtered through a 40 µm cell strainer. Bacteria suspensions were centrifuged at 3500 rpm for 15min and pellets were collected. An appropriate volume of lysis buffer (8M urea, 500mM bicarbonate, PH=8.5) was used to lyse the bacteria on ice for 1h, followed by centrifugation and collection of supernatants. Protein concentration was determined using Pierce BCA Protein Assay Kit according to the manual. For in vitro stimulation experiments, BPZE1 was cultivated in THIJS medium (1) overnight at 37°C in shaking incubator. Bacterial concentration was determined by measuring the optical density (OD) at 600 nm wavelength and calculated according to an established standard curve.

### *Multiplex assay*

The concentration of IL-1β, IL-6, and TNF in the supernatants collected from in-vitro stimulation cultures was measured using a customized MILLIPLEX MAP Multiplex Kit (Merck Millipore) according to the manufacturer's protocol. Data was analyzed using MAGPIX system (Merck Millipore).

### *Antibody avidity assay*

IgG and IgA avidities were evaluated according to (2) with little modifications. 96-well half-area plates (Greiner bio-one, Germany) were coated with BPZE1 lysates (500ng/well) overnight at 4°C, followed by blocking with PBS-T containing 2% BSA at room temperature for 2h. After that, serum samples were diluted in PBS-T containing 0.2% BSA and added into plates. The dilution factor of each serum sample corresponding to OD value around 1.0 was used. Following primary serum incubation for 2h and washing steps, 50 µl of ammonium thiocyanate ($NH_4SCN$) solution were added at different concentrations (0M, 0.25M, 0.5M, 1M, 2M, 4M, and 8M) for 30min at room temperature. The plates were then washed with PBS-T and further processed according to the description under ELISA assay. The concentration of $NH_4SCN$ that dissociates 50% of the antibody-antigen binding (EC50) was calculated and used as avidity index.

### *Memory B cell ELISpot*

Antigen-specific memory B cells were evaluated as previously described with some modifications (3). Briefly, MAIPSWU 96-well plates (Millipore) were coated with BPZE1 lysates (50 µg/ml), a mixture of antigens (FHA, PT, PRN, FIM, 200 µg/ml each), or PT alone (200 µg/ml). PBMCs (1x$10^6$ cells/ml) were stimulated with CpG ODN 2006 (5 µg/ml, Invivogen), Pokeweed mitogen (5 µg/ml, Sigma-Aldrich) and Protein A from Staphylococcus aureus Cowan strain (1:10000, Sigma-Aldrich) for 4 days. Stimulated cells were added in a three-fold serial dilution and cultured overnight at 37°C. Following washing steps with PBS-T, plates were incubated with biotinylated goat anti-human IgG Fcγ or anti-human IgA (0.25 µg/ml, Jackson ImmunoResearch Laboratories) in PBS-T for 1.5h, followed by incubation with streptavidin-conjugated alkaline phosphatase (1:1000, Mabtech) in PBS-T. Spots were developed with BCIP/NBT substrate (Mabtech) and counted using an AID ELISpot Reader (Autoimmun Diagnostika). Unspecific spots were subtracted from antigen-specific wells, as defined by spots counted in samples incubated in ovalbumin-coated wells. Results were depicted as spot-forming cells (SFC) per million stimulated cells.

### *Antigen recall T cell assay*

A total of 1 x $10^6$ PBMCs were seeded per well into 96-well U-bottom plates and incubated with 1 x $10^7$ heat-inactivated BPZE1 (56°C for 30min) in the presence of brefeldin A (5 µg) overnight. Cytokine production of memory T cells were evaluated by surface and intracellular staining with antibody cocktails using Fixation/Permeabilization Solution Kit (BD Biosciences) as previously described (3). Frequency of cytokine-producing $CD4^+$ T cells was determined by FACS analysis. Background cytokine staining was subtracted, as defined by staining in the samples incubated with PBS. Polyfunctionality of BPZE1-specific $CD4^+$ T cells was analyzed using FlowJo V.10.1 (Tree Star) and SPICE software (v.6.0).

### *Stimulation of neutrophils with Ab-opsonized BPZE1*

Opsonization of BPZE1 by antibodies was performed by incubating $10^7$ CFU of live BPZE1 with serum samples at 37°C for 25min. Fresh neutrophils ($1x10^6$ cells) were isolated as described above, and then added into the culture subsequently. After 1h of incubation, cells were evaluated by FACS analysis to measure the activation and maturation. Production of reactive oxygen species was measured using cellular ROS Assay Kit (Abcam) according to the manual.

### *Complement bactericidal activity*

Culture of BPZE1 was harvested after overnight shaking incubation to a concentration of about $10^9$ CFU/ml (OD value of 0.5). Serum samples were heated at 56°C for 30 min to inactivate the complement system. $10^7$ CFU of BPZE1 were incubated with 10% pooled serum or heat-inactivated serum from BPZE1- or aPV- vaccinees for 1.5h at 37°C. A 50-µl aliquot of culture was diluted in an appropriate volume of Hanks' Balanced Salt Solution (HBSS). 10µl of the diluted culture was plated in triplicates onto charcoal agar plates supplemented with 10% horse blood. Colonies were counted after 3 days of growth at 37°C. The average count of colonies was calculated back to the concentration as CFU/ml. BPZE1 cultured without serum was treated as control.

### *Neutrophil bactericidal assay*

$10^7$ CFU of BPZE1 were pre-incubated with or without 10% serum or heat-inactivated serum for 25min at 37°C, followed by co-culture with fresh neutrophils ($1x10^6$ cells). Control sample containing only $10^7$ CFU of BPZE1 was incubated in parallel. After 2h of incubation, saponin (0.5 mg/ml) was added to lyse the neutrophils. Then an aliquot of culture was diluted and plated onto agar plates as described above. Colonies were counted after 3 days of growth at 37°C.

The count of colonies was calculated back to the concentration as CFU/ml. Neutrophil bactericidal activity was shown as the percentage of survived bacteria of the initial inoculum.

### *In-solution Protein Digestion for MS analysis*

Bacteria pellets were suspended in 200 µL of 8M urea (Sigma-Aldrich) in 100 mM NaCl and 100 µL of 0.2% ProteaseMax (Promega) in 100 mM ammonium bicarbonate (AmBic) and 20% acetonitrile (AcN) was added. The samples were sonicated using VibraCell probe (Sonics & Materials, Inc.) for 1 min, with pulse 2/2, at 40% amplitude, and sonicated in bath for 5 minutes, followed by vortexing and centrifugation for 5 min at 13,000 rpm. The supernatants were transferred to new tubes and concentration determination was performed in a 1:2 dilution in water. Samples with 20 µg protein in 10 µL of lysis buffer were incubated at 37°C for 10 min and 30 µL of 100 mM AmBic was added to decrease urea concentration to about 1M. Proteins were reduced with 1 µL of 200 mM dithiothreitol (Sigma) in 50 mM AmBic and incubated at 37°C for 60 min. Alkylation was completed with 1 µL of 600 mM iodoacetamide (Sigma) in 50 mM AmBic at room temperature for 20 min. Then 0.5 µg of sequencing grade modified trypsin (Promega, Madison, WI, USA) was added to each sample (trypsin: protein = 1: 20) and incubated for 16 h at 37°C. The digestion was stopped by adding of formic acid at final concentration of 5% and incubating the solution at 37°C for 20 min. Then the samples were cleaned by C18 Hypersep plate (Thermo Scientific), dried using a speedvac and resuspended in 40 µl 0.1% formic acid and 2% AcN.

### *In-gel Protein Digestion for MS analysis*

Protein spots were excised manually from polyacrylamide gel and placed in Eppendorf tubes for in-gel digestion. Gel warping and spot detection were performed using Delta2D software (DECODON GmbH) to ensure the correct spot matching. Washing of gel pieces was carried out in 0.2M ammonium bicarbonate (AmBic) containing 50% acetonitrile. Proteins were reduced with 20 mM dithiothreitol in 100 mM AmBic for 60 min at 37°C followed by alkylation with 55 mM iodoacetamide in 100 mM AmBic for 20 min at 25°C and digested with 0.2 µg trypsin (modified, Promega, Madison, WI, USA) in 0.2 M AmBic overnight at 37°C. The tryptic peptides were acidified with formic acid and extracted twice using 0.1% formic acid in 50% and 100% acetonitrile, respectively. The solutions were dried and the peptides were cleaned up on C-18 Stage Tips (Thermo Scientific).

### ***LC-MS/MS analysis***

The reconstituted peptides in solvent A were separated on a 50 cm long EASY-spray column (Thermo Scientific) connected to an Ultimate-3000 nano-LC system (Thermo Scientific) using a 60 min gradient from 4-26% of solvent B (98% acetonitrile, 0.1% formic acid) in 55 min and up to 95% of solvent B in 5 min at a flow rate of 300 nL/min. Mass spectra were acquired on a Fusion Orbitrap mass spectrometer (Thermo Scientific) in m/z 350 to 1800 at resolution of 120,000 (at m/z 200) for full mass, followed by data-dependent HCD fragmentations from most intense precursor ions with a charge state 2+ to 7+. The tandem mass spectra were acquired with a resolution of 30,000, targeting $5x10^4$ ions, setting quadrupole isolation width to m/z 1.6 and normalized collision energy to 30%. Acquired raw data files were analyzed using the Mascot search engine v.2.5.1 (Matrix Science Ltd., UK) and searched against *B. pertussis* protein database from UniProt (6,516 entries, downloaded in April 2019). Maximum of three missed cleavage sites were allowed for trypsin, while setting the precursor and the fragment ion mass tolerance to 10 ppm and 0.02, respectively. Dynamic modifications of oxidation on methionine, deamidation of asparagine and glutamine and acetylation of N-termini were set. Initial search results were filtered with 5% FDR using Percolator to recalculate Mascot scores.

### *Bioinformatics analysis*

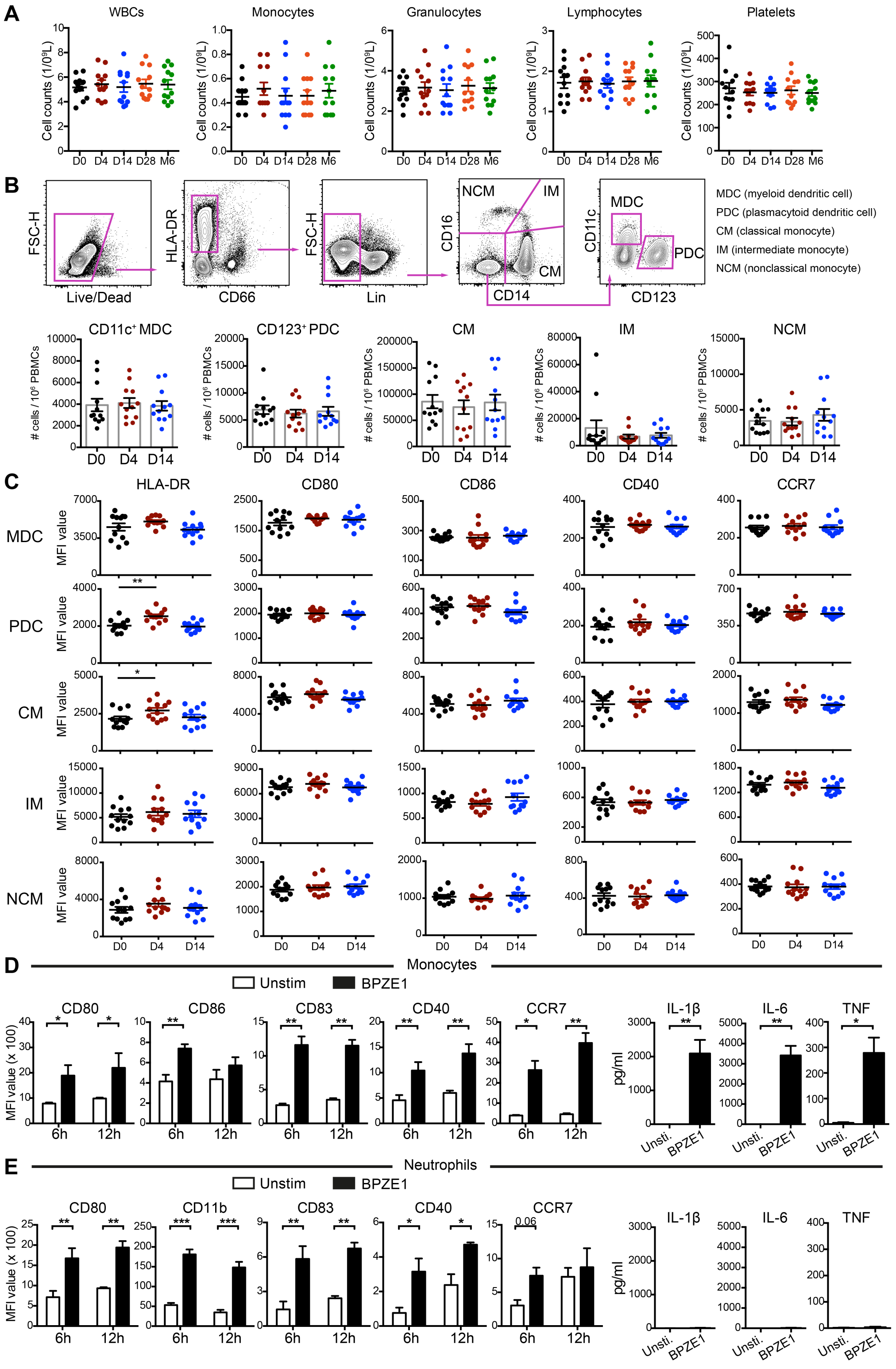
Gene ontology (GO) analysis of identified proteins was performed using the Database for Annotation, Visualization and Integrated Discovery (DAVID) v6.8 (4). KEGG pathway profiles of identified proteins were categorized based on KEGG BRITE database (http://www.genome.jp/kegg/brite.html) using clusterProfiler (5), programmed by R software.

## References

1. Thalen M, van den IJ, Jiskoot W, Zomer B, Roholl P, de Gooijer C, Beuvery C, and Tramper J. Rational medium design for Bordetella pertussis: basic metabolism. *J Biotechnol.* 1999;75(2-3):147-59.
2. Ibrahim NM, El-Kady EM, Eissa SA, and Wahby AF. Assessment of antibody level and avidity against Bordetella pertussis in a cohort of Egyptian individuals aged 1-18 years. *J Adv Res.* 2016;7(1):105-11.
3. Thompson EA, Ols S, Miura K, Rausch K, Narum DL, Spangberg M, Juraska M, Wille-Reece U, Weiner A, Howard RF, et al. TLR-adjuvanted nanoparticle vaccines differentially influence the quality and longevity of responses to malaria antigen Pfs25. *JCI Insight.* 2018;3(10).
4. Huang da W, Sherman BT, and Lempicki RA. Systematic and integrative analysis of large gene lists using DAVID bioinformatics resources. *Nat Protoc.* 2009;4(1):44-57.
5. Yu G, Wang LG, Han Y, and He QY. clusterProfiler: an R package for comparing biological themes among gene clusters. *OMICS.* 2012;16(5):284-7.

## Supplemental figures:

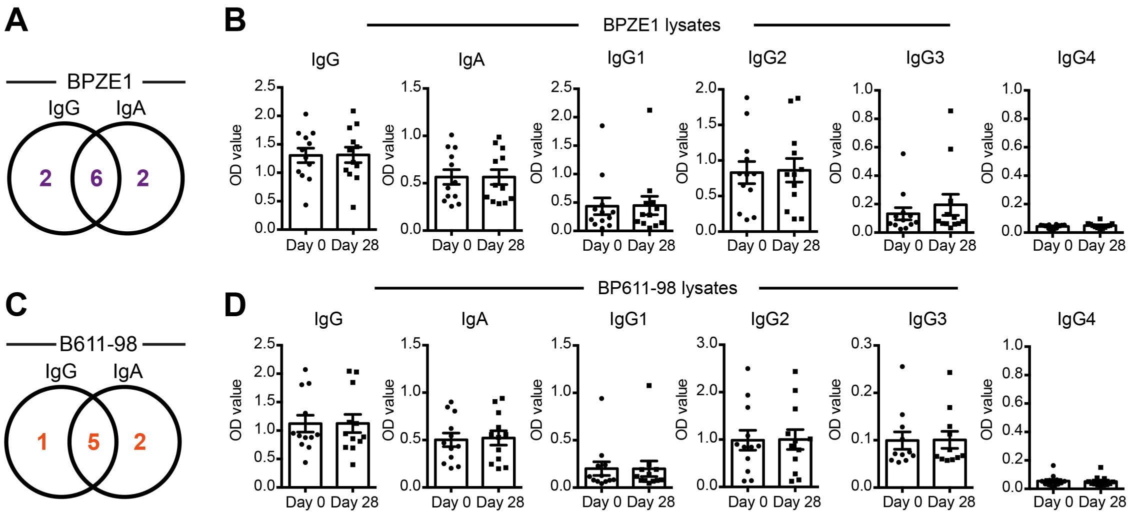
## Supplemental Figure 1.



**Supplemental Figure 1. Innate immune responses induced by BPZE1 vaccination.** **(A).** Absolute cell counts of total white blood cells and different cell subsets in the blood of BPZE1 vaccinees (n=12). **(B).** Phenotypic identification of different innate cell subsets in

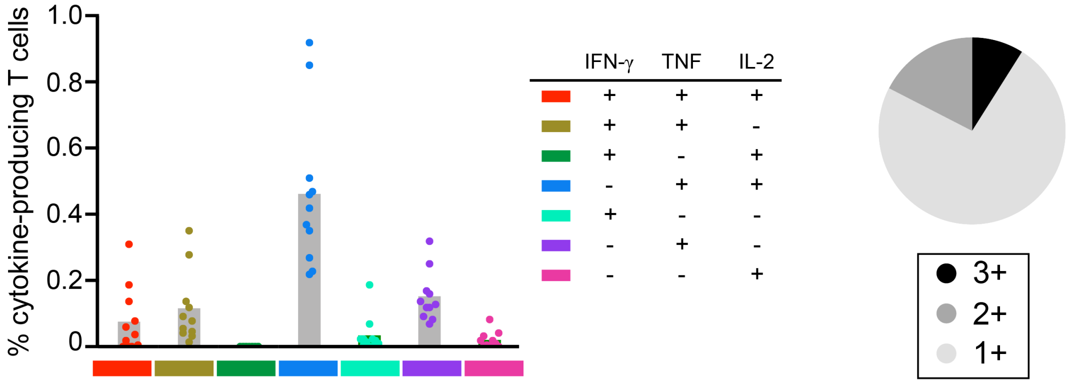
PBMCs by flow cytometry according to the indicated gating strategy (upper panel). Frequency of each cell subset in the blood of BPZE1 vaccinees at different time points after vaccination is shown (lower panel). **(C).** Expression of HLA-DR, CD80, CD86, CD40 and CCR7 on different innate immune cell subsets of individuals receiving BPZE1 immunization was evaluated by flow cytometry (n=12). MFI values of the indicated markers are shown. Wilcoxon matched-pairs signed rank test was used. **(D-E).** Surface expression levels of indicated markers on human monocytes or neutrophils upon stimulation by BPZE1 (Bacteria/cell ratio = 10:1) for 6h and 12h. Monocytes or neutrophils were stimulated with BPZE1 (Bacteria/cell ratio = 10:1) for 12h. Levels of IL-1β, IL-6 and TNF in supernatants collected from cell culture were measured. Compiled data is from four independent experiments. Two-tailed paired *t* test was used. $^*p \leq 0.05$, $^{**}p \leq 0.01$, $^{***}p \leq 0.001$.

**Supplemental Figure 2.**



**Supplemental Figure 2. Antibody responses in the subjects receiving BPZE1 or placebo. (A, C).** The number of BPZE1-immunized individuals showing at least 1.5-fold induction of BPZE1- or BP611-98-specific IgG and IgA titers. **(B, D).** Antibody titers of IgG, IgA, and four IgG subclasses directed against BPZE1 or BP611-98 lysates in individuals receiving placebo were evaluated (n=12). Optical density (OD) value is shown.

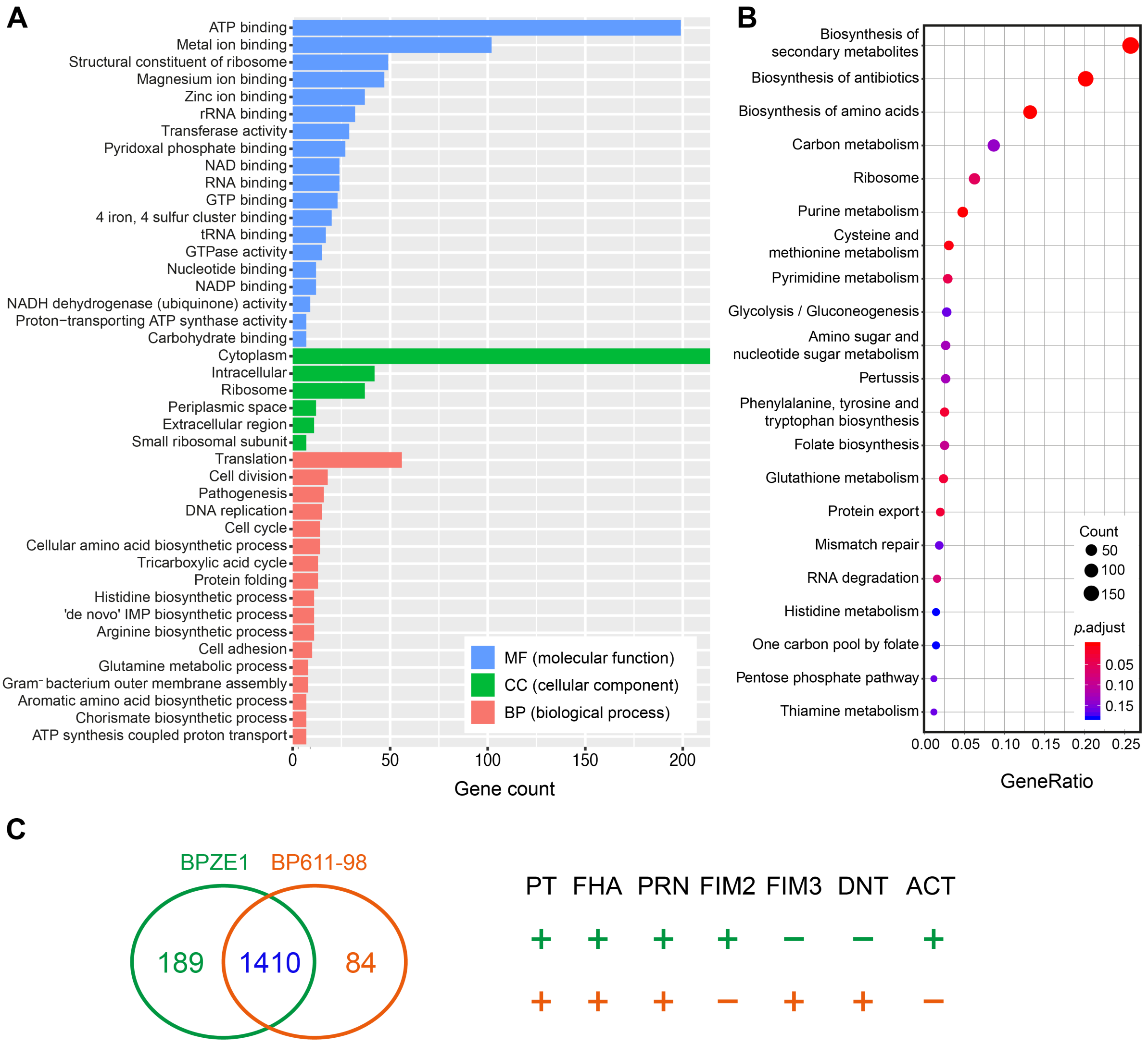
**Supplemental Figure 3.**



**Supplemental Figure 3. Polyfunctionality of BPZE1-specific CD4$^+$ T cells at 28 days after vaccination.**

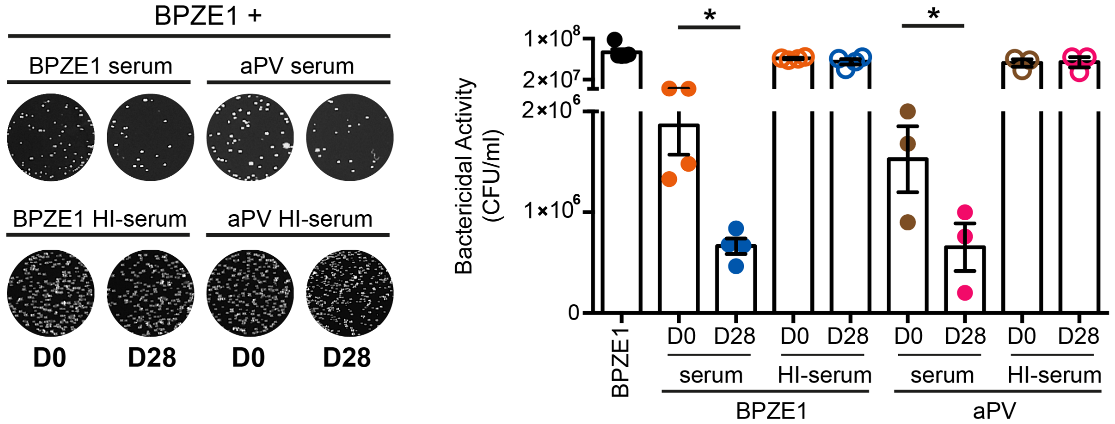
Polyfunctionality of BPZE1-specific CD4$^+$ T cells as measured by the co-expression of IFN-γ, TNF or IL-2. Pie chart shows proportion of total memory T cells producing triple, double or single cytokines.

## Supplemental Figure 4.



**Supplemental Figure 4. Proteomic characterization of BPZE1 and BP611-98.**
**(A).** Composition of BPZE1 was determined using in-solution mass spectrometric analysis. Gene ontology (GO) enrichment analysis of the identified proteins is shown. Count shows the number of genes enriched in each term. **(B).** Functional categories of the identified proteins were determined using KEGG BRITE database. Bubble chart represents the enrichment of differentially expressed genes in signaling pathways. Size and color of the bubble show the amount of differentially expressed genes enriched in pathways and the enrichment significance. **(C).** The amounts of proteins identified from BPZE1 and BP611-98 are shown. The presence or absence of key immunogenic antigens inside BPZE1 and BP611-98 is indicated.

## Supplemental Figure 5.



**Supplemental Figure 5. Complement killing of *B. pertussis* in the presence of vaccine-induced antibodies.** Live BPZE1 ($10^7$ CFU) were incubated with 10% pooled serum or HI-serum collected from BPZE1 or aPV vaccinees for 1.5h at 37°C. Live BPZE1 cultured alone is used as control. Survival of bacteria is calculated and shown. Compiled data is from at least three independent experiments. Two-tailed paired *t* test was used. $*p \leq 0.05$.

