CATÓLICA
INSTITUTO DE CIÊNCIAS DA SAÚDE
LISBOA · PORTO · VISEU

MESTRADO INTEGRADO EM MEDICINA DENTÁRIA

O PROTEOMA NAS INFEÇÕES ENDODÔNTICAS

Dissertação apresentada à Universidade Católica Portuguesa para obtenção
do grau de mestre em Medicina Dentária

Por:

Luís Miguel Marques Monteiro

Viseu, 2016

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THE PROTEOME OF ENDODONTIC INFECTIONS

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Por:
Luís Miguel Marques Monteiro

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Viseu, 2016

“A imaginação é mais importante que a ciência, porque a
ciência é limitada, ao passo que a imaginação
abrange o mundo inteiro”.
(Albert Einstein)

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Resumo

A cavidade oral apresenta uma grande diversidade de proteínas humanas e microbianas. O presente trabalho tem como objetivo identificar e anotar as proteínas humanas e microbianas que na bibliografia foram associadas à infeção endodontica. O estudo desenvolvido permitiu identificar 523 proteínas sendo 385 microbianas e 138 humanas, das quais 96 são proteinas exclusivas da patologia endôdontica. A informação relativa a estas proteínas foi anotada na base de dados OralOme a qual pode ser acedida via web pela interface OralCard. A caracterização funcional do OralOma da patologia endodôntica permitiu inferir um aumento do número de proteínas envolvidas nos processos moleculares *receptor activity* e *transport activity*.

A determinação das interações proteína-proteína entre as proteínas humanas e as proteínas microbianas permitiu identificar que um grande número de interações está associado a funções de defesa e à tentativa de invasão dos tecidos do hospedeiro. O facto de as proteínas identificadas na patologia endodontica não apresentarem dados de quantificação limita a identificação de potenciais biomarcadores para a patologia endodôntica. Sugerem-se novos estudos de proteómica que permitam esta quantificação.

Palavras-chave: “infeções endodônticas”, “proteómica”, “microbioma oral”, “diagnóstico salivar”, “OralCard”

Abstract:

The oral cavity presents a wide range of human and microbial proteins. This study aims to identify and annotate the human and microbial proteins in the literature associated with endodontic infection. The study developed identified 523 proteins being 385 microbial and 138 human, of which 96 are unique proteins of endodontic pathology. The information on these proteins has been noted in the database OralOme which can be accessed via the web by OralCard interface. Functional characterization of the endodontic OralOma disease possible to infer an increased number of molecular processes involved in protein activity and receptor transport activity.

The determination of protein-protein interactions between human proteins and microbial proteins identified that a large number of interactions are associated with defense functions and attempt invasion of host tissues. Many proteins identified in the endodontic disease don’t present quantification data and merely identifying potential biomarkers for endodontic disease. This suggest new studies of proteomics to enable this quantification.

Palavras-chave:“Endodontic infections”, “Salivar diagnosis”, “Proteomics”, “Oral microbiome”, ”OralCard”.

Nota prévia

Ao longo deste trabalho aparecem expressões em língua Inglesa, escritas em itálico, sendo exemplo disso, os termos de classificação de ontologias e nomes de proteínas assim como a explicação dos mecanismos biológicos das tabelas finais. Decidiu-se não traduzir essas expressões o que poderia implicar a alteração do seu significado original e assim a interpretação imprecisa do conceito biológico.

Índice

1.Introdução - 20 -

1.1 Patologia endodôntica - 20 -
1.1.1Conceito, etiologia e tratamento - 20 -
1.1.2 Microbiologia das infeções endodônticas - 21 -
1.1.3 Proteoma em Infeções endodônticas - 24 -
1.1.4 Relação da Endodontia com outras patologias como a doença periodontal - 26 -
1.1.5 Resposta imune - 26 -
1.1.6 Fluido Crevicular na patologia endodôntica - 28 -
1.1.7 Saliva como fluido diagnóstico - 29 -

1.2 Ferramentas bioinformáticas - 30 -

2.OBJETIVOS - 33 -

3. MATERIAIS E MÉTODOS - 35 -

3.1 Proteoma humano e microbiano em patologia endodôntica - 35 -

3.2 Obtenção da listagem de Proteínas - 35 -
3.2.1 Anotação manual da informação de proteínas da patologia endodôntica - 36 -
3.2.2 Identificação das proteínas da cavidade oral em patologia endodôntica - 37 -
3.2.3 Origem das proteínas orais da patologia endodôntica - 38 -
3.2.4 Relação com os estados de saúde e de doença - 38 -
3.2.5 Caraterização do dador da amostra analisada - 39 -
3.2.6 Métodos de amostragem e análise - 40 -
3.2.7 Outras informações - 40 -
3.2.8 Atualização do OralCard - 40 -

3.3 Caraterização funcional das proteínas orais em Patologia endodôntica - 41 -
3.3.1 Caracterização funcional com a ferramenta PANTHER - 41 -
3.3.2 Comparação com o OralOma Normal - 44 -

3.4 ***Caraterização funcional das proteínas microbianas recorrendo ao AgBase*** - 46 -

3.5 Relação com outras patologias - 50 -

3.6 Interactoma oral em Patologia endodôntica - 51 -

4. Resultados e Discussão - 54 -

4.1 Proteoma Humano e microbiano em patologia endodôntica - 54 -

4.2 Obtenção da listagem de proteinas - 54 -
4.2.1 Anotação manual de informação relativa às proteínas da patologia endodôntica - 56 -
4.2.2 Origem das proteínas orais da patologia endodôntica - 57 -
4.2.3 Relação com estados de saúde e de doença - 58 -
4.2.4 Caraterização do dador da amostra - 60 -
4.2.5 Métodos de amostragem e análise - 61 -

4.3 Caraterização funcional das proteínas orais em patologia endodôntica - 61 -
4.3.1 Caraterização funcional das proteínas humanas envolvidas em patologia endodontica com o auxílio da ferramenta PANTHER - 61 -

4.3.2 Comparação com o OralOma Normal ....- 64 -
4.3.3 Caraterização funcional das proteínas microbianas com a ferramenta PANTHER- 73 -

4.4 Caraterização funcional das proteínas microbianas recorrendo à Ferramenta AgBase..- *74* -

4.5 Relação de comparação com outras Patologias (periodontite crónica, gengivite e periodontite agressiva)..- *78* -

4.6 Interactoma oral da Patologia endodôntica...- *84* -

5. CONCLUSÃO..**- 92 -**

6. Bibliografia ....**- 95 -**

7. Anexos ....**- 105 -**

Lista de abreviaturas:

SCR – Sistema de canais radiculares

PE – Patologia endodôntica

PC– Periodontite crónica

PA– Periodontite agressiva

G– Gengivite

ADN – Ácido Desoxirribonucleico

MeSH – *Medical Subject Headings*

OMIM – *Online Mendelian Inheritance in Man*

PANTHER – *Protein Analysis Through Evolutionary Relationships*

STRING –*Functional protein association networks*

OMS – Organização Mundial de Saúde

PPI – *Protein-protein interaction*

UniProtKB – *Universal Protein Knowledge Base*

Índice deFiguras e tabelas

Tabela 1: Infeções endodônticas e microrganismos mais frequentemente detetados .... - 22 -
Figura 1: Cabeçalhos que permitem a organização da informação recolhida dos diferentes estudos de proteómica da cavidade oral (proteínas associadas á patologia anotadas manualmente) numa tabela em Microsoft Excel 2010. ...... - 36 -
Figura 2: Cabeçalhos das colunas da base de dados do proteoma oral em patologia endodôntica referentes à identificação de cada proteína. .... - 37 -
Figura 3: Exemplo ilustrativo da visualização do site da UniProt durante a atribuição do código UniProtKb AC, nome e organismo a uma determina da proteína. .... - 37 -
Figura 4: Cabeçalho da base de dados OralOme relativa à origem das proteínas da patologia endodôntica.......... - 38 -
Figura 5: Cabeçalho da base de dados OralOme referente à relação das proteínas anotadas da patologia endodôntica com os estados de saúde e doença. .... - 39 -
Figura 6: Cabeçalho do OralOme referente à caracterização do dador da amostra. .... - 39 -
Figura 7: Cabeçalho do OralOme referente aos métodos de amostragem e análise das proteínas associadas á patologia endodôntica. .... - 40 -
Figura 8: Home Page da página web do OralCard.......... - 41 -
(http://bioinformatics.ua.pt/OralCard/home) .... - 41 -
Figura 9: Sistema de análise em grupo da ferramenta de classificação do PANTHER. As opções selecionadas correspondem às definições utilizadas para analisar os conjuntos de proteínas. .... - 42 -
Figura 10: Seleção do tipo de classificação por ontologia desejado, na ferramenta PANTHER. .... - 43 -
Figura 11: Portal *AgBase* e seleção da ferramenta de classificação funcional GoRetriever (http://www.agbase.msstate.edu/). .... - 46 -
Figura 12: Página web do AgBase e seleção do tipo de acesso na ferramenta de classificação funcional GoRetriever (http://www.agbase.msstate.edu/cgi-bin/tools/goretriever_select.pl) .... - 47 -
Figura 13: Ferramenta GoSlimViewer em que se submetem os resultados obtidos no GoRetriever através do GoSummary File no AgBase. .... - 48 -
(http://www.agbase.msstate.edu/cgibin/tools/goslimviewer_select.pl) .... - 48 -
Figura 14: Portal do AgBase e demonstração da seleção do GoSummary file.. - 48 -
(http://www.agbase.msstate.edu/cgi-bin/tools/goretriever_select.pl) .... - 48 -
Figura 15: Página web do AgBase e seleção do tipo de acesso na ferramenta de classificação funcional GoSlimViewer, para proteínas microbianas. .... - 49 -
(http://www.agbase.msstate.edu/cgi-bin/tools/goslimviewer_select.pl) .... - 49 -
Figura 16: Ferramenta informática do *AgBase* e visualização dos resultados obtidos no GoSlimViewer.......... - 49 -
(http://www.agbase.msstate.edu/cgi-bin/tools/goslimviewer.pl) .... - 49 -

Figura 17: Número de artigos e de proteínas orais anotadas e catalogadas no OralCard identificadas na patologia endodôntica. ....- 55 -
Figura 18: Percentagem de proteínas humanas e microbianas anotadas e catalogadas no OralCard e que foram associadas a patologia endodôntica. ..- 56 -
Figura 19: Gráfico que ilustra a origem das amostras das proteínas em estudo. ..- 57 -
Figura 20: Representação do número de proteínas humanas distribuídas de acordo com a sua identificação em estados de saúde, de outras doenças e em patologia endodontica (endo humanas). Gráfico obtido com recurso ao programa Venny. (http://bioinfogp.cnb.csic.es/tools/venny/) ....- 59 -
Figura 21: Ilustração das proteínas microbianas provenientes de amostras da Patologia endodôntica e amostras encontradas no OralOme microbiano. Grafico obtido pelo programaVenny. ....- 60 -
(http://bioinfogp.cnb.csic.es/tools/venny/)..- 60 -
Figura 22: Distribuição das proteínas de patologia endodôntica anotadas ao nível da ontologia *Biological process* do PANTHER. ....- 62 -
Figura 23: Distribuição das proteínas de Patologia endodôntica anotadas no nível da ontologia *immune system process* do PANTHER. ....- 63 -
Figura 24: Distribuição das proteínas de patologia endodôntica anotadas no nível da ontologia *Molecular function* do PANTHER. ....- 64 -
Figura 25: Distribuição das proteínas orais de pacientes com patologia endodôntica segundo os processos biológicos em que intervêm, recorrendo à ferramenta PANTHER (Mi 2010, Thomas 2003). É mostrada a diferença fraccional entre as proteínas da patologia endodôntica e o OralOma normal. No gráfico estão indicados os processos biológicos com uma alteração em relação ao OralOma normal considerada estatisticamente significativa (p≤0.05). ....- 66 -
Figura 26: Distribuição das proteínas de pacientes com patologia endodontica segundo as funções moleculares que desempenham, recorrendo à ferramenta *PANTHER* (Mi 2010, Thomas 2003). É mostrada a diferença fracional entre as proteínas da patologia endodôntica e o oraloma normal. As barras azuis marcadas com uma estrela estão indicadas as funções moleculares com uma alteração em relação ao OralOma normal considerada estatisticamente significativa (p≤0.05)...- 69 -
Figura 27: Distribuição das proteínas microbianas da Patologia endodôntica anotadas ao nível da ontologia *Biological process* do PANTHER. ....- 73 -
Figura 28: Distribuição das proteínas microbianas de Patologia endodôntica anotadas no nível da ontologia *Molecular function* do PANTHER. ....- 74 -
Figura 29: Distribuição de proteínas, obtido pelo *AgBase*, anotadas na ontologia Biological process. ....- 75 -
Analisando a figura 29 podemos inferir que os processos biológicos que apresentam mais proteínas envolvidas correspondem a *metabolic process*, 116 proteínas, seguido de *biological process* 92 proteínas. ....- 76 -
Figura 30: Distribuição das proteínas orais por patologia endontica e outras patologias orais. Gráfico obtido com recurso ao programa Venny. (http://bioinfogp.cnb.csic.es/tools/venny/)..- 79 -
Tabela 3 – Proteínas humanas alteradas e que foram identificadas na patologia endodôntica, gengivite, periodontite crónica e agressiva ....- 80 -

Figura 31: Rede de interações entre proteínas humanas e microbianas em patologia endodôntica, gerada pelo algoritmo OralInt e visualizada com a ferramenta Cytoscape. Representação a cores das proteinas humanas que desempenham mais interações com *Enterococcus faecalis* (representadas a verde), o *streptococcus sanguinis* (representado a amarelo), *pseudomonas* (representado a cor de laranja) *bacteroides fragilis* (repesentado a cor de rosa). .- 85 -
Figura 32: Rede de interações entre proteínas humanas (retângulos verdes) e as proteínas de E. faecalis (retângulos azuis), geradas com a ferramenta Cytoscape. ....- 88 -
Anexo A - Proteínas humanas identificadas no âmbito do estudo de patologia endodontica e analisadas ao longo deste trabalho anotadas por ordem alfabética de código UniProtKBAC. 106
Anexo B - Proteínas microbianas identificadas no âmbito do estudo de patologia endodontica e analisadas ao longo deste trabalho anotadas por ordem alfabética de código UniProtKBAC. 112
Anexo C - Lista de proteinas excluivas da patologia endodôntica. 181

1. Introdução

*1.*Introdução

1.1 Patologia endodôntica

1.1.1Conceito, etiologia e tratamento

A endodontia é uma área da Medicina Dentária que se preocupa com a prevenção, diagnóstico e tratamento de doenças da polpa dentária e região perirradicular. O tratamento endodôntico constitui um processo seguro e eficaz de preservar os dentes que de outra forma seriam perdidos (1).

A cavidade oral está sujeita a uma complexa comunidade bacteriana, no entanto o tecido pulpar é normalmente protegido da infeção pela presença dos tecidos mineralizados coronários esmalte, dentina e radiculares representados pela dentina e pelo cemento. Se estas barreiras forem ultrapassadas, ou seja, afetadas principalmente pelo processo de cárie e fraturas coronárias que é o mais frequente, cria-se uma via de acesso para os microrganismos e os seus subprodutos atingirem a cavidade pulpar.

De acordo com a situação clínica estabelecida, as infeções endodônticas podem ser classificadas em infecções primárias ou secundárias. A infeção primária representa a infeção inicial decorrente da colonização do sistema de canais radiculares (SCR), após a necrose do tecido pulpar. A infeção secundária é caraterizada por ser desencadeada por microrganismos que não estavam presentes na infeção primária e que foram introduzidos no SCR durante o TER (tratamento endodôntico radical), quer entre as sessões do tratamento ou mesmo após a conclusão do tratamento. A microbiota envolvida nestes dois tipos de infeção é diferente podendo variar também de acordo com a função do tempo de infeção (28), e da exposição do SCR ao meio oral ou não (14), (26).

O sucesso clinico é o resultado esperado do tratamento endodôntico, depende da ausência de doença, ou seja, de infeções canalares ou inflamação periapical (2).

1.1.2 Microbiologia das infeções endodônticas

A inflamação periapical representa uma resposta biológica de defesa natural, causada por vários agentes etiológicos (4).

Vários microrganismos com diferentes características (estruturais, metabólicas e patogénicas) atingem a zona periapical e estimulam respostas inflamatórias e imunológicas. As defesas orgânicas e o grau de virulência dos microrganismos vão criar vários tipos de alterações periapicais, que são dependentes do potencial de infeção dos microrganismos presentes (5,6).

Foi reportado por vários autores que as infeções dos canais radiculares não são um envento aleatório, ou seja, o tipo de microbiota é desenvolvido de acordo com o ambiente envolvente (7). Existem também fatores de natureza química ou física que podem induzir uma patologia pulpar ou perirradicular. Os microrganismos presentes numa lesão de cárie ou no SCR representam uma fonte de agressão persistente que além de induzirem alterações tecidulares são capazes de perpetuá-las (8).

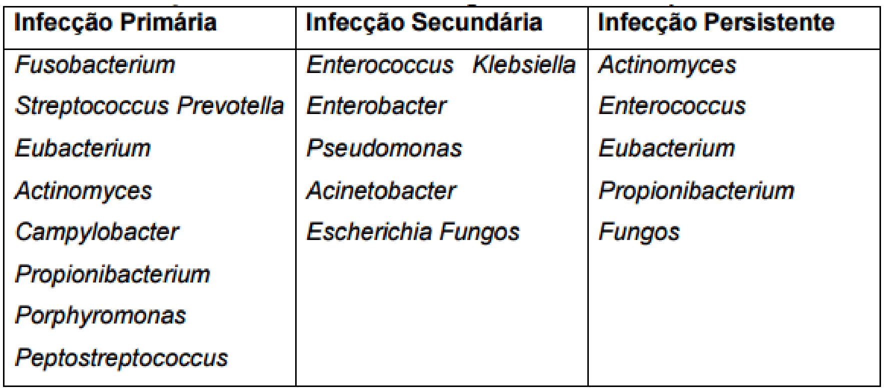
Em certas situações, esses microrganismos podem invadir locais normalmente estéreis do nosso organismo, tornando-os assim oportunistas (9).

Um dos primeiros estudos que contribuiu principalmente para a compreensão do papel dos microrganismos na etiopatogenia das alterações pulpares e periapicais irreversíveis evidenciou que quando polpas de ratos gnotobióticos foram deixadas expostas à cavidade oral, as polpas permaneceram vitais e nenhuma patologia periapical foi observada radiograficamente. Entretanto, após terem sido contaminados com a flora normal de polpas expostas desenvolveram necrose pulpar seguida de periapicopatias (10).

Dez anos mais tarde, foi demonstrado em dentes humanos necróticos intactos que lesões periapicais só se desenvolviam em dentes cujo SCR se apresentava contaminado por bactérias (11).

A principal via de acesso para a infeção do SCR é representada pela exposição dos túbulos dentinários, ou da própria cavidade pulpar, devido ao processo de cárie ou após fraturas coronárias. Entretanto outras vias de infeção do SCR como a via retrógrada ou anacorética foram também propostas (12).

Tabela 1: Infeções endodônticas e microrganismos mais frequentemente detetados (64).



Infecção Primária	Infecção Secundária	Infecção Persistente
Fusobacterium	*Enterococcus Klebsiella*	*Actinomyces*
Streptococcus Prevotella	*Enterobacter*	*Enterococcus*
Eubacterium	*Pseudomonas*	*Eubacterium*
Actinomyces	*Acinetobacter*	*Propionibacterium*
Campylobacter	*Escherichia Fungos*	*Fungos*
Propionibacterium		
Porphyromonas		
Peptostreptococcus		

Fonte: Siqueira Júnior e Lopes (1999)

A grande maioria dos microrganismos presentes nas infeções endodônticas são bactérias (15), embora os fungos e vírus também tenham sido ocasionalmente relatados (16).

Estima-se que cerca de 700 espécies microbianas habitem na cavidade oral humana sendo que, em princípio todas essas espécies têm a possibilidade de chegarem ao SCR (17).

A caraterização e identificação dos microorganismos em patologia endodôntica a nível do SCR foi relatado por alguns autores.

Os primeiros estudos de microrganismos no SCR advêm já do século passado, e foram realizados por Miller, em que foi descrita a presença de uma microbiota característico do SCR que variava de acordo com a exposição ou não da cavidade pulpar e de acordo com a região do canal radicular uma vez que a flora microbiana era diferente nos terços coronal, médio e apical. Estes estudos deram origem a uma primeira fase do estudo da microbiota endodôntica cujos resultados ressaltavam a presença de microrganismos facultativo e/ou aerotolerantes, compreendendo, principalmente, *estreptococos alfa e gama e enterococos, e com menos frequência, estafilococos coagulase-positivos e estreptococos β-hemolíticos* (18).

Depois uma segunda fase das pesquisas em microbiologia endodôntica, teve início com os trabalhos clássicos de Möller (1966) e Sundqvist (1976) a partir do aperfeiçoamento da técnica bacteriológica. Procedimentos assépticos de colheita de amostras, métodos de transporte do material capaz de proteger os microrganismos oxigênio-lábeis, meios de cultura ricos em nutrientes e técnicas anaeróbias de manipulação e incubação do material, o que permitiu reconhecer a presença e a importância dos microrganismos anaeróbios nas infeções endodônticas e periapicais.

Mais recentemente, o advento de métodos avançados de biologia molecular (9) deu início à terceira fase da pesquisa sobre microrganismos relacionados com a patologia endodôntica. Estes métodos não só confirmaram a maioria dos estudos anteriores usando o método de cultura, como também permitiram expandir significativamente a lista de agentes patogénicos endodônticos, uma vez que permitiu o reconhecimento de novos patógenos que nunca tinham sido identificados em canais pelos métodos de cultura (19).

Inúmeras espécies bacterianas só foram identificadas a partir da utilização de métodos moleculares (9).

A reação em cadeia da polimerase (PCR) seguida do sequenciamento de nucleótidos é um dos métodos citados na literatura para a identificação de microrganismos presentes no canal radicular. Foi descrito que através da utilização da abordagem por PCR era possível identificar uma nova espécie de *actinomiceto*, o *Actinomycesradicidentis*, que estava relacionado com um caso de insucesso terapêutico. O mesmo se deu com o *Treponemadenticola*, localizado em infeções endodônticas (20).

A microscopia eletrónica também é uma técnica que permite a observação de cocos e de fungos no forame apical (21).

Técnicas como a eletroforese em gel por gradiente de desnaturação (DGGE), e o polimorfismo no comprimento de fragmentos de restrição (T-RFLP), também têm sido empregues com eficácia para identificar as comunidades microbianas. A hibridização por fluorescência *in situ* (FISH) pode quantificar a abundância de espécies e determinar a sua distribuição espacial nos tecidos. Entre outras aplicações, os micros e macro ensaios de hibridização DNA-DNA, PCR espécie-específica, nested PCR, Multiplex PCR, e real-time PCR são técnicas que podem ser utilizadas para avaliar um grande número de amostras clínicas por comparação com várias espécies alvo.

O CheckerboardDNA – DNAhybridization é uma técnica molecular que permite a identificação de uma grande variedade de espécies bacterianas de várias amostras clínicas. Esta técnica tem sido utilizada com sucesso no estudo da microbiota da saliva, na placa supragengival, placa subgengival, tecidos moles orais, implantes e infeções endodônticas (22), (23), (24), (35), (26), (27), (28).

As infeções endodônticas apresentam uma natureza polimicrobiana com um evidente predomínio de bactérias anaeróbias estritas, principalmente nas infeções primárias, independentemente da metodologia adotada. A composição da microbiota pode variar entre indivíduos, entre os tipos de infeção, se primária ou secundária, de acordo com o tempo de infeção, de acordo com o quadro clínico e ainda de acordo com a localização geográfica (28).

Métodos de cultura e de biologia molecular têm coletivamente revelado a natureza polimicrobiana das infeções endodônticas, com um evidente predomínio de bactérias anaeróbias estritas principalmente nas infeções primárias. Entretanto, outros tipos de microrganismos também foram identificados em menor quantidade nas infeções endodônticas.

Fungos, particularmente espécies de Cândida, foram encontrados em infeções primárias (29) (30) (31) (32). Archeias, e procariotas diferentes das bactérias também foram identificadas no SCR de dentes portadores de lesões peri-radiculares crônicas primárias (33) (34).

A presença de vírus no SCR foi descrita em dentes vitais de pacientes portadores da SIDA, evírus herpes foi identificado em lesões peri-radiculares tendo sido implicados na etiopatogenia das lesões peri-radiculares, seja através de um mecanismo de ação direta da infeção viral, seja através de um mecanismo indireto reduzindo as defesaslocais e favorecendo a proliferação bacteriana na porção mais apical do canal radicular (35) (21).

1.1.3 Proteoma em Infeções endodônticas

As infeções endodônticas são muito prevalentes e tem etiologia polimicrobiana complexa, justificando-se a utilização de tecnologias como a proteómica e a metaproteómica no sentido de caracterizar as proteínas presentes e cuja identificação possa contribuir para o esclarecimento dos mecanismos de patogenicidade presentes, bem como o papelde interações multifatoriais existentes entre as bactérias dos canais radiculares (36).

Um estudo realizado utilizou a espectrometria de massa acoplada a cromatografia líquida (LC-MS / MS) para a identificação de proteínas de origem bacteriana presente nas infeções endodôntia (36). Verificou-se neste estudo que as proteínas eram da parede celular de espécies bacterianas como: *Enterococcus faecalis, Enterococcus faecium, Porphyromonas gingivalis, Fusobacterium nucleatum, e Treponema denticola*. As proteinas identificadas incluíram adesinas, autolisinas, proteases, fatores de virulência, e proteínas de resistência a antibióticos.

É óbvio que as proteínas identificadas neste estudo representam apenas uma fração do universo possível presente, uma vez que o estudo tinha como limitação o pequeno tamanho da amostra e o facto de que os genomas de muitas bactérias orais não estarem ainda totalmente anotados. No entanto estes resultados fornecem uma nova avenida para caracterizar diretamente as proteínas associadas à virulência comumente presentes em infecções endodônticas, e assim permitir fazer uma caracterização das espécies patogênicas nesta patologiao que pode levar a melhores estratégias de tratamento (36).

A análise do metaproteoma de comunidades microbianas é importante para fornecer uma visão da fisiologia e patogenicidade.

Estudos mais recentes avaliaram o metaproteoma de infeções endodônticas associadas a abcessos agudos e lesões de periodontite apical assintomática. Nesta base foram avaliadas as proteínas expressas ou persistentes após tratamento endodôntico (37).

A grande maioria das proteínas microbianas encontradas em amostras de endodôntia foi relacionada com processos metabólicos incluindo processos de síntese de proteínas, metabolismo energético e processos de síntese de DNA. Além disso, várias outras proteínas relacionadas com a patogenicidade e resistência / sobrevivência foram encontradas, incluindo as proteínas envolvidas na adesão, formação de biofilme e de resistência a antibióticos, proteínas de stress, exotoxinas, invasinas, proteases e endopeptidases (principalmente nos abscessos), e uma proteína de archaea ligada à produção de metano.

Contudo são necessários novos estudos que esclareçam os mecanismos envolvidos na associação desta patologia com o proteoma oral e para isso o diagnóstico do fluido crevicular e da saliva tornam-se essenciais para a identificação das proteínas presentes em situações distintas de patologia endodontica.

1.1.4 Relação da Endodontia com outras patologias como a doença periodontal

Os problemas pulpares e periodontais são responsáveis por mais de 50% das perdas dentárias (40).

A associação de tais patologias origina lesões endoperiodontais. A relação entre as doenças endodôntica e periodontal tem em comum a causa de processos de destruição tecidual que se inicia no ápice dentário e segue para a região da gengiva marginal. Estas doenças têm sido estudadas isoladamente, sendo que cada uma delas quando designadas de primárias pode simular as carateristicas uma da outra. Isto ocorre em função dos tecidos pulpar e do ligamento periodontal uma vez que possuem a mesma natureza embrionária, ou seja, mesenquimal, conferindo semelhanças durante as agressões.

Posto isto deverá ser feito um correto diagnóstico destas lesões. Os fatores etiológicos, em especial da microbiota desempenham um papel muito importante no desenvolvimento e progressão destas doenças (76).

1.1.5 Resposta imune

A nível geral a resposta imune tem papel fundamental na defesa contra agentes infeciosos e constitui o principal impedimento para a ocorrência de infeções disseminadas, habitualmente associadas com alto índice de mortalidade. É também conhecido o facto que para a quase totalidade das doenças infeciosas, o número de indivíduos expostos à infeção é bem superior ao dos que apresentam doença, indicando que a maioria das pessoas tem condições de destruir esses microorganismos e impedir a progressão da infeção. Em contraste, as deficiências imunológicas, sejam da imunidade inata (disfunções de células fagocíticas e deficiência de complemento) ou da imunidade adaptativa (deficiência de produção de anticorpos ou deficiência da função de células T), são fortemente associadas com aumento de susceptibilidade a infeções (42).

Na endodontia a infeção periapical está relacionada com a virulência e com as combinações de microorganismos presentes nos tecidos periapicais. Foram identificadas bactérias nos tecidos perirradiculares inflamados as quais são eliminadas por mecanismos de defesa do hospedeiro aquando da instrumentação mecânica, irrigação antisséptica e medicação intracanalar.

A infeção primária em canais radiculares não tratados é uma mistura de polimicrobiana de espécies gram-positivas e gram negativas denominada por anaérobios estritos. Neste sentido, quando a polpa está infetada muitas células da imunidade inata libertam quantidades elevadas de diversos mediadores inflamatórios incluindo citosinas, quimiocinas, neuropeptideos. À medida que a inflamação pulpar se espalha os mediadores inflamatórios começam a atuar e a fisiologia dos tecidos periapicais reagem com alargamento do espaço do ligamento periodontal devido área absorção óssea.

