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## Identificação *in silico* de potenciais alvos antigênicos de *Corynebacterium pseudotuberculosis*

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**Resumo.** *Corynebacterium pseudotuberculosis* é uma bactéria Gram-positiva causadora da linfadenite caseosa. A linfadenite caseosa acomete principalmente pequenos ruminantes como caprinos e ovinos. O controle da doença é muito difícil, uma vez que a doença já está estabelecida no rebanho. **Objetivo:** O proteoma do *Corynebacterium pseudotuberculosis* foi submetido a avaliação *in silico* da localização subcelular e topologia proteica. A predição *in silico* dos epítópos lineares de células B foi efetuada e realizada a análise de conservação desses epítópos em outros proteomas do *C. pseudotuberculosis* depositada na base de dados do UNIPROT. **Resultados:** 111 proteínas foram selecionadas a partir da avaliação subcelular e topologia proteica, com a posterior submissão dessas proteínas a uma predição de epítópos lineares de células B e análise de conservação desses em outros proteomas de *C. pseudotuberculosis*, resultando em 9 proteínas com uma ou mais regiões de epítópos conservados numa mesma proteína. **Conclusão:** Regiões conservadas favorecem um reconhecimento maior de抗ígenos quando avaliados. Além disso, neste trabalho é fornecida uma lista de epítópos que podem ser sintetizados e testados *in vitro*.

**Palavras chave:** *Corynebacterium pseudotuberculosis*, epítópos, imunoinformática

## *In silico* identification of potential antigenic targets of *Corynebacterium pseudotuberculosis*

**Abstract:** *Corynebacterium pseudotuberculosis* is a gram-positive bacterium that causes caseous lymphadenitis. Caseous lymphadenitis mainly affects small ruminants such as goats and sheep. Controlling the disease is very difficult, since the disease is already established in the herd. **Objective:** The proteome of *Corynebacterium pseudotuberculosis* was subjected to *in silico* evaluation of subcellular localization and protein topology. The *in silico* prediction of linear B cell epitopes was performed and the conservation analysis of these epitopes was performed on other *C. pseudotuberculosis* proteomes deposited in the UNIPROT database. **Results:** 111 proteins were selected from the subcellular evaluation and protein topology, with the subsequent submission of these proteins to a prediction of linear B cell epitopes and their conservation analysis in other proteases of *C. pseudotuberculosis*, resulting in 9 proteins with one or more regions of epitopes conserved in the same protein. **Conclusion:** Conserved regions favor a greater recognition of antigens

when evaluated. In addition, a list of epitopes that can be synthesized and tested *in vitro* is provided in this paper.

**Key words:** *Corynebacterium pseudotuberculosis*, epitopes, immunoinformatic

## Identificación *in silico* de posibles objetivos antigenicos de *Corynebacterium pseudotuberculosis*

**Resumen.** *Corynebacterium pseudotuberculosis* es una bacteria gram-positiva causante de la linfadenitis caseosa. La linfadenitis caseosa afecta principalmente a pequeños rumiantes como los caprinos y los ovinos. El control de la enfermedad es muy difícil, ya que la enfermedad ya está establecida en el rebaño. **Objetivo:** El proteoma del *Corynebacterium pseudotuberculosis* fue sometido a la evaluación *in silico* de la localización subcelular y topología proteica. La predicción *in silico* de los epítopenos lineales de células B fue efectuada y realizada el análisis de conservación de estos epítopenos en otros proteomas de la *C. pseudotuberculosis* depositada en la base de datos del UNIPROT. **Resultados:** 111 proteínas fueron seleccionadas a partir de la evaluación subcelular y topología proteica, con la posterior sumisión de esas proteínas a una predicción de epítopenos lineales de células B y análisis de conservación de estos en otros proteomas de *C. pseudotuberculosis*, resultando en 9 proteínas con una o más regiones de epítopenos conservados en una misma proteína. **Conclusión:** Las regiones conservadas favorecen un mayor reconocimiento de antígenos cuando se los evalúan. Además, en este trabajo se proporciona una lista de epítopenos que pueden ser sintetizados y probados *in vitro*.

**Palabras clave:** *Corynebacterium pseudotuberculosis*, epítopenos, imunoinformática

### Introdução

*Corynebacterium pseudotuberculosis* (*Cp*) é uma bactéria bacilar Gram-positiva, intracelular facultativa, imóvel, não esporulada e com capacidade fermentativa que causa a linfadenite caseosa em pequenos ruminantes, principalmente em caprinos e ovinos (Brum et al., 2017; Zhou et al., 2019). A linfadenite caseosa é caracterizada pelo aparecimento de granulomas contendo material caseoso nos linfonodos superficiais ou em vísceras (Corrêa et al., 2018; Eckersall & Bell, 2010; Santos Junior & Gomes, 2014). Como relatado na literatura, a transmissão pode ocorrer pelo material caseoso contaminado, tendo a via oral, nasal e cutânea como vias de transmissão (Othman et al., 2016; Varela-Castro et al., 2017).

O controle da linfadenite caseosa é de extrema importância para evitar perdas econômicas em muitos países, incluindo o Brasil (Batey, 1986; Nairn & Robertson, 1974). Entretanto, o tratamento existente ainda é pouco eficiente e se baseia na drenagem do abscesso e cauterização química, ou tratamento com antibiótico, este por sua vez possui custo elevado e muitas vezes o antibiótico não consegue alcançar as bactérias devido a sua localização, dentro dos piogranulomas (Batey, 1986; Brum et al., 2017; Nairn & Robertson, 1974). Abordagens recentes estão sendo desenvolvidas para a confecção de novos testes de diagnósticos mais sensíveis e específicos para a linfadenite caseosa. Essas novas abordagens envolvem o uso da bioinformática, enriquecendo ainda mais os novos estudos e os estudos existentes para os potenciais alvos terapêuticos, como proteínas com fator de virulência, mapas genéticos, dentre outros (Guimarães et al., 2011; Sobrinho Santos et al., 2018). A maioria dos determinantes genéticos de virulência do *Cp* é, até o momento, pouco caracterizados, podendo ter as proteínas em sua maioria como um fator de virulência ou até mesmo serem codificadoras dos fatores de virulência (Dorella et al., 2006). O principal fator de virulência é atribuído à exotoxina Fosfolipase D (PLD), se fazendo necessário para a comunidade científica a descoberta de proteínas e genes que tenham a função de líderes na virulência do *Cp* (Fontaine & Baird, 2008; Merchant & Packer, 1975; Muckle & Gyles, 1982; Songer et al., 1988; Souza et al., 2011; Sutherland et al., 1996).

O objetivo deste estudo foi identificar *in silico* os principais epítopenos como potenciais antigenicos de proteínas de *Corynebacterium pseudotuberculosis C231* a partir de base de dados públicas.

## Materiais e métodos

### Obtenção dos proteomas

Foi utilizado o proteoma completo da cepa de *C. pseudotuberculosis* C231 do UNIPROT (<http://www.uniprot.org/>) sendo arquivada em formato FASTA. Esta cepa possui 2090 proteínas. Em etapas posteriores do trabalho, também foram utilizados outros 70 proteomas *C. pseudotuberculosis* depositados na base de dados do UNIPROT, todos foram arquivados em formato FASTA.

### Avaliação in silico de localização subcelular

Nesta etapa, o proteoma da cepa C231 de *C. pseudotuberculosis* foi submetido à análise de localização sub-cellular no software público online CELLO2GO (<http://cello.life.nctu.edu.tw>). Com base nas sequências das proteínas, a plataforma online identifica a ontologia gênica de cada proteína, ou seja, o local em que cada proteína do proteoma se encontra.

### Avaliação in silico da topologia proteica

As topologias de proteínas foram avaliadas usando o software TOPCONS (<http://topcons.cbr.su.se/>). Esse software suporta sequências de aminoácidos formatada em FASTA ou um arquivo com múltiplas sequências, tendo os resultados apresentados aos usuários graficamente na tela, tendo a opção do download em formato de texto simples e também receber os resultados por e-mail, caso fornecidos. Com base na sequência de aminoácidos de cada proteína, o algoritmo do programa identifica a presença de peptídeo sinal e hélices transmembrana, sendo mapeadas as proteínas exportadas para o ambiente extracelular e as proteínas ancoradas na membrana e parede celular. Moléculas que apresentam exposição extracelular são acessíveis às células do sistema imunológico, constituindo potenciais alvos para uso como抗ígenos em ensaios de imunodiagnóstico.

### Predição in silico de epítópos lineares de células B

As proteínas selecionadas nas etapas anteriores foram submetidas ao mapeamento *in silico* de epítópos lineares de células B, utilizando diferentes modelos preditivos: Bepipred, LBtope, Método Chou & Fasman Beta, Emini Surface Accessibility, Karplus & Schulz Flexibility e Parker para a identificação de padrões de hidrofilicidade dos aminoácidos e estruturas secundárias das proteínas, prever e projetar epítópos lineares de células B, calcular a probabilidade de um trecho de resíduos de aminoácidos fazer parte da estrutura secundária β-turn (alças-β), calcular a acessibilidade à superfície da proteína e a probabilidade dos aminoácidos estarem expostos nessa superfície, avaliar a flexibilidade e mobilidade dos segmentos proteicos e avaliar em escalas de hidrofilicidade dos conjuntos de resíduos de aminoácidos em uma proteína, respectivamente.

Foram considerados potencialmente antigênicos aqueles peptídeos que apresentaram afinidade de ligação por anticorpos em todos os modelos preditivos utilizados. Desta forma, foi confeccionado um novo arquivo FASTA contendo todos os epítópos selecionados para posterior utilização.

### Análise de conservação dos epítópos no proteoma de outras cepas de *C. pseudotuberculosis*

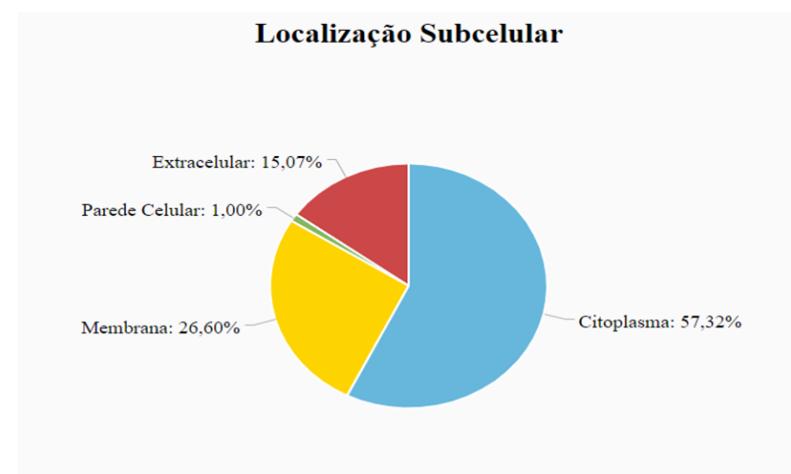
Os epítópos selecionados foram submetidos a uma análise de conservação entre os diferentes proteomas de *C. pseudotuberculosis* depositados na base de dados do UNIPROT. Foi utilizado o software “**Epitope Conservancy Analysis**” (<http://tools.iedb.org/conservancy/>) para calcular o grau de conservação dos epítopo dentro de um determinado grupo de sequências de proteínas em diferentes graus de identidade.

Além da análise de conservação, os epítópos preditos também foram submetidos a uma análise de sobreposição de sequências, por meio do programa online *Epitope Cluster Analysis* (<http://tools.immuneepitope.org/cluster/>). Posterior aos alinhamentos dos peptídeos, foram identificados os epítópos que compartilham sequências de aminoácidos idênticas em uma de suas extremidades, sendo agrupados em *clusters* de acordo com essas sobreposições, permitindo em momento futuro a confecção de uma sequência consenso, que contenha os diferentes epítópos simultaneamente. Os epítópos

conservados e presentes em todos os proteomas de *C. pseudotuberculosis* podem ser selecionados para uma etapa de síntese química e posterior validação experimental da antigenicidade.

## Resultados

A predição da análise da localização subcelular de proteínas e anotações sobre a função molecular e a função que cada gene tem no processo biológico do proteoma da cepa de *Corynebacterium pseudotuberculosis C231* ao software público CELLO2GO (<http://cello.life.nctu.edu.tw/>) teve como resultado 315 proteínas extracelulares (Anexo 1), tendo o proteoma um total de 2090 proteínas. As proteínas extracelulares correspondem a aproximadamente 15,07% do proteoma total (Figura 1).



**Figura 1. Análise da localização subcelular.** O software mostra a localização e a quantidade de proteínas que existe em cada compartimento, além do gráfico com proporções em porcentagem de cada proteína de acordo com a localização. O *Corynebacterium pseudotuberculosis C231* possui, aproximadamente, 15,07% de proteínas extracelulares; 57,32% de proteínas citoplasmáticas; 26,60% de proteínas de membrana; e 1% de proteínas de parede celular.

## Avaliação da topologia proteica

A plataforma online TOPCONS foi utilizada para a previsão e avaliação da topologia de cada proteína e avaliação da presença de peptídeo sinal nas 315 proteínas que o CELLO2GO sinalizou como proteínas extracelulares. O algoritmo do TOPCONS sinalizou 205 proteínas como extracelulares e possuíam o peptídeo sinal (Anexo 1). Foram selecionadas apenas proteínas que foram positivas aos dois softwares, ou seja, que eram proteínas extracelulares e que possuíam peptídeo sinal, totalizado um total de 111 proteínas selecionadas (Anexo 1).

## Predição de epítópos de células B

As proteínas extracelulares selecionadas na etapa anterior foram submetidas ao mapeamento *in silico* de epítópos lineares de células B e as regiões com afinidade de ligação ao epítopo em todos os testes foram selecionadas, ou seja, regiões comuns a todas as proteínas, dessa forma, 76 proteínas foram selecionadas. Algumas dessas proteínas continham mais de um epítopo de 10 aminoácidos (Anexo 2).

## Análise da conservação de epítópos

A conservação dos 76 epítópos foi avaliada em outros 75 proteomas existentes do *C. pseudotuberculosis*. Foram consideradas regiões de epítópos com grau de identidade acima de 97% para a análise de conservação dos epítópos em questão, resultando em nove proteínas com uma ou mais regiões de epítópos conservados (Tabela 1).

A análise da função gênica, função molecular e dos processos biológicos que cada proteína participa foi realizada, dessa forma, foi efetuada a comparação da similaridade que as mesmas possuem com as cepas do *Cp* e outras bactérias. Partindo desses critérios, foram selecionados 4 melhores epítópos para ser sintetizados individualmente para serem confrontados de acordo a sua eficiência no reconhecimento do antígeno (Tabela 2).

**Tabela 1.** Seleção dos epítópos no software *Epitope Conservancy Analysis*. Foram consideradas regiões que continham uma sequência de 10 aminoácidos, entretanto, em algumas proteínas foram selecionadas regiões contendo de 12-16 aminoácidos. O grau de conservação dessas regiões varia de 97,1 a 98,6% de conservação dentro dos proteomas.

Entrada da proteína no UNIPROT	Região Conservada
D9QBT2	PQVDAGTVAL
D9QAT6	GKEDQRPAWL PAFSKDKLDP
D9QCX3	AKPTPGESFS
D9Q954	VDDAQNYAAA
D9Q9L5	TRTPAKDFSS
	SSNPKTRHP KSSDTPPVER SDTPPVERAI
D9QBC2	KQGTFNPTAP QGTFNPTAPS FNPTAPSGGE NPTAPSGGEV
	GNKSNNQIES PLEGQRQAGK PQATPDTPNY
D9QBZ2	QATPDTPNYY ATPDTPNYP TPDTPNYPG PDTPNYPGG TPNYPGGMV
D9QCZ5	TWKDDQGKIT TPSLEQQDTH
D9QBC3	SSDDKGSSSS DAAAQPPAPD AAQPPAPDAP QPPAPDAPAA
	KSSDTPPVERAI KQGTFNPTAPSGGEV PQATPDTPNYYPGGMV DAAAQPPAPDAPAA

**Tabela 2. Epítópos selecionados.** 4 epítópos foram selecionados de três proteínas diferentes com base na conservação dessas sequências de aminoácidos em 69 dos 75 proteomas analisados, dois epítópos estavam presentes numa mesma proteína. Esses epítópos foram selecionados para o uso em estudos posteriores.

Código da Proteína no UNIPROT	Sequência do Epítopo	Gene	Função Molecular	Processo biológico	Similaridade com microrganismos
D9QAT6	GKEDQRPAWL	CPC231_1186	Atividade da oxirreductase; Ligação de íon	Transporte; resposta ao estresse; processo homeostático	<i>C. ulcerans</i> ; <i>C. ulcerans</i> NCTC 12077; <i>C. pseudotuberculosis</i> ; <i>Pseudomonas Aeruginosa</i>
D9QAT6	PAFSKDKLDP	CPC231_1186	Atividade da oxirreductase; Ligação de íon	Transporte; resposta ao estresse; processo homeostático	<i>C. ulcerans</i> ; <i>C. ulcerans</i> NCTC 12077; <i>C. pseudotuberculosis</i> ; <i>Pseudomonas Aeruginosa</i>
D9Q954	VDDAQNYAAA	rpfA	Ligação de proteínas; Atividade de hidrolase	Patogênese; simbiose (abrangendo o mutualismo através do parasitismo); processo catabólico; organização da parede celular ou biogênese	<i>Mycobacterium tuberculosis</i> ; <i>M. bovis</i> ; <i>Macacine betaherpesvirus</i>
D9Q9L5	TRTPAKDFSS	oppA3	Atividade transportadora transmembrana; Ligação de íon	Transporte; diferenciação celular; formação de estrutura anatômica envolvida na morfogênese; desenvolvimento de estrutura anatômica; locomoção	<i>C. ulcerans</i> ; <i>C. ulcerans</i> NCTC 12077; <i>C. pseudotuberculosis</i> ; <i>Pseudomonas Aeruginosa</i>

## Discussão

Os resultados mostram que a combinação de algoritmos de análises de bioinformática podem ser ferramentas úteis e muito importantes para a identificação de epítópos como potenciais alvos de antigenicidade a partir de genomas já sequenciados. O sequenciamento de genomas de patógenos tornou possível conhecer e analisar os principais抗ígenos que estão relacionados à doença com uma maior rapidez e menor custo, como é o caso do *Corynebacterium pseudotuberculosis* (Droppa-Almeida et al., 2018). Essas análises fornecem informações teóricas muito importantes para testar a hipótese em laboratório.

Dentre as 315 das proteínas extracelulares, o que equivale a 15,1% do proteoma da *Cp C231* (Figura 1), 191 delas são proteínas não caracterizada e não possuíam função experimental estudada (Anexo 1). Sendo a localização subcelular das proteínas uma informação importante para a evidência da função biológica, isso pode realizado de forma rápida e precisa (Spetale et al., 2018; Yu et al., 2004).

A partir da predição de epítópos *in silico* de células B realizada neste trabalho, foi gerada uma lista de epítópos (Anexo 2) que podem ser sintetizados quimicamente e testada a sua antigenicidade. Estudos já realizados demonstram que a descoberta de novos抗ígenos levou ao desenvolvimento de novas estratégias para o desenho de novas vacinas (Duthie et al., 2016; Koff et al., 2014). Estudos também mostram a importância de epítópos conservados em vários isolados diferentes (Marana et al., 2009). A escolha dos epítópos (Tabela 2) com base no grau de conservação dessas regiões em outros proteomas do *Corynebacterium pseudotuberculosis* pode fornecer um maior reconhecimento imunogênico quando testados *in vitro*.

Em conclusão, vale ressaltar que é de extrema importância a identificação dessas regiões em proteínas determinantes para o estabelecimento da linfadenite caseosa. O presente trabalho também pode contribuir com a academia para o desenvolvimento de novos testes de imunodiagnóstico com resultados mais satisfatórios, tendo então uma especificidade e sensibilidade maior.

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# Anexo 1

#	Uniprot entry	Uniprot annotation information		Gene names	Protein Length	Subcellular localization	Prediction of subcellular localization using Cello2GO software	Prediction of protein topology using TopCons software
		Protein names					Number of transmembrane helices	Presence of signal peptide
1	P48288	Protein RecA		RecA	369	Cytoplasmic;	0	No
2	P96749	3-dehydroquinate synthase		aroB	359	Cytoplasmic;	0	No
3	P96750	3-dehydroquinate dehydratase		aroQ	146	Cytoplasmic;	0	No
4	D9QB58	ATP-dependent protease		CpC231_1312	645	Membrane;	0	No
5	D9QBM2	Glutamine synthetase II		glnA2	446	Cytoplasmic;	0	No
6	D9Q957	Glutamine cyclotransferase		CpC231_0598	313	Cytoplasmic;	1	No
7	D9QE99	Response regulator		cstA	234	Cytoplasmic;	0	No
8	D9Q9I9	Uncharacterized protein		CpC231_0733	213	Extracellular;	0	Yes
9	D9Q9T7	Diaminopimelate decarboxylase		lysA	443	Cytoplasmic;	0	No
10	D9QDD3	Uncharacterized protein		CpC231_2069	59	Cytoplasmic;	0	No
11	D9QCR0	Uncharacterized protein		CpC231_1882	364	Membrane;	0	Yes
12	D9QCG6	tRNA(Ile)-lysidine synthase		tilS	280	Cytoplasmic;	0	No
13	D9Q9Z8	Uncharacterized protein		CpC231_0895	522	Membrane;	0	Yes
14	D9QA49	Phenylalanine-tRNA ligase beta subunit		pheT	836	Cytoplasmic;	0	No
15	D9QB41	Mycothione/glutathione reductase		CpC231_1293	463	Membrane;	0	No
16	D9QCV5	Arabinofuranosyltransferase		CpC231_1930	1087	Membrane;	15	No
17	D9QEN4	NlpC/P60 family protein		CpC231_0470	288	Membrane;	0	No
18	D9QCN6	Orotate phosphoribosyltransferase		pyrE	181	Cytoplasmic;	0	No
19	D9QAT2	Lipid A biosynthesis lauroyl acyltransferase		CpC231_1182	305	Cytoplasmic;	0	No
20	D9QEAE8	30S ribosomal protein S7		rpsG	155	Cytoplasmic;	0	No
21	D9Q9Y2	Iron(3+)-hydroxamate import ATP-binding protein FhuC		fhuC	255	Membrane;	0	No
22	D9QBD7	UDP-N-acetylmuramoylalanine-D-glutamate ligase		murD	461	Cytoplasmic;	0	No
23	D9QCZ9	Amidase		CpC231_1974	385	Cytoplasmic;	0	No
24	D9QDH0	Magnesium transporter mgtE		mgtE1	460	Membrane;	5	No
25	D9QCK8	Uncharacterized protein		CpC231_1828	389	Cytoplasmic;	0	No
26	D9QCI3	Uncharacterized protein		CpC231_1803	779	Extracellular;	0	Yes
27	D9Q9R8	Uncharacterized protein		CpC231_0812	139	Membrane;	1	No
28	D9Q995	Glucose-6-phosphate isomerase		pgi	547	Cytoplasmic;	0	No
29	D9QDA2	Formamidopyrimidine-DNA glycosylase		mutM2	273	Cytoplasmic;	0	No
30	D9QCP8	ABC transporter domain-containing ATP-binding subunit		CpC231_1869	268	Membrane;	0	No
31	D9QES4	Uncharacterized protein		CpC231_0510	133	Cytoplasmic;	0	No
32	D9QCQ6	ATP-bindingABC transporter domain-containing protein		CpC231_1878	244	Cytoplasmic;	0	No
33	D9Q981	Oligopeptide transport system permease protein oppB		oppB2	318	Membrane;	6	No
34	D9QB42	Cobyrinic acid synthase		cobQ	481	Cytoplasmic;	0	Yes
35	D9QCK2	ABC transporter glutamine-binding protein glnH		glnH	323	Membrane;	0	Yes
36	D9QA05	Menaquinone-specific isochorismate synthase		menF	372	Cytoplasmic;	0	No
37	D9QEM7	Endonuclease/Exonuclease/phosphatase family		CpC231_0463	299	Extracellular;	0	No
38	D9QEL2	Manganese ABC transporter membrane protein		mntD	269	Membrane;	9	No
39	D9QB01	Competence-damage inducible protein		cinA	171	Cytoplasmic;	0	No
40	D9QE48	Porphobilinogen deaminase		hemC	296	Cytoplasmic;	0	No
41	D9Q960	tRNA/rRNA methyltransferase, SpoU		spoU	290	Cytoplasmic;	0	No
42	D9QEG2	30S ribosomal protein S4		rpsD	201	Cytoplasmic;	0	No
43	D9QAU5	1-deoxy-D-xylulose-5-phosphate synthase		dxs	640	Membrane;	0	No
44	D9QD64	DNA gyrase subunit A		gyrA	854	Cytoplasmic;	0	No
45	D9Q9M2	Uncharacterized protein		CpC231_0766	236	Extracellular;	0	Yes
46	D9QE89	50S ribosomal protein L3		rplC	218	Cytoplasmic;	0	No
47	D9QBV3	Uncharacterized protein		CpC231_1567	197	Membrane;	1	No
48	D9QDI0	Choline transport system permease protein		opuBB	220	Membrane;	5	No
49	D9QA51	Arginine biosynthesis bifunctional protein ArgJ		argJ	386	Membrane;	0	No
50	D9QE29	UDP-N-acetylglucosamine reductase		murB	379	Cytoplasmic;	0	No
51	D9QD00	Uncharacterized protein		CpC231_1975	253	Membrane;	7	No
52	D9QEVS3	Uncharacterized protein		CpC231_0539	401	Extracellular;	1	No
53	D9Q9Q4	2-oxoglutarate dehydrogenase E1 component		odhA	1228	Cytoplasmic;	0	No
54	D9QDJ3	Abhydrolase domain-containing protein 6		CpC231_0067	286	Cytoplasmic;	0	No
55	D9Q9T3	Lactate utilization protein B		lutB	514	Cytoplasmic;	0	No

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56 D9QCP7	Chaperone protein ClpB	clpB	849	Cytoplasmic;	0	No
57 D9QAX1	Transcriptional repressor NrdR	nrdR	151	Cytoplasmic;	0	No
58 D9QAS3	Crossover junction endodeoxyribonuclease RuvC	ruvC	193	Cytoplasmic;	0	No
59 D9QE6	Adenylate kinase	adk	181	Cytoplasmic;	0	Yes
60 D9QE9	Manganese ABC transporter substrate-binding protein	CpC231_0443	318	Extracellular;	0	Yes
61 D9QDZ1	GPPII	gspE	373	Cytoplasmic;	0	No
62 D9QCD8	DNA repair protein RadA	radA	467	Membrane;	0	No
63 D9QDE2	Anthranilate phosphoribosyltransferase	trpD	341	Cytoplasmic;	0	No
64 D9QB9	Uncharacterized protein	CpC231_1458	543	Cytoplasmic;	0	No
65 D9QEC5	30S ribosomal protein S3	rpsC	248	Cytoplasmic;	0	No
66 D9QAU0	Uncharacterized protein	CpC231_1190	435	Membrane;	12	No
67 D9QE27	Uncharacterized protein	CpC231_0256	275	Cytoplasmic;	0	No
68 D9QAK5	Glyceraldehyde-3-phosphate dehydrogenase	gap	334	Cytoplasmic;	0	No
69 D9QA35	Phosphotransferase system II Component	ptsG	670	Membrane;	10	No
70 D9QDW8	Uncharacterized protein	CpC231_0196	468	Extracellular;	0	Yes
71 D9QDE1	Anthranilate synthase component II	trpG	215	Cytoplasmic;	0	No
72 D9QD58	DNA replication and repair protein RecF	recF	404	Cytoplasmic;	0	No
73 D9QCP3	Sortase B	srtB	319	Membrane;	2	No
74 D9QAI2	Uncharacterized protein	CpC231_1082	709	Extracellular;	1	Yes
75 D9QB99	Uncharacterized protein	CpC231_1354	430	Membrane;	12	No
76 D9QDN8	Manganese/zinc/iron transport system	mntC	175	Membrane;	6	No
77 D9QCP0	Uncharacterized protein	CpC231_1861	773	Extracellular;	0	No
78 D9QDN3	GtrA-like integral membrane protein	CpC231_0108	152	Extracellular;	4	No
79 D9QCT9	Urease subunit alpha	ureC	565	Cytoplasmic;	0	No
80 D9QAP4	Putative pre-16S rRNA nuclease	CpC231_1144	197	Cytoplasmic;	0	No
81 D9QDT3	2-isopropylmalate synthase	leuA	605	Cytoplasmic;	0	No
82 D9QE83	50S ribosomal protein L11	rplk	143	Cytoplasmic;	0	No
83 D9QDR3	Glutamyl-tRNA synthetase	gltX	270	Cytoplasmic;	0	No
84 D9QAW4	Proteasome assembly chaperones 2 (PAC2)	pac2	337	Cytoplasmic;	0	No
85 D9QAL4	Riboflavin biosynthesis protein RibD	ribD	353	Membrane;	0	No
86 D9QCT2	Iron(III) dicitrate transport permease-like protein yusV	phuC	256	Membrane;	0	No
87 D9Q9D5	Methionine--tRNA ligase	metG	610	Cytoplasmic;	0	No
88 D9QBT9	ABC-type dipeptide transport system, periplasmic compon	oppA5	513	Extracellular;	0	Yes
89 D9QB7	Uncharacterized protein	CpC231_1455	70	Cytoplasmic;	0	No
90 D9QAN5	Elongation factor P	efp	187	Cytoplasmic;	0	No
91 D9QBY7	Endopeptidase Clp	clpP	199	Cytoplasmic;	0	No
92 D9QEPI	Pyruvate carboxylase	pyc	1141	Cytoplasmic;	0	No
93 D9QCF5	Choline dehydrogenase	betA	582	Cytoplasmic;	0	No
94 D9QBW5	Probable nicotinate-nucleotide adenyllyltransferase	nadD	218	Cytoplasmic;	0	No
95 D9QC89	Phosphate transport system permease protein	pstC	343	Membrane;	6	No
96 D9QE79	FAD-linked oxidoreductase	CpC231_0308	425	Extracellular;	0	No
97 D9QB8	DNA methylase	CpC231_1456	656	Cytoplasmic;	0	No
98 D9QDF0	Branched-chain amino acid permease	azlC	238	Membrane;	6	No
99 D9QB53	Elongation factor Ts	tsf	275	Cytoplasmic;	0	No
100 D9QAV8	Methyltransferase	CpC231_1209	508	Cytoplasmic;	0	No
101 D9QD90	PP2C-family Ser/Thr phosphatase	pstP	503	Cytoplasmic;	1	No
102 D9QEL5	Bifunctional protein FolD	folD	281	Cytoplasmic;	0	No
103 D9Q9W2	Alpha-1,4-glucan:maltose-1-phosphate maltosyltransferase	glgE	671	Cytoplasmic;	0	No
104 D9QAI9	FeS cluster assembly protein sulfB	sufB	484	Cytoplasmic;	0	No
105 D9Q938	Inositol-1-monophosphatase ImpA	impA	294	Cytoplasmic;	0	No
106 D9QD54	Universal stress protein UspA	uspA4	325	Membrane;	0	No
107 D9QA32	DNA polymerase I	polA	886	Cytoplasmic;	0	No
108 D9QCL9	Tetratricopeptide TPR	CpC231_1839	241	Cytoplasmic;	1	No
109 D9QB60	Ribonuclease HII	rnhB	240	Cytoplasmic;	0	No
110 D9QES5	Phosphomannomutase ManB	manB	459	Cytoplasmic;	0	No
111 D9QA61	Haloacid dehalogenase (HAD) superfamily hydrolase	nagD	327	Cytoplasmic;	0	No
112 D9QE40	DNA-binding (Excisionase) protein	xis	63	Cytoplasmic;	0	No
113 D9QCM4	Uncharacterized protein	CpC231_1844	366	Membrane;	5	No
114 D9QDF1	Uncharacterized protein	CpC231_2087	198	Membrane;	0	No
115 D9QD68	Uncharacterized protein	CpC231_0013	86	Extracellular;	0	No
116 D9QAL3	Riboflavin synthase alpha chain	ribE	213	Cytoplasmic;	0	No
117 D9QE08	dTDP-glucose 4,6-dehydratase	rmlB	334	Cytoplasmic;	0	No
118 D9QBR0	Uncharacterized protein	CpC231_1520	366	Membrane;	5	No
119 D9Q9J1	Drug transport membrane protein	CpC231_0735	524	Membrane;	14	No
120 D9QC58	Ribonucleoside-diphosphate reductase subunit beta	nrdF2	328	Membrane;	0	No
121 D9QCQ4	Uncharacterized protein	CpC231_1875	174	Membrane;	4	No
122 D9QCZ3	Serine--tRNA ligase	serS	419	Cytoplasmic;	0	No