## Supplemental Table 1. List of antibodies used for FACS analysis

| Antibody | Clone | Fluorophore |
|---|---|---|
| HLA-DR | Tü36 | PE-Texas Red |
| CD3 | SP34-2 | APC-Cy7 |
| CD20 | L27 | APC-Cy7 |
| CD56 | HCD56 | APC-Cy7 |
| CD14 | M5E2 | BV510 |
| CD66abce | TET2 | PE |
| CD11c | 3,9 | PE-Cy7 |
| CD123 | 7G3 | BV650 |
| CD16 | 3G8 | Alexa Fluor 700 |
| CCR7 | G043H7 | BV421 |
| CD80 | 2D10 | BV605 |
| CD86 | 2331 | APC |
| CD40 | 5C3 | FITC |
| CD83 | HB15e | Percp-Cy5.5 |
| CD95 | DX2 | PE-Cy5 |
| CD28 | CD28.2 | ECD |
| CXCR5 | MU5UBEE | Percp-efluor 710 |
| PD-1 | EH12.2H7 | BV421 |
| CD4 | S3.5 | PE-Cy5.5 |
| CD123 | 6H6 | BV510 |
| CXCR3 | G025H7 | Alexa647 |
| CD19 | HIB19 | BV570 |
| CD38 | HIT2 | Alexa488 |
| ICOS | C398.4A | PE-Cy7 |
| CD27 | M-T271 | BV650 |
| CD8 | RPA-T8 | BV570 |
| CD45RA | 5H9 | PE-Cy5 |
| CD69 | TP1.55.3 | ECD |
| IL-13 | JES10-5A2 | PE |
| IL-17A | BL168 | BV785 |
| IL-2 | MQ1-17H12 | BV605 |
| TNF | Mab11 | Alexa Fluor 488 |
| IL-21 | 3A3-N2.1 | Alexa Fluor 647 |
| IFN-γ | B27 | Alexa Fluor 700 |
| CD62L | SK11 | Brilliant Violet 785 |
| CD10 | HI10a | Brilliant Violet 605 |
| CD66abce | TET2 | APC |
| CD11b | ICRF44 | Pacific blue |
| CD63 | H5C6 | FITC |

**Supplemental Table 2. Proteome composition of BPZE1**

| Protein_description | Score | Mass | Matches | Sequences | Cover |
|---|---|---|---|---|---|
| Filamentous hemagglutinin OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=fhaB PE=1 SV=4 | 24939 | 367471 | 726 | 132 | 51,6 |
| Adhesin OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=fhaS PE=4 SV=1 | 2673 | 263712 | 97 | 68 | 40,9 |
| Pertactin autotransporter OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=prn PE=1 SV=3 | 2296 | 93396 | 74 | 22 | 40,8 |
| Aminotransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=tyrB PE=3 SV=1 | 886 | 43238 | 26 | 16 | 48,2 |
| Putative thiolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2759 PE=3 SV=1 | 100 | 41731 | 8 | 8 | 29,9 |
| Citrate synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=prpC PE=3 SV=1 | 99 | 44335 | 5 | 5 | 18,2 |
| Ribosomal protein S12 methylthiotransferase RimO OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rimO PE=3 SV=1 | 99 | 49498 | 7 | 5 | 24,1 |
| Putative hydrolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2713 PE=4 SV=1 | 99 | 31245 | 9 | 8 | 36,7 |
| Putative transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0924 PE=4 SV=1 | 99 | 33194 | 5 | 4 | 14,8 |
| Putative potassium channel protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3606 PE=4 SV=1 | 99 | 42287 | 7 | 4 | 22,5 |
| Succinyl-diaminopimelate desuccinylase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=dapE PE=3 SV=1 | 98 | 41196 | 5 | 5 | 14 |
| Putative branched-chain amino acid transporter, ATP-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0304 PE=4 SV=1 | 98 | 28548 | 4 | 4 | 22 |
| Glycerol-3-phosphate acyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=plsY PE=3 SV=1 | 98 | 22720 | 3 | 3 | 18,1 |
| Putative CDP-diacylglycerol--serine O-phosphatidyltransferase protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=pssA PE=3 SV=1 | 98 | 28699 | 4 | 3 | 9,7 |
| Adenylosuccinate lyase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=purB PE=3 SV=1 | 872 | 50282 | 26 | 17 | 55 |
| Cytokinin riboside 5~-monophosphate phosphoribohydrolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0547 PE=3 SV=1 | 98 | 21449 | 5 | 4 | 33,3 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1304 PE=4 SV=1 | 98 | 12393 | 3 | 3 | 32,4 |
| Putative cytochrome C OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3650 PE=4 SV=1 | 97 | 24548 | 5 | 4 | 18 |
| MarR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1946 PE=4 SV=1 | 97 | 17804 | 2 | 1 | 8,1 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2651 PE=4 SV=1 | 97 | 28974 | 7 | 5 | 29,2 |
| Putative TetR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1651 PE=4 SV=1 | 97 | 23214 | 4 | 4 | 22,5 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3435 PE=4 SV=1 | 97 | 40336 | 4 | 3 | 9,3 |
| ATP synthase epsilon chain OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=atpC PE=3 SV=1 | 97 | 14675 | 4 | 3 | 35 |
| Probable glutathione S-transferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0075 PE=4 SV=1 | 97 | 22888 | 2 | 2 | 17 |
| Probable nicotinate-nucleotide adenylyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=nadD PE=3 SV=1 | 96 | 21348 | 3 | 3 | 38,6 |
| Probable cytosol aminopeptidase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=pepA PE=3 SV=1 | 866 | 52096 | 30 | 19 | 49,1 |
| Spermidine/putrescine import ATP-binding protein PotA OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=potA PE=3 SV=1 | 96 | 41605 | 2 | 2 | 7,2 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2918 PE=4 SV=1 | 96 | 15550 | 2 | 1 | 10,9 |
| 3-deoxy-manno-octulosonate cytidylyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=kdsB PE=3 SV=1 | 95 | 27200 | 6 | 6 | 28 |
| High-affinity choline transport protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=betT PE=3 SV=1 | 95 | 72206 | 4 | 4 | 8,3 |
| Thiamine-monophosphate kinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=thiL PE=3 SV=1 | 95 | 34954 | 5 | 4 | 19,5 |
| Putative TetR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0381 PE=4 SV=1 | 95 | 21177 | 3 | 3 | 25,1 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2373 PE=3 SV=1 | 94 | 52330 | 3 | 3 | 8,2 |
| GTP 3~,8-cyclase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=moaA PE=3 SV=1 | 94 | 40104 | 10 | 8 | 29,6 |
| Glycolate oxidase iron-sulfur subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=glcF PE=4 SV=1 | 94 | 45679 | 4 | 4 | 15,9 |
| Ribosomal RNA large subunit methyltransferase E OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rlmE PE=3 SV=1 | 94 | 23333 | 3 | 3 | 13,8 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3568 PE=4 SV=1 | 863 | 40457 | 25 | 12 | 51,4 |

| | | | | | |
|---|---|---|---|---|---|
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0325 PE=4 SV=1 | 94 | 43745 | 6 | 6 | 13,5 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3584 PE=4 SV=1 | 94 | 12522 | 7 | 5 | 70,7 |
| NADH-ubiquinone oxidoreductase, chain L OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=nuoL PE=4 SV=1 | 93 | 73357 | 4 | 3 | 5,1 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1896 PE=4 SV=1 | 93 | 38052 | 5 | 5 | 18,7 |
| Putative c~cytochrome OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2889 PE=4 SV=1 | 93 | 16453 | 5 | 5 | 36,2 |
| Putative glycosyl transferases OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3727 PE=4 SV=1 | 93 | 39213 | 8 | 8 | 20,1 |
| Flavin prenyltransferase UbiX OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ubiX PE=3 SV=1 | 93 | 20201 | 6 | 4 | 19,4 |
| UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=murG PE=3 SV=1 | 93 | 38168 | 11 | | |
| Glutaredoxin OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0680 PE=3 SV=1 | 93 | 11961 | 4 | 3 | 25 |
| Probable carboxylesterase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2966 PE=4 SV=1 | 92 | 24421 | 3 | 2 | 14,3 |
| 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=metE PE=3 SV=1 | 861 | 84763 | 44 | 26 | 37,2 |
| GTPase HflX OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hflX PE=3 SV=1 | 92 | 40199 | 3 | 3 | 9,8 |
| 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (flavodoxin) OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ispG PE=3 SV=1 | 92 | 47133 | 11 | 10 | 26,7 |
| Putative 5~(3~)-deoxyribonucleotidase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0294 PE=3 SV=1 | 92 | 21779 | 2 | 1 | 7,5 |
| Putative Xaa-Pro aminopeptidase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3411 PE=3 SV=1 | 92 | 48891 | 6 | 6 | 18,4 |
| 7-methyl-GTP pyrophosphatase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2447 PE=3 SV=1 | 92 | 21151 | 4 | 3 | 21,6 |
| GntR family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3452 PE=4 SV=1 | 92 | 26685 | 5 | 5 | 28,4 |
| Putative regulatory protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bcrH2 PE=4 SV=1 | 91 | 16806 | 4 | 4 | 37,9 |
| DNA-directed DNA polymerase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=dnaE PE=4 SV=1 | 91 | 130965 | 8 | 8 | 6,7 |
| Putative integral membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2986 PE=4 SV=1 | 91 | 20998 | 3 | 2 | 7,9 |
| Putative peptidase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0608 PE=4 SV=1 | 91 | 55878 | 14 | 11 | 21,3 |
| Multifunctional fusion protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=murE PE=3 SV=1 | 858 | 99874 | 36 | 28 | 43,3 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0707 PE=4 SV=1 | 91 | 10118 | 3 | 2 | 60,8 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0162 PE=4 SV=1 | 90 | 35090 | 9 | 7 | 35,9 |
| Putative nicotinate-nucleotide pyrophosphorylase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=nadC PE=3 SV=1 | 90 | 31428 | 6 | 4 | 18,9 |
| Putative GntR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2364 PE=4 SV=1 | 90 | 30509 | 6 | 5 | 27,9 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2141 PE=4 SV=1 | 90 | 16519 | 3 | 3 | 30,9 |
| Leucine-responsive regulatory protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=lrp PE=4 SV=1 | 90 | 19565 | 4 | 4 | 24,3 |
| Type IV secretion system protein PtlF OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ptlF PE=1 SV=1 | 90 | 29510 | 8 | 5 | 31,1 |
| Sec-independent protein translocase protein TatA OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=tatA PE=3 SV=1 | 90 | 8159 | 2 | 2 | 29,3 |
| Ribosome maturation factor RimM OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rimM PE=3 SV=1 | 90 | 22575 | 7 | 5 | 30,4 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0597 PE=4 SV=1 | 16 | 59093 | 1 | 1 | 1,3 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1489 PE=4 SV=1 | 89 | 59610 | 3 | 2 | 5,6 |
| Putative outer membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1428 PE=3 SV=1 | 853 | 20921 | 27 | 10 | 40,1 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0450 PE=4 SV=1 | 89 | 9148 | 1 | 1 | 18,5 |
| LysR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0498 PE=3 SV=1 | 89 | 34293 | 9 | 7 | 23,5 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1194 PE=4 SV=1 | 89 | 22742 | 3 | 3 | 24,4 |
| Ribosomal RNA small subunit methyltransferase A OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rsmA PE=3 SV=1 | 89 | 29262 | 9 | 7 | 39,6 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3507 PE=1 SV=1 | 89 | 52842 | 6 | 5 | 14,5 |

| | | | | | |
|---|---|---|---|---|---|
| HTH-type transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0258 PE=3 SV=1 | 88 | 20987 | 6 | 6 | 39,2 |
| Gluconate 5-dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=idnO PE=4 SV=1 | 88 | 26902 | 5 | 3 | 14,3 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0548 PE=4 SV=1 | 88 | 22329 | 2 | 2 | 20 |
| Putative thioredoxin OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2500 PE=4 SV=1 | 88 | 14312 | 5 | 4 | 38,9 |
| Putative phytoene synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1220 PE=4 SV=1 | 87 | 31487 | 7 | 6 | 28,3 |
| Pyruvate dehydrogenase E1 component OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=aceE PE=4 SV=1 | 845 | 100995 | 44 | 33 | 44 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1805 PE=4 SV=1 | 87 | 7325 | 2 | 2 | 67,2 |
| Probable acyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0036 PE=4 SV=1 | 87 | 27610 | 4 | 4 | 21,9 |
| Ferredoxin OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3582 PE=4 SV=1 | 87 | 12517 | 5 | 3 | 29 |
| Probable fatty acid desaturase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1758 PE=4 SV=1 | 87 | 46055 | 2 | 2 | 7,7 |
| Phosphoribosyl-AMP cyclohydrolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hisI PE=3 SV=1 | 86 | 15233 | 4 | 3 | 32,1 |
| Putative binding-protein-dependent transport permease OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2394 PE=3 SV=1 | 86 | 32049 | 3 | 3 | 12,4 |
| Cyclolysin secretion/processing ATP-binding protein CyaB OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=cyaB PE=3 SV=1 | 86 | 78225 | 5 | 5 | 12,4 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3001 PE=4 SV=1 | 86 | 22319 | 6 | 4 | 26,9 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1600 PE=3 SV=1 | 86 | 25224 | 2 | 2 | 12,1 |
| Oxygen-dependent coproporphyrinogen-III oxidase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hemF PE=3 SV=1 | 86 | 34335 | 7 | 6 | 24,4 |
| Inosine-5~-monophosphate dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=guaB PE=3 SV=1 | 842 | 52019 | 33 | 17 | 47,9 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2200 PE=4 SV=1 | 86 | 17920 | 4 | 4 | 36,9 |
| Putative IclR-family regulatory protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2645 PE=4 SV=1 | 86 | 26779 | 4 | 4 | 19,1 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2359 PE=4 SV=1 | 85 | 10144 | 5 | 4 | 31,4 |
| Putative phosphomethylpyrimidine kinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=thiD PE=4 SV=1 | 85 | 30345 | 5 | 5 | 29,3 |
| Molybdenum cofactor guanylyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=mobA PE=3 SV=1 | 84 | 21394 | 1 | 1 | 8,6 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1766 PE=4 SV=1 | 84 | 11367 | 7 | 4 | 57,8 |
| Putative cytochrome OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2490 PE=4 SV=1 | 84 | 12565 | 8 | 5 | 58,3 |
| Putative transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1899 PE=4 SV=1 | 84 | 26929 | 6 | 5 | 23,4 |
| Putative phage repressor protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3390 PE=3 SV=1 | 84 | 23144 | 4 | 4 | 40,4 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2156 PE=4 SV=1 | 84 | 24008 | 3 | 3 | 16,2 |
| Dihydroxy-acid dehydratase 1 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ilvD1 PE=3 SV=1 | 838 | 66348 | 25 | 16 | 41,5 |
| 50S ribosomal protein L20 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rplT PE=3 SV=1 | 83 | 13290 | 6 | 4 | 32,8 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0870 PE=4 SV=1 | 83 | 23731 | 4 | 4 | 15,1 |
| Putative iron-sulfur binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1470 PE=4 SV=1 | 83 | 75510 | 5 | 5 | 7,8 |
| Possible membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2994 PE=4 SV=1 | 82 | 39164 | 7 | 7 | 31,5 |
| Putative efflux system inner membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2075 PE=3 SV=1 | 82 | 47555 | 10 | 7 | 23,9 |
| Putative ABC transport protein, ATP-binding component OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2745 PE=3 SV=1 | 82 | 38916 | 7 | 5 | 16,6 |
| Putative asparagine synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3146 PE=4 SV=1 | 82 | 71734 | 6 | 5 | 8,3 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0682 PE=1 SV=1 | 82 | 34751 | 5 | 3 | 19,7 |
| Peptide chain release factor 1 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=prfA PE=3 SV=1 | 81 | 40219 | 6 | 5 | 23,6 |
| NADH-quinone oxidoreductase subunit A OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=nuoA PE=3 SV=1 | 81 | 13643 | 1 | 1 | 12,6 |
| Probable TonB-dependent receptor BfrD OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bfrD PE=1 SV=2 | 2200 | 81645 | 97 | 46 | 65,7 |
| Bifunctional hemolysin/adenylate cyclase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=cya PE=1 SV=1 | 138 | 177414 | 13 | 11 | 8,6 |

| | | | | | |
|---|---|---|---|---|---|
| Virulence sensor protein BvgS OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bvgS PE=1 SV=3 | 834 | 135317 | 30 | 26 | 29,6 |
| Probable GntR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0776 PE=4 SV=1 | 81 | 26832 | 6 | 5 | 17,4 |
| Sec-independent protein translocase protein TatC OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=tatC PE=3 SV=1 | 81 | 29293 | 1 | 1 | 9 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0060 PE=4 SV=1 | 80 | 45300 | 2 | 2 | 7,1 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3585 PE=4 SV=1 | 80 | 18051 | 4 | 3 | 29,6 |
| sn-glycerol-3-phosphate transport system permease protein UgpE OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ugpE PE=3 SV=1 | 80 | 31382 | 3 | 2 | 8,1 |
| Glycolate oxidase subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=glcE PE=4 SV=1 | 80 | 38941 | 5 | 4 | 12,5 |
| Cystathionine beta-lyase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=metC PE=3 SV=1 | 80 | 42214 | 6 | 4 | 14,6 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2502 PE=4 SV=1 | 79 | 8643 | 2 | 1 | 27,5 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1849 PE=4 SV=1 | 79 | 28735 | 4 | 4 | 23,4 |
| Heptosyltransferase II OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=waaF PE=4 SV=1 | 79 | 34373 | 6 | 5 | 18,1 |
| Arginine--tRNA ligase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=argS PE=3 SV=2 | 834 | 61577 | 26 | 21 | 45,9 |
| Lipoprotein-releasing system ATP-binding protein LolD OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=lolD PE=3 SV=1 | 79 | 25070 | 4 | 4 | 26 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0247 PE=4 SV=1 | 79 | 19472 | 7 | 4 | 39,3 |
| Small ribosomal subunit biogenesis GTPase RsgA OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rsgA PE=3 SV=1 | 79 | 32945 | 4 | 3 | 22,7 |
| Putative extracellular solute-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3159 PE=4 SV=1 | 78 | 57187 | 6 | 6 | 20 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1059 PE=4 SV=1 | 78 | 13377 | 5 | 4 | 35,3 |
| Glutamate uptake regulatory protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=grp PE=4 SV=1 | 78 | 17585 | 4 | 4 | 37,2 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1239 PE=4 SV=1 | 78 | 12065 | 3 | 2 | 21,6 |
| Putative integral membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2927 PE=4 SV=1 | 77 | 18495 | 2 | 2 | 12,7 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1837 PE=3 SV=1 | 77 | 9233 | 3 | 3 | 48,8 |
| Histone deacetylase family protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0960 PE=4 SV=1 | 76 | 33994 | 2 | 2 | 8,5 |
| 4,5-dihydroxyphthalate decarboxylase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0683 PE=4 SV=1 | 821 | 38061 | 22 | 14 | 58,6 |
| Putative ABC-transport protein, ATP-binding component OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1707 PE=4 SV=1 | 76 | 28331 | 4 | 4 | 18,6 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3540 PE=4 SV=1 | 76 | 10856 | 7 | 6 | 53,1 |
| Putative phospholipase D protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3092 PE=4 SV=1 | 76 | 56659 | 7 | 7 | 12,2 |
| Biotin carboxylase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=accC PE=4 SV=1 | 75 | 50337 | 4 | 4 | 11,8 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1413 PE=4 SV=1 | 75 | 23868 | 5 | 4 | 32,3 |
| Putative esterase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0300 PE=4 SV=1 | 75 | 32617 | 4 | 4 | 15,9 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0469 PE=4 SV=1 | 75 | 35250 | 2 | 2 | 7,9 |
| Lipid-A-disaccharide synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=lpxB PE=3 SV=1 | 75 | 42922 | 17 | 8 | 26,5 |
| Putative acetyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0213 PE=4 SV=1 | 74 | 19481 | 3 | 3 | 17 |
| Phosphate regulon sensor protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=phoR PE=4 SV=1 | 74 | 48923 | 4 | 4 | 17,2 |
| Probable orn/arg/lys decarboxylase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0190 PE=4 SV=1 | 817 | 85828 | 38 | 29 | 45,5 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1448 PE=4 SV=1 | 74 | 15816 | 1 | 1 | 11 |
| Malonyl-[acyl-carrier protein] O-methyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bioC PE=3 SV=1 | 74 | 33206 | 4 | 3 | 16,9 |
| Putative inner membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3393 PE=4 SV=1 | 74 | 29452 | 2 | 2 | 13,9 |
| Putative succinylglutamate desuccinylase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=astE PE=4 SV=1 | 74 | 36427 | 7 | 5 | 23,7 |
| Putative oxidoreductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0208 PE=4 SV=1 | 73 | 51334 | 4 | 4 | 18,5 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1291 PE=4 SV=1 | 73 | 18880 | 1 | 1 | 9,7 |

| | | | | | |
|---|---|---|---|---|---|
| Cys/Met metabolism PLP-dependent enzyme OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3528 PE=3 SV=1 | 73 | 45081 | 2 | 2 | 5,6 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2583 PE=4 SV=1 | 73 | 28352 | 4 | 4 | 26,2 |
| Putative RNA methyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1434 PE=4 SV=1 | 73 | 27824 | 4 | 4 | 17,5 |
| Phosphoenolpyruvate-protein phosphotransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ptsI PE=3 SV=1 | 73 | 60820 | 3 | 3 | 7,8 |
| DNA gyrase subunit B OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=gyrB PE=3 SV=1 | 816 | 90179 | 35 | 30 | 43,5 |
| 5~-nucleotidase SurE OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=surE PE=3 SV=1 | 73 | 26885 | 3 | 3 | 16,7 |
| Protein translocase subunit SecY OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=secY PE=3 SV=1 | 72 | 48345 | 6 | 4 | 10,4 |
| Putative polysaccharide deacetylase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2326 PE=4 SV=1 | 72 | 27472 | 3 | 3 | 19,9 |
| Enoyl-CoA hydratase/isomerase-like protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2093 PE=4 SV=1 | 72 | 28751 | 4 | 4 | 24,1 |
| Putative cytochrome OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2491 PE=4 SV=1 | 72 | 11664 | 1 | 1 | 25,2 |
| Putative ABC transport ATP-binding subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3339 PE=4 SV=1 | 72 | 27485 | 5 | 4 | 22 |
| Probable D-alanyl-D-alanine carboxypeptidase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1051 PE=4 SV=1 | 72 | 50901 | 3 | 3 | 7,7 |
| Uroporphyrinogen decarboxylase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hemE PE=3 SV=1 | 72 | 39473 | 7 | 7 | 17,9 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3686 PE=4 SV=1 | 72 | 17704 | 2 | 2 | 15,9 |
| Amino-acid ABC transporter binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0057 PE=4 SV=1 | 71 | 32539 | 7 | 7 | 37,5 |
| Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=odhB PE=3 SV=1 | 810 | 41799 | 27 | 12 | 43,1 |
| Putative aldehyde dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2303 PE=3 SV=1 | 71 | 54112 | 3 | 3 | 13,7 |
| Ornithine carbamoyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=argF PE=3 SV=1 | 71 | 35339 | 3 | 3 | 13,1 |
| Putative secreted protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1047 PE=4 SV=1 | 71 | 12181 | 5 | 3 | 40,4 |
| Putative lipoprotein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0793 PE=4 SV=1 | 70 | 19765 | 1 | 1 | 7,4 |
| Filamentous hemagglutinin transporter protein FhaC OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=fhaC PE=1 SV=1 | 70 | 64463 | 12 | 10 | 24 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0048 PE=4 SV=1 | 70 | 23268 | 3 | 3 | 22,1 |
| Putative citrate lyase beta chain OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=citE PE=3 SV=1 | 70 | 31651 | 4 | 4 | 21,1 |
| tRNA dimethylallyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=miaA PE=3 SV=1 | 70 | 34256 | 9 | 7 | 24,6 |
| Glycine--tRNA ligase alpha subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=glyQ PE=3 SV=1 | 70 | 34493 | 6 | 5 | 21,1 |
| Probable iron-sulfur binding oxidase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0141 PE=4 SV=1 | 70 | 145428 | 26 | 19 | 19,1 |
| Glycine--tRNA ligase beta subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=glyS PE=3 SV=1 | 809 | 76107 | 31 | 22 | 38,3 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0807 PE=4 SV=1 | 69 | 34112 | 3 | 3 | 12,2 |
| UPF0301 protein BP0319 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0319 PE=3 SV=1 | 69 | 21381 | 1 | 1 | 12,9 |
| ATP-dependent RNA helicase RhlE OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rhlE PE=3 SV=1 | 69 | 50740 | 4 | 4 | 11,8 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1290 PE=4 SV=1 | 69 | 17566 | 4 | 4 | 26,1 |
| Conserved hypothetical lipoprotein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2341 PE=4 SV=1 | 69 | 49727 | 8 | 8 | 19 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1903 PE=4 SV=1 | 69 | 58209 | 3 | 3 | 6,4 |
| 50S ribosomal protein L31 type B OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpmE2 PE=3 SV=1 | 69 | 10081 | 4 | 3 | 39,8 |
| 3-methyl-2-oxobutanoate hydroxymethyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=panB PE=3 SV=1 | 69 | 29455 | 2 | 2 | 12,9 |
| Co-chaperone protein HscB homolog OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hscB PE=3 SV=1 | 68 | 19608 | 3 | 3 | 21,8 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1699 PE=4 SV=1 | 68 | 32343 | 2 | 2 | 9,2 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2936 PE=4 SV=1 | 807 | 37469 | 32 | 14 | 43,3 |
| tRNA (guanine-N(7)-)-methyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=trmB PE=3 SV=1 | 68 | 28090 | 5 | 3 | 22,4 |

| | | | | | |
|---|---|---|---|---|---|
| Putative AsnC-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2981 PE=4 SV=1 | 68 | 16917 | 5 | 3 | 25,3 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2567 PE=4 SV=1 | 68 | 13885 | 1 | 1 | 18,1 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1698 PE=4 SV=1 | 68 | 17904 | 2 | 1 | 13 |
| Magnesium transporter MgtE OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2806 PE=3 SV=1 | 67 | 54012 | 4 | 4 | 12 |
| ABC transport protein, periplasmic component OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2616 PE=4 SV=1 | 67 | 35008 | 5 | 5 | 15,4 |
| Putative ribonuclease OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2317 PE=4 SV=1 | 66 | 54896 | 6 | 5 | 22,6 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0562 PE=4 SV=1 | 66 | 17177 | 4 | 4 | 33,7 |
| Iron-sulfur cluster assembly scaffold protein IscU OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=iscU PE=3 SV=1 | 66 | 14604 | 3 | 2 | 16,9 |
| Phosphate regulon transcriptional regulatory protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=phoB PE=4 SV=1 | 66 | 25952 | 3 | 3 | 24,1 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2815 PE=3 SV=1 | 798 | 81305 | 27 | 21 | 40,5 |
| Probable MerR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3110 PE=4 SV=1 | 66 | 30359 | 6 | 5 | 22,2 |
| Putative cell division protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ftsK PE=3 SV=1 | 66 | 85698 | 8 | 8 | 11,3 |
| Endonuclease III OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=nth PE=3 SV=1 | 66 | 23798 | 2 | 2 | 15,6 |
| Low molecular weight protein-tyrosine-phosphatase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ptpA PE=3 SV=1 | 65 | 18418 | 3 | 2 | 17,8 |
| Adenine phosphoribosyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=apt PE=3 SV=1 | 65 | 20247 | 4 | 2 | 17,6 |
| Putative TetR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2720 PE=4 SV=1 | 65 | 21863 | 5 | 4 | 23,5 |
| Putative chorismate-binding enzyme OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3241 PE=4 SV=1 | 64 | 41150 | 6 | 6 | 22,4 |
| Heat-inducible transcription repressor HrcA OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hrcA PE=3 SV=1 | 64 | 36634 | 6 | 4 | 12,6 |
| High-affinity branched-chain amino acid transporter, ATP-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0305 PE=4 SV=1 | 64 | 25614 | 3 | 3 | 21,4 |
| 2-nonaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=coq7 PE=3 SV=1 | 64 | 24171 | 3 | 3 | 24,3 |
| Acetoacetyl-CoA reductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=phbB PE=3 SV=1 | 798 | 26367 | 25 | 11 | 62,4 |
| Putative lipoprotein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0017 PE=4 SV=1 | 64 | 14400 | 2 | 2 | 28,4 |
| Probable ABC transporter, ATP-binding component OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0781 PE=4 SV=1 | 64 | 30874 | 3 | 3 | 12,9 |
| Putative two component system response regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2934 PE=4 SV=1 | 64 | 20245 | 4 | 4 | 24,5 |
| Cytidylate kinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=cmk PE=3 SV=1 | 64 | 24003 | 5 | 4 | 16,6 |
| TetR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1202 PE=4 SV=1 | 64 | 25148 | 3 | 3 | 13,9 |
| Nucleoid-associated protein BP1550 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1550 PE=3 SV=1 | 64 | 11596 | 6 | 4 | 40,7 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0241 PE=3 SV=1 | 64 | 25328 | 6 | 4 | 21,9 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3003 PE=4 SV=1 | 64 | 32680 | 1 | 1 | 8 |
| MerR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1726 PE=4 SV=1 | 64 | 14993 | 2 | 2 | 21,2 |
| Holliday junction ATP-dependent DNA helicase RuvA OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ruvA PE=3 SV=1 | 63 | 20108 | 5 | 5 | 42,1 |
| DNA-directed RNA polymerase subunit beta~ OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpoC PE=3 SV=1 | 2046 | 156884 | 87 | 60 | 51,9 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3440 PE=1 SV=1 | 794 | 34683 | 30 | 14 | 50,2 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0976 PE=4 SV=1 | 63 | 24413 | 2 | 2 | 10,9 |
| Glutaredoxin OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=grxC PE=3 SV=1 | 63 | 9668 | 3 | 2 | 39,5 |
| Exodeoxyribonuclease 7 small subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=xseB PE=1 SV=1 | 62 | 9673 | 2 | 1 | 20,5 |
| Putative acetyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1299 PE=4 SV=1 | 62 | 16894 | 2 | 2 | 13,6 |
| Putative integral membrane zinc-metalloprotease OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2688 PE=3 SV=1 | 62 | 47139 | 4 | 3 | 12,6 |
| Putative apolipoprotein N-acyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=lnt PE=5 SV=1 | 62 | 58666 | 3 | 2 | 5,3 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2486 PE=4 SV=1 | 62 | 45598 | 2 | 2 | 5,6 |