A reabsorção óssea é induzida pela inflamação nos tecidos periapicais e é acompanhada pelo recrutamento das células do sistema imunológico que constituem uma linha de defesa contra a invasão microbiana a partir do canal radicular.

Esta patologia envolve também resposta imune inata adaptativa, assim como resposta nervosa sensorial nos tecidos periapicais. As células do sistema imunológico presentes nestas lesões em seres humanos consistem em leucócitos, macrófagos, plasmócitos, neutrófilos e células natural Killer (NK) sendo a maioria dos dois primeiros tipos celulares (40).

Alguns destes tipos celulares como os neutrófilos têm ação microbicida fundamental contra bactérias; os macrófagos são células importantes na defesa contra agentes intracelulares (protozoários e bactérias intracelulares); e os eosinófilos, não tanto pela atividade fagocítica, mas pela atividade citotóxica contra parasitas. A resposta mediada pelas células T é extremamente efetiva no mecanismo de defesa contra agentes intracelulares, como vírus, protozoários, fungos e bactérias intracelulares. As células T podem exercer sua função através da citotoxicidade mediada por células CD8+ ou através da secreção de citocinas que vão ativar macrófagos para destruir os agentes intracelulares (43).

1.1.6 Fluido Crevicular na patologia endodôntica

O fluido crevicular é um exsudado originário do plasma sanguíneo que passa para a gengiva através do epitélio juncional e que banha o sulco gengival e flui ao longo dos dentes. A difusão do fluido gengival em indivíduos saudáveis é baixa, mas aumenta durante situações de inflamação.

A composição do fluido crevicular é similar ao plasma e contém proteínas, leucócitos, anticorpos, interleucinas, complemento, fatores de crescimentos e hormonas (38).

Este é composto principalmente por eletrólitos sanguíneos e moléculas orgânicas como, albumina, globulinas, lipoproteinas ou fibrogénio e componentes celulares. Além disso o fluido crevicular também contêm péptidos, bactérias e enzimas e enzimas (86).

Um estudo recente teve como objetivo investigar os níveis de metaloproteinase de matriz-8 (MMP-8) e substância P (SP) recorrendo a amostras do fluido crevicular gengival (GCF) durante o tratamento endodôntico (RCT) de dentes não vitais, em que foi verificado que a inflamação perirradicular de origem endodôntica pode elevar os níveis de SP e MMP-8 no GCF (39).

1.1.7 Saliva como fluido diagnóstico

Com os avanços significativos em espetrometria de massa e tecnologias associadas aos estudos de proteómica, a descoberta de biomarcadores tem-se tornado uma das suas principais aplicações (41).

A possibilidade de monitorização de estados de saúde bem como do surgimento, progressão e prognóstico de doenças, através de meios não invasivos é um dos grandes objetivos no que toca à promoção e cuidados de saúde oral (57).

Uma grande barreira na utilização da saliva como fluido diagnóstico tem sido a noção de que elementos informativos (analitos) se encontram em menores quantidades na saliva do que no soro. Com o desenvolvimento de novas e mais sensíveis técnicas de análise, no entanto, a pequena quantidade de analitos na saliva, deixou de ser uma limitação, com a possibilidade de quase todos os elementos passíveis de serem encontrados numa análise sanguínea, poderem-no ser igualmente na saliva. Assim, a capacidade de deteção de doenças quer orais como sistémicas a partir de análises salivares tem sido demostrada nos últimos anos para várias patologias, nomeadamente, cancro oral, Síndrome de Cushing, HIV 1 e 2 e Hepatites virais tipo A, B e C (58).

Enquanto fluido de diagnóstico a saliva oferece bastantes vantagens em comparação com o soro podendo ser recolhida de forma não-invasiva por indivíduos não especializados, facilmente armazenada e transportada, e oferecendo um custo-benefício favorável na recolha de quantidades suficientes para análise (65).

Para além disso, a recolha salivar está associada a um risco mínimo de infeções, podendo ser efetuada até em situações mais complicadas, como em crianças não cooperantes ou pacientes ansiosos, nos quais a recolha de sangue pode ser de difícil execução (65).

Nas últimas duas décadas várias técnicas que utilizam saliva como fluido de diagnóstico foram utilizadas para a avaliação do risco dos pacientes para determinadas doenças, entre as quais, como a doença periodontal e a cárie dentária (66).

Espera-se que a curto prazo este seja também uma ferramenta de diagnóstico com aplicação na patologia endodôntica.

1.2 Ferramentas bioinformáticas

A pesquisa e coleção de dados de proteomas e de genomas humano e microbiano em diversas situações clinicas presente nas infeções endodônticas levou à necessidade de desenvolver novos métodos de integração e análise de dados que permitissem identificar os mecanismos alterados na doença e as interações das proteínas produzidas pelos microrganismos presentes na patologia endodontica com as proteínas humanas.

As proteínas orais estudadas ao longo deste trabalho são o produto genético dos organismos que as produzem e são elas que regulam a maioria dos processos biológicos.

Neste contexto as ferramentas bioinformáticas em articulação com as bases de dados têm um papel muito importante na análise de dados estudados.

O ***OralCard*** é uma ferramenta bioinformática dedicada à investigação científica em Saúde Oral. Esta ferramenta resulta da parceria do Departamento de Ciências da Saúde da Universidade Católica Portuguesa com o grupo de Bioinformática da Universidade de Aveiro.
Esta ferramenta criada após o projeto ***OralOme*** que compila toda a informação sobre o proteoma oral, permite analisar e integrar os dados do ***OralOme***, contribuindo para a elucidação da biologia oral e para o desenho de estratégias para a identificação de biomarcadores de patologias orais e sistémicas.
Encontra-se disponível em http://bioinformatics.ua.pt/OralCard/ e está subdividido em 3 bases diferentes que se podem aceder através da pesquisa pelos nomes das proteínas salivares (código Uniprot), pelo nome da doença (termo MeSH da doença) e pelo organismo especifico.

Funciona assim como um recurso chave para os investigadores da área a compreender a função molecular implicada na biologia dos mecanismos das diversas patologias da cavidade oral (45).

A ferramenta bioinformática ***Panther***, permite a obtenção de informação acerca de um gene de interesse; explorar famílias de proteínas, funções moleculares, processos biológicos, componentes celulares e vias de sinalização (47). Permite com isto, essencialmente fazer uma análise funcional das proteínas em estudo.

O **Oralint** é um algoritmo que permite determinar PPI´s (interações proteína – proteina) entre espécies distintas. Pode ser usado para determinar as interações entre as proteínas humanas e microbianas, e identificar desta forma possíveis mecanismos de virulencia (46).

Cytoscape, software para a integração, visualização e análise de redes biológicas (51).

UniProt, repositório de proteínas que mantém as suas sequências primárias e armazena outro tipo de informação como, aspetos funcionais e informação taxonómica (48).

Uma vez que a patologia endodôntica afeta um grande número de pessoas em todo o mundo, torna-se importante esclarecer os mecanismos biológicos e moleculares envolvidos, permitindo uma posterior identificação de potenciais proteínas biomarcadoras que permitam identificar a potencial suscetibilidade à doença. Desta forma, poderão ser desenvolvidos novos métodos de diagnóstico, bem como de tratamento e prevenção da patologia endodôntica.

2. Objetivos

2.OBJETIVOS

A realização do presente trabalho tem como base a catalogação de toda a informação relativa às proteínas identificadas como estando presentes e alteradas em estudos de proteómica de amostras de indivíduos com patologia endodôntica, bem como a sua catalogação.

Deste modo, foram objectivos deste trabalho:

1. Efetuar a revisão da literatura dedicada a estudos de proteómica ou estudos dirigidos que identificam as proteínas humanas e as microbianas presentes na cavidade oral em pacientes com patologia endodôntica em diferentes condições clinicas;
2. Com a catalogação da informação recolhida em 1) será atualizada a base de dados OralOme criando-se uma nova sessão dedicada às proteínas humanas e microbianas identificadas em doença endodontica;
3. Estudo *in silico* por recurso a diferentes ferramentas bioinformáticas visando a caracterização de aspectos funcionais associados às proteínas humanas identificadas como estando alteradas no proteoma oral da patologia endodôntica;
4. Comparação das várias proteínas envolvidadas na patologia endodôntica com outras patologias como a doença periodontal e gengivite.
5. Estabelecer o interactoma estabelecido entre as proteínas humanas e as do microbioma presente na patologia endodôntica, visando a identificação de potenciais mecanismos moleculares comprometidos na doença endodontica.

3. Materiais e Métodos

3. MATERIAIS E MÉTODOS

Esta secção inclui todas as metodologias realizadas no decurso do presente trabalho de modo a atingir os objetivos propostos.

3.1 Proteoma humano e microbiano em patologia endodôntica

De modo a fazer a catalogação das proteínas humanas e microbianas identificadas na cavidade oral de pacientes com patologia endodôntica em diferentes condições clínicas e anotar a informação relevante para a interpretação destes dados foram seguidos os procedimentos descritos abaixo.

3.2 Obtenção da listagem de Proteínas

Foi realizada uma pesquisa bibliográfica com recurso à ferramenta de pesquisa avançada do portal PubMed, usando como palavras-chave os termos Mesh (*Medical Subject Headings*): “endodontic infections”, “crevicular fluid”, ”salivar diagnosis”, “proteomics”, “oral microbiome”, ”immune response”. Foram incluídos os artigos com resultados experimentais referentes a espécies microbianas e *Homo sapiens* com data de publicação até 2016. A seleção de artigos a analisar incluiu os resultados experimentais de estudos de proteómica a nível da cavidade oral. Foram excluídos artigos que não fossem referentes à patologia endodôntica ou estudos experimentais com amostras não provenientes da cavidade oral de pacientes pertencentes à espécie *Homo sapiens*.

3.2.1 Anotação manual da informação de proteínas da patologia endodôntica

A análise de cada um dos estudos experimentais permitiu anotar manualmente uma série de informações consideradas essenciais para a interpretação dos dados catalogados. Esta inclui dados de identificação de cada uma das proteínas, o local de obtenção da amostra, a relação de cada proteína com os estados de saúde e de doença, a caracterização do dador da amostra, a caracterização dos métodos de amostragem e de análise, bem como a presença de modificações pós-tradução associadas a cada proteína (Figura 1). Esta informação pode ser igualmente útil em casos onde seja necessário realizar uma análise comparativa de discrepâncias de resultados de estudos.

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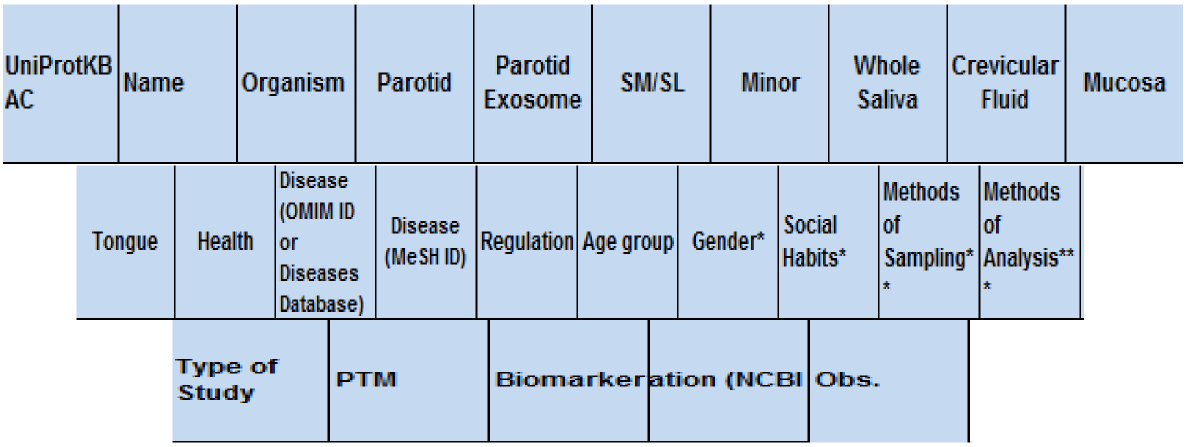


UniProtKB AC	Name	Organism	Parotid	Parotid Exosome	SM/SL	Minor	Whole Saliva	Crevicular Fluid	Mucosa

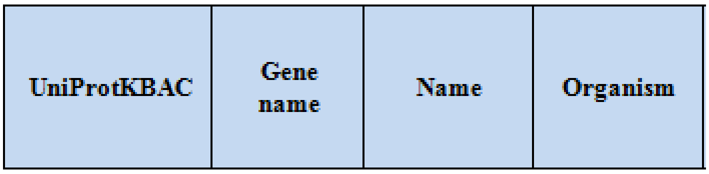
Tongue	Health	Disease (OMIM ID or Diseases Database)	Disease (MeSH ID)	Regulation	Age group	Gender*	Social Habits*	Methods of Sampling**	Methods of Analysis***

Type of Study	PTM	Biomarker	ation (NCBI	Obs.

Figura 1: Cabeçalhos que permitem a organização da informação recolhida dos diferentes estudos de proteómica da cavidade oral (proteínas associadas á patologia anotadas manualmente) numa tabela em Microsoft Excel 2010.

3.2.2 Identificação das proteínas da cavidade oral em patologia endodôntica

A primeira abordagem no registo das proteínas da cavidade oral foi a sua identificação (Figura 2).



UniProtKBAC	Gene name	Name	Organism

Figura 2: Cabeçalhos das colunas da base de dados do proteoma oral em patologia endodôntica referentes à identificação de cada proteína.

A cada proteína foi atribuído o seu código de identificação universal (UniProtKB), através da pesquisa e seleção na base de dados online *UniProt* (48) (http://www.uniprot.org/) (Figura 3).

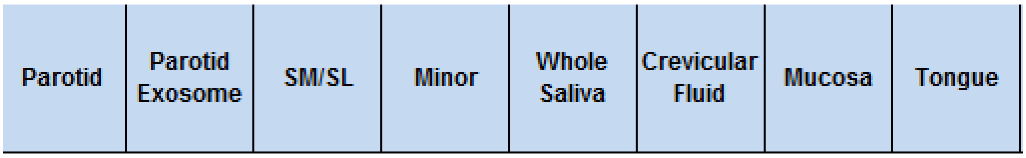
☐	Entry	Protein names	Entry name	Gene names	Organism
☐	Q99714	3-hydroxyacyl-CoA dehydrogenase typ...	HCD2_HUMAN	**HSD17B10** ERAB,HADH2,MRPP2,SCHAD,SDR5C1	Homo sapiens (Human)
☐	Q03393	6-pyruvoyl tetrahydrobiopterin synt...	PTPS_HUMAN	**PTS**	Homo sapiens (Human)
☐	P11021	78 kDa glucose-regulated protein	GRP78_HUMAN	**HSPA5** GRP78	Homo sapiens (Human)
☐	Q96QF7	Acidic repeat-containing protein	ACRC_HUMAN	**ACRC**	Homo sapiens (Human)
☐	A6NL76	Actin, alpha skeletal muscle	A6NL76_HUMAN	**ACTA1**	Homo sapiens (Human)
☐	C9JUM1	Actin, cytoplasmic 1	C9JUM1_HUMAN	**ACTB**	Homo sapiens (Human)
☐	F8SVK3	Cytoplasmic actin	F8SVK3_9METZ		Tethya wilhelma
☐	P63261	Actin, cytoplasmic 2	ACTG_HUMAN	**ACTG1** ACTG	Homo sapiens (Human)
☐	Q9UJY4	ADP-ribosylation factor-binding pro...	GGA2_HUMAN	**GGA2** KIAA1080	Homo sapiens (Human)

Figura 3: Exemplo ilustrativo da visualização do site da UniProt durante a atribuição do código UniProtKb AC, nome e organismo a uma determina da proteína.

Utilizando a plataforma UniProt, obtivemos dados importantes para a caracterização da proteina: com base no nome da(s) proteína(s) recolhido durante a fase de análise bibliográfica, obtivemos as informações referentes ao código de entrada da base de dados, nome do gene associado e organismo correspondente.

3.2.3 Origem das proteínas orais da patologia endodôntica

As possíveis origens das proteínas orais anotadas são as glândulas parótidas, o exossoma da glândula parótida, glândulas submandibulares e sublinguais, glândulas minor, fluído crevicular, mucosa oral, saliva total e língua (Figura 4).

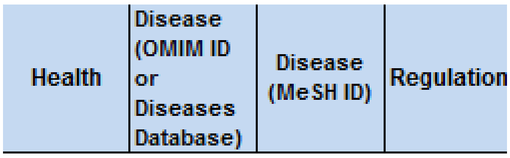


Parotid	Parotid Exosome	SM/SL	Minor	Whole Saliva	Crevicular Fluid	Mucosa	Tongue

Figura 4: Cabeçalho da base de dados OralOme relativa à origem das proteínas da patologia endodôntica.

3.2.4 Relação com os estados de saúde e de doença

A anotação da relação das proteínas da patologia endodôntica com os estados de saúde ou doença permite inferir se as proteínas em análise estão presentes exclusivamente em indivíduos saudáveis, se apenas são produzidas ou estão presentes em indivíduos com uma determinada patologia (neste caso, patologia endodôntica) ou se estão presentes em ambos os casos. Para identificar a patologia foi anotado o seu OMIM ID (*Online Mendelian Inheritance in Man*) e o seu código MESH que no caso da doença endodotica é indicado por D004708 (Figura 5).



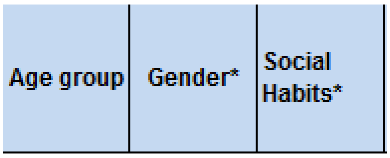
Health	Disease (OMIM ID or Diseases Database)	Disease (MeSH ID)	Regulation

Figura 5: Cabeçalho da base de dados OralOme referente à relação das proteínas anotadas da patologia endodôntica com os estados de saúde e doença.

Os artigos utilizados no presente trabalho não forneceram dados de quantificação das proteínas.

3.2.5 Caraterização do dador da amostra analisada

A caracterização do dador da amostra inclui a sua faixa etária, género e hábitos sociais (por exemplo o tabagismo), uma vez que estes fatores podem ser modificadores da expressão das proteínas nos indivíduos. Os critérios de exclusão definidos pelos autores de cada estudo analisado foram igualmente anotados (Figura 6).

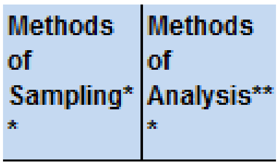


Age group	Gender*	Social Habits*

Figura 6: Cabeçalho do OralOme referente à caracterização do dador da amostra.

3.2.6 Métodos de amostragem e análise

Os métodos de amostragem e análise permitem caracterizar a metodologia utilizada na colheita, na identificação e na análise das proteínas da cavidade oral. Esta informação é essencial para interpretar dados de proteómica uma vez que se sabe que diferentes técnicas de amostragem ou diferentes metodologias de análise permitem identificar diferentes proteínas (Figura 7).



Methods of Sampling**	Methods of Analysis***

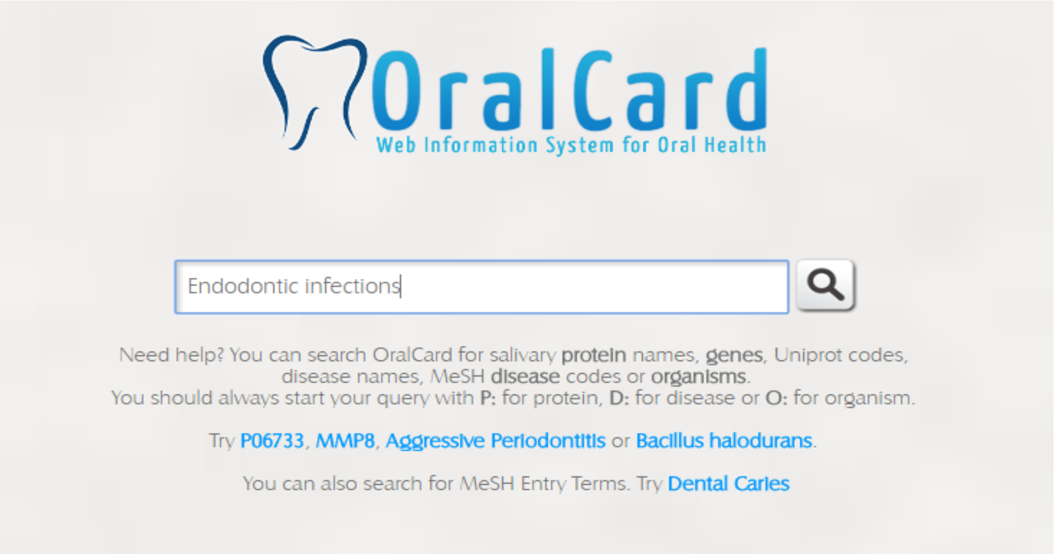
Figura 7: Cabeçalho do OralOme referente aos métodos de amostragem e análise das proteínas associadas á patologia endodôntica.

3.2.7 Outras informações

Foram ainda anotadas informações acerca do tipo de estudo, presença de modificações pós-tradução nas proteínas identificadas e sugestão do autor do estudo, para que a proteína possa ser utilizada como biomarcador da patologia.

3.2.8 Atualização do OralCard

Numa segunda fase, depois da anotação manual, procedeu-se à atualização da base de dados OralOme/OralCard (52) (Figura 8), disponibilizando-se à comunidade científica a lista de proteínas humanas e microbianas presentes na cavidade oral como estando associadas à patologia endodôntica.



OralCard
Web Information System for Oral Health

Endodontic infections

Need help? You can search OralCard for salivary **protein** names, **genes**, Uniprot codes, disease names, MeSH **disease** codes or **organisms**.
You should always start your query with **P:** for protein, **D:** for disease or **O:** for organism.

Try P06733, MMP8, Aggressive Periodontitis or Bacillus halodurans.

You can also search for MeSH Entry Terms. Try Dental Caries

Figura 8: Home Page da página web do OralCard (http://bioinformatics.ua.pt/OralCard/home)

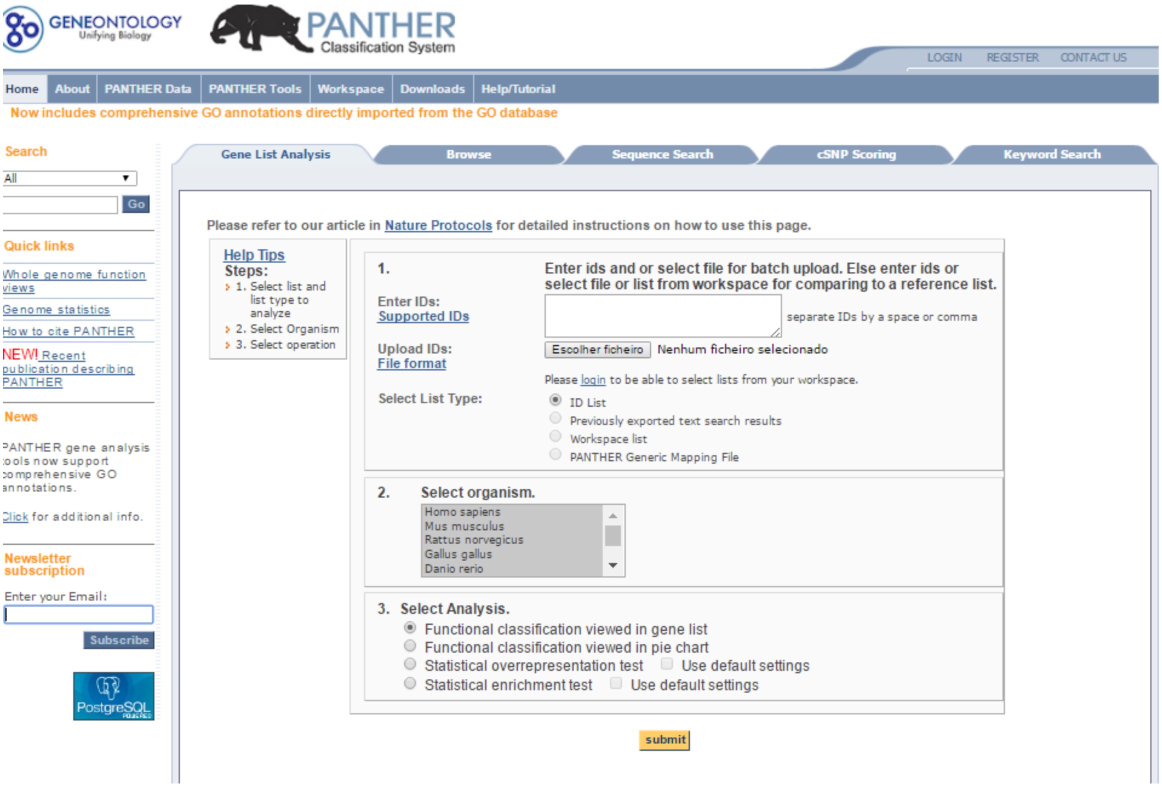
3.3 Caraterização funcional das proteínas orais em Patologia endodôntica

De modo a conseguir alcançar os objetivos deste trabalho procedeu-se a uma análise *in silico* com recurso a diferentes ferramentas bioinformáticas para uma caraterização dos aspetos funcionais associados às proteínas identificadas como estando alteradas no proteoma oral da patologia endodôntica.

3.3.1 Caracterização funcional com a ferramenta PANTHER

Com o objetivo de compreender o papel fisiológico das proteínas orais humanas presentes em patologia endodôntica, estas foram classificadas funcionalmente de acordo com a sua ontologia, nomeadamente no que concerne ao processo biológico em que intervêm, e a função molecular que desempenham. Esta classificação foi realizada com recurso à ferramenta *online* *PANTHER* (*Protein ANalysis THroughEvolutionary Relationships*) (http://pantherdb.org/) (Figura9). (53,54). São múltiplas as funcionalidades do *PANTHER* fundamentais no desenvolvimento deste trabalho, nomeadamente: obter informação organizada sobre uma proteína de interesse; explorar famílias de proteínas, funções moleculares, processos biológicos, componentes celulares e vias de sinalização; gerar listas de proteínas que pertencem a determinadas famílias ou subfamílias, de acordo com a sua função molecular, participação em processo (s) biológico(s) ou via(s) de sinalização; analisar listas de genes, proteínas ou transcritos de acordo com categorias baseadas na família, função molecular, processo biológico, componente celular e/ou via de sinalização.

Para compreender a distribuição das proteínas identificadas em patologia endodôntica pelas diferentes ontologias, recorreu-se à ferramenta de classificação funcional do *Panther*.



Now includes comprehensive GO annotations directly imported from the GO database

PANTHER gene analysis tools now support comprehensive GO annotations.

Click for additional info.

Please refer to our article in Nature Protocols for detailed instructions on how to use this page.

Steps:
- 1. Select list and list type to analyze
- 2. Select Organism
- 3. Select operation

1. Enter ids and or select file for batch upload. Else enter ids or select file or list from workspace for comparing to a reference list.

Enter IDs: Supported IDs — separate IDs by a space or comma

Upload IDs: File format — Escolher ficheiro Nenhum ficheiro selecionado

Please login to be able to select lists from your workspace.

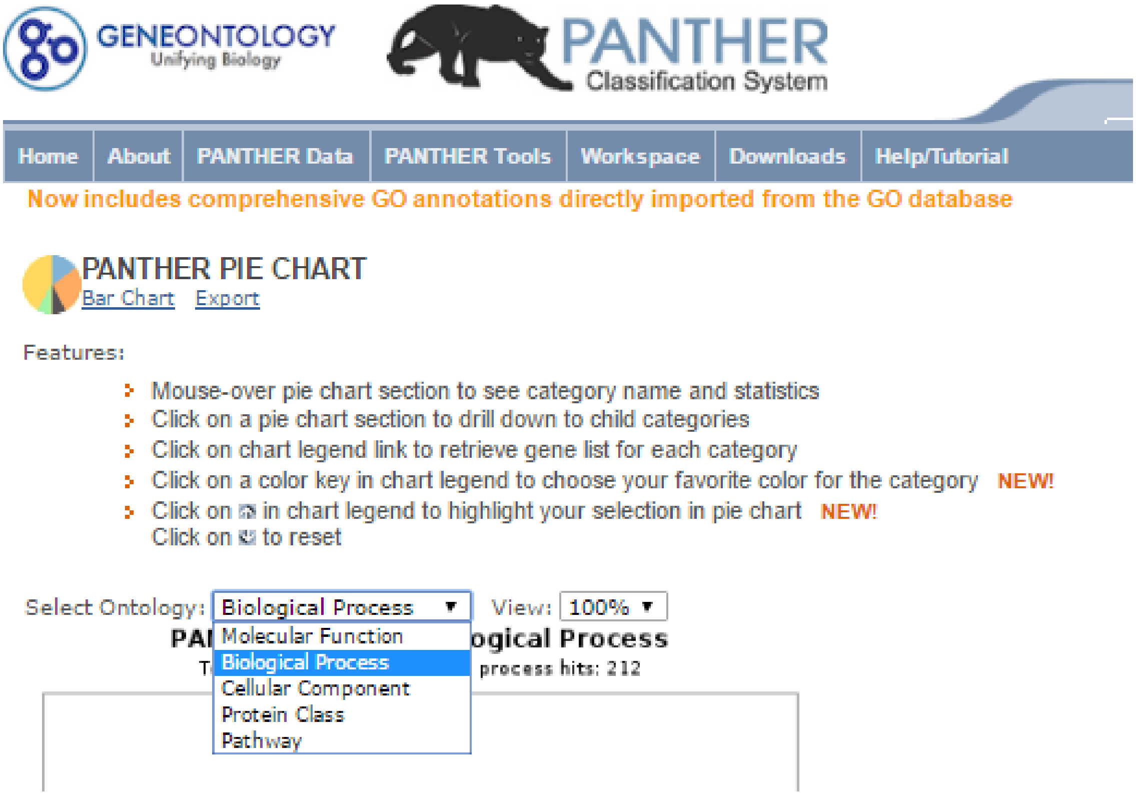
Select List Type:
● ID List
○ Previously exported text search results
○ Workspace list
○ PANTHER Generic Mapping File

2. Select organism.
Homo sapiens
Mus musculus
Rattus norvegicus
Gallus gallus
Danio rerio

3. Select Analysis.
● Functional classification viewed in gene list
○ Functional classification viewed in pie chart
○ Statistical overrepresentation test ☐ Use default settings
○ Statistical enrichment test ☐ Use default settings

Figura 9: Sistema de análise em grupo da ferramenta de classificação do PANTHER. As opções selecionadas correspondem às definições utilizadas para analisar os conjuntos de proteínas.