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123 D9QEG0	30S ribosomal protein S13	rpsM	122 Cytoplasmic;	0	No
124 D9QCP4	Collagen-binding surface protein Cna-like, B-type domain	CpC231_1865	480 Cellwall;	1	Yes
125 D9QDT1	UDP-N-acetylmuramoylalanine--D-glutamate ligase	murD	431 Cytoplasmic;	0	Yes
126 D9QB97	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylide]	hisA	242 Cytoplasmic;	0	No
127 D9QED1	Oligopeptide transport system permease protein oppC	oppC1	346 Membrane;	6	No
128 D9QA38	UvrABC system protein B	uvrB	699 Cytoplasmic;	0	No
129 D9QAJ6	Transketolase	tkt	697 Cytoplasmic;	0	No
130 D9Q9P4	Glycosyl transferase	glgA	390 Cytoplasmic;	0	No
131 D9QBR4	Pyridoxal kinase PdxY	pdxY	283 Cytoplasmic;	0	No
132 D9QBT0	Uncharacterized protein	CpC231_1541	516 Cytoplasmic;	0	No
133 D9QD13	Uncharacterized protein	CpC231_1989	403 Membrane;	12	No
134 D9QBA6	Uncharacterized protein	CpC231_1361	219 Extracellular;	0	Yes
135 D9Q9D8	Ribosomal RNA small subunit methyltransferase A	rsmA	290 Cytoplasmic;	0	No
136 D9QDF6	RNA polymerase sigma factor sigM	sigM	222 Cytoplasmic;	0	No
137 D9QBV5	PemK-like protein	CpC231_1569	184 Cytoplasmic;	0	No
138 D9QB83	Glutamate dehydrogenase	gdh	448 Cytoplasmic;	0	No
139 D9QAF9	Uncharacterized protein	CpC231_1059	317 Cytoplasmic;	0	No
140 D9QAL1	6,7-dimethyl-8-ribityllumazine synthase	ribH	157 Cytoplasmic;	0	No
141 D9Q9W7	Electron transfer flavo protein subunit alpha	etfA	318 Membrane;	0	No
142 D9QC65	NH(3)-dependent NAD(+) synthetase	nadE	276 Cytoplasmic;	0	No
143 D9QEP9	Uncharacterized protein	CpC231_0485	138 Cytoplasmic;	0	No
144 D9QD21	Two-component system sensor kinase protein	tcsS	441 Membrane;	6	No
145 D9QER8	dTDP-Rha:alpha-D-GlcNAc-pyrophosphate polypropenol, alp	wbbL	316 Extracellular;	0	No
146 D9Q9Y1	Iron(3+)-hydroxamate import system permease protein fhu	fhuG	344 Membrane;	10	No
147 D9QAZ3	Regulatory protein RecX	recX	201 Cytoplasmic;	0	No
148 D9QAT1	GDP-mannose-dependent alpha-(1-2)-phosphatidylinositol	pimA	366 Cytoplasmic;	0	No
149 D9Q9J7	Exodeoxyribonuclease 7 large subunit	xseA	413 Cytoplasmic;	0	No
150 D9QEK3	Methionine import system permease protein metI	metI	225 Membrane;	5	No
151 D9QA73	Uncharacterized transporter yclF	yclF	501 Membrane;	14	No
152 D9QC13	Copper resistance D domain-containing protein/Cytochrom	copD	681 Membrane;	16	No
153 D9QA41	Metallo-beta-lactamase superfamily protein	CpC231_0939	242 Cytoplasmic;	0	No
154 D9QEG5	tRNA pseudouridine synthase A	truA	291 Cytoplasmic;	0	No
155 D9QCH4	Mycosubtilin synthase subunit B	mycB	1276 Cellwall;	10	No
156 D9QAD8	M18 family aminopeptidase	pepC2	438 Cytoplasmic;	0	No
157 F9Y364	Phosphoribosyl-ATP pyrophosphatase	hisE	87 Cytoplasmic;	0	No
158 D9QBW2	DegV family protein	CpC231_1576	276 Cytoplasmic;	0	No
159 D9Q9Y5	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subuni	gatB	501 Cytoplasmic;	0	No
160 D9QEC0	50S ribosomal protein L4	rplD	217 Cytoplasmic;	0	No
161 D9QD40	Cation-transporting P-type ATPase A	ctpA	790 Membrane;	8	No
162 D9QCM5	Uncharacterized protein	CpC231_1845	375 Cytoplasmic;	0	Yes
163 D9QCH0	Aerobic C4-dicarboxylate transport protein	dctA	480 Membrane;	10	No
164 D9QBS6	Peptidyl-dipeptidase	dcp	692 Cytoplasmic;	0	No
165 D9QAG3	Methylmalonyl-CoA mutase small subunit	mutA	603 Cytoplasmic;	0	No
166 D9QBQ3	Uncharacterized protein	CpC231_1513	690 Extracellular;	1	Yes
167 D9QD98	UPF0176 protein CpC231	CpC231_2034	337 Cytoplasmic;	0	Yes
168 D9QAX3	LexA repressor	lexA	235 Cytoplasmic;	0	No
169 D9QEES	30S ribosomal protein S5	rpsE	208 Cytoplasmic;	0	No
170 D9QA06	Glutamate-tRNA ligase	gltX1	475 Cytoplasmic;	0	No
171 D9QCK3	Serine/threonine-protein kinase PknG	pknG	749 Cytoplasmic;	0	No
172 D9QEG3	DNA-directed RNA polymerase subunit alpha	rpoA	338 Cytoplasmic;	0	No
173 D9QDU0	Serine-aspartate repeat-containing protein	sdrC	723 Cellwall;	0	Yes
174 D9QCT3	Iron(III) dicitrate transport system permease fecD	CpC231_1907	355 Membrane;	10	No
175 D9Q951	UvrABC system protein B	uvrB	549 Cytoplasmic;	0	No
176 D9QCA7	Glutathione peroxidase	CpC231_1723	157 Cytoplasmic;	0	No
177 D9QBA3	Histidinol dehydrogenase	hisD	441 Cytoplasmic;	0	No
178 D9QER2	Maltose transport system permease protein malG	malG	278 Membrane;	6	No
179 D9QE00	OPT family protein	opt	657 Membrane;	18	No
180 D9QCA8	Protease II	ptrB	708 Cytoplasmic;	0	No
181 D9QDR1	Uncharacterized protein	mmpL11	795 Membrane;	11	Yes
182 D9QAF0	Prolipoprotein LppL	lppL	340 Extracellular;	0	Yes
183 D9QCE5	Uncharacterized protein	CpC231_1764	228 Membrane;	6	No
184 D9QAJ5	Protoheme IX farnesyltransferase	ctaB	310 Membrane;	9	No
185 D9QEUS	Anti-sigma factor	CpC231_0535	93 Cytoplasmic;	0	No
186 D9Q9W1	1,4-alpha-glucan branching enzyme GlgB	glgB	732 Extracellular;	0	No
187 D9QAR2	Thiol peroxidase	tpx	168 Cytoplasmic;	0	No
188 D9QDX4	Penicillin binding protein transpeptidase	pbpB	790 Extracellular;	0	Yes
189 D9QDZ0	Pilus assembly protein CpaE	cpaE	342 Cytoplasmic;	0	No

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190 D9QD73	Peptidyl-prolyl cis-trans isomerase	ppiA	178	Cytoplasmic;	0	No
191 D9QD24	Sortase-like protein	srtB	295	Membrane;	1	No
192 D9QBU0	Oligopeptide transport system permease protein oppB	oppB4	316	Membrane;	6	No
193 D9Q9A4	Glutamate-binding protein GluB	gluB	293	Extracellular;	0	Yes
194 D9QBA1	Imidazoleglycerol-phosphate dehydratase	hisB	202	Cytoplasmic;	0	No
195 D9QAZ2	tRNA-2-methylthio-N(6)-dimethylallyladenosine synthase	miaB	512	Cytoplasmic;	0	No
196 D9QCFO	Lysine--tRNA ligase	lysS	518	Cytoplasmic;	0	No
197 D9Q9L5	Oligopeptide-binding protein oppA	oppA3	526	Extracellular;	0	Yes
198 D9QA16	Glycerol-3-phosphate dehydrogenase [NAD(P)+]	gpsA	338	Cytoplasmic;	0	No
199 D9QDD1	Uncharacterized protein	CpC231_2067	212	Membrane;	0	No
200 D9QBL4	Uncharacterized protein	CpC231_1473	69	Cytoplasmic;	0	No
201 D9QBP7	DNA primase	dnaG	638	Cytoplasmic;	0	No
202 D9QB13	Polyribonucleotide nucleotidyltransferase	pnp	767	Cytoplasmic;	0	No
203 D9QE84	50S ribosomal protein L1	rplA	236	Cytoplasmic;	0	No
204 D9QD09	L-lactate dehydrogenase	ldh	316	Cytoplasmic;	0	No
205 D9QER7	Transcriptional regulator lytR	lytR	522	Extracellular;	1	No
206 D9QC11	Uncharacterized protein	CpC231_1625	252	Membrane;	6	No
207 D9QCZ4	GntR family transcriptional regulator	CpC231_1969	257	Cytoplasmic;	0	No
208 D9Q932	Methylmalonyl-CoA carboxyltransferase 5S subunit	CpC231_0571	493	Cytoplasmic;	0	No
209 D9QB28	Uncharacterized protein	CpC231_1280	308	Extracellular;	0	Yes
210 D9QEJ6	GMP synthase [glutamine-hydrolyzing]	guaA	525	Cytoplasmic;	0	No
211 D9Q946	Periplasmic binding protein	fecB	330	Cytoplasmic;	0	Yes
212 D9QB24	Translation initiation factor IF-2	infB	976	Cytoplasmic;	0	No
213 D9QBR8	Ribosomal RNA small subunit methyltransferase E	rsmE	256	Cytoplasmic;	1	No
214 D9QD56	Chromosomal replication initiator protein DnaA	dnaA	603	Cytoplasmic;	0	No
215 D9QDU1	Serine-aspartate repeat-containing protein D	sdrD	367	Extracellular;	1	No
216 D9QEBO	Elongation factor Tu	tuf	396	Cytoplasmic;	0	No
217 D9QB04	YCI-related domain protein	CpC231_1256	97	Extracellular;	0	No
218 D9QBC6	Isoleucine--tRNA ligase	ileS	1052	Cytoplasmic;	0	No
219 D9QAY2	FMN-dependent NADPH-azoreductase	azoR	277	Membrane;	0	Yes
220 D9QC07	Lantibiotic dehydratase, N terminus/C terminus family	CpC231_1621	867	Membrane;	0	No
221 D9QEC3	30S ribosomal protein S19	rpsS	92	Cytoplasmic;	0	No
222 D9QD70	Ribose transport system permease protein rbsC	rbsC	361	Membrane;	10	No
223 D9QEC8	30S ribosomal protein S17	rpsQ	92	Cytoplasmic;	0	No
224 D9QEI6	Uncharacterized protein	CpC231_0419	224	Cytoplasmic;	0	No
225 D9QA67	Uncharacterized protein	CpC231_0965	317	Extracellular;	0	Yes
226 D9QCA5	Phosphoribosylformylglycinamide synthase subunit PurC	purQ	223	Cytoplasmic;	0	No
227 D9QEF3	FNT family formate-nitrite transporter	nirC	265	Membrane;	6	No
228 D9QA36	Depospho-CoA kinase	coaE	204	Cytoplasmic;	0	No
229 D9Q9E8	Glyceraldehyde-3-phosphate dehydrogenase	gapA	476	Cytoplasmic;	0	No
230 D9QDR2	Queuine tRNA-ribosyltransferase	tgt	413	Cytoplasmic;	0	No
231 D9QAA6	Thioesterase	CpC231_1005	166	Membrane;	0	No
232 D9QA95	Hydrolase alpha/beta superfamily	CpC231_0993	395	Cytoplasmic;	0	No
233 D9QA39	Stress related protein	uspA3	146	Cytoplasmic;	0	No
234 D9QED8	Serine transporter	sdaC	447	Membrane;	11	No
235 D9Q9W3	Ferric enterobactin transport ATP-binding protein FepC	fepC1	282	Cytoplasmic;	0	No
236 D9Q9R6	Galactokinase	galK	407	Cytoplasmic;	0	No
237 D9QB29	Proline--tRNA ligase	proS	585	Cytoplasmic;	0	No
238 D9QAA3	Hemolysin-related protein	tlyC	467	Membrane;	4	No
239 D9Q965	Peptidyl-prolyl cis-trans isomerase	fkbp	119	Cytoplasmic;	0	No
240 D9QB57	Rossmann-fold nucleotide-binding protein/SMF	CpC231_1311	391	Cytoplasmic;	0	No
241 D9QBW3	Phosphoglycerate mutase	gpmB	247	Extracellular;	0	No
242 D9QAI6	Cysteine desulfurase	csdA	429	Cytoplasmic;	0	No
243 D9QD49	Uncharacterized protein	CpC231_2026	511	Membrane;	10	No
244 D9QB40	Lysophospholipase L2	CpC231_1292	332	Cytoplasmic;	0	No
245 D9QE88	50S ribosomal protein L7/L12	rplL	127	Cytoplasmic;	0	No
246 D9Q9B8	Serine protease	pepD	484	Extracellular;	1	No
247 D9QDB3	Uncharacterized protein	CpC231_2049	773	Cellwall;	0	Yes
248 D9QCZ1	HAD-family hydrolase	CpC231_1966	271	Cytoplasmic;	0	No
249 D9QBK0	DNA helicase	CpC231_1459	297	Cytoplasmic;	0	No
250 D9QA96	Protein translocase subunit SecA	secA	765	Cytoplasmic;	0	No
251 D9QBE9	Acetyltransferase	CpC231_1404	202	Cytoplasmic;	0	No
252 D9QEP2	Lincomycin resistance protein	lmrB	485	Membrane;	14	No
253 D9QC35	Two component transcriptional regulator	tcsR5	208	Cytoplasmic;	0	No
254 D9QDJ7	Uncharacterized iron-regulated membrane protein	piuB	492	Membrane;	6	No
255 F9Y379	Uncharacterized protein	CpC231_1669a	211	Extracellular;	0	Yes
256 D9QEI9	10 kDa chaperonin	groS	98	Cytoplasmic;	0	No

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257	D9QAR0	Histidine--tRNA ligase	hisS	423	Cytoplasmic;	0	No
258	D9QBE6	Uncharacterized protein	CpC231_1401	131	Membrane;	2	No
259	D9QE80	Polypropenyl synthetase	ispB	339	Cytoplasmic;	0	No
260	D9QC72	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	murA	418	Cytoplasmic;	0	No
261	D9QBP9	Guanyl-specific ribonuclease Sa3	CpC231_1509	175	Extracellular;	0	Yes
262	D9QD41	MFS family major facilitator transporter	CpC231_2018	450	Membrane;	12	No
263	D9QAA5	6-phosphogluconate dehydrogenase, decarboxylating	gnd	498	Cytoplasmic;	0	No
264	D9QA60	Tetratricopeptide TPR2	CpC231_0958	405	Cytoplasmic;	0	No
265	D9QAE8	Undecaprenyl-diphosphatase	uppP	295	Membrane;	6	No
266	D9QD20	Two-component system transcriptional regulatory protein	tcsR	212	Cytoplasmic;	0	No
267	D9QDC4	Oligopeptide transport ATP-binding protein OppD	oppCD2	677	Membrane;	6	No
268	D9QEY9	DNA helicase, UvrD/REP type	uvrD	1074	Cytoplasmic;	0	No
269	D9QD07	Cytidine deaminase	cdd	156	Cytoplasmic;	0	No
270	D9QB55	M23 peptidase domain-containing protein	CpC231_1309	187	Extracellular;	0	Yes
271	D9QEN8	Phosphoglucomutase/phosphomannomutase	manB	533	Cytoplasmic;	0	No
272	D9QAG2	Methylmalonyl-CoA mutase large subunit	sbm	735	Cytoplasmic;	0	No
273	D9QDH1	Oligo-1,6-glucosidase 1	mall	532	Extracellular;	0	No
274	D9QEFO	Maltose transport system permease protein	malF	468	Membrane;	8	No
275	D9QCU1	Urease subunit gamma	ureA	100	Cytoplasmic;	0	No
276	D9Q998	ATP-dependent DNA helicase	pcrA	846	Membrane;	0	No
277	D9QCW1	Phosphoenolpyruvate carboxykinase [GTP]	pckG	645	Cytoplasmic;	0	No
278	D9QAW5	Uncharacterized protein	CpC231_1216	846	Cytoplasmic;	0	No
279	D9QE4	Propionyl CoA carboxylase beta chain 1	pccB1	543	Cytoplasmic;	0	No
280	D9QED5	50S ribosomal protein L14	rplN	122	Cytoplasmic;	0	No
281	D9QDG0	Uncharacterized protein	CpC231_2096	199	Cytoplasmic;	0	No
282	D9QDA4	Glycopeptide antibiotics resistance protein	CpC231_2040	173	Membrane;	5	No
283	D9QB45	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (fla	ispG	391	Cytoplasmic;	0	No
284	D9QC83	ATP-binding/permease protein cydC	cydC	521	Membrane;	6	No
285	D9QDK4	Uncharacterized protein	CpC231_0079	198	Extracellular;	0	Yes
286	D9QB07	DNA translocase ftsK	ftsK	1045	Membrane;	4	No
287	D9QBG4	Ubiquinol-cytochrome C reductase cytochrome B subunit	qcrB	540	Membrane;	10	No
288	D9QB33	CobW/HypB/UreG, nucleotide-binding domain protein	CpC231_1285	371	Cytoplasmic;	0	No
289	D9QBE0	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminc	murE	503	Cytoplasmic;	0	No
290	D9QBS3	4-alpha-glucanotransferase	malQ	728	Cytoplasmic;	0	No
291	D9QAI5	NifU	nifU	149	Cytoplasmic;	0	No
292	D9QE57	Phosphoglycerate mutase	gpmB	202	Cytoplasmic;	0	No
293	D9QE37	Uncharacterized protein	CpC231_0266	368	Cytoplasmic;	3	No
294	D9Q9Q0	Iron-sulfur cluster carrier protein	mrp	380	Cytoplasmic;	0	No
295	D9Q9N1	Aromatic amino acid transport protein	aroP1	469	Membrane;	12	No
296	D9QB94	Phosphoribosyl-AMP cyclohydrolase	hisI	118	Cytoplasmic;	0	No
297	D9QBQ1	Deoxyguanosinetriphosphate triphosphohydrolase-like pro	dgt	424	Cytoplasmic;	0	No
298	D9QEUS	3-phosphoshikimate 1-carboxyvinyltransferase	aroA	424	Extracellular;	0	No
299	D9QC53	Transposase for IS3511a	CpC231_1667	167	Cytoplasmic;	0	No
300	D9QCA2	Ribonucleoside-diphosphate reductase beta chain 2	nrdF	340	Extracellular;	0	No
301	D9QAN0	Aspartate carbamoyltransferase	pyrB	313	Cytoplasmic;	0	No
302	D9Q9U4	Release factor glutamine methyltransferase	hemK	272	Cytoplasmic;	0	No
303	D9QAG6	SPFH domain, band 7 integral membrane protein	CpC231_1066	403	Membrane;	1	No
304	D9QAQ1	SNF2 family DNA/RNA helicase	CpC231_1151	920	Cytoplasmic;	0	No
305	D9Q9W0	Thioredoxin TrxA	trxA	297	Cytoplasmic;	0	No
306	D9QE61	Methyltransferase	CpC231_0290	253	Cytoplasmic;	0	No
307	D9Q948	ABC transporter iron (III)	fecC	352	Membrane;	10	No
308	D9QAK2	Phosphoenolpyruvate carboxylase	ppc	893	Cytoplasmic;	0	No
309	D9Q9J8	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	ispH	341	Cytoplasmic;	0	No
310	D9QDF7	Thioredoxin reductase	trxB	315	Cytoplasmic;	0	No
311	D9QDD6	Na+/H+-dicarboxylate symporter	CpC231_2072	439	Membrane;	10	No
312	D9QDA3	ADP-dependent (S)-NAD(P)H-hydrate dehydratase	nnrD	500	Extracellular;	0	No
313	D9QEG8	Subtilisin-like serine protease	mycP	392	Membrane;	2	Yes
314	D9QB91	Prolipoprotein diacylglycerol transferase	lgt	300	Membrane;	7	No
315	D9Q982	Oligopeptide transport system permease protein oppC	oppC2	258	Membrane;	6	No
316	D9QB90	Pyruvate kinase	pyk	472	Cytoplasmic;	0	No
317	D9QEPO	Flavoprotein disulfide reductase	lpdA	489	Cytoplasmic;	0	No
318	D9QET4	Sensor histidine kinase mtrB	mtrB	524	Membrane;	1	No
319	D9QE12	Alanine racemase	alr	370	Cytoplasmic;	0	No
320	D9QB08	Uncharacterized protein	CpC231_1260	220	Cytoplasmic;	0	No
321	D9QCF4	Betaine aldehyde dehydrogenase	gbsA	501	Cytoplasmic;	0	No
322	D9QDG1	Chromosome partitioning protein ParB	parB	350	Cytoplasmic;	0	No
323	D9QEX2	Uncharacterized protein	CpC231_0558	328	Cytoplasmic;	0	No

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324 D9QDH4 Uncharacterized protein	CpC231_0048	69 Cytoplasmic;	0	No
325 D9QC32 Fatty acid synthase	fas	3032 Cellwall;	0	No
326 D9Q9L0 HMP/thiamine permease protein ykoE	ykoE	204 Membrane;	6	No
327 D9QBM6 Galactokinase	CpC231_1486	429 Cytoplasmic;	0	No
328 D9Q977 Diaminopimelate decarboxylase	lysA	452 Extracellular;	0	No
329 D9QCQ3 Oxidoreductase	CpC231_1874	378 Cytoplasmic;	0	No
330 D9Q9W8 Cysteine desulfurase	nifS	375 Cytoplasmic;	0	No
331 D9QAK6 Putative sporulation transcription regulator WhiA	whiA	329 Cytoplasmic;	0	No
332 D9QED6 50S ribosomal protein L24	rplX	104 Cytoplasmic;	0	No
333 D9Q9L6 Oligopeptide transport system permease protein oppB	oppB3	308 Membrane;	6	No
334 D9QBIO Aminomethyltransferase	gcvT	377 Cytoplasmic;	0	No
335 D9QCU4 Aminotransferase AlaT	aspC	428 Cytoplasmic;	0	No
336 D9QER5 Maltose/maltodextrin transport system substrate-binding p	malE	419 Extracellular;	0	Yes
337 D9QD55 Uncharacterized protein	CpC231_2032	222 Membrane;	0	No
338 D9QB78 Formamidopyrimidine-DNA glycosylase	mutM1	285 Cytoplasmic;	0	No
339 D9QEG1 30S ribosomal protein S11	rpsK	134 Cytoplasmic;	0	No
340 D9Q978 Ornithine cyclodeaminase	arcB	328 Membrane;	0	No
341 D9QA59 Tyrosine-tRNA ligase	tyrS	426 Cytoplasmic;	0	No
342 D9QEWA Uncharacterized protein	CpC231_0554	167 Cytoplasmic;	0	No
343 D9QDY2 Thioredoxin-related protein	CpC231_0211	201 Membrane;	0	Yes
344 D9QBC7 Uncharacterized protein	CpC231_1382	62 Membrane;	2	No
345 D9QBP6 Thiamine biosynthesis protein X	thiX	193 Extracellular;	0	Yes
346 D9Q9Q9 Uncharacterized protein	CpC231_0803	263 Cytoplasmic;	0	No
347 D9QBQ2 Uncharacterized protein	CpC231_1512	258 Membrane;	1	No
348 D9QCG2 Dihydropteroate synthase	folP1	260 Cytoplasmic;	0	No
349 D9QBU1 Oligopeptide transport system permease protein oppC	oppC4	287 Membrane;	6	No
350 D9QBL3 Inosine 5-monophosphate dehydrogenase	CpC231_1472	477 Cytoplasmic;	0	No
351 D9QDC9 Uncharacterized protein	CpC231_2065	88 Extracellular;	0	No
352 D9QC94 UPF0678 fatty acid-binding protein-like protein CpC231	CpC231_1710	214 Cytoplasmic;	0	No
353 D9QE14 Dihydrolipoil dehydrogenase	lpd	469 Cytoplasmic;	0	No
354 D9Q9A6 Glutamate transport system permease protein gluD	gluD	312 Membrane;	6	No
355 D9QDM8 Decaprenylphosphoryl-beta-D-ribose oxidase	dprE1	488 Extracellular;	0	No
356 D9QDH7 Uncharacterized protein	CpC231_0051	97 Extracellular;	0	Yes
357 D9QBV1 MFS-type drug efflux transporter	CpC231_1564	410 Membrane;	12	No
358 D9QBK7 ABC transporter ATP-binding protein	CpC231_1466	236 Membrane;	0	No
359 D9Q9A1 Phosphoribosylglycinamide formyltransferase	purN	208 Cytoplasmic;	0	No
360 D9QD67 Uncharacterized protein	CpC231_0012	171 Extracellular;	0	Yes
361 D9QEUV Stearyl-CoA 9-desaturase electron transfer partner	CpC231_0528	352 Cytoplasmic;	0	No
362 D9QEG9 Uncharacterized protein	CpC231_0402	478 Membrane;	11	No
363 D9QAC1 Precorrin-8X methyl mutase	cobH	216 Cytoplasmic;	0	No
364 D9QEKA4 Methionine import ATP-binding protein MetN	metN	340 Cytoplasmic;	0	No
365 D9QAS9 8-amino-7-oxononanoate synthase/2-amino-3-ketobutyrate	bioF	342 Membrane;	0	No
366 D9QCN7 Uncharacterized protein	CpC231_1857	332 Cytoplasmic;	1	No
367 D9QEKA1 Uncharacterized protein	CpC231_0435	210 Extracellular;	0	Yes
368 D9Q9G0 Bifunctional protein glmU	glmU	487 Cytoplasmic;	0	Yes
369 D9QAW3 Uncharacterized protein	CpC231_1214	355 Cytoplasmic;	0	No
370 D9QER3 Maltose transport system permease protein malF	malF	361 Membrane;	6	No
371 D9QAE7 L-cysteine:1D-myo-inositol 2-amino-2-deoxy-alpha-D-gluc	mshC	416 Cytoplasmic;	0	No
372 D9Q9K1 Ribosome-binding ATPase YchF	ychF	361 Cytoplasmic;	0	No
373 D9QCD2 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	ispF	159 Cytoplasmic;	0	No
374 D9QBD2 Cell division protein FtsZ	ftsZ	409 Cytoplasmic;	0	No
375 D9QB88 Alpha-1,4 glucan phosphorylase	glgP	802 Cytoplasmic;	0	No
376 D9QE32 2,3-bisphosphoglycerate-dependent phosphoglycerate mu	gpmA	248 Cytoplasmic;	0	No
377 D9QCB0 Phosphoribosylaminoimidazole-succinocarboxamide synth	purC	297 Cytoplasmic;	0	No
378 D9Q9N8 Glycosyl transferase group 2	CpC231_0782	244 Cytoplasmic;	0	No
379 D9QBF5 Phospho-2-dehydro-3-deoxyheptonate aldolase	aroG	462 Cytoplasmic;	0	No
380 D9QBA2 Histidinol-phosphate aminotransferase	hisC	371 Cytoplasmic;	0	No
381 D9QDV6 Spermidine/putrescine transport system permease protein	potC	466 Membrane;	10	No
382 D9Q9S5 Exonuclease, SbcD-family	sbcD	372 Cytoplasmic;	0	No
383 D9QBI4 Lipoyl synthase	lipA	348 Cytoplasmic;	0	No
384 D9Q996 Succinate-semialdehyde dehydrogenase [NADP+]	gabD	495 Cytoplasmic;	0	No
385 D9QBH1 Iron-sulfur cluster insertion protein erpA	CpC231_1426	115 Extracellular;	0	No
386 D9QBY2 Malate dehydrogenase	mdh	326 Cytoplasmic;	0	No
387 D9QDV5 Spermidine/putrescine import ATP-binding protein PotA	potA	350 Membrane;	0	No
388 D9QEJ5 Uncharacterized protein	CpC231_0429	617 Membrane;	11	No
389 D9QE17 Succinate dehydrogenase flavoprotein subunit	sdhA	671 Cytoplasmic;	0	No
390 D9QDE6 Iron-sulfur protein	CpC231_2082	116 Membrane;	0	Yes