| | | | | | |
|---|---|---|---|---|---|
| Putative peptidoglycan binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0020 PE=4 SV=1 | 62 | 38260 | 3 | 3 | 9,2 |
| Putative GntR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0198 PE=4 SV=1 | 62 | 27066 | 6 | 6 | 27,2 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2863 PE=4 SV=1 | 61 | 32705 | 2 | 2 | 7,1 |
| Acetylornithine aminotransferase 2 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=argD2 PE=3 SV=1 | 792 | 43081 | 31 | 17 | 52,5 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2402 PE=4 SV=1 | 61 | 17213 | 1 | 1 | 7,4 |
| 30S ribosomal protein S20 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpsT PE=3 SV=1 | 61 | 9466 | 5 | 5 | 39,1 |
| Putative sodium:alanine symporter OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2306 PE=3 SV=1 | 61 | 47039 | 3 | 3 | 6 |
| Chromosomal replication initiator protein DnaA OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=dnaA PE=3 SV=1 | 61 | 52477 | 2 | 2 | 9,4 |
| tRNA-2-methylthio-N(6)-dimethylallyladenosine synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=miaB PE=3 SV=1 | 61 | 49993 | 1 | 1 | 2,9 |
| Phenylacetic acid degradation protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=paaI PE=4 SV=1 | 61 | 16460 | 2 | 2 | 14,1 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2144 PE=4 SV=1 | 60 | 20051 | 2 | 2 | 16,4 |
| Primosomal protein N~ OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=priA PE=3 SV=1 | 60 | 75090 | 10 | 9 | 16,9 |
| Probable transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1590 PE=3 SV=1 | 60 | 33024 | 5 | 4 | 22,6 |
| Putative ABC transporter substrate binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0301 PE=4 SV=1 | 791 | 41662 | 24 | 16 | 49,9 |
| Probable TetR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1924 PE=4 SV=1 | 60 | 24359 | 6 | 5 | 32,1 |
| Putative taurine dioxygenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3455 PE=4 SV=1 | 60 | 34463 | 5 | 5 | 22,8 |
| Queuine tRNA-ribosyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=tgt PE=3 SV=1 | 60 | 42445 | 5 | 5 | 11,1 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2387 PE=4 SV=1 | 60 | 10709 | 7 | 5 | 54,3 |
| Bis(5~-nucleosyl)-tetraphosphatase, symmetrical OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=apaH PE=3 SV=1 | 60 | 30918 | 3 | 3 | 10,1 |
| Molybdopterin converting factor OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=moaD PE=4 SV=1 | 60 | 8826 | 2 | 2 | 34,9 |
| Putative phospholipase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2225 PE=4 SV=1 | 60 | 53490 | 11 | 9 | 19,8 |
| UPF0337 protein BP1738 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1738 PE=3 SV=1 | 59 | 7576 | 3 | 3 | 45,5 |
| Putative LacI-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2590 PE=4 SV=1 | 59 | 38150 | 3 | 3 | 9,3 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3058 PE=4 SV=1 | 59 | 44532 | 6 | 3 | 8,6 |
| Phosphoribosylformylglycinamidine cyclo-ligase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=purM PE=3 SV=1 | 790 | 36995 | 29 | 13 | 55,3 |
| Putative Sodium:sulfate symportert OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0380 PE=4 SV=1 | 59 | 52491 | 3 | 3 | 7 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2299 PE=1 SV=1 | 59 | 10711 | 5 | 3 | 57,3 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0411 PE=4 SV=1 | 58 | 11874 | 3 | 3 | 43 |
| Cytochrome c oxidase subunit 1 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ctaD PE=3 SV=1 | 58 | 59694 | 4 | 4 | 15,3 |
| Nod factor export ATP-binding protein I OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=nodI PE=3 SV=1 | 58 | 34651 | 1 | 1 | 9,2 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2060 PE=4 SV=1 | 58 | 28767 | 2 | 2 | 12,1 |
| Type IV secretion system protein PtlG OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ptlG PE=2 SV=1 | 58 | 39618 | 4 | 4 | 15,2 |
| Shikimate kinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=aroK PE=3 SV=1 | 57 | 23252 | 4 | 4 | 18 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1123 PE=4 SV=1 | 57 | 70658 | 2 | 2 | 3,1 |
| Putative oxidoreductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2906 PE=4 SV=1 | 57 | 51374 | 7 | 6 | 18,1 |
| Isoleucine--tRNA ligase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ileS PE=3 SV=1 | 784 | 106148 | 27 | 22 | 37,7 |
| Probable ornithine cyclodeaminase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0354 PE=1 SV=1 | 57 | 32451 | 4 | 4 | 21,6 |
| Probable enoyl-CoA hydratase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=paaG PE=4 SV=1 | 57 | 28051 | 4 | 3 | 16,8 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2344 PE=3 SV=1 | 57 | 13391 | 4 | 3 | 28,8 |
| Tw-component sensor kinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0992 PE=4 SV=1 | 56 | 66367 | 7 | 7 | 12,2 |

| | | | | | |
|---|---|---|---|---|---|
| Phosphoglycolate phosphatase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=gph PE=3 SV=1 | 56 | 24828 | 3 | 3 | 20,9 |
| Putative cytochrome c asssembly protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3652 PE=4 SV=1 | 56 | 49270 | 1 | 1 | 5 |
| Putative acetyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3524 PE=4 SV=1 | 56 | 16089 | 1 | 1 | 21,1 |
| 50S ribosomal protein L3 glutamine methyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=prmB PE=3 SV=1 | 56 | 32964 | 5 | 5 | 12,1 |
| UPF0339 protein BP0521 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0521 PE=3 SV=1 | 56 | 11947 | 4 | 3 | 52,3 |
| Probable oxidoreductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bplA PE=1 SV=1 | 56 | 39107 | 3 | 3 | 12,3 |
| Adenylosuccinate synthetase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=purA PE=3 SV=1 | 781 | 47089 | 24 | 12 | 41,8 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1907 PE=4 SV=1 | 56 | 24782 | 7 | 7 | 32,6 |
| Putative outer protein N OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bopN PE=4 SV=1 | 56 | 39083 | 3 | 3 | 16,2 |
| Periplasmic solute-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3674 PE=4 SV=1 | 56 | 34412 | 4 | 4 | 17,1 |
| Probable two-component response regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1091 PE=4 SV=1 | 56 | 25953 | 7 | 5 | 23,1 |
| GntR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0888 PE=4 SV=1 | 55 | 29538 | 5 | 4 | 15,6 |
| Probable glutathione S-transferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0519 PE=4 SV=1 | 55 | 26848 | 3 | 2 | 7,7 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0708 PE=4 SV=1 | 54 | 24001 | 3 | 2 | 14 |
| UDP-3-O-acyl-N-acetylglucosamine deacetylase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=lpxC PE=3 SV=1 | 54 | 34135 | 8 | 8 | 28,3 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0452 PE=4 SV=1 | 54 | 33184 | 1 | 1 | 4 |
| Putative transferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2329 PE=4 SV=1 | 54 | 27946 | 4 | 3 | 12,4 |
| UvrABC system protein A OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=uvrA2 PE=3 SV=1 | 778 | 208883 | 33 | 28 | 19,6 |
| UvrABC system protein A OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=uvrA PE=3 SV=1 | 548 | 105439 | 24 | 20 | 29,2 |
| Probable L-aspartate dehydrogenase 2 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=nadX2 PE=3 SV=1 | 54 | 27890 | 2 | 1 | 6,7 |
| Cell division protein FtsB OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ftsB PE=3 SV=1 | 53 | 13115 | 4 | 4 | 31,4 |
| Phospho-N-acetylmuramoyl-pentapeptide-transferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=mraY PE=3 SV=1 | 53 | 41402 | 3 | 3 | 5,8 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3823 PE=4 SV=1 | 53 | 7426 | 4 | 3 | 46,8 |
| Probable transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0220 PE=4 SV=1 | 53 | 31240 | 5 | 4 | 18,4 |
| Probable LysR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0433 PE=3 SV=1 | 53 | 35871 | 4 | 3 | 15,2 |
| Putative transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2319 PE=4 SV=1 | 52 | 19983 | 1 | 1 | 9,4 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1231 PE=4 SV=1 | 52 | 64212 | 3 | 3 | 8 |
| Probable hydrolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0478 PE=4 SV=1 | 52 | 24082 | 4 | 4 | 15,2 |
| Magnesium and cobalt efflux protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=corC PE=4 SV=1 | 52 | 32958 | 8 | 6 | 24,7 |
| Putative aldehyde dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3624 PE=4 SV=1 | 776 | 51960 | 34 | 19 | 50,9 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0043 PE=4 SV=1 | 52 | 20101 | 4 | 4 | 44,5 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0732 PE=4 SV=1 | 52 | 46208 | 5 | 4 | 9 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2475 PE=4 SV=1 | 52 | 23982 | 4 | 4 | 16,2 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1898 PE=4 SV=1 | 51 | 30151 | 1 | 1 | 7,2 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2024 PE=4 SV=1 | 51 | 11133 | 3 | 3 | 41,7 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1438 PE=4 SV=1 | 50 | 14905 | 3 | 3 | 21,3 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1561 PE=4 SV=1 | 50 | 47483 | 4 | 4 | 9,9 |
| Putative lipoate-protein ligase A OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1297 PE=4 SV=1 | 50 | 28336 | 3 | 3 | 9,3 |
| UPF0250 protein BP0104 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0104 PE=3 SV=1 | 50 | 10205 | 2 | 2 | 22 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3097 PE=4 SV=1 | 49 | 20531 | 1 | 1 | 12,4 |

| | | | | | |
|---|---|---|---|---|---|
| Probable aldehyde dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0465 PE=3 SV=1 | 765 | 50902 | 29 | 22 | 64,6 |
| LysR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1599 PE=3 SV=1 | 49 | 33822 | 3 | 2 | 8,3 |
| DNA-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=fis PE=3 SV=1 | 49 | 9226 | 3 | 3 | 38 |
| ATP synthase subunit c OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=atpE PE=3 SV=1 | 49 | 8256 | 1 | 1 | 13,8 |
| 2-methylcitrate dehydratase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=prpD PE=4 SV=1 | 49 | 54274 | 2 | 2 | 6 |
| UDP-N-acetylenolpyruvoylglucosamine reductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=murB PE=3 SV=1 | 49 | 37683 | 3 | 3 | 10,5 |
| Glutamine transport system permease protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=glnP PE=3 SV=1 | 49 | 23756 | 1 | 1 | 5 |
| Putative pH adaptation potassium efflux protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=phaA PE=4 SV=1 | 49 | 104833 | 3 | 3 | 4,8 |
| Lipoyl synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=lipA PE=3 SV=1 | 49 | 37479 | 2 | 2 | 6,3 |
| SsrA-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=smpB PE=3 SV=1 | 49 | 18234 | 7 | 5 | 28,4 |
| MotA/TolQ/ExbB proton channel family protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=exbB PE=3 SV=1 | 49 | 33833 | 2 | 2 | 6,5 |
| Proline--tRNA ligase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=proS PE=3 SV=1 | 764 | 63988 | 32 | 23 | 51,4 |
| Peptide methionine sulfoxide reductase MsrA OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=msrA PE=3 SV=1 | 49 | 20994 | 2 | 2 | 11,3 |
| S-formylglutathione hydrolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3750 PE=3 SV=1 | 49 | 31598 | 2 | 2 | 10,3 |
| Lipopolysaccharide biosynthesis protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bplL PE=4 SV=1 | 49 | 69227 | 6 | 6 | 11,5 |
| Protein translocase subunit SecE OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=secE PE=3 SV=1 | 48 | 13727 | 2 | 2 | 21,4 |
| Putative amino acid ABC transporter permease protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3829 PE=3 SV=1 | 48 | 40464 | 2 | 2 | 7,1 |
| Putative type III secretion protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bscU PE=4 SV=1 | 48 | 38196 | 3 | 3 | 13,5 |
| Putative GntR-family transcriptional regulatory protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2825 PE=4 SV=1 | 48 | 26181 | 3 | 3 | 22,5 |
| Putative biopolymer transport protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2764 PE=3 SV=1 | 48 | 22638 | 6 | 4 | 18,4 |
| Phosphate starvation-inducible protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=psiF PE=4 SV=1 | 48 | 11985 | 6 | 4 | 39,3 |
| Putative ferredoxin OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0353 PE=4 SV=1 | 48 | 11431 | 2 | 2 | 20,8 |
| Alkyl hydroperoxide reductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ahpC PE=4 SV=1 | 2014 | 20331 | 66 | 10 | 80,8 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3276 PE=4 SV=1 | 759 | 65352 | 24 | 16 | 35,6 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2869 PE=4 SV=1 | 48 | 40755 | 3 | 3 | 9,1 |
| Integration host factor subunit alpha OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ihfA PE=3 SV=1 | 48 | 12451 | 3 | 3 | 31,9 |
| Autotransporter OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=phg PE=4 SV=1 | 47 | 45435 | 4 | 4 | 10,3 |
| 6-carboxy-5,6,7,8-tetrahydropterin synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2660 PE=3 SV=1 | 47 | 16717 | 1 | 1 | 14,3 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0181 PE=4 SV=1 | 47 | 9773 | 4 | 4 | 38,9 |
| Probable GntR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3176 PE=4 SV=1 | 47 | 29316 | 6 | 6 | 39 |
| Pertussis toxin subunit 5 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ptxE PE=1 SV=1 | 47 | 14718 | 1 | 1 | 7,5 |
| Molybdate-binding periplasmic protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=modB PE=4 SV=1 | 47 | 26436 | 8 | 6 | 21,9 |
| Cystathionine beta-lyase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=metC PE=3 SV=1 | 47 | 43524 | 3 | 3 | 10,1 |
| Probable ABC transporter, ATP-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0723 PE=3 SV=1 | 47 | 60822 | 6 | 5 | 13,3 |
| Aconitate hydratase B OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=acnB PE=3 SV=1 | 757 | 93799 | 39 | 30 | 40,8 |
| Probable ATP-binding component of ABC transporter OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0263 PE=4 SV=1 | 46 | 57819 | 6 | 6 | 11,1 |
| Putative alcohol dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2864 PE=4 SV=1 | 46 | 36945 | 2 | 2 | 9,2 |
| Putative cold-shock protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2757 PE=4 SV=1 | 46 | 8635 | 2 | 2 | 17,3 |
| Putative ABC transporter, ATP-binding subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2178 PE=4 SV=1 | 46 | 33562 | 7 | 5 | 18,2 |
| 7-carboxy-7-deazaguanine synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=queE PE=3 SV=1 | 46 | 22964 | 2 | 2 | 21 |

| | | | | | |
|---|---|---|---|---|---|
| Cytokinin riboside 5~-monophosphate phosphoribohydrolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1253 PE=3 SV=1 | 45 | 22317 | 3 | 2 | 12,4 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3051 PE=4 SV=1 | 45 | 53012 | 2 | 2 | 4 |
| 3-deoxy-D-manno-octulosonic acid transferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=kdtA PE=3 SV=1 | 45 | 45605 | 7 | 6 | 16,4 |
| Phosphate import ATP-binding protein PstB OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=pstB PE=3 SV=3 | 45 | 29228 | 7 | 6 | 22,1 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2862 PE=4 SV=1 | 45 | 13384 | 2 | 2 | 16,4 |
| Putative cyclase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3130 PE=4 SV=1 | 753 | 35848 | 24 | 12 | 51,4 |
| Putative restriction endonuclease OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0204 PE=4 SV=1 | 45 | 37608 | 4 | 4 | 14,1 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2513 PE=4 SV=1 | 45 | 34960 | 5 | 5 | 19,2 |
| Probable TonB-dependent receptor for iron transport OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bfrE PE=3 SV=1 | 45 | 81464 | 5 | 5 | 7,3 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1223 PE=4 SV=1 | 45 | 24815 | 4 | 2 | 11,3 |
| Putative membrane transport ATPase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2722 PE=3 SV=1 | 45 | 81468 | 2 | 2 | 5,1 |
| Anti-sigma factor antagonist OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2226 PE=3 SV=1 | 45 | 12772 | 4 | 3 | 25,9 |
| Conserved hypothetical membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2323 PE=4 SV=1 | 45 | 27311 | 4 | 4 | 24,4 |
| Cardiolipin synthase B OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=clsB PE=3 SV=1 | 45 | 45926 | 5 | 5 | 11 |
| Putative periplasmic solute binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3080 PE=3 SV=1 | 45 | 33389 | 4 | 4 | 11,6 |
| Probable glycosyl transferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bplE PE=4 SV=1 | 44 | 46967 | 8 | 6 | 17,2 |
| Phosphoglucosamine mutase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=glmM PE=3 SV=1 | 751 | 48512 | 24 | 14 | 44,2 |
| tRNA (guanine-N(1)-)-methyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=trmD PE=3 SV=1 | 44 | 27888 | 1 | 1 | 8,6 |
| Putative LysR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2894 PE=3 SV=1 | 44 | 34376 | 1 | 1 | 6,2 |
| Ribose-5-phosphate isomerase A OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpiA PE=3 SV=1 | 44 | 23789 | 5 | 4 | 31,4 |
| Putative glycosyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3144 PE=4 SV=1 | 43 | 40846 | 1 | 1 | 2,6 |
| Putative DNA polymerase III, delta subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=holA PE=4 SV=1 | 43 | 37643 | 6 | 4 | 13,7 |
| Putative phosphoglycolate phosphatase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0941 PE=3 SV=1 | 43 | 24283 | 1 | 1 | 7,1 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2116 PE=4 SV=1 | 43 | 33776 | 3 | 3 | 14,9 |
| DNA helicase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=uvrD PE=3 SV=1 | 42 | 84547 | 3 | 3 | 6,1 |
| Integral membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2586 PE=4 SV=1 | 42 | 38439 | 4 | 3 | 10,8 |
| Putative mechanosensitive channel protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0785 PE=4 SV=1 | 42 | 33962 | 2 | 2 | 7,4 |
| Membrane protein insertase YidC OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=yidC PE=3 SV=1 | 747 | 61706 | 23 | 15 | 46,9 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2652 PE=4 SV=1 | 42 | 17443 | 2 | 2 | 9,6 |
| L-2,4-diaminobutyric acid acetyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ectA PE=3 SV=1 | 42 | 20916 | 3 | 3 | 22,6 |
| AsnC-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0468 PE=4 SV=1 | 42 | 17966 | 6 | 4 | 19,6 |
| tRNA-dihydrouridine(20/20a) synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=dusA PE=3 SV=1 | 42 | 37706 | 2 | 2 | 6,5 |
| Putative regulatory protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3083 PE=3 SV=1 | 42 | 18941 | 2 | 2 | 12,9 |
| Type IV secretion system protein PtlE OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ptlE PE=1 SV=1 | 41 | 25978 | 4 | 3 | 16,3 |
| tRNA pseudouridine synthase B OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=truB PE=3 SV=1 | 41 | 26393 | 4 | 3 | 13,9 |
| Putative transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3482 PE=4 SV=1 | 41 | 28834 | 2 | 2 | 9,1 |
| Putative alcohol dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2820 PE=4 SV=1 | 41 | 39333 | 1 | 1 | 7,6 |
| Putative branched-chain amino acid transport permease OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3573 PE=3 SV=1 | 41 | 35012 | 1 | 1 | 3,1 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0385 PE=4 SV=1 | 745 | 28506 | 29 | 18 | 67,2 |
| Putative transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3064 PE=3 SV=1 | 41 | 36960 | 7 | 7 | 31,6 |

| | | | | | |
|---|---|---|---|---|---|
| Putative DNA-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1798 PE=4 SV=1 | 41 | 18706 | 3 | 2 | 16,5 |
| LysR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0419 PE=3 SV=1 | 41 | 33456 | 1 | 1 | 5,9 |
| Deoxyuridine 5~-triphosphate nucleotidohydrolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=dut PE=3 SV=1 | 41 | 15951 | 5 | 3 | 29,5 |
| Putative type III secretion pore protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bcrD PE=4 SV=1 | 40 | 75611 | 4 | 3 | 4 |
| Putative type III secretion protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bscQ PE=4 SV=1 | 40 | 38072 | 6 | 4 | 13,6 |
| Probable GTP-binding protein EngB OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=engB PE=3 SV=1 | 40 | 22732 | 3 | 3 | 21,7 |
| Succinate-semialdehyde dehydrogenase [NADP+] OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=gabD PE=3 SV=1 | 40 | 52381 | 6 | 5 | 13,1 |
| Bacteriophage-related DNA polymerase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3556 PE=4 SV=1 | 40 | 31497 | 4 | 4 | 12,8 |
| Putative D-amino acid dehydrogenase small subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3009 PE=4 SV=1 | 40 | 45027 | 2 | 2 | 10 |
| Glutamate dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=gdhA PE=3 SV=1 | 740 | 46409 | 24 | 12 | 42 |
| Glutamine transport ATP-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=glnQ PE=4 SV=1 | 40 | 27776 | 4 | 3 | 17,1 |
| Type IV secretion system protein PtlH OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ptlH PE=1 SV=1 | 40 | 37591 | 9 | 5 | 17,1 |
| Probable short-chain dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0813 PE=4 SV=1 | 40 | 28653 | 2 | 2 | 7,7 |
| Probable transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0541 PE=4 SV=1 | 40 | 24988 | 5 | 5 | 22,3 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3586 PE=3 SV=1 | 40 | 30744 | 4 | 4 | 17,7 |
| Putative ferredoxin OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0351 PE=4 SV=1 | 40 | 11935 | 4 | 3 | 23,8 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2037 PE=4 SV=1 | 39 | 10231 | 2 | 2 | 30 |
| N-acetylmuramoyl-L-alanine amidase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=amiC PE=4 SV=1 | 39 | 45531 | 4 | 4 | 12,8 |
| Threonylcarbamoyl-AMP synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1528 PE=3 SV=1 | 39 | 36048 | 3 | 3 | 16,9 |
| UPF0761 membrane protein BP1088 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1088 PE=3 SV=1 | 39 | 47600 | 2 | 2 | 5,5 |
| Site-determining protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=minD PE=3 SV=1 | 739 | 29777 | 29 | 17 | 63,8 |
| Glutamyl-tRNA reductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hemA PE=3 SV=1 | 39 | 46964 | 3 | 3 | 11,1 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0518 PE=4 SV=1 | 39 | 13663 | 1 | 1 | 14,5 |
| Putative DNA-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2589 PE=4 SV=1 | 38 | 18475 | 3 | 3 | 16,1 |
| dTDP-glucose 4,6-dehydratase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rfbB PE=3 SV=1 | 38 | 39337 | 3 | 3 | 9,6 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2865 PE=4 SV=1 | 38 | 15291 | 2 | 2 | 18,1 |
| 50S ribosomal protein L13 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rplM PE=3 SV=1 | 38 | 16037 | 4 | 3 | 19,7 |
| Putative lipoprotein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3544 PE=4 SV=1 | 38 | 34083 | 1 | 1 | 7,7 |
| Phosphoribosyl-ATP pyrophosphatase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hisE PE=3 SV=1 | 38 | 12681 | 2 | 2 | 21,7 |
| Probable periplasmic solute-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0128 PE=4 SV=1 | 38 | 36553 | 6 | 4 | 12,8 |
| UPF0434 protein BP2767 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2767 PE=3 SV=1 | 37 | 6978 | 3 | 3 | 46,8 |
| Protein translocase subunit SecD OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=secD PE=3 SV=1 | 729 | 67801 | 28 | 18 | 38,3 |
| N-acetylmuramoyl-L-alanine amidase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ampD PE=4 SV=1 | 37 | 21609 | 2 | 2 | 9,3 |
| Putative restriction endonuclease OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3117 PE=4 SV=1 | 37 | 117810 | 6 | 6 | 6,6 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0183 PE=4 SV=1 | 37 | 68837 | 4 | 3 | 12,8 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1218 PE=4 SV=1 | 36 | 47990 | 4 | 4 | 10,8 |
| Nitrogen regulation protein NR(II) OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=glnL PE=4 SV=1 | 36 | 39523 | 5 | 5 | 19 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1342 PE=4 SV=1 | 36 | 22720 | 3 | 2 | 17,1 |
| 30S ribosomal protein S12 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpsL PE=3 SV=1 | 36 | 14064 | 4 | 3 | 31,2 |
| Peptide methionine sulfoxide reductase MsrB OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=msrB PE=3 SV=1 | 36 | 15368 | 2 | 2 | 17,3 |

| | | | | | |
|---|---|---|---|---|---|
| Putative periplasmic divalent cation tolerance protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=cutA PE=4 SV=1 | 36 | 12484 | 1 | 1 | 14,2 |
| Large-conductance mechanosensitive channel OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=mscL PE=3 SV=1 | 36 | 16522 | 2 | 2 | 13,8 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2953 PE=4 SV=1 | 729 | 23980 | 19 | 6 | 64,2 |
| Microcystinase C OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2111 PE=3 SV=1 | 35 | 53423 | 4 | 4 | 13,8 |
| RNA pyrophosphohydrolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rppH PE=3 SV=1 | 35 | 22721 | 2 | 2 | 12,6 |
| Phosphatidylserine decarboxylase proenzyme OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=psd PE=3 SV=1 | 35 | 32764 | 2 | 2 | 8,1 |
| Putative monooxygenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3269 PE=4 SV=1 | 35 | 42152 | 7 | 6 | 20,8 |
| Putative transcriptional regulator (MarR family) OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2216 PE=4 SV=1 | 35 | 19474 | 2 | 2 | 12,7 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1257 PE=4 SV=1 | 35 | 58742 | 9 | 7 | 13,4 |
| Probable thiol:disulfide interchange protein DsbC OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=dsbC PE=1 SV=1 | 35 | 30924 | 4 | 4 | 16,5 |
| Putative LysR-family regulatory protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2520 PE=3 SV=1 | 35 | 37942 | 5 | 5 | 14,4 |
| Adenylyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=thiF PE=4 SV=1 | 34 | 28503 | 2 | 2 | 8 |
| Alanine racemase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=alr PE=3 SV=1 | 34 | 41836 | 1 | 1 | 2,6 |
| Chaperone protein ClpB OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=clpB PE=3 SV=1 | 1963 | 96332 | 87 | 50 | 65,7 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0454 PE=4 SV=1 | 722 | 33434 | 20 | 8 | 36,6 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3521 PE=3 SV=1 | 34 | 60512 | 3 | 3 | 5,8 |
| Type IV secretion system protein PtlC OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ptlC PE=1 SV=1 | 34 | 93435 | 2 | 2 | 2,4 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=smf PE=4 SV=1 | 34 | 38906 | 5 | 4 | 12,4 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1815 PE=4 SV=1 | 33 | 32686 | 2 | 2 | 8,3 |
| 50S ribosomal protein L29 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpmC PE=3 SV=1 | 33 | 7094 | 1 | 1 | 11,1 |
| Putative hemin binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bhuT PE=4 SV=1 | 33 | 29658 | 2 | 2 | 9 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1469 PE=4 SV=1 | 33 | 23483 | 1 | 1 | 7,5 |
| Putative acetyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1010 PE=4 SV=1 | 33 | 17676 | 3 | 3 | 18 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3522 PE=4 SV=1 | 33 | 45860 | 1 | 1 | 2,5 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3153 PE=4 SV=1 | 33 | 15461 | 1 | 1 | 7,6 |
| Outer membrane protein A OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ompA PE=3 SV=1 | 714 | 21089 | 31 | 10 | 44 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0816 PE=4 SV=1 | 33 | 36305 | 2 | 2 | 11,1 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0114 PE=4 SV=1 | 33 | 23528 | 5 | 4 | 28,2 |
| Probable transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0727 PE=4 SV=1 | 33 | 29522 | 6 | 3 | 11,4 |
| Probable MarR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0575 PE=4 SV=1 | 32 | 17808 | 10 | 5 | 31 |
| TetR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3679 PE=4 SV=1 | 32 | 23760 | 4 | 4 | 22,4 |
| Probable aminotransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1062 PE=4 SV=1 | 32 | 41580 | 2 | 2 | 6,2 |
| Putative secreted protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bsp22 PE=4 SV=1 | 32 | 22231 | 4 | 4 | 25,4 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2937 PE=3 SV=1 | 32 | 30599 | 5 | 4 | 21,2 |
| Putative ferredoxin OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2173 PE=4 SV=1 | 32 | 55846 | 5 | 4 | 10,5 |
| D-3-phosphoglycerate dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=serA PE=3 SV=1 | 32 | 43014 | 5 | 3 | 8,6 |
| Leucine--tRNA ligase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=leuS PE=3 SV=1 | 712 | 99585 | 30 | 23 | 31,5 |
| Probable heptosyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rfaC PE=4 SV=1 | 32 | 37216 | 3 | 3 | 14,9 |
| dTDP-4-dehydrorhamnose reductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rfbD PE=3 SV=1 | 31 | 32572 | 3 | 3 | 10,4 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1704 PE=4 SV=1 | 31 | 23628 | 1 | 1 | 5,3 |