Inicialmente, inserem-se os códigos UniprotKB AC de identificação de proteínas anotadas, seleciona-se a espécie (humana) e o tipo de análise desejado, obtendo-se como resultado uma lista com uma série de informações acerca das proteínas inseridas. Posteriormente, escolhe-se o tipo de classificação desejado: segundo as funções moleculares, os processos biológicos, as vias de sinalização, classe proteica ou componentes celulares. (Figura10).



Now includes comprehensive GO annotations directly imported from the GO database

PANTHER PIE CHART

Features:

- Mouse-over pie chart section to see category name and statistics
- Click on a pie chart section to drill down to child categories
- Click on chart legend link to retrieve gene list for each category
- Click on a color key in chart legend to choose your favorite color for the category NEW!
- Click on ▨ in chart legend to highlight your selection in pie chart NEW!
  Click on ▨ to reset

Select Ontology: Biological Process ▼ View: 100% ▼

Figura 10: Seleção do tipo de classificação por ontologia desejado, na ferramenta PANTHER.

3.3.2 Comparação com o OralOma Normal

O objetivo desta análise foi determinar se as diferentes ontologias das proteínas orais em patologia endodôntica, resultantes da classificação obtida com recurso à ferramenta PANTHER, se encontravam acima ou abaixo dos valores esperados comparativamente ao verificado em indivíduos saudáveis (OralOma Normal). Para tal, cada lista de proteínas da patologia endodôntica classificada segundo uma determinada ontologia PANTHER (função molecular ou processo biológico) foi comparada com uma lista de referência (OralOma normal). Por cálculo de proporção direta, inferiu-se o valor espectável para cada uma das categorias caso se verificasse proporção direta entre as entidades comparadas.

Para quantificar a diferença entre os valores observados e os valores esperados para cada categoria, procedeu-se ao cálculo da diferença fracional, segundo a seguinte fórmula:

$$DF = \left(\frac{Z_t - \hat{Z}_t}{\hat{Z}_t}\right)$$

em que Zt representa o valor observado, $\hat{Z}t$ o valor esperado e DF a diferença fracional (metodologia adaptada do PANTHER O*verrepresentation Test).*

Assim, a diferença fracional consiste no valor cuja multiplicação pelo valor esperado traduz a fração que deveria ser adicionada ou subtraída ao valor observado para que este igualasse o valor teoricamente esperado.

Posteriormente foi aplicado um teste binominal, descrito por Cho & Campbell, TIGs, em 2000 (55), de forma a obter a significância estatística dos resultados expressa segundo um nível de significância (*p-value*). O “*p-value”* representa a probabilidade de erro envolvida em aceitar o resultado observado como válido, isto é, como representativo da “população”. Dizer que um resultado é estatisticamente significativo significa que as diferenças encontradas são grandes o suficiente para não serem atribuídas ao acaso, com uma certeza estabelecida.

A lista de referência (OralOma normal) derivou da base de dados do OralCard (http://bioinformatics.ua.pt/OralCard/)(56). Esta ferramenta bioinformática, em constante atualização, reúne os dados de proteómica salivar, provenientes de amostras de componentes da cavidade oral, identificados a partir de estudos experimentais, permitindo a caracterização das proteínas segundo o local de produção da proteína, a sua função molecular, a presença de modificações pós-tradução, a sua associação a doenças, entre outros. Para este trabalho, foi considerado o OralOma normal como o conjunto total de proteínas exclusivamente presentes na cavidade oral de indivíduos saudáveis e não identificadas em situação de patologia.

Nesta abordagem foram apenas utilizadas as classificações segundo os processos biológicos e funções moleculares.

De modo a conseguir resultados mais específicos para a patologia endodôntica, selecionou-se de todas as classificações obtidas, aquelas que segundo a análise são mais relevantes para a patologia.

1. Processos biológicos

2. Funções moleculares

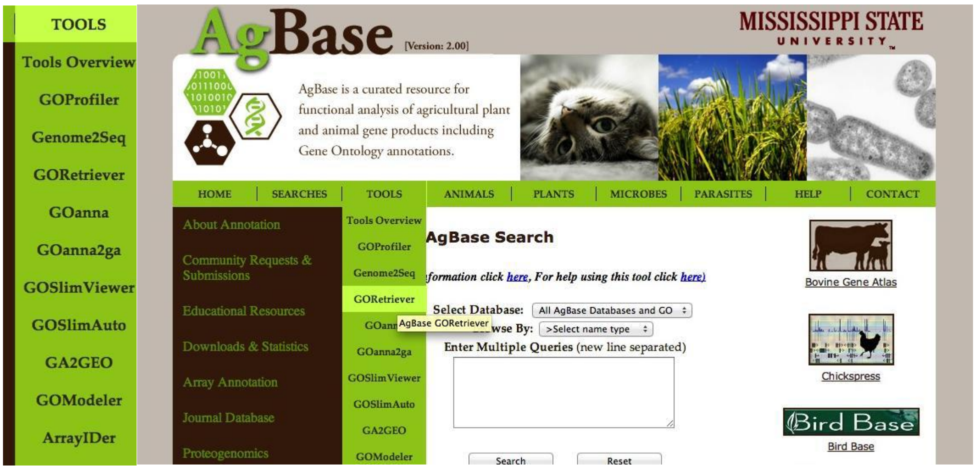
Ao saber em que processos biológicos e funções moleculares estão envolvidos cada proteína implicada na doença endodontica.

3.4 *Caraterização funcional das proteínas microbianas recorrendo ao AgBase*

No sentido de realizar uma caraterização funcional das proteínas microbianas, obtendo as ontologias génicas (GOs), recorreu-se à ferramenta online *AgBase* (http://www.agbase.msstate.edu/). Esta ferramenta, foi utilizada em substituição do PANTHER, pois apresenta um maior número de microrganismos identificados, permitindo uma análise mais completa.

O *AgBase* é uma plataforma *online* de recurso público, que permite a anotação funcional e estrutural de uma grande parte dos microrganismos presentes na cavidade oral. A sua base de dados inclui ferramentas computacionais para anotações de GOs (85).

A Figura 11 apresenta a página inicial do *AgBase*, onde se prossegiu para a ferramenta Tools e posteriormente para GORetrivier.



AgBase is a curated resource for functional analysis of agricultural plant and animal gene products including Gene Ontology annotations.

formation click here, For help using this tool click here)

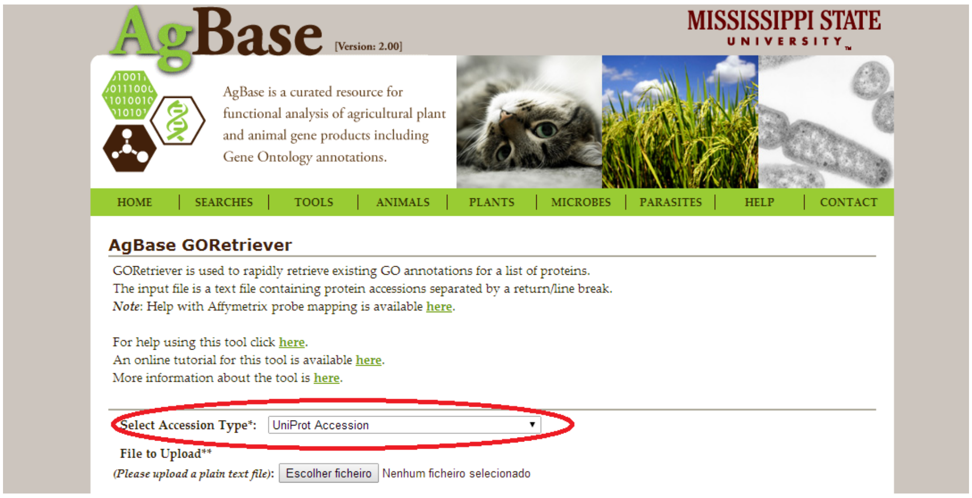
Select Database: All AgBase Databases and GO

Browse By: >Select name type

Enter Multiple Queries (new line separated)

Figura 11: Portal *AgBase* e seleção da ferramenta de classificação funcional GoRetriever (http://www.agbase.msstate.edu/).

Nesta ferramenta foi necessário o upload do ficheiro em formato TXT da lista de proteínas microbianas e escolher o tipo de acesso “*UniProt Accession*” (Figura 12), para submeter as proteínas à pesquisa.



AgBase is a curated resource for functional analysis of agricultural plant and animal gene products including Gene Ontology annotations.

AgBase GORetriever

GORetriever is used to rapidly retrieve existing GO annotations for a list of proteins.
The input file is a text file containing protein accessions separated by a return/line break.
Note: Help with Affymetrix probe mapping is available here.

For help using this tool click here.
An online tutorial for this tool is available here.
More information about the tool is here.

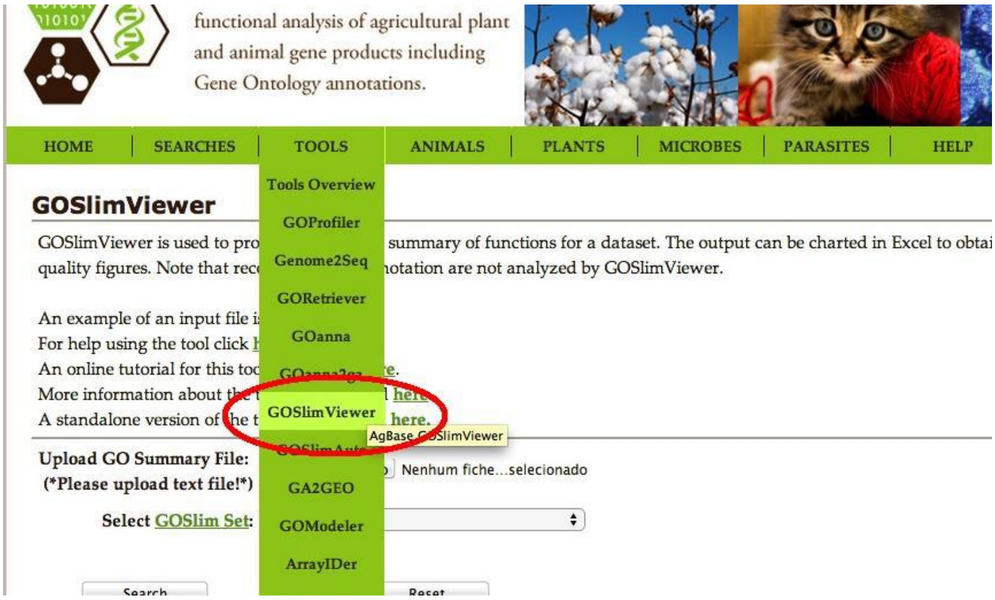
Select Accession Type*: UniProt Accession

File to Upload**
(Please upload a plain text file): Escolher ficheiro Nenhum ficheiro selecionado

Figura 12: Página web do AgBase e seleção do tipo de acesso na ferramenta de classificação funcional GoRetriever (http://www.agbase.msstate.edu/cgi-bin/tools/goretriever_select.pl)

De seguida selecionou-se a opção GoSummaryFile (for use in GOSlimViewer), onde se obteve um novo documento em formato texto, que para ser visualizado é necessário recorrer à ferramenta GoSlimViewer (Tools> GoSlimViewer).
Nesta ferramenta podémos observar os processos biológicos em que as proteínas microbianas estão envolvidas.

Todo o procedimento está exemplificado na Figura 13 e Figura 14.



GOSlimViewer

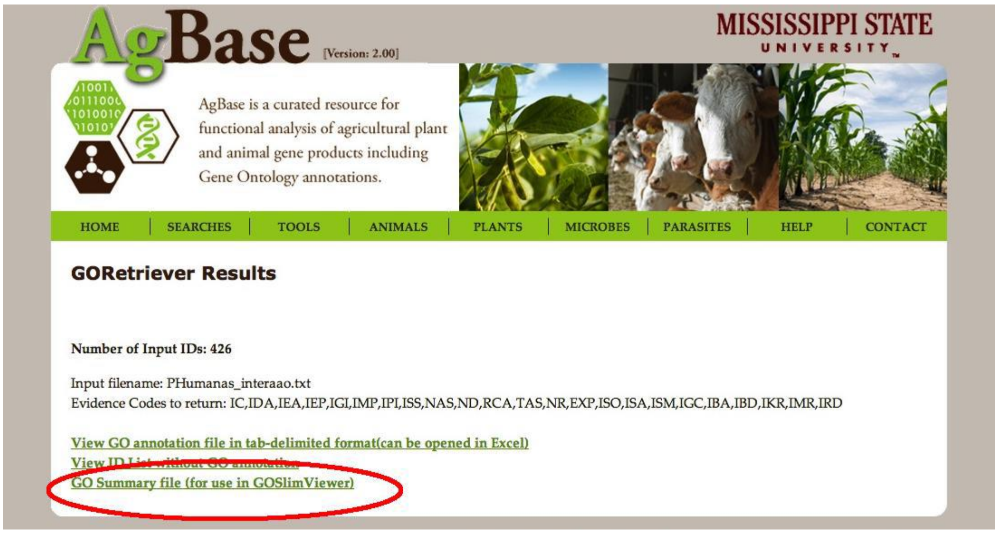
GOSlimViewer is used to pro summary of functions for a dataset. The output can be charted in Excel to obtai quality figures. Note that rec otation are not analyzed by GOSlimViewer.

An example of an input file i
For help using the tool click
An online tutorial for this to e.
More information about t l here
A standalone version of he t here.

Upload GO Summary File: Nenhum fiche...selecionado
(*Please upload text file!*)

Select GOSlim Set:

Figura 13: Ferramenta GoSlimViewer em que se submetem os resultados obtidos no GoRetriever através do GoSummary File no AgBase. (http://www.agbase.msstate.edu/cgibin/tools/goslimviewer_select.pl)



GORetriever Results

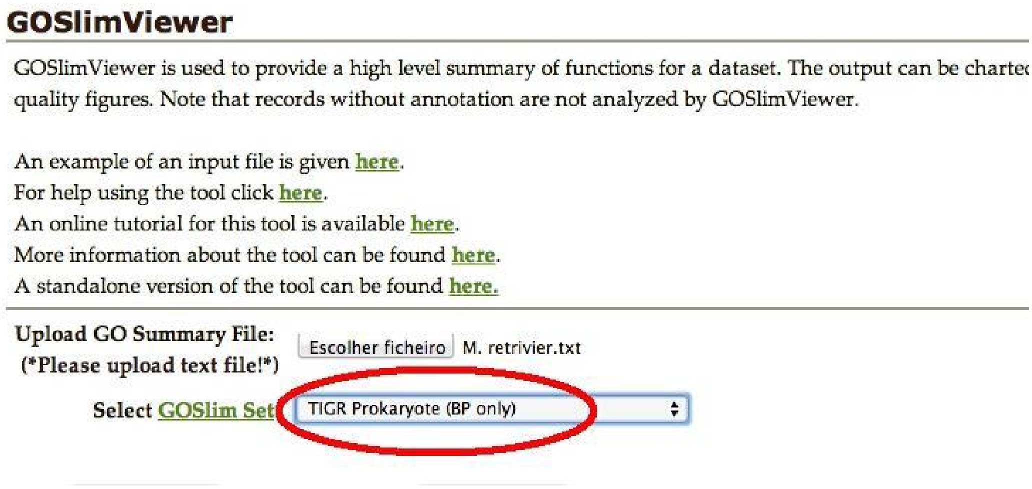
Number of Input IDs: 426

Input filename: PHumanas_interaao.txt
Evidence Codes to return: IC,IDA,IEA,IEP,IGI,IMP,IPI,ISS,NAS,ND,RCA,TAS,NR,EXP,ISO,ISA,ISM,IGC,IBA,IBD,IKR,IMR,IRD

View GO annotation file in tab-delimited format(can be opened in Excel)
View ID List without GO annotation
GO Summary file (for use in GOSlimViewer)

Figura 14: Portal do AgBase e demonstração da seleção do GoSummary file.
(http://www.agbase.msstate.edu/cgi-bin/tools/goretriever_select.pl)

Na ferramenta GoSlimViewer, *Select GOSlim Set,* a análise foi realizada utilizando a opção *TIGR Prokaryote (BP only)* para proteínas microbianas, de modo a eliminar GOs sem significado em organismos procariontes (por exemplo processos biológicos relativos a mitocôndria) (Figura 15).



GOSlimViewer

GOSlimViewer is used to provide a high level summary of functions for a dataset. The output can be charte
quality figures. Note that records without annotation are not analyzed by GOSlimViewer.

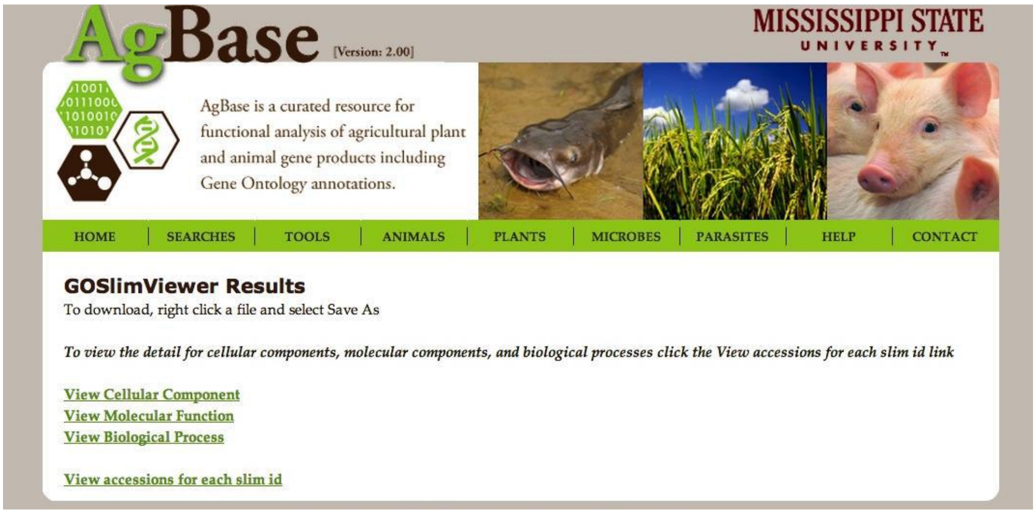
An example of an input file is given here.
For help using the tool click here.
An online tutorial for this tool is available here.
More information about the tool can be found here.
A standalone version of the tool can be found here.

Upload GO Summary File: (*Please upload text file!*) Escolher ficheiro M. retrivier.txt

Select GOSlim Set: TIGR Prokaryote (BP only)

Figura 15: Página web do AgBase e seleção do tipo de acesso na ferramenta de classificação funcional GoSlimViewer, para proteínas microbianas. (http://www.agbase.msstate.edu/cgi-bin/tools/goslimviewer_select.pl)

Obteve-se assim a listagem de processos biológicos em que as proteínas microbianas estão envolvidas (Figura 16).



AgBase is a curated resource for functional analysis of agricultural plant and animal gene products including Gene Ontology annotations.

GOSlimViewer Results

To download, right click a file and select Save As

To view the detail for cellular components, molecular components, and biological processes click the View accessions for each slim id link

View Cellular Component
View Molecular Function
View Biological Process

View accessions for each slim id

Figura 16: Ferramenta informática do *AgBase* e visualização dos resultados obtidos no GoSlimViewer. (http://www.agbase.msstate.edu/cgi-bin/tools/goslimviewer.pl)

A visualização de todos os processos biológicos que envolvem proteínas microbianas, será apresentada no capítulo dos RESULTADOS E DISCUSSÃO.

3.5 Relação com outras patologias

Com o propósito de perceber quais as proteínas exclusívas da patologia endodôntica, foi estabelecida uma relação de comparação com outras patologias que estão associadas à cavidade oral como:

1. **Periodontite crónica;**

2. **Gengivite;**

3. **Periodontite agressiva.**

Para isso, foi elaborada uma tabela para cada patologia com o Código UniprotKB AC, nome da proteína e organismo.

As proteínas anotadas para as patologias periodontite crónica, gengivite e periodontite agressiva foram identificadas a partir da base de dados do OralOma (52).

Esta representação foi feita com a ajuda de um diagrama de Venny (74) onde se fez a visualização das interações das 4 patologias.

3.6 Interactoma oral em Patologia endodôntica

Com o objetivo de compreender o interactoma oral (humano-microbioma) na patologia endodôntica realizou-se uma análise de interactómica, descrita abaixo.

O conjunto de proteínas do proteoma de patologia endodôntica, identificado pelos métodos acima descritos, foi posteriormente submetido a uma análise de interatómica, através do algoritmo *Oralint*. O ***Oralint*** é um algoritmo computacional que permitiu a previsão do interactoma oral. A principal inovação desta ferramenta é o facto de permitir determinar o interactoma interespecífico (humano-microbiano e microbiano-microbiano). Este algoritmo foi desenvolvido pelo grupo de Biomedicina Computacional e Diagnóstico em saliva do Instituto de Ciências da Saúde da UCP em parceria com o grupo de Bioinformática da Universidade de Aveiro e o Departamento de Engenharia Informática da Universidade de Coimbra. Uma das aplicações do conhecimento gerado consiste na identificação de proteínas-chave envolvidas em patologias orais, que podem ser utilizadas no diagnóstico (como biomarcadores moleculares) ou no tratamento (como alvos terapêuticos) (46).

Do total das interações obtidas, selecionaram-se as interações proteína-proteína (PPIs) com *score* igual ou superior a 0,9, limitando a análise a pares com nível elevado de confiança de existência da interação.

Para visualização e validação destas redes de interações recorreu-se à utilização da ferramenta *Cytoscape*, capaz de realizar a integração biomolecular de redes com diferentes dados (47).

4. Resultados e Discussão

4. Resultados e Discussão

4.1 Proteoma Humano e microbiano em patologia endodôntica

A identificação do proteoma oral de patologia endodôntica constitui um passo importante para a compreensão dos mecanismos biológicos e moleculares da patologia, permitindo uma posterior identificação de potenciais proteínas biomarcadoras para identificação da doença, sua monitorização e eventualmente para definição de estratégias para avaliação da suscetibilidade à doença. Adicionalmente o proteoma da doença endodôntica permite esclarecer os mecanismos moleculares que se encontram comprometidos nesta doença.

4.2 Obtenção da listagem de proteinas

A identificação das proteínas alteradas presentes na cavidade oral de pacientes com patologia endodôntica foi conseguida recorrendo a uma alargada pesquisa e análise de resultados de estudos abrangentes que recorrem a abordagens por proteómica. A análise dos resultados dos estudos abaixo referidos permitiu identificar as proteínas que se encontram alteradas em pacientes com patologia endodôntica e realizar estudos sobre os mecanismos moleculares que se encontram comprometidos nessas situações.

A pesquisa bibliográfica efetuada indica que até ao ano 2016 apenas foram identificados 2 artigos dedicados à identificação das proteínas em doença endodontica e esses artigos utilizaram como estratégia metodológica a proteómica. Os 2 artigos permitiram a identificação de 523 proteinas associadas a patologia endodôntica (figura 17). No anexo A e B são apresentadas as proteínas humanas e microbianas identificadas e a informação associada a cada proteína de acordo com os critérios necessários a cumprir para a sua inserção na base de dados OralOme/OralCard.

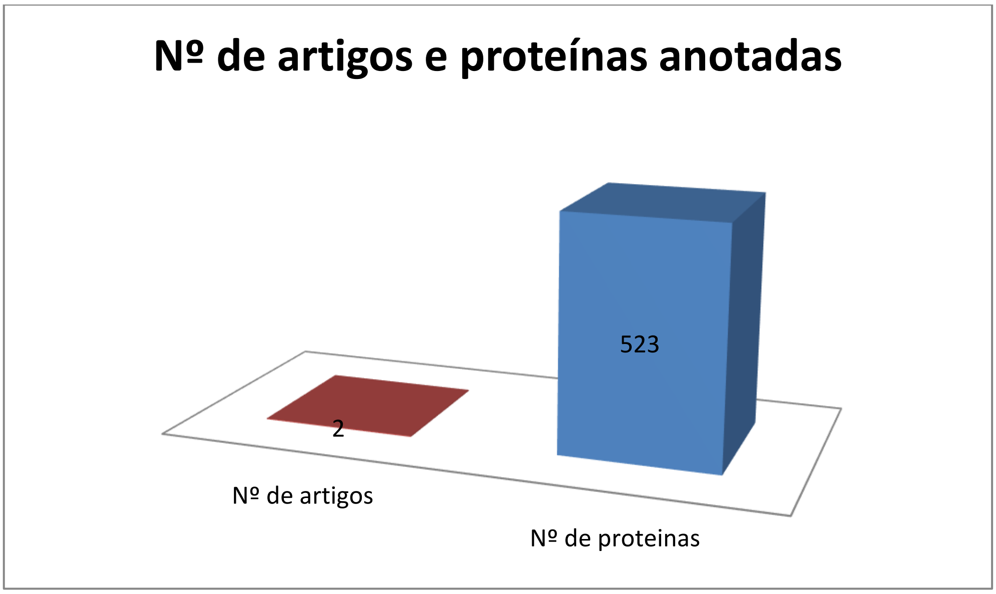


Figura 17: Número de artigos e de proteínas orais anotadas e catalogadas no OralCard identificadas na patologia endodôntica.

A figura 18 mostra que foram catalogas e anotadas no OralCard 523 proteínas para a patologia endodôntica das quais 138 (26%) são humanas, sendo que as restantes 385 (74%) são proteínas microbianas.

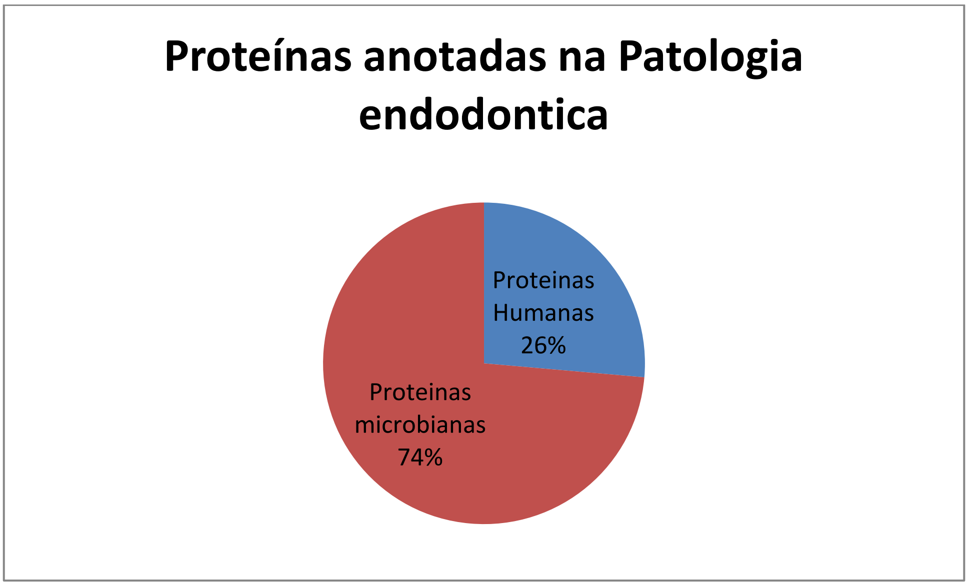


Figura 18: Percentagem de proteínas humanas e microbianas anotadas e catalogadas no OralCard e que foram associadas a patologia endodôntica.

4.2.1 Anotação manual de informação relativa às proteínas da patologia endodôntica

A anotação das proteínas caraterísticas da patologia endodontica conjuntamente com toda a informação associada a cada proteína (como descrito no Material e Métodos) permitiu criar uma nova seção na base de dados do *OralCard* (45) dedicada à doença endodôntica. A atualização da informação constante no OralCard com uma nova secção permitirá que esta base de dados se torne ainda mais robusta e permita estudos alargados de comparação dos perfis de proteínas que se encontram alteradas em diversas patologias da cavidade oral.

4.2.2 Origem das proteínas orais da patologia endodôntica

Dos estudos de proteómica analisados para a doença foram identificadas proteínas com origem em doentes com periodontite apical aguda, abcesso apical agudo, infeções do canal radicular e após tratamento endodôntico. (37)
A quando da anotação destas proteínas na base de dados *Oralcard* foi feita a distinção das várias condições clínicas no campo (*disease name*). (ANEXO A e B)

A análise da figura 19 indica que das 138 proteínas humanas identificadas para a patologia endodôntica, todas são provenientes de amostras de fluido crevicular. Ou seja estudos posteriores em fluido crevicular podem vir a ser importantes para a deteção de potenciais fatores patológicos e fisiológicos para o diagnóstico e tratamento da patologia endodôntica.