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391 D9QAF8	ABC transporter ATP-binding protein	CpC231_1058	91 Cytoplasmic;	0	No
392 D9QED2	Oligopeptide transport system permease protein oppB	oppB1	327 Membrane;	6	No
393 D9QD76	Uncharacterized protein	CpC231_0021	115 Cytoplasmic;	0	No
394 D9QCM2	Adenylosuccinate synthetase	purA	428 Cytoplasmic;	0	No
395 D9QB15	30S ribosomal protein S15	rpsO	89 Cytoplasmic;	0	No
396 D9QDM1	Metalloendopeptidase	pepO	623 Cytoplasmic;	0	No
397 D9Q9B0	30S ribosomal protein S18	rpsR	77 Cytoplasmic;	0	No
398 D9QDU8	Catalase	katA	512 Extracellular;	0	No
399 D9QC49	Nicotinate phosphoribosyltransferase	pncB	452 Membrane;	0	No
400 D9QA57	Argininosuccinate lyase	argH	477 Cytoplasmic;	0	No
401 D9QB37	Magnesium chelatase subunit D	chII	254 Cytoplasmic;	0	No
402 D9QB20	Calcineurin-like phosphoesterase	CpC231_1272	291 Cytoplasmic;	0	No
403 D9QBY5	Para-aminobenzoate synthase component I	pabB	934 Cytoplasmic;	0	No
404 D9QDP5	Cysteine desulfurase	csd	397 Cytoplasmic;	0	No
405 D9QEW2	DNA helicase	uvrD	683 Cytoplasmic;	0	No
406 D9Q970	Enoyl-CoA hydratase echA6	echA6	228 Cytoplasmic;	0	No
407 D9QAT0	Uncharacterized protein	CpC231_1180	152 Membrane;	1	No
408 D9QF0	Proline iminopeptidase	pip	339 Cytoplasmic;	0	No
409 D9QET1	Adenosylhomocysteinase	ahcY	479 Cytoplasmic;	0	No
410 D9QE14	AspT/YidE/YbjL antiporter duplication domain-containing p	CpC231_0417	535 Membrane;	12	No
411 D9Q9X1	Uncharacterized protein	CpC231_0866	323 Cytoplasmic;	0	No
412 D9Q9H2	Ppx/GppA phosphatase family	gppA2	323 Cytoplasmic;	0	No
413 D9Q9T6	Arginine-tRNA ligase	argS	550 Cytoplasmic;	0	No
414 D9QCR5	Chaperone protein DnaJ	dnaJ	396 Cytoplasmic;	0	No
415 D9Q9G2	C4-dicarboxylate transporter/malic acid transport protein	tehA	379 Membrane;	10	No
416 D9QB67	Ribosome maturation factor RimM	rimM	167 Cytoplasmic;	0	No
417 D9QET8	Protein translocase subunit SecA	secA	847 Cytoplasmic;	0	No
418 D9Q9H8	Mycothiol S-conjugate amidase	mca	296 Cytoplasmic;	0	No
419 D9QAA9	NADH dehydrogenase	ndh	452 Cytoplasmic;	3	No
420 D9QE15	HTH-type transcriptional regulator	CpC231_0244	475 Cytoplasmic;	0	No
421 D9QBR7	Phosphate starvation-inducible protein PhoH	phoH	345 Cytoplasmic;	0	No
422 D9QE81	Uncharacterized protein	CpC231_0342	209 Cytoplasmic;	0	No
423 D9QAB4	Uncharacterized protein	CpC231_1013	108 Cytoplasmic;	0	No
424 D9QAX4	Galactitol utilization operon repressor	gatR	258 Membrane;	0	No
425 D9QAC8	ATP-dependent DNA helicase	helY	918 Cytoplasmic;	0	No
426 D9Q9L7	Oligopeptide transport system permease protein oppC	oppC3	319 Membrane;	6	No
427 D9QAP8	Phosphotransferase enzyme family protein	CpC231_1148	443 Cytoplasmic;	0	No
428 D9QD63	Uncharacterized protein	CpC231_0008	70 Cytoplasmic;	0	No
429 D9QA45	50S ribosomal protein L20	rplT	127 Cytoplasmic;	0	No
430 D9QA88	Siderophore biosynthesis related protein	ciuE	1129 Cytoplasmic;	0	No
431 D9QB56	Tyrosine recombinase XerC	xerC	293 Cytoplasmic;	0	No
432 D9QCT4	ABC transporter domain-containing permease component	CpC231_1908	336 Extracellular;	0	Yes
433 D9QDK0	Multiple antibiotic resistance protein marR	marR	138 Cytoplasmic;	0	No
434 D9QEP8	O-acetyltransferase OatA	oatA	704 Membrane;	11	No
435 D9QCX1	Long-chain-fatty-acid-AMP ligase FadD32	fadD32	615 Cytoplasmic;	0	No
436 D9QDN9	Manganese/zinc/iron transport system permease protein	mntD	291 Membrane;	9	No
437 D9QBD6	Cell division protein ftsW	ftsW1	544 Membrane;	10	No
438 D9QCY8	ABC-type cobalamin/Fe3+-siderophores transport system,	CpC231_1963	347 Membrane;	10	No
439 D9QCE1	A/G-specific DNA glycosylase	mutY	295 Cytoplasmic;	0	No
440 D9QCS2	Oligopeptide transport system permease protein oppC	oppCD1	509 Membrane;	4	No
441 D9QAB7	Apolipoprotein N-acyltransferase	Int	518 Membrane;	8	No
442 D9QA71	Segregation and condensation protein A	scpA	272 Cytoplasmic;	0	No
443 D9QAI0	Archaeal ATPase	CpC231_1080	369 Cytoplasmic;	0	No
444 D9Q9P5	Glucose-1-phosphate adenylyltransferase	glgC	429 Cytoplasmic;	0	No
445 D9Q9J9	Uncharacterized protein	CpC231_0743	267 Membrane;	2	No
446 D9QDN4	UDP-galactofuranosyl transferase GlfT1	glfT1	300 Cytoplasmic;	0	No
447 D9QCF3	Na+/H+-dicarboxylate symporter	CpC231_1772	429 Membrane;	9	No
448 D9QAB9	Cobaltochelatase	cobN	1204 Cytoplasmic;	0	No
449 D9QEL1	Manganese ABC transporter membrane protein	mntC	280 Membrane;	9	No
450 D9QDT2	DNA polymerase III subunit epsilon	dnaQ1	348 Cytoplasmic;	0	No
451 D9QDN7	Manganese/zinc/iron transport system ATP-binding protein	mntB	241 Membrane;	0	No
452 D9QE73	o-succinylbenzoate synthase	menC	345 Cytoplasmic;	0	No
453 D9QEQQ1	Ribokinase	rbsK	300 Cytoplasmic;	0	No
454 D9QA84	Iron ABC transporter substrate-binding protein	ciuA	301 Membrane;	0	Yes
455 D9QB79	Ribonuclease 3	rnc	249 Membrane;	0	No
456 D9QBS0	Oxygen-independent coproporphyrinogen-III oxidase-like p	hemN	384 Cytoplasmic;	0	No
457 D9QAJ1	Uncharacterized protein	CpC231_1091	612 Membrane;	14	No

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458 D9Q9Y8	LysR family transcriptional regulator	lysG	296	Cytoplasmic;	0	No
459 D9QDA5	ABC-2 type transporter family protein	CpC231_2041	633	Membrane;	6	No
460 D9QBM1	Heme oxygenase	hmuO	212	Cytoplasmic;	0	No
461 D9QEQQ2	Ribose operon repressor	rbsR	354	Cytoplasmic;	0	No
462 D9QCN8	Glycerol-3-phosphate dehydrogenase	glpD	573	Cytoplasmic;	0	No
463 D9QAM2	DNA-directed RNA polymerase subunit omega	rpoZ	95	Cytoplasmic;	0	No
464 D9Q959	Xanthine permease	pbuX	492	Membrane;	13	No
465 D9QCH9	60 kDa chaperonin	groL	546	Cytoplasmic;	0	No
466 D9QAD6	AAA ATPase forming ring-shaped complexes	arc	526	Cytoplasmic;	0	No
467 D9QB96	Inositol monophosphate phosphatase	impA	260	Cytoplasmic;	0	No
468 D9QE97	DNA-directed RNA polymerase subunit beta;	rpoC	1350	Cytoplasmic;	0	No
469 D9QCM6	Uncharacterized protein	CpC231_1846	384	Membrane;	6	No
470 D9QD83	Uncharacterized protein	fagA	355	Membrane;	9	No
471 D9QC56	Cytochrome c oxidase subunit 1	ctaD	573	Membrane;	12	No
472 D9QD82	Iron-enterobactin transporter	fagB	328	Membrane;	10	No
473 D9Q9U8	ATP synthase subunit a	atpB	261	Membrane;	7	No
474 D9QCS3	Oligopeptide transport system permease protein oppB	oppB5	331	Membrane;	6	No
475 D9QBT8	Auxin Efflux Carrier	CpC231_1550	306	Membrane;	10	No
476 D9QDM6	Arabinofuranosyl transferase A	aftA	691	Membrane;	13	No
477 D9Q9A3	Glutamate ABC transporter domain-containing ATP-bindin	gluA	252	Cytoplasmic;	0	No
478 D9QE74	2-succinyl-5-enopyruvyl-6-hydroxy-3-cyclohexene-1-carbo	menD	537	Cytoplasmic;	0	No
479 D9QCR7	Chaperone protein DnaK	dnaK	610	Cytoplasmic;	0	No
480 D9QCI4	Na(+)/H(+) antiporter subunit A	mrpA1	952	Membrane;	23	Yes
481 D9QBQ6	Glycine-tRNA ligase	glyS	461	Cytoplasmic;	0	No
482 D9QBZ7	Small-conductance mechanosensitive channel	CpC231_1611	224	Membrane;	2	No
483 D9QB11	Flavin-dependent thymidylate synthase	thyX	252	Cytoplasmic;	0	No
484 D9Q9Z0	Uncharacterized protein	CpC231_0885	474	Extracellular;	5	No
485 D9QBL0	Cell-surface hemin receptor	CpC231_1469	733	Extracellular;	1	No
486 D9QE47	Glutamyl-tRNA reductase	hemA	456	Cytoplasmic;	0	No
487 D9QAZ9	Phage shock protein A (IM30)	pspA	280	Cytoplasmic;	0	No
488 D9QB31	Uroporphyrinogen-III methylase	cobA	250	Cytoplasmic;	0	No
489 D9Q989	Thymidylate synthase	thyA	265	Cytoplasmic;	0	No
490 D9Q9V1	ATP synthase subunit delta	atpH	273	Cytoplasmic;	0	No
491 D9QAQ3	Uncharacterized protein	CpC231_1153	270	Cytoplasmic;	0	No
492 D9QC91	Mycothiol acetyltransferase	mshD	304	Cytoplasmic;	0	No
493 D9QD31	Ribosomal pseudouridine synthase	rluC	327	Cytoplasmic;	0	No
494 D9QCC2	Acetolactate synthase large subunit IlvB1	ilvB1	578	Cytoplasmic;	0	No
495 D9QB86	Galactose-1-phosphate uridylyltransferase	CpC231_1341	447	Cytoplasmic;	0	No
496 D9QBE4	Transcriptional regulator MraZ	mraZ	143	Cytoplasmic;	0	No
497 D9QBC0	Pseudouridine synthase	rulD	307	Cytoplasmic;	0	No
498 D9Q9J2	TetR family transcriptional regulator	tetR3	216	Cytoplasmic;	0	No
499 D9QDE5	Tryptophan synthase alpha chain	trpA	279	Cytoplasmic;	0	No
500 D9QBD8	Phospho-N-acetylmuramoyl-pentapeptide-transferase	mraY	366	Membrane;	10	No
501 D9QDC6	Dihydrodipicolinate synthase	nanL	307	Cytoplasmic;	0	No
502 D9QAK3	Triosephosphate isomerase	tpiA	259	Cytoplasmic;	0	No
503 D9QEX3	UvrABC system protein B	uvrB	1648	Cellwall;	0	No
504 D9QD71	Ribose import ATP-binding protein RbsA	rbsA	257	Cytoplasmic;	0	No
505 D9Q9K9	2-dehydropantoate 2-reductase	panE	294	Cytoplasmic;	0	No
506 D9QAM7	Carbamoyl-phosphate synthase large chain	carB	1120	Cytoplasmic;	0	No
507 D9QBY8	Trigger factor	tig	450	Cytoplasmic;	0	No
508 D9QBR9	Chaperone protein DnaJ	dnaJ1	378	Cytoplasmic;	0	No
509 D9QCV1	Aldehyde dehydrogenase	CpC231_1926	463	Cytoplasmic;	0	No
510 D9Q988	Dihydrofolate reductase	folA	175	Membrane;	0	No
511 D9Q9X6	Glutamyl-tRNA(Gln) amidotransferase subunit A	gatA	494	Cytoplasmic;	0	No
512 D9QE54	Protoporphyrinogen oxidase	hemY	461	Cytoplasmic;	0	Yes
513 D9Q9F3	Peptidyl-tRNA hydrolase	pth	217	Cytoplasmic;	0	No
514 D9Q9I3	Serine hydroxymethyltransferase	glyA	429	Cytoplasmic;	0	No
515 D9QAX6	Glycerol-3-phosphate regulon repressor	glpR	267	Cytoplasmic;	0	No
516 D9QCS9	Protein fadF	fadF	887	Membrane;	5	No
517 D9QDD7	Phytoene synthase	crtB	397	Membrane;	0	No
518 D9Q9E7	Uncharacterized protein	CpC231_0691	416	Cytoplasmic;	0	No
519 D9QE56	Glutamate-1-semialdehyde 2,1-aminomutase	hemL	441	Cytoplasmic;	0	No
520 D9QBB1	RelA/SpoT domain-containing protein	CpC231_1366	338	Cytoplasmic;	0	No
521 D9QCT6	Urease accessory protein UreG	ureG	204	Cytoplasmic;	0	No
522 D9QB35	Hydrogenobyrinate a,c-diamide synthase	cobB	457	Cytoplasmic;	0	Yes
523 D9QDF5	Uncharacterized protein	CpC231_2091	1157	Cellwall;	15	No
524 D9QBC1	Lipoprotein signal peptidase	ispA	186	Membrane;	4	No

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525 D9QA91	Uncharacterized protein	CpC231_0989	523	Extracellular;	0	Yes
526 D9QCD0	SpoU rRNA Methylase family protein	CpC231_1749	313	Cytoplasmic;	0	No
527 D9QEN2	Adenosine deaminase	add	296	Cytoplasmic;	0	No
528 D9QAG5	DNA-binding protein	CpC231_1065	190	Cytoplasmic;	0	No
529 D9QB95	Imidazole glycerol phosphate synthase subunit HisF	hisF	264	Cytoplasmic;	0	No
530 D9QDD2	UPF0371 protein CpC231	CpC231_2068	497	Cytoplasmic;	0	No
531 D9QE86	N-ethylmaleimide reductase	nema	357	Cytoplasmic;	0	No
532 D9QEN1	D-alanyl-D-alanine carboxypeptidase dacA	dacA	404	Extracellular;	1	Yes
533 D9Q9Z5	Ketol-acid reductoisomerase (NADP(+))	ilvC	337	Cytoplasmic;	0	No
534 D9QEY0	Uncharacterized protein	CpC231_0566	455	Membrane;	10	No
535 D9QB19	4-phosphopantetheinyl transferase entD	entD	223	Cytoplasmic;	0	No
536 D9QDY8	Phosphoserine phosphatase	serB	290	Membrane;	1	No
537 D9Q9C1	Large-conductance mechanosensitive channel	mscl	140	Membrane;	2	No
538 D9QC38	Uncharacterized protein	CpC231_1652	109	Extracellular;	0	Yes
539 D9QC51	Ribosomal-protein-alanine acetyltransferase	CpC231_1665	165	Membrane;	0	No
540 D9QBR6	Endoribonuclease YbeY	ybeY	196	Cytoplasmic;	0	No
541 D9QDY1	Endonuclease III	nth	268	Cytoplasmic;	0	No
542 D9QDF9	N-Acetylmuramyl-L-Alanine Amidase	cwlM	398	Cytoplasmic;	0	No
543 D9QE43	Permease	CpC231_0334	320	Membrane;	11	No
544 D9Q9A2	Bifunctional purine biosynthesis protein PurH	purH	525	Cytoplasmic;	0	No
545 D9QCK5	Phosphotransacetylase	eutD	462	Cytoplasmic;	0	No
546 D9Q9N6	Cytokinin riboside 5;	CpC231_0780	263	Cytoplasmic;	0	No
547 D9QE05	Secreted hydrolase	CpC231_0234	269	Extracellular;	0	Yes
548 D9QE47	30S ribosomal protein S12	rpsL	128	Cytoplasmic;	0	No
549 D9QAC4	Precorrin-4 C11-methyltransferase	cobM	257	Cytoplasmic;	0	No
550 D9QDX9	CRP/FNR family transcriptional regulator	glxR	227	Cytoplasmic;	0	No
551 D9Q9P9	Sec-independent protein translocase protein TatB	tatB	147	Cytoplasmic;	1	No
552 D9QEY8	DNA helicase	uvrD	1062	Cytoplasmic;	0	No
553 D9QB62	50S ribosomal protein L19	rplS	113	Cytoplasmic;	0	No
554 D9QDB6	Uncharacterized protein	CpC231_2052	1135	Cellwall;	1	Yes
555 D9QB27	Ribosome maturation factor RimP	rimP	184	Cytoplasmic;	0	No
556 D9QC08	Uncharacterized protein	CpC231_1622	337	Extracellular;	0	No
557 D9QCA4	Phosphoribosylformylglycinamide synthase subunit PurL	purL	766	Cytoplasmic;	0	No
558 D9QCQ9	UPF0012 hydrolase	CpC231_1881	278	Cytoplasmic;	0	No
559 D9QC46	Rhomboid family protein	CpC231_1660	272	Membrane;	6	No
560 D9QB22	DHH subfamily 1 protein	CpC231_1274	330	Cytoplasmic;	0	No
561 D9QA29	ABC transporter domain-containing protein	CpC231_0926	318	Membrane;	6	No
562 D9Q9F9	Ribose-phosphate pyrophosphokinase	prsA	326	Cytoplasmic;	0	No
563 D9QDL8	Glycerol kinase	glpK	509	Cytoplasmic;	0	No
564 F9Y365	Haloacid dehalogenase-like hydrolase	CpC231_1044	234	Cytoplasmic;	0	No
565 D9QDV3	Uncharacterized protein	CpC231_0181	207	Cytoplasmic;	0	No
566 D9QB44	Serine/threonine protein kinase	pknL	752	Membrane;	1	No
567 D9Q947	FecCD family membrane transport protein	fecCD	321	Membrane;	10	No
568 D9QBH0	Asparagine synthetase	asnB	640	Cytoplasmic;	0	No
569 D9QE42	Uncharacterized protein	CpC231_0333	241	Membrane;	3	No
570 D9QBN9	Alpha/beta hydrolase	CpC231_1499	321	Cytoplasmic;	0	No
571 D9QB55	Uncharacterized protein	CpC231_1452	377	Cytoplasmic;	0	No
572 D9QDI1	Choline transport system permease protein opuBD	opuBD	212	Membrane;	5	No
573 D9QC74	Transcriptional regulator, LuxR family	CpC231_1689	279	Cytoplasmic;	0	No
574 D9QEJ2	Uncharacterized protein	CpC231_0425	293	Extracellular;	0	No
575 D9Q9Z6	Cadmium, cobalt and zinc/H(+)-K(+) antiporter	czcD	361	Membrane;	6	No
576 D9QE07	dTDP-4-dehydrorhamnose reductase	rmlD	460	Extracellular;	0	No
577 D9QBZ6	Aminopeptidase N	pepN	871	Cytoplasmic;	0	No
578 D9Q9V0	ATP synthase subunit b	atpF	188	Cytoplasmic;	1	No
579 D9QB39	Probable malate:quinone oxidoreductase	mqa	499	Cytoplasmic;	0	No
580 D9QE87	50S ribosomal protein L10	rplJ	171	Cytoplasmic;	0	No
581 D9QAR1	Metallo-beta-lactamase superfamily protein	gloB1	182	Cytoplasmic;	0	No
582 D9QA83	Uncharacterized protein	CpC231_0981	898	Membrane;	12	No
583 D9QD25	Uncharacterized protein	oxaA	415	Membrane;	6	No
584 D9QEP4	Acyl coenzyme A carboxylase	accBC	591	Cytoplasmic;	0	No
585 D9QA14	7,8-dihydro-8-oxoguanine-triphosphatase	mutT2	333	Cytoplasmic;	0	No
586 D9QBB8	RarD protein	rarD	294	Membrane;	10	No
587 D9QEC6	50S ribosomal protein L16	rplP	138	Cytoplasmic;	0	No
588 D9QDW7	Uncharacterized protein	CpC231_0195	477	Extracellular;	5	Yes
589 D9QBA8	Glycogen debranching protein	glgX	745	Cytoplasmic;	0	No
590 D9QB84	Glycerate kinase	glxK	396	Extracellular;	0	No
591 D9QET6	Phosphoribosyl transferase	CpC231_0522	201	Cytoplasmic;	0	No

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592 D9QEL3	DtxR family transcriptional regulator	mntR	213	Cytoplasmic;	0	No
593 D9QCN2	Sdr family related adhesin	CpC231_1852	1269	Cellwall;	2	Yes
594 D9QAK9	UvrABC system protein C	uvrC	675	Cytoplasmic;	0	No
595 D9Q9B7	Two component system sensor kinase protein	tcsS4	514	Membrane;	2	No
596 D9QBK8	ABC transporter inner membrane protein	CpC231_1467	484	Membrane;	10	No
597 D9QAI7	FeS assembly ATPase SufC	sufC	252	Cytoplasmic;	0	No
598 D9QAS4	Probable transcriptional regulatory protein CpC231	CpC231_1174	250	Cytoplasmic;	0	No
599 D9QE04	Acetyl-coenzyme A synthetase	acsA	548	Membrane;	0	No
600 D9QED7	50S ribosomal protein L5	rplE	187	Cytoplasmic;	0	No
601 D9Q9R5	Galactose-1-phosphate uridylyltransferase	galT	371	Cytoplasmic;	0	No
602 D9QD29	Universal stress protein A	uspA	299	Cytoplasmic;	0	No
603 D9QEG4	50S ribosomal protein L17	rplQ	161	Cytoplasmic;	0	No
604 D9QE18	Succinate dehydrogenase iron-sulfur subunit	sdhB	249	Cytoplasmic;	0	No
605 D9QCC7	Trehalose 6-phosphate phosphatase	otsB	241	Cytoplasmic;	0	No
606 D9QCN4	Glycoside hydrolase family 76 protein	CpC231_1854	380	Cytoplasmic;	0	No
607 D9QAJ0	Iron-sulfur cluster biosynthesis transcriptional regulator Su	sufR	257	Cytoplasmic;	0	No
608 D9QCD3	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	ispD	245	Membrane;	0	No
609 D9QE43	Thiol:disulfide interchange protein DsbA	dsbA	293	Membrane;	0	Yes
610 D9Q9X8	Multidrug resistance protein B	embB	482	Membrane;	14	No
611 D9QC96	Glycine cleavage T protein	CpC231_1712	376	Cytoplasmic;	0	No
612 D9QC31	Holo-[acyl-carrier-protein] synthase	acpS	129	Cytoplasmic;	0	No
613 D9QCE6	Permease, major facilitator family	CpC231_1765	467	Membrane;	14	No
614 D9QBF0	Methylenetetrahydrofolate reductase	metF	327	Cytoplasmic;	0	No
615 D9Q9A5	Glutamate transport system permease protein gluC	gluC	228	Membrane;	5	No
616 D9QE20	Uncharacterized protein yjiN	yjiN	435	Membrane;	3	No
617 D9QCS0	Predicted permease	CpC231_1894	453	Membrane;	10	No
618 D9Q9H3	HTH-type transcriptional repressor of iron protein A	ripA	368	Membrane;	0	No
619 D9Q9Z2	Small-conductance mechanosensitive channel	mscS	564	Membrane;	4	No
620 D9QCJ0	Uncharacterized protein	CpC231_1810	430	Membrane;	12	No
621 D9Q997	Chorismate mutase	csm	100	Cytoplasmic;	0	No
622 D9QES8	Uncharacterized protein	CpC231_0514	255	Extracellular;	1	No
623 D9Q972	Cation/acetate symporter ActP	actP	547	Membrane;	13	No
624 D9Q9M5	1D-myo-inositol 2-acetamido-2-deoxy-alpha-D-glucopyranose	mshB	294	Cytoplasmic;	0	No
625 D9QDS5	3-hydroxyisobutyrate dehydrogenase	mmsB	302	Cytoplasmic;	0	Yes
626 D9Q9R3	Sodium/solute symporter	CpC231_0807	552	Membrane;	14	No
627 D9QET2	Thymidylate kinase	tmk	206	Cytoplasmic;	0	No
628 D9QC42	dITP/XTP pyrophosphatase	CpC231_1656	207	Cytoplasmic;	0	No
629 D9Q9U6	Undecaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate acetyltransferase	rfe	384	Membrane;	11	No
630 D9QCZ6	Uncharacterized protein	CpC231_1971	115	Cytoplasmic;	0	No
631 D9QBU6	Uncharacterized protein	CpC231_1558	440	Membrane;	9	No
632 D9QAD0	Sec-independent protein translocase protein TatA	tatA	92	Cytoplasmic;	1	No
633 D9QDR9	Aspartate transaminase	aspB	451	Cytoplasmic;	0	No
634 D9Q9D2	Glycine betaine transporter	betP	663	Membrane;	12	No
635 D9QCP9	Transport protein	CpC231_1870	528	Membrane;	5	No
636 D9QAU6	RNA methyltransferase, TrmA family	trmA	439	Cytoplasmic;	0	No
637 D9QDG8	Fe(3+) dicitrate transport ATP-binding protein FecE	fecE	256	Membrane;	0	No
638 D9QEHI1	ESX-3 secretion system protein eccC3	eccC3	1283	Cytoplasmic;	1	No
639 D9QAR8	Protein-export membrane protein SecF	secF	373	Membrane;	6	No
640 D9Q9V7	Endonuclease NucS	nucS	227	Cytoplasmic;	0	No
641 D9Q9S6	ATP-binding protein	CpC231_0820	857	Cytoplasmic;	0	No
642 D9QDJ8	Uncharacterized protein	CpC231_0073	356	Cytoplasmic;	0	No
643 D9QCB4	Phosphoribosylamine-glycine ligase	purD	422	Cytoplasmic;	0	No
644 D9QA37	Coenzyme PQQ synthesis protein E	pqqE	412	Cytoplasmic;	0	No
645 D9QEQQ9	N5-carboxyaminoimidazole ribonucleotide mutase	purE	166	Membrane;	0	No
646 D9QAX9	PTS system fructose-specific EIIBC component	fruA	38	Extracellular;	0	No
647 D9QAC5	Precorrin-6Y C5,15-methyltransferase	cobL	422	Membrane;	0	No
648 D9QA42	UvrABC system protein A	uvrA	954	Cytoplasmic;	0	No
649 D9QEPT7	Uncharacterized protein	CpC231_0483	356	Cytoplasmic;	0	No
650 D9QBY4	ATP-dependent Clp protease ATP-binding subunit ClpX	clpX	428	Cytoplasmic;	0	No
651 D9QBH3	Bifunctional adenosylcobalamin biosynthesis protein CobL	cobU	184	Cytoplasmic;	0	No
652 D9QA43	Translation initiation factor IF-3	infC	148	Cytoplasmic;	0	No
653 D9QC88	Phosphate import ATP-binding protein PstB	pstB	257	Cytoplasmic;	0	No
654 D9QE38	Pyroline-5-carboxylate reductase	proC	267	Membrane;	0	No
655 D9Q9C6	Ribosomal-protein-alanine acetyltransferase	rimJ	238	Cytoplasmic;	0	No
656 D9QE60	Cytochrome C biosynthesis protein ResB	ccsB	535	Membrane;	4	No
657 D9QC84	Succinyl-CoA Coenzyme A transferase	cat1	501	Cytoplasmic;	0	No
658 D9QAI3	ABC transporter ATP-binding protein	CpC231_1083	543	Cytoplasmic;	0	No

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659 D9QBV1	ABC-type oligopeptide transport system	CpC231_1565	235 Membrane;	0	No
660 D9Q9U9	ATP synthase subunit c	atpE	79 Cytoplasmic;	2	No
661 D9QBI3	Octanoyltransferase	lipB	251 Cytoplasmic;	0	No
662 D9QDS1	DNA polymerase III subunit gamma/tau	dnaX	849 Cytoplasmic;	0	No
663 D9QAH4	Aconitate hydratase	acnA	939 Cytoplasmic;	0	No
664 D9QBR3	GTPase Era	era	305 Cytoplasmic;	0	No
665 D9QBX8	Ornithine cyclodeaminase	arcB	316 Membrane;	0	No
666 D9QCX0	Phthiocerol synthesis polyketide synthase type I PpsA	ppsA	1611 Cellwall;	0	No
667 D9Q950	Uncharacterized protein	CpC231_0591	213 Membrane;	2	No
668 D9QBD3	Cell division protein FtsQ	ftsQ	218 Membrane;	1	No
669 D9QAQ9	CaiB/baiF CoA-transferase family protein	CpC231_1159	379 Cytoplasmic;	0	No
670 D9QD16	Uncharacterized protein	CpC231_1993	452 Membrane;	13	No
671 D9QE8	Uncharacterized protein	CpC231_0379	151 Cytoplasmic;	0	Yes
672 D9QBX0	Glutamate 5-kinase	proB	417 Cytoplasmic;	0	No
673 D9QBL8	Threonine synthase	thrC	480 Cytoplasmic;	0	No
674 D9Q9E4	Transcriptional regulatory protein PvdS	pvdS	287 Cytoplasmic;	0	No
675 D9QAL2	Riboflavin biosynthesis protein RibBA	ribA	451 Cytoplasmic;	0	No
676 D9QA75	ATP-dependent dethiobiotin synthetase BioD	bioD	229 Membrane;	0	Yes
677 D9QE1	PAP2 superfamily protein	CpC231_0372	410 Extracellular;	0	Yes
678 D9QCR9	Fimbrial associated sortase-like protein	srtA	291 Cytoplasmic;	2	No
679 D9QDK8	ATP-dependent RNA helicase hrpB	hrpB	818 Membrane;	0	No
680 D9QAK0	6-phosphogluconolactonase	pgl	236 Cytoplasmic;	0	No
681 D9QEFS	Protein translocase subunit SecY	secY	440 Membrane;	10	No
682 D9Q9Y9	Uncharacterized protein	CpC231_0884	273 Extracellular;	0	Yes
683 D9QB74	Uncharacterized protein	CpC231_1328	1201 Membrane;	3	No
684 D9QAX7	1-phosphofructokinase	fruK	326 Extracellular;	0	No
685 D9QA21	Dihydroxyacetone kinase 2	dak2	571 Cytoplasmic;	0	No
686 D9QAK4	Phosphoglycerate kinase	pgk	404 Cytoplasmic;	0	No
687 D9QDS7	2-hydroxyhepta-2,4-diene-1,7-dioatesomerase	hpaF	282 Cytoplasmic;	0	No
688 D9QBL5	Na+/H+ antiporter NhaC	CpC231_1474	456 Membrane;	13	No
689 D9QA50	N-acetyl-gamma-glutamyl-phosphate reductase	argC	347 Membrane;	0	No
690 D9QA77	Pseudouridine synthase	rluB	373 Cytoplasmic;	0	No
691 D9Q9Y4	ATP-dependent 6-phosphofructokinase	pfkA	342 Cytoplasmic;	0	No
692 D9QBH9	Glycine dehydrogenase (aminomethyl-transferring)	gcvP	951 Cytoplasmic;	0	No
693 D9QAW8	Transcriptional activator protein lysR	lysR1	313 Cytoplasmic;	0	No
694 D9QA85	Iron ABC transporter domain-containing permease protein	ciuB	322 Membrane;	9	No
695 D9QBY6	ATP-dependent Clp protease proteolytic subunit	clpP	209 Cytoplasmic;	0	No
696 D9QE3	50S ribosomal protein L6	rplF	178 Cytoplasmic;	0	No
697 D9QE26	Formate acetyltransferase 1	pflB	698 Cytoplasmic;	0	No
698 D9QDW0	Sensor-like histidine kinase senX3	senX3	261 Membrane;	0	Yes
699 D9QBA4	Uncharacterized protein	CpC231_1359	401 Membrane;	0	No
700 D9Q9A0	Uncharacterized protein	CpC231_0643	579 Membrane;	10	No
701 D9QBP8	Glutamine--fructose-6-phosphate aminotransferase [isome	glmS	624 Cytoplasmic;	4	No
702 D9QBH4	Nicotinate-nucleotide--dimethylbenzimidazole phosphoribc	cobT	354 Cytoplasmic;	0	No
703 D9QES6	Uncharacterized protein	CpC231_0512	328 Membrane;	0	No
704 D9QD01	LytR family transcriptional regulator	lytR	427 Extracellular;	1	No
705 D9QD72	Uncharacterized protein	CpC231_0017	223 Cytoplasmic;	1	No
706 D9QBD9	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine liga:	murF	516 Cytoplasmic;	0	No
707 D9QBX7	Nucleoside diphosphate kinase	ndk	136 Cytoplasmic;	0	No
708 D9QDV2	Uncharacterized protein	CpC231_0180	244 Extracellular;	0	No
709 D9Q9R7	ATP-dependent RNA helicase DeaD	deaD1	650 Cytoplasmic;	0	No
710 D9QE03	Uncharacterized protein	CpC231_0232	78 Extracellular;	1	No
711 D9QEAI	ABC transporter inner membrane protein	CpC231_0332	253 Membrane;	6	No
712 D9QE45	Haloacid dehalogenase-like hydrolase	CpC231_0274	347 Cytoplasmic;	1	No
713 D9QCR6	Protein GrpE	grpE	214 Cytoplasmic;	0	No
714 D9QEX6	Uncharacterized protein	CpC231_0562	350 Membrane;	11	No
715 D9QEHI6	30S ribosomal protein S9	rpsI	177 Cytoplasmic;	0	No
716 D9QD61	Uncharacterized protein	CpC231_0006	144 Cytoplasmic;	0	No
717 D9QDT8	Phosphoglucosamine mutase	pmmb	554 Cytoplasmic;	0	No
718 D9QD43	Glycoside hydrolase 15-related protein	CpC231_2020	654 Cytoplasmic;	0	No
719 D9QCB7	Sensor histidine kinase mtrB	mtrB	501 Membrane;	3	No
720 D9QA74	Adenosylmethionine-8-amino-7-oxononanoate aminotrans	bioA	432 Cytoplasmic;	0	No
721 D9QEAI6	Uncharacterized protein	CpC231_0337	146 Cytoplasmic;	0	No
722 D9QB63	Transcriptional accessory protein	CpC231_1317	767 Cytoplasmic;	0	No
723 D9QEIQ7	Uncharacterized protein	CpC231_0493	156 Membrane;	0	No
724 D9QC95	4-Amino-4-deoxychorismate lyase	pabC	305 Cytoplasmic;	0	No
725 D9QEJ0	60 kDa chaperonin	groL	540 Cytoplasmic;	0	No