| | | | | | |
|---|---|---|---|---|---|
| Putative LysR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2416 PE=3 SV=1 | 31 | 35227 | 5 | 5 | 17 |
| Peptide deformylase 1 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=def1 PE=3 SV=1 | 31 | 20097 | 2 | 1 | 6,8 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0077 PE=4 SV=1 | 31 | 9112 | 2 | 2 | 42,2 |
| Histidine kinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3137 PE=4 SV=1 | 31 | 47884 | 6 | 6 | 19,8 |
| Putative AsnC-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1749 PE=4 SV=1 | 31 | 17811 | 3 | 2 | 12,7 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2150 PE=4 SV=1 | 31 | 13358 | 3 | 2 | 11 |
| TetR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3190 PE=4 SV=1 | 31 | 25196 | 2 | 2 | 7 |
| Citrate synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=gltA PE=3 SV=1 | 705 | 48945 | 20 | 13 | 39,7 |
| Gamma-glutamylcyclotransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3250 PE=3 SV=1 | 31 | 25037 | 1 | 1 | 5,5 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0616 PE=4 SV=1 | 31 | 31650 | 1 | 1 | 6,4 |
| Probable aldehyde dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0360 PE=3 SV=1 | 30 | 52181 | 4 | 4 | 12,6 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0570 PE=4 SV=1 | 30 | 23148 | 5 | 5 | 24,6 |
| Putative peptidoglycan-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1746 PE=4 SV=1 | 30 | 44186 | 8 | 7 | 17,8 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2436 PE=4 SV=1 | 30 | 17825 | 1 | 1 | 8,9 |
| Putative inositol monophosphatase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1975 PE=4 SV=1 | 30 | 30500 | 2 | 2 | 9,9 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2006 PE=4 SV=1 | 30 | 17234 | 3 | 3 | 33,5 |
| Putative lipoprotein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1463 PE=3 SV=1 | 30 | 29677 | 5 | 5 | 21,6 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2153 PE=4 SV=1 | 30 | 48060 | 6 | 6 | 15,5 |
| ADP-L-glycero-D-manno-heptose-6-epimerase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hldD PE=3 SV=1 | 703 | 36965 | 21 | 14 | 62 |
| Nitroreductase family protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3845 PE=4 SV=1 | 30 | 27266 | 4 | 3 | 17,6 |
| Putative IIa component of sugar transport PTS system OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1500 PE=4 SV=1 | 30 | 13897 | 5 | 3 | 19,7 |
| Probable ATP-binding component of ABC transporter OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0262 PE=4 SV=1 | 30 | 61367 | 4 | 4 | 8,4 |
| Shikimate dehydrogenase (NADP(+)) OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=aroE PE=3 SV=1 | 29 | 29670 | 2 | 2 | 8 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3391 PE=4 SV=1 | 29 | 8160 | 1 | 1 | 18,6 |
| Cytochrome D ubiquinol oxidase subunit II OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=cydB PE=4 SV=1 | 29 | 41649 | 5 | 4 | 10,9 |
| 7,8-dihydroneopterin aldolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=folB PE=3 SV=1 | 29 | 13753 | 1 | 1 | 11,8 |
| Probable LysR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0135 PE=3 SV=1 | 29 | 34162 | 4 | 4 | 10,5 |
| Succinate dehydrogenase cytochrome B subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=sdhC PE=4 SV=1 | 28 | 14858 | 2 | 1 | 8 |
| Dihydrofolate reductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=folA PE=3 SV=1 | 28 | 17904 | 3 | 3 | 16,8 |
| Lipoprotein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2818 PE=3 SV=1 | 703 | 28725 | 29 | 15 | 58,5 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0819 PE=4 SV=1 | 28 | 35514 | 3 | 3 | 13,3 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bscW PE=4 SV=1 | 28 | 14244 | 2 | 2 | 22 |
| Putative LysR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3133 PE=3 SV=1 | 28 | 33339 | 6 | 6 | 22,5 |
| Type IV secretion system protein PtlA OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ptlA PE=2 SV=1 | 28 | 10863 | 1 | 1 | 8,8 |
| Transcriptional regulatory protein btr OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=btr PE=4 SV=2 | 28 | 27398 | 8 | 7 | 22,7 |
| Putative heme receptor OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hemC PE=3 SV=1 | 28 | 82301 | 5 | 5 | 10,6 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0882 PE=4 SV=1 | 27 | 48528 | 2 | 2 | 3,8 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1894 PE=4 SV=1 | 27 | 18869 | 3 | 3 | 19,4 |
| SURF1-like protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2727 PE=3 SV=1 | 27 | 28244 | 1 | 1 | 3 |
| Putative molybdenum-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2071 PE=4 SV=1 | 27 | 27788 | 2 | 2 | 16,4 |

| | | | | | |
|---|---|---|---|---|---|
| 4-hydroxy-tetrahydrodipicolinate synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=dapA PE=3 SV=1 | 696 | 31128 | 17 | 10 | 50,3 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0770 PE=4 SV=1 | 27 | 20241 | 1 | 1 | 4,8 |
| Leucine-responsive regulatory protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=lrp PE=4 SV=1 | 26 | 18587 | 10 | 7 | 35,2 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0918 PE=4 SV=1 | 26 | 50952 | 2 | 2 | 14,6 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2949 PE=4 SV=1 | 26 | 23568 | 2 | 2 | 19,2 |
| Putative autotransporter OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bapA PE=4 SV=1 | 25 | 91270 | 5 | 5 | 8,1 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2422 PE=4 SV=1 | 25 | 16693 | 2 | 2 | 13,2 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3402 PE=4 SV=1 | 25 | 54233 | 7 | 6 | 17,4 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2609 PE=4 SV=1 | 25 | 49347 | 6 | 5 | 14,4 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3394 PE=4 SV=1 | 25 | 16585 | 1 | 1 | 14,2 |
| Probable sugar transferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bplG PE=4 SV=1 | 25 | 22245 | 4 | 3 | 20,3 |
| Probable class IV aminotransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0103 PE=4 SV=1 | 696 | 32447 | 20 | 12 | 48,8 |
| Phage-related protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0937 PE=4 SV=1 | 24 | 14138 | 2 | 2 | 13,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0202 PE=4 SV=1 | 24 | 35764 | 4 | 4 | 16,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1711 PE=4 SV=1 | 24 | 35780 | 5 | 5 | 22,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0023 PE=4 SV=1 | 24 | 35749 | 4 | 4 | 16,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0676 PE=4 SV=1 | 24 | 35763 | 4 | 4 | 16,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2672 PE=4 SV=1 | 24 | 35724 | 4 | 4 | 16,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2087 PE=4 SV=1 | 24 | 35755 | 4 | 4 | 16,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0080 PE=4 SV=1 | 24 | 35750 | 5 | 5 | 22,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0049 PE=4 SV=1 | 24 | 35710 | 5 | 5 | 22,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0041 PE=4 SV=1 | 24 | 35779 | 4 | 4 | 16,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1134 PE=4 SV=1 | 24 | 35819 | 4 | 4 | 16,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0514 PE=4 SV=1 | 24 | 35790 | 4 | 4 | 16,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0166 PE=4 SV=1 | 24 | 35776 | 4 | 4 | 16,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2214 PE=4 SV=1 | 24 | 35736 | 4 | 4 | 16,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0031 PE=4 SV=1 | 24 | 35737 | 4 | 4 | 16,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0058 PE=4 SV=1 | 24 | 35777 | 4 | 4 | 16,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1080 PE=4 SV=1 | 24 | 35778 | 5 | 5 | 22,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0210 PE=4 SV=1 | 24 | 35739 | 4 | 4 | 16,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0517 PE=4 SV=1 | 24 | 35776 | 5 | 5 | 22,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0365 PE=4 SV=1 | 24 | 35808 | 5 | 5 | 22,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3806 PE=4 SV=1 | 24 | 35737 | 4 | 4 | 16,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3548 PE=4 SV=1 | 24 | 35778 | 5 | 5 | 22,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3478 PE=4 SV=1 | 24 | 35812 | 4 | 4 | 16,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3311 PE=4 SV=1 | 24 | 35791 | 4 | 4 | 16,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3220 PE=4 SV=1 | 24 | 35731 | 5 | 5 | 22,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2763 PE=4 SV=1 | 24 | 35768 | 5 | 5 | 22,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2415 PE=4 SV=1 | 24 | 35719 | 4 | 4 | 16,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2390 PE=4 SV=1 | 24 | 35666 | 4 | 4 | 16,8 |

| | | | | | |
|---|---|---|---|---|---|
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2355 PE=4 SV=1 | 24 | 35767 | 4 | 4 | 16,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2105 PE=4 SV=1 | 24 | 35754 | 4 | 4 | 16,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1911 PE=4 SV=1 | 24 | 35723 | 4 | 4 | 16,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1450 PE=4 SV=1 | 24 | 35709 | 4 | 4 | 16,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1086 PE=4 SV=1 | 24 | 35741 | 5 | 5 | 22,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0897 PE=4 SV=1 | 24 | 35780 | 5 | 5 | 22,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0891 PE=4 SV=1 | 24 | 35729 | 5 | 5 | 22,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0867 PE=4 SV=1 | 24 | 35740 | 5 | 5 | 22,8 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0704 PE=4 SV=1 | 24 | 35759 | 4 | 4 | 17,1 |
| Transposase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0110 PE=4 SV=1 | 24 | 35776 | 5 | 5 | 22,8 |
| N-ethylmaleimide reductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=nemA PE=4 SV=1 | 24 | 39512 | 1 | 1 | 6,5 |
| Putative two component system, histidine kinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2935 PE=4 SV=1 | 24 | 42900 | 2 | 2 | 4,2 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3118 PE=4 SV=1 | 24 | 39183 | 1 | 1 | 5,2 |
| NADH-quinone oxidoreductase subunit J OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=nuoJ PE=3 SV=1 | 23 | 23462 | 2 | 2 | 5,6 |
| Putative 3-oxoacyl-CoA or-ACP reductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2094 PE=4 SV=1 | 23 | 24595 | 1 | 1 | 6,2 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3506 PE=4 SV=1 | 23 | 23565 | 4 | 3 | 22,8 |
| Putative membrane transport protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2716 PE=4 SV=1 | 23 | 49761 | 1 | 1 | 3 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3334 PE=4 SV=1 | 23 | 43426 | 3 | 3 | 10,3 |
| Glutamine--fructose-6-phosphate aminotransferase [isomerizing] OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=glmS PE=3 SV=3 | 693 | 67264 | 29 | 22 | 46,4 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2040 PE=4 SV=1 | 23 | 15435 | 1 | 1 | 6,9 |
| 3-dehydroquinate dehydratase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=aroQ PE=3 SV=1 | 23 | 15376 | 1 | 1 | 10,4 |
| Probable transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0630 PE=4 SV=1 | 22 | 30376 | 2 | 2 | 8,3 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2063 PE=4 SV=1 | 22 | 28648 | 1 | 1 | 4,9 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0237 PE=4 SV=1 | 22 | 33098 | 1 | 1 | 9,1 |
| Putative conserved DNA-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2211 PE=4 SV=1 | 22 | 16342 | 1 | 1 | 8,3 |
| Flagellar hook-associated protein 2 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=fliD PE=3 SV=1 | 22 | 47748 | 7 | 6 | 16,2 |
| Putative cytochrome c oxidase, subunit III OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=coIII PE=3 SV=1 | 21 | 32779 | 1 | 1 | 4,5 |
| Putative membrane transport protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2701 PE=4 SV=1 | 21 | 50328 | 4 | 4 | 11,4 |
| ATP synthase subunit a OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=atpB PE=3 SV=1 | 21 | 32138 | 1 | 1 | 5,5 |
| Serine hydroxymethyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=glyA PE=3 SV=1 | 692 | 44840 | 16 | 12 | 60,7 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2873 PE=4 SV=1 | 21 | 34558 | 1 | 1 | 4,6 |
| Putative transcriptional regulator (MarR family) OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2286 PE=4 SV=1 | 21 | 18092 | 3 | 3 | 22,2 |
| dTTP/UTP pyrophosphatase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2314 PE=3 SV=1 | 21 | 22367 | 2 | 1 | 5,3 |
| Putative integral membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2424 PE=3 SV=1 | 21 | 25075 | 1 | 1 | 5,5 |
| LysR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0650 PE=3 SV=1 | 21 | 35529 | 4 | 4 | 15,3 |
| Putative integral membrane transport protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3062 PE=4 SV=1 | 21 | 49205 | 1 | 1 | 3,5 |
| Putative lipoprotein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0876 PE=4 SV=1 | 21 | 24426 | 1 | 1 | 8 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0642 PE=4 SV=1 | 20 | 41260 | 3 | 1 | 2,1 |
| Probable membrane efflux protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2620 PE=4 SV=1 | 20 | 49158 | 1 | 1 | 1,7 |
| Formamidopyrimidine-DNA glycosylase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=mutM PE=3 SV=3 | 20 | 30838 | 3 | 3 | 15,6 |

| | | | | | |
|---|---|---|---|---|---|
| Malate synthase G OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=glcB PE=3 SV=1 | 1763 | 78812 | 66 | 26 | 55,2 |
| Electron transfer flavoprotein alpha-subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=etfA PE=4 SV=1 | 690 | 31000 | 22 | 7 | 33 |
| Putative iron-sulfur protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2804 PE=4 SV=1 | 20 | 44273 | 3 | 3 | 7,6 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1089 PE=4 SV=1 | 20 | 13457 | 2 | 2 | 15,4 |
| Putative LuxR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1517 PE=4 SV=1 | 20 | 41873 | 4 | 4 | 10,9 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0576 PE=4 SV=1 | 20 | 35956 | 10 | 9 | 26 |
| Autotransporter OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1344 PE=4 SV=1 | 19 | 88998 | 7 | 6 | 8,9 |
| Protease OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=degQ PE=4 SV=1 | 19 | 38982 | 6 | 6 | 15,9 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2895 PE=4 SV=1 | 19 | 34187 | 6 | 5 | 17,1 |
| GntR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1319 PE=4 SV=1 | 19 | 47387 | 5 | 5 | 14,9 |
| Putative outer protein B OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bopB PE=4 SV=1 | 19 | 40512 | 3 | 3 | 7,7 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0064 PE=4 SV=1 | 19 | 21616 | 2 | 2 | 18,7 |
| Threonine--tRNA ligase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=thrS PE=3 SV=1 | 689 | 73791 | 28 | 19 | 36,8 |
| Probable class-I glutamine amidotransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1437 PE=4 SV=1 | 18 | 24738 | 2 | 2 | 22,2 |
| [Fe-S] cluster formation/repair protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=iscA PE=3 SV=1 | 18 | 11789 | 1 | 1 | 18,7 |
| Probable ABC transporter, periplasmic binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0726 PE=4 SV=1 | 18 | 58595 | 6 | 5 | 11,7 |
| Putative dehydratase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2318 PE=4 SV=1 | 18 | 32001 | 1 | 1 | 3,3 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3212 PE=4 SV=1 | 18 | 29107 | 3 | 3 | 7,8 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1211 PE=4 SV=1 | 18 | 28855 | 1 | 1 | 7,9 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3296 PE=4 SV=1 | 17 | 33238 | 1 | 1 | 3 |
| Putative hydrolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2896 PE=4 SV=1 | 17 | 32492 | 1 | 1 | 14,1 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3723 PE=4 SV=1 | 17 | 8369 | 2 | 2 | 62,3 |
| Putative hydrolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2838 PE=4 SV=1 | 17 | 25147 | 5 | 5 | 23,3 |
| 3-oxoacyl-[acyl-carrier-protein] synthase 2 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=fabF PE=3 SV=1 | 681 | 43608 | 44 | 15 | 45,7 |
| Putative transport system periplasmic protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3704 PE=4 SV=1 | 17 | 37797 | 3 | 3 | 17,4 |
| Rubredoxin OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rubA PE=3 SV=1 | 16 | 6470 | 1 | 1 | 16,7 |
| Endolytic peptidoglycan transglycosylase RlpA OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rlpA PE=3 SV=1 | 16 | 32886 | 1 | 1 | 8,2 |
| DNA polymerase III subunit epsilon OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=dnaQ PE=4 SV=1 | 16 | 26604 | 2 | 2 | 12,7 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3808 PE=4 SV=1 | 16 | 32772 | 1 | 1 | 2,4 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1188 PE=4 SV=1 | 16 | 30634 | 4 | 4 | 15 |
| DNA helicase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1980 PE=3 SV=1 | 16 | 77034 | 5 | 3 | 3,6 |
| HipA-like protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hipA PE=4 SV=1 | 16 | 49830 | 4 | 4 | 6,7 |
| Putative GntR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1349 PE=4 SV=1 | 16 | 25184 | 4 | 4 | 20,8 |
| LysR family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3446 PE=3 SV=1 | 16 | 33786 | 6 | 5 | 15,8 |
| Probable D-aminopeptidase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2393 PE=4 SV=1 | 676 | 40389 | 25 | 11 | 41,1 |
| Thiopurine S-methyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=tpm PE=3 SV=1 | 16 | 24902 | 2 | 2 | 9,1 |
| Putative inner membrane component of binding-protein-dependent transport system OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1533 PE=3 SV=1 | 15 | 25488 | 3 | 2 | 7 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3837 PE=4 SV=1 | 15 | 30428 | 4 | 4 | 18,2 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2752 PE=4 SV=1 | 15 | 42817 | 2 | 2 | 3,8 |

| | | | | | |
|---|---|---|---|---|---|
| Putative oxidoreductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3275 PE=4 SV=1 | 15 | 31836 | 4 | 4 | 22,7 |
| Putative glycosyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3143 PE=4 SV=1 | 15 | 40668 | 1 | 1 | 3,7 |
| Putative membrane transport protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2451 PE=4 SV=1 | 15 | 44029 | 1 | 1 | 1,7 |
| NADH-quinone oxidoreductase subunit K OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=nuoK PE=3 SV=1 | 15 | 11220 | 4 | 2 | 14,7 |
| Probable dioxygenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0153 PE=4 SV=1 | 15 | 15750 | 1 | 1 | 11,2 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3497 PE=4 SV=1 | 14 | 23905 | 4 | 4 | 32,1 |
| 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=dapD PE=3 SV=1 | 676 | 29417 | 17 | 10 | 57,5 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3437 PE=4 SV=1 | 14 | 29486 | 4 | 3 | 13,7 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0886 PE=4 SV=1 | 14 | 29598 | 2 | 2 | 13 |
| Putative hemin transport protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bhuS PE=4 SV=1 | 14 | 38336 | 3 | 3 | 12,9 |
| Probable chorismate pyruvate-lyase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ubiC PE=3 SV=1 | 14 | 20978 | 2 | 2 | 12,1 |
| Probable LysR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1242 PE=3 SV=1 | 13 | 33298 | 1 | 1 | 2,6 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2469 PE=4 SV=1 | 13 | 13194 | 3 | 3 | 40,4 |
| Ribose-phosphate pyrophosphokinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=prs PE=3 SV=2 | 591 | 33831 | 17 | 12 | 61,6 |
| Probable short-chain dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2770 PE=3 SV=1 | 672 | 26267 | 23 | 9 | 52,8 |
| Pyruvate kinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=pykA PE=3 SV=1 | 671 | 52791 | 19 | 12 | 42,2 |
| Threonine synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=thrC PE=4 SV=1 | 670 | 50899 | 20 | 15 | 44,4 |
| Putative peptidase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1721 PE=4 SV=1 | 663 | 30089 | 21 | 8 | 59,2 |
| Tol-Pal system protein TolB OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=tolB PE=3 SV=1 | 1740 | 47119 | 54 | 24 | 68,3 |
| 6,7-dimethyl-8-ribityllumazine synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ribH PE=3 SV=1 | 661 | 18536 | 18 | 4 | 48,6 |
| Succinate--CoA ligase [ADP-forming] subunit alpha OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=sucD PE=3 SV=1 | 658 | 30890 | 21 | 7 | 30 |
| Probable zinc-binding dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0800 PE=4 SV=1 | 652 | 33898 | 21 | 11 | 72,9 |
| ATP synthase gamma chain OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=atpG PE=3 SV=1 | 652 | 33348 | 20 | 15 | 59,1 |
| Ribonuclease R OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rnr PE=3 SV=1 | 650 | 92358 | 25 | 24 | 39,3 |
| Autotransporter OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0529 PE=4 SV=1 | 650 | 222792 | 32 | 25 | 19,4 |
| Peptidoglycan-associated protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=pal PE=3 SV=1 | 648 | 17942 | 15 | 6 | 63 |
| Probable acyl-CoA dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1445 PE=3 SV=1 | 645 | 41859 | 17 | 12 | 45,3 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2909 PE=4 SV=1 | 645 | 51438 | 28 | 21 | 47,3 |
| Methionine--tRNA ligase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=metG PE=3 SV=1 | 644 | 76908 | 24 | 19 | 35,1 |
| Chaperone protein HtpG OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=htpG PE=3 SV=1 | 1712 | 71225 | 57 | 30 | 55,7 |
| DNA gyrase subunit A OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=gyrA PE=3 SV=1 | 642 | 99019 | 35 | 28 | 38,6 |
| Triosephosphate isomerase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=tpiA PE=3 SV=1 | 639 | 26030 | 15 | 10 | 53,6 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3761 PE=4 SV=1 | 638 | 22972 | 21 | 6 | 48,8 |
| Fructose-1,6-bisphosphate aldolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=fba PE=3 SV=1 | 638 | 38562 | 25 | 14 | 48,9 |
| Putative aminotransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3571 PE=4 SV=1 | 636 | 31282 | 16 | 10 | 48,7 |
| Histidinol dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hisD PE=3 SV=1 | 634 | 46336 | 21 | 16 | 54,4 |
| Cell division protein ZipA OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3559 PE=3 SV=1 | 634 | 37922 | 22 | 15 | 56 |
| Phosphate-binding protein PstS OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=pstS PE=3 SV=1 | 631 | 36575 | 17 | 13 | 52,6 |
| Aminopeptidase N OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=pepN PE=4 SV=1 | 629 | 100084 | 27 | 24 | 32,4 |
| Putative L-lactate dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ldh PE=3 SV=1 | 629 | 37476 | 19 | 11 | 51,9 |

| | | | | | |
|---|---|---|---|---|---|
| ATP synthase subunit beta OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=atpD PE=3 SV=1 | 1705 | 50670 | 48 | 23 | 73,2 |
| Cell division coordinator CpoB OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=cpoB PE=3 SV=1 | 628 | 24992 | 19 | 6 | 44,1 |
| Putative gamma-glutamyltranspeptidase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3052 PE=4 SV=1 | 164 | 57450 | 6 | 6 | 13,3 |
| Cell division protein FtsA OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ftsA PE=3 SV=1 | 627 | 44360 | 22 | 14 | 42,9 |
| 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hisA PE=3 SV=1 | 625 | 26234 | 20 | 12 | 58,9 |
| CTP synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=pyrG PE=3 SV=1 | 625 | 60848 | 23 | 15 | 36,4 |
| ABC transporter ATP-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3460 PE=3 SV=1 | 130 | 67546 | 9 | 8 | 15,3 |
| Putative ABC transporter ATP-binding subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2397 PE=3 SV=1 | 624 | 69428 | 25 | 17 | 35,2 |
| Carbamoyl-phosphate synthase small chain OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=carA PE=3 SV=1 | 619 | 39573 | 18 | 10 | 48,5 |
| Protein-export protein SecB OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=secB PE=3 SV=1 | 616 | 19127 | 30 | 4 | 56,6 |
| Ribonucleoside-diphosphate reductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=nrdA PE=3 SV=1 | 615 | 108675 | 22 | 19 | 27,3 |
| Glutamate synthase [NADPH] small chain OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3754 PE=4 SV=1 | 613 | 54725 | 24 | 18 | 44,7 |
| 3-oxoacyl-[acyl-carrier-protein] synthase 3 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=fabH PE=3 SV=1 | 611 | 35240 | 17 | 11 | 56,1 |
| DNA-directed RNA polymerase subunit beta OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpoB PE=3 SV=1 | 1695 | 153343 | 81 | 57 | 46,6 |
| Molybdopterin molybdenumtransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=moeA PE=3 SV=1 | 610 | 45608 | 15 | 10 | 45,6 |
| Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=gatB PE=3 SV=1 | 609 | 52414 | 15 | 11 | 32,6 |
| Argininosuccinate synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=argG PE=1 SV=1 | 608 | 49349 | 26 | 17 | 43,6 |
| Formate-dependent phosphoribosylglycinamide formyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=purT PE=3 SV=1 | 604 | 43365 | 20 | 15 | 47,3 |
| Leu/ile/val-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=livJ PE=4 SV=1 | 604 | 39488 | 18 | 8 | 28,6 |
| Transcription termination factor Rho OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rho PE=3 SV=1 | 602 | 47213 | 29 | 20 | 46,7 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2788 PE=4 SV=1 | 602 | 61839 | 19 | 13 | 34,2 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1843 PE=4 SV=1 | 600 | 15962 | 13 | 6 | 65 |
| Putative glutamine-binding periplasmic protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1852 PE=3 SV=1 | 598 | 27136 | 16 | 7 | 29,6 |
| Aromatic-amino-acid aminotransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=tyrB PE=4 SV=1 | 594 | 43403 | 18 | 11 | 40,4 |
| 60 kDa chaperonin OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=groL PE=3 SV=1 | 7757 | 57446 | 239 | 39 | 70 |
| Glycine dehydrogenase (decarboxylating) OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=gcvP PE=3 SV=1 | 1675 | 102811 | 74 | 36 | 48,2 |
| Outer membrane protein assembly factor BamA OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bamA PE=3 SV=1 | 594 | 86470 | 24 | 19 | 36,1 |
| Putative extracellular solute-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3862 PE=4 SV=1 | 588 | 57391 | 27 | 18 | 50,6 |
| Glutathione reductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=gor PE=3 SV=1 | 586 | 49476 | 21 | 13 | 44,7 |
| Anthranilate synthase component II OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=trpG PE=4 SV=1 | 580 | 20476 | 22 | 6 | 75,9 |
| CDP-6-deoxy-L-threo-D-glycero-4-hexulose-3-dehy drase reductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ascD PE=4 SV=1 | 575 | 38367 | 16 | 13 | 58,3 |
| Aspartate-semialdehyde dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=asd PE=3 SV=1 | 574 | 40535 | 16 | 9 | 34 |
| DNA topoisomerase 4 subunit A OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=parC PE=3 SV=1 | 574 | 84504 | 30 | 21 | 33,9 |
| 2-isopropylmalate synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=leuA PE=3 SV=1 | 573 | 63320 | 27 | 20 | 42 |
| 3-hydroxyisobutyrate dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=mmsB PE=3 SV=1 | 571 | 29757 | 18 | 10 | 48,1 |
| Transcription termination/antitermination protein NusA OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=nusA PE=3 SV=1 | 568 | 54977 | 24 | 14 | 31,5 |
| DNA-binding protein Bph2 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bph2 PE=3 SV=1 | 1610 | 11340 | 45 | 8 | 63,8 |
| Acyl carrier protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=acpP PE=3 SV=1 | 565 | 8893 | 16 | 4 | 40,5 |
| Gamma-glutamyltranspeptidase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ggt PE=4 SV=1 | 565 | 62437 | 26 | 16 | 36 |