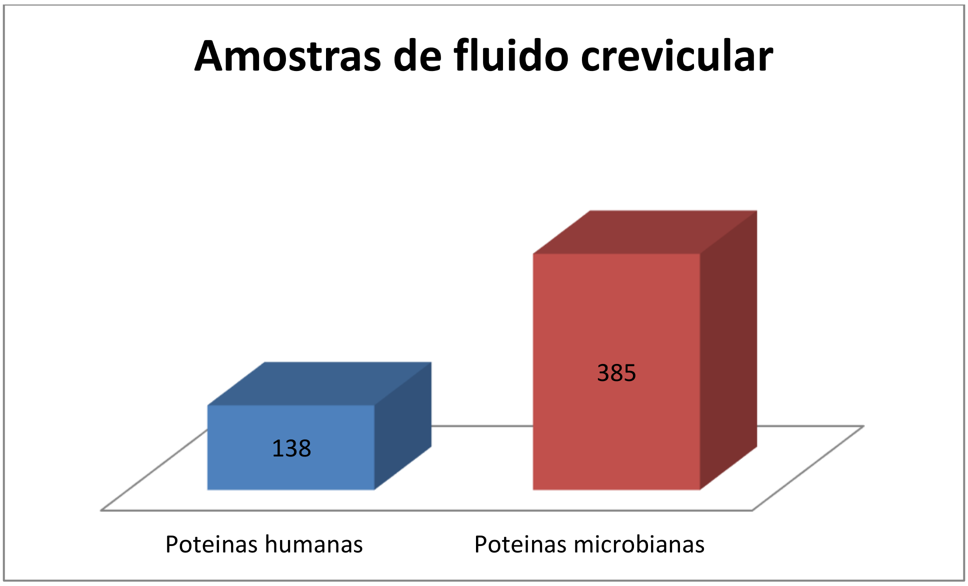


Figura 19: Gráfico que ilustra a origem das amostras das proteínas em estudo.

4.2.3 Relação com estados de saúde e de doença

O conjunto total de proteínas identificadas em estudos relacionados com patologia endodôntica permitiu estabelecer uma relação entre essas proteínas e outras proteínas que foram identificadas noutras patologias, recorrendo-se para o efeito ao OralOma total em estados de saúde.

A análise foi elaborada separadamente por proteínas humanas e microbianas.

4.2.3.1 Proteínas Humanas

A análise da figura 20 indica que existem 88 proteinas humanas exclusivas de doença endodontica e 171 em outras doenças. Pode ainda verificar-se que apenas uma proteína é comum a doença endodontica e a outras doenças, e 3786 são comuns a OralOma normal e outras doenças. Existem ainda 49 proteínas presentes em comum tanto em outras patologias, como no OralOma normal e doença endodôntica.

De destacar a proteína **Q5VU65** (*Nuclear pore membrane glycoprotein 210-like)* que está presente na patologia endodôntica e em outras patologias e é sugerida como importante formador do poro nuclear (87). Esta proteína é prevalentemente encontrada em pacientes com cirrose biliar primária (88).

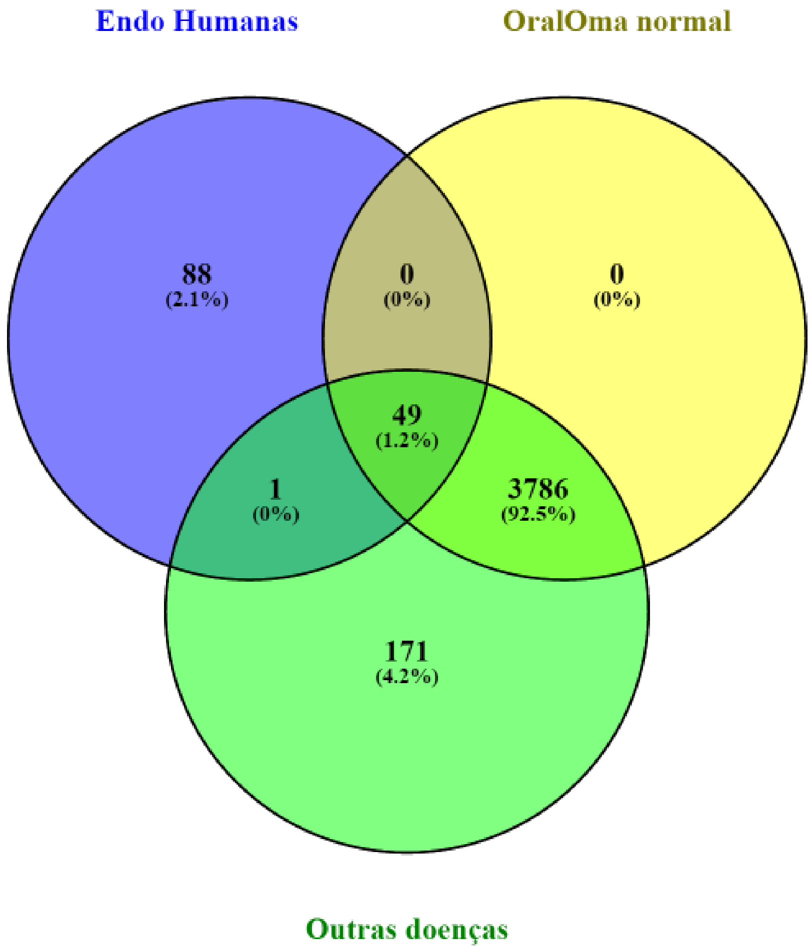


Figura 20: Representação do número de proteínas humanas distribuídas de acordo com a sua identificação em estados de saúde, de outras doenças e em patologia endodontica (endo humanas)**.** Gráfico obtido com recurso ao programa Venny. (http://bioinfogp.cnb.csic.es/tools/venny/)

4.2.3.2 Proteínas microbianas

A análise da figura 21 indica que das 385 proteínas microbianas 362 são exclusivas da patologia endodontica e 23 proteínas microbianas têm relação em comum com proteínas da patologia endodôntica e o OralOma microbiano.

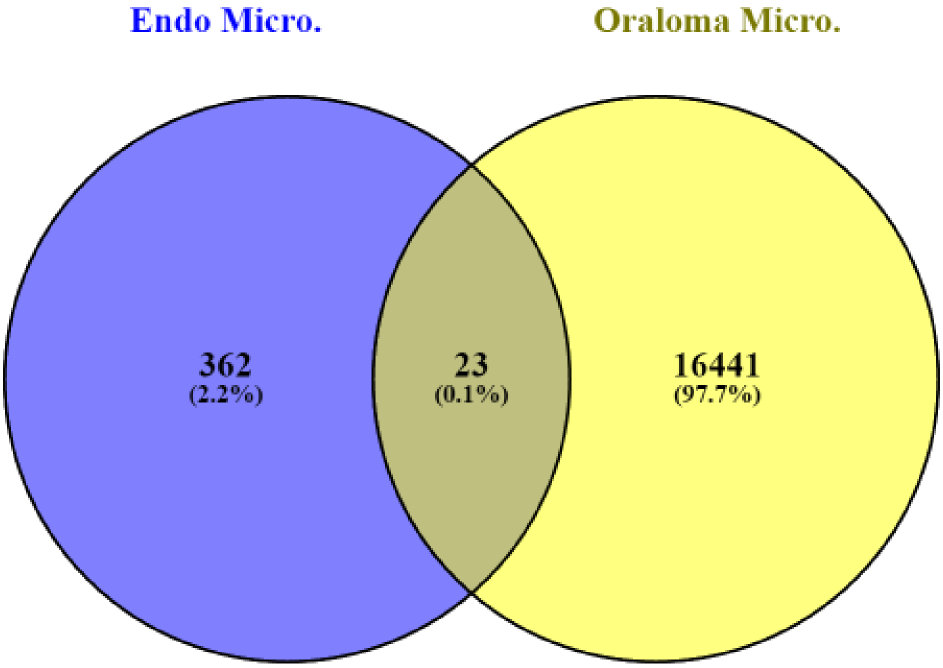


Figura 21: Ilustração das proteínas microbianas provenientes de amostras da Patologia endodôntica e amostras encontradas no OralOme microbiano. Grafico obtido pelo programaVenny.
(http://bioinfogp.cnb.csic.es/tools/venny/)

4.2.4 Caraterização do dador da amostra

A caracterização do dador da amostra inclui a análise da sua faixa etária, do seu género e hábitos sociais relevantes. O intervalo de variação geral da faixa etária das populações incluídas nos estudos analisados está compreendido entre os 20 e os 39 anos, enquanto outros não foram especificados. De notar a variabilidade em termos de raça e de género, uma vez que foram incluídos, nas populações dos estudos experimentais, indivíduos de raça caucasiana e afro-americana, e indivíduos do sexo feminino e masculino. Nos artigos consultados para o trabalho não foi apresentada informação relativa à presença de hábitos sociais como tabagismo ou alcoolismo.

4.2.5 Métodos de amostragem e análise

Como já foi dito anteriormente a pesquisa bibliográfica realizada obteve como resultados estudos de proteómica geral, com a identificação de proteínas orais no âmbito da patologia endodôntica. A realização de estudos gerais de proteómica oral, a nivel quantitiativo, isto é, mais abrangentes, com desenhos similares entre eles poderá apresentar vantagens na identificação de um vasto leque de proteínas, permitindo relacionar as variações da expressão proteica na patologia endodôntica comparativamente ao OralOma normal.

4.3 Caraterização funcional das proteínas orais em patologia endodôntica

4.3.1 Caraterização funcional das proteínas humanas envolvidas em patologia endodontica com o auxílio da ferramenta PANTHER

Com o intuito de compreender o papel fisiológico das proteínas humanas foi feita uma caraterização no qual se pretendeu verificar quais os processos biológicos e funções moleculares que se encontram alterados em relação ao OralOma normal e para isso recorreu-se à ferramenta *PANTHER* (47).

4.3.1.1 Processos Biológicos

De forma a catalogar as proteínas de acordo com a ontologia *Biological Process*, recorreu-se também à ferramenta *PANTHER*. Com base nesta análise foi possível catalogar os processos biológicos em que participam 116 das 138 proteínas humanas identificadas em patologia endodontica, tal como nas funções moleculares (Figura 22).

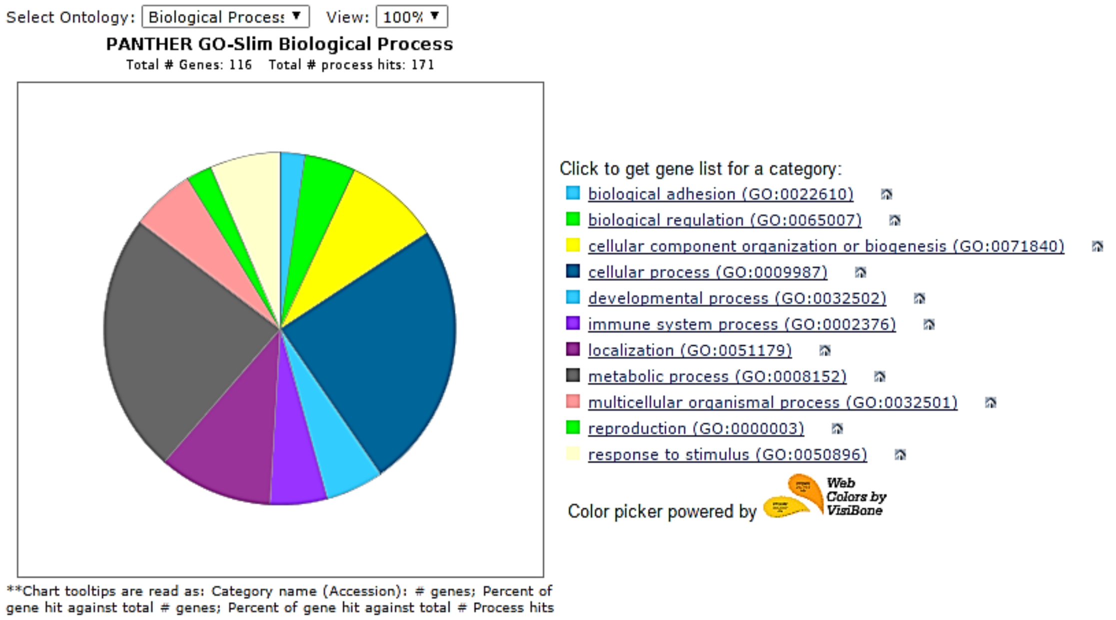
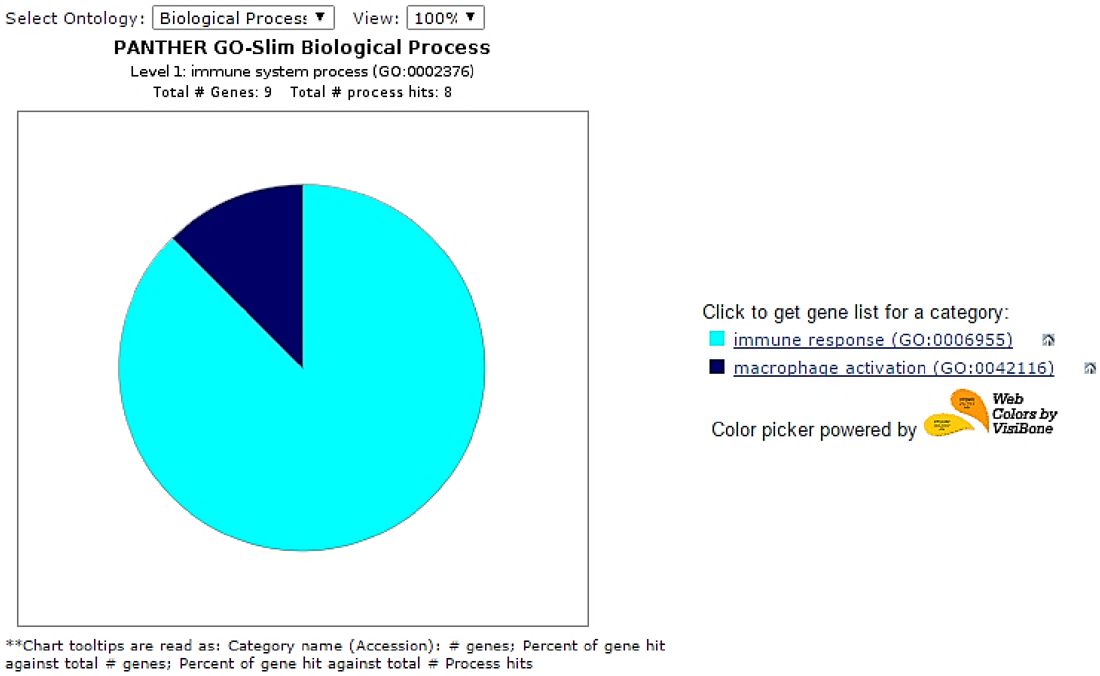


**Chart tooltips are read as: Category name (Accession): # genes; Percent of gene hit against total # genes; Percent of gene hit against total # Process hits

Figura 22: Distribuição das proteínas de patologia endodôntica anotadas ao nível da ontologia *Biological process* do PANTHER.

A análise da Figura 22 permite inferir que a distribuição das proteínas de Patologia endodôntica anotadas no nível da ontologia *Biological process* do PANTHER são identificadas como ativas na presença de patologia endodôntica. Os processos biológicos que apresentam um maior número de proteínas envolvidas correspondem a *Metabolic process,* seguido de *celular process.* Estes processos são bastante abrangentes e pouco informativos.

No contexto deste trabalho, e merecendo particular atenção devido à sua possível relação com a doença endodôntica foi avaliada a subdivisão (*PANTHER*) das proteínas que apresentam atividade de "*imune system process*" obtemos o seguinte gráfico (Figura 23).



Select Ontology: Biological Process

View: 100%

PANTHER GO-Slim Biological Process

Level 1: immune system process (GO:0002376)

Total # Genes: 9 Total # process hits: 8

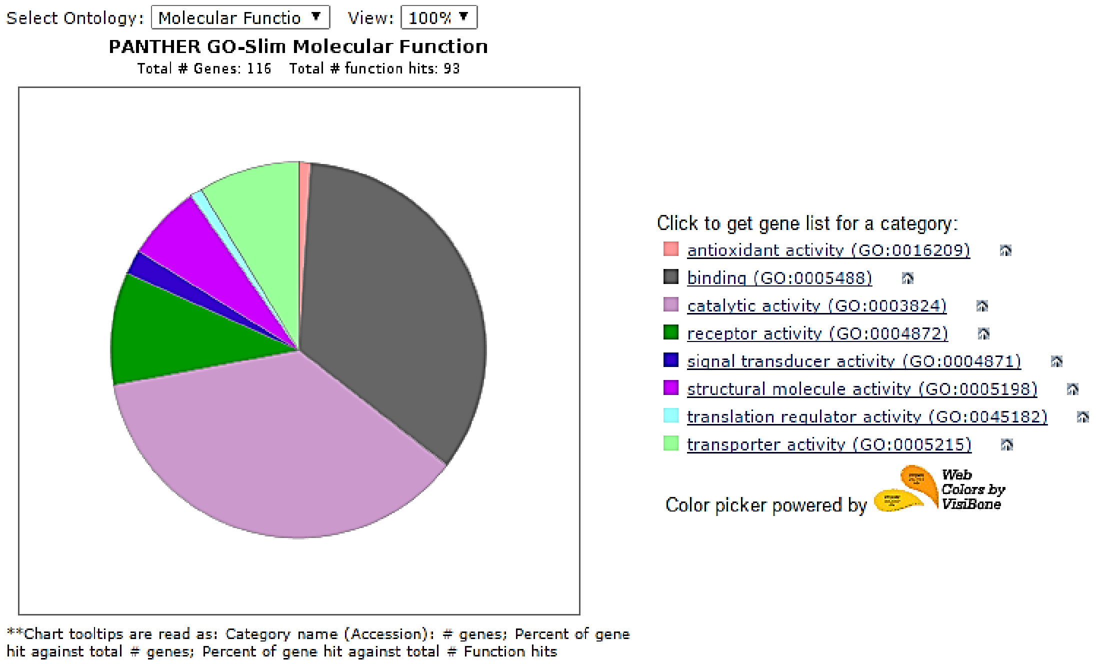
**Chart tooltips are read as: Category name (Accession): # genes; Percent of gene hit against total # genes; Percent of gene hit against total # Process hits

Figura 23: Distribuição das proteínas de Patologia endodôntica anotadas no nível da ontologia *immune system process* do PANTHER.

A análise da Figura 23 indica que das 116 proteínas humanas identificadas no âmbito dos processos biológicos, apenas 8 estão envolvidas e apresentam atividade de resposta imune seguida de ativação de macrófagos.

4.3.1.2 Funções moleculares

De forma a catalogar as proteínas de acordo com a ontologia *Molecular Function*, recorreu-se também à ferramenta PANTHER. Com base nesta análise foi possível catalogar as funções moleculares em que participam 116 das 138 proteínas humanas identificadas em patologia endodontica (Figura 24).



Select Ontology: Molecular Functio ▼ View: 100% ▼

Click to get gene list for a category:

**Chart tooltips are read as: Category name (Accession): # genes; Percent of gene hit against total # genes; Percent of gene hit against total # Function hits

Figura 24: Distribuição das proteínas de patologia endodôntica anotadas no nível da ontologia *Molecular function* do PANTHER.

A análise da figura 24 permite inferir que da distribuição das proteínas de patologia endodôntica anotadas no nível da ontologia "molecular function" do *PANTHER* são identificadas como ativas na presença de patologia endodontica, apresentam várias funções específicas. A grande maioria das proteínas envolvidas fazem parte de funções de *catalytic activity*, seguido de *binding* e *receptor activity.*

4.3.2 Comparação com o OralOma Normal

Como referido em Materiais e Métodos, cada lista de proteínas de patologia endodôntica, classificada segundo a ontologia processo biológico e função molecular, foi comparada com o OralOma Normal. Consideraram-se valores estatisticamente significativos ($p \leq 0.05$).

4.3.2.1 Processos biológicos das proteínas envolvidas em patologia endodontica

A caracterização funcional das proteínas identificadas na patologia endodontica, foi realizada recorrendo à ferramenta *PANTHER* (Mi 2010, Thomas 2003) de acordo com “Material e Métodos – secção Caraterização funcional”. A figura 25 apresenta os resultados obtidos referentes à ontologia *Biological Process*. Nos dados apresentados é mostrada a diferença fracional entre as proteínas da patologia endodôntica e o OralOme normal. No gráfico estão indicados os processos biológicos com uma alteração em relação ao proteoma normal considerada estatisticamente significativa (p≤0.05).

Esta análise permitiu identificar os processos biológicos em que intervêm o total das proteínas identificadas na doença endodontica.

A caracterização funcional das proteínas identificadas na patologia endodontica, foi realizada recorrendo à ferramenta *PANTHER* (Mi 2010, Thomas 2003) de acordo com “Material e Métodos – secção Caraterização funcional”. A figura 25 apresenta os resultados obtidos referentes à ontologia *Biological Process*. Nos dados apresentados é mostrada a diferença fracional entre as proteínas da patologia endodôntica e o OralOme normal. No gráfico estão indicados os processos biológicos com uma alteração em relação ao OralOma normal considerada estatisticamente significativa (p≤0.05).

Esta análise permitiu identificar os processos biológicos em que intervêm o total das proteínas identificadas na doença endodontica.

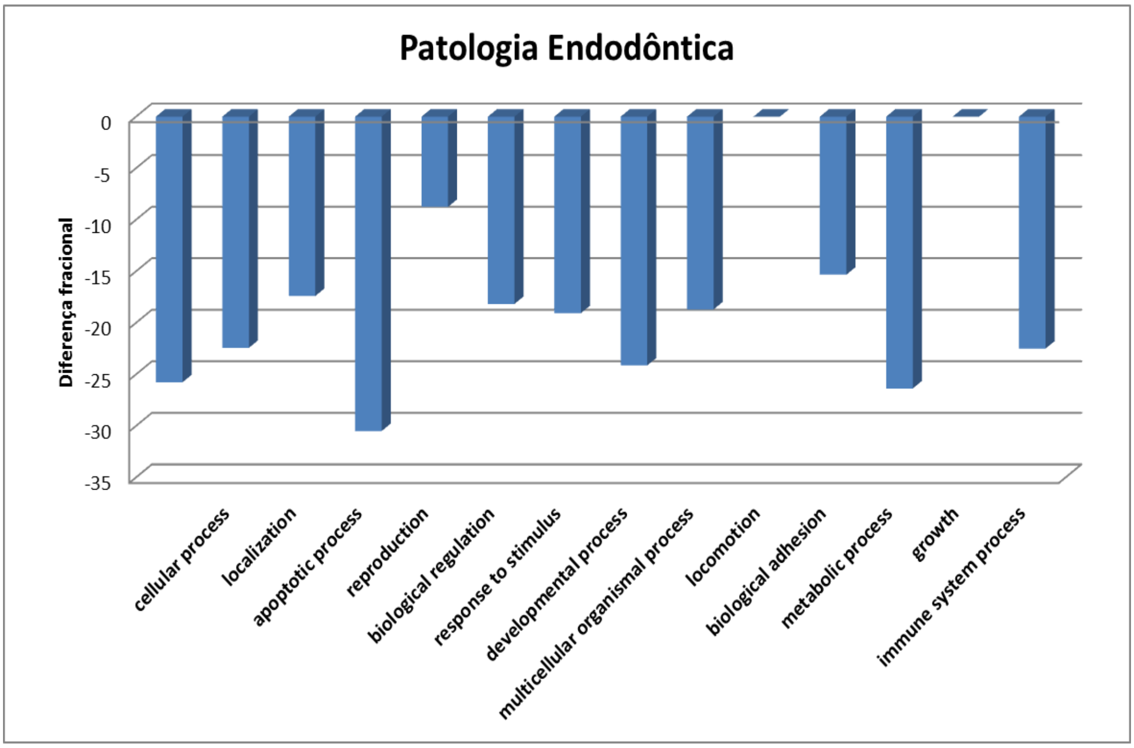


Figura 25: Distribuição das proteínas orais de pacientes com patologia endodôntica segundo os processos biológicos em que intervêm, recorrendo à ferramenta PANTHER (Mi 2010, Thomas 2003). É mostrada a diferença fraccional entre as proteínas da patologia endodôntica e o OralOma normal. No gráfico estão indicados os processos biológicos com uma alteração em relação ao OralOma normal considerada estatisticamente significativa (p≤0.05).

A análise da Figura 25 permite inferir que os processos biológicos que apresentam um maior número de proteínas envolvidas correspondem *metabolic process e cellular process* seguido de *localization e biological regulation*. Estes processos são bastante abrangentes e pouco informativos. No âmbito deste trabalho, o processo imune system process merece particular atenção devido à sua potencial relação a patologia endodôntica.

Analisando as proteínas envolvidas nos processos de *imune system process*, verificou-se que todas elas estão envolvidas nas respostas de defesa do hospedeiro que se verificam no desenvolvimento de patologia endodôntica. Assim, as proteínas identificadas ao longo deste estudo e ativas nos processos biológicos acima mencionados serão analisadas no âmbito do processo geral *imune system process*.

Ig alpha-1 chain C region (P01876), constitui a molécula do colágeno fibrilar e é a principal classe de imunoglobulina nas secreções corporais. Pode servir tanto para defender contra a infeção local como para impedir o acesso de antígenos estranhos ao sistema imunológico em geral (48). Sabe-se que está associada a casos de estados iniciais de doênça endodôntica (37).

A Interleukin enhancer-binding factor 2 (Q12905), funciona predominantemente como um complexo heterodimérico com a ILF3. Este complexo pode regular a transcrição do gene de IL2 durante a ativação de células-T (48). Ligada a casos de pós tratamento da infeção endodôntica (37).

A *Ig alpha-1 chain C region* (P01834), é a principal classe de imunoglobulina das secreções corporais. Atua como defesa contra as infeções locais e para impedir o acesso de antígenos estranhos ao sistema imunológico (48). Esta proteína está presente em estados iniciais, abcessos e pós tratamento de infeções endodônticas (37).

A Myeloperoxidase (P05164), faz parte do sistema de defesa do hospedeiro de leucócitos polimorfonucleares. É responsável pela atividade microbicida contra um amplo espectro de organismos. É a principal enzima constituinte dos grânulos azurófilos primários dos neutrófilos e pode originar ácido hipocloroso. Quando ocorre estimulação ou desgranulação dos neutrófilos, a mieloperoxidase é libertada para o espaço extracelular. Esta enzima, após libertação, consegue ativar de forma oxidativa MMP-8 e MMP-9 e ainda inativar TIMP-1 (77). Apesar desta ação estar só identificada em periodontite, o mesmo se poderá desenrolar em patologia endodôntica. Presente em casos de abcessos. (37)

***Beta-2-glycoprotein* 1** (P02749), liga-se a vários tipos de substâncias carregadas negativamente, tais como a heparina, fosfolípidos, e sulfato de dextrano. Evitam a ativação da cascata de coagulação sanguínea intrínseca através da ligação a fosfolípidos na superfície das células danificadas *(48).*

O Complement C3 (P01024), reage como um quimioatrativo para neutrófilos na inflamação crónica. Uma deficiência no complemento pode aumentar a susceptibilidade a infeções (42,48). Esta proteína foi identificada em abcessos (37).

O aumento do número de proteínas associadas a resposta imune do hospedeiro pode ser esperado em patologia endodontica. Sabe-se, que perante uma invasão bacteriana, ocorrem mecanismos de resposta contra essas mesmas bactérias. As bactérias estão localizadas nos tecidos perirradiculares inflamados no qual são eliliminados por mecanismos de defesa do hospedeiro, a quando da instrumentação mecânica, irrigação antisséptica e medicação intracanalar.

4.3.2.2 Funções moleculares das proteínas envolvidas em patologia endodontica

Os dados do OralOme normal dos pacientes com patologia endodontica foram catalogados de acordo com a ontologia *Molecular Function*, recorrendo à ferramenta *PANTHER* (Mi 2010, Thomas 2003) de acordo com "Material e Métodos – secção Caraterização funcional". Esta análise permitiu identificar as funções moleculares desempenhadas pelo total de proteínas identificadas nestes pacientes (Figura 26).

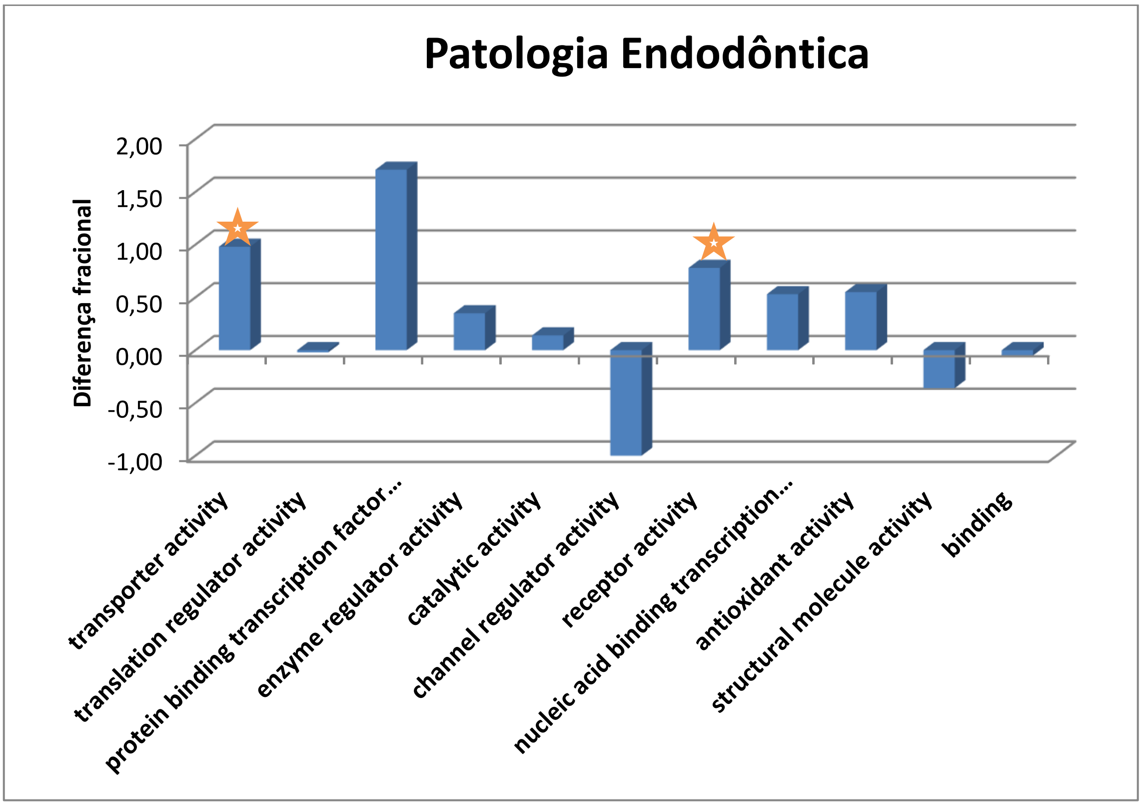


Figura 26: Distribuição das proteínas de pacientes com patologia endodontica segundo as funções moleculares que desempenham, recorrendo à ferramenta *PANTHER* (Mi 2010, Thomas 2003). É mostrada a diferença fracional entre as proteínas da patologia endodôntica e o oraloma normal. As barras azuis marcadas com uma estrela estão indicadas as funções moleculares com uma alteração em relação ao OralOma normal considerada estatisticamente significativa (p≤0.05).