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726 D9QDQ4	HTH-type pyridoxine biosynthesis transcriptional regulator	pdxR	464	Membrane;	0	No
727 D9QB77	Na+/alanine symporter family	CpC231_1331	488	Membrane;	11	No
728 D9QE10	Serine proteases of the peptidase family S9A	CpC231_0239	693	Cytoplasmic;	0	No
729 D9QERO	Uncharacterized protein	CpC231_0496	155	Membrane;	0	No
730 D9QEY1	Non-ribosomal peptide synthetase	CpC231_0567	1332	Cellwall;	10	No
731 D9QB43	Methionine aminopeptidase	map	297	Cytoplasmic;	0	No
732 D9QEC1	50S ribosomal protein L23	rplW	101	Cytoplasmic;	0	No
733 D9Q994	Uncharacterized protein	CpC231_0637	137	Membrane;	4	No
734 D9QDZ7	DEAD-box ATP dependent DNA helicase	CpC231_0226	785	Membrane;	0	No
735 D9QA20	Uracil-DNA glycosylase	ung	207	Cytoplasmic;	0	No
736 D9QBW6	Gamma-glutamyl phosphate reductase	proA	428	Cytoplasmic;	0	No
737 D9QBI7	Glutamine synthetase	glnA	478	Cytoplasmic;	0	No
738 D9QAE5	Methionine synthase	metH	1199	Cytoplasmic;	0	No
739 D9QA64	NAD kinase	nadK	319	Cytoplasmic;	0	No
740 D9QCD5	Lipoprotein LpqE	lpqE	191	Extracellular;	0	Yes
741 D9QDI2	Choline transport ATP-binding protein OpuBA	opuBA	295	Cytoplasmic;	0	No
742 D9QE35	Uncharacterized protein	CpC231_0264	310	Cytoplasmic;	0	No
743 D9QDA6	Leucine-tRNA ligase	leuS	953	Cytoplasmic;	0	No
744 D9QEC9	Oligopeptide-binding protein oppA	oppA1	558	Extracellular;	0	Yes
745 D9QDP7	Putative phenylalanine aminotransferase	pat	343	Cytoplasmic;	0	No
746 D9QAB3	Protein ycel	ycel	230	Extracellular;	1	No
747 D9QDX8	Metallo-beta-lactamase superfamily protein	CpC231_0207	277	Cytoplasmic;	0	No
748 D9QUEL7	Uncharacterized protein	CpC231_0451	366	Cytoplasmic;	0	No
749 D9QAM9	Dihydroorotate	pyrC	452	Cytoplasmic;	0	No
750 D9QA33	SAM-dependent methyltransferase	CpC231_0930	262	Cytoplasmic;	0	No
751 D9QBF6	3;	CpC231_1411	167	Cytoplasmic;	0	No
752 D9QE09	Peptidase family M1 containing protein	CpC231_0238	457	Cytoplasmic;	0	No
753 D9QCK7	Acetyltransferase	CpC231_1827	161	Cytoplasmic;	0	No
754 D9QA10	Guanosine-3;	spoT	191	Cytoplasmic;	0	No
755 D9QAH0	Ferrochelatase	hemH	376	Cytoplasmic;	0	No
756 D9QEM2	Hemin import ATP-binding protein HmuV	hmuV	280	Membrane;	0	No
757 D9QCB1	Adenylosuccinate lyase	purB	479	Cytoplasmic;	0	No
758 D9Q952	Uncharacterized protein	CpC231_0593	832	Membrane;	0	Yes
759 D9QE64	Membrane permease protein	CpC231_0293	350	Membrane;	10	No
760 D9QDK5	Probable membrane transporter protein	CpC231_0080	270	Membrane;	9	No
761 D9QAV9	D-aminoacyl-tRNA deacylase	dtd	144	Cytoplasmic;	0	No
762 D9QA11	IclR family transcriptional regulator	ltbR	241	Membrane;	0	No
763 D9QAU9	Deoxyuridine 5;	dut	153	Cytoplasmic;	0	No
764 D9QAM0	S-adenosylmethionine synthase	metK	409	Cytoplasmic;	0	No
765 D9Q9I2	Pantothenate kinase	coA	308	Cytoplasmic;	0	No
766 D9QA44	50S ribosomal protein L35	rpmI	64	Cytoplasmic;	0	No
767 D9QCK1	Uncharacterized protein	CpC231_1821	471	Membrane;	4	No
768 D9QE93	Manganese transport system membrane protein mntD	mntD	293	Membrane;	8	No
769 D9QEM9	Tryptophan-tRNA ligase	trpS	387	Cytoplasmic;	0	No
770 D9QDC3	Oligopeptide transport system permease protein oppB	oppB6	321	Membrane;	6	No
771 D9QEY2	Secreted hydrolase	CpC231_0538	290	Cytoplasmic;	0	Yes
772 D9QAY8	tRNA dimethylallyltransferase	miaA	323	Cytoplasmic;	0	No
773 D9QBG6	Ubiquinol-cytochrome C reductase cytochrome C subunit	qcrC	298	Membrane;	2	No
774 D9Q9D4	Ribosomal RNA small subunit methyltransferase I	rsml	301	Cytoplasmic;	0	No
775 D9QCL4	Uncharacterized protein	CpC231_1834	84	Extracellular;	0	No
776 D9QDB5	ChrA, CheY/winged-helix DNA-binding domain-containing	chrA	199	Cytoplasmic;	0	No
777 D9QAL7	Methionyl-tRNA formyltransferase	fmt	313	Cytoplasmic;	0	No
778 D9QEY8	N5-carboxyaminoimidazole ribonucleotide synthase	purK	401	Cytoplasmic;	0	No
779 D9QBU5	Pyridoxal phosphate homeostasis protein	CpC231_1557	232	Cytoplasmic;	0	No
780 D9QC79	Glycerol dehydrogenase	gldA	358	Cytoplasmic;	0	No
781 D9QE85	Aminopeptidase C	pepC1	433	Extracellular;	0	No
782 D9QEJ3	Inosine-5;	guaB	506	Membrane;	0	No
783 D9QCL8	Cytochrome c biogenesis protein resB	resB	466	Membrane;	4	No
784 D9QDZ9	DNA topoisomerase 1	topA	984	Cytoplasmic;	0	No
785 D9QEY3	Uncharacterized protein	CpC231_0569	92	Extracellular;	0	Yes
786 D9Q9X3	DNA ligase	ligA	694	Cytoplasmic;	0	No
787 D9QDM0	Alpha/beta hydrolase family protein	CpC231_0095	286	Cytoplasmic;	0	No
788 D9QE52	Cation-transporting P-type ATPase A	ctpA	796	Membrane;	8	No
789 D9QC23	Dihydrodipicolinate synthase	dapA1	275	Cytoplasmic;	0	No
790 D9Q9F4	Nitronate monooxygenase	yrpB	349	Membrane;	0	No
791 D9QB10	4-hydroxy-tetrahydrodipicolinate synthase	dapA	301	Cytoplasmic;	0	No
792 D9QEM1	Hemin import ATP-binding protein	hmuU	321	Membrane;	9	Yes

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793 D9QA86	Iron ABC transporter permease	ciuC	343 Membrane;	10	No
794 D9QCK6	Ferredoxin/ferredoxin-NADP reductase	CpC231_1826	450 Cytoplasmic;	0	No
795 D9QC50	ATP-dependent helicase dinG-like protein	dinG	664 Cytoplasmic;	0	No
796 D9QC82	ATP-binding/permease protein cydD	cydD	522 Membrane;	6	No
797 D9QE82	Transcription termination/antitermination protein NusG	nusG	276 Cytoplasmic;	0	No
798 D9Q9D0	Dolichyl-phosphate-mannose-protein mannosyltransferase	CpC231_0673	577 Membrane;	11	No
799 D9QC66	Uncharacterized protein	CpC231_1680	144 Cytoplasmic;	0	No
800 D9QET5	Lipoprotein LpqB	lpqB	561 Extracellular;	0	No
801 D9QBP1	N-acetyl glucosamine related protein	CpC231_1501	273 Cytoplasmic;	0	No
802 D9Q9G1	Multicopper oxidase	CpC231_0705	547 Cytoplasmic;	0	Yes
803 D9QAT5	Threonine-tRNA ligase	thrS	689 Cytoplasmic;	0	No
804 D9QCQ0	Uncharacterized protein	CpC231_1871	304 Cytoplasmic;	1	Yes
805 D9QBA5	Uncharacterized protein	CpC231_1360	225 Membrane;	4	No
806 D9QEX4	Uncharacterized protein	CpC231_0560	51 Extracellular;	0	No
807 D9Q9A9	Nucleotidyltransferase substrate binding domain protein	CpC231_0652	298 Cytoplasmic;	0	No
808 D9QAZ0	Uncharacterized protein	CpC231_1241	450 Cytoplasmic;	0	No
809 D9QD84	Iron siderophore binding protein	fagD	350 Membrane;	0	Yes
810 D9QEX8	Trypsin	sprT	224 Membrane;	0	Yes
811 D9Q9B9	Molybdenum cofactor biosynthesis protein B	moaB	212 Cytoplasmic;	0	No
812 D9QC12	ABC transporter ATP-binding protein	CpC231_1626	307 Cytoplasmic;	0	No
813 D9QA04	2-hydroxyhepta-2,4-diene-1,7-dioate isomerase	mhpD	265 Cytoplasmic;	0	No
814 D9QB17	Riboflavin biosynthesis protein	ribF	332 Cytoplasmic;	0	No
815 D9QDB2	LPxTG domain-containing protein	CpC231_2048	62 Extracellular;	1	No
816 D9QDW3	Na(+)/H(+) antiporter subunit E	mrpE	139 Membrane;	1	No
817 D9QA17	D-alanine-D-alanine ligase	ddl	363 Cytoplasmic;	0	No
818 D9QBI2	Glyoxalase/bleomycin resistance protein/dioxygenase	CpC231_1438	164 Membrane;	0	No
819 D9QDL0	DNA-3-methyladenine glycosylase 1	tagA	220 Cytoplasmic;	0	No
820 D9QCS8	Oxidoreductase	CpC231_1902	170 Cytoplasmic;	0	Yes
821 D9QDG2	Chromosome partitioning protein parA	parA	330 Cytoplasmic;	0	No
822 F9Y363	Uncharacterized protein	CpC231_1042a	32 Extracellular;	0	No
823 D9QD34	ABC transporter ATP-binding protein	CpC231_2011	292 Cytoplasmic;	0	No
824 D9QC30	HTH-type transcriptional regulator EthR	ethR	217 Cytoplasmic;	0	No
825 D9QA22	ATP-dependent DNA helicase	recG	704 Membrane;	0	No
826 D9QCV9	Glycosyltransferase	CpC231_1934	401 Cytoplasmic;	0	No
827 D9QDQ9	tRNA-specific adenosine deaminase	tadA	158 Cytoplasmic;	0	No
828 D9QB34	Methylated-DNA-protein-cysteinemethyltransferase	ada	173 Cytoplasmic;	0	No
829 D9QCS6	Phosphate transporter	pitB	534 Membrane;	13	No
830 D9QDV0	Uncharacterized protein	CpC231_0178	233 Cytoplasmic;	0	No
831 D9QC85	tRNA-dihydrouridine synthase	CpC231_1700	384 Cytoplasmic;	0	Yes
832 D9QBC2	Uncharacterized protein	CpC231_1377	332 Extracellular;	0	Yes
833 D9QD86	Serine/threonine-protein kinase	pknB	664 Membrane;	1	No
834 D9QCJ9	ABC superfamily ATP binding cassette transporter protein	CpC231_1819	309 Cytoplasmic;	0	No
835 D9QA94	UPF0225 protein	CpC231_0992	129 Cytoplasmic;	0	No
836 D9QBK1	Uncharacterized protein	CpC231_1460	59 Cytoplasmic;	0	No
837 D9QAX5	Phosphoenolpyruvate-protein phosphotransferase	ptsI	567 Cytoplasmic;	0	No
838 D9QE88	30S ribosomal protein S10	rpsJ	101 Cytoplasmic;	0	No
839 D9QC06	Nitroreductase	CpC231_1620	492 Cytoplasmic;	0	No
840 D9QD60	DNA gyrase subunit B	gyrB	681 Cytoplasmic;	0	No
841 D9QC29	Bacterioferritin comigratory protein	bcp	159 Cytoplasmic;	0	No
842 D9QAA4	DEAD-box helicase	deaD2	435 Membrane;	0	No
843 D9QD39	Cation transport protein	CpC231_2016	67 Cytoplasmic;	0	No
844 D9QE22	Deoxyribose-phosphate aldolase	deoC	197 Cytoplasmic;	0	No
845 F9Y381	Uncharacterized protein	CpC231_1753a	37 Extracellular;	0	Yes
846 D9QAC0	Precorrin-3B synthase	cobG	438 Cytoplasmic;	0	Yes
847 D9QAF4	Phosphatidylethanolamine-binding protein	CpC231_1054	178 Extracellular;	0	No
848 D9Q984	Uncharacterized protein	CpC231_0627	59 Cytoplasmic;	0	No
849 D9QBZ3	Pirin C-terminal domain-containing protein	CpC231_1607	336 Cytoplasmic;	0	No
850 D9QCR2	Membrane protein	CpC231_1885	202 Extracellular;	0	Yes
851 D9QDY6	Uncharacterized protein	CpC231_0215	166 Membrane;	2	No
852 D9QAS2	Holliday junction ATP-dependent DNA helicase RuvA	rvuA	203 Membrane;	0	No
853 D9QE84	Uncharacterized protein	CpC231_0345	153 Cytoplasmic;	0	No
854 D9QCI5	Na(+)/H(+) antiporter subunit C	mrpC1	160 Membrane;	3	No
855 D9QCV4	Uncharacterized protein	CpC231_1929	62 Cytoplasmic;	1	No
856 D9QBX2	50S ribosomal protein L27	rpmA	88 Cytoplasmic;	0	No
857 F9Y350	Uncharacterized protein	CpC231_0691a	97 Cytoplasmic;	0	No
858 D9Q9X5	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit	gatC	97 Cytoplasmic;	0	No
859 D9QDW6	Na(+)/H(+) antiporter subunit A	mrpA	989 Membrane;	0	No

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860	D9Q9L4	MutT-like protein	mutT1	128	Cytoplasmic;	0	No
861	F9Y333	Uncharacterized protein	CpC231_0021b	32	Extracellular;	0	Yes
862	D9QAP6	Alanine-ttRNA ligase	alaS	890	Cytoplasmic;	0	No
863	D9QB36	Cob (I) yinic acid a,c-diamide adenosyltransferase	cobO	206	Cytoplasmic;	0	No
864	D9QAV0	Uncharacterized protein	CpC231_1200	165	Membrane;	2	No
865	D9QEPM	Uncharacterized protein	CpC231_0482	52	Cytoplasmic;	0	No
866	D9QAL6	Ribosomal RNA small subunit methyltransferase B	fmu	504	Cytoplasmic;	0	No
867	D9Q9G7	Transcriptional regulator, MazG family	CpC231_0711	205	Cytoplasmic;	0	No
868	D9QDB0	ABC-type antimicrobial peptide transport system, ATPase	CpC231_2046	227	Membrane;	0	No
869	D9QEM0	Hemin-binding periplasmic protein hmuT	hmuT	351	Cytoplasmic;	0	Yes
870	D9QCP6	Sortase A	srtA	296	Membrane;	2	No
871	D9Q934	Uncharacterized protein	CpC231_0573	87	Cytoplasmic;	0	No
872	D9QE13	Uncharacterized protein	CpC231_0242	71	Extracellular;	0	No
873	D9Q9X2	DNA polymerase III subunit epsilon	dnaQ2	232	Cytoplasmic;	0	No
874	D9QA34	30S ribosomal protein S1	rpsA	487	Cytoplasmic;	0	No
875	D9QDE7	Predicted Na+-dependent transporter	CpC231_2083	322	Membrane;	10	No
876	D9QAV1	Uncharacterized protein	CpC231_1201	97	Cytoplasmic;	0	No
877	D9Q9I5	TetR family transcriptional regulator	tetR2	209	Cytoplasmic;	0	No
878	D9QCN0	Uncharacterized protein	CpC231_1850	187	Membrane;	2	No
879	D9QCE3	Uncharacterized protein	CpC231_1762	56	Extracellular;	0	No
880	D9QA68	ADP-ribose pyrophosphatase (ADPRase)	nudF	222	Cytoplasmic;	0	No
881	D9QAR7	Oligopeptide-binding protein oppA	oppA4	546	Cytoplasmic;	0	Yes
882	D9QDM9	Uncharacterized protein	CpC231_0104	74	Cytoplasmic;	0	No
883	D9QBB6	L-threonine dehydratase	ilvA	434	Cytoplasmic;	0	No
884	D9QCG9	Rhodanese-related sulfurtransferase	CpC231_1789	94	Cytoplasmic;	0	No
885	D9QAH8	UPF0210 protein CpC231	CpC231_1078	454	Cytoplasmic;	0	No
886	D9Q9M3	GTP-binding protein TypA/BipA	typA	636	Cytoplasmic;	0	No
887	D9QAD7	tRNA (adenine(58)-N(1))-methyltransferase Trml	pimT	278	Cytoplasmic;	0	No
888	D9QDX2	Uncharacterized metallophosphoesterase ykuE	ykuE	312	Cytoplasmic;	0	Yes
889	D9Q9H6	Transcription elongation factor GreA	greA	173	Cytoplasmic;	0	No
890	D9QBP0	Acyl carrier protein	acp	101	Cytoplasmic;	0	No
891	D9Q9S1	Uncharacterized protein	CpC231_0815	194	Membrane;	0	Yes
892	D9QB00	Transcriptional regulator ClgR	clgR	129	Cytoplasmic;	0	No
893	D9QAI1	Uncharacterized protein	CpC231_1081	51	Extracellular;	0	No
894	D9Q9Y3	Iron(3+)-hydroxamate-binding protein fhuD	fhuD	355	Extracellular;	0	Yes
895	D9QA23	Biotin/lipoyl attachment protein	yngHB	74	Cytoplasmic;	0	No
896	D9QE34	Sensory transduction protein regX3	regX3	231	Cytoplasmic;	0	No
897	D9QC15	Uncharacterized protein	CpC231_1629	39	Extracellular;	0	No
898	D9QCW6	Uncharacterized protein	CpC231_1941	115	Membrane;	4	No
899	D9QC71	LPxTG domain-containing protein	CpC231_1686	725	Extracellular;	0	Yes
900	D9QDB7	Glucosamine-6-phosphate deaminase	nagB	259	Cytoplasmic;	0	No
901	D9QCF1	SPFH domain/Band 7 family protein	CpC231_1770	314	Membrane;	2	No
902	D9QEE4	50S ribosomal protein L18	rplR	135	Cytoplasmic;	0	No
903	D9QDQ6	Pyridoxal 5;	pdxT	188	Cytoplasmic;	0	No
904	D9Q9W4	NUDIX hydrolase	CpC231_0859	268	Cytoplasmic;	0	No
905	D9QC43	Ribonuclease PH	rph	247	Cytoplasmic;	0	No
906	D9Q9P0	Uncharacterized protein	CpC231_0784	55	Cytoplasmic;	0	No
907	D9QA78	Cytidylate kinase	cmk	238	Cytoplasmic;	0	No
908	D9QDG3	Ribosomal RNA small subunit methyltransferase G	gidB	223	Cytoplasmic;	0	No
909	D9QDU6	Aspartate-semialdehyde dehydrogenase	asd	343	Cytoplasmic;	0	No
910	D9Q945	Carbonic anhydrase	cynT	240	Cytoplasmic;	0	Yes
911	D9Q9F2	Short chain dehydrogenase	CpC231_0696	284	Cytoplasmic;	0	No
912	D9QAX2	Uncharacterized protein	CpC231_1223	138	Cytoplasmic;	1	No
913	D9QET0	Uncharacterized protein	CpC231_0516	117	Cytoplasmic;	0	No
914	D9QEQQ3	Uncharacterized protein	CpC231_0489	82	Extracellular;	0	No
915	D9QBC5	DNA polymerase IV	dinB	464	Cytoplasmic;	0	No
916	D9QD87	Serine/threonine-protein kinase	pknA	506	Membrane;	1	No
917	D9Q9T9	Homoserine kinase	thrB	307	Cytoplasmic;	0	No
918	D9QCL2	Uncharacterized protein	CpC231_1832	55	Extracellular;	1	No
919	D9QDP4	O-antigen export system ATP-binding protein R	rfbD	301	Membrane;	6	No
920	D9Q985	Uncharacterized protein	CpC231_0628	92	Cytoplasmic;	0	No
921	D9Q9A8	TetR family regulatory protein	amtR	227	Cytoplasmic;	0	No
922	D9QCM1	Cytochrome c nitrate reductase, small subunit	nrfC	161	Extracellular;	1	No
923	D9QCV8	Uncharacterized protein	CpC231_1933	489	Membrane;	12	No
924	D9QDT7	Deoxyribose-phosphate aldolase	deoC	221	Cytoplasmic;	0	No
925	D9QCG7	D-alanyl-D-alanine carboxypeptidase	pbp4	394	Membrane;	0	Yes
926	D9QBC8	Antigen 84	ag84	338	Cytoplasmic;	0	No

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927	D9Q9K8	Uncharacterized protein	CpC231_0752	308	Membrane;	4	No
928	D9QA01	Predicted signal-transduction protein containing cAMP-bin	CpC231_0898	637	Membrane;	0	No
929	D9QD81	ATP binding cytoplasmic membrane protein	fagC	288	Membrane;	0	No
930	D9QE19	Uncharacterized protein	CpC231_0248	116	Extracellular;	2	No
931	D9QC09	Uncharacterized protein	CpC231_1623	326	Membrane;	0	No
932	D9Q9F6	Peptidyl-tRNA hydrolase 1	pth1	135	Cytoplasmic;	0	No
933	D9QCJ3	Transcriptional regulator, Fis family	CpC231_1813	92	Cytoplasmic;	0	No
934	D9QA08	Uncharacterized protein	CpC231_0905	469	Extracellular;	0	Yes
935	D9QAD9	RecB family nuclease	recB	303	Cytoplasmic;	0	No
936	D9QAW7	Alkyl hydroperoxide reductase subunit C	ahpC	198	Cytoplasmic;	0	No
937	D9QBR2	DNA repair protein RecO	recO	242	Cytoplasmic;	0	No
938	D9QD92	Uncharacterized protein	CpC231_0037	317	Cytoplasmic;	0	No
939	D9Q9L8	Oligopeptide transport ATP-binding protein OppD	oppD2	558	Membrane;	0	No
940	D9QC19	Na(+)/H(+) antiporter subunit G	mrpG1	120	Membrane;	3	No
941	D9QBZ2	Uncharacterized protein	CpC231_1606	258	Extracellular;	0	Yes
942	D9Q9B6	Two component system response regulator	tcsR4	230	Cytoplasmic;	0	No
943	D9QAQ6	L-serine dehydratase	sdaB	468	Cytoplasmic;	0	No
944	D9QDM2	Uncharacterized protein	CpC231_0097	180	Membrane;	0	Yes
945	D9Q9J6	Exodeoxyribonuclease 7 small subunit	xseB	98	Cytoplasmic;	0	No
946	D9QBQ5	Uncharacterized protein	CpC231_1515	175	Extracellular;	1	No
947	D9QD93	CAAX amino terminal protease family	CpC231_0038	237	Membrane;	7	No
948	D9QAS1	Holliday junction ATP-dependent DNA helicase RuvB	rvuB	365	Cytoplasmic;	0	No
949	D9QCS7	Uncharacterized protein	CpC231_1901	37	Extracellular;	1	No
950	D9QE69	O-succinylbenzoic acid--CoA ligase	menE	375	Cytoplasmic;	0	No
951	D9Q987	Glutaredoxin	CpC231_0630	84	Extracellular;	0	No
952	D9QDM7	Decaprenylphosphoryl-D-2-keto erythropentose reductase	CpC231_0102	253	Cytoplasmic;	0	No
953	D9QAH9	Uncharacterized protein	CpC231_1079	75	Cytoplasmic;	2	No
954	D9QD94	Uncharacterized protein	CpC231_0039	176	Membrane;	2	No
955	D9QAW9	Uncharacterized protein	CpC231_1220	342	Membrane;	6	No
956	D9QCU0	Urease subunit beta	ureB	103	Cytoplasmic;	0	No
957	D9QB64	PTS system mannose-specific EIIBCA component	manP	677	Membrane;	10	No
958	D9QDL1	Short-chain dehydrogenase/reductase yusR	yusR	233	Membrane;	0	Yes
959	D9QC03	Uncharacterized protein	CpC231_1617	50	Extracellular;	0	No
960	D9QC22	Oligoribonuclease	om	219	Cytoplasmic;	0	No
961	D9QAT8	Copper resistance protein CopC	copC	190	Extracellular;	1	Yes
962	D9QE50	Delta-aminolevulinic acid dehydratase	hemB	335	Cytoplasmic;	0	No
963	D9QBH5	Adenosylcobinamide-GDP ribazoletransferase	cobS	273	Membrane;	7	No
964	D9QAV6	Uncharacterized protein	CpC231_1207	79	Cytoplasmic;	0	No
965	D9Q9U7	Uncharacterized protein	CpC231_0842	144	Membrane;	4	No
966	D9QCJ4	Peptide deformylase	def	197	Cytoplasmic;	0	No
967	D9Q967	Superoxide dismutase [Cu-Zn]	sodC	206	Extracellular;	0	Yes
968	D9Q9P3	Alpha-acetolactate decarboxylase	alsD	246	Cytoplasmic;	0	No
969	D9QB54	30S ribosomal protein S2	rpsB	276	Cytoplasmic;	0	No
970	D9QDA8	Uncharacterized protein	CpC231_2044	33	Extracellular;	0	No
971	D9QBV7	LysE type translocator	CpC231_1571	215	Membrane;	6	No
972	D9QCB3	Trk system potassium uptake protein trkH	trkH	444	Membrane;	9	No
973	D9QEN3	Uncharacterized protein	CpC231_0469	411	Cytoplasmic;	0	No
974	D9QCX5	Uncharacterized protein	CpC231_1950	473	Membrane;	11	No
975	D9Q9K4	Phosphonoacetate hydrolase	phnA	98	Cytoplasmic;	0	No
976	D9QDE4	Tryptophan synthase beta chain	trpB	416	Cytoplasmic;	0	No
977	D9QBN8	Pyruvate dehydrogenase E1 component	aceE	911	Cytoplasmic;	0	No
978	D9QC34	Two-component system sensor kinase protein	tcsS5	368	Membrane;	6	No
979	D9QEEO	L-asparaginase	ansA	358	Cytoplasmic;	0	Yes
980	D9QDQ0	Glyoxalase/Bleomycin resistance protein/Dihydroxybiphen	CpC231_0126	267	Cytoplasmic;	0	No
981	D9QCH3	Multiple antibiotic resistance protein marR	marR2	146	Cytoplasmic;	0	No
982	D9Q9I1	Uncharacterized protein	CpC231_0725	166	Cytoplasmic;	0	No
983	D9QEJ8	Phage shock protein C	pspC	350	Membrane;	4	No
984	D9QAF5	Fructose-specific phosphotransferase enzyme IIA compon	levD	229	Cytoplasmic;	0	No
985	D9QCP2	Gram-positive anchor	CpC231_1863	271	Membrane;	1	Yes
986	D9Q9F8	Pullulanase	pulA	624	Extracellular;	0	No
987	D9QAS8	6-carboxyhexanoate--CoA ligase	bioW	243	Cytoplasmic;	0	No
988	D9QDI5	Biotin synthase	bioB	331	Cytoplasmic;	0	No
989	D9Q966	Acetyl-CoA carboxylase carboxyl transferase	accDA	391	Membrane;	0	No
990	F9Y371	Uncharacterized protein	CpC231_1417a	53	Cytoplasmic;	0	No
991	D9QER1	Uncharacterized protein	CpC231_0497	67	Cytoplasmic;	2	No
992	D9QBE5	Uncharacterized protein	CpC231_1400	104	Extracellular;	0	No
993	D9QAR5	GTP pyrophosphokinase	relA	759	Cytoplasmic;	0	No