| | | | | | |
|---|---|---|---|---|---|
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2964 PE=4 SV=1 | 564 | 48489 | 16 | 12 | 37,2 |
| DNA polymerase I OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=polA PE=3 SV=1 | 564 | 99516 | 23 | 22 | 34,1 |
| Putative iron binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1605 PE=1 SV=1 | 561 | 37491 | 21 | 13 | 49,6 |
| Glutamate dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=gdhA PE=3 SV=1 | 560 | 48981 | 20 | 15 | 49,7 |
| Putative gamma-glutamyltranspeptidase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2693 PE=4 SV=1 | 559 | 59184 | 17 | 15 | 35,6 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3128 PE=4 SV=1 | 557 | 68722 | 21 | 18 | 40,8 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1440 PE=4 SV=1 | 554 | 33518 | 28 | 10 | 35,1 |
| Putative oxygenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3131 PE=4 SV=1 | 553 | 62339 | 20 | 13 | 41,9 |
| Superoxide dismutase [Fe] OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=sodB PE=3 SV=2 | 1601 | 21331 | 44 | 12 | 83,3 |
| Cysteine synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=cysM PE=3 SV=1 | 552 | 32240 | 15 | 9 | 46,2 |
| 10 kDa chaperonin OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=groS PE=3 SV=1 | 547 | 10266 | 26 | 7 | 65,3 |
| Protein HflC OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hflC PE=3 SV=1 | 547 | 33412 | 26 | 20 | 51,2 |
| 5-oxoprolinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=oplaH PE=4 SV=1 | 544 | 130360 | 24 | 21 | 22,6 |
| Cytochrome C1 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=petC PE=4 SV=1 | 543 | 31542 | 13 | 8 | 44,7 |
| Thioredoxin reductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=trxB PE=3 SV=1 | 542 | 34437 | 12 | 8 | 50,5 |
| Rod shape-determining protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=mreB PE=4 SV=1 | 539 | 37050 | 18 | 10 | 42,4 |
| Probable acyl-CoA dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0964 PE=3 SV=1 | 538 | 64968 | 15 | 11 | 32,7 |
| GMP synthase [glutamine-hydrolyzing] OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=guaA PE=3 SV=1 | 536 | 58119 | 23 | 16 | 42,5 |
| Chaperone protein HscA homolog OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hscA PE=3 SV=1 | 533 | 65334 | 24 | 14 | 34,2 |
| Aconitate hydratase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=acnA PE=3 SV=1 | 1587 | 98073 | 68 | 28 | 40,6 |
| Single-stranded DNA-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ssb PE=3 SV=1 | 531 | 18146 | 17 | 7 | 64,5 |
| Probable Zinc-binding dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0777 PE=4 SV=1 | 530 | 36314 | 18 | 14 | 56,1 |
| Putative amidase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3321 PE=4 SV=1 | 528 | 46709 | 18 | 13 | 51,4 |
| Probable aminotransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0721 PE=3 SV=1 | 527 | 50837 | 17 | 15 | 46,4 |
| Putative DNA-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=dps PE=3 SV=1 | 527 | 18512 | 25 | 7 | 39,2 |
| Orotate phosphoribosyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=pyrE PE=3 SV=1 | 523 | 23300 | 13 | 9 | 57,6 |
| UDP-N-acetylmuramate--L-alanine ligase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=murC PE=3 SV=1 | 519 | 49557 | 13 | 9 | 30,8 |
| Thioredoxin 1 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=trxA PE=4 SV=1 | 516 | 15400 | 17 | 5 | 47,5 |
| Iron-sulfur cluster carrier protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1467 PE=3 SV=1 | 515 | 38289 | 15 | 10 | 46,6 |
| Iron-sulfur cluster carrier protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0182 PE=3 SV=1 | 408 | 37751 | 12 | 9 | 46,1 |
| Tresponse regulator protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=risA PE=4 SV=1 | 514 | 27779 | 20 | 10 | 46,3 |
| Putative ABC transport solute-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2747 PE=4 SV=1 | 1541 | 40709 | 63 | 18 | 64,8 |
| Putative carbohydrate kinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2993 PE=4 SV=1 | 512 | 33133 | 13 | 10 | 47,6 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3819 PE=4 SV=1 | 510 | 26484 | 20 | 10 | 78,5 |
| Two-component response regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0991 PE=4 SV=1 | 508 | 23152 | 14 | 8 | 48,6 |
| Putative translational inhibitor OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1611 PE=4 SV=1 | 508 | 13295 | 18 | 7 | 88,3 |
| Imidazole glycerol phosphate synthase subunit HisF OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hisF PE=3 SV=1 | 505 | 28475 | 17 | 13 | 68,8 |
| Tryptophan synthase alpha chain OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=trpA PE=3 SV=1 | 503 | 29856 | 16 | 12 | 56,8 |
| ATP-dependent clp protease ATP-binding OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=clpA PE=3 SV=1 | 497 | 84622 | 20 | 19 | 34,8 |
| Outer membrane usher protein FimC OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=fimC PE=3 SV=1 | 492 | 93540 | 20 | 15 | 27,3 |

| | | | | | |
|---|---|---|---|---|---|
| Quinone oxidoreductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=qor PE=4 SV=1 | 491 | 35058 | 19 | 16 | 59,9 |
| GTP-binding elongation factor OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=typA PE=4 SV=1 | 491 | 67660 | 25 | 21 | 41,3 |
| Translation initiation factor IF-2 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=infB PE=3 SV=1 | 1531 | 106209 | 58 | 32 | 51,7 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3689 PE=4 SV=1 | 491 | 19407 | 26 | 11 | 57,4 |
| Succinate dehydrogenase iron-sulfur subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=sdhB PE=3 SV=1 | 490 | 27822 | 27 | 12 | 41,6 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1480 PE=4 SV=1 | 489 | 29129 | 23 | 13 | 58,1 |
| Putative glutathione transferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1300 PE=3 SV=1 | 489 | 26413 | 12 | 8 | 39,9 |
| Thiazole synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=thiG PE=3 SV=1 | 489 | 28318 | 14 | 8 | 36,2 |
| Lysine--tRNA ligase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=lysS PE=3 SV=1 | 488 | 56708 | 22 | 17 | 42,5 |
| Uridylate kinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=pyrH PE=3 SV=1 | 486 | 25593 | 12 | 8 | 45 |
| NAD(P) transhydrogenase, subunit alpha part 1 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=pntaA PE=4 SV=1 | 485 | 39282 | 18 | 13 | 51,9 |
| Putative binding-protein-dependent transport protein (Periplasmic) OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3237 PE=4 SV=1 | 483 | 59026 | 16 | 15 | 43,8 |
| 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=gpmA PE=3 SV=1 | 481 | 28250 | 15 | 10 | 61,2 |
| 2-oxoglutarate dehydrogenase E1 component OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=odhA PE=4 SV=1 | 1522 | 106691 | 56 | 38 | 53,1 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1151 PE=4 SV=1 | 481 | 21633 | 10 | 6 | 48,7 |
| NADP-dependent malic enzyme OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=maeB PE=4 SV=1 | 431 | 82999 | 13 | 12 | 22,4 |
| NADP-dependent malic enzyme OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=maeB PE=4 SV=1 | 477 | 83113 | 14 | 13 | 25,7 |
| Isocitrate dehydrogenase [NADP] OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=icd PE=4 SV=1 | 477 | 45936 | 26 | 16 | 40 |
| Putative carboxy-terminal processing protease OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ctpA PE=3 SV=1 | 477 | 51139 | 16 | 12 | 30,6 |
| Putative ABC transporter ATP-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3034 PE=4 SV=1 | 470 | 66309 | 18 | 13 | 33,6 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3012 PE=4 SV=1 | 470 | 37383 | 19 | 13 | 40,1 |
| Putative pyruvate dehydrogenase E1 beta subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0628 PE=4 SV=1 | 468 | 34793 | 11 | 8 | 41,7 |
| Protein HflK OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hflK PE=3 SV=1 | 468 | 47456 | 23 | 15 | 49,8 |
| 4-aminobutyrate aminotransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=goaG PE=3 SV=1 | 467 | 45059 | 23 | 16 | 47,5 |
| Azurin OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0824 PE=3 SV=1 | 466 | 16134 | 13 | 5 | 45,3 |
| Adhesin OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=fhaL PE=4 SV=1 | 1518 | 438124 | 52 | 41 | 15,4 |
| Phosphomethylpyrimidine synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=thiC PE=3 SV=1 | 460 | 71323 | 16 | 13 | 30,1 |
| Serine--tRNA ligase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=serS PE=3 SV=1 | 460 | 50071 | 15 | 13 | 37,9 |
| Putative 2-hydroxyacid dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2304 PE=4 SV=1 | 460 | 33939 | 14 | 11 | 51 |
| 50S ribosomal protein L4 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rplD PE=3 SV=1 | 459 | 22707 | 15 | 7 | 42 |
| Trk system potassium uptake protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=trkA PE=4 SV=1 | 456 | 50273 | 19 | 12 | 39,4 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3827 PE=4 SV=1 | 453 | 35389 | 20 | 10 | 38,2 |
| Hydroxymethylglutaryl-CoA lyase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hmgcL PE=4 SV=1 | 451 | 32088 | 15 | 10 | 47,7 |
| Glutamyl-tRNA(Gln) amidotransferase subunit A OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=gatA PE=3 SV=1 | 447 | 53669 | 14 | 10 | 35 |
| Acetyl-coenzyme A synthetase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=acsA PE=3 SV=1 | 446 | 72792 | 24 | 17 | 31,7 |
| Efflux pump membrane transporter OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=acrB PE=3 SV=1 | 445 | 113817 | 15 | 10 | 15 |
| Efflux pump membrane transporter OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2076 PE=3 SV=1 | 354 | 115453 | 20 | 15 | 20,1 |
| Anthranilate phosphoribosyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=trpD PE=3 SV=1 | 1497 | 36648 | 43 | 11 | 37,9 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0117 PE=4 SV=1 | 444 | 12752 | 11 | 6 | 60,5 |
| NADH-quinone oxidoreductase subunit F OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=nuoF PE=3 SV=1 | 444 | 50480 | 17 | 14 | 46,4 |

| | | | | | |
|---|---|---|---|---|---|
| Aspartokinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ask PE=3 SV=1 | 443 | 45336 | 20 | 14 | 46,6 |
| S-adenosylmethionine synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=metK PE=3 SV=1 | 443 | 42318 | 17 | 13 | 43,7 |
| Glutamate-1-semialdehyde 2,1-aminomutase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hemL PE=3 SV=1 | 442 | 45101 | 15 | 13 | 38,9 |
| Putative extracellular solute-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3802 PE=4 SV=1 | 440 | 59281 | 19 | 17 | 36,7 |
| LPS-assembly protein LptD OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=lptD PE=3 SV=1 | 440 | 88761 | 16 | 15 | 26,3 |
| RNA polymerase sigma factor RpoD OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpoD PE=3 SV=1 | 439 | 84030 | 22 | 20 | 34,9 |
| Phosphoglycerate kinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=pgk PE=3 SV=1 | 439 | 41210 | 10 | 8 | 26,7 |
| Dihydroorotase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=pyrC PE=3 SV=1 | 439 | 39331 | 15 | 11 | 38,7 |
| Anthranilate synthase component 1 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=trpE PE=3 SV=1 | 1475 | 55574 | 63 | 24 | 62,8 |
| Putative inner membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3326 PE=4 SV=1 | 434 | 26098 | 15 | 11 | 66,5 |
| Putative lipoprotein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2072 PE=4 SV=1 | 432 | 21563 | 12 | 6 | 48 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3481 PE=4 SV=1 | 429 | 37450 | 11 | 9 | 39,1 |
| Phenylalanine--tRNA ligase beta subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=pheT PE=3 SV=1 | 427 | 88515 | 20 | 17 | 28,6 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3599 PE=4 SV=1 | 427 | 24874 | 11 | 7 | 53,1 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0561 PE=4 SV=1 | 426 | 33634 | 15 | 11 | 40,5 |
| Uracil phosphoribosyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=upp PE=3 SV=1 | 425 | 23012 | 15 | 8 | 55,9 |
| Putative hydrolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3857 PE=4 SV=1 | 425 | 43496 | 15 | 9 | 41,6 |
| Putative hydrolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3036 PE=4 SV=1 | 251 | 42666 | 6 | 6 | 26,2 |
| Fumarate hydratase class II OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=fumC PE=3 SV=1 | 424 | 49589 | 14 | 12 | 42,1 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0782 PE=4 SV=1 | 424 | 39928 | 12 | 10 | 35,3 |
| BrkA autotransporter OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=brkA PE=1 SV=1 | 3945 | 103372 | 130 | 32 | 53,5 |
| Protein translocase subunit SecA OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=secA PE=3 SV=1 | 1439 | 103465 | 66 | 39 | 53,9 |
| Branched-chain-amino-acid aminotransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ilvE PE=3 SV=1 | 421 | 33817 | 16 | 11 | 50 |
| Biotin carboxylase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=fabG PE=4 SV=1 | 420 | 50045 | 18 | 15 | 44,4 |
| p-protein [includes: chorismate mutase and prephenate dehydratase] OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=pheA PE=4 SV=1 | 419 | 39218 | 16 | 10 | 51,8 |
| Dihydroorotate dehydrogenase (quinone) OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=pyrD PE=3 SV=1 | 419 | 37208 | 15 | 10 | 44,4 |
| RNA polymerase-binding transcription factor DksA OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=dksA PE=3 SV=1 | 419 | 17620 | 10 | 7 | 74 |
| Porphobilinogen deaminase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hemC PE=3 SV=1 | 419 | 33465 | 14 | 10 | 41,1 |
| Bacterioferritin OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bfr PE=3 SV=1 | 418 | 18371 | 21 | 5 | 46,8 |
| 30S ribosomal protein S11 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpsK PE=3 SV=1 | 418 | 14040 | 16 | 7 | 67,7 |
| Conserved ATP-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2307 PE=4 SV=1 | 417 | 57247 | 15 | 13 | 28,6 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1887 PE=1 SV=1 | 416 | 35622 | 34 | 13 | 34,6 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0589 PE=3 SV=1 | 53 | 40471 | 5 | 4 | 14,4 |
| Putative periplasmic solute-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=smoM PE=3 SV=1 | 1432 | 40224 | 46 | 19 | 70,3 |
| ATP-dependent protease ATPase subunit HslU OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hslU PE=3 SV=1 | 416 | 49671 | 20 | 16 | 35,4 |
| Putative acetolactate synthase large subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ilvG PE=3 SV=1 | 414 | 61085 | 15 | 11 | 33,5 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3320 PE=4 SV=1 | 414 | 21464 | 18 | 9 | 74,5 |
| Putative solute-binding periplasmic protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3572 PE=4 SV=1 | 413 | 36781 | 13 | 9 | 42,5 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1057 PE=4 SV=1 | 409 | 11574 | 10 | 2 | 22,9 |
| NADH-quinone oxidoreductase subunit D OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=nuoD PE=3 SV=1 | 406 | 47713 | 17 | 14 | 45,5 |

| | | | | | |
|---|---|---|---|---|---|
| Stringent starvation protein A OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=sspA PE=4 SV=1 | 398 | 23997 | 16 | 8 | 46,8 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1358 PE=4 SV=1 | 397 | 34330 | 17 | 10 | 45 |
| Putative aminohydrolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3063 PE=4 SV=1 | 397 | 37806 | 15 | 9 | 45,4 |
| L-lactate dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=lldD PE=3 SV=1 | 396 | 42388 | 16 | 13 | 43,9 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0250 PE=1 SV=1 | 1420 | 34627 | 49 | 18 | 60,6 |
| Glutamine synthetase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=glnA PE=3 SV=1 | 395 | 52122 | 20 | 14 | 45,5 |
| Tryptophan synthase beta chain OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=trpB PE=3 SV=1 | 395 | 43714 | 18 | 14 | 58,4 |
| Putative ABC transport protein, substrate-binding component OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2418 PE=4 SV=1 | 394 | 43194 | 17 | 9 | 27,2 |
| Branched-chain amino acid-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1948 PE=4 SV=1 | 393 | 44392 | 13 | 10 | 35,8 |
| Probable chromosome partitioning protein ParB OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=parB PE=3 SV=1 | 393 | 32667 | 12 | 9 | 42 |
| Putative sugar transport protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2549 PE=4 SV=1 | 392 | 60588 | 12 | 5 | 15,6 |
| Homoserine dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2784 PE=3 SV=1 | 392 | 46368 | 13 | 9 | 29 |
| 50S ribosomal protein L10 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rplJ PE=3 SV=1 | 391 | 18474 | 13 | 8 | 67,8 |
| Fructose-1,6-bisphosphatase class 1 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=fbp PE=3 SV=1 | 391 | 37345 | 9 | 7 | 29,2 |
| Probable short chain dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1103 PE=4 SV=1 | 390 | 26156 | 10 | 9 | 43,8 |
| Glyceraldehyde-3-phosphate dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=gap PE=3 SV=1 | 1401 | 36433 | 44 | 15 | 64 |
| Tyrosine--tRNA ligase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=tyrS PE=3 SV=1 | 389 | 45112 | 18 | 13 | 44,5 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2471 PE=4 SV=1 | 389 | 48951 | 15 | 10 | 37 |
| Diaminopimelate decarboxylase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=lysA PE=3 SV=1 | 389 | 46643 | 12 | 10 | 28,9 |
| Protein GrpE OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=grpE PE=3 SV=1 | 384 | 19613 | 15 | 7 | 72,3 |
| Acetylornithine aminotransferase 1 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=argD1 PE=3 SV=1 | 383 | 41640 | 15 | 12 | 45,3 |
| Thiol:disulfide interchange protein DsbD OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=dsbD PE=3 SV=1 | 383 | 67555 | 8 | 6 | 11,6 |
| 4-hydroxy-3-methylbut-2-enyl diphosphate reductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ispH PE=3 SV=1 | 383 | 34740 | 10 | 7 | 33,5 |
| 30S ribosomal protein S16 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpsP PE=3 SV=1 | 382 | 9579 | 10 | 4 | 53,5 |
| 50S ribosomal protein L19 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rplS PE=3 SV=1 | 381 | 13938 | 11 | 7 | 70,6 |
| Argininosuccinate lyase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=argH PE=3 SV=1 | 380 | 52314 | 19 | 15 | 34,2 |
| DNA topoisomerase iii OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=topB PE=4 SV=1 | 1382 | 97100 | 50 | 41 | 54,5 |
| Polyphosphate kinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ppk PE=3 SV=1 | 378 | 78553 | 18 | 16 | 30,2 |
| Enoly-CoA hydratase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1446 PE=4 SV=1 | 375 | 42412 | 20 | 14 | 44,6 |
| Pyrroline-5-carboxylate reductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=proC PE=3 SV=1 | 373 | 28640 | 15 | 9 | 57,8 |
| Probable septum site-determining protein MinC OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=minC PE=3 SV=1 | 373 | 30741 | 12 | 9 | 46,6 |
| Putative ABC transport protein, ATP-binding component OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2743 PE=4 SV=1 | 372 | 26147 | 11 | 10 | 46,9 |
| Enoyl-[acyl-carrier-protein] reductase [NADH] OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=fabI PE=3 SV=1 | 372 | 27697 | 14 | 12 | 49 |
| 50S ribosomal protein L2 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rplB PE=3 SV=1 | 371 | 30341 | 13 | 8 | 34,5 |
| UPF0246 protein BP2452 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2452 PE=3 SV=1 | 370 | 28689 | 13 | 7 | 41,2 |
| Beta sliding clamp OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=dnaN PE=3 SV=1 | 370 | 41288 | 15 | 10 | 31,2 |
| Ferric uptake regulation protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=fur PE=3 SV=1 | 368 | 15946 | 14 | 5 | 48,9 |
| Carbamoyl-phosphate synthase large chain OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=carB PE=3 SV=1 | 1361 | 118808 | 48 | 35 | 48,3 |
| ATP-dependent Clp protease proteolytic subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=clpP PE=3 SV=1 | 368 | 23817 | 14 | 6 | 30 |
| Protein-methionine-sulfoxide reductase catalytic subunit MsrP OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=msrP PE=3 SV=1 | 366 | 35696 | 17 | 12 | 47,3 |

| | | | | | |
|---|---|---|---|---|---|
| ATP phosphoribosyltransferase regulatory subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hisZ PE=3 SV=1 | 366 | 42001 | 18 | 15 | 48,8 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0663 PE=4 SV=1 | 366 | 32297 | 14 | 10 | 40,7 |
| 50S ribosomal protein L25 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rplY PE=3 SV=1 | 365 | 22292 | 11 | 6 | 41,3 |
| Thymidylate synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=thyA PE=3 SV=1 | 365 | 36576 | 8 | 5 | 22,6 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1722 PE=4 SV=1 | 364 | 29673 | 13 | 11 | 48,6 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0279 PE=4 SV=1 | 363 | 27923 | 14 | 10 | 61,6 |
| Molybdopterin molybdenumtransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=moeA PE=3 SV=1 | 363 | 42666 | 10 | 7 | 33,7 |
| ATP phosphoribosyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hisG PE=3 SV=1 | 363 | 24056 | 13 | 9 | 50,2 |
| Periplasmic serine endoprotease DegP-like OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=mucD PE=3 SV=1 | 1330 | 52102 | 39 | 16 | 42,6 |
| 50S ribosomal protein L9 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rplI PE=3 SV=1 | 362 | 16373 | 19 | 9 | 54,3 |
| Holliday junction ATP-dependent DNA helicase RuvB OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ruvB PE=3 SV=1 | 362 | 39023 | 11 | 10 | 44 |
| Oligopeptidase A OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=prlC PE=3 SV=1 | 361 | 76438 | 14 | 12 | 27,1 |
| RNA-binding protein Hfq OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hfq PE=3 SV=1 | 361 | 8808 | 10 | 6 | 82,1 |
| Chaperone protein DnaJ OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=dnaJ PE=3 SV=1 | 355 | 41700 | 16 | 13 | 45,5 |
| ABC-transport protein, solute-binding component OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2692 PE=4 SV=1 | 353 | 55909 | 14 | 10 | 29,9 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3013 PE=4 SV=1 | 353 | 26605 | 9 | 8 | 48,5 |
| Cysteine--tRNA ligase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=cysS PE=3 SV=1 | 353 | 53413 | 13 | 9 | 29,8 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1845 PE=4 SV=1 | 349 | 35382 | 10 | 8 | 37,3 |
| Ribosomal RNA small subunit methyltransferase H OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rsmH PE=3 SV=1 | 349 | 39013 | 14 | 11 | 40,7 |
| ATP synthase subunit alpha OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=atpA PE=3 SV=1 | 1321 | 55558 | 45 | 26 | 45,8 |
| ParA family protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=parA PE=4 SV=1 | 348 | 29064 | 11 | 11 | 46,8 |
| Putative outer protein D OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bopD PE=4 SV=1 | 348 | 31820 | 12 | 9 | 44,7 |
| ADP-dependent (S)-NAD(P)H-hydrate dehydratase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=nnrD PE=3 SV=1 | 347 | 28926 | 11 | 7 | 54,7 |
| Probable enoyl-CoA hydratase/isomerase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0627 PE=4 SV=1 | 347 | 28043 | 11 | 7 | 35,6 |
| Thiol:disulfide interchange protein DsbA OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=dsbA PE=1 SV=1 | 347 | 22884 | 15 | 7 | 42,6 |
| Putative glycerol-3-phosphate dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2644 PE=4 SV=1 | 346 | 57245 | 13 | 11 | 31,3 |
| Chaperone SurA OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=surA PE=3 SV=1 | 345 | 56822 | 21 | 15 | 38 |
| Phenylalanine--tRNA ligase alpha subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=pheS PE=3 SV=1 | 223 | 39263 | 12 | 11 | 36,8 |
| 3-isopropylmalate dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=leuB PE=3 SV=1 | 344 | 38590 | 14 | 10 | 31 |
| Putative AMP-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2377 PE=4 SV=1 | 343 | 62593 | 17 | 15 | 37,8 |
| Acetyltransferase component of pyruvate dehydrogenase complex OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=aceF PE=3 SV=1 | 1315 | 57264 | 39 | 21 | 60,4 |
| Dihydrolipoyl dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=lpdA PE=3 SV=1 | 1239 | 62566 | 48 | 29 | 52,5 |
| Putative glutathione S-transferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3659 PE=4 SV=1 | 343 | 24375 | 12 | 9 | 50,7 |
| Putative sigma factor regulatory protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=mucB PE=4 SV=1 | 343 | 39358 | 16 | 12 | 39,8 |
| 30S ribosomal protein S8 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpsH PE=3 SV=1 | 343 | 14309 | 13 | 7 | 56,5 |
| Integrase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0502 PE=4 SV=1 | 342 | 37619 | 18 | 13 | 38 |
| Glutamine-dependent NAD(+) synthetase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=nadE PE=3 SV=1 | 342 | 59453 | 12 | 10 | 30,1 |
| Ribonucleoside-diphosphate reductase subunit beta OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=nrdB PE=3 SV=1 | 342 | 45538 | 12 | 11 | 41,5 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0664 PE=4 SV=1 | 340 | 35891 | 13 | 10 | 32,4 |
| UDP-3-O-acylglucosamine N-acyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=lpxD PE=3 SV=1 | 340 | 37930 | 12 | 10 | 38,6 |

| | | | | | |
|---|---|---|---|---|---|
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1900 PE=4 SV=1 | 339 | 34558 | 12 | 9 | 34,5 |
| Methionine synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=metH PE=4 SV=1 | 338 | 138893 | 19 | 18 | 17,4 |
| Glutamate synthase [NADPH] large chain OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=gltB PE=4 SV=1 | 1308 | 173540 | 62 | 44 | 39,3 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3605 PE=4 SV=1 | 338 | 28442 | 14 | 11 | 54,7 |
| Probable two-component histidine kinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1092 PE=4 SV=1 | 337 | 105220 | 15 | 14 | 19,3 |
| Putative mandelate racemase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1359 PE=3 SV=1 | 337 | 42079 | 13 | 10 | 38,8 |
| 33 kDa chaperonin OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hslO PE=3 SV=1 | 337 | 33829 | 8 | 6 | 41,8 |
| Adenylate kinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=adk PE=3 SV=1 | 337 | 23829 | 11 | 10 | 65,1 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1838 PE=4 SV=1 | 336 | 20347 | 17 | 9 | 60,1 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0116 PE=4 SV=1 | 331 | 13894 | 5 | 4 | 53,2 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3441 PE=4 SV=1 | 330 | 19819 | 8 | 6 | 52,6 |
| Serotype 2 fimbrial subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=fim2 PE=3 SV=1 | 330 | 22107 | 10 | 6 | 48,3 |
| Glucose-6-phosphate isomerase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=pgi PE=3 SV=1 | 330 | 57356 | 16 | 11 | 31,5 |
| Chaperone protein DnaK OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=dnaK PE=3 SV=1 | 3451 | 69720 | 110 | 42 | 67,4 |
| NADH-quinone oxidoreductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=nuoG PE=3 SV=1 | 1298 | 81931 | 36 | 22 | 39,5 |
| Putative electron transfer flavoprotein-ubiquinone oxidoreductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2403 PE=4 SV=1 | 328 | 59322 | 14 | 12 | 33 |
| Acetylglutamate kinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=argB PE=3 SV=1 | 328 | 31792 | 13 | 9 | 31,3 |
| Orotidine 5~-phosphate decarboxylase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=pyrF PE=3 SV=1 | 328 | 29630 | 11 | 10 | 57,1 |
| Putative mannose-6-phosphate isomerase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=pmi PE=4 SV=1 | 327 | 42205 | 11 | 6 | 25,9 |
| Capsular polysaccharide biosynthesis protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=wbpP PE=4 SV=1 | 326 | 37589 | 18 | 14 | 41,6 |
| Putative amidohydrolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2301 PE=4 SV=1 | 326 | 45239 | 12 | 10 | 36 |
| Amino-acid acetyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=argA PE=3 SV=1 | 326 | 51164 | 12 | 9 | 23,8 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3037 PE=4 SV=1 | 324 | 10182 | 13 | 4 | 47,8 |
| Putative D-isomer specific 2-hydroxyacid dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3543 PE=3 SV=1 | 324 | 33949 | 12 | 9 | 43,8 |
| Peptidyl-prolyl cis-trans isomerase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ppiB PE=3 SV=1 | 324 | 18554 | 17 | 7 | 52,1 |
| Succinate--CoA ligase [ADP-forming] subunit beta OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=sucC PE=3 SV=1 | 1285 | 41141 | 40 | 18 | 53,4 |
| Putative toxin OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1251 PE=4 SV=1 | 323 | 26755 | 9 | 6 | 57,7 |
| NADPH-dependent 7-cyano-7-deazaguanine reductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=queF PE=3 SV=1 | 322 | 30830 | 9 | 7 | 39,9 |
| Putative hydrolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2810 PE=4 SV=1 | 322 | 43628 | 15 | 11 | 33,7 |
| 50S ribosomal protein L14 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rplN PE=3 SV=1 | 321 | 13285 | 13 | 9 | 54,1 |
| Putative oxidoreductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2454 PE=4 SV=1 | 320 | 26599 | 7 | 5 | 33,1 |
| 2-dehydropantoate 2-reductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1360 PE=3 SV=1 | 320 | 31779 | 12 | 7 | 29,8 |
| Transcriptional repressor NrdR OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=nrdR PE=3 SV=1 | 319 | 18327 | 7 | 5 | 41,2 |
| 30S ribosomal protein S3 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpsC PE=3 SV=1 | 318 | 29438 | 14 | 8 | 40,7 |
| Putative ATP-binding component of ABC transporter OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1534 PE=4 SV=1 | 60 | 28195 | 6 | 6 | 30 |
| Putative amino acid ABC transporter ATP-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3828 PE=4 SV=1 | 318 | 28254 | 17 | 9 | 43,5 |
| Glutamine--tRNA ligase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=glnS PE=3 SV=1 | 318 | 66999 | 19 | 16 | 35,6 |
| Virulence factors putative positive transcription regulator BvgA OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bvgA PE=1 SV=1 | 1282 | 23051 | 46 | 15 | 81,8 |
| Homogentisate 1,2-dioxygenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hmgA PE=3 SV=1 | 315 | 48301 | 12 | 11 | 36,1 |
| D-alanine--D-alanine ligase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ddl PE=3 SV=1 | 315 | 33765 | 12 | 9 | 40,5 |