A análise da Figura 26 permite identificar as funções moleculares estatisticamente aumentadas na patologia endodôntica (p≤0,05) (barras assinaladas), comparativamente com o OralOma normal. As proteínas envolvidas em processos de *receptor activity, transporter activity possuem* um aumento estatisticamente significativo na patologia endodôntica com um p-value <0,05.

Analisando as proteínas envolvidas nas funções moleculares podemos dizer que os processos que envolvem um maior número de proteinas são *"protein binding transcription factor activity" e "channel regulator activity".*

Assim, as proteínas identificadas ao longo deste estudo e ativas nas funções moleculares acima mencionadas serão analisadas no âmbito do processo geral ***receptor activity*** *e* ***transporter activity***.

Como referido na caraterização funcional, proteínas humanas com a função de ***receptor activity*** podem apresentar características importantes durante o processo patológico da patologia endodôntica.

A ***Polymeric immunoglobulin receptor, (PIgR)*** (P01833) *desempenha um processo de detection chemical stimulos involved in sensory perception of bitter taste*. É uma proteína que, em seres humanos é codificada pelo gene *pIgR* . Este receptor de Fc liga-se à imunoglobulina A e imunoglobulina M (48).

Transient receptor potential cation channel subfamily M member 3 (Q9HCF6), tem a função de mediar a entrada do ião cálcio. A sua atividade é aumentada pela redução da osmolaridade extracelular, por eliminação do armazenamento e a ativação do receptor muscarínico. (48) Presente em abcessos na patologia endodôntica (37).

ATP synthase subunit alpha, mitochondrial (P25705), produz ATP a partir de ADP na presença de um gradiente de protões através da membrana, que é gerado por complexos de transporte de electrões da cadeia respiratória. Esta proteína está associada a casos de pós tratamento na patologia endodôntica (37,48).

Neuropilin-2 (O60462), receptor de alta afinidade para 3C semaforina, 3F, VEGF-165 e VEGF-145 isoformas de VEGF e o PIGF-2 isoforma de PGF. Esta proteína está ligada a estados de abcessos na enfeção endodôntica (37,48).

Cadherin EGF LAG seven-pass G-type receptor 1 (Q9NYQ6), receptor que pode ter um papel importante na sinalização celular durante a formação do sistema nervoso. Presente em casos de abcessos (37,48).

Gamma-aminobutyric acid receptor subunit rho-3 (A8MPY1), GABA, o principal neurotransmissor inibitório no cérebro dos vertebrados, medeia a inibição neuronal através da ligação ao receptor de GABA / benzodiazepina e a abertura de um canal de cloreto de integrante. Presente em abcessos (37,48).

Leucine-rich repeat transmembrane neuronal protein 2 (O43300), envolvida no desenvolvimento e manutenção de sinapses excitatórias no sistema nervoso dos vertebrados. Regula a expressão de superfície de receptores AMPA. Atua como um ligando para os receptores pré-sinápticos NRXN1-A e B-NRXN1 (por similaridade). Presente em abcessos (37,48).

PAS domain-containing serine/threonine-protein kinase (Q96RG2), envolvida na homeostase e aumenta a eficiência da tradução da proteína. Aparece em casos de abcessos (37,48).

Leucine-rich repeat, immunoglobulin-like domain and transmembrane domain-containing protein 1 (Q9P2V4), papel na fototransdução. Esta proteína associa-se a casos iniciais da infeção e pós tratamento do canal (37,48).

A função de **transport activity** também podem apresentar caraterísticas importantes durante o processo patológico da patologia endodôntica.

TOM1-like protein 2 (Q6ZVM7), tem um papel de transporte de proteínas e pode regular o crescimento *factor-induced* de sinalização mitogênica, presente em abcessos (37,48).

Transient receptor potential cation channel subfamily M member 3 (Q9HCF6),), com função e tipo de condição clinica já referida atrás (pág.70) (37,48).

ATP synthase subunit alpha, mitochondrial (P25705), com função e tipo de condição clinica já referida atrás (pág.70) (37,48).

Neuropilin-2 (O60462), com função e tipo de condição clinica já referida atrás (pág.70) (37,48).

Short transient receptor potential channel 4 (Q9UBN4), atua como um canal de entrada de cálcio endotelial dependente de contacto célula-célula. Provavelmente, executado por um segundo sistema mensageiro fosfatidilinositol ativado por tirosina-quinases receptoras ou receptores acoplados à proteína G. Medeia a entrada de cátions, com uma permeabilidade aumentada ao bário sobre o cálcio. Também pode ser activado por depleção de armazenamento de cálcio intracelular. Presente em abcessos (37,48).

ADP-ribosylation factor-binding protein GGA2 (Q9UJY4), estabelece um papel em triagem de proteínas e tráfico entre a rede trans-Golgi (TGN) e endossomas. Associada a abcessos (37,48).

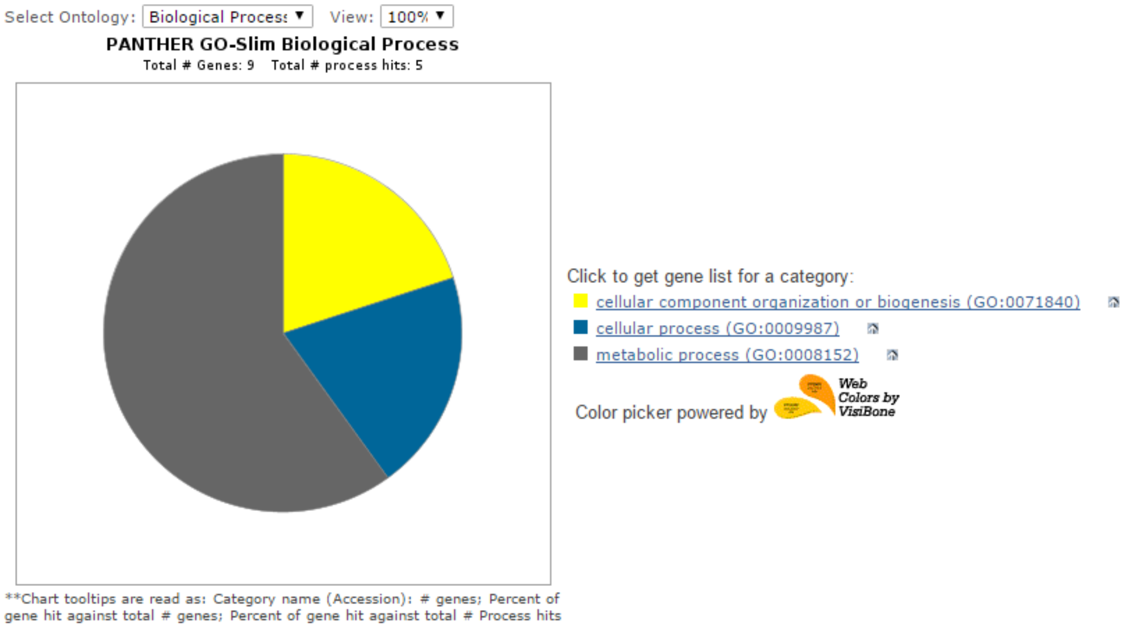
Solute carrier organic anion transporter family member 1B3 (Q9NPD5), medeia a absorção independente de Na^+ de aniões orgânicos. Presente em abcessos (37,48).

V-type proton ATPase 116 kDa subunit a isoform 1 (Q93050), necessária para a atividade da ATPase vacuolar e tem um potencial papel na segmentação diferencial e regulação da enzima para uma organela específica. Associada a pós tratamento do canal em enfeções endodônticas (37,48).

As proteínas ***Transient receptor potential cation channel subfamily M member 3*** (Q9HCF6), ***ATP synthase subunit alpha, mitochondrial*** (P25705), **Neuropilin-2** (O60462) estão presentes nas duas ontologias identificadas segundo as funções moleculares em patologia endodôntica.

No sentido de esclarecer a importância funcional das proteínas microbianas envolvidas em patologia endodontica, estas foram agrupadas na ontologia *Biological Process* e *Molecular Function* e para isso recorreu-se á ferramenta PANTHER. (47)

4.3.3.1 Processos Biológicos



Select Ontology: Biological Process View: 100%

PANTHER GO-Slim Biological Process

Total # Genes: 9 Total # process hits: 5

Click to get gene list for a category:

- 🟨 cellular component organization or biogenesis (GO:0071840)
- 🟦 cellular process (GO:0009987)
- ⬛ metabolic process (GO:0008152)

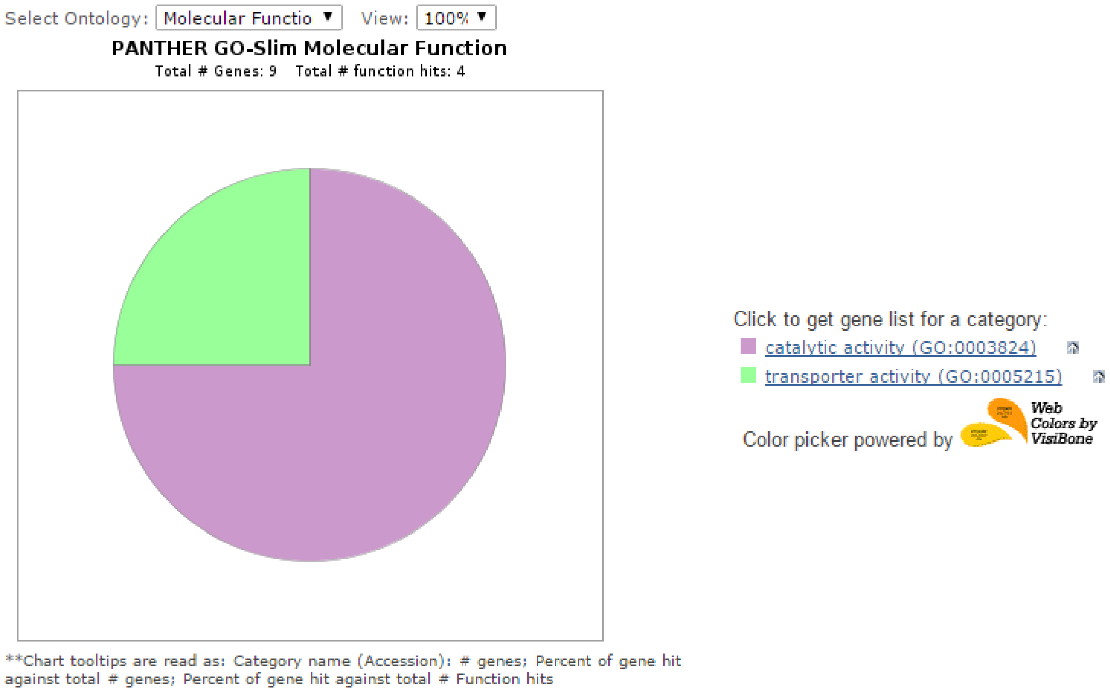
Color picker powered by Web Colors by VisiBone

**Chart tooltips are read as: Category name (Accession): # genes; Percent of gene hit against total # genes; Percent of gene hit against total # Process hits

Figura 27: Distribuição das proteínas microbianas da Patologia endodôntica anotadas ao nível da ontologia *Biological process* do PANTHER.

A análise da Figura 27 permite inferir que da distribuição das proteínas de Patologia endodôntica anotadas ao nível da ontologia Biological process do PANTHER são identificadas como ativas na presença de patologia endodôntica e apresentam várias funções específicas.

4.3.3.2 Funções moleculares


Select Ontology: Molecular Functio ▼ View: 100% ▼

PANTHER GO-Slim Molecular Function

Total # Genes: 9 Total # function hits: 4

Click to get gene list for a category:

🟪 catalytic activity (GO:0003824)

🟩 transporter activity (GO:0005215)

Color picker powered by Web Colors by VisiBone

**Chart tooltips are read as: Category name (Accession): # genes; Percent of gene hit against total # genes; Percent of gene hit against total # Function hits

Figura 28: Distribuição das proteínas microbianas de Patologia endodôntica anotadas no nível da ontologia *Molecular function* do PANTHER.

A análise da Figura 28 permite inferir que da distribuição das proteínas de patologia endodôntica anotadas no nível da ontologia *Molecular function* do PANTHER são identificadas como ativas na presença de patologia endodontica, apresentam várias funções específicas como *catalytic activity* e *transporter activity*.

4.4 Caraterização funcional das proteínas microbianas recorrendo à Ferramenta AgBase

Recorreu-se também à ferramenta *AgBase* para visualizar o número de proteínas de acordo com a ontologia *Biological Process*.

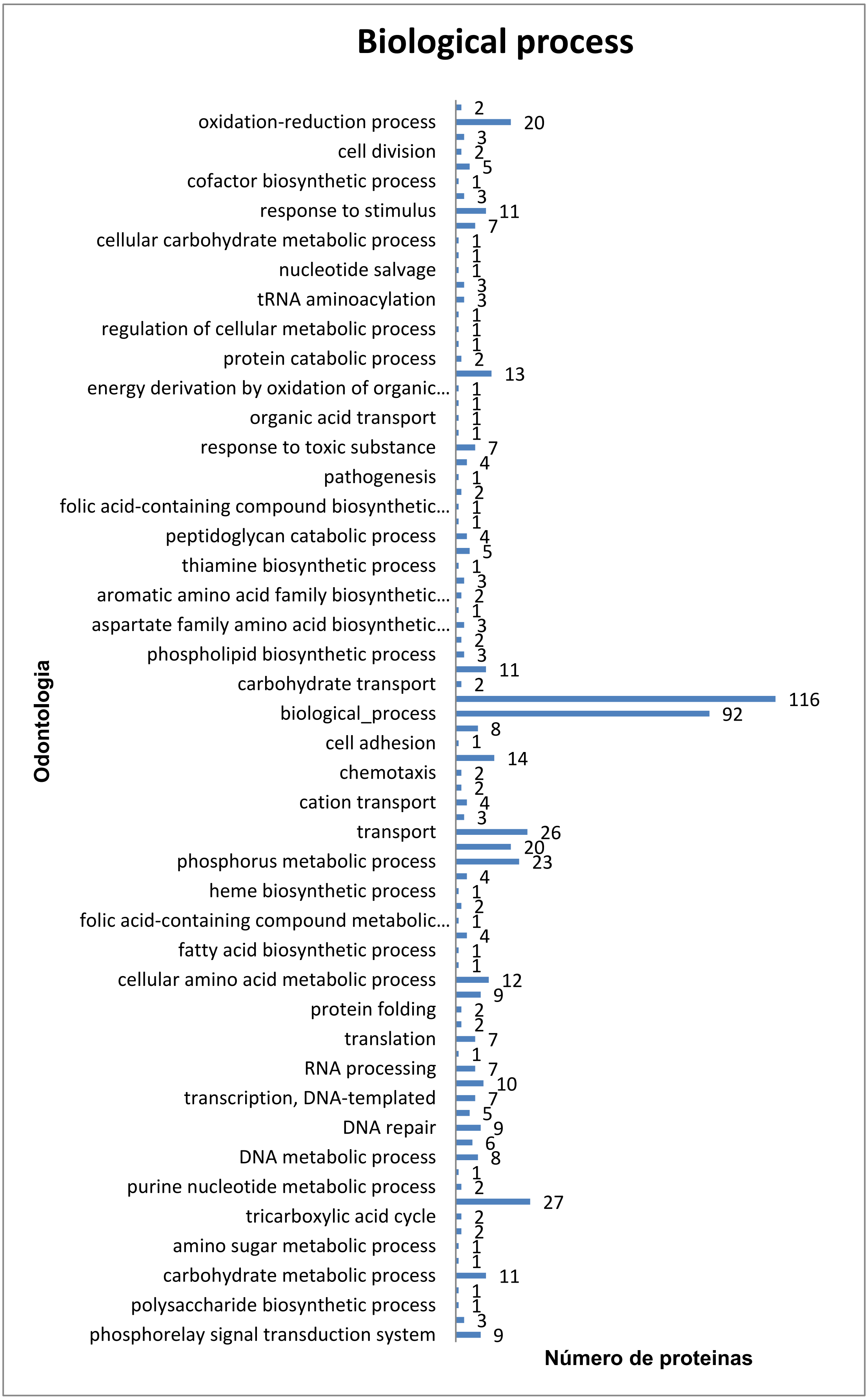


Figura 29: Distribuição de proteínas, obtido pelo *AgBase*, anotadas na ontologia Biological process.

Analisando a figura 29 podemos inferir que os processos biológicos que apresentam mais proteínas envolvidas correspondem a *metabolic process*, 116 proteínas, seguido de *biological process* 92 proteínas.

Retirando informação acerca dos processos biológicos mais relevantes para a este trabalho destacam-se ***multi-organism process*** *com 3 proteinas,* ***response to stimulus*** *com 14 proteinas,* ***pathogenesis*** com 1 proteina, **phosphoenolpyruvate-*dependent sugar phosphotransferase system*** *com 2 proteinas,* ***cell adhesion*** com 1, ***response to stress*** com 17*,* ***conjugation*** com 1, ***peptidoglycan biosynthetic process*** com 5 e ***phosphorelay signal transduction system*** com 9 proteinas.

Posto isto, destacam-se ***TraG family protein*** *(*Q832B2), que faz parte dos processos *multi-organism process e conjugaction* e tem como organismo associado o *enterococcus faecalis.*

CRISPR-associated endonuclease Cas1 (G2SLM4), participa no sistema imune adaptativo que proporciona protecção contra elementos genéticos móveis (vírus, elementos transponíveis e plasmídeos conjugativos) (48). que entra em *multi-organism process, response to stimulus e response to stress.*

Autolysin (P37710), pode desempenhar um papel importante no crescimento da parede celular e separação das células (48) e entra em *multi-organism process, response to stimulus e response to stress.* Tem como organismo associado o *enterococcus faecalis*.

Thioredoxin reductase *(*A3CPZ1), com função de remoção de radicais superóxido e que entra em processos de response to stimulus e response to stress.

UvrABC system protein B (A1STV6), ***UvrABC system protein C*** (A3VEV1), ***DNA ligase*** (A9NHW0), ***Single-stranded DNA-binding protein (SSB)*** (B9DIB9), ***RecBCD enzyme subunit RecC*** (D2PR48), ***Holliday junction ATP-dependent DNA helicase RuvB*** (I4ECD9), ***ATP-dependent helicase/nuclease subunit A*** (Q88U41), que desempenham uma resposta celular a danos no DNA e que entram em processos de response to stimulus e response to stress.

2,3-dihydroxyphenylpropionate/2,3-dihydroxicinnamic acid 1,2-dioxygenase (A7IDU0), que também desempenha uma resposta celular a danos no DNA e que entra em processos de response to stimulus.

Putative NAD (+)--arginine ADP-ribosyltransferase (A0QLI5), que está associada a *pathogenesis*.

Phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2 (D3MPG4) e é associado a metabolismo de açucares.

PTS system, IIC component (Q837M0), envolvida em processos de *Phosphoenolpyruvate-dependent sugar phosphotransferase system e que tem como organismo associado o enterococcus faecalis*.

Putative invasin (D3UXC7), envolvida em processos de *cell adhesion.*

Transport associated protein (B5HF16), Putative ***toxin-antitoxin system, toxin component*** (D9WI88), ***Possible universal stress protein*** (Q0S9R0), ***Catalase*** (Q82ID4), envolvida em processos de *response to stress*.

Glutamate racemase *(*A6VX99), ***D-alanine--D-alanine ligase A*** *(*Q8PDW3), e FemAB ***family protein*** *(*B5I692), com funções de fornecer glutamato- (R) necessário para a biossíntese da parede celular estão envolvidas em *peptidoglycan biosynthetic process.*

UDP-N-acetylmuramoylalanine--D-glutamate ligase *(*O07108) e **D-alanine--D-alanine ligase** (Q93A46), com funções de fornecer glutamato- (R) necessário para a biossíntese da parede celular e estão envolvidas em *peptidoglycan biosynthetic process* e ligadas á bactéria *enterococcus faecalis*.

Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain (D5HJ19), ***Response regulator receiver: ATP-binding region, ATPase-like: Histidine kinase A, N-terminal*** (E0TFX1), ***Two component transcriptional regulator*** (E7DPN6), ***Uncharacterized protein*** (J2T720), ***Periplasmic sensor signal transduction histidine kinase***

(Q11JY3), ***Chemotaxis response regulator protein-glutamate methylesterase*** (Q8XQ83), e ***Sensory box sensor histidine kinase*** (A4BWF2), estão envolvidas em processos *de phosphorelay signal transduction system.*

VanSG2 (Q30BF3), ***Sensor protein VanSB*** (Q47745) e ***Sensor protein VanSB*** (Q47745), estão envolvidas em processos de *phosphorelay signal transduction system*. Têm como organismo associado o *Enterococcus faecalis.*

4.5 Relação de comparação com outras Patologias (periodontite crónica, gengivite e periodontite agressiva)

Com base nas 138 proteínas humanas identificadas na doença endodontica foi realizada a comparação com outras patologias em que há implicação de ação microbiana e que estão associadas à cavidade oral.

As proteínas anotadas para as patologias periodontite crónica, gengivite e periodontite agressiva foram identificadas a partir da base de dados do OralOma (figura 30).

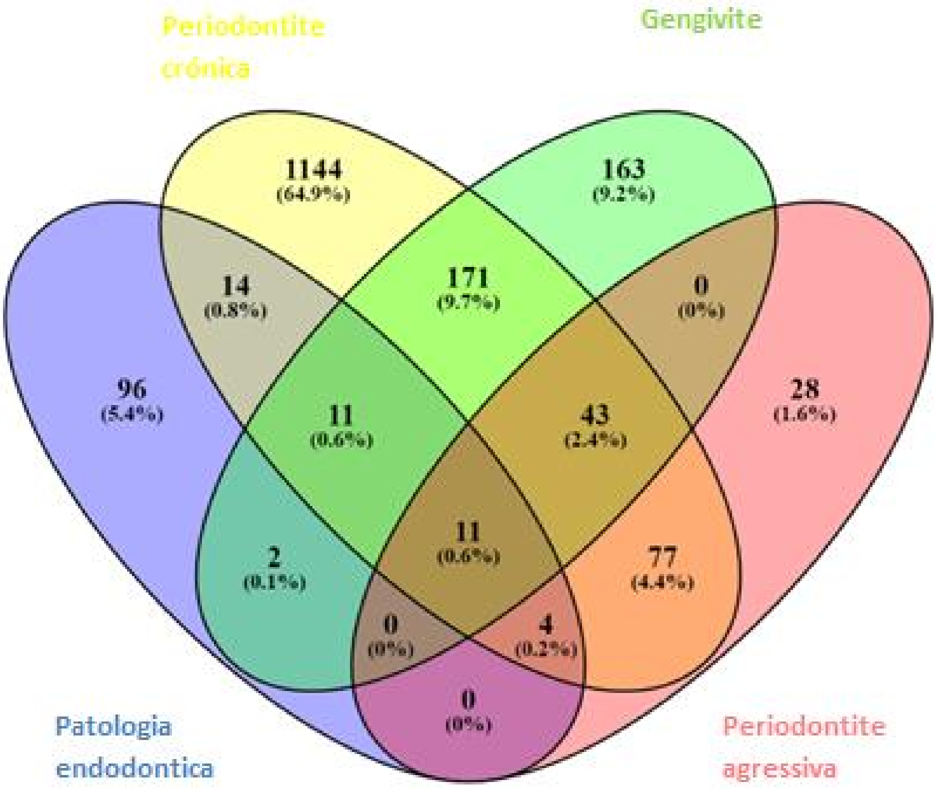


Figura 30: Distribuição das proteínas orais por patologia endontica e outras patologias orais. Gráfico obtido com recurso ao programa Venny. (http://bioinfogp.cnb.csic.es/tools/venny/)

Pela análise da figura 30 podemos inferir que estão designadas patologias como a gengivite, (cor verde) periodontite agressiva, (cor vermelha) patologia endodôntica, (cor azul) e periodontite crónica, (cor amarela) o que permite verificar a existência de algumas proteínas comuns entre patologias.

Estes resultados demonstram que 96 das 138 proteinas humanas são exclusivas de patologia endodôntica e 11 proteinas são comuns a todas a patologias estudadas.

Assim sendo, foi feita uma análise mais detalhada em relação às proteinas em comum a todas as patologias e às exclusivas à doênca endodôntica.

Para apresentação das várias proteínas estas são expostas na tabela seguinte (tabela 3) e anexo C, tabelas essas que contemplam o código Uniprot, nome da proteína e organismo associado.

Na **tabela 3** são apresentadas as 11 proteinas humanas comuns à patologia endodôntica, gengivite, periodontite crónica e periodontite agressiva.

Tabela 3 – Proteínas humanas alteradas e que foram identificadas na patologia endodôntica, gengivite, periodontite crónica e agressiva

Codigo UniprotKB	Protein names
A6NL76	Actin, alpha skeletal muscle
C9JUM1	Actin, cytoplasmic 1 (Fragment)
P63261	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]
P16401	Histone H1.5 (Histone H1a) (Histone H1b) (Histone H1s-3)
P05204	Non-histone chromosomal protein HMG-17 (High mobility group nucleosome-binding domain-containing protein 2)
P01036	Cystatin-S (Cystatin-4) (Cystatin-SA-III) (Salivary acidic protein 1)
P09228	Cystatin-SA (Cystatin-2) (Cystatin-S5)
P59666	Neutrophil defensin 3 (Defensin, alpha 3) (HNP-3) (HP-3) (HP3) [Cleaved into: HP 3-56; Neutrophil defensin 2 (HNP-2) (HP-2) (HP2)]
P01833	Polymeric immunoglobulin receptor (PIgR) (Poly-Ig receptor) (Hepatocellular carcinoma-associated protein TB6) [Cleaved into: Secretory component]
P12273	Prolactin-inducible protein (Gross cystic disease fluid protein 15) (GCDFP-15) (Prolactin-induced protein) (Secretory actin-binding protein) (SABP) (gp17)
P02814	Submaxillary gland androgen-regulated protein 3B (Proline-rich peptide P-B) (Proline-rich protein 3) [Cleaved into: Peptide P-A; Peptide D1A]

A **actina**, (C9JUM1 e P63261), é um alvo chave de numerosos agentes patogénicos. Em particular, as bactérias produzem fatores de virulência que atuam nas células hospedeiras sequestrando a actina permitindo assim a invasão bateriana, e atuando também no bloqueio da fagocitose (78).

As **histonas** (P05204) são um componente importante dos *neutrophil extracelular traps* (NETs). Quando os neutrófilos são ativados, os NETs são libertados e apresentam capacidade de aprisionar agentes patogénicos evitando assim a sua disseminação ou contribuindo para a sua morte (79).

Outras proteínas como a ***Cystatin-S*** (P01036)*,* ***Cystatin-SAThiol protease inhibitor*** (P09228)*,* estão presentes na película adquirida e ligam-se às bactérias e aos lipossacarídeos bacterianos (80). De um modo geral, as cistatinas são essenciais ao organismo, e nos tecidos orais fornecem proteção contra a proteólise inadequada dos tecidos que facilita a infeção microbiana (81). ***Neutrophil defensin 3*** (P59666)*, e também a Defensin 2* têm atividade antibiótica, fungicida e antiviral. Contêm também atividade antimicrobiana contra bactérias Gram-negativas e Gram-positivas. As defensinas estão relacionadas com o aumento da saúde gengival. O seu aumento está relacionado com a diminuição da saúde periodontal uma vez que a proteína está relacionada com a inflamação e a destruição do osso e tecido conjuntivo na doença periodontal (73,75).

No Anexo C são apresentadas as proteinas **exclusivas** da patologia endodôntica, e que pela análise da figura 30 foi obtido um resultado de 96 proteinas comuns encontradas.

Das 96 proteinas exclusivas da PE foram selecionadas algumas que se pensa terem um papel mais importante no proteoma oral da patologia. As proteínas selecionadas estão ligadas a uma função biológica e associadas a um tipo de condição clínica em que é recolhida a amostra, ou seja, abcesso, pós tratamento ou estado inicial. (37).
Recorrendo a base de dados Uniprot (48) foram caraterizadas algumas proteínas consoante a sua função e interesse para a patologia. Das proteínas de interesse (sublinhadas na tabela do anexo A) identificamos as proteinas com os códigos Uniprot:

A proteina ***S100-A9*** (P06702) faz ligação ao zinco e desempenha um papel proeminente na regulação de processos inflamatórios e resposta imune. Pode induzir quimiotaxia de neutrófilos, adesão e pode aumentar a actividade bactericida de neutrófilos através da promoção de fagocitose por meio de activação de *SYK, PI3K / AKT e ERK1 / 2*, pode também induzir a desgranulação de neutrófilos por um mecanismo *MAPK-dependent.* Esta foi encontrada em estados iniciais (asymptomatic) da patologia (37).