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994	D9QCM8	ABC transporter ATP-binding protein YxlF	yxlF	271	Membrane;	0	Yes
995	D9QBX9	Uncharacterized protein	CpC231_1593	142	Membrane;	4	No
996	D9QEVT	Uncharacterized protein	CpC231_0543	279	Cytoplasmic;	0	No
997	F9Y342	Uncharacterized protein	CpC231_0558a	152	Membrane;	2	Yes
998	D9QCM7	Uncharacterized transmembrane protein yxlG	yxlG	226	Membrane;	5	No
999	D9QEL6	Uncharacterized protein	CpC231_0450	108	Membrane;	3	No
1000	D9QDX6	Uncharacterized protein	CpC231_0205	51	Extracellular;	0	No
1001	D9QED4	Uncharacterized protein	CpC231_0365	39	Extracellular;	0	Yes
1002	D9QAE9	Aldo/keto reductase family oxidoreductase	CpC231_1049	302	Cytoplasmic;	0	No
1003	D9QA00	3-isopropylmalate dehydrogenase	leuB	339	Cytoplasmic;	0	No
1004	D9QAC7	Dipeptidase pepE	pepE	380	Cytoplasmic;	0	No
1005	D9QE68	1,4-dihydroxy-2-naphthoate octaprenyltransferase	menA	291	Membrane;	9	No
1006	D9QAX0	ATP-dependent RNA helicase hrpA	hrpA	1332	Cytoplasmic;	0	No
1007	D9QCY0	Glycosyltransferase	glfT1	663	Cytoplasmic;	0	No
1008	D9QBJ3	rRNA biogenesis protein rrp5	CpC231_1449	140	Cytoplasmic;	0	No
1009	D9QEF8	L,D-transpeptidase catalytic domain, region YkuD	CpC231_0391	246	Extracellular;	0	Yes
1010	D9QC44	Metal-dependent hydrolase	CpC231_1658	265	Cytoplasmic;	0	Yes
1011	D9QDX1	Uncharacterized protein	CpC231_0199	159	Extracellular;	0	No
1012	D9QEET	50S ribosomal protein L15	rplO	148	Cytoplasmic;	0	No
1013	D9QC37	Uncharacterized protein	CpC231_1651	252	Cytoplasmic;	0	No
1014	D9QDM4	Glycine betaine-binding protein	opoAC	291	Cytoplasmic;	0	Yes
1015	D9QDC8	CAAX amino terminal protease	CpC231_2064	209	Membrane;	7	No
1016	D9QBL1	Uncharacterized protein	CpC231_1470	44	Extracellular;	0	No
1017	D9QDA0	Uncharacterized protein	CpC231_2036	257	Membrane;	5	No
1018	F9Y330	Uncharacterized protein	CpC231_0006a	28	Extracellular;	0	No
1019	D9QAD4	Prokaryotic ubiquitin-like protein Pup	pup	64	Extracellular;	0	No
1020	D9QEUT	Cys-tRNA(Pro)/Cys-tRNA(Cys) deacylase	ybaK	167	Cytoplasmic;	0	No
1021	D9QED3	Uncharacterized protein	CpC231_0364	53	Cytoplasmic;	0	No
1022	D9QEJ9	Two-component system sensor kinase	tcsS3	398	Membrane;	6	No
1023	D9QBV6	30S ribosomal protein S20	rpsT	87	Cytoplasmic;	0	No
1024	D9QA13	3-isopropylmalate dehydratase small subunit	leuD	196	Cytoplasmic;	0	No
1025	D9QER4	Uncharacterized protein	CpC231_0500	36	Extracellular;	0	No
1026	D9QBL6	MutT/NUDIX family protein	CpC231_1475	178	Cytoplasmic;	0	No
1027	D9QAJ9	OxPP cycle protein opcA	CpC231_1099	319	Cytoplasmic;	0	No
1028	D9QBJ1	Phage-associated protein	CpC231_1447	130	Extracellular;	0	No
1029	D9QDX5	Transcriptional regulator WhiB	whiB	115	Cytoplasmic;	0	No
1030	D9QEA0	Uncharacterized protein	CpC231_0330	58	Cytoplasmic;	1	No
1031	D9QA19	Thiamine-monophosphate kinase	thiL	326	Cytoplasmic;	0	No
1032	D9QE23	Uncharacterized protein	CpC231_0252	282	Membrane;	1	No
1033	D9QAE6	Uncharacterized protein	CpC231_1046	145	Cytoplasmic;	0	No
1034	D9QEN7	HTH-type transcriptional regulator	CpC231_0473	158	Membrane;	0	No
1035	D9QAJ8	Glucose-6-phosphate 1-dehydrogenase	zwf	531	Cytoplasmic;	0	No
1036	D9Q975	Multidrug resistance protein norM	norM	472	Membrane;	12	No
1037	D9QD27	Probable queuosine precursor transporter	CpC231_2004	258	Membrane;	6	No
1038	D9QDQ7	Prephenate dehydrogenase	tyrA	337	Cytoplasmic;	1	Yes
1039	D9QEJ7	Uncharacterized protein	CpC231_0431	149	Cytoplasmic;	0	No
1040	D9QEUT3	Stearoyl-CoA 9-desaturase	desA3	424	Cytoplasmic;	0	No
1041	D9QCY7	Spermidine/putrescine import ATP-binding protein PotA	potA	258	Membrane;	0	No
1042	D9QAP3	Endolytic murein transglycosylase	yceG	382	Extracellular;	1	No
1043	D9QDV1	Uncharacterized protein	CpC231_0179	68	Extracellular;	0	No
1044	D9QEE2	30S ribosomal protein S8	rpsH	132	Cytoplasmic;	0	No
1045	D9QBI1	Glycine cleavage system H protein	gcvH	128	Cytoplasmic;	0	No
1046	D9Q937	Histidinol-phosphatase	hisN	268	Cytoplasmic;	0	No
1047	D9QAQ5	NADPH-dependent FMN reductase	CpC231_1155	178	Membrane;	0	Yes
1048	D9QCA1	Protein Nrdl	nrdl	141	Cytoplasmic;	0	No
1049	D9Q969	2,5-diketo-D-gluconic acid reductase A	dkgA	286	Cytoplasmic;	0	No
1050	D9QAM6	Orotidine 5';	pyrF	279	Cytoplasmic;	0	No
1051	D9QBV8	Ankyrin domain-containing protein	CpC231_1572	133	Cytoplasmic;	0	No
1052	D9QC48	ATP-dependent Clp protease adapter protein ClpS	clpS	126	Cytoplasmic;	0	No
1053	F9Y368	Uncharacterized protein	CpC231_1158a	57	Extracellular;	0	No
1054	D9Q990	3;	cysQ	294	Cytoplasmic;	0	No
1055	D9QDT9	Uncharacterized protein	CpC231_0167	518	Extracellular;	2	Yes
1056	D9QEE6	50S ribosomal protein L30	rpmD	61	Cytoplasmic;	0	No
1057	D9QBN3	Low molecular weight protein-tyrosine-phosphatase	ptpA	141	Cytoplasmic;	0	No
1058	D9QCA6	Phosphoribosylformylglycinamidine synthase subunit PurS	purS	79	Cytoplasmic;	0	No
1059	D9QDA1	DNA protection during starvation protein	dps	163	Cytoplasmic;	0	No
1060	D9QDD0	Aldose 1-epimerase	CpC231_2066	179	Membrane;	0	No

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1061	D9Q9K3	Uncharacterized protein	CpC231_0747	179	Cytoplasmic;	0	No
1062	D9QES9	Uncharacterized protein	CpC231_0515	57	Extracellular;	0	No
1063	D9Q9K2	Uncharacterized protein	CpC231_0746	87	Cytoplasmic;	0	No
1064	F9Y373	Uncharacterized protein	CpC231_1467a	31	Extracellular;	0	Yes
1065	D9QAP5	Uncharacterized protein	CpC231_1145	36	Extracellular;	0	No
1066	D9QCT0	Uncharacterized protein	CpC231_1904	218	Cytoplasmic;	2	No
1067	D9Q9C5	Molybdopterin molybdenumtransferase	moeA	421	Cytoplasmic;	0	No
1068	F9Y354	Uncharacterized protein	CpC231_0886a	55	Extracellular;	0	No
1069	D9Q980	Oligopeptide-binding protein oppA	oppA2	510	Extracellular;	0	Yes
1070	D9QAH3	1-deoxy-D-xylulose-5-phosphate synthase	CpC231_1073	195	Cytoplasmic;	1	No
1071	D9QCD9	Uncharacterized protein	CpC231_1758	235	Extracellular;	1	No
1072	D9QCI8	Na(+)/H(+) antiporter subunit F	mrpF1	90	Membrane;	3	No
1073	D9QAV5	Type III restriction endonuclease, res subunit	CpC231_1206	569	Cytoplasmic;	0	No
1074	D9QAE2	Aspartate ammonia-lyase	aspA	476	Cytoplasmic;	0	No
1075	D9QCM3	Uncharacterized protein	CpC231_1843	284	Cytoplasmic;	0	No
1076	D9QCR3	Uncharacterized protein	CpC231_1886	379	Extracellular;	0	Yes
1077	D9QAY6	Uncharacterized protein	CpC231_1237	174	Membrane;	0	No
1078	D9QD14	Abi family protein	CpC231_1990	290	Cytoplasmic;	0	No
1079	D9QD96	Zinc ABC transporter substrate-binding protein	fecB	332	Extracellular;	0	Yes
1080	D9QC62	Protein Nrdl	nrdl	145	Membrane;	0	No
1081	D9QEN9	Aminobenzoyl-glutamate utilization protein B	abgB	398	Cytoplasmic;	0	No
1082	D9QAY9	Uncharacterized protein	CpC231_1240	234	Cytoplasmic;	0	No
1083	D9QB69	30S ribosomal protein S16	rpsP	154	Cytoplasmic;	0	No
1084	F9Y358	Uncharacterized protein	CpC231_0969a	31	Cytoplasmic;	0	No
1085	D9QB92	Indole-3-glycerol phosphate synthase	trpC2	273	Cytoplasmic;	0	No
1086	D9Q991	ATP-dependent helicase Ihr	ihr	1673	Cellwall;	0	No
1087	D9QCN3	Fructose-bisphosphate aldolase class 2	fbaA	344	Cytoplasmic;	0	No
1088	D9QE30	Long-chain-fatty-acid-CoA ligase	lcfA1	506	Membrane;	2	No
1089	D9Q9Y7	Lysine exporter protein	lysE	243	Membrane;	6	No
1090	F9Y375	Uncharacterized protein	CpC231_1487a	106	Extracellular;	0	No
1091	D9Q961	Uncharacterized protein	CpC231_0602	300	Cytoplasmic;	0	No
1092	D9Q979	Alpha-ketoglutarate-dependent taurine dioxygenase	tauD	322	Cytoplasmic;	0	No
1093	D9QC75	Uncharacterized protein	CpC231_1690	50	Cytoplasmic;	0	No
1094	D9QE78	L-lactate dehydrogenase	ldh	320	Membrane;	0	No
1095	D9QCW3	Uncharacterized protein	CpC231_1938	219	Cytoplasmic;	0	No
1096	D9QAS6	Acyl-CoA thioesterase II	tesB	298	Cytoplasmic;	0	No
1097	D9QDL7	Uncharacterized protein	CpC231_0092	331	Cytoplasmic;	0	No
1098	D9QAA7	Magnesium/cobalt transporter CorA	corA	356	Cytoplasmic;	2	No
1099	D9Q974	Na(+)/H(+) antiporter-like protein	CpC231_0616	424	Membrane;	13	No
1100	D9QE67	Uncharacterized protein	CpC231_0296	111	Membrane;	2	No
1101	D9QD02	Uncharacterized protein	CpC231_1977	374	Cellwall;	1	Yes
1102	D9QCD1	Cysteine-tRNA ligase	cysS	465	Cytoplasmic;	0	No
1103	D9QCE8	Hydrolase, alpha/beta fold family	pldB1	261	Cytoplasmic;	0	No
1104	D9Q9H5	Uncharacterized protein	CpC231_0719	146	Extracellular;	0	No
1105	D9QBN5	Cobalamin biosynthesis protein CobD	cobD	287	Membrane;	5	No
1106	D9QBN2	Phosphoglycolate phosphatase	pgp	214	Cytoplasmic;	0	No
1107	D9QCN5	tRNA/rRNA methyltransferase	CpC231_1855	223	Cytoplasmic;	0	No
1108	D9QDD8	Phytoene Dehydrogenase (Desaturase)	crtl2	543	Extracellular;	0	Yes
1109	D9QEW6	Endopeptidase La	lon	351	Cytoplasmic;	0	Yes
1110	D9QBG1	Cell-wall peptidase NlpC/P60 protein	CpC231_1416	334	Extracellular;	0	Yes
1111	D9QE33	Signal-transduction histidine kinase senX3	senX3	412	Membrane;	1	No
1112	D9QBX3	50S ribosomal protein L21	rplU	101	Cytoplasmic;	0	No
1113	D9QB30	Uncharacterized protein	CpC231_1282	245	Membrane;	0	No
1114	D9QDZ8	Cold-shock protein	cspA	67	Cytoplasmic;	0	No
1115	D9QC99	Amidophosphoribosyltransferase	purF	520	Cytoplasmic;	0	No
1116	D9QAB1	MFS family major facilitator transporter	CpC231_1010	461	Membrane;	12	No
1117	D9QEQ6	Biotin-(Acetyl-CoA carboxylase) ligase	birA	281	Cytoplasmic;	0	No
1118	D9QCJ1	Putative glutamate-cysteine ligase 2	CpC231_1811	372	Cytoplasmic;	0	No
1119	D9QD46	Single-stranded DNA-binding protein	ssb1	189	Extracellular;	0	No
1120	D9QBW0	Competence protein ComE-like protein	comE	555	Membrane;	12	No
1121	D9Q9V5	ATP synthase epsilon chain	atpC	123	Cytoplasmic;	0	No
1122	D9Q9G9	Enolase	eno	425	Cytoplasmic;	0	No
1123	D9QDG9	Fe(3+) dicitrate transport system permease protein fecD	fecD	374	Membrane;	10	No
1124	D9QE53	Uroporphyrinogen decarboxylase	hemE	371	Cytoplasmic;	0	No
1125	D9QDD5	UDP-N-acetylglucosamine diphosphorylase	CpC231_2071	304	Cytoplasmic;	0	No
1126	D9QA54	Ornithine carbamoyltransferase	argF	333	Cytoplasmic;	0	No
1127	D9QB09	Ribonuclease J	rnj	683	Cytoplasmic;	0	No

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1128	D9QEF1	Maltose transport system permease	malG	292	Membrane;	6	No
1129	F9Y370	Uncharacterized protein	CpC231_1199a	56	Extracellular;	0	No
1130	D9QBN7	Uncharacterized protein	CpC231_1497	145	Cytoplasmic;	0	No
1131	D9QA24	Ribosomal RNA small subunit methyltransferase D	rsmD	192	Cytoplasmic;	0	No
1132	F9Y382	Uncharacterized protein	CpC231_1864a	28	Extracellular;	0	No
1133	D9Q9W5	Uncharacterized protein	CpC231_0860	403	Cytoplasmic;	0	No
1134	D9QAC9	Sec-independent protein translocase protein TatC	tatC	362	Membrane;	6	No
1135	D9QA26	Probable membrane transporter protein	CpC231_0923	247	Membrane;	9	No
1136	D9QAF6	Dihydroxyacetone kinase family protein	dhaL	215	Cytoplasmic;	0	No
1137	D9Q9I4	Major facilitator superfamily permease	CpC231_0728	566	Membrane;	14	No
1138	D9Q9M8	N-succinylaminopimelate aminotransferase	dapC	364	Cytoplasmic;	0	No
1139	D9QC24	L,D-transpeptidase YkuD	ykuD	396	Extracellular;	0	Yes
1140	D9QAB5	RNA polymerase-binding protein RbpA	rpbA	130	Cytoplasmic;	0	No
1141	D9QBM8	Bifunctional RNase H/acid phosphatase	CpC231_1488	385	Cytoplasmic;	0	No
1142	D9QBX4	Ribonuclease E/G family	rne	1134	Cellwall;	0	No
1143	D9QCZ0	Peptidoglycan recognition protein	CpC231_1965	675	Extracellular;	0	Yes
1144	D9QC25	Oxidoreductase	CpC231_1639	332	Cytoplasmic;	0	No
1145	D9QA55	Arginine repressor	argR	163	Cytoplasmic;	0	No
1146	D9Q9T4	Lactate utilization protein A	lutA	261	Cytoplasmic;	0	No
1147	D9QE75	Uncharacterized protein	CpC231_0304	151	Membrane;	2	No
1148	D9Q9H0	Septum formation initiator protein	CpC231_0714	180	Membrane;	1	No
1149	D9QCU8	Uncharacterized protein	CpC231_1922	221	Membrane;	6	No
1150	D9QBT1	Uncharacterized protein	CpC231_1542	222	Membrane;	1	No
1151	D9QBB3	Ribosome-associated heat shock protein/S4	CpC231_1368	124	Cytoplasmic;	0	No
1152	D9QEL8	Cell-surface hemin receptor	htaB	167	Membrane;	2	No
1153	D9QDS8	Uncharacterized protein	CpC231_0155	78	Cytoplasmic;	0	No
1154	D9QEP5	Sulfurtransferase	cysA	292	Cytoplasmic;	0	No
1155	D9QDH8	Protein dipZ	dipZ	545	Membrane;	6	No
1156	F9Y359	Uncharacterized protein	CpC231_0987a	48	Cytoplasmic;	1	No
1157	D9QCF6	Pantoate--beta-alanine ligase	panC	222	Cytoplasmic;	0	No
1158	D9QE36	Ppx/GppA phosphatase family	gppA1	290	Cytoplasmic;	0	No
1159	D9QDD9	Tryptophan-specific permease, 5-methyltryptophan resista	trpF	160	Membrane;	3	No
1160	D9QDM3	Uncharacterized protein	CpC231_0098	300	Membrane;	8	No
1161	D9Q9X7	Mycothiol acetyltransferase	mshD	164	Extracellular;	0	No
1162	D9QAT7	Lipoprotein	CpC231_1187	201	Membrane;	0	Yes
1163	D9Q9C7	Uncharacterized protein	CpC231_0670	387	Cytoplasmic;	3	No
1164	D9QAR9	Protein translocase subunit SecD	secD	622	Membrane;	6	No
1165	D9QBT7	Uncharacterized protein	CpC231_1549	182	Membrane;	2	No
1166	D9QA48	Phenylalanine-tRNA ligase alpha subunit	pheS	351	Cytoplasmic;	0	No
1167	D9QBK9	Uncharacterized protein htaC	CpC231_1468	299	Extracellular;	1	Yes
1168	D9Q944	Uncharacterized protein	CpC231_0584	41	Extracellular;	0	No
1169	D9QC80	Cytochrome d ubiquinol oxidase subunit 1	cydA	507	Membrane;	9	No
1170	D9QAL5	Ribulose-phosphate 3-epimerase	rpe	224	Cytoplasmic;	0	No
1171	D9QEWT1	NADH pyrophosphatase	nudC	219	Membrane;	0	No
1172	D9QDF4	Uncharacterized protein	CpC231_2090	948	Cellwall;	1	Yes
1173	F9Y357	Uncharacterized protein	CpC231_0938a	36	Extracellular;	0	No
1174	D9QAB6	Polyprenol-phosphate-mannose synthase domain 1	ppm1	265	Cytoplasmic;	0	No
1175	D9QDB9	N-acylglucosamine-6-phosphate 2-epimerase	nanE	229	Cytoplasmic;	0	No
1176	F9Y337	Uncharacterized protein	CpC231_0416a	33	Cytoplasmic;	0	No
1177	D9QDJ0	Lysozyme M1	CpC231_0064	389	Extracellular;	0	Yes
1178	D9QAZ8	Cobalt transport protein cbiQ	bioN	204	Membrane;	6	No
1179	D9QBB5	Uncharacterized protein	CpC231_1370	211	Cytoplasmic;	0	No
1180	D9Q9Q3	Uncharacterized protein	CpC231_0797	220	Membrane;	0	Yes
1181	D9QAN2	Epimerase family protein yfcH	CpC231_1132	459	Membrane;	0	No
1182	D9QCY6	UDP-galactopyranose mutase	glf	411	Cytoplasmic;	0	No
1183	D9Q942	Cell division protein FtsX	ftsX	300	Membrane;	4	No
1184	D9QC45	Glutamate racemase	murl	297	Membrane;	0	No
1185	D9QEP3	Uncharacterized protein	CpC231_0479	128	Cytoplasmic;	0	No
1186	D9QCT7	Urease accessory protein UreF	ureF	228	Cytoplasmic;	0	No
1187	D9QBM5	Uncharacterized protein	CpC231_1485	61	Cytoplasmic;	0	No
1188	D9QBF2	Alpha mannopyranosyltransferase	mptA	490	Membrane;	14	No
1189	D9QC47	Uncharacterized protein	CpC231_1661	178	Cytoplasmic;	0	No
1190	D9QEWT0	Trk system potassium uptake protein trkA	trkA	359	Membrane;	2	No
1191	D9QCN9	Uncharacterized protein	CpC231_1860	31	Extracellular;	1	No
1192	D9QEC2	50S ribosomal protein L2	rplB	280	Cytoplasmic;	0	No
1193	D9QCG8	Inorganic pyrophosphatase	ppa	158	Cytoplasmic;	0	No
1194	D9QB65	Uncharacterized protein	CpC231_1319	134	Cytoplasmic;	0	No

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1195	D9QDC5	Oligopeptide transport ATP-binding protein OppF	oppF	277	Cytoplasmic;	0	No
1196	D9Q9Q6	Uncharacterized protein	CpC231_0800	275	Membrane;	2	No
1197	F9Y331	Uncharacterized protein	CpC231_0019a	35	Extracellular;	0	Yes
1198	D9QEY2	Uncharacterized protein	CpC231_0568	60	Extracellular;	0	No
1199	D9Q9H9	Uncharacterized protein	CpC231_0723	95	Cytoplasmic;	0	No
1200	D9QB73	Signal recognition particle receptor FtsY	ftsY	548	Cytoplasmic;	1	No
1201	D9Q9H4	Uncharacterized protein	CpC231_0718	273	Membrane;	7	No
1202	D9QC02	Single-strand binding protein	CpC231_1616	186	Extracellular;	0	No
1203	D9QD75	Uncharacterized protein	CpC231_0020	52	Extracellular;	0	No
1204	D9QD44	Uncharacterized protein	CpC231_2021	76	Extracellular;	1	No
1205	D9QD78	CRISPR-associated protein Cas5	cas5	117	Cytoplasmic;	0	No
1206	D9QBE3	Ribosomal RNA small subunit methyltransferase H	mraW	351	Cytoplasmic;	0	No
1207	D9QAB2	Uncharacterized protein	CpC231_1011	66	Membrane;	2	No
1208	D9QCZ5	Uncharacterized protein	CpC231_1970	338	Extracellular;	0	Yes
1209	D9Q9W6	Electron transfer flavo protein subunit beta	etfB	264	Cytoplasmic;	0	No
1210	D9QE4	Glycerol-3-phosphate-transporting ATPase	malK	378	Cytoplasmic;	0	No
1211	D9QBV9	DNA polymerase III subunit delta	holA	324	Cytoplasmic;	0	No
1212	D9QBF1	Geranylgeranyl pyrophosphate synthase	idsA	372	Cytoplasmic;	0	No
1213	D9QAV7	Uncharacterized protein	CpC231_1208	168	Cytoplasmic;	2	No
1214	D9QAU3	Uncharacterized protein	CpC231_1193	202	Cytoplasmic;	0	No
1215	D9QCH5	Uncharacterized protein	CpC231_1795	54	Extracellular;	0	No
1216	D9QE28	Uncharacterized protein	CpC231_0257	167	Cytoplasmic;	0	No
1217	D9QC98	Phosphoribosylformylglycinamide cyclo-ligase	purM	353	Cytoplasmic;	0	No
1218	D9QCP5	Uncharacterized protein	CpC231_1866	33	Extracellular;	0	Yes
1219	D9QCY5	Glycerol-3-phosphate transporter	glpT1	461	Membrane;	12	No
1220	D9QBW7	Phosphoglycerate dehydrogenase	CpC231_1581	304	Cytoplasmic;	0	No
1221	D9Q9C0	Uncharacterized protein	CpC231_0663	69	Cytoplasmic;	0	No
1222	D9QBF3	Transcription regulator	CpC231_1408	122	Cytoplasmic;	0	No
1223	D9QAS0	Preprotein translocase subunit YajC	secN	111	Membrane;	1	No
1224	D9QCB6	Uncharacterized protein	CpC231_1732	205	Membrane;	0	No
1225	D9QA87	Iron ABC transporter ATP-binding protein	ciuD	273	Membrane;	0	No
1226	D9QD05	Glycerophosphoryl diester phosphodiesterase	glpQ	239	Cytoplasmic;	0	No
1227	D9QBQ8	HTH-type transcriptional regulator	CpC231_1518	133	Cytoplasmic;	0	No
1228	F9Y360	Uncharacterized protein	CpC231_0987b	52	Cytoplasmic;	0	No
1229	D9QCE2	Uncharacterized protein	CpC231_1761	433	Membrane;	11	No
1230	D9QAU1	Peptide-methionine (R)-S-oxide reductase	msrB	136	Cytoplasmic;	0	No
1231	D9Q9R4	Uncharacterized protein	CpC231_0808	102	Membrane;	2	No
1232	D9QDY0	Uncharacterized protein	CpC231_0209	71	Extracellular;	1	No
1233	D9QE62	ABC transporter ATP-binding protein	CpC231_0291	256	Membrane;	0	No
1234	D9Q9N9	Uncharacterized protein	CpC231_0783	95	Membrane;	1	No
1235	D9Q9B2	50S ribosomal protein L33	rpmG	54	Cytoplasmic;	0	No
1236	D9QCQ2	Uncharacterized protein	CpC231_1873	251	Extracellular;	1	No
1237	D9QDC1	GntR family regulatory protein	CpC231_2057	258	Cytoplasmic;	0	No
1238	D9QDH5	Anti-sigma factor	cskE	214	Cytoplasmic;	1	No
1239	D9QE77	Demethylmenaquinone methyltransferase	menG	232	Cytoplasmic;	0	No
1240	D9QA72	Dethiobiotin synthase	bioD	201	Membrane;	0	Yes
1241	D9QCG0	2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphate synthase	folK	151	Cytoplasmic;	0	No
1242	D9QAD2	Protein pafB	pafB	329	Cytoplasmic;	0	No
1243	D9QDR4	Gluconate permease	gntP	462	Membrane;	13	No
1244	D9Q9K6	ABC transporter ATP-binding protein	CpC231_0750	564	Membrane;	6	No
1245	D9QC36	Uncharacterized protein	CpC231_1650	343	Membrane;	10	No
1246	D9QDB1	ABC transporter inner membrane protein	CpC231_2047	350	Membrane;	4	No
1247	D9QA02	DNA polymerase III subunit epsilon	dnaQ3	172	Cytoplasmic;	0	No
1248	D9QD89	Cell division protein ftsW	ftsW	457	Membrane;	12	No
1249	D9QEL9	Cell-surface hemin receptor	htaA	615	Extracellular;	1	Yes
1250	D9QA98	MerR family transcriptional regulator	merR2	250	Cytoplasmic;	0	No
1251	D9QEN6	Uracil phosphoribosyltransferase	upp	211	Cytoplasmic;	0	No
1252	D9QCX7	Uncharacterized protein	CpC231_1952	641	Membrane;	11	No
1253	D9QDJ1	Inositol-3-phosphate synthase	ino1	361	Cytoplasmic;	0	No
1254	D9Q9X9	Uncharacterized protein	CpC231_0874	120	Extracellular;	4	No
1255	D9QCQ7	Secretion protein HlyD	hlyD	563	Extracellular;	0	No
1256	D9QA09	Biotin synthase	bioB2	334	Cytoplasmic;	0	No
1257	D9QD38	Thioredoxin	trxA1	122	Cytoplasmic;	0	No
1258	D9Q9C4	UTP--glucose-1-phosphate uridylyltransferase	galU	318	Cytoplasmic;	0	No
1259	D9QDI6	Uncharacterized protein	CpC231_0060	84	Cytoplasmic;	0	No
1260	D9Q9D9	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	ispE	319	Cytoplasmic;	0	No
1261	D9QEY5	Uncharacterized protein	CpC231_0541	75	Extracellular;	0	No

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1262	D9QAT9	Riboflavin biosynthesis protein RibD	CpC231_1189	265	Extracellular;	0	No
1263	D9QA03	Uncharacterized protein	CpC231_0900	107	Membrane;	1	No
1264	F9Y348	Uncharacterized protein	CpC231_0599a	32	Extracellular;	0	No
1265	D9QE86	Uncharacterized protein	CpC231_0347	112	Cytoplasmic;	0	No
1266	D9Q9B1	30S ribosomal protein S14	rpsN	101	Cytoplasmic;	0	No
1267	D9QE11	Surface layer protein A	slpA	359	Extracellular;	0	Yes
1268	D9QA82	Esterase	CpC231_0980	414	Extracellular;	4	No
1269	D9QAG4	Uncharacterized protein	CpC231_1064	170	Membrane;	5	No
1270	D9QD15	MazG nucleotide pyrophosphohydrolase	mazG	106	Cytoplasmic;	0	No
1271	D9QED0	Oligopeptide transport ATP-binding protein	oppDF1	690	Membrane;	0	No
1272	F9Y384	Uncharacterized protein	CpC231_1964a	40	Cytoplasmic;	0	No
1273	D9QER9	Uncharacterized protein	CpC231_0505	34	Extracellular;	0	No
1274	D9QDH9	Uncharacterized protein	CpC231_0053	253	Cytoplasmic;	0	No
1275	D9QBG5	Ubiquinol-cytochrome c reductase iron-sulfur subunit	qcrA	406	Membrane;	3	No
1276	D9QD57	Beta sliding clamp	dnaN	395	Cytoplasmic;	0	No
1277	D9Q9R9	Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl	CpC231_0813	148	Cytoplasmic;	0	No
1278	D9QC87	Uncharacterized protein	CpC231_1702	67	Extracellular;	0	No
1279	D9QC68	HTH-type transcriptional regulator CmtR	cmtR	132	Cytoplasmic;	0	No
1280	D9QE59	Cytochrome c-type biogenesis protein CcdA	ccdA	268	Membrane;	6	No
1281	D9QC19	Uncharacterized protein	CpC231_1633	44	Extracellular;	0	No
1282	D9Q9Y6	Aldo-keto reductase	yghZ	379	Cytoplasmic;	0	No
1283	D9QE51	Uncharacterized protein	CpC231_0280	193	Membrane;	2	No
1284	D9QCZ2	1-acyl-sn-glycerol-3-phosphate acyltransferase	plsC1	282	Cytoplasmic;	0	No
1285	D9QB46	Zinc metalloprotease	CpC231_1299	404	Membrane;	4	No
1286	D9QES2	Transcriptional regulator WhiB	whiB	99	Cytoplasmic;	0	No
1287	D9QAR4	Uncharacterized protein	CpC231_1164	113	Extracellular;	1	Yes
1288	D9Q9B3	50S ribosomal protein L28	rpmB	78	Cytoplasmic;	0	No
1289	D9QBF9	Glucose kinase	glk	317	Cytoplasmic;	0	No
1290	D9QDP9	PtsGHI operon antiterminator	glcT	282	Cytoplasmic;	0	No
1291	D9QCA9	Uncharacterized protein	CpC231_1725	69	Extracellular;	0	No
1292	D9QCJ5	Acetyltransferase	CpC231_1815	320	Cytoplasmic;	0	No
1293	D9Q9N5	Succinyl-diaminopimelate desuccinylase	dapE	357	Cytoplasmic;	0	No
1294	D9QEHI3	ESAT-6-like protein	CpC231_0406	94	Extracellular;	0	No
1295	D9QAG0	Dehydrogenase/oxidoreductase	CpC231_1060	490	Cytoplasmic;	0	No
1296	D9QBQ9	Ferric uptake regulatory protein	furB	141	Cytoplasmic;	0	No
1297	D9QC60	Ferritin	ftn	173	Cytoplasmic;	0	No
1298	D9QD91	FHA domain-containing protein	CpC231_0036	159	Membrane;	1	No
1299	D9QA69	Tyrosine recombinase XerD	xerD	310	Cytoplasmic;	0	No
1300	D9QB23	Ribosome-binding factor A	rbfA	145	Cytoplasmic;	0	No
1301	D9QAL9	Probable primosomal protein N;	priA	681	Cytoplasmic;	0	No
1302	D9QET9	Uncharacterized protein	CpC231_0525	177	Membrane;	0	No
1303	D9QCV6	Acyltransferase	CpC231_1931	363	Membrane;	10	No
1304	D9Q9T1	Uncharacterized protein	CpC231_0826	114	Cytoplasmic;	0	Yes
1305	D9QDV7	Spermidine/putrescine-binding periplasmic protein	potD	333	Extracellular;	0	Yes
1306	D9QBP3	Beta-lactamase transpeptidase-like protein	bla	269	Membrane;	0	No
1307	D9QC76	Cysteine synthase	cysK	311	Cytoplasmic;	0	No
1308	D9QDK2	Uncharacterized protein	CpC231_0077	278	Cytoplasmic;	0	No
1309	D9QCD4	Transcriptional regulator	carD	193	Cytoplasmic;	0	No
1310	D9QDS0	Uncharacterized protein	CpC231_0146	189	Cytoplasmic;	0	No
1311	D9QBG8	Cytochrome c oxidase polypeptide 4	ctaF	143	Membrane;	4	No
1312	D9Q993	DNA glycosylase	nei	257	Cytoplasmic;	0	No
1313	D9QCI7	Na(+)/H(+) antiporter subunit E	mrpE1	171	Membrane;	4	No
1314	D9QD48	Uncharacterized protein	CpC231_2025	60	Extracellular;	2	No
1315	D9QE8U	RNA polymerase sigma factor	sigH	223	Cytoplasmic;	0	No
1316	D9QAH7	UPF0237 protein CpC231	CpC231_1077	89	Extracellular;	0	No
1317	D9QA70	Chromosome partitioning ATPase protein	soj	289	Cytoplasmic;	0	No
1318	D9QDV8	Glycerol-3-phosphate transporter	glpT	465	Membrane;	12	No
1319	D9QBU8	Uncharacterized protein	CpC231_1560	43	Extracellular;	0	No
1320	D9Q9H7	Uncharacterized protein	CpC231_0721	150	Membrane;	1	No
1321	D9QBQ4	Uncharacterized protein	CpC231_1514	142	Cytoplasmic;	0	No
1322	D9QDK3	Ammonia monooxygenase	abrB	360	Membrane;	10	No
1323	D9QC16	Carbon starvation protein A	pcsA	761	Membrane;	16	No
1324	D9QBD1	Polyphenol oxidase	CpC231_1386	239	Cytoplasmic;	0	No
1325	F9Y374	Uncharacterized protein	CpC231_1472a	35	Extracellular;	0	No
1326	D9QDI4	Peptidase family M20/M25/M40	CpC231_0058	445	Cytoplasmic;	0	No
1327	D9QCX2	Cutinase	CpC231_1947	308	Cytoplasmic;	1	No
1328	D9Q9U0	Uncharacterized protein	CpC231_0835	221	Cytoplasmic;	0	No