| | | | | | |
|---|---|---|---|---|---|
| Methionyl-tRNA formyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=fmt PE=3 SV=1 | 315 | 32823 | 14 | 11 | 48,1 |
| Translation initiation factor IF-3 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=infC PE=3 SV=1 | 315 | 18794 | 8 | 4 | 39 |
| Putative two-component sensor kinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0571 PE=4 SV=1 | 315 | 83472 | 13 | 12 | 21,1 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3752 PE=4 SV=1 | 314 | 27619 | 11 | 5 | 49,6 |
| Probable aminotransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0559 PE=4 SV=1 | 313 | 44681 | 7 | 6 | 26,2 |
| Putative universal stress protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0410 PE=4 SV=1 | 311 | 16449 | 10 | 4 | 48,1 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1601 PE=3 SV=1 | 309 | 32621 | 11 | 8 | 47,2 |
| 30S ribosomal protein S4 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpsD PE=3 SV=1 | 309 | 23465 | 11 | 8 | 40,6 |
| Elongation factor Ts OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=tsf PE=3 SV=1 | 1277 | 30999 | 45 | 17 | 58,2 |
| 50S ribosomal protein L22 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rplV PE=3 SV=1 | 308 | 11832 | 7 | 5 | 45,9 |
| Haloacid dehalogenase-like hydrolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3483 PE=4 SV=1 | 307 | 29105 | 9 | 7 | 34 |
| Inositol-1-monophosphatase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=suhB PE=3 SV=1 | 306 | 28443 | 10 | 8 | 26,2 |
| Glutaryl-CoA dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=gcdH PE=3 SV=1 | 306 | 43616 | 14 | 7 | 30,2 |
| Nitrogen regulatory IIA protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpoP PE=4 SV=1 | 306 | 16297 | 7 | 5 | 45 |
| Methionine aminopeptidase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=map PE=3 SV=1 | 305 | 30031 | 16 | 11 | 57,9 |
| UTP--glucose-1-phosphate uridylyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3403 PE=3 SV=1 | 305 | 32634 | 10 | 6 | 26,2 |
| dCTP deaminase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=dcd PE=3 SV=1 | 304 | 21215 | 14 | 9 | 65,2 |
| Probable oxidoreductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0900 PE=4 SV=1 | 304 | 29536 | 14 | 9 | 53,8 |
| Putative NADH dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ndh PE=4 SV=1 | 304 | 47750 | 15 | 12 | 32,6 |
| Lon protease OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=lon PE=2 SV=1 | 1259 | 90507 | 51 | 34 | 42,4 |
| Putative integral membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2959 PE=4 SV=1 | 301 | 26623 | 12 | 9 | 51,6 |
| Poly-beta-hydroxybutyrate polymerase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=phbC PE=4 SV=1 | 301 | 60324 | 12 | 11 | 28,4 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2751 PE=4 SV=1 | 301 | 60122 | 25 | 20 | 50,6 |
| Outer-membrane lipoprotein LolB OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=lolB PE=3 SV=1 | 301 | 21479 | 6 | 4 | 34,2 |
| Tryptophan--tRNA ligase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=trpS PE=3 SV=1 | 300 | 49551 | 10 | 10 | 29,7 |
| Glutamate 5-kinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=proB PE=3 SV=2 | 300 | 40495 | 9 | 9 | 31,7 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2534 PE=4 SV=1 | 299 | 57842 | 13 | 10 | 25,4 |
| DNA topoisomerase 4 subunit B OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=parE PE=3 SV=1 | 299 | 71556 | 18 | 17 | 36 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1506 PE=4 SV=1 | 299 | 40769 | 16 | 8 | 31,1 |
| GTPase Der OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=der PE=3 SV=1 | 298 | 49397 | 15 | 12 | 30,2 |
| Malate dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=mdh PE=3 SV=1 | 1253 | 35699 | 41 | 17 | 57,8 |
| Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=accA PE=3 SV=1 | 298 | 35843 | 15 | 10 | 35,2 |
| Putative regulatory lipoprotein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2271 PE=4 SV=1 | 296 | 47455 | 19 | 12 | 35,5 |
| L-threonine dehydratase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ilvA PE=3 SV=1 | 296 | 55555 | 18 | 15 | 37,8 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0169 PE=4 SV=1 | 296 | 23233 | 9 | 8 | 45,9 |
| Phosphoribosylaminoimidazole-succinocarboxamide synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=purC PE=3 SV=1 | 296 | 32402 | 15 | 10 | 38,6 |
| Universal stress family protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1315 PE=4 SV=1 | 295 | 15240 | 8 | 5 | 43,3 |
| Putative lipoprotein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=pcp PE=4 SV=1 | 295 | 16577 | 9 | 5 | 48,5 |
| 3-isopropylmalate dehydratase large subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=leuC PE=3 SV=1 | 294 | 51085 | 14 | 11 | 31 |
| DNA repair protein RecN OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2506 PE=3 SV=1 | 294 | 59775 | 13 | 11 | 28,8 |

| | | | | | |
|---|---|---|---|---|---|
| Putative membrane-bound transglycolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3268 PE=4 SV=1 | 293 | 47001 | 9 | 9 | 31,5 |
| Tracheal colonization factor OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=tcfA PE=4 SV=1 | 1252 | 66310 | 70 | 21 | 54,7 |
| Phenylacetate-coenzyme A ligase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=paaK PE=3 SV=1 | 293 | 48437 | 10 | 6 | 18,3 |
| 30S ribosomal protein S6 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpsF PE=3 SV=1 | 293 | 14325 | 13 | 6 | 73 |
| Coenzyme A biosynthesis bifunctional protein CoaBC OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=dfp PE=3 SV=1 | 291 | 42683 | 10 | 8 | 27,4 |
| Transaldolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=tal PE=3 SV=1 | 290 | 35003 | 13 | 11 | 44,1 |
| 1-deoxy-D-xylulose-5-phosphate synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=dxs PE=3 SV=1 | 290 | 66504 | 9 | 9 | 20,8 |
| Indole-3-glycerol phosphate synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=trpC PE=3 SV=1 | 289 | 28715 | 22 | 13 | 43,5 |
| Phosphoribosylformylglycinamidine synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=purL PE=3 SV=1 | 289 | 145427 | 18 | 16 | 18,8 |
| Nucleotide-binding protein BP0690 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0690 PE=3 SV=1 | 288 | 32725 | 13 | 9 | 42,8 |
| ADP-heptose synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rfaE PE=4 SV=1 | 287 | 33802 | 14 | 11 | 51,1 |
| Putative ferredoxin--NADP reductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3581 PE=4 SV=1 | 287 | 29778 | 13 | 11 | 46 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2068 PE=4 SV=1 | 1232 | 33690 | 29 | 15 | 51,5 |
| Putative binding-protein-dependent transport permease OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2395 PE=3 SV=1 | 287 | 33851 | 6 | 4 | 17,3 |
| tRNA modification GTPase MnmE OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=mnmE PE=3 SV=1 | 287 | 49069 | 12 | 8 | 23,8 |
| Lipoprotein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2750 PE=4 SV=1 | 286 | 23397 | 9 | 6 | 39,2 |
| Putrescine-binding periplasmic protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2348 PE=3 SV=1 | 285 | 41056 | 14 | 9 | 34,6 |
| DNA ligase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ligA PE=3 SV=1 | 285 | 75825 | 13 | 13 | 24 |
| 50S ribosomal protein L24 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rplX PE=3 SV=1 | 285 | 11339 | 11 | 8 | 61,3 |
| Methylglyoxal synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1806 PE=3 SV=1 | 285 | 32879 | 9 | 7 | 32 |
| Glycerol-3-phosphate dehydrogenase [NAD(P)+] OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=gpsA PE=3 SV=1 | 285 | 35984 | 7 | 6 | 31,3 |
| Putative transferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2187 PE=4 SV=1 | 284 | 20530 | 10 | 6 | 53,6 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2924 PE=4 SV=1 | 284 | 10194 | 8 | 2 | 24,5 |
| Antioxidant protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0965 PE=4 SV=1 | 1219 | 23819 | 43 | 15 | 62,9 |
| Hydroxyacylglutathione hydrolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=gloB PE=3 SV=1 | 283 | 28803 | 10 | 8 | 41,4 |
| 50S ribosomal protein L6 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rplF PE=3 SV=1 | 283 | 19217 | 13 | 8 | 53,1 |
| Protein RecA OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=recA PE=3 SV=1 | 283 | 38040 | 16 | 11 | 41,9 |
| 50S ribosomal protein L11 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rplK PE=3 SV=1 | 283 | 14904 | 9 | 6 | 38,5 |
| Signal peptidase I OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=lep PE=3 SV=1 | 283 | 33793 | 7 | 6 | 21,4 |
| Sugar ABC transporter, ATP-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0122 PE=3 SV=1 | 280 | 37268 | 10 | 7 | 36,7 |
| 3~,5~-cyclic adenosine monophosphate phosphodiesterase CpdA OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=cpdA PE=3 SV=1 | 279 | 29785 | 9 | 5 | 33 |
| ATP-dependent zinc metalloprotease FtsH OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ftsH PE=3 SV=1 | 279 | 69073 | 8 | 8 | 18,5 |
| ATP-dependent Clp protease ATP-binding subunit ClpX OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=clpX PE=3 SV=1 | 278 | 47477 | 13 | 9 | 32,7 |
| ATP synthase subunit delta OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=atpH PE=3 SV=1 | 278 | 19387 | 10 | 7 | 53,1 |
| Putative exported solute binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2963 PE=3 SV=1 | 1198 | 40405 | 36 | 16 | 49,3 |
| Putative ABC transporter, ATP-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1986 PE=3 SV=1 | 278 | 60459 | 14 | 11 | 25,8 |
| Prephenate dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=tyrA PE=4 SV=1 | 276 | 31307 | 8 | 7 | 34,8 |
| Putative oxidoreductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3139 PE=4 SV=1 | 276 | 49961 | 7 | 5 | 28,2 |
| Probable ATP-dependent RNA helicase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=dbpA PE=3 SV=1 | 276 | 50971 | 13 | 11 | 32,9 |
| 2-dehydro-3-deoxyphosphooctonate aldolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=kdsA PE=3 SV=1 | 276 | 30872 | 8 | 6 | 31,2 |

| | | | | | |
|---|---|---|---|---|---|
| Guanylate kinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=gmk PE=3 SV=2 | 245 | 23780 | 13 | 8 | 52,1 |
| Putative aminotransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2785 PE=4 SV=1 | 275 | 44447 | 17 | 11 | 37 |
| DNA mismatch repair protein MutS OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=mutS PE=3 SV=1 | 274 | 96529 | 12 | 12 | 19,6 |
| Phosphoribosylamine--glycine ligase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=purD PE=3 SV=1 | 274 | 47678 | 10 | 6 | 22,9 |
| Putative lipoprotein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2564 PE=4 SV=1 | 274 | 15556 | 7 | 4 | 29,9 |
| Putative outer membrane ligand binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bipA PE=4 SV=1 | 3422 | 137111 | 120 | 52 | 54,6 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3575 PE=4 SV=1 | 1191 | 43273 | 32 | 13 | 41,1 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2755 PE=4 SV=1 | 273 | 189093 | 18 | 16 | 13,4 |
| Lipoprotein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1189 PE=4 SV=1 | 273 | 15732 | 7 | 4 | 54,9 |
| Putative haloacid-type dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2017 PE=4 SV=1 | 272 | 27076 | 9 | 5 | 32 |
| Putative acetolactate synthase large subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ilvB PE=3 SV=1 | 270 | 60049 | 14 | 10 | 30,1 |
| Putative binding-protein-dependent transport periplasmic protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2396 PE=4 SV=1 | 268 | 57572 | 14 | 11 | 35 |
| Chorismate synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=aroC PE=3 SV=1 | 268 | 37566 | 10 | 7 | 35,7 |
| 23S rRNA (uracil(1939)-C(5))-methyltransferase RlmD OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rlmD PE=3 SV=1 | 267 | 51549 | 13 | 11 | 28,8 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2977 PE=4 SV=1 | 267 | 89183 | 12 | 12 | 21,4 |
| Cytochrome D ubiquinol oxidase subunit I OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=cydA PE=4 SV=1 | 267 | 59448 | 9 | 5 | 14,3 |
| Carbonic anhydrase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3425 PE=3 SV=1 | 266 | 23872 | 17 | 8 | 52,8 |
| Putative peptidase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0906 PE=4 SV=1 | 1166 | 71146 | 41 | 32 | 59,5 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3515 PE=4 SV=1 | 266 | 36062 | 7 | 6 | 23,5 |
| Ribosome-recycling factor OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=frr PE=3 SV=1 | 266 | 20696 | 9 | 5 | 40,3 |
| MttA/Hcf106 family protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3776 PE=4 SV=1 | 266 | 13191 | 6 | 4 | 50,8 |
| ATP-dependent protease subunit HslV OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hslV PE=3 SV=1 | 265 | 19572 | 5 | 3 | 27,4 |
| Segregation and condensation protein B OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1243 PE=3 SV=1 | 265 | 38083 | 12 | 11 | 33,4 |
| Transketolase 1 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=tktA PE=3 SV=1 | 263 | 72256 | 16 | 10 | 22,3 |
| Malonyl CoA-acyl carrier protein transacylase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=fabD PE=3 SV=1 | 262 | 31534 | 7 | 4 | 20,9 |
| 1-deoxy-D-xylulose 5-phosphate reductoisomerase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=dxr PE=3 SV=1 | 262 | 42413 | 5 | 5 | 18,5 |
| Aspartate transcarbamoylase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=pyrB PE=3 SV=1 | 262 | 47771 | 13 | 10 | 31,8 |
| Glutamate--tRNA ligase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=gltX PE=3 SV=1 | 262 | 51278 | 14 | 10 | 31,3 |
| Putative lipoprotein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1569 PE=4 SV=1 | 1163 | 41527 | 43 | 22 | 63,2 |
| Putative ABC transporter, ATP-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3757 PE=4 SV=1 | 261 | 29663 | 10 | 6 | 34,9 |
| Ubiquinol-cytochrome c reductase iron-sulfur subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=petA PE=4 SV=1 | 260 | 23177 | 9 | 5 | 43,2 |
| Putative hydrolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2910 PE=4 SV=1 | 258 | 30201 | 5 | 4 | 19,6 |
| 50S ribosomal protein L15 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rplO PE=3 SV=1 | 257 | 15358 | 9 | 7 | 56,2 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0516 PE=4 SV=1 | 256 | 22950 | 11 | 5 | 24,9 |
| Delta-aminolevulinic acid dehydratase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hemB PE=3 SV=1 | 256 | 36872 | 7 | 4 | 18,9 |
| Octaprenyl-diphosphate synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ispB PE=3 SV=1 | 256 | 34909 | 8 | 7 | 33,6 |
| Phosphoglucomutase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=pgm PE=3 SV=1 | 256 | 49411 | 15 | 12 | 36,1 |
| Pyridoxine/pyridoxamine 5~-phosphate oxidase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=pdxH PE=3 SV=1 | 256 | 24266 | 7 | 4 | 31,4 |
| Alkyl hydroperoxide reductase AhpD OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ahpD PE=3 SV=1 | 255 | 18487 | 10 | 7 | 34,9 |
| Bifunctional purine biosynthesis protein PurH OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=purH PE=3 SV=1 | 1161 | 56113 | 36 | 19 | 59,2 |

| | | | | | |
|---|---|---|---|---|---|
| Probable zinc-binding dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0659 PE=4 SV=1 | 255 | 34577 | 11 | 7 | 34,3 |
| Putative lipoprotein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2569 PE=4 SV=1 | 254 | 20398 | 9 | 6 | 36,4 |
| Signal recognition particle protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ffh PE=3 SV=1 | 254 | 50633 | 11 | 9 | 29,2 |
| Putative oxidoreductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1581 PE=3 SV=1 | 252 | 27524 | 12 | 9 | 48,8 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3731 PE=4 SV=1 | 251 | 23882 | 8 | 3 | 12,2 |
| Putative aminopeptidase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2391 PE=4 SV=1 | 251 | 64811 | 13 | 11 | 23 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2125A PE=4 SV=1 | 251 | 11931 | 11 | 5 | 71,9 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2891 PE=4 SV=1 | 250 | 22905 | 10 | 7 | 40,9 |
| 3,4-dihydroxy-2-butanone 4-phosphate synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ribB PE=3 SV=1 | 250 | 42529 | 12 | 10 | 30,7 |
| PhoH-like protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1040 PE=4 SV=1 | 248 | 37733 | 12 | 10 | 49,7 |
| Peptidylprolyl isomerase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ppiD PE=4 SV=1 | 1142 | 70367 | 30 | 23 | 59,8 |
| GTPase Obg OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=obg PE=3 SV=1 | 248 | 40611 | 7 | 7 | 24,7 |
| Putative ABC-transporter substrate-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2090 PE=4 SV=1 | 248 | 39708 | 7 | 6 | 28,2 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0240 PE=1 SV=1 | 248 | 25768 | 6 | 5 | 31 |
| Carboxynorspermidine/carboxyspermidine decarboxylase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=nspC PE=3 SV=1 | 248 | 41430 | 12 | 9 | 32,1 |
| Imidazole glycerol phosphate synthase subunit HisH OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hisH PE=3 SV=1 | 248 | 24668 | 8 | 5 | 35,1 |
| D-amino acid dehydrogenase small subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=dadA PE=4 SV=1 | 248 | 46165 | 11 | 10 | 39,7 |
| Diaminopimelate epimerase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=dapF PE=3 SV=1 | 247 | 33032 | 9 | 6 | 38 |
| 3-oxoadipate CoA-transferase subunit A OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=catI PE=4 SV=1 | 247 | 24227 | 9 | 6 | 34,2 |
| Gamma-glutamyl phosphate reductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=proA PE=3 SV=1 | 247 | 44585 | 8 | 6 | 22,7 |
| Dephospho-CoA kinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=coaE PE=3 SV=1 | 247 | 22718 | 8 | 7 | 44,4 |
| Probable parvulin-type peptidyl-prolyl cis-trans isomerase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3561 PE=2 SV=2 | 1126 | 29003 | 44 | 11 | 60,9 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2446 PE=4 SV=1 | 246 | 21648 | 10 | 7 | 58,4 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2012 PE=4 SV=1 | 246 | 44341 | 6 | 6 | 23,5 |
| Probable hydrolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0700 PE=4 SV=1 | 245 | 21135 | 10 | 5 | 40,6 |
| Outer membrane protein assembly factor BamE OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=omlA PE=3 SV=1 | 245 | 20533 | 16 | 10 | 63,2 |
| Response regulator protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=basR PE=4 SV=1 | 244 | 24409 | 5 | 3 | 20,6 |
| Putative amino acid ABC transporter permease protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3830 PE=3 SV=1 | 244 | 42795 | 12 | 9 | 27,5 |
| Putative GTP pyrophosphokinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=relA PE=3 SV=1 | 244 | 81656 | 16 | 13 | 22,3 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3217 PE=4 SV=1 | 244 | 14257 | 7 | 6 | 62,3 |
| Transcription termination/antitermination protein NusG OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=nusG PE=3 SV=1 | 244 | 20192 | 17 | 12 | 66,1 |
| ATP synthase subunit b OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=atpF PE=3 SV=1 | 244 | 17282 | 9 | 5 | 39,1 |
| Putative amino-acid ABC transporter, periplasmic amino acid-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1364 PE=3 SV=1 | 1114 | 28260 | 30 | 17 | 56,1 |
| 30S ribosomal protein S19 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpsS PE=3 SV=1 | 244 | 10169 | 11 | 7 | 64,8 |
| Putative glutathione-S-transferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1238 PE=4 SV=1 | 243 | 23663 | 10 | 8 | 52,8 |
| Ribosome-binding factor A OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rbfA PE=3 SV=1 | 243 | 14716 | 10 | 7 | 69,2 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3732 PE=4 SV=1 | 243 | 21804 | 7 | 5 | 46,7 |
| Histidine--tRNA ligase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hisS PE=3 SV=2 | 243 | 47888 | 5 | 5 | 21,3 |
| AsnC-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0667 PE=4 SV=1 | 243 | 18072 | 6 | 5 | 50,6 |

| | | | | | |
|---|---|---|---|---|---|
| Cell division ATP-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ftsE PE=4 SV=1 | 243 | 24385 | 12 | 10 | 62,8 |
| Putative amino-acid ABC transporter, ATP-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1362 PE=4 SV=1 | 241 | 27576 | 9 | 8 | 34,8 |
| Two-component sensor kinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3223 PE=4 SV=1 | 241 | 52424 | 11 | 11 | 27,4 |
| 3-oxoadipate CoA-transferase subunit B OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=catJ PE=4 SV=1 | 241 | 23069 | 7 | 5 | 37,9 |
| Trigger factor OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=tig PE=3 SV=1 | 1103 | 47587 | 39 | 28 | 65,4 |
| Acetolactate synthase small subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ilvH PE=4 SV=1 | 241 | 18116 | 7 | 6 | 47,9 |
| Putative pyruvate dehydrogenase E1 component, alpha subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=pdhA PE=4 SV=1 | 241 | 35081 | 10 | 9 | 25,7 |
| Poly(A) polymerase I OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=pcnB PE=3 SV=1 | 241 | 52060 | 8 | 7 | 21,7 |
| Tol-Pal system protein TolQ OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=tolQ PE=3 SV=1 | 239 | 24890 | 9 | 6 | 27,4 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2532 PE=4 SV=1 | 239 | 25045 | 6 | 4 | 29,9 |
| Putative amidase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2039 PE=3 SV=1 | 237 | 48832 | 8 | 7 | 26,3 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3084 PE=4 SV=1 | 236 | 41974 | 10 | 9 | 21,8 |
| Putative TonB-dependent receptor OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bfrG PE=3 SV=1 | 236 | 79325 | 14 | 11 | 19,9 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bscE PE=4 SV=1 | 235 | 10704 | 7 | 6 | 73,7 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2661 PE=3 SV=1 | 234 | 39621 | 9 | 7 | 29,5 |
| Aminomethyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=gcvT PE=3 SV=1 | 1101 | 39609 | 36 | 13 | 54,1 |
| Lipopolysaccharide export system protein LptA OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=lptA PE=3 SV=1 | 233 | 22343 | 11 | 6 | 30,6 |
| 30S ribosomal protein S2 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpsB PE=3 SV=1 | 233 | 27550 | 13 | 8 | 44,6 |
| Putative lipoprotein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3760 PE=4 SV=1 | 232 | 28249 | 10 | 6 | 35 |
| Putative serine/threonine dehydratase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3420 PE=4 SV=1 | 232 | 34077 | 11 | 8 | 37,3 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2411 PE=4 SV=1 | 231 | 13678 | 9 | 5 | 40,7 |
| Putative penicillin-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0102 PE=3 SV=1 | 231 | 44908 | 8 | 8 | 23,7 |
| Putative bacterioferritin comigratory protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1307 PE=4 SV=1 | 231 | 19479 | 6 | 5 | 28,5 |
| Exopolyphosphatase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ppx PE=4 SV=1 | 230 | 55203 | 10 | 10 | 23,1 |
| Cell division protein FtsZ OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ftsZ PE=3 SV=1 | 229 | 41632 | 16 | 12 | 36,3 |
| Putative short-chain dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2841 PE=4 SV=1 | 229 | 25376 | 6 | 5 | 26 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1485 PE=4 SV=1 | 1082 | 51625 | 38 | 19 | 61,3 |
| Pertussis toxin subunit 1 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ptxA PE=1 SV=1 | 227 | 30127 | 11 | 6 | 37,9 |
| Type III pantothenate kinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=coaX PE=3 SV=1 | 227 | 27942 | 5 | 5 | 37,8 |
| 50S ribosomal protein L3 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rplC PE=3 SV=2 | 226 | 24447 | 12 | 3 | 20,2 |
| Phosphoserine aminotransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=serC PE=3 SV=1 | 226 | 41003 | 7 | 5 | 19,1 |
| Serine acetyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=srpH PE=4 SV=1 | 226 | 34551 | 11 | 10 | 40,1 |
| Ribonuclease PH OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rph PE=3 SV=1 | 225 | 26247 | 10 | 9 | 41,5 |
| Putative DNA-binding protein (Histone) OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bph3 PE=4 SV=1 | 224 | 13645 | 9 | 6 | 37,4 |
| Putative two-component response regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0572 PE=4 SV=1 | 224 | 25414 | 6 | 3 | 21,8 |
| Putative phosphoenolpyruvate synthase regulatory protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1435 PE=3 SV=1 | 223 | 30821 | 13 | 9 | 38,2 |
| Putative chromate reductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1563 PE=4 SV=1 | 223 | 20297 | 7 | 6 | 53,3 |
| Autotransporter OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=vag8 PE=4 SV=1 | 2674 | 94824 | 98 | 28 | 51,4 |
| Succinate dehydrogenase flavoprotein subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=sdhA PE=3 SV=1 | 1077 | 65157 | 38 | 20 | 47,3 |
| Alkyl hydroperoxide reductase AhpD OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0535 PE=3 SV=1 | 222 | 11671 | 9 | 2 | 18,9 |