60 kDa heat shock protein **(P10809)**, implicada na importação de proteína mitocondrial e organização macromolecular. Está associada a patologia como *Spastic paraplegia 13, autosomal dominant (SPG13)* *(57)* *e Leukodystrophy, hypomyelinating, 4 (HLD4)* (58).

Myeloperoxidase **(P05164),** produzida por leucócitos polimorfonucleares, faz parte do sistema de defesa do hospedeiro. É responsável pela atividade microbicida contra um amplo espectro de organismos. Está associada a patologia como *Myeloperoxidase deficiency* (MPOD) que é caracterizada pela desordem na diminuição da atividade da mieloperoxidase em neutrófilos e monócitos que resulta em candidíase disseminada (59). Esta proteína foi encontrada em casos de abcesso (37).

Liprin-alpha**-4 (O75335)**, que regula a desagregação de adesões focais. Pode localizar os *receptores* tirosina fosfatases 2A em locais específicos na membrana plasmática, e regulam possivelmente a sua interação com o ambiente extracelular e a sua associação com substratos.

Neutrophil defensin 1 **(P59665**) ***e Neutrophil defensin 3*** **(P59666)***, Defensin 1 e uma defensin 2* têm atividade antibacteriana, fungicida e antiviral. Tem também actividade antimicrobiana contra bactérias Gram-negativas e Gram-positivas. Neste caso esta ligada a casos de abcessos, estados iniciais (asymptomatic) e pós tratamento (NaOCl) da patologia (37).

V-type proton ATPase 116 kDa subunit a isoform 1 **(Q93050)**, esta é necessária para a atividade da ATPase vacuolar e tem um papel potencial na segmentação diferencial e regulação da enzima em cada tipo de organelo.

***78 kDa glucose-regulated protein* (P11021)**, provavelmente desempenha um papel em facilitar a organização de complexos de proteínas multiméricas no interior do retículo endoplasmático (60).

***Beta-2-glycoprotein 1* (P02749)**, liga-se a vários tipos de substâncias carregadas negativamente, tais como a *heparin, phospholipids, e dextran sulfate*. Podem evitar a ativação da cascata de coagulação sanguínea intrínseca através da ligação a fosfolípidos na superfície de células danificadas.

***Cystatin-S* (P01036)**, esta proteína inibe fortemente a papaína e a ficina, inibe parcialmente a cathepsina bovina C, mas não inibe a cathepsina B e a clostripaina tem uma função de inibição da protéase e está ligada a casos de estados iniciais e pós tratamento da patologia endodôntica (37).

O aumento do número de proteínas associadas a resposta imune do hospedeiro como ***Neutrophil defensin 1* (P59665**), ***Neutrophil defensin 3* (P59666) e *Myeloperoxidase* (P05164),** podem ser esperadas em patologia endodôntica. Sabe-se, que perante uma invasão bacteriana, ocorrem mecanismos de resposta contra essas mesmas bactérias.

4.6 Interactoma oral da Patologia endodôntica

O conhecimento do papel das interações do proteoma oral do hospedeiro com o proteoma do microbioma em patologia endodôntica, tem uma importância vital para o entendimento dos mecanismos de virulência que possam estar implicados na patologia endodontica. Estas interações são importantes não apenas no estabelecimento e manutenção da flora oral capaz de desencadear desenvolvimento das infeções, mas também, como discutido anteriormente, nos próprios mecanismos de defesa do hospedeiro a estímulos.

Para se obter o interactoma em patologia endodontica, realizou-se uma lista no Microsoft Excel com todas as proteínas humanas exclusivas da doença endodontica, (no total de 96) identificadas na secção anterior e com proteinas microbianas envolvidas na patologia endodôntica que foi submetida ao algoritmo OralInt (*http://bioinformatics.ua.pt/software/oralint/)* para permitir a previsão do Interactoma oral.

Através do algoritmo OralInt realizou-se o levantamento dessas interações que foram posteriormente visualizadas em detalhe através da ferramenta Cytoscape. (Figura 31)

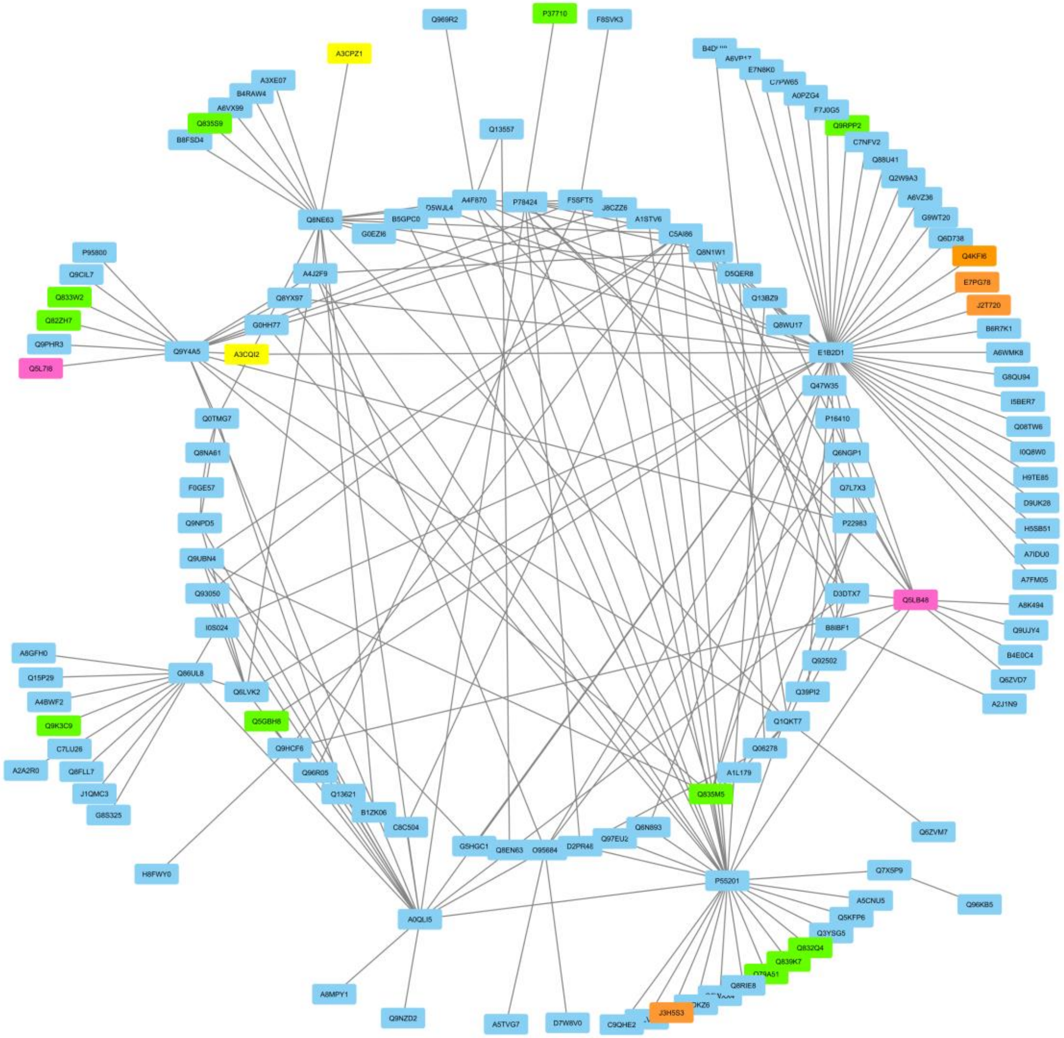


Figura 31: Rede de interações entre proteínas humanas e microbianas em patologia endodôntica, gerada pelo algoritmo OralInt e visualizada com a ferramenta Cytoscape. Representação a cores das proteinas humanas que desempenham mais interações com *Enterococcus faecalis* (representadas a verde), o *streptococcus sanguinis* (representado a amarelo), *pseudomonas* (representado a cor de laranja) *bacteroides fragilis* (repesentado a cor de rosa).

Na figura 31 estão representadas as proteinas da patologia endodôntica que foram submetidas e geradas através do algoritmo OralInt, posto isto só 37 proteinas fizeram ppi´s (interação proteína-proteina) com um score acima de 0,9, ou seja, com elevado grau de confiança.
Estas proteínas interagem (interação representada pelas linhas a cinzento) com as proteínas do microbioma oral, com base na determinação do algoritmo OralInt. A grande condensação de linhas a cinzento confirma a existência de uma grande rede de interações existente entre as proteínas do proteoma de PE com proteínas microbianas. É de salientar que só foram consideradas as interações com um score acima de 0, 9.

Posto isto e pela análise da figura 31 pode ser dito que as proteínas que fazem um maior número de interções são:
a proteína humana ***Hemoglobin*** **(E1B2D1)**, que está associada ao sistema circulatório e envolvida no transporte de oxigênio dos pulmões para os vários tecidos periféricos, pode estar envolvida na sinalização de dor, ou seja, como um regulador da dor e da inflamação e desempenhar um papel anti-inflamatório, e pode ser um parâmetro de diagnóstico valioso para monitorizar a ativação de macrófagos em condições inflamatórias e no caso de doença endodôntica, (37,48) está ligada a 8 proteínas microbianas como a ***Collagenase A*** **(F7J0G5)**, que desempenha uma função de proteólise e pode desempenhar um papel importante em vários efeitos patogénicos, incluindo a invasão de tecidos, a aquisição de nutrientes a partir de proteínas, a destruição da matriz do tecido conjuntivo, e de inactivação de moléculas de defesa do hospedeiro e está ligada a casos de abcessos em PE, (37;48) *a* ***Enolase*** **(I0S024)**, que tem um papel de metabolismo energético e está presente em abcessos, (37;48) a ***Extracellular solute-binding protein family 3*** **(B8IBF1)**, que está presente na membrana e em casos iniciais de PE, (37;48) ***Extracellular solute-binding protein, family 5*** **(Q13BZ9)**, tem função de transporte e é ligada a casos iniciais de PE, (37;48) ***Putative ABC transport system*****,** ***membrane protein*** **(Q5LB48),** com função de transporte e presente em estados iniciais de PE, (37;48) ***TetR family transcriptional regulator*** **(I5BER7)**, com função de

resistência a antibióticos e a proteína ***Tet*** **(Q5GBH8)**, com resistência a tetraciclinas.

A proteína humana ***Peregrin*** **(P55201)**, que pode funcionar como componente do complexo *MOZ / MORF* que tem uma actividade de acetiltransferase de histona H3. Regula positivamente a transcrição de *RUNX1* e *RUNX2* que está associada a estados iniciais da PE, (37) e liga-se a 6 proteinas microbianas tais como a ***Endopeptidase*** **(Q5KFP6)**, com função de proteólise, patogenicidade e resistência / sobrevivência e presente principalmente em abcessos PE, (37;48) **Extracellular *solute-binding protein, family 5* (Q13BZ9)**, ligada ao transporte e envolvida em estados iniciais de PE, ***Minor extracellular protease (F5SFT5),*** ligada á função de proteólise presente em casos de abcessos de PE, (37;48) ***Outer-membrane lipoprotein LolB*** **(G2DKZ6)**, envolvida no transporte e ligada a casos de abcesso, (37;48) ***Putative ABC transport system,*** membrane protein, também com funções de transporte (37;48) e por fim a **Putative ABC transport system, membrane protein (Q5LB48)**, envolvida na resistência a antibióticos. (37;48)

Pela análise da Figura 31 pode constatar-se que o microorganismo que representa mais interações com proteínas humanas são o ***Enterococcus faecalis*** que repesenta um total de 11 proteínas diferentes (representadas a verde), que estabelecem 18 interações, o ***streptococcus sanguinis*** (representado a amarelo) que fazem interações com 2 proteinas, ***pseudomonas*** (representado a cor de laranja) que fazem igualmente 2 interações e o ***bacteroides fragilis*** (repesentado a cor de rosa) também com um total de 2 interações.

E. faecalis, é referido como sendo altamente prevalente (12-90%) em infeções endodônticas e têm o propósito de desempenhar um papel que é responsavel em falhas de tratamento. (70, 71)

Devido ao elevado número de interações e não sendo exequível fazer um estudo exaustivo de cada uma delas, restringiu-se o estudo a bactérias que são conhecidas como tendo influência no desenvolvimento da patologia endodontica. Com isto, tem se como objetivo, perceber de que forma estes agentes possam estar a influenciar o hospedeiro.

Na figura 32 está representada de uma forma mais pormenorizada e restrita a rede de interações entre proteínas humanas (retângulos verdes) que interagem com proteínas *E. faecalis (*retângulos azuis), que foi elaborada com auxílio da ferramenta cytoscape e tendo em conta o número de interações que foram visualizadas para o organismo *E. faecalis* na figura 31.

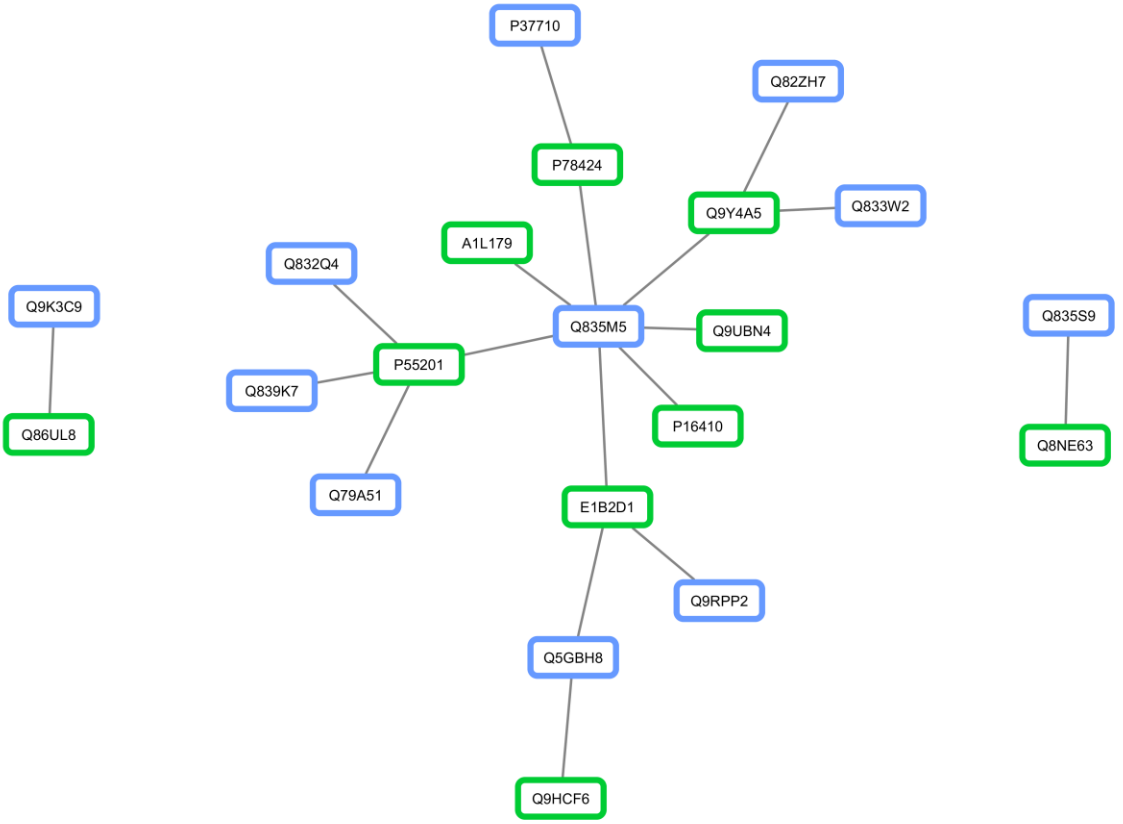


Figura 32: Rede de interações entre proteínas humanas (retângulos verdes) e as proteínas de E. faecalis (retângulos azuis), geradas com a ferramenta Cytoscape.

Pela análise da figura 32 pode ser dito que, a proteína, ***Magnesium-translocating P-type ATPase*** (Q835M5) implicada em processos de transporte de membrana que são mediadas através de ATPases tipo P, com a maioria das ATPases do tipo P a servir processos celulares cruciais, a sua alteração pode estar associada a várias condições fisiopatológicas em seres humanos, (82) interage com 7 proteinas humanas nomeadamente **Peregrin** (P55201), **Short transient receptor potential channel 4** (Q9UBN4), **POU domain, class 6, transcription factor 2** (P78424), **transformation/transcription domain-associated protein** (Q9Y4A5), **Kinesin-like protein** (A1L179), **Cytotoxic T-lymphocyte protein 4** (P16410), **Hemoglobin alpha-1 globin chain variant** (E1B2D1).

As proteínas **Membrane protein, putative** (Q8 32Q4), *Conjugal transfer protein, putative* (Q839K7) e **Nickase** (Q79A51) interage com 1 proteina humana **Peregrin** (P55201).

A proteína **Peptidase T** (Q82ZH7), protease que pode desempenhar um papel importante em vários efeitos patogénicos, incluindo a invasão de tecidos, a aquisição de nutrientes a partir de proteínas, a destruição da matriz do tecido conjuntivo, e a inactivação de moléculas de defesa do hospedeiro, (83) **Sulfatase domain protein** (Q833W2), estas interagem com 1 proteina humana **transformation/transcription domain-associated protein** (Q9Y4A5).
A proteína **Probable protease eep** (Q9RPP2), **TetT** (Q5GBH8) interage com 1 proteina humana **Hemoglobin alpha-1 globin chain variant** (E1B2D1). A proteína **TetT** (Q5GBH8) de resistência à tetraciclina é encontrada em casos de pacientes com *Enterococcus* e pode ser importante do ponto de vista do tratamento porque os antibióticos são conhecidos por não ser muito eficazes no tratamento de infeções endodônticas, (36,37) interage com 1 proteina humana **Transient receptor potential cation channel subfamily M member 3** (Q9HCF6).

A proteína **Autolysin** (P37710),hidrolisa a parede celular de *E. faecalis* e *M. lysodeikticus*. Tem um papel importante no crescimento e separação da parede celular. Participa ainda em processos de doenças infeciosas em endodontia por *E. faecalis*. Estas proteinas existem em todas as bactérias contendo peptidoglicano quebrando esta matriz para que o crescimento e divisão celular possa ocorrer. Quantidades excessivas destas proteínas podem levar a matriz de peptidoglicano a rebentar devido à pressão osmótica (84). Esta proteína interage com 1 proteina humana ***POU domain, class 6, transcription factor 2*** (P78424).

A proteína ***Endolysin*** (Q835S9) interage com 1 proteina humana ***Homeodomain-interacting protein kinase 4*** (Q8NE63).

A proteína ***PBP4 protein*** (Q9K3C9) interage com 1 proteina humana ***Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 2*** (Q86UL8).

5. Conclusão

5. CONCLUSÃO

Este trabalho teve como objetivo a compilação de dados do proteoma em patologia endodôntica e a anotação dessa informação na base de dados do OralOme.

No total foram identificadas 523 novas proteínas, sendo 138 humanas e 385 microbianas o que constitui um contributo importante para o avanço do conhecimento molecular acerca da patologia endodôntica, potenciando a identificação de mecanismos moleculares implicados e futura identificação de biomarcadores.

O facto de as proteínas catalogadas não apresentarem dados de quantificação limita as conclusões, nomeadamente a proposta de potenciais biomarcadores. Sugere-se que sejam realizados novos estudos de proteómica quantitativa.

A caraterização funcional das proteínas implicadas em patologia endodôntica, comparada com o OralOme normal, permitiu inferir um aumento do número de proteínas envolvidas nos processos moleculares como *receptor activity* e *transport activity*.

A comparação das proteínas implicadas na doença endodôntica, identificadas no presente trabalho com as proteínas identificadas como estando alteradas noutras patologias como a periodontite e a gengivite (OralCard), permitiu perceber que das 138 proteinas humanas implicadas em doença endodôntica, 96 são exclusivas desta doença e que as restantes 11 já foram também identificadas noutras patologias orais.

A análise da rede de interações proteína-proteina (interactómica) estabelecida entre as proteínas humanas e microbianas implicadas na doença endodontica, mostra que existe um elevado número de proteínas microbianas a interagir com proteínas do hospedeiro. Verificou-se que existem várias espécies microbianas que interagem com as proteínas humanas hemoglobina (E1B2D1) e peregrin (P55201), ambas associadas a funções de defesa do hospedeiro como a respostas inflamatória contra os agentes patogénicos.

Identificou-se adicionalmente que são possíveis iinterações entre várias proteínas humanas com proteínas de *E. faecalis* nomeadamente com as proteínas ***Magnesium-translocating P-type ATPase, Peptidase T, TetT,***

Autolysin. Estas interações podem ajudar a identificar mecanismos de virulência, e, assim, auxiliar na identificação de potenciais alvos terapêuticos.

As proteínas microbianas estudadas neste trabalho representam apenas uma pequena fração das proteínas envolvidas na doença endodontica, facto este dependente da pouca anotação disponível atualmente sobre as proteínas bacterianas.

6. Bibliografia

6. Bibliografia

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7. Anexos

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Anexo A

Proteínas humanas identificadas no âmbito do estudo do proteoma da patologia endodôntica.

Anexo B

Proteínas microbianas identificadas no âmbito do estudo do proteoma da patologia endodôntica.

Anexo C

Lista de proteinas exclusivas da patologia endodôntica.

Anexo A

Proteínas humanas identificadas no âmbito do estudo de patologia endodôntica e analisadas ao longo deste trabalho anotadas por ordem alfabética de código UniProtKBAC.

UniProtKB AC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling**	Methods of Analysis***	Type of Study	Citation (NCBI ID)
A1L179	Homo sapiens	Kinesin-like protein	x	x	initial (asymptomatic); post-treatment (CHX)	D005057	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A2A2R0	Homo sapiens	BPI fold-containing family B member 1	x	x	post-treatment (NaOCl)	D005028	20 - 39	M/F	"	"	Proteomics	24143178
A2J1N9	Homo sapiens	Rheumatoid factor RF-ET12	x	x	abscess	D005149	20 - 39	M/F	"	"	Proteomics	24143178
A2MYD4	Homo sapiens	V2-7 protein	x	x	post-treatment (NaOCl)	D005153	20 - 39	M/F	"	"	Proteomics	24143178
A3KMH1	Homo sapiens	von Willebrand factor A domain-containing protein 8	x	x	abscess	D005099	20 - 39	M/F	"	"	Proteomics	24143178
A6NKG5	Homo sapiens	Retrotransposon-like protein 1	x	x	initial (asymptomatic)	D005082	20 - 39	M/F	"	"	Proteomics	24143178
A6NL76	Homo sapiens	Actin, alpha skeletal muscle	x	x	initial (asymtpmatic)	D005020	20 - 39	M/F	"	"	Proteomics	24143178
A8K494	Homo sapiens	cDNA FLJ78440, highly similar to Human lactoferrin	x	x	post-treatment (NaOCl)	D005034	20 - 39	M/F	"	"	Proteomics	24143178
A8K964	Homo sapiens	cDNA FLJ75071, highly similar to Homo sapiens pinin, desmosome associated protein	x	x	abscess	D005142	20 - 39	M/F	"	"	Proteomics	24143178
A8MPY1	Homo sapiens	Gamma-aminobutyric acid receptor subunit rho-3	x	x	abscess	D005049	20 - 39	M/F	"	"	Proteomics	24143178
B1ANS9	Homo sapiens	WD repeat-containing protein 64	x	x	abscess	D005154	20 - 39	M/F	"	"	Proteomics	24143178
B2RBS8	Homo sapiens	cDNA, FLJ95666, highly similar to Homo sapiens albumin	x	x	abscess	D005035	20 - 39	M/F	"	"	Proteomics	24143178
B3KS49	Homo sapiens	cDNA FLJ35478 fis, clone SMINT2007796, highly similar to Gelsolin	x	x	abscess	D005140	20 - 39	M/F	"	"	Proteomics	24143178
B4DUI8	Homo sapiens	cDNA FLJ52761, highly similar to Actin, aortic smooth muscle	x	x	abscess	D005105	20 - 39	M/F	"	"	Proteomics	24143178
B4DYU2	Homo sapiens	cDNA FLJ55996, highly similar to Conserved oligomeric Golgi complex component 8	x	x	abscess	D005141	20 - 39	M/F	"	"	Proteomics	24143178
B4E0C4	Homo sapiens	Poly [ADP-ribose] polymerase	x	x	post-treatment (CHX)	D005033	20 - 39	M/F	"	"	Proteomics	24143178
B4E1B2	Homo sapiens	cDNA FLJ53691, highly similar to Serotransferrin	x	x	post-treatment (NaOCl)	D005032	20 - 39	M/F	"	"	Proteomics	24143178
B4E1D3	Homo sapiens	cDNA FLJ53952, highly similar to Fibrinogen beta	x	x	initial (asymptomatic)	D005106	20 - 39	M/F	"	"	Proteomics	24143178

UniProtKB AC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling**	Methods of Analysis***	Type of Study	Citation (NCBI ID)
		chain										
B7Z7W2	Homo sapiens	cDNA FLJ55558, highly similar to Regulating synaptic membrane exocytosis protein 1	x	x	abscess	D005079	20 - 39	M/F	"	"	Proteomics	24143178
C8C504	Homo sapiens	Beta-globin	x	x	post-treatment (CHX)	D005104	20 - 39	M/F	"	"	Proteomics	24143178
G5E940	Homo sapiens	RING finger protein 32	x	x	initial (asymptomatic)	D005150	20 - 39	M/F	"	"	Proteomics	24143178
O00461	Homo sapiens	Golgi integral membrane protein 4	x	x	abscess	D005051	20 - 39	M/F	"	"	Proteomics	24143178
O15355	Homo sapiens	Protein phosphatase 1G	x	x	abscess	D005076	20 - 39	M/F	"	"	Proteomics	24143178
O43300	Homo sapiens	Leucine-rich repeat transmembrane neuronal protein 2	x	x	abscess	D005058	20 - 39	M/F	"	"	Proteomics	24143178
O43805	Homo sapiens	Sjoegren syndrome nuclear autoantigen 1	x	x	post-treatment (NaOCl)	D005086	20 - 39	M/F	"	"	Proteomics	24143178
O60462	Homo sapiens	Neuropilin-2	x	x	abscess	D005110	20 - 39	M/F	"	"	Proteomics	24143178
O60869	Homo sapiens	Endothelial differentiation-related factor 1	x	x	post-treatment (CHX)	D005043	20 - 39	M/F	"	"	Proteomics	24143178
O75335	**Homo sapiens**	**Liprin-alpha-4**	**x**	**x**	**abscess**	**D005060**	**20 - 39**	**M/F**	"	"	**Proteomics**	**24143178**
O94827	Homo sapiens	Pleckstrin homology domain-containing family G member 5	x	x	initial (asymptomatic)	D005070	20 - 39	M/F	"	"	Proteomics	24143178
O95067	Homo sapiens	G2/mitotic-specific cyclin-B2	x	x	abscess	D005121	20 - 39	M/F	"	"	Proteomics	24143178
O95684	Homo sapiens	FGFR1 oncogene partner	x	x	abscess	D005045	20 - 39	M/F	"	"	Proteomics	24143178
P00738	Homo sapiens	Haptoglobin	x	x	abscess; initial (asymptomatic)	D005122	20 - 39	M/F	"	"	Proteomics	24143178
P01024	Homo sapiens	Complement C3	x	x	abscess	D005116	20 - 39	M/F	"	"	Proteomics	24143178
P01036	**Homo sapiens**	**Cystatin-S**	**x**	**x**	**initial (asymptomatic); post-treatment (CHX/NaOCl)**	**D005117**	**20 - 39**	**M/F**	"	"	**Proteomics**	**24143178**
P01037	Homo sapiens	Cystatin-SN	x	x	abscess; initial (asymptomatic); post-treatment (CHX/NaOCl)	D005119	20 - 39	M/F	"	"	Proteomics	24143178
P01833	Homo sapiens	Polymeric immunoglobulin receptor	x	x	initial (asymptomatic); post-treatment (CHX/NaOCl)	D005135	20 - 39	M/F	"	"	Proteomics	24143178
P01834	Homo sapiens	Ig kappa chain C region	x	x	abscess; initial (asymptomatic); post-treatment (CHX/NaOCl)	D005126	20 - 39	M/F	"	"	Proteomics	24143178
P01860	Homo sapiens	Ig gamma-3 chain C region	x	x	abscess;initial (asymptomatic); post-treatment (NaOCl)	D005125	20 - 39	M/F	"	"	Proteomics	24143178
P01876	Homo sapiens	Ig alpha-1 chain C region	x	x	initial (asymptomatic)	D005124	20 - 39	M/F	"	"	Proteomics	24143178
P02042	Homo sapiens	Hemoglobin subunit delta	x	x	abscess, initial (asymptomatic)	D005109	20 - 39	M/F	"	"	Proteomics	24143178
P02452	Homo sapiens	Collagen alpha-1	x	x	initial (asymptomatic); post-treatment (CHX)	D005112	20 - 39	M/F	"	"	Proteomics	24143178
P02679	Homo sapiens	Fibrinogen gamma chain	x	x	abscess	D005107	20 - 39	M/F	"	"	Proteomics	24143178
P02749	**Homo sapiens**	**Beta-2-glycoprotein 1**	**x**	**x**	**abscess**	**D005103**	**20 - 39**	**M/F**	"	"	**Proteomics**	**24143178**
P02768	Homo sapiens	Serum albumin	x	x	abscess; initial	D005111	20 - 39	M/F	"	"	Proteomics	24143178