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1329	D9Q9I6	Uncharacterized protein	CpC231_0730	111	Cytoplasmic;	0	No
1330	F9Y353	Uncharacterized protein	CpC231_0852a	94	Cytoplasmic;	0	No
1331	D9QDI7	Metallopeptidase MepB	mepB	143	Extracellular;	0	No
1332	D9QDZ3	Bacterial type II secretion system protein F domain protein	gspF	207	Membrane;	2	No
1333	D9QBY0	Bifunctional protein folC	folC	520	Cytoplasmic;	0	No
1334	D9Q9R1	Uncharacterized protein	CpC231_0805	177	Cytoplasmic;	0	No
1335	F9Y332	Uncharacterized protein	CpC231_0021a	34	Extracellular;	0	No
1336	D9QBS4	Uncharacterized protein	CpC231_1535	46	Extracellular;	1	No
1337	D9QBM7	Ribonuclease R	rnr	461	Cytoplasmic;	0	No
1338	D9QC90	Phosphate-binding protein PstS	pstS	368	Extracellular;	0	Yes
1339	D9QCU2	Uncharacterized protein	CpC231_1916	396	Membrane;	10	No
1340	D9QCG3	GTP cyclohydrolase 1	folE	187	Cytoplasmic;	0	No
1341	D9QCG5	Hypoxanthine phosphoribosyltransferase	hpt	193	Cytoplasmic;	0	No
1342	D9QE94	Uncharacterized protein	CpC231_0324	653	Cellwall;	1	Yes
1343	D9QA15	Uncharacterized protein	CpC231_0912	40	Extracellular;	0	Yes
1344	D9QBH2	Uncharacterized protein	CpC231_1427	243	Membrane;	2	No
1345	D9QBT4	Uncharacterized protein	yvbT	331	Cytoplasmic;	0	No
1346	D9QDL3	Uncharacterized protein yaaA	yaaA	96	Cytoplasmic;	0	No
1347	D9QC59	Uncharacterized protein	CpC231_1673	57	Cytoplasmic;	1	No
1348	D9QBI5	Uncharacterized protein	CpC231_1441	256	Membrane;	2	No
1349	F9Y351	Uncharacterized protein	CpC231_0691b	40	Cytoplasmic;	0	Yes
1350	D9Q9E0	ABC transporter ATP-binding protein	CpC231_0683	604	Cytoplasmic;	0	No
1351	D9QBG2	Uncharacterized protein	CpC231_1417	209	Extracellular;	0	Yes
1352	D9QDJ2	Fe(2+)/Mn(2+) transporter pcl1	CpC231_0066	245	Membrane;	5	No
1353	D9QC93	Diacylglycerol kinase, catalytic region	CpC231_1709	344	Cytoplasmic;	0	No
1354	D9QDU4	Aspartokinase	lysC	429	Cytoplasmic;	0	No
1355	D9Q9R0	Uncharacterized protein	CpC231_0804	262	Cytoplasmic;	0	No
1356	D9QCV2	VanW family protein	CpC231_1927	553	Extracellular;	1	No
1357	D9Q9V3	ATP synthase gamma chain	atpG	326	Cytoplasmic;	0	No
1358	F9Y366	Uncharacterized protein	CpC231_1057a	42	Extracellular;	0	No
1359	D9Q9E9	Uncharacterized protein	CpC231_0693	217	Membrane;	6	No
1360	D9QBZ0	Uncharacterized protein	CpC231_1604	39	Cytoplasmic;	0	No
1361	D9QES1	Uncharacterized protein	CpC231_0507	100	Extracellular;	0	No
1362	D9QBJ4	Uncharacterized protein	CpC231_1450	79	Cytoplasmic;	0	No
1363	D9QEJ1	RNA polymerase sigma-D factor	sigD	196	Cytoplasmic;	0	No
1364	D9Q9V6	Uncharacterized protein	CpC231_0851	164	Membrane;	1	No
1365	D9QBM0	Uncharacterized protein	CpC231_1479	86	Extracellular;	0	No
1366	D9QDU3	Uncharacterized protein	CpC231_0171	281	Membrane;	9	No
1367	D9QDW1	Na(+)/H(+) antiporter subunit G	mrpG	102	Membrane;	3	No
1368	D9QB03	Putative membrane protein	CpC231_1255	26	Extracellular;	0	No
1369	D9QCU7	Hydrolase/acyltransferase	CpC231_1921	203	Cytoplasmic;	0	No
1370	D9Q9Z1	Low molecular weight protein antigen 6	cfp6	179	Membrane;	2	No
1371	D9Q9Y0	Uncharacterized protein	CpC231_0875	48	Extracellular;	0	No
1372	D9QAA0	MerR family transcriptional regulator	merR3	185	Cytoplasmic;	0	No
1373	D9QDF8	Thioredoxin	trxA1	107	Cytoplasmic;	0	No
1374	D9QE46	Glutaredoxin-like domain protein	CpC231_0275	84	Cytoplasmic;	0	No
1375	D9Q9N0	Uncharacterized protein	CpC231_0774	390	Cytoplasmic;	0	No
1376	D9QDJ9	Uncharacterized protein	CpC231_0074	556	Cytoplasmic;	0	No
1377	D9QE31	D-inositol-3-phosphate glycosyltransferase	mshA	420	Cytoplasmic;	0	No
1378	D9QE39	Uncharacterized protein	CpC231_0268	62	Extracellular;	0	No
1379	D9QAR6	Adenine phosphoribosyltransferase	apt	201	Cytoplasmic;	0	No
1380	D9QCW9	Propionyl-CoA carboxylase beta chain 5	accD	515	Cytoplasmic;	0	No
1381	D9QDE9	Branched-chain amino acid transport protein	azlD	117	Membrane;	4	No
1382	D9QDE8	Uncharacterized protein	CpC231_2084	104	Cytoplasmic;	0	No
1383	D9QD59	Uncharacterized protein	CpC231_0004	190	Cytoplasmic;	0	No
1384	D9QEF2	Protein traX	traX	247	Membrane;	8	No
1385	D9QCK0	7,8-dihydro-8-oxoguanine-triphosphatase	mutT	192	Cytoplasmic;	0	No
1386	D9QAL0	Uncharacterized protein	CpC231_1110	188	Cytoplasmic;	2	No
1387	D9QE02	DNA polymerase III subunit gamma/tau	dnaX	400	Cytoplasmic;	0	No
1388	D9QDV4	Uncharacterized protein	CpC231_0182	317	Cytoplasmic;	0	No
1389	D9QB89	Uncharacterized protein	CpC231_1344	191	Membrane;	1	No
1390	D9QDP1	Periplasmic zinc-binding protein troA	troA	330	Extracellular;	0	Yes
1391	D9QAH1	Invasion-associated protein p60	CpC231_1071	580	Extracellular;	0	No
1392	D9QBS9	Isopentenyl-diphosphate Delta-isomerase	idi	184	Cytoplasmic;	0	No
1393	D9QC86	Phosphate uptake regulator	phoU	250	Cytoplasmic;	0	No
1394	D9Q9U3	Peptide chain release factor 1	prfA	356	Cytoplasmic;	0	No
1395	D9QA40	DoxX family protein	doxX	269	Cytoplasmic;	0	No

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1396 D9QBW8	Uncharacterized protein	CpC231_1582	115 Membrane;	4	No
1397 D9Q9E6	Enoyl-CoA hydratase	echA	355 Cytoplasmic;	0	No
1398 D9QBT5	Endonuclease	CpC231_1547	395 Cytoplasmic;	0	No
1399 D9QD74	Rhomboid family protein	ybhB	256 Membrane;	7	No
1400 D9QD77	Uncharacterized protein	CpC231_0022	42 Extracellular;	1	No
1401 D9QD47	30S ribosomal protein S6	rpsF	95 Cytoplasmic;	0	No
1402 D9Q983	Oligopeptide transport ATP-binding protein OppD	oppD1	480 Membrane;	0	No
1403 D9QDY9	Uncharacterized protein	CpC231_0218	71 Extracellular;	0	No
1404 D9QC55	Uncharacterized protein	CpC231_1669	74 Extracellular;	0	No
1405 D9QD42	Replicative DNA helicase	dnaB	492 Cytoplasmic;	0	No
1406 D9QBA7	TetR family transcriptional regulator	tetR	205 Cytoplasmic;	0	No
1407 D9QDN2	Uncharacterized protein	CpC231_0107	295 Cytoplasmic;	0	No
1408 D9QBB2	Uncharacterized protein	CpC231_1367	41 Extracellular;	0	No
1409 D9QAV4	Uncharacterized protein	CpC231_1205	173 Membrane;	2	No
1410 D9QBZ1	Uncharacterized protein	CpC231_1605	83 Cytoplasmic;	0	No
1411 D9QBB7	DNA-directed DNA polymerase	dnaE	1186 Cytoplasmic;	0	No
1412 D9QCL7	Cytochrome c biogenesis protein resC	resC	269 Membrane;	8	No
1413 D9QDU9	Uncharacterized protein	CpC231_0177	39 Cytoplasmic;	0	No
1414 D9QEL4	Putative tRNA (cytidine(34)-2;	spoU	176 Cytoplasmic;	0	No
1415 D9QE65	Cytochrome c biogenesis protein CcsA	ccsA	333 Membrane;	8	No
1416 D9Q9J0	Phosphinothricin acetyltransferase YwnH	ywnH	186 Cytoplasmic;	0	No
1417 D9QDL9	Glycerol uptake facilitator protein	glpF	257 Membrane;	6	No
1418 D9QAA8	Methyltransferase type 11	CpC231_1007	195 Cytoplasmic;	0	No
1419 D9QCH6	Polyphosphate kinase 2	CpC231_1796	301 Cytoplasmic;	0	No
1420 D9QDT4	Deoxyribonucleoside regulator	deoR	312 Cytoplasmic;	0	No
1421 D9QAT3	CDP-diacylglycerol-inositol 3-phosphatidyltransferase	pgsA	229 Membrane;	6	No
1422 D9QCE4	ATP-dependent Clp protease ATP-binding subunit	clpC	885 Cytoplasmic;	0	No
1423 D9QB81	Uncharacterized protein	CpC231_1335	244 Cytoplasmic;	0	No
1424 D9Q9M9	Uncharacterized protein	CpC231_0773	185 Membrane;	4	No
1425 D9Q9V4	ATP synthase subunit beta	atpD	481 Cytoplasmic;	0	No
1426 D9QCC4	Uncharacterized protein	CpC231_1743	118 Cytoplasmic;	0	No
1427 D9QDC2	Oligopeptide-binding protein oppA	oppA7	540 Extracellular;	0	Yes
1428 D9QBM4	Chad domain-containing protein	CpC231_1484	551 Cytoplasmic;	0	No
1429 F9Y340	Uncharacterized protein	CpC231_0441a	160 Cytoplasmic;	0	Yes
1430 D9Q956	Uncharacterized protein	CpC231_0597	175 Membrane;	1	No
1431 D9QB59	Uncharacterized protein	CpC231_1313	101 Cytoplasmic;	0	No
1432 D9QB52	Uridylate kinase	pyrH	243 Cytoplasmic;	0	No
1433 D9QB21	Multidrug resistance protein norM	norM	451 Membrane;	12	No
1434 D9QDZ2	Uncharacterized protein	CpC231_0221	251 Membrane;	4	No
1435 D9QEM8	Uncharacterized protein	CpC231_0464	59 Cytoplasmic;	2	No
1436 D9Q9Q5	ABC transporter domain-containing ATP-binding protein	CpC231_0799	1231 Cellwall;	12	No
1437 D9QB71	Bifunctional uridylyltransferase/uridylyl-removing enzyme	glnD	745 Cytoplasmic;	0	No
1438 D9QBH6	Branched-chain-amino-acid aminotransferase	ilvE	366 Cytoplasmic;	0	No
1439 D9QA97	Oxoglutarate dehydrogenase inhibitor	odhl	143 Cytoplasmic;	0	No
1440 D9QA56	Argininosuccinate synthase	argG	399 Cytoplasmic;	0	No
1441 D9QC78	Acetyltransferase	CpC231_1693	100 Cytoplasmic;	0	No
1442 D9QA65	DNA repair protein RecN	recN	582 Cytoplasmic;	0	No
1443 D9QAP2	Shikimate dehydrogenase	aroE1	307 Extracellular;	0	Yes
1444 D9Q949	Fe(3+) dicitrate transport ATP-binding protein FecE	fecE	251 Cytoplasmic;	0	No
1445 D9QA52	Acetylglutamate kinase	argB	311 Cytoplasmic;	0	No
1446 D9QBZ4	Ribose-5-phosphate isomerase B	rpiB	157 Cytoplasmic;	0	No
1447 D9Q9R2	Aldose 1-epimerase	yihR	295 Cytoplasmic;	0	No
1448 D9QAG9	Uncharacterized protein	CpC231_1069	260 Cytoplasmic;	0	No
1449 D9QC27	Antibiotic biosynthesis monooxygenase	CpC231_1641	116 Cytoplasmic;	0	No
1450 D9QE42	Uncharacterized protein	CpC231_0271	33 Cytoplasmic;	0	No
1451 D9QAU2	Chlorite dismutase	CpC231_1192	259 Cytoplasmic;	0	No
1452 D9QEVO	Transcriptional regulator WhiB	whiB	86 Cytoplasmic;	0	No
1453 D9QA31	Uncharacterized protein	CpC231_0928	313 Membrane;	9	No
1454 D9QB12	4-hydroxy-tetrahydrodipicolinate reductase	dapB	248 Cytoplasmic;	0	No
1455 D9QCU9	Uncharacterized protein	CpC231_1923	77 Cytoplasmic;	0	No
1456 D9QDW4	Na(+)/H(+) antiporter subunit D	mrpD	512 Membrane;	14	No
1457 D9QBL7	Uncharacterized protein	CpC231_1476	46 Extracellular;	0	No
1458 D9QD26	TetR family transcriptional regulator	mcbR	208 Cytoplasmic;	0	No
1459 D9QAD5	Proteasome accessory factor PafA2	pafA1	510 Cytoplasmic;	0	No
1460 D9QDZ6	Uncharacterized protein	CpC231_0225	88 Cytoplasmic;	0	Yes
1461 D9QB47	1-deoxy-D-xylulose 5-phosphate reductoisomerase	dxr	388 Membrane;	0	Yes
1462 D9Q9L2	Cobalt transport protein CbiQ	cbiQ	251 Membrane;	7	No

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1463 D9QAE3	Anaerobic C4-dicarboxylate transporter	dcuA	435	Membrane;	13	No
1464 D9QC21	Short chain dehydrogenase	CpC231_1635	267	Cytoplasmic;	0	No
1465 D9QDG4	Inner membrane protein translocase component YidC	yidC1	318	Membrane;	5	No
1466 D9QEX5	Uncharacterized protein	CpC231_0561	98	Cytoplasmic;	0	No
1467 D9QE90	ABC-type metal ion transport system, periplasmic compon	CpC231_0320	541	Cytoplasmic;	0	Yes
1468 D9Q9P7	RNA polymerase sigma factor SigE	sigE	213	Cytoplasmic;	0	No
1469 D9QDC7	Uncharacterized protein	CpC231_2063	139	Extracellular;	0	Yes
1470 D9QEY4	L-asparagine permease	ansP	479	Membrane;	12	No
1471 D9Q9D7	Resuscitation-promoting factor RpfB	rpfB	383	Extracellular;	1	No
1472 D9QAY4	GTPase HflX	hflX	546	Cytoplasmic;	0	No
1473 D9QBV4	Elongation factor 4	leP	615	Cytoplasmic;	0	No
1474 D9QCM9	YxlE	yxlE	90	Membrane;	2	No
1475 D9QE95	Uncharacterized protein	CpC231_0325	313	Membrane;	1	Yes
1476 D9QAP7	Uncharacterized AAA domain-containing protein Rv2559c/	CpC231_1147	445	Membrane;	0	No
1477 D9QB02	Phosphatidylglycerophosphate synthase	pgsA1	197	Membrane;	6	No
1478 D9QBE7	Uncharacterized protein	CpC231_1402	140	Cytoplasmic;	0	No
1479 D9QBU3	Uncharacterized protein	CpC231_1555	44	Extracellular;	0	No
1480 D9QC70	Uncharacterized protein	CpC231_1685	82	Extracellular;	0	No
1481 D9QDW2	Na(+)/H(+) antiporter subunit F	mrpF	88	Membrane;	3	No
1482 D9QEK8	Uncharacterized protein	CpC231_0442	24	Extracellular;	0	No
1483 D9QBP2	Uncharacterized protein	CpC231_1502	120	Cytoplasmic;	0	No
1484 D9QA99	Uncharacterized protein	CpC231_0997	202	Cytoplasmic;	0	No
1485 D9QAV3	RNA polymerase sigma factor SigA	sigA	517	Cytoplasmic;	0	No
1486 D9QA30	Serine/threonine-protein kinase PknD	pknD	298	Membrane;	0	Yes
1487 D9QD11	Superoxide dismutase	sodA	213	Extracellular;	0	No
1488 D9QCW8	DedA family protein	dedA	213	Membrane;	5	No
1489 F9Y380	Uncharacterized protein	CpC231_1684a	110	Extracellular;	1	No
1490 F9Y329	Uncharacterized protein	CpC231_0001a	48	Extracellular;	0	No
1491 D9QAM8	Carbamoyl-phosphate synthase small chain	carA	410	Cytoplasmic;	0	No
1492 D9QBG7	Cytochrome c oxidase subunit III	ctaE	196	Membrane;	5	No
1493 D9QBX1	GTPase Obg	obgE	508	Cytoplasmic;	0	No
1494 F9Y334	Uncharacterized protein	CpC231_0021c	48	Extracellular;	0	No
1495 D9QC05	Uncharacterized protein ycaO	ycaO	512	Cytoplasmic;	0	No
1496 D9QCY9	ABC transporter substrate-binding lipoprotein yvrC	yvrC	337	Cytoplasmic;	0	Yes
1497 D9QD28	Transglycosylase associated protein	CpC231_2005	85	Membrane;	3	No
1498 D9QE83	Uncharacterized protein	CpC231_0344	183	Membrane;	2	No
1499 D9QBP5	Uncharacterized protein	CpC231_1505	80	Extracellular;	0	No
1500 D9QBT3	Branched-chain amino acid transport system carrier protein	brnQ	439	Membrane;	12	No
1501 D9QDF3	MutT/NUDIX family protein	CpC231_2089	368	Cytoplasmic;	0	No
1502 D9QBA0	Uncharacterized protein	CpC231_1355	67	Extracellular;	2	No
1503 D9QDY5	Alpha/beta hydrolase family	mhpC	305	Membrane;	0	No
1504 D9QC97	Uncharacterized protein	CpC231_1713	108	Extracellular;	0	No
1505 D9QE86	Putative SOS response-associated peptidase	CpC231_0532	219	Extracellular;	0	No
1506 D9QBS1	Uncharacterized protein	CpC231_1532	226	Cytoplasmic;	0	No
1507 D9QBB4	Uncharacterized protein	CpC231_1369	77	Extracellular;	2	No
1508 D9QD30	Uncharacterized protein	CpC231_2007	47	Extracellular;	0	No
1509 D9QEL0	Manganese ABC transporter ATP-binding protein	mntB	240	Cytoplasmic;	0	No
1510 D9QAQ8	MaoC-like dehydratase	CpC231_1158	181	Extracellular;	0	No
1511 D9QAS7	Uncharacterized protein	CpC231_1177	491	Membrane;	9	Yes
1512 F9Y386	Uncharacterized protein	CpC231_2024a	82	Cytoplasmic;	0	No
1513 D9QC92	Uncharacterized protein	CpC231_1708	262	Extracellular;	0	Yes
1514 D9QBI6	Uncharacterized protein	CpC231_1442	157	Membrane;	3	No
1515 D9QAD3	Pup--protein ligase	pafA	485	Cytoplasmic;	0	No
1516 D9QBK3	Uncharacterized protein	CpC231_1462	66	Cytoplasmic;	0	No
1517 D9QC26	Isochorismatase family protein yddQ	yddQ	204	Cytoplasmic;	0	No
1518 D9QBE8	Uncharacterized protein	CpC231_1403	37	Extracellular;	0	No
1519 D9QAT6	Dyp-type peroxidase family protein	CpC231_1186	436	Extracellular;	0	Yes
1520 D9QDP8	Sodium-dependent dicarboxylate transporter sdcS	sdcS	524	Membrane;	15	No
1521 D9QCC1	Uncharacterized protein	CpC231_1739	294	Cytoplasmic;	0	No
1522 D9Q9N7	Dihydropteroate synthase	folP	285	Cytoplasmic;	0	No
1523 D9QD51	Penicillin-binding protein	pbp1A	721	Extracellular;	1	No
1524 D9QB85	Uncharacterized protein	CpC231_1340	143	Cytoplasmic;	0	No
1525 D9Q940	Topology modulation protein	flaR	157	Cytoplasmic;	0	No
1526 D9QDS6	Galactonate operon transcriptional repressor	dgoR	234	Cytoplasmic;	0	No
1527 D9Q976	Cystathionine beta-synthase	cbs	356	Cytoplasmic;	0	No
1528 D9QCH1	Uncharacterized protein	CpC231_1791	63	Cytoplasmic;	0	No
1529 D9QDK7	Ascorbate-specific permease IIC component ulaA	ulaA	513	Membrane;	11	No

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1530 F9Y372	RNA polymerase factor sigma 70	CpC231_1451	183	Cytoplasmic;	0	No
1531 D9QEK7	Uncharacterized protein	CpC231_0441	134	Cytoplasmic;	1	No
1532 D9QAF7	Dihydroxyacetone kinase subunit	dhaK	345	Cytoplasmic;	0	No
1533 D9QDZ5	Uncharacterized protein	CpC231_0224	90	Extracellular;	0	Yes
1534 D9Q9F1	Peptide chain release factor 3	prfC	544	Cytoplasmic;	0	No
1535 D9QER6	Uncharacterized protein	CpC231_0502	225	Cytoplasmic;	0	No
1536 D9QE25	Formate acetyltransferase	pfl	83	Cytoplasmic;	0	No
1537 D9QCL6	Thiol-disulfide oxidoreductase resA	resA	174	Cytoplasmic;	0	Yes
1538 D9QAN4	Transcription antitermination protein NusB	nusB	208	Cytoplasmic;	0	No
1539 D9QE18	tRNA N6-adenosine threonylcarbamoyltransferase	tsaD	351	Cytoplasmic;	0	No
1540 D9QAZ1	Uncharacterized protein	CpC231_1243	223	Membrane;	2	No
1541 D9QC61	Ribonucleoside-diphosphate reductase	nrdE	719	Cytoplasmic;	0	No
1542 D9QA76	Segregation and condensation protein B	scpB	207	Cytoplasmic;	0	No
1543 D9QD22	Uncharacterized protein	CpC231_1999	190	Extracellular;	0	Yes
1544 D9QBS7	Carboxylic ester hydrolase	CpC231_1538	423	Extracellular;	0	No
1545 D9QD12	Flavin reductase	CpC231_1988	194	Cytoplasmic;	0	No
1546 D9QAJ2	Nod factor export ATP-binding protein I	nodI	318	Membrane;	0	No
1547 D9QCC0	Corynomycolyl transferase	CpC231_1737	393	Extracellular;	0	Yes
1548 D9QBC4	L-asparaginase	ansA	358	Cytoplasmic;	0	No
1549 F9Y347	Uncharacterized protein	CpC231_0595a	47	Extracellular;	0	No
1550 D9QBK5	Uncharacterized protein	CpC231_1464	57	Extracellular;	0	No
1551 D9Q9U1	Long-chain-fatty-acid-CoA ligase	lcfA2	577	Membrane;	0	No
1552 D9QD06	Nucleoside transporter	yutK	404	Membrane;	10	No
1553 D9QD50	Uncharacterized protein	CpC231_2027	28	Extracellular;	0	No
1554 D9Q9E2	Uncharacterized protein	CpC231_0685	92	Extracellular;	0	Yes
1555 D9QD79	Insertion element protein	CpC231_0024	346	Membrane;	0	No
1556 D9Q9C8	Oxidoreductase mhqP	mhqP	137	Membrane;	4	No
1557 D9QES3	Uncharacterized protein	CpC231_0509	151	Cytoplasmic;	0	No
1558 D9QCI6	Na(+)/H(+) antiporter subunit D	mrpD1	556	Membrane;	14	No
1559 D9Q9P8	Anti-sigma factor	cseE	143	Cytoplasmic;	0	No
1560 D9QDT5	Purine-nucleoside phosphorylase	deoD	238	Membrane;	0	No
1561 D9QBC9	YggT	yggT	98	Membrane;	2	No
1562 D9QBK6	Uncharacterized protein	CpC231_1465	61	Extracellular;	0	No
1563 D9QEC7	50S ribosomal protein L29	rpmC	76	Cytoplasmic;	0	No
1564 D9QAN9	Shikimate kinase	aroK	198	Cytoplasmic;	0	No
1565 D9QDA7	Uncharacterized protein	CpC231_2043	39	Extracellular;	0	No
1566 D9QEWS5	Uncharacterized protein	CpC231_0551	462	Membrane;	0	No
1567 D9QDI8	AMP nucleosidase	amn	471	Cytoplasmic;	0	No
1568 F9Y367	Uncharacterized protein	CpC231_1133a	134	Cytoplasmic;	0	No
1569 D9QA25	Phosphopantetheine adenyllyltransferase	coaD	162	Cytoplasmic;	0	No
1570 D9QEX7	Copper-containing nitrite reductase	aniA	877	Membrane;	13	No
1571 D9Q941	Cell division ATP-binding protein FtsE	ftsE	229	Cytoplasmic;	0	No
1572 D9QAP0	Chorismate synthase	aroC	428	Cytoplasmic;	0	No
1573 D9QDL6	Uncharacterized protein	CpC231_0091	81	Extracellular;	0	No
1574 D9Q9S3	Helicase helZ	helZ	1031	Membrane;	0	No
1575 D9Q9V9	Uncharacterized protein	CpC231_0854	122	Cytoplasmic;	0	Yes
1576 D9QAN3	Uncharacterized protein	CpC231_1133	157	Extracellular;	0	No
1577 D9QEX1	Abi-like protein	CpC231_0557	278	Cytoplasmic;	0	No
1578 D9QD88	Penicillin-binding protein A	pbpA	486	Extracellular;	0	Yes
1579 D9QBE1	Penicillin-binding protein	ftsI	627	Membrane;	1	No
1580 D9QBY3	TetR-family regulatory protein	CpC231_1597	252	Cytoplasmic;	0	No
1581 D9QB44	Secreted penicillin-binding protein	pbpB	613	Extracellular;	0	Yes
1582 D9QDZ4	Uncharacterized protein	CpC231_0223	64	Extracellular;	1	No
1583 D9QAC6	Oxidoreductase	CpC231_1025	246	Membrane;	0	No
1584 D9QEFT7	Neuraminidase (Sialidase)	nanH	694	Cytoplasmic;	1	Yes
1585 D9QAW2	UDP-glucose 4-epimerase	galE	327	Cytoplasmic;	0	Yes
1586 D9Q9W9	Spermidine synthase	speE	289	Cytoplasmic;	0	No
1587 D9QEKF6	D-methionine-binding lipoprotein metQ	metQ1	334	Membrane;	1	No
1588 D9QCW2	tRNA (guanine-N(7)-)methyltransferase	trmB	269	Cytoplasmic;	0	No
1589 D9QAH5	HTH-type transcriptional repressor AcnR	acnR	192	Cytoplasmic;	0	No
1590 D9QCB2	Trk system potassium uptake protein trkA	trkA	218	Membrane;	0	No
1591 D9QAY0	Phosphocarrier protein HPr	ptsH	88	Cytoplasmic;	0	No
1592 D9QE66	Uncharacterized protein	CpC231_0295	101	Membrane;	0	Yes
1593 D9QD33	Uncharacterized protein	CpC231_2010	349	Membrane;	10	No
1594 D9QEX0	Transcription regulator BetR, N-terminal	betR	56	Cytoplasmic;	0	No
1595 D9QD66	Uncharacterized protein	CpC231_0011	259	Membrane;	9	No
1596 D9QCH7	Cell wall channel	porH	60	Extracellular;	0	No