| | | | | | |
|---|---|---|---|---|---|
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3306 PE=4 SV=1 | 222 | 34638 | 3 | 2 | 13,9 |
| 30S ribosomal protein S13 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpsM PE=3 SV=1 | 222 | 13562 | 9 | 7 | 56,2 |
| 50S ribosomal protein L16 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rplP PE=3 SV=1 | 222 | 15499 | 7 | 6 | 52,2 |
| GTP cyclohydrolase FolE2 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=folE2 PE=3 SV=1 | 220 | 29517 | 10 | 7 | 38,5 |
| UDP-N-acetylglucosamine 2-epimerase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bplD PE=3 SV=1 | 220 | 39349 | 7 | 5 | 19,1 |
| Ferredoxin, 2Fe-2S OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=fdx PE=4 SV=1 | 220 | 12831 | 6 | 5 | 59,3 |
| Phosphopantetheine adenylyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=coaD PE=3 SV=1 | 220 | 19172 | 10 | 7 | 37,9 |
| Outer membrane protein assembly factor BamD OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=comL PE=3 SV=1 | 219 | 29879 | 7 | 7 | 38,3 |
| Outer-membrane lipoprotein carrier protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=lolA PE=3 SV=1 | 219 | 22285 | 7 | 6 | 42,4 |
| Enolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=eno PE=3 SV=1 | 1075 | 46056 | 29 | 16 | 47,4 |
| Inositol-1-monophosphatase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2813 PE=3 SV=1 | 218 | 35656 | 5 | 4 | 18,1 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0500 PE=4 SV=1 | 217 | 68607 | 13 | 10 | 16,8 |
| UPF0234 protein BP2916 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2916 PE=3 SV=1 | 217 | 17890 | 10 | 7 | 50,6 |
| UPF0307 protein BP2965 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2965 PE=3 SV=2 | 217 | 20989 | 9 | 7 | 37,2 |
| Chaperone protein FimB/FhaD OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=fimB PE=3 SV=2 | 217 | 26420 | 7 | 5 | 26,2 |
| Glutathione synthetase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=gshB PE=3 SV=1 | 217 | 34791 | 9 | 7 | 27,4 |
| Proline-rich inner membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3344 PE=4 SV=1 | 217 | 35149 | 10 | 9 | 33,6 |
| Putative transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0744 PE=4 SV=1 | 216 | 16203 | 8 | 4 | 36,1 |
| 3-oxoadipate enol-lactone hydrolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=catD2 PE=4 SV=1 | 215 | 28590 | 6 | 4 | 23,9 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1204 PE=4 SV=1 | 215 | 29589 | 6 | 5 | 28,3 |
| Autotransporter subtilisin-like protease OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=sphB1 PE=4 SV=1 | 1073 | 99701 | 44 | 28 | 39,4 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1565 PE=4 SV=1 | 215 | 7874 | 6 | 3 | 59,2 |
| 30S ribosomal protein S10 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpsJ PE=3 SV=1 | 214 | 11799 | 5 | 4 | 32 |
| Long-chain-fatty-acid--CoA ligase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=fadD PE=4 SV=1 | 214 | 61316 | 7 | 7 | 23,3 |
| Ribosome-binding ATPase YchF OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ychF PE=3 SV=1 | 214 | 39667 | 10 | 8 | 28,9 |
| ABC transporter OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0697 PE=4 SV=1 | 214 | 28404 | 10 | 9 | 51 |
| Peptidyl-tRNA hydrolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=pth PE=3 SV=2 | 213 | 23658 | 7 | 6 | 42,8 |
| Sulfate-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=sbp PE=4 SV=1 | 212 | 37891 | 8 | 8 | 29,7 |
| NADH-quinone oxidoreductase subunit I OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=nuoI PE=3 SV=1 | 212 | 19278 | 5 | 4 | 37 |
| Histone protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bpH1 PE=4 SV=1 | 212 | 17386 | 8 | 2 | 18,3 |
| 30S ribosomal protein S18 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpsR PE=3 SV=1 | 212 | 10762 | 10 | 5 | 44,4 |
| Outer membrane porin protein BP0840 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0840 PE=1 SV=1 | 1071 | 41020 | 31 | 10 | 39,2 |
| Putative enoyl-CoA hydratase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3277 PE=3 SV=1 | 211 | 30158 | 10 | 6 | 25,1 |
| Glycerol kinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=glpK PE=3 SV=1 | 211 | 54908 | 7 | 4 | 10,8 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3511 PE=4 SV=1 | 211 | 9410 | 4 | 3 | 68,2 |
| Pertussis toxin subunit 3 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ptxC PE=1 SV=1 | 210 | 25314 | 8 | 7 | 32,6 |
| Pertussis toxin subunit 2 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ptxB PE=1 SV=2 | 177 | 25183 | 7 | 6 | 31,9 |
| Two component response regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ompR PE=4 SV=1 | 209 | 26015 | 9 | 7 | 37,8 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0701 PE=3 SV=1 | 208 | 34510 | 7 | 5 | 21,9 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2197 PE=4 SV=1 | 208 | 22805 | 6 | 4 | 22,6 |

| | | | | | |
|---|---|---|---|---|---|
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1016 PE=4 SV=1 | 208 | 12004 | 7 | 5 | 60,4 |
| Transcription antitermination protein NusB OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=nusB PE=3 SV=1 | 208 | 17155 | 7 | 4 | 31,8 |
| Putative modification methylase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3116 PE=4 SV=1 | 207 | 111480 | 15 | 13 | 16,2 |
| Adenosylhomocysteinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ahcY PE=3 SV=1 | 1050 | 51997 | 38 | 18 | 52,8 |
| Nicotinate phosphoribosyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=pncB PE=3 SV=1 | 207 | 47140 | 8 | 6 | 21,5 |
| GTPase Era OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=era PE=3 SV=1 | 206 | 33126 | 12 | 9 | 39,9 |
| dTDP-4-dehydrorhamnose 3,5-epimerase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rfbC PE=3 SV=1 | 206 | 20871 | 9 | 6 | 47,3 |
| LPS-assembly lipoprotein LptE OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=lptE PE=3 SV=1 | 205 | 24273 | 10 | 9 | 44,3 |
| Cell shape-determining protein MreC OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=mreC PE=3 SV=1 | 205 | 31618 | 8 | 6 | 31 |
| Probable geranyltranstransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2799 PE=3 SV=1 | 204 | 31907 | 8 | 6 | 36,3 |
| sn-glycerol-3-phosphate import ATP-binding protein UgpC OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ugpC PE=3 SV=1 | 204 | 40107 | 9 | 8 | 22,7 |
| Signal recognition particle receptor FtsY OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ftsY PE=3 SV=1 | 204 | 38703 | 8 | 5 | 31,7 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0606 PE=4 SV=1 | 204 | 15008 | 10 | 6 | 62,1 |
| Putative thiamine-pyrophosphate-requiring enzyme OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1535 PE=4 SV=1 | 202 | 55308 | 7 | 6 | 17,3 |
| 3-oxoacyl-[acyl-carrier protein] reductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=fabG PE=4 SV=1 | 1046 | 25720 | 20 | 7 | 52,8 |
| 50S ribosomal protein L27 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpmA PE=3 SV=1 | 202 | 8952 | 5 | 4 | 59,3 |
| Putative TolR-like translocation protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3345 PE=3 SV=1 | 201 | 16354 | 10 | 6 | 49,3 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0779 PE=4 SV=1 | 201 | 41777 | 11 | 7 | 23,4 |
| Molybdopterin converting factor OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=moaE PE=4 SV=1 | 201 | 18097 | 9 | 9 | 69,9 |
| Nitrogen regulatory protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=glnB PE=3 SV=1 | 201 | 12232 | 7 | 5 | 53,6 |
| tRNA-specific 2-thiouridylase MnmA OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=mnmA PE=3 SV=1 | 200 | 41183 | 12 | 8 | 32,9 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0499 PE=4 SV=1 | 200 | 13966 | 7 | 4 | 31,8 |
| Thioredoxin OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=trxC PE=3 SV=1 | 199 | 13976 | 4 | 3 | 35,4 |
| UbiE/COQ5 methyltransferase family protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3838 PE=4 SV=1 | 199 | 27940 | 9 | 8 | 35 |
| 50S ribosomal protein L1 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rplA PE=3 SV=1 | 199 | 23965 | 8 | 8 | 40,9 |
| Putative cell surface protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2219 PE=4 SV=1 | 1044 | 35715 | 42 | 13 | 65,6 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0735 PE=3 SV=1 | 198 | 21173 | 4 | 4 | 28,1 |
| Inorganic pyrophosphatase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ppa PE=3 SV=1 | 198 | 20143 | 12 | 8 | 51,1 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0189 PE=4 SV=1 | 198 | 18415 | 4 | 3 | 17,6 |
| Putative dioxygenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2333 PE=4 SV=1 | 197 | 35661 | 12 | 10 | 41,9 |
| Putative ATP-dependent RNA helicase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3395 PE=3 SV=1 | 197 | 52051 | 14 | 9 | 23,7 |
| Probable short-chain dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1222 PE=4 SV=1 | 197 | 25380 | 8 | 6 | 26,5 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3132 PE=4 SV=1 | 197 | 7465 | 4 | 2 | 46,4 |
| Formyltetrahydrofolate deformylase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=purU PE=3 SV=1 | 196 | 32110 | 7 | 6 | 28,2 |
| Putative thioesterase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2807 PE=4 SV=1 | 195 | 14668 | 6 | 5 | 54,4 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3218 PE=4 SV=1 | 193 | 23397 | 8 | 5 | 33,6 |
| Valine--tRNA ligase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=valS PE=3 SV=1 | 1039 | 107827 | 35 | 26 | 37,1 |
| Putative phytoene synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1219 PE=4 SV=1 | 193 | 33224 | 8 | 7 | 28,9 |
| Putative transcriptional regulatory protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2571 PE=4 SV=1 | 192 | 15308 | 7 | 5 | 52,9 |
| 3-octaprenyl-4-hydroxybenzoate carboxy-lyase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ubiD PE=3 SV=2 | 192 | 56974 | 12 | 9 | 28,2 |

| | | | | | |
|---|---|---|---|---|---|
| Two component response regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3350 PE=4 SV=1 | 192 | 25381 | 7 | 7 | 39,9 |
| 3-dehydroquinate synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=aroB PE=3 SV=1 | 192 | 38308 | 4 | 3 | 12,6 |
| Elongation factor P OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=efp PE=3 SV=1 | 191 | 20969 | 8 | 7 | 35,1 |
| Carboxyvinyl-carboxyphosphonate phosphorylmutase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0718 PE=4 SV=1 | 191 | 31372 | 8 | 7 | 33,8 |
| Putative sulfurtransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2280 PE=4 SV=1 | 191 | 29761 | 4 | 3 | 19,4 |
| Replicative DNA helicase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=dnaB PE=3 SV=1 | 191 | 50382 | 10 | 8 | 24,7 |
| 3-isopropylmalate dehydratase small subunit 2 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=leuD2 PE=3 SV=1 | 191 | 24589 | 11 | 10 | 40,3 |
| Chromosome partition protein Smc OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=smc PE=3 SV=1 | 1038 | 130767 | 39 | 35 | 37,4 |
| Cytochrome b OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=petB PE=3 SV=1 | 190 | 52122 | 7 | 6 | 13,7 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3399 PE=4 SV=1 | 190 | 7504 | 5 | 3 | 85,7 |
| Cytochrome c oxidase subunit 2 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3744 PE=3 SV=1 | 190 | 43254 | 9 | 6 | 28,6 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3075 PE=4 SV=1 | 190 | 25359 | 6 | 5 | 33,9 |
| Putative response regulator protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3865 PE=4 SV=1 | 189 | 25396 | 4 | 3 | 18,6 |
| Putative biotin protein ligase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=birA PE=4 SV=1 | 189 | 29819 | 6 | 6 | 30,2 |
| Pseudouridine synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1244 PE=3 SV=1 | 189 | 60768 | 13 | 10 | 18,9 |
| Probable enoyl-CoA hydratase/isomerase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1702 PE=4 SV=1 | 189 | 28823 | 6 | 4 | 28 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3048 PE=4 SV=1 | 188 | 19818 | 7 | 5 | 26,7 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3651 PE=4 SV=1 | 188 | 76344 | 12 | 8 | 16,6 |
| Glutamine-binding periplasmic protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=glnH PE=3 SV=1 | 1038 | 26758 | 40 | 13 | 54,8 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1305 PE=4 SV=1 | 188 | 51959 | 8 | 7 | 22,8 |
| Probable extracellular solute-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0363 PE=4 SV=1 | 187 | 25822 | 8 | 7 | 27,6 |
| Superoxide dismutase [Cu-Zn] OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2067 PE=3 SV=1 | 187 | 17525 | 11 | 6 | 45,3 |
| Lipid A export ATP-binding/permease protein MsbA OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=msbA PE=3 SV=1 | 187 | 67573 | 7 | 7 | 13,2 |
| Putative tautomerase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2058 PE=3 SV=1 | 187 | 12882 | 9 | 6 | 60,5 |
| Cysteine desulfurase IscS OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=iscS PE=3 SV=1 | 187 | 45021 | 8 | 7 | 24,8 |
| Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=gatC PE=3 SV=1 | 187 | 11230 | 6 | 3 | 57,8 |
| N-(5~-phosphoribosyl)anthranilate isomerase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=trpF PE=3 SV=1 | 187 | 23110 | 4 | 2 | 17 |
| DNA mismatch repair protein MutL OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=mutL PE=3 SV=1 | 186 | 68079 | 6 | 5 | 20,7 |
| Ribulose-phosphate 3-epimerase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpe PE=3 SV=1 | 186 | 26523 | 7 | 5 | 31,4 |
| Elongation factor Tu OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=tuf1 PE=3 SV=1 | 2652 | 43003 | 91 | 19 | 58,8 |
| Dihydrolipoyl dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=odhL PE=1 SV=1 | 1038 | 50357 | 36 | 22 | 65,3 |
| Putative arginase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1531 PE=3 SV=1 | 186 | 32353 | 7 | 7 | 32,6 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2581 PE=4 SV=1 | 185 | 10275 | 5 | 3 | 50,5 |
| AMP nucleosidase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=amn PE=3 SV=1 | 185 | 56092 | 9 | 6 | 22,2 |
| Bifunctional protein FolD 1 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=folD1 PE=3 SV=1 | 185 | 29699 | 8 | 7 | 30,4 |
| Fumarylacetoacetase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=fahA PE=4 SV=1 | 184 | 47557 | 5 | 4 | 13 |
| Pyridoxal phosphate homeostasis protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1320 PE=3 SV=1 | 184 | 29819 | 10 | 9 | 29,2 |
| Cell division protein ZapA OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3047 PE=4 SV=1 | 184 | 11174 | 6 | 5 | 43,7 |
| 3-hydroxybutyryl-CoA dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0217 PE=4 SV=1 | 183 | 33805 | 10 | 8 | 27,1 |
| Lipoprotein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bscJ PE=3 SV=1 | 183 | 28730 | 7 | 6 | 25,9 |

| | | | | | |
|---|---|---|---|---|---|
| Putative endonuclease OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0369 PE=4 SV=1 | 183 | 30350 | 5 | 5 | 25,2 |
| N-acetyl-gamma-glutamyl-phosphate reductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=argC PE=3 SV=1 | 1035 | 38034 | 42 | 19 | 62,1 |
| Outer membrane porin protein OmpQ OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ompQ PE=4 SV=1 | 182 | 39117 | 4 | 4 | 17 |
| Protein-export membrane protein SecF OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=secF PE=3 SV=1 | 182 | 34519 | 8 | 4 | 19 |
| Putative transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2399 PE=4 SV=1 | 182 | 31171 | 6 | 6 | 27,6 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1127 PE=4 SV=1 | 181 | 44067 | 10 | 8 | 27,1 |
| Probable transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0533 PE=4 SV=1 | 181 | 26477 | 5 | 5 | 27,2 |
| 30S ribosomal protein S5 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpsE PE=3 SV=1 | 180 | 18103 | 9 | 8 | 54,6 |
| Transcriptional regulator MraZ OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=mraZ PE=3 SV=1 | 180 | 15779 | 9 | 6 | 45,8 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3465 PE=4 SV=1 | 180 | 19025 | 9 | 5 | 49,4 |
| High-affinity branched-chain amino acid transport, ATP-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=livG PE=4 SV=1 | 180 | 28526 | 11 | 9 | 39,2 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1471 PE=4 SV=1 | 180 | 22964 | 4 | 3 | 22 |
| Putative L-asparaginase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2398 PE=4 SV=1 | 1034 | 33763 | 32 | 14 | 75,5 |
| Transcription-repair-coupling factor OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=mfd PE=3 SV=1 | 179 | 127060 | 9 | 9 | 9,9 |
| ATP-dependent DNA helicase RecG OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=recG PE=3 SV=1 | 162 | 72272 | 11 | 11 | 24,4 |
| 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ispF PE=3 SV=1 | 179 | 16558 | 10 | 6 | 34 |
| Probable aminotransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3870 PE=4 SV=1 | 178 | 43006 | 7 | 6 | 28,1 |
| Glycerophosphoryl diester phosphodiesterase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ugpQ PE=4 SV=1 | 178 | 27003 | 9 | 7 | 37,8 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2233 PE=4 SV=1 | 177 | 25132 | 8 | 5 | 31,9 |
| Bifunctional uridylyltransferase/uridylyl-removing enzyme OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=glnD PE=3 SV=1 | 177 | 98691 | 15 | 13 | 19,2 |
| SCO1/SenC family protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3734 PE=4 SV=1 | 177 | 21504 | 6 | 6 | 34,5 |
| DNA-binding protein Hu-beta OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hupB PE=3 SV=1 | 177 | 9397 | 11 | 5 | 55,6 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3002 PE=4 SV=1 | 176 | 69660 | 8 | 8 | 22 |
| Putative solute-binding transport protein (Periplasmic) OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2293 PE=4 SV=1 | 176 | 58938 | 10 | 9 | 23,9 |
| Bifunctional protein GlmU OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=glmU PE=3 SV=1 | 1031 | 48655 | 30 | 15 | 37,2 |
| Oligoribonuclease OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=orn PE=3 SV=1 | 175 | 20705 | 7 | 6 | 30,4 |
| UvrABC system protein B OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=uvrB PE=3 SV=1 | 175 | 76553 | 20 | 17 | 26,1 |
| 3-phosphoshikimate 1-carboxyvinyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=aroA PE=3 SV=2 | 175 | 46861 | 7 | 5 | 17 |
| 50S ribosomal protein L5 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rplE PE=3 SV=1 | 174 | 20259 | 13 | 9 | 48 |
| Putative dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3682 PE=4 SV=1 | 174 | 40740 | 6 | 4 | 13,6 |
| Pertussis toxin subunit 4 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ptxD PE=1 SV=1 | 174 | 16761 | 9 | 6 | 49,3 |
| Putative glutamate--cysteine ligase 2 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0598 PE=3 SV=1 | 172 | 46170 | 7 | 5 | 20,6 |
| LysR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3503 PE=3 SV=1 | 172 | 36974 | 7 | 6 | 25,2 |
| HPr kinase/phosphorylase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hprK PE=3 SV=1 | 172 | 33781 | 10 | 8 | 34,1 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1116 PE=4 SV=1 | 171 | 30262 | 5 | 5 | 27,8 |
| Electron transfer flavoprotein beta-subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=etfB PE=4 SV=1 | 1026 | 26917 | 26 | 13 | 54,2 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1512 PE=4 SV=1 | 171 | 14990 | 4 | 4 | 47 |
| UPF0261 protein BP1203 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1203 PE=3 SV=1 | 170 | 43195 | 8 | 6 | 20,4 |
| Protein FhaE OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=fhaE PE=3 SV=1 | 169 | 40788 | 7 | 7 | 23,9 |
| Cell division protein ZapD OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=zapD PE=3 SV=1 | 169 | 28704 | 11 | 9 | 55,3 |

| | | | | | |
|---|---|---|---|---|---|
| Dihydropteroate synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=folP PE=3 SV=1 | 169 | 30116 | 7 | 6 | 42,5 |
| Peroxiredoxin OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2715 PE=3 SV=1 | 168 | 17787 | 8 | 5 | 55,7 |
| Ubiquinone/menaquinone biosynthesis C-methyltransferase UbiE OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ubiE PE=3 SV=1 | 168 | 28516 | 9 | 8 | 35,7 |
| Protein-export membrane protein SecG OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=secG PE=3 SV=1 | 167 | 14908 | 7 | 3 | 46,6 |
| Putative transferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2328 PE=4 SV=1 | 167 | 40823 | 8 | 8 | 33,2 |
| Acetylornithine deacetylase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3588 PE=3 SV=1 | 166 | 42918 | 13 | 7 | 25,4 |
| Putative substrate-CoA ligase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0624 PE=4 SV=1 | 1023 | 54869 | 27 | 16 | 38 |
| GntR-family transcription regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0356 PE=4 SV=1 | 166 | 26157 | 7 | 7 | 48,8 |
| N5-carboxyaminoimidazole ribonucleotide synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=purK PE=3 SV=1 | 166 | 41924 | 4 | 4 | 17,4 |
| Putative periplasmic substrate-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2055 PE=4 SV=1 | 165 | 37291 | 6 | 6 | 28,8 |
| Kynurenine formamidase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=kynB PE=3 SV=1 | 165 | 22933 | 5 | 4 | 34,9 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0132 PE=4 SV=1 | 165 | 23954 | 6 | 5 | 27,9 |
| 50S ribosomal protein L23 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rplW PE=3 SV=1 | 164 | 11152 | 7 | 5 | 44,9 |
| DNA polymerase III subunit gamma/tau OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=dnaX PE=3 SV=1 | 164 | 73323 | 10 | 9 | 23,9 |
| Putative carboxymethylenebutenolidase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1256 PE=4 SV=1 | 163 | 28068 | 7 | 5 | 51,9 |
| Acetolactate synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ilvI PE=3 SV=1 | 163 | 63538 | 13 | 11 | 18,6 |
| Phosphoheptose isomerase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=gmhA PE=3 SV=1 | 163 | 21541 | 5 | 2 | 24,5 |
| Leu/ile/val-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=livJ PE=4 SV=1 | 1015 | 39697 | 28 | 11 | 46,1 |
| Cold shock-like protein CspA OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=cspA PE=3 SV=1 | 163 | 7344 | 11 | 3 | 55,2 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2703 PE=4 SV=1 | 163 | 21287 | 5 | 4 | 19,1 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2787 PE=4 SV=1 | 162 | 17211 | 6 | 3 | 33,8 |
| Phosphate acetyl/butaryl transferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1004 PE=4 SV=1 | 162 | 32838 | 9 | 6 | 26,9 |
| Pyridoxine 5~-phosphate synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=pdxJ PE=3 SV=1 | 162 | 26677 | 5 | 4 | 19,4 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0649 PE=4 SV=1 | 161 | 33155 | 7 | 6 | 27,6 |
| Homoserine kinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=thrB PE=3 SV=1 | 161 | 37025 | 12 | 10 | 41,5 |
| 23S rRNA (guanosine-2~-O-)-methyltransferase RlmB OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rlmB PE=3 SV=1 | 161 | 26833 | 8 | 5 | 32,2 |
| UDP-N-acetylmuramoylalanine--D-glutamate ligase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=murD PE=3 SV=1 | 160 | 54264 | 7 | 5 | 11,4 |
| Putative hemolysin OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bllY PE=4 SV=1 | 160 | 42011 | 4 | 4 | 12,4 |
| Arginine biosynthesis bifunctional protein ArgJ OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=argJ PE=3 SV=1 | 1013 | 42829 | 30 | 13 | 46,1 |
| ABC transporter ATP-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3576 PE=4 SV=1 | 160 | 25665 | 7 | 5 | 24,6 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3248 PE=4 SV=1 | 160 | 30057 | 4 | 4 | 21,6 |
| Ribosome maturation factor RimP OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rimP PE=3 SV=1 | 160 | 18777 | 11 | 8 | 45,2 |
| Putative lipoprotein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1296 PE=4 SV=1 | 160 | 30249 | 6 | 5 | 28,4 |
| Ubiquinol oxidase subunit 2 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=cyoA PE=3 SV=1 | 159 | 33560 | 3 | 3 | 18,4 |
| Lipopolysaccharide assembly protein B OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=lapB PE=3 SV=1 | 158 | 46259 | 10 | 10 | 37,2 |
| LexA repressor OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=lexA PE=3 SV=1 | 158 | 23203 | 10 | 9 | 58,8 |
| 50S ribosomal protein L18 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rplR PE=3 SV=1 | 158 | 12940 | 4 | 4 | 43,3 |
| UDP-N-acetylmuramate--L-alanyl-gamma-D-glutamyl-meso-2,6-diaminoheptandioate ligase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=mpl PE=3 SV=1 | 158 | 48697 | 10 | 8 | 23,7 |
| Riboflavin biosynthesis protein RibD OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2948 PE=3 SV=1 | 157 | 41500 | 15 | 13 | 43,8 |

| | | | | | |
|---|---|---|---|---|---|
| Phosphoenolpyruvate synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ppsA PE=3 SV=1 | 1013 | 86639 | 45 | 30 | 41,9 |
| Putative transport protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2338 PE=4 SV=1 | 157 | 30400 | 10 | 9 | 35,1 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1727 PE=4 SV=1 | 157 | 6897 | 4 | 3 | 60,6 |
| HlyD family secretion protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3815 PE=3 SV=1 | 157 | 44815 | 8 | 8 | 28,6 |
| Peptide chain release factor 3 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=prfC PE=3 SV=2 | 157 | 59341 | 7 | 7 | 19,4 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3499 PE=4 SV=1 | 157 | 23797 | 4 | 4 | 27,5 |
| 50S ribosomal protein L33 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpmG PE=3 SV=1 | 157 | 6492 | 6 | 4 | 61,8 |
| Putative GTP-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2632 PE=4 SV=1 | 155 | 96665 | 25 | 20 | 25,5 |
| Putative lipoprotein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2886 PE=4 SV=1 | 155 | 26714 | 9 | 9 | 46 |
| Polyphenol oxidase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1148 PE=3 SV=1 | 154 | 24772 | 4 | 3 | 19,7 |
| Transcription elongation factor GreB OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=greB PE=3 SV=1 | 153 | 20650 | 4 | 4 | 35,3 |
| DNA-directed RNA polymerase subunit alpha OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpoA PE=3 SV=1 | 1012 | 36250 | 40 | 15 | 57 |
| NADH-quinone oxidoreductase subunit C OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=nuoC PE=3 SV=1 | 153 | 24133 | 6 | 6 | 28 |
| Sec-independent protein translocase protein TatB OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=tatB PE=3 SV=1 | 153 | 15866 | 9 | 6 | 40,8 |
| Maleate isomerase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=maiA PE=3 SV=1 | 152 | 26837 | 3 | 3 | 24 |
| Glycolate oxidase subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=glcD PE=4 SV=1 | 151 | 53858 | 8 | 7 | 18,8 |
| Peptide chain release factor 2 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=prfB PE=3 SV=1 | 151 | 41611 | 7 | 6 | 21,8 |
| Glycerol-3-phosphate regulon repressor protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=glpR PE=4 SV=1 | 151 | 28848 | 4 | 3 | 18,7 |
| Arsenate reductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=arsC PE=3 SV=1 | 151 | 13664 | 6 | 4 | 38,8 |
| ABC transporter ATP-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3577 PE=4 SV=1 | 150 | 28295 | 12 | 8 | 25,7 |
| Conserved inner membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2220 PE=4 SV=1 | 150 | 92467 | 5 | 5 | 9 |
| 50S ribosomal protein L28 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpmB PE=3 SV=1 | 150 | 8897 | 9 | 6 | 42,3 |
| Elongation factor G OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=fusA PE=3 SV=1 | 2501 | 77352 | 77 | 32 | 65 |
| NADP-dependent malic enzyme OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=maeB PE=4 SV=1 | 1009 | 82818 | 43 | 20 | 39,5 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2258 PE=4 SV=1 | 150 | 13292 | 3 | 3 | 42,4 |
| Putative ATP-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2493 PE=4 SV=1 | 148 | 33363 | 7 | 7 | 26,1 |
| Isoprenyl transferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=uppS PE=3 SV=1 | 148 | 29118 | 6 | 6 | 29,5 |
| Probable acetyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bplB PE=4 SV=1 | 148 | 20955 | 5 | 4 | 30,9 |
| Probable oxidoreductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0977 PE=4 SV=1 | 147 | 38781 | 7 | 7 | 23,2 |
| 3~,5~-cyclic adenosine monophosphate phosphodiesterase CpdA OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=cpdA PE=3 SV=1 | 147 | 30721 | 7 | 5 | 34,1 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1587 PE=4 SV=1 | 147 | 34235 | 13 | 11 | 45,8 |
| CCA-adding enzyme OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=cca PE=3 SV=1 | 147 | 39688 | 10 | 8 | 29,7 |
| Putative conserved exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3253 PE=1 SV=1 | 146 | 38737 | 6 | 6 | 30,9 |
| Putative regulator (SIS family) OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2217 PE=4 SV=1 | 146 | 36498 | 6 | 5 | 21,6 |
| Catalase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=katA PE=1 SV=1 | 1006 | 54588 | 32 | 17 | 48,5 |
| Putative aldehyde dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0207 PE=3 SV=1 | 146 | 50793 | 9 | 8 | 19,5 |
| Protein tex OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=tex PE=4 SV=2 | 146 | 85959 | 14 | 13 | 16,4 |
| Putative glycosyl transferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bplH PE=4 SV=1 | 145 | 42936 | 7 | 7 | 22,3 |
| Histidinol-phosphate aminotransferase 1 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hisC1 PE=3 SV=1 | 144 | 38985 | 16 | 11 | 38,5 |
| Glutathione peroxidase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1301 PE=3 SV=1 | 144 | 18638 | 6 | 5 | 38 |