UniProtKB AC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling**	Methods of Analysis***	Type of Study	Citation (NCBI ID)
					(asymptomatic); post-treatment (NaOCl)							
P02812	Homo sapiens	Basic salivary proline-rich protein 2	x	x	abscess	D005139	20 - 39	M/F	"	"	Proteomics	24143178
P02814	Homo sapiens	Submaxillary gland androgen-regulated protein 3B	x	x	abscess	D005151	20 - 39	M/F	"	"	Proteomics	24143178
P04745	Homo sapiens	Alpha-amylase 1	x	x	initial (asymtpmatic); post-treatment (CHX/NaOCl)	D005024	20 - 39	M/F	"	"	Proteomics	24143178
P05164	**Homo sapiens**	**Myeloperoxidase**	**x**	**x**	**abscess**	**D005131**	**20 - 39**	**M/F**	"	"	**Proteomics**	**24143178**
P05204	Homo sapiens	Non-histone chromosomal protein HMG-17	x	x	abscess; initial (asymptomatic)	D005063	20 - 39	M/F	"	"	Proteomics	24143178
P06702	**Homo sapiens**	**Protein S100-A9**	**x**	**x**	**initial (asymptomatic)**	**D005137**	**20 - 39**	**M/F**	"	"	**Proteomics**	**24143178**
P06733	Homo sapiens	Alpha-enolase	x	x	post-treatment (NaOCl)	D005025	20 - 39	M/F	"	"	Proteomics	24143178
P07737	Homo sapiens	Profilin-1	x	x	initial (asymptomatic); post-treatment (NaOCl)	D005073	20 - 39	M/F	"	"	Proteomics	24143178
P08670	Homo sapiens	Vimentin	x	x	post-treatment (NaOCl)	D005100	20 - 39	M/F	"	"	Proteomics	24143178
P09228	Homo sapiens	Cystatin-SA	x	x	initial (asymptomatic); post-treatment (NaOCl)	D005118	20 - 39	M/F	"	"	Proteomics	24143178
P09661	Homo sapiens	U2 small nuclear ribonucleoprotein A'	x	x	post-treatment (NaOCl)	D005096	20 - 39	M/F	"	"	Proteomics	24143178
P0CG04	Homo sapiens	Ig lambda-1 chain C regions	x	x	abscess; initial (asymptomatic)	D005127	20 - 39	M/F	"	"	Proteomics	24143178
P10809	**Homo sapiens**	**60 kDa heat shock protein, mitochondrial**	**x**	**x**	**post-treatment (NaOCl)**	**D005114**	**20 - 39**	**M/F**	"	"	**Proteomics**	**24143178**
P11021	**Homo sapiens**	**78 kDa glucose-regulated protein**	**x**	**x**	**post-treatment (NaOCl)**	**D005018**	**20 - 39**	**M/F**	"	"	**Proteomics**	**24143178**
P12273	Homo sapiens	Prolactin-inducible protein	x	x	initial (asymptomatic); post-treatment (NaOCl)	D005136	20 - 39	M/F	"	"	Proteomics	24143178
P13797	Homo sapiens	Plastin-3	x	x	abscess	D005069	20 - 39	M/F	"	"	Proteomics	24143178
P16401	Homo sapiens	Histone H1.5	x	x	initial (asymptomatic)	D005053	20 - 39	M/F	"	"	Proteomics	24143178
P16410	Homo sapiens	Cytotoxic T-lymphocyte protein 4	x	x	abscess	D005120	20 - 39	M/F	"	"	Proteomics	24143178
P18583	Homo sapiens	Protein SON	x	x	abscess	D005077	20 - 39	M/F	"	"	Proteomics	24143178
P25705	Homo sapiens	ATP synthase subunit alpha, mitochondrial	x	x	post-treatment (NaOCl)	D005026	20 - 39	M/F	"	"	Proteomics	24143178
P29400	Homo sapiens	Collagen alpha-5	x	x	abscess	D005113	20 - 39	M/F	"	"	Proteomics	24143178
P32314	Homo sapiens	Forkhead box protein N2	x	x	abscess	D005046	20 - 39	M/F	"	"	Proteomics	24143178
P42356	Homo sapiens	Phosphatidylinositol 4-kinase alpha	x	x	initial (asymptomatic)	D005068	20 - 39	M/F	"	"	Proteomics	24143178
P55201	Homo sapiens	Peregrin	x	x	initial (asymptomatic)	D005067	20 - 39	M/F	"	"	Proteomics	24143178
P57053	Homo sapiens	Histone H2B type F-S	x	x	abscess; initial (asymptomatic)	D005123	20 - 39	M/F	"	"	Proteomics	24143178
P59665	**Homo sapiens**	**Neutrophil defensin 1**	**x**	**x**	**abscess; initial (asymptomatic); post-treatment (NaOCl)**	**D005133**	**20 - 39**	**M/F**	"	"	**Proteomics**	**24143178**

UniProtKB AC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling**	Methods of Analysis***	Type of Study	Citation (NCBI ID)
P59666	**Homo sapiens**	**Neutrophil defensin 3**	**x**	**x**	**abscess;initial (asymptomatic); post-treatment (NaOCl)**	**D005134**	**20 - 39**	**M/F**	"	"	**Proteomics**	**24143178**
P63261	Homo sapiens	Actin, cytoplasmic 2	x	x	abscess; initial (asymptomatic)	D005022	20 - 39	M/F	"	"	Proteomics	24143178
P69905	Homo sapiens	Hemoglobin subunit alpha	x	x	abscess; initial (asymptomatic); post-treatment (CHX)	D005108	20 - 39	M/F	"	"	Proteomics	24143178
P78424	Homo sapiens	POU domain, class 6, transcription factor 2	x	x	initial (asymptomatic)	D005072	20 - 39	M/F	"	"	Proteomics	24143178
Q03393	Homo sapiens	6-pyruvoyl tetrahydrobiopterin synthase	x	x	abscess	D005017	20 - 39	M/F	"	"	Proteomics	24143178
Q06278	Homo sapiens	Aldehyde oxidase	x	x	abscess	D005115	20 - 39	M/F	"	"	Proteomics	24143178
Q12905	Homo sapiens	Interleukin enhancer-binding factor 2	x	x	post-treatment (NaOCl)	D005128	20 - 39	M/F	"	"	Proteomics	24143178
Q13557	Homo sapiens	Calcium/calmodulin-dependent protein kinase type II subunit delta	x	x	abscess	D005031	20 - 39	M/F	"	"	Proteomics	24143178
Q13621	Homo sapiens	Solute carrier family 12 member 1	x	x	abscess	D005087	20 - 39	M/F	"	"	Proteomics	24143178
Q14376	Homo sapiens	UDP-glucose 4-epimerase	x	x	abscess	D005097	20 - 39	M/F	"	"	Proteomics	24143178
Q14623	Homo sapiens	Indian hedgehog protein	x	x	abscess	D005055	20 - 39	M/F	"	"	Proteomics	24143178
Q15080	Homo sapiens	Neutrophil cytosol factor 4	x	x	abscess	D005132	20 - 39	M/F	"	"	Proteomics	24143178
Q562F6	Homo sapiens	Shugoshin 2	x	x	abscess	D005085	20 - 39	M/F	"	"	Proteomics	24143178
Q5VU65	Homo sapiens	Nuclear pore membrane glycoprotein 210-like	x	x	abscess	D005064	20 - 39	M/F	"	"	Proteomics	24143178
Q693B1	Homo sapiens	BTB/POZ domain-containing protein KCTD11	x	x	abscess	D005029	20 - 39	M/F	"	"	Proteomics	24143178
Q6ICB4	Homo sapiens	Sesquipedalian-2	x	x	abscess	D005074	20 - 39	M/F	"	"	Proteomics	24143178
Q6PIF6	Homo sapiens	Unconventional myosin-VIIb	x	x	abscess	D005062	20 - 39	M/F	"	"	Proteomics	24143178
Q6ZVD7	Homo sapiens	Storkhead-box protein 1	x	x	abscess	D005091	20 - 39	M/F	"	"	Proteomics	24143178
Q6ZVM7	Homo sapiens	TOM1-like protein 2	x	x	abscess	D005092	20 - 39	M/F	"	"	Proteomics	24143178
Q7L7X3	Homo sapiens	Serine/threonine-protein kinase TAO1	x	x	abscess	D005083	20 - 39	M/F	"	"	Proteomics	24143178
Q7Z517	Homo sapiens	Transgelin	x	x	initial (asymptomatic)	D005145	20 - 39	M/F	"	"	Proteomics	24143178
Q86UL8	Homo sapiens	Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 2	x	x	abscess	D005061	20 - 39	M/F	"	"	Proteomics	24143178
Q86Y26	Homo sapiens	NUT family member 1	x	x	abscess	D005075	20 - 39	M/F	"	"	Proteomics	24143178
Q8IVB5	Homo sapiens	LIX1-like protein	x	x	abscess	D005143	20 - 39	M/F	"	"	Proteomics	24143178
Q8IW40	Homo sapiens	Coiled-coil domain-containing protein 103	x	x	initial (asymtomatic)	D005036	20 - 39	M/F	"	"	Proteomics	24143178
Q8N1W1	Homo sapiens	Rho guanine nucleotide exchange factor 28	x	x	post-treatment (CHX)	D005056	20 - 39	M/F	"	"	Proteomics	24143178
Q8N4C9	Homo sapiens	Uncharacterized protein C17orf78	x	x	abscess	D005098	20 - 39	M/F	"	"	Proteomics	24143178
Q8NA61	Homo sapiens	Spermatid-associated protein	x	x	abscess	D005089	20 - 39	M/F	"	"	Proteomics	24143178
Q8NDV7	Homo sapiens	Trinucleotide repeat-containing gene 6A protein	x	x	abscess	D005095	20 - 39	M/F	"	"	Proteomics	24143178
Q8NE09	Homo sapiens	Regulator of G-protein signaling 22	x	x	abscess	D005080	20 - 39	M/F	"	"	Proteomics	24143178
Q8NE63	Homo sapiens	Homeodomain-interacting protein kinase 4	x	x	abscess	D005054	20 - 39	M/F	"	"	Proteomics	24143178
Q8NEM8	Homo sapiens	Cytosolic carboxypeptidase 3	x	x	abscess	D005037	20 - 39	M/F	"	"	Proteomics	24143178

UniProtKB AC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling**	Methods of Analysis***	Type of Study	Citation (NCBI ID)
Q8NFI4	Homo sapiens	Putative protein FAM10A5	x	x	abscess	D005147	20 - 39	M/F	"	"	Proteomics	24143178
Q8TD57	Homo sapiens	Dynein heavy chain 3, axonemal	x	x	abscess	D005040	20 - 39	M/F	"	"	Proteomics	24143178
Q8TDJ6	Homo sapiens	DmX-like protein 2	x	x	abscess	D005039	20 - 39	M/F	"	"	Proteomics	24143178
Q8TE73	Homo sapiens	Dynein heavy chain 5, axonemal	x	x	abscess	D005041	20 - 39	M/F	"	"	Proteomics	24143178
Q8TF21	Homo sapiens	Ankyrin repeat domain-containing protein 24	x	x	initial (asymptomatic)	D005138	20 - 39	M/F	"	"	Proteomics	24143178
Q8WU17	Homo sapiens	E3 ubiquitin-protein ligase RNF139	x	x	initial (asymptomatic)	D005042	20 - 39	M/F	"	"	Proteomics	24143178
Q8WUD1	Homo sapiens	Ras-related protein Rab-2B	x	x	abscess	D005078	20 - 39	M/F	"	"	Proteomics	24143178
Q8WUE5	Homo sapiens	Cancer/testis antigen 55	x	x	abscess	D005152	20 - 39	M/F	"	"	Proteomics	24143178
Q92499	Homo sapiens	ATP-dependent RNA helicase DDX1	x	x	abscess	D005027	20 - 39	M/F	"	"	Proteomics	24143178
Q92502	Homo sapiens	StAR-related lipid transfer protein 8	x	x	abscess	D005090	20 - 39	M/F	"	"	Proteomics	24143178
Q93050	**Homo sapiens**	**V-type proton ATPase 116 kDa subunit a isoform 1**	**x**	**x**	**post-treatment (CHX)**	**D005101**	**20 - 39**	**M/F**	"	"	**Proteomics**	**24143178**
Q969R2	Homo sapiens	Oxysterol-binding protein 2	x	x	abscess	D005065	20 - 39	M/F	"	"	Proteomics	24143178
Q96KB5	Homo sapiens	Lymphokine-activated killer T-cell-originated protein kinase	x	x	abscess	D005130	20 - 39	M/F	"	"	Proteomics	24143178
Q96QF7	Homo sapiens	Acidic repeat-containing protein	x	x	abscess	D005019	20 - 39	M/F	"	"	Proteomics	24143178
Q96R05	Homo sapiens	Retinoid-binding protein 7	x	x	abscess	D005081	20 - 39	M/F	"	"	Proteomics	24143178
Q96RG2	Homo sapiens	PAS domain-containing serine/threonine-protein kinase	x	x	abscess	D005066	20 - 39	M/F	"	"	Proteomics	24143178
Q99714	Homo sapiens	3-hydroxyacyl-CoA dehydrogenase type-2	x	x	abscess	D005016	20 - 39	M/F	"	"	Proteomics	24143178
Q9GZV4	Homo sapiens	Eukaryotic translation initiation factor 5A-2	x	x	post-treatment (CHX)	D005044	20 - 39	M/F	"	"	Proteomics	24143178
Q9H040	Homo sapiens	SprT-like domain-containing protein Spartan	x	x		D005102	20 - 39	M/F	"	"	Proteomics	24143178
Q9H3Q3	Homo sapiens	Galactose-3-O-sulfotransferase 2	x	x	abscess	D005048	20 - 39	M/F	"	"	Proteomics	24143178
Q9H5Q4	Homo sapiens	Dimethyladenosine transferase 2, mitochondrial	x	x	abscess	D005038	20 - 39	M/F	"	"	Proteomics	24143178
Q9HCF6	Homo sapiens	Transient receptor potential cation channel subfamily M member 3	x	x	abscess	D005094	20 - 39	M/F	"	"	Proteomics	24143178
Q9HCH0	Homo sapiens	Nck-associated protein 5-like	x	x	abscess	D005144	20 - 39	M/F	"	"	Proteomics	24143178
Q9NPD5	Homo sapiens	Solute carrier organic anion transporter family member 1B3	x	x	abscess	D005088	20 - 39	M/F	"	"	Proteomics	24143178
Q9NRZ9	Homo sapiens	Lymphoid-specific helicase	x	x	abscess	D005129	20 - 39	M/F	"	"	Proteomics	24143178
Q9NW75	Homo sapiens	G patch domain-containing protein 2	x	x	abscess	D005047	20 - 39	M/F	"	"	Proteomics	24143178
Q9NYQ6	Homo sapiens	Cadherin EGF LAG seven-pass G-type receptor 1	x	x	abscess	D005030	20 - 39	M/F	"	"	Proteomics	24143178
Q9NZD2	Homo sapiens	Glycolipid transfer protein	x	x	abscess	D005050	20 - 39	M/F	"	"	Proteomics	24143178
Q9P2V4	Homo sapiens	Leucine-rich repeat, immunoglobulin-like domain and transmembrane domain-containing protein 1	x	x	initial (asymptomatic);post-treatment (NaOCl)	D005059	20 - 39	M/F	"	"	Proteomics	24143178
Q9UBN4	Homo sapiens	Short transient receptor potential channel 4	x	x	abscess	D005084	20 - 39	M/F	"	"	Proteomics	24143178
Q9UJY4	Homo sapiens	ADP-ribosylation factor-binding protein GGA2	x	x	abscess	D005023	20 - 39	M/F	"	"	Proteomics	24143178
Q9UKA9	Homo sapiens	Polypyrimidine tract-binding	x	x	abscess	D005071	20 - 39	M/F	"	"	Proteomics	24143178

UniProtKB AC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling**	Methods of Analysis***	Type of Study	Citation (NCBI ID)
		protein 2										
Q9ULV5	Homo sapiens	Heat shock factor protein 4	x	x	abscess	D005052	20 - 39	M/F	"	"	Proteomics	24143178
Q9Y2G0	Homo sapiens	Protein EFR3 homolog B	x	x	abscess	D005146	20 - 39	M/F	"	"	Proteomics	24143178
Q9Y4A5	Homo sapiens	Transformation/transcription domain-associated protein	x	x	abscess	D005093	20 - 39	M/F	"	"	Proteomics	24143178

Anexo B

Proteínas microbianas identificadas no âmbito do estudo de patologia endodôntica e analisadas ao longo deste trabalho anotadas por ordem alfabética de código UniProtKBAC.

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis***	Type of Study	Citation (NCBI ID)
A0A0D7LTZ2	Citrobacter freundii	Tail protein	x	x	abscess	D004940	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A0A0E0UZZ5	Listeria monocytogenes serotype 4a	Putative gp69	x	x	abscess	D004947	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A0A0G3CVE3	Acinetobacter baumannii	Uncharacterized protein	x	x	initial (asymptomatic)	D004950	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A0A0K2E6R3	Streptococcus suis	Phosphate transport system permease protein	x	x	endodontic infections (initial)	D005183		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
A0A0K9UZH8	Vibrio cholerae 2740-80	Oligoendopeptidase F	x	x	abscess	D004893	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
									malaise.			
A0A0M1T4F4	Klebsiella pneumoniae subsp. pneumoniae	Hydrolase	x	x	post-treatment (CHX)	D004827	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A0A0M7PC69	Achromobacter sp.	Phosphoheptose isomerase	x	x	abscess	D004868	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A0A0T5XCA0	Anaerobaculum hydrogeniformans ATCC BAA-1850	Probable endonuclease 4	x	x	abscess	D004793	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A0A0T6FJS9	Clostridium sporogenes	ATP-dependent helicase	x	x	post-treatment (CHX)	D004838	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A0A0T9B796	Mycobacterium tuberculosis	Cutinase	x	x	abscess	D004849	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178

UniProtKB AC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
									malaise.			
A0A0U0YFC9	Mycobacterium abscessus	Probable 3-oxoacyl-	x	x	abscess	D004846	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A0A140PSG7	Fusobacterium nucleatum subsp. animalis 7_1	Uncharacterized protein	x	x	abscess	D004830	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A0PZG4	Clostridium novyi	UPF0758 protein NT01CX_1687	x	x	initial (asymptomatic)	D004807	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A0QLI5	Mycobacterium avium	Putative NAD	x	x	post-treatment (NaOCl)	D004888	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A1STV6	Psychromonas ingrahamii	UvrABC system protein B	x	x	abscess	D004808	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis***	Type of Study	Citation (NCBI ID)
									malaise.			
A1YGU1	Enterococcus faecalis	Serine protease	x	x	endodontic infections (initial)	D005199		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
A2SIW6	Methylibium petroleiphilum	Uncharacterized protein	x	x	abscess	D004986	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A3CPZ1	Streptococcus sanguinis	Thioredoxin reductase	x	x	endodontic infections (initial)	D005185		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
A3CQI2	Streptococcus sanguinis	DNA polymerase III PolC-type	x	x	initial (asymptomatic)	D004780	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A3I6E1	Bacillus sp. B14905	Microbial collagenase metalloprotease, peptidase M9A family protein	x	x	endodontic infections (initial)	D005156		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
A3PFE3	Prochlorococcus marinus	Trigger factor	x	x	initial (asymtomatic); post-treatment (NaOCl)	D004773	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A3VEV1	Maritimibacter alkaliphilus HTCC2654	UvrABC system protein C	x	x	initial (asymptomatic)	D004809	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion	Proteomics	24143178

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
									which showed localized swelling, fever, lymphadenopathy, and malaise.	trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
A3XE07	Roseobacter sp. MED193	ATPase of the AAA+ class	x	x	abscess	D004819	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A3XLN6	Leeuwenhoekiella blandensis	Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase	x	x	abscess	D004939	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A4BWF2	Polaribacter irgensii 23-P	Sensory box sensor histidine kinase	x	x	initial (asymptomatic)	D004730	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A4EBZ4	Collinsella aerofaciens ATCC 25986	Imidazoleglycerol-phosphate dehydratase	x	x	abscess	D004756	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A4F870	Saccharopolyspora erythraea	Probable DNA ligase	x	x	abscess	D004792	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion	Proteomics	24143178

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis***	Type of Study	Citation (NCBI ID)
									which showed localized swelling, fever, lymphadenopathy, and malaise.	trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
A4J2F9	Desulfotomaculum reducens	Probable glycine dehydrogenase	x	x	abscess	D004944	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A4VQY0	Pseudomonas stutzeri	Glutamate-1-semialdehyde 2,1-aminomutase	x	x	initial (asymptomatic)	D004936	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A4X9C9	Salinispora tropica	Uncharacterized protein	x	x	abscess	D004969	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A5CNU5	Clavibacter michiganensis subsp. michiganensis	Putative beta lactamase/penicillin-binding protein	x	x	endodontic infections (initial)	D005161		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
A5EYL9	Vibrio cholerae serotype O1	GMP reductase	x	x	initial (asymptomatic)	D004873	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A5IYP9	Mycoplasma	ABC transporter, permease protein	x	x	initial	D00491	20 -	M/F	canals of 12 teeth with	Clinical samples were processed for	Proteomi	241431

UniProtKB AC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling**	Methods of Analysis***	Type of Study	Citation (NCBI ID)
	agalactiae				(asymptomatic)	0	39		asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	cs	78
A5M6N5	Streptococcus pneumoniae SP14-BS69	Single-stranded-DNA-specific exonuclease RecJ	x	x	post-treatment (NaOCl)	D004803	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A5TVG7	Fusobacterium nucleatum subsp. polymorphum ATCC 10953	N-acylneuraminate cytidylyltransferase	x	x	endodontic infections (initial)	D005168		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
A6EP73	unidentified eubacterium SCB49	Peptidoglycan-binding LysM	x	x	initial (asymtomatic)	D004769	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A6F384	Marinobacter algicola DG893	Uncharacterized protein	x	x	post-treatment (NaOCl)	D004952	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A6FL05	Roseobacter sp. AzwK-3b	Probable insertion sequence transposase protein	x	x	initial (asymtomatic); post-treatment (CHX)	D004794	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and	Proteomics	24143178

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
									swelling, fever, lymphadenopathy, and malaise.	liquid chromatography-quadrupole time-of-flight.		
A6FT75	Roseobacter sp. AzwK-3b	Uncharacterized protein	x	x	abscess	D004959	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A6GBD0	Plesiocystis pacifica SIR-1	Histidine ammonia-lyase	x	x	abscess	D004755	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A6L076	Bacteroides vulgatus	Penicillin-binding protein	x	x	endodontic infections (initial)	D005160		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
A6L2G6	Bacteroides vulgatus	Putative outer membrane protein, probably involved in nutrient binding	x	x	post-treatment (CHX)	D004864	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A6U8F8	Sinorhizobium medicae	Bifunctional enzyme IspD/IspF [Includes: 2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	x	x	abscess	D004932	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A6VP17	Actinobacillus succinogenes	Glucose-1-phosphate adenylyltransferase	x	x	abscess	D004825	20 - 39	M/F	canals of 12 teeth with asymptomatic apical	Clinical samples were processed for analysis of the exoproteome by using	Proteomics	24143178

UniProtKB AC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis***	Type of Study	Citation (NCBI ID)
									periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
A6VX99	Marinomonas sp.	Glutamate racemase	x	x	abscess	D004764	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A6VZ36	Marinomonas sp.	Succinate dehydrogenase hydrophobic membrane anchor subunit	x	x	abscess	D004843	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A6WMK8	Shewanella baltica	Probable hydrogenase nickel incorporation protein HypA	x	x	post-treatment (NaOCl)	D004945	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A7FM05	Yersinia pseudotuberculosis serotype O:1b	Vitamin B12-binding protein	x	x	post-treatment (NaOCl)	D004928	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A7HA60	Anaeromyxobacter sp.	Bifunctional purine biosynthesis protein PurH [Includes:	x	x	initial (asymptomatic)	D004872	20 - 39	M/F	canals of 12 teeth with asymptomatic apical	Clinical samples were processed for analysis of the exoproteome by using	Proteomics	24143178

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
		Phosphoribosylaminoimidazolecarboxamide formyltransferase							periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
A7IDU0	Xanthobacter autotrophicus	2,3-dihydroxyphenylpropionate/2,3-dihydroxicinnamic acid 1,2-dioxygenase	x	x	post-treatment (NaOCl)	D004810	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A7INN1	Xanthobacter autotrophicus	Serine--tRNA ligase	x	x	post-treatment (NaOCl)	D004742	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A7MMY9	Cronobacter sakazakii	Uncharacterized protein	x	x	abscess	D004985	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A7MZE8	Vibrio campbellii	Uncharacterized protein	x	x	abscess	D004974	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A7NHN0	Roseiflexus castenholzii	Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen	x	x	abscess	D004900	20 - 39	M/F	canals of 12 teeth with asymptomatic apical	Clinical samples were processed for analysis of the exoproteome by using	Proteomics	24143178

UniProtK BAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
									periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
A7NL32	Roseiflexus castenholzii	Mandelate racemase/muconate lactonizing protein	x	x	abscess	D004757	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A8AXJ4	Streptococcus gordonii	Lipoprotein, putative	x	x	endodontic infections (initial)	D005182		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
A8GFH0	Serratia proteamaculans	Ribonuclease D	x	x	abscess	D004728	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A8H6I8	Shewanella pealeana	Amidohydrolase	x	x	initial (asymptomatic)	D004930	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A8ZRB5	Deinococcus geothermalis	Antitoxin	x	x	abscess	D004941	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole	Proteomics	24143178

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
									lymphadenopathy, and malaise.	time-of-flight.		
A9NHW0	Acholeplasma laidlawii	DNA ligase	x	x	abscess	D004779	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
A9WPI2	Renibacterium salmoninarum	Lipoprotein	x	x	abscess	D004869	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
B0NFJ8	[Clostridium] scindens ATCC 35704	Cysteine desulfurase family protein	x	x	abscess	D004753	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
B1I3T1	Desulforudis audaxviator	Malate dehydrogenase	x	x	initial (asymptomatic)	D004829	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
B1TBS9	Burkholderia ambifaria MEX-5	Aminotransferase	x	x	abscess	D004713	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole	Proteomics	24143178

UniProtK BAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
									lymphadenopathy, and malaise.	time-of-flight.		
B1XSN0	Polynucleobacter necessarius subsp. necessarius	Protease HtpX homolog	x	x	abscess	D004894	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
B1YIY3	Exiguobacterium sibiricum	Methylthioribose kinase	x	x	abscess	D004721	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
B1ZK06	Methylobacterium populi	Uncharacterized protein	x	x	abscess	D004966	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
B2RKT2	Porphyromonas gingivalis	Protein translocase subunit SecA	x	x	endodontic infections (initial)	D005175		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
B2UMZ4	Akkermansia muciniphila	ABC transporter related	x	x	post-treatment (CHX)	D004815	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
B2UQE4	Akkermansia muciniphila	Coagulation factor 5/8 type domain protein	x	x	abscess	D004886	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry	Proteomics	24143178

UniProtKB AC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling**	Methods of Analysis***	Type of Study	Citation (NCBI ID)
									aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
B2VIL6	Erwinia tasmaniensis	Ubiquinone biosynthesis O-methyltransferase	x	x	abscess	D004811	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
B3F5G1	Streptococcus dysgalactiae subsp. equisimilis	DNA topoisomerase	x	x	post-treatment (NaOCl)	D004804	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
B4RAW4	Phenylobacterium zucineum	DNA polymerase III, delta prime subunit	x	x	abscess	D004781	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
B5GPC0	Streptomyces clavuligerus	tRNA	x	x	abscess	D004751	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
B5HF16	Streptomyces pristinaespiralis ATCC 25486	Transport associated protein	x	x	initial (asymptomatic)	D004907	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry	Proteomics	24143178

UniProtKB AC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age grou	Gender*	Methods of Sampling **	Methods of Analysis***	Type of Study	Citation (NCBI ID)
									aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
B5I692	Streptomyces sviceus ATCC 29083	FemAB family protein	x	x	abscess	D004913	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
B5ZFN7	Gluconacetobacter diazotrophicus	Uncharacterized protein	x	x	abscess	D004964	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
B6R7K1	Pseudovibrio sp. JE062	Polyphosphate kinase	x	x	initial (asymptomatic)	D004835	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
B7AQT9	[Bacteroides] pectinophilus ATCC 43243	Putative uncharacterized protein	x	x	initial (asymptomatic)	D004726	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
B7GGW0	Anoxybacillus flavithermus	L-arabinose isomerase	x	x	initial (asymptomatic)	D004828	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry	Proteomics	24143178

UniProtKB AC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
									aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
B7KZ66	Methylobacterium extorquens	Methylthioribose-1-phosphate isomerase	x	x	initial (asymptomatic)	D004722	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
B8CMJ8	Shewanella piezotolerans	Tight adherence TadB-like transmembrane protein, putative	x	x	abscess	D004865	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
B8D065	Halothermothrix orenii	ATP-dependent zinc metalloprotease FtsH	x	x	abscess	D004890	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
B8FMD3	Desulfatibacillum alkenivorans	Uncharacterized protein	x	x	post-treatment (CHX)	D004962	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
B8FSD4	Desulfitobacterium hafniense	Diaminopimelate epimerase	x	x	initial (asymptomatic)	D004738	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry	Proteomics	24143178

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling**	Methods of Analysis***	Type of Study	Citation (NCBI ID)
									aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
B8IBF1	Methylobacterium nodulans	Extracellular solute-binding protein family 3	x	x	abscess	D004857	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
B8L3R0	Stenotrophomonas sp. SKA14	TonB-dependent receptor	x	x	abscess	D004923	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
B9BK48	Burkholderia multivorans CGD2	Putative transposase for insertion sequence	x	x	abscess	D004797	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
B9DIB9	Staphylococcus carnosus	Single-stranded DNA-binding protein	x	x	abscess	D004802	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
C0DA64	[Clostridium asparagiforme] DSM 15981	Uncharacterized protein	x	x	abscess	D004994	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry	Proteomics	24143178