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1597	D9QC14	Uncharacterized protein	CpC231_1628	50	Extracellular;	0	No
1598	D9Q9B4	50S ribosomal protein L31 type B	rpmE	88	Cytoplasmic;	0	No
1599	D9QCE0	Carbonic anhydrase	bca	209	Cytoplasmic;	0	No
1600	D9QBZ5	DSBA oxidoreductase	CpC231_1609	206	Cytoplasmic;	0	No
1601	D9QA28	ABC transporter ATP-binding protein	atrC	257	Cytoplasmic;	0	No
1602	D9Q9G6	L-Lysine transport protein	lysI	496	Membrane;	13	No
1603	D9QBB9	Uncharacterized protein	CpC231_1374	179	Cytoplasmic;	0	Yes
1604	D9QE16	Succinate dehydrogenase cytochrome b556 subunit	sdhC	252	Membrane;	5	No
1605	D9QCP1	Uncharacterized protein	CpC231_1862	403	Membrane;	0	Yes
1606	D9QC40	Uncharacterized protein	CpC231_1654	148	Cytoplasmic;	0	No
1607	D9Q9X4	Uncharacterized protein	CpC231_0869	220	Cytoplasmic;	0	No
1608	D9QAU8	Uncharacterized protein	CpC231_1198	267	Cytoplasmic;	0	No
1609	D9QBE2	Uncharacterized protein	CpC231_1397	235	Cytoplasmic;	1	No
1610	D9QB98	Imidazole glycerol phosphate synthase subunit HisH	hisH	210	Cytoplasmic;	0	No
1611	D9Q9Q8	Carboxylic ester hydrolase	lipT	532	Cytoplasmic;	0	No
1612	D9QDH3	Major Facilitator Superfamily (MFS)	CpC231_0047	424	Membrane;	12	No
1613	D9QEA4	Anaerobic ribonucleoside-triphosphate reductase activatin	nrdG	193	Cytoplasmic;	0	No
1614	D9QB16	Pyrimidine-specific ribonucleoside hydrolase rihA	rihA	321	Cytoplasmic;	0	No
1615	D9QEY4	ATP-dependent RNA helicase rhlE	rhlE	441	Cytoplasmic;	0	No
1616	F9Y376	Uncharacterized protein	CpC231_1596a	55	Cytoplasmic;	1	No
1617	D9QAA1	Uncharacterized protein	CpC231_0999	476	Extracellular;	1	No
1618	D9QC73	Cob(I)yrinic acid a,c-diamide adenosyltransferase	yvqK	190	Cytoplasmic;	0	No
1619	D9Q9Q1	Uncharacterized protein	CpC231_0795	199	Cytoplasmic;	2	No
1620	D9QA07	Poly(3-hydroxybutyrate) depolymerase	lpqC	377	Cytoplasmic;	1	No
1621	D9QE89	Uncharacterized protein	CpC231_0319	317	Extracellular;	1	Yes
1622	D9QB48	Uncharacterized protein	CpC231_1301	141	Cytoplasmic;	2	No
1623	D9QD03	Uncharacterized protein	CpC231_1978	666	Extracellular;	1	Yes
1624	D9QEG7	Uncharacterized protein	CpC231_0400	140	Membrane;	3	No
1625	D9QAZ6	Biotin transporter BioY	bioY	197	Membrane;	6	No
1626	D9QAC3	Precorrin-6A reductase	cobK	226	Cytoplasmic;	0	No
1627	D9QDP3	O-antigen export system, ATP-binding protein	rfbE	264	Cytoplasmic;	0	No
1628	D9QDG6	Ribonuclease P protein component	rnpA	118	Cytoplasmic;	0	No
1629	D9QD45	50S ribosomal protein L9	rplI	150	Cytoplasmic;	0	No
1630	D9Q9T5	L-lactate permease	lutP	550	Membrane;	14	No
1631	D9QCJ2	Uncharacterized protein	CpC231_1812	183	Extracellular;	1	No
1632	F9Y352	Uncharacterized protein	CpC231_0709a	36	Extracellular;	0	No
1633	D9QB38	Magnesium chelatase	CpC231_1290	360	Membrane;	0	No
1634	F9Y355	Uncharacterized protein	CpC231_0928a	39	Cytoplasmic;	0	No
1635	D9QCY3	LPxTG domain-containing protein	CpC231_1958	1029	Cellwall;	1	Yes
1636	F9Y378	Hemoglobin-like protein	glbO	130	Cytoplasmic;	0	No
1637	D9QE87	Uncharacterized protein	CpC231_0348	155	Cytoplasmic;	0	No
1638	D9QCA0	Uncharacterized protein	CpC231_1716	145	Cytoplasmic;	0	No
1639	D9QDK1	Uncharacterized protein	CpC231_0076	118	Membrane;	4	No
1640	D9Q955	Cold shock protein B	cspB	130	Cytoplasmic;	0	No
1641	D9QBH7	Probable cytosol aminopeptidase	pepB	505	Cytoplasmic;	0	No
1642	D9QDL4	Antigen Cfp30B	cfp30B	274	Cytoplasmic;	0	No
1643	D9QC10	YcaO-like family protein	CpC231_1624	491	Membrane;	0	Yes
1644	D9QBQ0	Uncharacterized protein	CpC231_1510	85	Cytoplasmic;	0	No
1645	D9QAU7	Uncharacterized protein	CpC231_1197	234	Membrane;	6	No
1646	D9QB70	Signal recognition particle protein	ffh	535	Cytoplasmic;	0	No
1647	D9QC64	50S ribosomal protein L36	rpmJ	40	Cytoplasmic;	0	No
1648	D9QEST7	Mannose-6-phosphate isomerase manA	manA	385	Cytoplasmic;	0	No
1649	D9QDE0	Anthranilate synthase component I	trpE	535	Cytoplasmic;	0	No
1650	D9QCL1	Disulfide bond formation protein, DsbB family	dsbB	496	Membrane;	5	No
1651	D9QB75	Chromosome partition protein Smc	smc	1160	Cellwall;	0	No
1652	D9QEM4	Isocitrate dehydrogenase [NADP]	icd	736	Cytoplasmic;	0	No
1653	D9QCH2	Secretory lipase	lipY	415	Extracellular;	0	Yes
1654	D9QA79	GTPase Der	engA	540	Cytoplasmic;	0	No
1655	D9QCK9	Formate-dependent phosphoribosylglycinamide formyltran	purT	354	Cytoplasmic;	0	No
1656	D9QCI1	Acetyl-CoA acetyltransferase	CpC231_1801	178	Extracellular;	0	No
1657	D9Q9A7	Citrate lyase subunit beta	citE	297	Cytoplasmic;	0	No
1658	D9QAP9	Aspartate--tRNA(Asp/Asn) ligase	aspS	600	Cytoplasmic;	0	No
1659	D9QBT6	Ectoine, glycine betaine and proline transport system merr	ectP	610	Membrane;	12	No
1660	D9QEY6	Uncharacterized protein	CpC231_0542	296	Extracellular;	1	No
1661	D9QEE9	Maltotriose-binding protein	malE	415	Extracellular;	0	Yes
1662	D9Q9K5	ABC transporter ATP-binding protein	CpC231_0749	546	Membrane;	6	No
1663	D9QBD4	UDP-N-acetylmuramate--L-alanine ligase	murC	485	Cytoplasmic;	0	No

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1664 D9QE96	DNA-directed RNA polymerase subunit beta	rpoB	1178	Cytoplasmic;	0	No
1665 D9QBW9	Transport YidE/YbjL family protein	CpC231_1583	530	Membrane;	11	No
1666 D9QCC8	LacI-family transcriptional regulator	CpC231_1747	363	Cytoplasmic;	0	No
1667 D9QCK4	Acetate kinase	ackA	400	Cytoplasmic;	0	No
1668 D9QEKO	Two-component system transcriptional regulatory protein	tcsR3	225	Cytoplasmic;	0	No
1669 D9QCG4	ATP-dependent zinc metalloprotease FtsH	ftsH	667	Membrane;	2	No
1670 D9QA53	Acetylornithine aminotransferase	argD	416	Cytoplasmic;	0	No
1671 D9QCU6	Lysine--tRNA ligase	lysS1	1083	Membrane;	8	No
1672 D9QDU5	Surface antigen	CpC231_0173	1071	Cellwall;	1	Yes
1673 D9QEFO	Translation initiation factor IF-1	infA	72	Cytoplasmic;	0	No
1674 D9QEG6	Uncharacterized protein	CpC231_0399	452	Membrane;	1	No
1675 D9QBU4	Proline iminopeptidase	CpC231_1556	423	Cytoplasmic;	0	No
1676 D9Q964	Citrate synthase	gltA	431	Cytoplasmic;	0	No
1677 D9QCV7	Uncharacterized protein	CpC231_1932	396	Membrane;	2	No
1678 D9QBY1	Valine--tRNA ligase	valS	911	Cytoplasmic;	1	No
1679 D9QDQ5	Pyridoxal 5;	pdxS	323	Cytoplasmic;	0	No
1680 D9QDB8	N-acetylglucosamine-6-phosphate deacetylase	nagA1	383	Cytoplasmic;	0	No
1681 D9Q963	Phosphoserine aminotransferase	serC	377	Membrane;	0	No
1682 D9QE21	Uncharacterized protein	CpC231_0250	96	Membrane;	3	No
1683 D9QDT6	MFS-type drug efflux transporter	CpC231_0164	459	Membrane;	14	No
1684 D9QD19	LSR2-like protein	CpC231_1996	106	Cytoplasmic;	0	No
1685 D9QCW7	Uncharacterized protein	CpC231_1942	209	Extracellular;	0	Yes
1686 F9Y349	Uncharacterized protein	CpC231_0604a	34	Extracellular;	0	No
1687 D9QCC6	Uncharacterized protein	CpC231_1745	159	Membrane;	0	Yes
1688 D9Q9T2	Uncharacterized protein	CpC231_0827	209	Cytoplasmic;	0	No
1689 D9QAM5	Uncharacterized protein	CpC231_1125	42	Extracellular;	0	No
1690 D9QCX6	Trehalose corynomycol transferase B	cmtB	341	Extracellular;	0	Yes
1691 D9QAM1	Coenzyme A biosynthesis bifunctional protein CoaBC	coaBC	417	Cytoplasmic;	0	No
1692 D9QD18	Uncharacterized protein	CpC231_1995	210	Cytoplasmic;	0	No
1693 D9QAY7	Diaminopimelate epimerase	dapF	297	Cytoplasmic;	0	No
1694 D9QC63	Glutaredoxin-like protein nrdH	nrdH	77	Cytoplasmic;	0	No
1695 D9QCT8	Urease accessory protein UreE	ureE	158	Cytoplasmic;	0	No
1696 D9Q9T0	Uncharacterized protein	CpC231_0824	119	Cytoplasmic;	0	No
1697 D9QDX3	Uncharacterized protein yqeY	yqeY	153	Cytoplasmic;	0	No
1698 F9Y369	Uncharacterized protein	CpC231_1188a	117	Extracellular;	0	No
1699 D9QEN0	Ribonuclease BN-like family	CpC231_0466	361	Membrane;	7	No
1700 D9QET7	Ribosome hibernation promoting factor	hpf	222	Cytoplasmic;	0	No
1701 D9Q968	Uncharacterized protein	CpC231_0609	53	Extracellular;	1	No
1702 D9Q939	Peptide chain release factor 2	prfB	366	Cytoplasmic;	0	No
1703 D9QAB8	FxsA cytoplasmic membrane protein	fxsA	176	Membrane;	4	No
1704 D9QDP6	Quinone oxidoreductase 1	qorA	319	Cytoplasmic;	0	No
1705 D9QCA3	Hemolysin III-like protein	CpC231_1719	225	Membrane;	7	No
1706 D9QCQ5	Macrolide export ATP-binding/permease protein macB	macB	423	Membrane;	4	No
1707 D9QB25	Predicted nucleic-acid-binding protein implicated in transci	ylxR	124	Cytoplasmic;	0	No
1708 D9QBG3	Uncharacterized protein	CpC231_1418	34	Extracellular;	0	No
1709 D9QCQ1	Sodium/glutamate symporter	gltT	449	Membrane;	13	No
1710 D9QC54	Uncharacterized protein	CpC231_1668	46	Extracellular;	0	No
1711 D9Q9K7	UvrABC system protein A	uvrA	734	Membrane;	0	No
1712 D9QBU2	Oligopeptide transport ATP-binding protein OppD	oppDF2	477	Membrane;	0	No
1713 F9Y338	Uncharacterized protein	CpC231_0423a	63	Cytoplasmic;	0	No
1714 D9Q9C3	5-formyltetrahydrofolate cyclo-ligase	CpC231_0666	205	Cytoplasmic;	0	No
1715 D9QD97	Uncharacterized protein	CpC231_2033	157	Membrane;	3	No
1716 D9Q9V2	ATP synthase subunit alpha	atpA	542	Cytoplasmic;	0	No
1717 D9QBX5	Uncharacterized protein	CpC231_1589	57	Extracellular;	0	No
1718 F9Y335	Uncharacterized protein	CpC231_0342a	34	Extracellular;	0	No
1719 D9Q9P1	Ribosomal RNA methyltransferase	rrmA	288	Cytoplasmic;	0	No
1720 D9QE91	Uncharacterized protein	CpC231_0321	344	Extracellular;	1	Yes
1721 D9QAF2	Uncharacterized protein	CpC231_1052	62	Cytoplasmic;	2	No
1722 D9QED9	L-serine dehydratase 1	sdaA	458	Cytoplasmic;	0	No
1723 D9Q9H1	Uncharacterized protein	CpC231_0715	188	Cytoplasmic;	0	No
1724 D9QD95	Transcription regulator padR	padR	107	Cytoplasmic;	0	No
1725 D9QDN1	Uncharacterized protein	CpC231_0106	176	Cytoplasmic;	0	No
1726 D9QC01	ABC transporter ATP-binding protein	CpC231_1615	570	Cytoplasmic;	0	No
1727 D9QD04	SEC-C domain-containing protein	CpC231_1980	303	Cytoplasmic;	0	No
1728 D9QC81	Cytochrome d ubiquinol oxidase subunit 2	cydB	327	Membrane;	9	No
1729 D9QC39	Caax amino protease	CpC231_1653	220	Membrane;	7	No
1730 D9QE49	Uroporphyrinogen-III synthase	hemD	562	Cytoplasmic;	0	No

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1731 D9QCL3	Uncharacterized protein	CpC231_1833	103	Extracellular;	0	No
1732 D9QCX4	Trehalose corynomycol transferase C	cmtC	644	Extracellular;	0	Yes
1733 D9QBI8	Uncharacterized protein	CpC231_1444	81	Membrane;	2	No
1734 D9QCM0	Cytochrome c-552	nrfA	483	Cytoplasmic;	1	No
1735 D9QEHI9	Uncharacterized protein	CpC231_0412	387	Membrane;	0	No
1736 D9QD17	RecB family nuclease	recB	520	Cytoplasmic;	0	No
1737 D9QDU7	RNA polymerase sigma factor	sigC	187	Cytoplasmic;	0	No
1738 D9Q962	Uncharacterized protein	CpC231_0603	361	Cytoplasmic;	0	No
1739 D9QBFI7	Acyltransferase	CpC231_1412	368	Membrane;	10	No
1740 F9Y344	Uncharacterized protein	CpC231_0569a	30	Extracellular;	0	Yes
1741 D9QBT2	Uncharacterized protein	CpC231_1543	168	Extracellular;	0	Yes
1742 D9QE81	Protein translocase subunit SecE	secE	108	Cytoplasmic;	1	No
1743 D9QAH6	Glutamine amidotransferase class-I	CpC231_1076	239	Cytoplasmic;	0	No
1744 D9QDF2	tRNA nucleotidyltransferase	cca	533	Cytoplasmic;	0	No
1745 D9QBF8	1-acyl-sn-glycerol-3-phosphate acyltransferase	plsC	242	Membrane;	0	No
1746 D9QDE3	N-(5;	trpC	495	Membrane;	0	No
1747 D9QC00	Thioesterase	CpC231_1614	142	Cytoplasmic;	0	No
1748 D9QAY3	Pyrimidine permease rutG	CpC231_1234	428	Membrane;	12	No
1749 D9QDG5	Putative membrane protein insertion efficiency factor	CpC231_2101	95	Extracellular;	0	No
1750 D9QB87	Metal-dependent amidase/aminoacylase/carboxypeptidase	amiB	420	Membrane;	0	No
1751 D9Q9L3	Uncharacterized protein	CpC231_0757	155	Cytoplasmic;	0	No
1752 D9QB26	Transcription termination/antitermination protein NusA	nusA	332	Cytoplasmic;	0	No
1753 D9Q9U5	tRNA threonylcarbamoyladenosine biosynthesis protein Yv	ywIC	216	Cytoplasmic;	0	No
1754 D9QAQ4	HTH-type transcriptional repressor KstR	kstR	200	Membrane;	0	No
1755 D9QBM9	Zn-ribbon protein	CpC231_1489	238	Cytoplasmic;	0	No
1756 D9Q943	SsrA-binding protein	smpB	163	Cytoplasmic;	0	No
1757 D9Q9T8	Homoserine dehydrogenase	thrA	449	Cytoplasmic;	0	No
1758 D9QCE9	Caax amino protease family	CpC231_1768	220	Membrane;	7	No
1759 D9QBN0	GTP cyclohydrolase 1 type 2 homolog	CpC231_1490	385	Cytoplasmic;	0	No
1760 D9QCI0	Thiol dipeptidase	tpdA	521	Membrane;	0	No
1761 D9QBH8	Oxidoreductase	CpC231_1433	131	Cytoplasmic;	0	No
1762 D9QDR6	Zinc-binding alcohol dehydrogenase	idnD	329	Membrane;	0	No
1763 D9QEHI5	50S ribosomal protein L13	rplM	147	Cytoplasmic;	0	No
1764 D9QCB8	Response regulator mprA	mprA	237	Cytoplasmic;	0	No
1765 D9QA27	PhzF family phenazine biosynthesis protein	phzF	272	Extracellular;	0	No
1766 D9QAQ2	Uncharacterized protein yhgE	CpC231_1152	673	Membrane;	6	No
1767 D9QCR4	Heat shock protein HspR	hspR	133	Cytoplasmic;	0	No
1768 D9Q9B5	50S ribosomal protein L32	rpmF	57	Cytoplasmic;	0	No
1769 D9QE55	3-hydroxyisobutyrate dehydrogenase	mmsB	278	Membrane;	0	No
1770 D9QDK6	PTS system, IIA component	sgaA	271	Cytoplasmic;	0	No
1771 D9Q936	Uncharacterized protein	CpC231_0575	394	Extracellular;	0	Yes
1772 D9QC77	Serine acetyltransferase	cysE	188	Cytoplasmic;	0	No
1773 D9QC28	Uncharacterized protein	CpC231_1642	91	Cytoplasmic;	1	No
1774 D9QAN1	Bifunctional protein PyrR	pyrR	221	Cytoplasmic;	0	No
1775 D9QBQ7	Uncharacterized protein	CpC231_1517	65	Cytoplasmic;	0	No
1776 D9QDJ4	Gamma-type carbonic anhydratase-like protein	gca	185	Cytoplasmic;	0	No
1777 D9QBL2	Regulatory protein	pfoS	356	Membrane;	10	No
1778 D9Q935	Methylmalonyl-CoA carboxyltransferase 1.3S subunit	CpC231_0574	120	Cytoplasmic;	0	No
1779 D9QA81	SAM-dependent methyltransferase	CpC231_0979	279	Extracellular;	0	No
1780 D9QDD4	Uncharacterized protein	CpC231_2070	378	Cytoplasmic;	0	No
1781 D9Q999	Uncharacterized metalloprotease	CpC231_0642	237	Extracellular;	0	Yes
1782 D9Q9V8	Methylmalonyl-CoA epimerase	CpC231_0853	152	Cytoplasmic;	0	No
1783 D9QDH2	Uncharacterized protein	CpC231_0046	96	Cytoplasmic;	0	No
1784 D9QAR3	Peptidyl-prolyl cis-trans isomerase B	ppiB	284	Extracellular;	1	No
1785 D9QD08	Thymidine phosphorylase	deoA	433	Cytoplasmic;	0	No
1786 D9QCJ7	Cardiolipin synthase	cls	497	Membrane;	2	No
1787 D9QBU9	Uncharacterized protein	CpC231_1561	57	Cytoplasmic;	0	No
1788 D9QAC2	Precorrin-3B C(17)-methyltransferase	cobj	501	Cytoplasmic;	0	No
1789 D9QB93	Uncharacterized protein	CpC231_1348	213	Membrane;	3	Yes
1790 D9QEM5	Arabinose efflux permease	araJ	409	Membrane;	12	No
1791 D9QD62	Uncharacterized protein	CpC231_0007	77	Extracellular;	0	No
1792 D9Q9F7	50S ribosomal protein L25	rplY	205	Cytoplasmic;	0	No
1793 D9QD53	Multiple antibiotic resistance protein marR	marR3	176	Membrane;	0	No
1794 D9QAE1	Formate-tetrahydrofolate ligase	fhs	550	Cytoplasmic;	0	No
1795 D9QBV2	ABC transporter ATP-binding protein	CpC231_1566	209	Cytoplasmic;	0	No
1796 D9Q9L9	Trypsin-like serine protease	sprX	246	Extracellular;	0	Yes
1797 D9QBJ6	Uncharacterized protein	CpC231_1453	75	Cytoplasmic;	0	No

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1798	D9Q9D6	TatD family hydrolase	tatD	280	Cytoplasmic;	0	No
1799	D9QDC0	N-acetylglucosamine kinase	nanK	297	Cytoplasmic;	0	No
1800	D9QAK1	Protein-export membrane protein secG	secG	78	Membrane;	2	No
1801	D9QC04	Uncharacterized protein	CpC231_1618	584	Membrane;	0	No
1802	D9QCY4	Glycerophosphoryl diester phosphodiesterase	glpQ	365	Cytoplasmic;	0	Yes
1803	D9QDI9	Uncharacterized protein	CpC231_0063	474	Extracellular;	0	Yes
1804	D9QB80	Metal-binding, possibly nucleic acid-binding protein	CpC231_1334	175	Cytoplasmic;	0	No
1805	D9QCF9	Uncharacterized protein	CpC231_1779	148	Membrane;	4	No
1806	D9QE00	Haloacid dehalogenase-like hydrolase	CpC231_0526	136	Cytoplasmic;	0	No
1807	F9Y387	Uncharacterized protein	CpC231_2063a	77	Cytoplasmic;	0	No
1808	D9QE11	Abhydrolase domain-containing protein 5	CpC231_0414	280	Membrane;	0	No
1809	D9QAE0	Virulence-associated protein I	vapl	100	Cytoplasmic;	0	No
1810	D9QDH6	ECF family sigma factor K	sigK	183	Cytoplasmic;	0	No
1811	D9Q9M6	Uncharacterized protein	CpC231_0770	133	Membrane;	4	No
1812	D9QEVI	Uncharacterized protein	CpC231_0537	140	Membrane;	3	No
1813	D9QD23	Uncharacterized protein	CpC231_2000	50	Extracellular;	1	No
1814	D9QE17	Ribosomal-protein-alanine N-acetyltransferase	riml	163	Cytoplasmic;	0	No
1815	D9Q9N4	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltran	dapD1	304	Cytoplasmic;	0	No
1816	D9Q9C9	Uncharacterized protein	CpC231_0672	221	Membrane;	4	No
1817	D9Q958	Uncharacterized protein	CpC231_0599	244	Cytoplasmic;	0	No
1818	D9QB12	Protein p51	CpC231_1448	337	Cytoplasmic;	0	No
1819	D9QAZ5	Uncharacterized protein	CpC231_1247	70	Cytoplasmic;	0	No
1820	D9Q9M7	Ferredoxin	fdxA	105	Cytoplasmic;	0	No
1821	D9Q9D1	Uncharacterized protein	CpC231_0674	70	Extracellular;	0	No
1822	D9QDB4	Two-component system histidine kinase ChrS	chrS	424	Membrane;	6	No
1823	D9Q9S0	Uncharacterized protein	CpC231_0814	156	Membrane;	4	No
1824	D9QDY7	Uncharacterized protein	CpC231_0216	221	Cytoplasmic;	0	No
1825	D9Q9G8	LpqU family protein	lpqU	261	Extracellular;	1	No
1826	D9QES0	Mannose-1-phosphate guanylyltransferase	manC	362	Cytoplasmic;	0	No
1827	D9QB49	Uncharacterized protein	CpC231_1303	144	Membrane;	2	No
1828	D9QA66	Thiamin pyrophosphokinase, catalytic domain-containing p	CpC231_0964	397	Cytoplasmic;	1	No
1829	D9QAU4	Ribonuclease D	rnd	401	Cytoplasmic;	0	No
1830	D9QEW3	Uncharacterized protein	CpC231_0549	283	Cytoplasmic;	0	No
1831	D9QAG7	NfeD-like protein	CpC231_1067	142	Membrane;	2	No
1832	D9QBM3	Uncharacterized protein	CpC231_1483	314	Membrane;	0	No
1833	D9QDX7	RutC family protein yabJ	yabJ	152	Cytoplasmic;	0	No
1834	D9QEQQ	Maf-like protein CpC231	maf	209	Cytoplasmic;	0	No
1835	D9QCQ8	Uncharacterized protein	CpC231_1880	55	Cytoplasmic;	0	No
1836	D9QEWF	Uncharacterized protein	CpC231_0550	183	Cytoplasmic;	0	No
1837	D9QDY4	Trypsin-like serine protease	htrA2	399	Membrane;	4	No
1838	D9QBR1	Isoprenyl transferase	uppS2	245	Cytoplasmic;	0	No
1839	D9QAS5	Uncharacterized protein	CpC231_1175	46	Extracellular;	1	No
1840	D9QE92	Manganese transport system ATP-binding protein MntB	mntB	257	Membrane;	0	No
1841	D9Q9G4	TetR family transcriptional regulator	tetR1	215	Cytoplasmic;	0	No
1842	D9Q9N2	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltran	dapD	324	Cytoplasmic;	0	No
1843	D9QC7	Inosine-uridine preferring nucleoside hydrolase	iunH2	330	Cytoplasmic;	0	No
1844	D9Q9K0	Uncharacterized protein	CpC231_0744	524	Membrane;	10	No
1845	D9Q9J4	Fructose-1,6-bisphosphatase	glpX	336	Cytoplasmic;	0	No
1846	D9QAM3	Guanylate kinase	gmk	191	Cytoplasmic;	0	No
1847	D9QCY2	Membrane-associated phospholipid phosphatase	CpC231_1957	168	Membrane;	4	No
1848	D9QAQ0	Zinc metallopeptidase	CpC231_1150	297	Extracellular;	1	No
1849	D9Q9Z4	Acetolactate synthase 3 regulatory subunit	ilvH	174	Membrane;	0	No
1850	D9QCR1	Alcohol dehydrogenase GroES-like protein	adhA	385	Cytoplasmic;	0	No
1851	D9QD80	Phospholipase D	pld	307	Extracellular;	0	Yes
1852	D9QAG8	Uncharacterized protein	CpC231_1068	280	Cytoplasmic;	0	No
1853	F9Y336	Uncharacterized protein	CpC231_0370a	41	Extracellular;	0	Yes
1854	D9QCW5	Uncharacterized protein	CpC231_1940	349	Membrane;	10	No
1855	D9QCX3	Uncharacterized protein	CpC231_1948	175	Extracellular;	0	Yes
1856	D9QC67	Uncharacterized protein	CpC231_1681	138	Cytoplasmic;	0	No
1857	D9QB68	Cupin domain-containing protein	CpC231_1322	193	Membrane;	0	No
1858	D9QDG7	50S ribosomal protein L34	rpmH	47	Cytoplasmic;	0	No
1859	D9Q9J3	Fumarate hydratase class II	fumC	467	Cytoplasmic;	0	No
1860	D9Q9U2	Transcription termination factor Rho	rho	714	Cytoplasmic;	0	No
1861	D9QCL5	Uncharacterized protein	CpC231_1835	85	Extracellular;	0	No
1862	D9QE15	Uncharacterized protein	CpC231_0418	158	Membrane;	0	Yes
1863	D9QB51	Ribosome-recycling factor	frr	185	Cytoplasmic;	0	No
1864	D9QEN5	Uncharacterized protein	CpC231_0471	89	Cytoplasmic;	0	No

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1865 D9QCW0 SAM-dependent methyltransferase	CpC231_1935	53 Extracellular;	0	No
1866 D9QDS9 Uncharacterized protein	CpC231_0156	41 Extracellular;	0	No
1867 D9Q9S8 Multiple antibiotic resistance protein marR	marR1	158 Cytoplasmic;	0	No
1868 D9QB82 Alanine dehydrogenase	ald	369 Membrane;	0	No
1869 D9QDT0 Cobyrinic acid synthase	cobQ	250 Cytoplasmic;	0	No
1870 D9QA80 Anaerobic C4-dicarboxylate transporter	dcuB	461 Membrane;	13	No
1871 D9QAQ7 Citrate lyase subunit beta-like protein	CpC231_1157	300 Cytoplasmic;	0	No
1872 D9QDQ1 Nitric-oxide reductase, cytochrome b-containing subunit I	norB	766 Membrane;	14	No
1873 D9QB05 TerC family	terC	331 Membrane;	8	No
1874 F9Y339 Uncharacterized protein	CpC231_0423b	30 Extracellular;	0	No
1875 D9Q9L1 HMP/thiamine import ATP-binding protein	ykoD	466 Membrane;	0	No
1876 D9QAA2 UPF0053 protein	CpC231_1001	350 Membrane;	4	No
1877 D9QCW4 Transmembrane transport protein MmpL	mmpL	874 Membrane;	12	No
1878 F9Y343 Uncharacterized protein	CpC231_0560a	56 Cytoplasmic;	0	No
1879 D9QC41 Uncharacterized protein	CpC231_1655	119 Membrane;	3	No
1880 D9QD37 Phage shock protein A	pspA1	295 Cytoplasmic;	0	No
1881 D9QCG1 7,8-dihydronopterin aldolase	folB	105 Cytoplasmic;	0	No
1882 D9QB18 tRNA pseudouridine synthase B	truB	303 Membrane;	0	No
1883 D9QCC5 Trehalose-6-phosphate synthase	otsA	491 Cytoplasmic;	0	No
1884 D9QD10 Peptide methionine sulfoxide reductase MsrA	mrsA	224 Cytoplasmic;	0	No
1885 D9QEK2 Sucrase ferredoxin-like protein	CpC231_0436	290 Cytoplasmic;	0	No
1886 D9QE63 ABC-type transporter	CpC231_0292	328 Cytoplasmic;	0	Yes
1887 D9QBW1 DNA uptake protein, SLBB domain protein	CpC231_1575	205 Cytoplasmic;	1	No
1888 D9QCU3 Uncharacterized protein	CpC231_1917	59 Extracellular;	0	No
1889 D9Q9S7 Metabolite transport protein ycel	ycel	175 Cytoplasmic;	0	No
1890 D9QB61 Signal peptidase I	lepB	271 Cytoplasmic;	1	No
1891 D9QEUI Ribosome biogenesis GTPase RsgA	rsgA	338 Cytoplasmic;	0	No
1892 D9QD85 Cell division protein CrgA	crgA	89 Extracellular;	2	No
1893 D9QD69 Periplasmic binding protein/LacI transcriptional regulator	CpC231_0014	333 Extracellular;	0	Yes
1894 F9Y383 Uncharacterized protein	CpC231_1890a	35 Extracellular;	0	No
1895 D9Q9S2 Sodium/proline symporter	putP	480 Membrane;	12	No
1896 F9Y362 Uncharacterized protein	CpC231_0993a	46 Extracellular;	0	No
1897 D9QB32 Uncharacterized protein	CpC231_1284	377 Cytoplasmic;	0	No
1898 D9QCC9 Poly(3-hydroxyalkanoate) depolymerase	CpC231_1748	285 Extracellular;	0	No
1899 D9QCF8 Uncharacterized protein	CpC231_1778	174 Membrane;	2	No
1900 D9QE13 UPF0079 ATP-binding protein	ydiB	164 Cytoplasmic;	0	No
1901 D9Q9M1 Uncharacterized protein	CpC231_0765	177 Cytoplasmic;	0	No
1902 D9QE58 Thiol-disulfide isomerase/thioredoxin	ccsX	194 Membrane;	0	Yes
1903 D9QAN6 Uncharacterized peptidase yqhT, Metallopeptidase family	CpC231_1136	363 Cytoplasmic;	0	No
1904 D9QBD5 UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptid	murG	361 Cytoplasmic;	0	No
1905 F9Y361 Uncharacterized protein	CpC231_0989a	58 Extracellular;	0	No
1906 D9QE44 Thiol:disulfide interchange protein DsbD	dsbD	274 Membrane;	7	No
1907 D9QE8 Uncharacterized protein	CpC231_0411	99 Cytoplasmic;	0	No
1908 D9QAB0 Cyclopropane fatty acid synthase	ufaA	435 Cytoplasmic;	0	No
1909 D9QC17 Uncharacterized protein	CpC231_1631	66 Extracellular;	0	No
1910 D9QAK8 Nucleotide-binding protein CpC231	CpC231_1108	299 Cytoplasmic;	0	No
1911 D9QBY9 Uncharacterized protein	CpC231_1603	44 Extracellular;	0	No
1912 D9QEM3 Uncharacterized protein	htAC	302 Extracellular;	1	Yes
1913 D9Q9Q2 Magnesium transporter mgtE	mgtE2	430 Cytoplasmic;	0	No
1914 D9QE98 Two-component system sensor kinase protein	cstS	382 Membrane;	5	No
1915 D9QA92 Uncharacterized protein	CpC231_0990	717 Cellwall;	1	No
1916 F9Y356 Uncharacterized protein	CpC231_0931a	30 Extracellular;	1	No
1917 D9QC33 Uncharacterized protein	CpC231_1647	101 Cytoplasmic;	0	No
1918 D9QEJ4 Inosine-5;	guaB2	380 Cytoplasmic;	0	No
1919 D9QCT1 Transcriptional regulatory protein	CpC231_1905	103 Cytoplasmic;	0	No
1920 D9QE12 Uncharacterized protein	CpC231_0241	44 Extracellular;	0	No
1921 D9QBX6 Uncharacterized protein	CpC231_1590	228 Membrane;	4	No
1922 D9QCV0 dCTP deaminase	dcd	188 Cytoplasmic;	0	No
1923 D9QDU2 Uncharacterized protein	CpC231_0170	368 Membrane;	11	No
1924 D9QCF7 Uncharacterized protein	CpC231_1777	128 Cytoplasmic;	0	No
1925 D9QEX9 Uncharacterized protein	CpC231_0565	218 Extracellular;	0	No
1926 D9QA47 rRNA methyltransferase	tsnR	289 Cytoplasmic;	0	No
1927 D9QBR5 CBS domain-containing protein	CpC231_1525	441 Membrane;	4	No
1928 D9QC20 Mycocerosic acid synthase	mas	334 Cytoplasmic;	0	No
1929 D9QDY3 Uncharacterized Nudix hydrolase nudL	nudL	259 Cytoplasmic;	0	No
1930 D9Q9P6 O-methyltransferase	CpC231_0790	210 Cytoplasmic;	0	No
1931 D9QBZ9 Uncharacterized protein	CpC231_1613	202 Membrane;	0	No