| | | | | | |
|---|---|---|---|---|---|
| N5-carboxyaminoimidazole ribonucleotide mutase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=purE PE=3 SV=1 | 144 | 16483 | 3 | 3 | 26,4 |
| Thiamine-phosphate synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=thiE PE=3 SV=1 | 144 | 22557 | 4 | 4 | 38,2 |
| 30S ribosomal protein S7 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpsG PE=3 SV=1 | 143 | 17712 | 9 | 6 | 44,2 |
| TetR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0617 PE=4 SV=1 | 143 | 22926 | 8 | 7 | 35,8 |
| PKHD-type hydroxylase BP3529 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3529 PE=3 SV=1 | 143 | 25118 | 6 | 6 | 38,1 |
| Alanine--tRNA ligase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=alaS PE=3 SV=1 | 991 | 95211 | 30 | 23 | 35,5 |
| Guanosine-3~,5~-bis(Diphosphate) 3~-pyrophosphohydrolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=spoT PE=3 SV=1 | 143 | 84227 | 6 | 6 | 7,5 |
| Putative RNA polymerase sigma factor OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=brpL PE=3 SV=1 | 143 | 22307 | 5 | 4 | 37 |
| Putative Ecf-type RNA polymerase sigma factor OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1225 PE=3 SV=1 | 142 | 21890 | 5 | 4 | 27,1 |
| Ribonuclease 3 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rnc PE=3 SV=1 | 141 | 27869 | 7 | 5 | 20,3 |
| DNA-directed RNA polymerase subunit omega OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpoZ PE=3 SV=1 | 140 | 7529 | 4 | 3 | 50,7 |
| Transcription elongation factor GreA OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=greA PE=3 SV=1 | 140 | 17032 | 8 | 5 | 41,8 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2213 PE=4 SV=1 | 140 | 16606 | 6 | 4 | 27,9 |
| Putative amino acid-binding periplasmic protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1532 PE=4 SV=1 | 140 | 28373 | 5 | 5 | 22,4 |
| UDP-glucose 6-dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rkpK PE=3 SV=1 | 140 | 47908 | 6 | 5 | 17,3 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1175 PE=4 SV=1 | 139 | 12589 | 5 | 4 | 54,7 |
| Glycerol-3-phosphate-binding periplasmic protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ugpB PE=4 SV=1 | 987 | 47781 | 40 | 22 | 54,9 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1736 PE=4 SV=1 | 139 | 11364 | 4 | 3 | 29,5 |
| Tryptophan 2,3-dioxygenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=kynA PE=3 SV=1 | 139 | 32921 | 10 | 8 | 25 |
| Ubiquinone biosynthesis O-methyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ubiG PE=3 SV=1 | 139 | 26146 | 4 | 3 | 20,7 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1555 PE=4 SV=1 | 139 | 30917 | 3 | 2 | 15,9 |
| Elongation factor 4 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=lepA PE=3 SV=2 | 138 | 66354 | 9 | 8 | 18,8 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0101B PE=4 SV=1 | 138 | 23252 | 4 | 4 | 33,2 |
| Probable phosphoglycerate mutase 2 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=gpmB PE=4 SV=1 | 138 | 23832 | 3 | 3 | 16,4 |
| Zinc metalloprotease OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1426 PE=3 SV=1 | 138 | 46824 | 9 | 7 | 21,2 |
| Tartrate dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2291 PE=4 SV=1 | 138 | 39047 | 8 | 8 | 24,2 |
| Putative isochorismatase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0582 PE=4 SV=1 | 138 | 21684 | 5 | 5 | 36,1 |
| Bifunctional protein PutA OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=putA PE=3 SV=1 | 979 | 137868 | 38 | 33 | 36,5 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0569 PE=3 SV=1 | 138 | 47617 | 6 | 6 | 22,1 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0224 PE=4 SV=1 | 137 | 11076 | 4 | 2 | 31,6 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1066 PE=4 SV=1 | 136 | 16995 | 6 | 5 | 50 |
| Riboflavin synthase alpha chain OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ribE PE=4 SV=1 | 136 | 25208 | 5 | 5 | 26,2 |
| Putative acyl-CoA dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3308 PE=3 SV=1 | 136 | 41749 | 8 | 7 | 25,1 |
| Segregation and condensation protein A OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3822 PE=3 SV=1 | 136 | 33463 | 6 | 4 | 26,4 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1556 PE=3 SV=1 | 136 | 22446 | 2 | 1 | 15,9 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2177 PE=4 SV=1 | 135 | 17498 | 6 | 5 | 41,6 |
| Methylenetetrahydrofolate reductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3066 PE=3 SV=1 | 135 | 30761 | 6 | 6 | 25,7 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3419 PE=4 SV=1 | 134 | 32751 | 6 | 5 | 30 |
| Polyribonucleotide nucleotidyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=pnp PE=3 SV=1 | 978 | 77351 | 31 | 17 | 35,2 |
| 30S ribosomal protein S9 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpsI PE=3 SV=1 | 134 | 14482 | 7 | 4 | 49,2 |

| | | | | | |
|---|---|---|---|---|---|
| Phosphoserine phosphatase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=serB PE=4 SV=1 | 133 | 30630 | 4 | 4 | 17,5 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1241 PE=3 SV=1 | 132 | 21956 | 5 | 5 | 31,3 |
| NAD kinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=nadK PE=3 SV=1 | 132 | 32320 | 5 | 4 | 21,7 |
| GntR family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0233 PE=4 SV=1 | 132 | 27060 | 4 | 4 | 29,1 |
| Putative periplasmic substrate-binding transport protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2352 PE=4 SV=1 | 132 | 34737 | 8 | 7 | 23,5 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1536 PE=4 SV=1 | 132 | 16076 | 5 | 3 | 34,7 |
| Ferrochelatase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hemH PE=3 SV=2 | 132 | 41293 | 4 | 3 | 15,7 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1252 PE=4 SV=1 | 131 | 14810 | 4 | 2 | 19,4 |
| 7-cyano-7-deazaguanine synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=queC PE=3 SV=2 | 131 | 27813 | 6 | 6 | 33,2 |
| Phospho-2-dehydro-3-deoxyheptonate aldolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=aroG PE=3 SV=1 | 959 | 39179 | 33 | 13 | 45,1 |
| UDP-2,3-diacylglucosamine hydrolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=lpxH PE=3 SV=2 | 131 | 28435 | 8 | 8 | 33,7 |
| Translation initiation factor IF-1 2 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=infA2 PE=3 SV=1 | 131 | 8258 | 6 | 5 | 77,8 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2553 PE=4 SV=1 | 131 | 38073 | 4 | 3 | 14,2 |
| Glutamine transport ATP-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=glnQ PE=4 SV=1 | 130 | 26645 | 6 | 5 | 27,3 |
| Aminobutyrate aminotransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2298 PE=3 SV=1 | 130 | 45602 | 4 | 4 | 12,3 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1012 PE=4 SV=1 | 130 | 11754 | 3 | 3 | 39 |
| Probable LacI-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1355 PE=4 SV=1 | 130 | 36157 | 5 | 5 | 25,1 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2423 PE=4 SV=1 | 130 | 11209 | 5 | 4 | 56,5 |
| Putative aldo/keto reductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1036 PE=4 SV=1 | 130 | 36903 | 5 | 3 | 22,1 |
| Uracil-DNA glycosylase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ung PE=3 SV=1 | 130 | 27035 | 6 | 6 | 45,6 |
| Ketol-acid reductoisomerase (NADP(+)) OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ilvC PE=3 SV=1 | 947 | 36411 | 37 | 16 | 57,7 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1058 PE=4 SV=1 | 130 | 14887 | 2 | 1 | 10,2 |
| RNA polymerase sigma factor OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=sigE PE=3 SV=1 | 129 | 22781 | 4 | 2 | 13,1 |
| 50S ribosomal protein L21 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rplU PE=3 SV=1 | 129 | 11540 | 6 | 5 | 68,9 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1298 PE=4 SV=1 | 129 | 10128 | 2 | 1 | 19,6 |
| S-(hydroxymethyl)glutathione dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=adhI PE=3 SV=1 | 129 | 39960 | 6 | 5 | 21,5 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3809 PE=3 SV=1 | 129 | 34221 | 6 | 4 | 18,1 |
| Imidazoleglycerol-phosphate dehydratase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=hisB PE=3 SV=2 | 129 | 21623 | 6 | 6 | 40,5 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1292 PE=4 SV=1 | 129 | 29653 | 3 | 3 | 20,7 |
| Putative iron-sulfur cluster insertion protein ErpA OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=erpA PE=3 SV=1 | 129 | 13304 | 5 | 5 | 54,5 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0403 PE=4 SV=1 | 128 | 52181 | 8 | 8 | 28 |
| Putative thiolase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2059 PE=3 SV=1 | 943 | 40843 | 41 | 21 | 62,5 |
| NADH-quinone oxidoreductase subunit B OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=nuoB PE=3 SV=1 | 128 | 17756 | 4 | 4 | 26,6 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0596 PE=4 SV=1 | 117 | 23498 | 5 | 3 | 12,9 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1488 PE=4 SV=1 | 128 | 23441 | 8 | 5 | 17,2 |
| Lipoprotein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2782 PE=4 SV=1 | 128 | 8108 | 3 | 3 | 68,5 |
| Ribosomal silencing factor RsfS OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rsfS PE=3 SV=1 | 128 | 14055 | 3 | 3 | 29,7 |
| Exodeoxyribonuclease 7 large subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=xseA PE=3 SV=1 | 128 | 50301 | 14 | 12 | 27,9 |
| Alanine racemase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=dadX PE=3 SV=1 | 128 | 39849 | 4 | 4 | 14,7 |
| Methylaspartate ammonia-lyase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0806 PE=4 SV=1 | 128 | 45213 | 5 | 5 | 14,1 |

| | | | | | |
|---|---|---|---|---|---|
| Probable acyl-CoA dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0625 PE=3 SV=1 | 127 | 42987 | 5 | 5 | 16,1 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2802 PE=4 SV=1 | 127 | 34185 | 4 | 4 | 16,2 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0506 PE=4 SV=1 | 127 | 42851 | 6 | 6 | 20,8 |
| Ribonuclease E OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rne PE=3 SV=1 | 940 | 113110 | 34 | 24 | 27,3 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2789 PE=3 SV=1 | 127 | 34214 | 9 | 8 | 41,8 |
| Putative type III secretion protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bscC PE=3 SV=1 | 127 | 63326 | 5 | 5 | 11,3 |
| Cyclic pyranopterin monophosphate synthase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=moaC PE=3 SV=1 | 127 | 17623 | 6 | 4 | 27,3 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0184 PE=4 SV=1 | 125 | 130231 | 14 | 14 | 13,6 |
| Putative two-component system response regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3138 PE=4 SV=1 | 125 | 25593 | 6 | 4 | 23,7 |
| 4-hydroxy-tetrahydrodipicolinate reductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=dapB PE=3 SV=1 | 125 | 28538 | 6 | 4 | 21,6 |
| Kynureninase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=kynU PE=3 SV=1 | 125 | 45951 | 3 | 3 | 8,9 |
| Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=accD PE=3 SV=1 | 124 | 31996 | 11 | 11 | 39 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1192 PE=4 SV=1 | 124 | 11660 | 5 | 3 | 26,9 |
| Ribosomal RNA small subunit methyltransferase I OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rsmI PE=3 SV=1 | 124 | 33044 | 6 | 6 | 24,7 |
| Putative zinc protease OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2497 PE=1 SV=1 | 2485 | 101044 | 84 | 44 | 58,5 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0205 PE=4 SV=1 | 933 | 19415 | 30 | 10 | 58 |
| Ribosomal RNA large subunit methyltransferase J OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rlmJ PE=3 SV=1 | 123 | 32707 | 7 | 6 | 22 |
| dITP/XTP pyrophosphatase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1593 PE=3 SV=1 | 123 | 22748 | 6 | 4 | 23,5 |
| Putative dioxygenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0783 PE=4 SV=1 | 123 | 32609 | 6 | 6 | 26,9 |
| Riboflavin biosynthesis protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ribF PE=3 SV=1 | 123 | 35665 | 5 | 5 | 23,1 |
| Probable LysR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1613 PE=3 SV=1 | 122 | 35124 | 7 | 6 | 19,9 |
| Putative monooxygenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3413 PE=4 SV=1 | 122 | 42120 | 4 | 4 | 13,7 |
| Stringent starvation protein B OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=sspB PE=4 SV=1 | 122 | 15903 | 4 | 3 | 32,9 |
| 2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ispD PE=3 SV=1 | 121 | 23818 | 6 | 5 | 34,8 |
| Regulatory protein BvgR OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bvgR PE=4 SV=1 | 121 | 32504 | 4 | 4 | 16,5 |
| Probable transcriptional regulatory protein BP2308 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2308 PE=3 SV=1 | 121 | 26417 | 7 | 6 | 32,5 |
| Amino acid-binding periplasmic protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0558 PE=3 SV=1 | 922 | 36346 | 23 | 14 | 58,6 |
| Putative extracellular solute-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1529 PE=4 SV=1 | 904 | 36766 | 29 | 17 | 53,8 |
| Putative ABC transporter periplasmic amino acid-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3831 PE=3 SV=1 | 865 | 36883 | 32 | 18 | 58,6 |
| Pantothenate synthetase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=panC PE=3 SV=1 | 121 | 31725 | 8 | 6 | 28,9 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2786 PE=1 SV=1 | 121 | 15779 | 3 | 2 | 25,3 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2735 PE=4 SV=1 | 121 | 10061 | 8 | 7 | 70,5 |
| Putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0459 PE=4 SV=1 | 120 | 94641 | 3 | 2 | 5,6 |
| Cell division topological specificity factor OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=minE PE=3 SV=1 | 120 | 9483 | 5 | 5 | 61,4 |
| 30S ribosomal protein S15 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpsO PE=3 SV=1 | 120 | 10262 | 4 | 4 | 38,2 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3867 PE=4 SV=1 | 120 | 35802 | 6 | 5 | 21 |
| Iron-sulfur cluster assembly protein CyaY OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=cyaY PE=3 SV=1 | 120 | 11899 | 2 | 1 | 18,3 |
| Putative oxidoreductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2726 PE=4 SV=1 | 119 | 24491 | 5 | 5 | 23,9 |
| D,D-heptose 1,7-bisphosphate phosphatase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0035 PE=3 SV=1 | 119 | 19308 | 6 | 5 | 43,6 |
| 30S ribosomal protein S1 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpsA PE=3 SV=1 | 917 | 63036 | 33 | 19 | 35,9 |

| | | | | | |
|---|---|---|---|---|---|
| Lipopolysaccharide biosynthesis protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bplC PE=3 SV=1 | 119 | 39993 | 6 | 5 | 26,5 |
| NADH-quinone oxidoreductase subunit N OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=nuoN PE=3 SV=1 | 118 | 52728 | 3 | 3 | 8,9 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3242 PE=4 SV=1 | 118 | 23697 | 6 | 5 | 29,3 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2972 PE=4 SV=1 | 118 | 14167 | 3 | 3 | 31 |
| Putative exodeoxyribonuclease III OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2110 PE=4 SV=1 | 118 | 29669 | 10 | 9 | 43,8 |
| 50S ribosomal protein L32 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpmF PE=3 SV=1 | 118 | 6817 | 5 | 2 | 55 |
| Putative GntR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0428 PE=4 SV=1 | 118 | 24176 | 4 | 4 | 22,4 |
| Glutathione S-transferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=gst PE=4 SV=1 | 117 | 22611 | 3 | 2 | 11,6 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1079 PE=4 SV=1 | 117 | 21215 | 7 | 5 | 38,5 |
| L-serine dehydratase 1 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=sdaA PE=4 SV=1 | 117 | 49622 | 8 | 8 | 20,1 |
| Outer membrane protein assembly factor BamB OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bamB PE=3 SV=1 | 910 | 40237 | 28 | 12 | 54,7 |
| Putative enoyl-CoA hydratase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3304 PE=3 SV=1 | 116 | 30068 | 5 | 5 | 22,3 |
| Putative oxidoreductase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0901 PE=4 SV=1 | 116 | 36631 | 4 | 4 | 14,1 |
| Muramoyltetrapeptide carboxypeptidase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ldcA PE=4 SV=1 | 116 | 36257 | 6 | 6 | 19,2 |
| Putative malonyl-CoA decarboxylase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2062 PE=4 SV=1 | 116 | 47938 | 8 | 7 | 20,8 |
| Phosphate acyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=plsX PE=3 SV=1 | 115 | 37779 | 9 | 7 | 24,4 |
| Recombination-associated protein RdgC OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rdgC PE=3 SV=1 | 115 | 33596 | 7 | 6 | 25,1 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2653 PE=4 SV=1 | 115 | 33379 | 6 | 6 | 26,3 |
| Putative glycosyl transferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3238 PE=4 SV=1 | 114 | 36068 | 8 | 7 | 28,3 |
| Thymidylate kinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=tmk PE=3 SV=1 | 114 | 23453 | 6 | 6 | 35,6 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3328 PE=4 SV=1 | 114 | 41167 | 8 | 7 | 18 |
| Polysaccharide biosynthesis protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=wbpO PE=3 SV=1 | 904 | 46872 | 32 | 18 | 57,8 |
| Capsular polysaccharide biosynthesis protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=wbpO PE=3 SV=1 | 904 | 47367 | 32 | 18 | 57,1 |
| Adenosylmethionine-8-amino-7-oxononanoate aminotransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=bioA PE=3 SV=1 | 113 | 46481 | 7 | 7 | 19,8 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3801 PE=4 SV=1 | 113 | 50772 | 8 | 7 | 12,4 |
| FolC bifunctional protein [includes: folylpolyglutamate synthase and dihydrofolate synthase] OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=folC PE=3 SV=1 | 113 | 46687 | 5 | 5 | 20,5 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0581 PE=4 SV=1 | 113 | 37359 | 11 | 8 | 28,6 |
| 50S ribosomal protein L17 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rplQ PE=3 SV=1 | 112 | 14781 | 7 | 6 | 51,1 |
| Respiratory-chain NADH dehydrogenase I, 24 kDa subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=nuoE PE=4 SV=1 | 112 | 18281 | 7 | 5 | 39,6 |
| Putative transcriptional regulator (Fragment) OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2618 PE=4 SV=1 | 112 | 28901 | 6 | 4 | 24,7 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3489 PE=3 SV=1 | 112 | 19218 | 6 | 4 | 19,1 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1087 PE=4 SV=1 | 112 | 16726 | 2 | 1 | 13,8 |
| Lipoprotein releasing system transmembrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=lolC PE=4 SV=1 | 111 | 44096 | 9 | 8 | 14,6 |
| Probable extracellular solute-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0121 PE=4 SV=1 | 903 | 47122 | 28 | 19 | 49,1 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2003 PE=4 SV=1 | 111 | 77184 | 2 | 2 | 7,9 |
| DNA repair protein RadA OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=radA PE=3 SV=1 | 111 | 48247 | 7 | 7 | 20,8 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1705 PE=3 SV=1 | 111 | 41262 | 6 | 6 | 18,4 |
| Protease HtpX homolog OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=htpX PE=3 SV=1 | 111 | 31427 | 3 | 3 | 16,7 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2231 PE=4 SV=1 | 111 | 43074 | 6 | 4 | 14,2 |

| | | | | | |
|---|---|---|---|---|---|
| Peptide deformylase 2 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=def2 PE=3 SV=1 | 110 | 19488 | 4 | 4 | 27,1 |
| Putative amidase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1874 PE=4 SV=1 | 110 | 46187 | 5 | 5 | 11,6 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3448 PE=4 SV=1 | 110 | 21791 | 2 | 2 | 17 |
| Phage-related putative membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3388 PE=4 SV=1 | 110 | 25718 | 4 | 3 | 22,4 |
| Putative integral membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2420 PE=4 SV=1 | 110 | 39982 | 2 | 2 | 9,7 |
| Aspartate--tRNA(Asp/Asn) ligase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=aspS PE=3 SV=1 | 900 | 67522 | 28 | 19 | 38,8 |
| Regulatory protein RecX OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=recX PE=3 SV=1 | 109 | 21132 | 3 | 3 | 20,7 |
| Putative sulfatase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3136 PE=4 SV=1 | 109 | 73286 | 8 | 6 | 10,6 |
| Nucleoside diphosphate kinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ndk PE=3 SV=1 | 109 | 15450 | 7 | 3 | 21,3 |
| DNA-binding transcriptional regulator NtrC OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=glnG PE=4 SV=1 | 109 | 53682 | 5 | 5 | 16,6 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3498 PE=4 SV=1 | 108 | 25367 | 4 | 4 | 18,9 |
| Beta-hexosaminidase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=nagZ PE=3 SV=1 | 108 | 38882 | 5 | 5 | 14,8 |
| Probable glutathione S-transferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1006 PE=4 SV=1 | 108 | 23390 | 5 | 5 | 35,2 |
| Putative transferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2378 PE=4 SV=1 | 108 | 18495 | 4 | 3 | 24,3 |
| Glycine cleavage system H protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=gcvH PE=3 SV=1 | 108 | 13110 | 4 | 3 | 28,2 |
| GntR family regulatory proteins OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3667 PE=4 SV=1 | 108 | 29109 | 4 | 4 | 30,3 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0387 PE=4 SV=1 | 895 | 24900 | 23 | 10 | 56,7 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0334 PE=4 SV=1 | 107 | 33836 | 6 | 6 | 35 |
| 30S ribosomal protein S21 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpsU PE=3 SV=1 | 107 | 8530 | 3 | 3 | 28,6 |
| Amidophosphoribosyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=purF PE=3 SV=1 | 107 | 55833 | 9 | 6 | 12,6 |
| Probable protein kinase UbiB OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=ubiB PE=3 SV=1 | 106 | 58522 | 11 | 8 | 20,2 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2147 PE=4 SV=1 | 106 | 16865 | 4 | 3 | 27 |
| Putative lipoprotein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2714 PE=4 SV=1 | 106 | 15370 | 3 | 3 | 35 |
| Two-component response regulatory protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2547 PE=4 SV=1 | 106 | 25085 | 2 | 2 | 13,1 |
| Probable Fe(2+)-trafficking protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2336 PE=3 SV=1 | 106 | 10618 | 8 | 6 | 76,7 |
| Lactoylglutathione lyase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=gloA PE=3 SV=1 | 105 | 14927 | 5 | 5 | 53,4 |
| MerR-family transcriptional regulator OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0441 PE=4 SV=1 | 105 | 14472 | 5 | 5 | 38,7 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2535 PE=4 SV=1 | 895 | 41327 | 30 | 18 | 59,1 |
| Primosomal replication protein N OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=priB PE=1 SV=1 | 105 | 11474 | 2 | 1 | 24,3 |
| Putative cytidylyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3602 PE=4 SV=1 | 105 | 17486 | 3 | 3 | 27,2 |
| Cell division protein FtsX OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3833 PE=3 SV=1 | 104 | 31891 | 3 | 3 | 14,9 |
| 30S ribosomal protein S17 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rpsQ PE=3 SV=1 | 104 | 10627 | 4 | 2 | 34,4 |
| Curved DNA-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=cbpA PE=4 SV=1 | 104 | 34728 | 6 | 5 | 29,8 |
| Probable short-chain dehydrogenase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1163 PE=4 SV=1 | 104 | 27082 | 5 | 5 | 27,4 |
| UDP-N-acetylglucosamine 1-carboxyvinyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=murA PE=3 SV=1 | 103 | 44641 | 7 | 7 | 19,7 |
| Putative extracellular solute-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1983 PE=4 SV=1 | 103 | 84368 | 9 | 9 | 21,1 |
| Uncharacterized protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3115 PE=4 SV=1 | 103 | 43920 | 7 | 5 | 14,9 |
| Putative ABC transport protein, ATP-binding component OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP2744 PE=4 SV=1 | 103 | 29141 | 6 | 5 | 24 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3467 PE=4 SV=1 | 895 | 87687 | 44 | 28 | 47,3 |
| 2-amino-4-hydroxy-6-hydroxymethyldihydropteridi ne pyrophosphokinase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=folK PE=4 SV=1 | 103 | 17506 | 3 | 2 | 20,9 |

| | | | | | |
|---|---|---|---|---|---|
| Cys-tRNA(Pro)/Cys-tRNA(Cys) deacylase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1541 PE=3 SV=1 | 103 | 17717 | 5 | 3 | 22,2 |
| Protein ApaG OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=apaG PE=1 SV=1 | 103 | 14714 | 4 | 2 | 22,9 |
| 50S ribosomal protein L7/L12 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=rplL PE=3 SV=1 | 103 | 12788 | 4 | 2 | 15 |
| Putative oligopeptide transport integral membrane protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP1985 PE=3 SV=1 | 102 | 53158 | 5 | 4 | 10,1 |
| Biotin carboxyl carrier protein of acetyl-CoA carboxylase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=fabE PE=4 SV=1 | 102 | 15568 | 1 | 1 | 11,4 |
| S-adenosylmethionine:tRNA ribosyltransferase-isomerase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=queA PE=3 SV=1 | 102 | 37617 | 5 | 5 | 23,6 |
| Putative acetyltransferase OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP3555 PE=4 SV=1 | 101 | 44522 | 5 | 4 | 15,4 |
| High-affinity branched-chain amino acid transport, ATP-binding protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=livF PE=4 SV=1 | 101 | 25459 | 10 | 9 | 57,5 |
| Putative exported protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) OX=257313 GN=BP0461 PE=4 SV=1 | 100 | 37973 | 6 | 6 | 28,8 |

**Supplemental Table 3. Annotation of LC/MS-identified antigens**

| Label | UniProt. ID | Annotation | Gene ontogeny |
|---|---|---|---|
| **1** | **Q7VZU0** | RNA processing, mRNA catabolic process | BP |
| | | cytoplasma | CC |
| | | 3'-5'-exoribonuclease activity, magnesium ion binding, RNA binding, polyribonucleotide nucleotidyltransferase activity | MF |
| **2** | **Q45340** | cell adhesion, pathogenesis | BP |
| | | extracellular region, cell outer membrane, cell surface, integral component of membrane, periplasmic space | CC |
| **3** | **Q7VZG0** | translation | BP |
| | | ribosome | CC |
| | | RNA binding, structural constituent of ribosome | MF |
| **4** | **P48210** | protein refolding | BP |
| | | cytoplasm | CC |
| | | ATP binding | MF |
| **5** | **P14283** | cell adhesion, pathogenesis, | BP |
| | | extracellular region, cell outer membrane, cell surface, integral component of membrane, periplasmic space | CC |
| **6** | **Q7VU66** | tryptophan biosynthetic process, cellular amino acid biosynthetic process | BP |
| | | magnesium ion binding, anthranilate phosphoribosyltransferase activity | MF |
| | **Q7VYN1** | amino acid transport | BP |
| | **Q7VVC9** | amino acid transport | BP |
| **7** | **Q7VZB0** | protein folding | BP |
| | | DNA binding | MF |
| **8** | **Q7VUV7** | transport | BP |
| | | outer membrane-bounded periplasmic space | CC |
| | | metal ion binding | MF |
| **9** | **Q7W0S2** | translation, regulation of translation | BP |
| | | large ribosomal subunit | CC |
| | | tRNA binding, structural constituent of ribosome, rRNA binding | MF |
| **10** | **Q7W0E4** | glycine decarboxylation via glycine cleavage system | BP |
| | | glycine cleavage complex | CC |
| | **Q7VW32** | cytoplasm | CC |
| | | ACP phosphopantetheine attachment site binding involved in fatty acid biosynthetic process | MF |
| **11** | **P12255** | cell surface | CC |
| **12** | **Q7VVJ2** | Uncharacterized | |

| | | | |
|---|---|---|---|
| **13** | **P14283** | cell adhesion, pathogenesis<br>extracellular region, cell outer membrane, cell surface, integral component of membrane, periplasmic space | BP<br>CC |
| **14** | **P04977** | pathogenesis<br>extracellular region<br>NAD+ ADP-ribosyltransferase activity | BP<br>CC<br>MF |
| **15** | **P04978**<br>**P04979** | pathogenesis<br>extracellular region | BP<br>CC |
| **16** | **Q7VVY2** | protein folding<br>ATP binding | BP<br>MF |
| **17** | **Q7VUE7** | polysaccharide biosynthetic process<br>oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor, oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor, NAD binding, | BP<br>MF |
| **18** | **P12255** | cell surface | CC |
| **19** | **Q7VWW8** | uncharacterized | |
| **20** | **Q7VXB3** | transport<br>outer membrane-bounded periplasmic space, | BP<br>CC |
| **21,22** | **P40415** | peptidyl-prolyl cis-trans isomerase activity | MF |
| **23** | **Q7VYH5** | transporter activity | MF |
| **24** | **P37369** | superoxide dismutase activity, metal ion binding | MF |
| | **Q7W0K2** | cell redox homeostasis<br>periplasmic space<br>protein disulfide oxidoreductase activity | BP<br>CC<br>MF |
| **25** | **Q7W0S4** | DNA-templated transcription, termination, DNA-templated transcription, elongation, transcription antitermination, regulation of DNA-templated transcription, elongation | BP |
| **26** | **Q7VX98** | protein folding<br>peptidyl-prolyl cis-trans isomerase activity | BP<br>MF |
| **27** | **P0A339** | protein folding<br>cytoplasm<br>DNA binding | BP<br>CC<br>MF |
| **28** | **LPS** | | |
| **29** | **P0A3R5** | pathogenesis<br>extracellular region, membrane, host cell plasma membrane | BP<br>CC |
| **30** | **Q7VW79** | glycolytic process<br>phosphopyruvate hydratase complex, extracellular region, cell surface<br>magnesium ion binding, phosphopyruvate hydratase activity | BP<br>CC<br>MF |
| **31** | **Q7VSR6** | transmembrane transport | BP |