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1932 D9QBG0 Mannosyltransferase	pimB	376	Cytoplasmic;	0	No
1933 D9QDV9 Response regulator mprA	mpmA	233	Cytoplasmic;	0	No
1934 D9QAK7 Putative gluconeogenesis factor	CpC231_1107	342	Cytoplasmic;	0	No
1935 D9QA58 Uncharacterized protein	CpC231_0956	61	Cytoplasmic;	0	No
1936 D9Q992 G/U mismatch-specific DNA glycosylase	mug	211	Membrane;	0	No
1937 D9QAE4 ATP phosphoribosyltransferase	hisG	281	Cytoplasmic;	0	No
1938 D9QBJ0 Uncharacterized protein	CpC231_1446	69	Cytoplasmic;	1	No
1939 D9Q9Z7 Uncharacterized protein	CpC231_0894	620	Cytoplasmic;	0	No
1940 D9QAI8 FeS cluster assembly protein SufD	sufD	393	Cytoplasmic;	0	No
1941 D9QAW0 RNA polymerase sigma factor	sigB	329	Cytoplasmic;	0	No
1942 D9QDQ8 Uncharacterized protein	CpC231_0134	160	Cytoplasmic;	0	No
1943 D9QCI2 Uncharacterized protein	CpC231_1802	355	Membrane;	2	No
1944 D9QBU7 Uncharacterized protein	CpC231_1559	71	Extracellular;	0	Yes
1945 D9QAW1 Diphtheria toxin repressor	dtxR	226	Cytoplasmic;	0	No
1946 D9QCZ8 Prephenate dehydratase	pheA	269	Cytoplasmic;	0	No
1947 D9QCX9 Membrane-associated phospholipid phosphatase	CpC231_1954	168	Membrane;	1	No
1948 D9QAV2 Polyphosphate glucokinase	ppgk	258	Cytoplasmic;	0	No
1949 D9Q9C2 Uncharacterized protein	CpC231_0665	250	Membrane;	0	Yes
1950 D9QE45 Anaerobic ribonucleoside triphosphate reductase	nrdD	598	Extracellular;	0	No
1951 D9Q9E1 Antibiotic biosynthesis monooxygenase	CpC231_0684	107	Cytoplasmic;	0	No
1952 D9Q9S4 Uncharacterized protein	CpC231_0818	261	Cytoplasmic;	0	No
1953 D9QAF3 Uncharacterized protein	CpC231_1053	130	Membrane;	4	No
1954 D9QBN4 SURF1-like protein	CpC231_1494	314	Membrane;	2	No
1955 D9QA89 Efflux protein	ciuF	430	Membrane;	12	No
1956 D9QAM4 Integration host factor MihF	mihF	107	Cytoplasmic;	0	No
1957 D9QDR5 Gluconokinase	idnK	163	Cytoplasmic;	0	No
1958 D9QBB0 Glycogen debranching protein	glgX	211	Membrane;	0	No
1959 D9QEUI Uncharacterized protein	CpC231_0527	168	Cytoplasmic;	0	No
1960 D9QAJ7 Transaldolase	tal	360	Cytoplasmic;	0	No
1961 D9QDR8 Uncharacterized protein	CpC231_0144	37	Extracellular;	0	Yes
1962 D9Q9P2 Sucrose-6-phosphate hydrolase	scrB	483	Cytoplasmic;	0	No
1963 D9QEBS Uncharacterized protein	CpC231_0346	68	Membrane;	2	No
1964 D9QAP1 Uncharacterized protein	CpC231_1141	176	Membrane;	6	No
1965 D9QB76 Acylphosphatase	acyP	105	Cytoplasmic;	0	No
1966 D9QAZ7 Cobalt import ATP-binding protein CbiO	bioM	230	Cytoplasmic;	0	No
1967 D9Q9M0 Arsenate reductase	arsC	114	Cytoplasmic;	0	No
1968 D9QAF1 Dihydroorotate dehydrogenase (quinone)	pyrD	348	Cytoplasmic;	0	No
1969 D9QBW4 Ribosomal silencing factor RsfS	rsfS	155	Cytoplasmic;	0	No
1970 D9QBA9 DNA polymerase III PolC	CpC231_1364	453	Extracellular;	0	No
1971 D9Q9Q7 Shikimate 5-dehydrogenase	aroE	271	Membrane;	0	No
1972 D9QD65 Uncharacterized protein	CpC231_0010	114	Membrane;	2	No
1973 D9QBZ8 Uncharacterized protein	CpC231_1612	298	Membrane;	10	No
1974 D9QCJ6 Exodeoxyribonuclease III	xthA	255	Cytoplasmic;	0	No
1975 D9QEKS D-methionine-binding lipoprotein metQ	metQ	285	Cytoplasmic;	0	Yes
1976 F9Y385 Uncharacterized protein	CpC231_1989a	37	Extracellular;	0	No
1977 D9QAY1 Luciferase-like monooxygenase	CpC231_1232	371	Cytoplasmic;	0	No
1978 D9QEHS Uncharacterized protein	CpC231_0405	344	Cytoplasmic;	1	No
1979 D9Q933 Methylmalonyl-CoA carboxyltransferase 12S subunit	CpC231_0572	518	Cytoplasmic;	0	No
1980 D9Q973 Uncharacterized protein	CpC231_0615	302	Extracellular;	0	Yes
1981 D9QEWS Uncharacterized protein	CpC231_0553	234	Extracellular;	0	Yes
1982 D9QA62 Uncharacterized protein	CpC231_0960	54	Cytoplasmic;	0	No
1983 D9QAW6 Alkyl hydroperoxide reductase AhpD	ahpD	174	Cytoplasmic;	0	No
1984 D9QB50 Phosphatidate cytidyltransferase	cdsA	292	Membrane;	9	No
1985 D9QDP2 Phosphatidylglycerophosphatase B	pgpB	244	Membrane;	6	No
1986 D9QBG9 Cytochrome c oxidase subunit II	ctaC	361	Membrane;	2	Yes
1987 D9QCV3 Beta-N-acetylglucosaminidase	nagA	371	Extracellular;	0	Yes
1988 D9QDS2 Nucleoid-associated protein CpC231	ybaB	106	Cytoplasmic;	0	No
1989 D9QDA9 Uncharacterized protein	CpC231_2045	32	Extracellular;	0	No
1990 D9QAL8 Peptide deformylase	def	169	Cytoplasmic;	0	No
1991 D9QCB5 HIT family protein	CpC231_1731	141	Cytoplasmic;	0	No
1992 D9QBD0 Cell division protein SepF	sepF	149	Cytoplasmic;	0	No
1993 D9QEWS UPF0182 protein CpC231	CpC231_0555	1010	Membrane;	7	No
1994 D9Q9E5 Nicotinamide riboside transporter pnuC	pnuC	236	Membrane;	7	No
1995 D9Q9D3 Uncharacterized protein	CpC231_0676	514	Membrane;	10	No
1996 D9QCD7 Uncharacterized protein	CpC231_1756	313	Membrane;	0	Yes
1997 D9QAD1 Protein pafC	pafC	329	Cytoplasmic;	0	No
1998 D9QEHS ESAT-6-like protein	esxT	93	Extracellular;	0	No

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1999 D9QC18	Peptidase, S8A (Subtilisin) family protein	CpC231_1632	608	Extracellular;	0	Yes
2000 D9Q9G5	Transcription-repair-coupling factor	mfd	1264	Cytoplasmic;	0	No
2001 D9QE82	Uncharacterized protein	CpC231_0343	181	Membrane;	1	No
2002 D9QCD6	Uncharacterized protein	CpC231_1755	162	Cytoplasmic;	1	No
2003 D9Q9X0	tRNA-specific 2-thiouridylase MnmA	mnmA	372	Cytoplasmic;	0	Yes
2004 D9Q9N3	Aromatic amino acid transport protein	aroP2	454	Membrane;	12	No
2005 D9QBK4	Uncharacterized protein	CpC231_1463	62	Cytoplasmic;	0	No
2006 D9Q9J5	Uncharacterized protein	CpC231_0739	189	Membrane;	1	No
2007 D9QAT4	Hit (Histidine triad) family protein	CpC231_1184	197	Cytoplasmic;	0	No
2008 D9QCC3	Threonine export carrier	CpC231_1741	489	Membrane;	10	No
2009 F9Y341	Uncharacterized protein	CpC231_0491a	53	Extracellular;	0	No
2010 D9QAJ3	Uncharacterized protein	CpC231_1093	266	Membrane;	6	No
2011 D9QE41	Uncharacterized protein	CpC231_0270	40	Extracellular;	0	Yes
2012 D9QEM6	HTH-type transcriptional activator tipA	tipA	256	Cytoplasmic;	0	No
2013 D9QAH2	Uncharacterized protein	CpC231_1072	31	Extracellular;	0	No
2014 D9QAJ4	Cytochrome oxidase assembly protein	CpC231_1094	331	Membrane;	8	No
2015 D9Q9F5	Uncharacterized protein	CpC231_0699	57	Cytoplasmic;	0	No
2016 D9QA63	Hemolysin A	tlyA	273	Cytoplasmic;	0	No
2017 F9Y377	Uncharacterized protein	CpC231_1610a	39	Extracellular;	0	Yes
2018 D9QDW5	Na(+) / H(+) antiporter subunit C	mrpC	151	Membrane;	3	No
2019 D9Q986	Precorrin-6A synthase [deacetylating]	cobF	251	Membrane;	0	No
2020 D9QBS5	Uncharacterized protein	CpC231_1536	73	Cytoplasmic;	1	No
2021 D9QEIO	Uncharacterized protein	CpC231_0413	101	Cytoplasmic;	0	No
2022 D9QCN1	Transcription regulator padR	padR1	129	Cytoplasmic;	0	No
2023 D9QDN0	Uncharacterized protein	CpC231_0105	153	Membrane;	1	No
2024 D9QE01	Adenylate cyclase	cyaA	505	Membrane;	6	No
2025 D9QBK2	Uncharacterized protein	CpC231_1461	72	Cytoplasmic;	0	No
2026 D9Q971	Uncharacterized protein	CpC231_0612	113	Cytoplasmic;	2	No
2027 D9Q9I0	Isoprenyl transferase	uppS1	265	Cytoplasmic;	0	No
2028 D9QAX8	PTS system fructose-specific EIABC component	ptsF	649	Membrane;	8	No
2029 D9QCJ8	ABC transporter	CpC231_1818	253	Membrane;	6	No
2030 D9QDR0	Uncharacterized protein	CpC231_0136	100	Cytoplasmic;	0	No
2031 D9QE76	Glycosyl transferase group 1	CpC231_0305	354	Cytoplasmic;	0	No
2032 D9QDI3	Uncharacterized protein	CpC231_0057	66	Cytoplasmic;	0	No
2033 D9QEC4	50S ribosomal protein L22	rplV	120	Cytoplasmic;	0	No
2034 D9QDL5	Methylated-DNA--protein-cysteine methyltransferase	ogt	96	Cytoplasmic;	0	No
2035 D9QC69	Uncharacterized protein	CpC231_1684	214	Extracellular;	3	No
2036 D9QDS4	Inner membrane permease ygbN	ygbN	445	Membrane;	13	No
2037 D9QCS1	Oligopeptide ABC transporter, ATP-binding protein	oppD3	221	Cytoplasmic;	0	No
2038 D9QC57	Uncharacterized protein	CpC231_1671	59	Extracellular;	0	No
2039 D9QCL0	Purine phosphoribosyltransferase	CpC231_1830	159	Cytoplasmic;	0	No
2040 D9QBI9	Uncharacterized protein	CpC231_1445	117	Cytoplasmic;	0	No
2041 D9QA12	3-isopropylmalate dehydratase large subunit	leuC	482	Cytoplasmic;	0	No
2042 D9QBS2	Long-chain-fatty-acid-CoA ligase	fadD15	611	Cytoplasmic;	0	No
2043 D9QBL9	Uncharacterized protein	CpC231_1478	266	Extracellular;	1	No
2044 D9QA46	Uncharacterized protein	CpC231_0944	180	Membrane;	3	No
2045 D9QA18	Uncharacterized protein	CpC231_0915	322	Extracellular;	1	No
2046 D9QCF2	Uncharacterized protein	CpC231_1771	66	Cytoplasmic;	0	No
2047 D9QDJ5	Transcription factor Rok	CpC231_0070	339	Membrane;	0	No
2048 D9QET3	DNA-binding response regulator mtrA	mtrA	232	Cytoplasmic;	0	No
2049 D9QE06	Glucose-1-phosphate thymidylyltransferase	rfaB	289	Membrane;	0	No
2050 D9QAG1	Arginine/ornithine transport system ATPase	CpC231_1061	365	Cytoplasmic;	0	No
2051 D9QDJ6	Uncharacterized protein	CpC231_0071	31	Extracellular;	0	No
2052 F9Y345	Uncharacterized protein	CpC231_0580a	48	Extracellular;	0	No
2053 D9QE70	1,4-dihydroxy-2-naphthoyl-CoA synthase	menB	335	Cytoplasmic;	0	No
2054 D9QC52	Phosphoserine phosphatase	serB	427	Cytoplasmic;	0	No
2055 D9QDL2	UPF0145 protein CpC231	CpC231_0087	106	Cytoplasmic;	0	No
2056 D9QCY1	Uncharacterized protein	CpC231_1956	451	Extracellular;	1	Yes
2057 D9QCZ7	Phosphoglycerate mutase	pgmB	218	Cytoplasmic;	0	No
2058 D9QE24	Pyruvate formate-lyase-activating enzyme	pflA	289	Cytoplasmic;	0	No
2059 D9QBN1	Aminotransferase	cobC	380	Cytoplasmic;	0	No
2060 D9QDK9	Alpha-ketoglutarate-dependent dioxygenase AlkB	alkB	247	Membrane;	0	No
2061 D9QEHI7	Phosphoglucosamine mutase	glmM	447	Cytoplasmic;	0	No
2062 D9QB66	tRNA (guanine-N(1)-)methyltransferase	trmD	289	Cytoplasmic;	0	No
2063 D9QEAI9	Elongation factor G	fusA	708	Cytoplasmic;	0	No
2064 D9QB72	Nitrogen regulatory protein P-II	glnB	112	Cytoplasmic;	0	No
2065 D9QBC3	Uncharacterized protein	CpC231_1378	197	Extracellular;	0	Yes

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2066	D9QA90	Uncharacterized protein	CpC231_0988	81	Extracellular;	0	No
2067	D9QA93	Integrase	CpC231_0991	88	Extracellular;	0	No
2068	D9Q9I7	Transcriptional regulator LysR family	lysR	253	Cytoplasmic;	0	No
2069	D9Q9S9	Phage shock protein C	pspC1	73	Membrane;	1	No
2070	D9QD36	Uncharacterized protein	CpC231_2013	460	Cytoplasmic;	0	No
2071	D9QCT5	Urease accessory protein UreD	ureD	275	Cytoplasmic;	0	No
2072	D9Q954	Resuscitation-promoting factor	rpfA	207	Extracellular;	0	Yes
2073	D9QDM5	Arabinosyltransferase C	embC	1070	Membrane;	14	Yes
2074	D9Q9M4	Monoacyl phosphatidylinositol tetramannoside-binding pro	lpqW	490	Extracellular;	0	No
2075	D9QDS3	Recombination protein RecR	recR	218	Cytoplasmic;	0	No
2076	D9QD35	GntR-family transcriptional regulator	CpC231_2012	124	Cytoplasmic;	0	No
2077	D9QD52	Uncharacterized protein	CpC231_2029	123	Cytoplasmic;	0	No
2078	D9QCH8	Cell wall channel	CpC231_1798	49	Extracellular;	0	No
2079	D9QDR7	Gluconate 5-dehydrogenase	idnO	249	Membrane;	0	No
2080	D9QCU5	YibE/F family protein	CpC231_1919	510	Membrane;	8	No
2081	D9QDQ3	Uncharacterized protein	CpC231_0129	228	Extracellular;	0	Yes
2082	D9QCB9	TetR-family regulatory protein	CpC231_1736	169	Extracellular;	0	No
2083	D9QBP4	Uncharacterized protein	CpC231_1504	249	Membrane;	7	No
2084	D9QCX8	4-hydroxybenzoate polyprenyltransferase-related prenyltra	ubiA	326	Membrane;	9	No
2085	D9QAY5	Uncharacterized protein	CpC231_1236	252	Membrane;	0	No
2086	D9QAI4	Uncharacterized protein	CpC231_1084	159	Cytoplasmic;	0	No
2087	D9QDW9	Protein yhaP	yhaP	275	Membrane;	5	No
2088	D9QE95	Propionyl-CoA carboxylase beta chain 2	pccB2	547	Cytoplasmic;	0	No
2089	D9Q9Z9	D-3-phosphoglycerate dehydrogenase	serA	531	Cytoplasmic;	0	No
2090	D9QD32	Uncharacterized protein	CpC231_2009	103	Extracellular;	0	No

## Anexo 2

#	Uniprot entry	B-cell Epitopes		
Epitope #	Epitope name	Epitope sequence	Position of first aa in protein sequence	Conservation among proteomes (%)
1	E1_D9Q9I9	SDLPRGDDDD	81	94,3
		DLPRGDDDDD	82	94,3
		LPRGDDDDDS	83	94,3
		RGDDDDDSAL	84	94,3
		YPKDGPSGNT	185	35,7
2	E5_D9QCI3	TQSNTANVNG	186	35,7
		QPDGSRTLAG	187	35,7
		ADPQYQRKEF	612	41,4
3	E9_D9QEK9	EGESQPEFTH	128	94,3
		GESQPEFTHD	129	94,3
4	E11_D9QDW8	PADAQPTPRA	406	92,9
		PGKFEQRKGG	176	80,0
		VTKNKPAPGS	177	51,4
		TKNKPAPGSI	178	51,4
5	E12_D9QAI2	FEPKQTGGFT	484	80,0
		IPRDRSSETP	578	80,0
		RDRSSETPLV	580	80,0
		DRSSETPLVI	581	80,0
		PVPPTDPWYQ	323	90,0
		VPPTDPWYQK	324	90,0
6	E19_D9QBT9	AEQYPFDPDR	334	90,0
		PFDPDRARQL	338	90,0
		FDPDRARQLM	339	90,0
		DPDRARQLMD	340	90,0
		SNGQSAAWLG	189	90,0
7	E25_D9QBQ3	ARKTTTDHAR	539	52,9
		RKTTTDHARQ	340	90,0
8	E28_D9QAF0	SGTAEPKRHY	229	88,6
		NLQDLTDGSA	46	84,3
		LQDLTDGSAP	47	84,3
9	E29_D9QDX4	TSNNNADEQAA	145	84,3
		KKGLSTEQIT	303	84,3
		SYSEKGFSFDQ	488	84,3
		YNTKYNRGSS	679	84,3
		SDGTPPPRTT	749	80,0
10	E37_D9Q9L5	DGTTPPRRTS	750	78,6
		TRTPAKDFSS	321	97,1
		DSSDAPYSAL	50	94,3
		DPSVNKLKSS	158	94,3
		SVNKLKSSDV	160	94,3
		VNKLKSSDVK	161	94,3
11	E38_D9QB28	PTGELPKPES	225	94,3
		TGELPKPESA	226	94,3
		GELPKPESAY	227	94,3
		ELPKPESAYE	228	94,3
		LPKPESAYEL	229	94,3
		LKKYQQPVDA	238	94,3
		KKYQQPVDAQ	239	94,3
		QPVDAQSTAD	243	94,3
		TNNSYSNNAD	81	54,3
		NNNSYSNNADA	82	54,3
12	E50_F9Y379	QDLTNRGINPD	153	52,9
		DLTNRGINPDG	154	52,9
		NRGIPDGPNY	157	55,7
		PNTAKGKKFS	9	50,0
		DPASGNRSAQ	43	55,7
13	E55_D9QB55	PASGNRSAQR	44	55,7
		ASGNRSAQRV	45	55,7

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		SGNRSAQRVL	46	55,7
		KDSTSAKTPP	63	51,4
14	E60_D9QDK4	TSAKTPPPAA	65	51,4
		TWKATSGNHP	115	92,9
15	E63_D9QER5	SDSSAPAPQN	26	91,4
16	E64_D9QBP6	AAPKPQTTHNH	44	57,1
17	E66_D9QDH7	APKPQTTHNH	46	57,1
		HREGMDGKD	73	55,7
18	E67_D9QD67	DKPETLDPDE	63	84,3
		KPETLDPDEK	64	84,3
		KTPEIDDRDD	73	84,3
19	E70_D9QCT4	CAKPEEDPYM	159	70,0
		AKPEEDPYMV	160	70,0
		IDTNRGYDSK	155	37,1
20	E72_D9QA91	DTNRGYDSKT	156	37,1
		TNRGYDSKTD	158	37,1
		ERKQGGSYTG	279	34,3
21	E76_D9QEN1	LADPTPRSSA	26	72,9
		PSELPTPPTP	351	81,4
22	E78_D9QC38	PGAPMRTELA	33	38,6
		VEGDADPACA	90	34,3
		STGEESAGAP	38	94,3
		GEESAGAPAV	39	94,3
		EESAGAPAVH	40	94,3
		ESAGAPAVHD	41	94,3
23	E80_D9QDW7	TSARDGAAKL	98	94,3
		SARDGAAKLA	99	94,3
		ARDGAAKLAD	100	94,3
		RDGAAKLADG	101	94,3
		ADGMNQLQAA	108	94,3
		DPKAAEFKPE	165	94,3
		NFEDLRQNHP	85	35,7
		FEDLRQNHPK	86	35,7
		EDLRQNHPKA	87	35,7
24	E90_D9QEE1	LRQNHPKAME	90	35,7
		RQNHPKAMEE	91	35,7
		QNHPKAMEEN	92	37,1
		GSIRQYRVSH	194	37,1
25	E97_D9Q9Y9	YTWDDAQKRRN	195	92,9
		TWDAQKRRNF	196	94,3
26	E99_D9QCD5	ESGTQDREVG	176	87,1
27	E100_D9QEC9	PYTEDPPGSL	143	87,1
		STYSPEPHSK	25	54,3
28	E101_D9QEY3	TYSPEPHSKE	26	54,3
		SPEPHSKEWC	28	54,3
		PEPHSKEWCH	29	54,3
		SSNPPKTRHP	15	97,1
		KSSDTPPVER	49	97,1
		SDTPPVERAI	51	97,1
29	E105_D9QBC2	KQGTFNPTAP	111	97,1
		QGTFNPTAPS	112	97,1
		FNPTAPSGGE	115	97,1
		NPTAPSGGEV	116	97,1
		PEKVTKGETF	61	55,7
30	E112_D9QCR2	SSCTTKPDVQ	183	92,9
		NSNTYVGPSN	88	40,0
31	E114_D9QC71	KIGEYRGFDE	214	47,1
		DKDEKVRSIG	472	44,3
		PLENPQDIFS	50	90,0
		ENPQDIFSFG	51	90,0
		NLTNNSAATT	176	90,0
32	E117_DaOAO8	TNNSAATTG	177	90,0

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		L117_D9QK600	GLTGPRPAGA	213	90,0
			LTGPRPAGAF	214	90,0
			TGPRPAGAFS	215	90,0
			EPQPVRDGFY	216	90,0
33	E125_D9QA08	PQPVRDGFYA	301	90,0	
		QPVRDGFYAA	302	90,0	
		GNKSNQQIES	21	97,1	
		NKSNQQIESD	22	60,0	
		PLEGQRQAGK	119	97,1	
		PQATPDTPNY	146	97,1	
34	E127_D9QBZ2	QATPDTPNYY	147	97,1	
		ATPDTPNYYP	148	97,1	
		TPDTPNYYPG	149	97,1	
		PDTPNYYPGG	150	97,1	
		TPNYYPGGMV	152	97,1	
		TSSDGHATRG	147	90,0	
		DRAEGASTSS	135	90,0	
35	E136_D9QAT8	EGASTSSDPN	138	57,1	
		STSSDPNDAT	141	57,1	
		TSSDPNDATK	142	57,1	
36	E141_D9Q967	TKDSADKAMT	31	95,7	
37	E142_D9QEF8	QERTAPPVVP	107	88,6	
		PTPPAFDTGS	124	48,6	
		DSFPSDTSBV	90	55,7	
		AGPNSNKIGQ	182	55,7	
		SVNPEDPTKP	247	41,4	
		VNPEDPTKPE	248	41,4	
38	E144_D9QDT9	EDPTKPEPK	249	41,4	
		PEPKKEPEPK	256	77,1	
		YKAEDKGTVV	374	52,9	
		PVENEDLFTP	403	77,1	
		TPEVPDDSSF	411	74,3	
		QTNPAYAAPV	451	77,1	
		ASAQRDPYKL	57	92,9	
39	E154_D9Q980	AQRDPYKLLP	59	92,9	
		GTGDPNIDSS	323	92,9	
		ESGQFYDNTW	392	92,9	
40	E158_D9QC90	KKWNDAIAAQ	162	77,1	
41	E159_D9QDD8	DVSSDPTALA	108	88,6	
42	E161_D9QB44	GSAESTAVRT	418	54,3	
43	E162_D9QDP1	SIEGETPLD	467	88,6	
		GGDPHTYQPS	69	81,4	
		PDKADTYKTN	179	80,0	
		SEKKYTRRDF	5	92,9	
44	E164_D9QDC2	KSTNATEQKN	479	94,3	
		STNATEQKNK	480	94,3	
45	E167_D9QDV7	NVDRFTRSGN	196	88,6	
		TRSGNAPSVD	201	88,6	
		EGKEMTSYKA	147	92,9	
46	E169_D9QEM3	DNEKLSFSGK	182	92,9	
		NSSKDASLGD	254	92,9	
		SNYADPSSGS	169	87,1	
		PKTENQTPPS	321	87,1	
47	E172_D9QEL9	KTENQTPPS	322	87,1	
		ASAKQGDKDD	542	85,7	
		SAKQGDKDDS	543	87,1	
		KQGDKDDSEE	545	87,1	
48	E178_D9QCH2	TDPDGFTSI	38	85,7	
		DNTGIDPIEA	41	72,9	
		QGKMGSRVTVK	73	10,0	
		GKMGSRTVKQ	74	10,0	
		GSRTVKQFHR	77	72,9	

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		DGTWSEWYDT	113	72,9
49	E179_D9QCZ0	SEWYDTEPLD	117	72,9
		QPAAGQPAAD	173	72,9
		TNNVSDFDVV	219	72,9
		HYSEGTSYTP	395	72,9
		NTPPRGDAPA	462	72,9
		TPPRGDAPAP	463	72,9
		PPRGDAPAPQ	464	72,9
50	E191_D9QDJ0	SSINWKDVKS	62	88,6
		GGVMPPSREE	102	55,7
51	E192_D9QD96	GVMPPSREEL	103	55,7
		VMPPSREELL	104	55,7
		MPPSREELLA	105	55,7
52	E196_D9QD88	GYYQRRYVTN	71	95,7
		DPTTAESTWA	185	95,7
53	E198_D9QBK9	AEYTKDDRTD	156	54,3
		EYTKDDRTDA	157	54,3
		EGEYLPSSTK	272	81,4
		EYLPSSTKGE	274	81,4
54	E200_D9QE91	YLPSSTKGEE	275	81,4
		LPSSTKGEEK	276	81,4
		PSSTKGEEKG	277	81,4
		SSRSTSRTT	250	84,3
55	E205_D9QE89	SRSTSRTTS	251	84,3
		RSTSRTTSS	252	84,3
		KYCKNTGKKD	112	82,9
56	E208_D9QD03	FKDSDGKISW	180	82,9
		SSERSIALPK	378	81,4
57	E211_D9QAR4	EQTPTASSLA	33	58,6
		SQPAPVSAWV	35	94,3
		QPAPVSAWVN	36	94,3
58	E212_D9Q936	TQKDAQGRTI	123	94,3
		NSPDVPAESL	179	94,3
		PDVPAESLAA	181	94,3
		SGAPKPPSAD	210	95,7
		GAPKPPSADA	211	95,7
59	E217_D9Q9L9	APKPPSADAP	212	95,7
		PKPPSADAPS	213	95,7
		KPPSADAPSP	214	95,7
		PPSADAPSPL	215	95,7
60	E223_D9QCW7	AEPKGSASNN	149	52,9
61	E224_D9QBT2	PQVDAGTVAL	117	98,6
62	E225_D9Q999	VSGKHRKQTS	8	95,7
		EPLKASPGRA	39	44,3
63	E226_D9QCR3	DDPWKDKLQV	80	71,4
		EVNKSGAMQV	307	71,4
		GKEDQRPAWL	156	98,6
64	E229_D9QAT6	PAFSKDKLDP	169	98,6
65	E231_D9QCZ5	TWKDDQGKIT	66	97,1
66	E233_D9QBU7	TPSLEQQDTH	231	97,1
		DCLSSRTDAS	35	48,6
67	E234_D9QBG1	DEAKSKEDVY	76	90,0
		EAKSKEDVYR	77	90,0
		ASAGPRDWLR	35	91,4
		SAGPRDWLRP	36	90,0
		RDWLRPDATG	40	90,0
68	E236_D9QCX6	DWLRPDATGT	41	90,0
		LRPDATGTCE	43	90,0
		RPDATGTCEW	44	90,0
		PDATGTCEWD	45	90,0
69	E243_D9QC24	KDLGKGVYGD	220	92,9
70	E244_D9QCX3	AKPTPGESFS	89	98,6

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71	E245_D9QC18	QRQSAAPAGE	49	85,7
		SDPKISQDHD	207	90,0
		PKISQDHGDR	209	90,0
		GNHNPGGIL	400	90,0
		NHNPGGGILS	401	90,0
		NRGLRGAEAS	413	54,3
		RQPKERSGRE	574	90,0
		TGKEQSKQQQ	585	90,0
		KEQSKQQQCT	587	90,0
		LGAPQNGLPS	267	77,1
72	E254_D9QCV3	GAPQNGLPST	268	77,1
		APQNGLPSTL	269	77,1
73	E257_D9Q954	VDDAQNYAAA	138	98,6
		TADWKQGAAG	111	94,3
74	E258_D9Q973	APPVSPGNPA	252	94,3
		PPVSPGNPAP	253	94,3
		PVSPGNPAPV	254	94,3
		SSDDKGSSSS	23	97,1
		SDDKGSSSSS	24	95,7
75	E262_D9QBC3	DDKGSSSSSS	25	95,7
		DAAAQPPAPD	171	97,1
		AAQPPAPDAP	173	97,1
		QPPAPDAPAA	175	97,1
		GTAETSSEKT	79	54,3
		ETSSEKTKKN	82	88,6
76	E268_D9QEWF7	QFDSCDANGV	112	88,6
		MACSGEKIGQ	125	88,6
		ACSGEKIGQF	126	88,6
		CSGEKIGQFQ	127	88,6