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
									aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
C0QR68	Persephonella marina	Anthranilate phosphoribosyltransferase	x	x	post-treatment (NaOCl)	D004737	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
C1CBS9	Streptococcus pneumoniae	Argininosuccinate lyase	x	x	abscess	D004714	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
C3JME0	Rhodococcus erythropolis SK121	Uncharacterized protein	x	x	abscess	D004988	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
C3SU72	Escherichia coli	Membrane protein YqiJ	x	x	post-treatment (NaOCl)	D004948	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
C4FJQ7	Sulfurihydrogenibium yellowstonense SS-5	Crispr-associated protein, Crm2 family	x	x	initial (asymptomatic)	D004935	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry	Proteomics	24143178

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
									aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
C4L5X0	Exiguobacterium sp.	Fibronectin-binding A domain protein	x	x	endodontic infections (initial)	D005163		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
C4LEY3	Tolumonas auensis	GPR1/FUN34/yaaH family protein	x	x	abscess	D004858	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
C5AI86	Burkholderia glumae	CBS domain containing membrane protein	x	x	abscess	D004856	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
C6C0P1	Desulfovibrio salexigens	ATP-dependent protease ATPase subunit HslU	x	x	initial (asymptomatic)	D004901	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
C6CTI9	Paenibacillus sp.	S-layer domain protein	x	x	endodontic infections (initial)	D005173		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
C6CYP0	Paenibacillus sp.	ABC transporter related	x	x	endodontic infections (initial)	D005172		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886

UniProtK BAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
C6PNE4	Clostridium carboxidivorans P7	Uncharacterized protein	x	x	initial (asymptomatic)	D004976	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
C6PXG7	Clostridium carboxidivorans P7	30S ribosomal protein S10	x	x	initial (asymptomatic)	D004708	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
C6RMB0	Acinetobacter radioresistens SK82	Uncharacterized protein	x	x	abscess	D005004	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
C7LU26	Desulfomicrobium baculatum	50S ribosomal protein L17	x	x	initial (asymptomatic)	D004710	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
C7NFV2	Kytococcus sedentarius	Predicted transcriptional regulator	x	x	abscess	D004770	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178

UniProtK BAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
C7PW65	Catenulispora acidiphila	Adenylyl-sulfate kinase	x	x	abscess	D004871	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
C8S212	Rhodobacter sp. SW2	Inositol monophosphatase	x	x	abscess	D004852	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
C9LTI6	Selenomonas sputigena	ATP/cobalamin adenosyltransferase	x	x	post-treatment (CHX)	D004924	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
C9LVC7	Selenomonas sputigena	POTRA domain protein, ShlB-type	x	x	abscess	D004862	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
C9QHE2	Vibrio orientalis CIP 102891 = ATCC 33934	Uncharacterized protein	x	x	abscess	D005013	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178

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D0X5C0	Vibrio harveyi	Ada regulatory protein	x	x	initial (asymptomatic)	D004711	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
D1A9M9	Thermomonospora curvata	N-acetylmuramoyl-L-alanine amidase family 2	x	x	initial (asymtomatic)	D004767	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
D1CAK5	Sphaerobacter thermophilus	Glycosyl transferase group 1	x	x	initial (asymptomatic)	D004884	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
D1YLV1	Lactobacillus gasseri 224-1	Uncharacterized protein	x	x	endodontic infections (initial)	D005169		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
D2J7P9	Staphylococcus aureus	Replication initiator protein	x	x	abscess	D004801	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
D2PR48	Kribbella flavida	RecBCD enzyme subunit RecC	x	x	post-treatment (CHX)	D004785	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion	Proteomics	24143178

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									which showed localized swelling, fever, lymphadenopathy, and malaise.	trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
D3MPG4	Peptostreptococcus anaerobius 653-L	Phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2	x	x	initial (asymptomatic)	D004836	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
D3Q9J9	Stackebrandtia nassauensis	Uncharacterized protein	x	x	post-treatment (CHX)	D004970	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
D3UXC7	Xenorhabdus bovienii	Putative invasin	x	x	abscess	D004887	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
D4FTX1	Streptococcus oralis ATCC 35037	Uncharacterized protein	x	x	abscess	D004992	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
D4FTZ7	Streptococcus oralis ATCC 35037	Nicotinate phosphoribosyltransferase	x	x	abscess	D004875	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion	Proteomics	24143178

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									which showed localized swelling, fever, lymphadenopathy, and malaise.	trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
D4ZTQ7	Arthrospira platensis	ABC transporter ATP-binding protein	x	x	abscess	D004814	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
D5HJ19	Coprococcus sp. ART55/1	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	x	x	abscess	D004758	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
D5QER8	Komagataeibacter hansenii ATCC 23769	N-acetylmuramic acid 6-phosphate etherase	x	x	post-treatment (CHX)	D004765	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
D5WJL4	Burkholderia sp.	Rieske	x	x	abscess	D004842	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
D5WM69	Burkholderia sp.	Phosphatidylserine decarboxylase-related protein	x	x	abscess	D004853	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion	Proteomics	24143178

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									which showed localized swelling, fever, lymphadenopathy, and malaise.	trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
D6H6L9	Neisseria gonorrhoeae DGI2	RecBCD enzyme subunit RecC	x	x	abscess	D004784	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
D6TSI1	Ktedonobacter racemifer DSM 44963	Mandelate racemase/muconate lactonizing protein	x	x	abscess	D004757	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
D6ZT43	Bifidobacterium longum subsp. longum	Transcriptional regulator	x	x	initial (asymptomatic)	D004732	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
D7C1X9	Streptomyces bingchenggensis	Secreted protein	x	x	abscess	D004996	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
D7HAI8	Vibrio cholerae RC385	Putative uncharacterized protein	x	x	abscess	D004845	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion	Proteomics	24143178

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
									which showed localized swelling, fever, lymphadenopathy, and malaise.	trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
D7W8V0	Chryseobacterium gleum ATCC 35910	ATPase, AAA family	x	x	abscess; pos-treatment (CHX)	D004813	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
D9PAM9	Actinobacillus pleuropneumoniae serovar 6 str. Femo	Uncharacterized protein	x	x	initial (asymptomatic)	D004990	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
D9PEH5	Actinobacillus pleuropneumoniae serovar 6 str. Femo	Uncharacterized protein	x	x	post-treatment (NaOCl)	D004885	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
D9PQI1	Finegoldia magna ACS-171-V-Col3	Alpha-1,4 glucan phosphorylase	x	x	abscess	D004834	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
D9SJG8	Gallionella capsiferriformans	PAS sensor protein	x	x	abscess	D004724	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion	Proteomics	24143178

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
									which showed localized swelling, fever, lymphadenopathy, and malaise.	trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
D9SJJ9	Gallionella capsiferriformans	FAD-dependent pyridine nucleotide-disulphide oxidoreductase	x	x	post-treatment (CHX)	D004786	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
D9UEM7	Streptomyces sp.	Predicted protein	x	x	initial (asymptomatic)	D004942	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
D9UK28	Streptomyces sp.	Secreted protein	x	x	initial (asymtomatic)	D004772	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
D9UQU3	Streptomyces sp.	Putative uncharacterized protein	x	x	abscess	D004977	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
D9WCB6	Streptomyces himastatinicus ATCC 53653	Pyrroloquinoline-quinone synthase	x	x	abscess	D004840	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion		

UniProtKB AC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis***	Type of Study	Citation (NCBI ID)
									which showed localized swelling, fever, lymphadenopathy, and malaise.	trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
D9WI88	Streptomyces himastatinicus ATCC 53653	Putative toxin-antitoxin system, toxin component	x	x	abscess	D004905	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
D9WYW4	Streptomyces viridochromogenes	Putative uncharacterized protein	x	x	abscess	D004972	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
E0TFX1	Parvularcula bermudensis	Response regulator receiver:ATP-binding region,ATPase-like:Histidine kinase A, N-terminal	x	x	post-treatment (CHX)	D004727	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
E1M101	Streptococcus mitis NCTC 12261	Membrane protein, putative	x	x	post-treatment (NaOCl)	D004860	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
E1RBP4	Spirochaeta smaragdinae	Metallophosphoesterase	x	x	abscess	D004874	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion	Proteomics	24143178

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									which showed localized swelling, fever, lymphadenopathy, and malaise.	trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
E1SJ96	Pantoea vagans	ABC transport system periplasmic protein yejA	x	x	abscess	D004909	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
E1TD79	Burkholderia sp.	Uncharacterized protein	x	x	post-treatment (CHX)	D004961	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
E2CRD5	Roseibium sp. TrichSKD4	Xanthine dehydrogenase accessory protein XdhC	x	x	abscess	D004881	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
E4LZP6	Clostridium sp. HGF2	Glycosyl hydrolase, family 1	x	x	abscess	D004818	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
E6RKB8	Pseudoalteromonas sp.	Uncharacterized protein	x	x	abscess	D004975	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion	Proteomics	24143178

UniProtKB AC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis***	Type of Study	Citation (NCBI ID)
									which showed localized swelling, fever, lymphadenopathy, and malaise.	trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
E7DPN6	Nostoc flagelliforme str. Sunitezuoqi	Two component transcriptional regulator	x	x	initial (asymptomatic)	D004735	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
E7FS96	Lactobacillus ruminis ATCC 25644	KxYKxGKxW signal domain protein	x	x	post-treatment (NaOCl)	D004766	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
E7N8K0	Actinomyces sp. oral taxon 171 str. F0337	Putative 6-phosphofructokinase	x	x	initial (asymptomatic)	D004837	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
E7PG78	Pseudomonas savastanoi pv. glycinea str. race 4	N5-carboxyaminoimidazole ribonucleotide synthase	x	x	post-treatment (NaOCl)	D004877	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
E7S8C2	Streptococcus australis ATCC 700641	Uncharacterized protein	x	x	abscess	D004991	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion	Proteomics	24143178

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									which showed localized swelling, fever, lymphadenopathy, and malaise.	trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
E8K1Q3	Streptococcus infantis ATCC 700779	Uncharacterized protein	x	x	initial (asymtomatic); post-treatment (CHX/ NaOCl)	D005012	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
E8LHR5	Succinatimonas hippei YIT 12066	Phosphoribosylformylglycinamidine synthase	x	x	abscess;initial (asymptomatic)	D004878	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
E8NE46	Microbacterium testaceum	Uncharacterized protein	x	x	abscess	D004967	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
F0GE57	Burkholderia sp. TJI49	Dihydroneopterin triphosphate pyrophosphatase	x	x	initial (asymptomatic);post-treatment (CHX)	D004778	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
F0NVW1	Lactobacillus helveticus	Leucine--tRNA ligase	x	x	initial (asymptomatic);post-treatment (NaOCl)	D004720	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion	Proteomics	24143178

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									which showed localized swelling, fever, lymphadenopathy, and malaise.	trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
F0TD35	Nitrosomonas sp. AL212	Uncharacterized protein	x	x	abscess	D004957	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
F1WPD0	Moraxella catarrhalis 12P80B1	Uncharacterized protein	x	x	post-treatment (CHX)	D004968	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
F2I8K9	Aerococcus urinae	Uncharacterized protein	x	x	initial (asymptomatic)	D004951	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
F2NRG9	Treponema succinifaciens	Type III restriction protein res subunit	x	x	initial (asymptomatic)	D004844	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
F3G779	Pseudomonas syringae pv. pisi str. 1704B	Uncharacterized protein	x	x	initial (asymptomatic); post-treatment (CHX/ NaOCl)	D004993	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion	Proteomics	24143178

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									which showed localized swelling, fever, lymphadenopathy, and malaise.	trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
F3NDV7	Streptomyces griseoaurantiacus M045	Uncharacterized protein	x	x	abscess	D004979	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
F3NR51	Streptomyces griseoaurantiacus M045	DNA-binding protein	x	x	initial (asymtomatic)	D004783	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
F3UP35	Streptococcus sanguinis SK355	Bifunctional purine biosynthesis protein PurH	x	x	initial (asymptomatic)	D004872	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
F5IUM9	Dysgonomonas gadei ATCC BAA-286	Uncharacterized protein	x	x	post-treatment (CHX)	D004956	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
F5KXI8	Veillonella parvula ACS-068-V-Sch12	Putative uncharacterized protein	x	x	abscess	D004978	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion		

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									which showed localized swelling, fever, lymphadenopathy, and malaise.	trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
F5SFT5	Desmospora sp. 8437	Minor extracellular protease vpr	x	x	abscess	D004895	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
F7J0G5	Clostridium perfringens	Collagenase A	x	x	abscess	D004891	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
F7VB68	Acetobacter tropicalis NBRC 101654	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	x	x	post-treatment (CHX)	D004847	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
F9MSG0	Peptoniphilus sp. oral taxon 375 str. F0436	4-phosphoerythronate dehydrogenase	x	x	abscess	D004925	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
F9PXP4	Streptococcus infantis SK970	Conserved domain protein	x	x	post-treatment (NaOCl)	D004933	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion	Proteomics	24143178

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age grou	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
									which showed localized swelling, fever, lymphadenopathy, and malaise.	trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
G0ERN5	Cupriavidus necator	Spermidine synthase SpeE	x	x	abscess	D004731	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
G0EZI6	Cupriavidus necator	Uncharacterized protein	x	x	abscess	D004800	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
G0G2U0	Amycolatopsis mediterranei	MutT-like protein	x	x	abscess	D004791	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
G0G4P8	Amycolatopsis mediterranei	Hydrolase	x	x	initial (asymptomatic)	D004937	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
G0HH77	Corynebacterium variabile	Arabinofuranosyltransferase A	x	x	abscess	D004762	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion	Proteomics	24143178

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
									which showed localized swelling, fever, lymphadenopathy, and malaise.	trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
G2DKZ6	Neisseria weaveri LMG 5135	Outer-membrane lipoprotein LolB	x	x	abscess	D004918	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
G2GMS3	Streptomyces zinciresistens K42	Methyltransferase NNMT/PNMT/TEMT	x	x	abscess	D004917	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
G2SLM4	Rhodothermus marinus SG0.5JP17-172	CRISPR-associated endonuclease Cas1	x	x	post-treatment (NaOCl)	D004934	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
G4CEP3	Neisseria shayeganii 871	Uncharacterized protein	x	x	abscess	D004955	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
G4CXS6	Propionibacterium avidum ATCC 25577	Uncharacterized protein	x	x	abscess	D004980	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion	Proteomics	24143178

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
									which showed localized swelling, fever, lymphadenopathy, and malaise.	trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
G4QMG0	Glaciecola nitratireducens	Putative signal transduction protein	x	x	abscess	D004949	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
G4SXK7	Methylomicrobium alcaliphilum	Nicotinamidase	x	x	abscess	D004926	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
G5HGC1	[Clostridium] citroniae WAL-17108	Uncharacterized protein	x	x	abscess, post-treatment (CHX)	D004798	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
G5IJI3	Hungatella hathewayi WAL-18680	Uncharacterized protein	x	x	post-treatment (CHX)	D004760	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
G8M7P9	Burkholderia sp. YI23	Translation initiation factor IF-3	x	x	abscess	D004733	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion	Proteomics	24143178

UniProtKB AC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis***	Type of Study	Citation (NCBI ID)
									which showed localized swelling, fever, lymphadenopathy, and malaise.	trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
G8PEV5	Pediococcus claussenii	ABC-type cation transporter, ATPase component	x	x	abscess	D004817	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
G8QU94	Sphaerochaeta pleomorpha	Succinyl-CoA synthetase, alpha subunit	x	x	abscess	D004854	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
G8S325	Actinoplanes sp.	PhoH-like ATPase	x	x	initial (asymptomatic)	D004831	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
G8ULB9	Tannerella forsythia	TonB-linked outer membrane protein, SusC/RagA family	x	x	initial (asymptomatic)	D004866	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
G9WT20	Oribacterium asaccharolyticum ACB7	Phosphoglucosamine mutase	x	x	abscess	D004833	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion		

UniProtKB AC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis***	Type of Study	Citation (NCBI ID)
									which showed localized swelling, fever, lymphadenopathy, and malaise.	trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
G9XAC6	Peptostreptococcaceae bacterium CM5	Uncharacterized protein	x	x	abscess	D004799	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
H0BRN6	Acidovorax sp. NO-1	NUDIX hydrolase	x	x	abscess	D004876	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
H0G1E7	Sinorhizobium meliloti CCNWSX0020	YjbE family integral membrane protein	x	x	post-treatment (NaOCl)	D004859	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
H0JFX6	Pseudomonas psychrotolerans L19	Putative uncharacterized protein	x	x	abscess	D004914	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
H0JFX6	Pseudomonas psychrotolerans L19	Putative uncharacterized protein	x	x	abscess	D004958	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion	Proteomics	24143178

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									which showed localized swelling, fever, lymphadenopathy, and malaise.	trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
H0SNN0	Bradyrhizobium sp. ORS 375	Uncharacterized protein	x	x	abscess	D004953	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
H0TEG1	Bradyrhizobium sp. STM 3843	Uncharacterized protein	x	x	abscess	D005000	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
H1D226	Dialister succinatiphilus YIT 11850	Uncharacterized protein	x	x	abscess	D004982	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
H1X994	Weissella confusa LBAE C39-2	Negative regulator of septation ring formation	x	x	initial (asymtomatic)	D004768	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
H3KFX4	Sutterella parvirubra YIT 11816	Hydrolase, TatD family	x	x	initial (asymptomatic)	D004788	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion	Proteomics	24143178

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									which showed localized swelling, fever, lymphadenopathy, and malaise.	trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
H3RHG4	Pantoea stewartii subsp. stewartii DC283	Methyl-accepting chemotaxis protein	x	x	initial (asymptomatic)	D004775	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
H3SBV6	Paenibacillus dendritiformis C454	3D domain-containing protein	x	x	initial (asymtomatic)	D004761	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
H4UI65	Escherichia coli DEC6A	Putative DNA-binding protein	x	x	abscess	D004796	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
H5SB51	uncultured Acetothermia bacterium	Branched-chain amino acid transport system ATP-binding protein	x	x	abscess	D004821	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
H5STP7	Candidatus Acetothermus autotrophicum	DNA-directed RNA polymerase subunit beta	x	x	initial (asymptomatic); post-treatment (CHX)	D004717	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion	Proteomics	24143178

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									which showed localized swelling, fever, lymphadenopathy, and malaise.	trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
H5UVQ1	Mobilicoccus pelagius NBRC 104925	Uncharacterized protein	x	x	initial (asymtomatic)	D005015	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
H5V6X6	Escherichia hermannii NBRC 105704	Beta-lactamase	x	x	initial (asymptomatic)	D004883	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
H5WI69	Burkholderiales bacterium JOSHI_001	Uncharacterized protein, possibly involved in utilization of glycolate and propanediol	x	x	initial (asymtomatic)	D005014	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
H6MWK8	Gordonia polyisoprenivorans	Uncharacterized protein	x	x	abscess	D005011	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
H8FWY0	Phaeospirillum molischianum DSM 120	Cytochrome C	x	x	abscess	D004822	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion	Proteomics	24143178

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									which showed localized swelling, fever, lymphadenopathy, and malaise.	trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
H8GFK9	Saccharomonospora azurea NA-128	Uncharacterized protein	x	x	initial (asymtomatic)	D005003	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
H8NYQ3	Rahnella aquatilis HX2	Adenine DNA glycosylase	x	x	abscess	D004776	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
H9TE85	Streptomyces flaveolus	MycA1	x	x	initial (asymptomatic)	D004938	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
I0L020	Micromonospora lupini str. Lupac 08	Uncharacterized protein	x	x	initial (asymtomatic)	D004998	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
I0Q8W0	Streptococcus oralis SK100	IgA-specific serine endopeptidase	x	x	post-treatment (NaOCl)	D004897	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion	Proteomics	24143178

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									which showed localized swelling, fever, lymphadenopathy, and malaise.	trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
I0S024	Mycobacterium xenopi RIVM700367	Enolase	x	x	abscess	D004824	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
I1D602	Saccharomonospora glauca K62	Uncharacterized protein	x	x	abscess	D005010	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
I1X956	uncultured methanogenic archaeon	Methyl coenzyme M reductase	x	x	initial (asymptomatic)	D004855	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
I2GSM3	Fibrisoma limi BUZ 3	Uncharacterized protein	x	x	initial (asymtomatic)	D004999	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
I3C080	Thiothrix nivea DSM 5205	Addiction module antidote protein, CC2985 family	x	x	initial (asymptomatic)	D004712	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion	Proteomics	24143178

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									which showed localized swelling, fever, lymphadenopathy, and malaise.	trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
I4ECD9	Nitrolancea hollandica Lb	Holliday junction ATP-dependent DNA helicase RuvB	x	x	abscess	D004787	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
I4MLL2	Hydrogenophaga sp. PBC	Carboxylic ester hydrolase	x	x	initial (asymptomatic)	D004848	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
I4X1V3	Planococcus antarcticus DSM 14505	Uncharacterized protein	x	x	abscess	D005009	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
I4Z978	Prevotella bivia DSM 20514		x	x	abscess	D004879	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
I5B125	Desulfobacter postgatei 2ac9	DNA topoisomerase III	x	x	post-treatment (CHX)	D004782	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion	Proteomics	24143178

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling**	Methods of Analysis***	Type of Study	Citation (NCBI ID)
									which showed localized swelling, fever, lymphadenopathy, and malaise.	trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
I5B8R0	Sphingobium indicum B90A	Glutamyl-tRNA	x	x	abscess	D004715	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
I5BER7	Sphingobium indicum B90A	TetR family transcriptional regulator	x	x	initial (asymptomatic)	D004882	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
J0P971	Saprospira grandis DSM 2844	Subtilisin-like serine protease	x	x	abscess	D004896	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
J0VVL6	Rhizobium leguminosarum bv. trifolii WSM2012	T5orf172 domain-containing protein	x	x	abscess	D004997	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
J1FBZ3	Thiovulum sp. ES	Uncharacterized protein	x	x	post-treatment (NaOCl)	D005002	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion		

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									which showed localized swelling, fever, lymphadenopathy, and malaise.	trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
J1GGD9	Enterobacter sp. Ag1	DNA-binding transcriptional regulator	x	x	abscess	D004754	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
J1QMC3	Alishewanella aestuarii B11	Type I restriction-modification system restriction subunit	x	x	abscess	D004806	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
J2T720	Pseudomonas sp. GM50	Uncharacterized protein	x	x	post-treatment (CHX)	D004736	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
J3H5S3	Pseudomonas sp. GM60	Arabinose efflux permease family protein	x	x	initial (asymptomatic)	D004911	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
J4JV55	Mycobacterium colombiense CECT 3035	ABC transporter ATP-binding protein	x	x	abscess	D004814	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion	Proteomics	24143178

UniProtK BAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
									which showed localized swelling, fever, lymphadenopathy, and malaise.	trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
J5L1X0	Campylobacter sp. FOBRC14	tRNA dimethylallyltransferase	x	x	abscess	D004759	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
J7ILM7	Desulfosporosinus meridiei	Uncharacterized protein	x	x	abscess	D005001	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
J8CZZ6	Bacillus cereus VD014	Uncharacterized protein	x	x	abscess	D005005	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
J8HZA5	Bacillus cereus VD078	Uncharacterized protein	x	x	post-treatment (NaOCl)	D005007	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
J8LAV7	Bacillus cereus VD166	Uncharacterized protein	x	x	initial (asymtomatic)	D005006	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion		

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age grou	Gender*	Methods of Sampling**	Methods of Analysis***	Type of Study	Citation (NCBI ID)
									which showed localized swelling, fever, lymphadenopathy, and malaise.	trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
O07108	Enterococcus faecalis	UDP-N-acetylmuramoylalanine--D-glutamate ligase	x	x	endodontic infections (initial)	D005234		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
O31216	Allochromatium vinosum	Cytochrome c1	x	x	post-treatment (NaOCl)	D004823	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
O84818	Chlamydia trachomatis	Probable outer membrane protein PmpD	x	x	abscess	D004863	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
P0A4M1	Enterococcus faecalis	Toxin zeta	x	x	endodontic infections (initial)	D005242		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
P0C0J1	Streptococcus pyogenes serotype M1	Streptopain	x	x	initial (asymptomatic)	D004889	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
P10728	Bacillus subtilis	Anti-sigma F factor	x	x	initial (asymptomatic)	D004898	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and	Proteomics	24143178

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
									swelling, fever, lymphadenopathy, and malaise.	liquid chromatography-quadrupole time-of-flight.		
P22983	Clostridium symbiosum	Pyruvate, phosphate dikinase	x	x	abscess	D004841	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
P37710	Enterococcus faecalis	Autolysin	x	x	endodontic infections (initial)	D005190		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
P48215	Neisseria flavescens	60 kDa chaperonin	x	x	initial (asymptomatic)	D004899	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
P74269	Synechocystis sp.		x	x	abscess	D004752	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
P94638	Corynebacterium glutamicum	Uncharacterized protein	x	x	abscess	D004989	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
P94638	Corynebacterium glutamicum	Uncharacterized protein	x	x	abscess	D004995	20 - 39	M/F	canals of 12 teeth with asymptomatic apical	Clinical samples were processed for analysis of the exoproteome by using	Proteomics	24143178

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
									periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
P95469	Paracoccus denitrificans	Protein RecA	x	x	abscess	D004795	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
P95800	Stenotrophomonas maltophilia	60 kDa chaperonin	x	x	endodontic infections (initial)	D005179		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
P96594	Bacillus subtilis	UPF0410 protein YdaS	x	x	abscess	D004867	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q03YI2	Leuconostoc mesenteroides subsp. mesenteroides	Elongation factor Tu	x	x	post-treatment (CHX)	D004739	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q08TW6	Stigmatella aurantiaca	Iron-sulfur cluster-binding protein, Rieske family	x	x	initial (asymptomatic)	D004826	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole	Proteomics	24143178

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis***	Type of Study	Citation (NCBI ID)
									lymphadenopathy, and malaise.	time-of-flight.		
Q0RU36	Frankia alni	Uncharacterized protein	x	x	abscess	D004963	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q0S9R0	Rhodococcus jostii	Possible universal stress protein	x	x	endodontic infections (initial)	D005178		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q0TMG7	Clostridium perfringens	Peptidyl-tRNA hydrolase	x	x	initial (asymptomatic)	D004725	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q11JY3	Chelativorans sp.	Periplasmic sensor signal transduction histidine kinase	x	x	initial (asymptomatic)	D004904	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q13BZ9	Rhodopseudomonas palustris	Extracellular solute-binding protein, family 5	x	x	initial (asymptomatic)	D004912	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q15P29	Pseudoalteromonas atlantica	tRNA pseudouridine synthase D	x	x	abscess	D004744	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry	Proteomics	24143178

UniProtKB AC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis***	Type of Study	Citation (NCBI ID)
									aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
Q1D8Z5	Myxococcus xanthus	Uncharacterized protein	x	x	abscess	D004987	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q1H2I8	Methylobacillus flagellatus	Phosphoribosylformylglycinamidine synthase	x	x	abscess;initial (asymptomatic)	D004878	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q1M5X3	Rhizobium leguminosarum bv. viciae	Rhamnose periplasmic binding protein	x	x	initial (asymtomatic)	D004921	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q1QKT7	Nitrobacter hamburgensis	Methyltransferase type 12	x	x	initial (asymptomatic)	D004790	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q2G7B1	Novosphingobium aromaticivorans	Conserved hypothetical membrane protein	x	x	endodontic infections (initial)	D005171		M/F	Endodontic specimens were aseptically obtained from seven patients with root	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–	Proteomics	2744886

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									canal infections.	MS/MS followed by a database search.		
Q2JJQ0	Synechococcus sp.	tRNA	x	x	post-treatment (NaOCl)	D004743	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q2KYY2	Bordetella avium	Chaperone protein HtpG	x	x	post-treatment (NaOCl)	D004903	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q2RR25	Rhodospirillum rubrum	Chorismate synthase	x	x	abscess	D004746	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q2UXR5	Enterococcus faecalis	Tetracycline resistance protein	x	x	endodontic infections (initial)	D005229		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q2W9A3	Magnetospirillum magneticum	Probable glycine dehydrogenase	x	x	initial (asymptomatic)	D004943	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q30BE9	Enterococcus faecalis	VanTG2	x	x	endodontic infections (initial)	D005239		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886

UniProtK BAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
Q30BF2	Enterococcus faecalis	VanWG2	x	x	endodontic infections (initial)	D005240		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q30BF3	Enterococcus faecalis	VanSG2	x	x	endodontic infections (initial)	D005238		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q39PI2	Burkholderia lata	Lipocalin-like protein	x	x	endodontic infections (initial)	D005155		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q3MER6	Anabaena variabilis	Uncharacterized protein	x	x	abscess	D004960	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q3XXB2	Enterococcus faecium DO	Bacteriocin-associated integral membrane protein	x	x	endodontic infections (initial)	D005235		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q3Y1R6	Enterococcus faecium DO	Probable cell wall amidase lytH	x	x	endodontic infections (initial)	D005192		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q3YSG5	Ehrlichia canis	Membrane protein insertase YidC	x	x	abscess	D004916	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q47745	Enterococcus faecalis	Sensor protein VanSB	x	x	endodontic infections (initial)	D005237		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q47779	Enterococcus faecalis	BacB protein	x	x	endodontic infections (initial)	D005191		M/F	Endodontic specimens were aseptically obtained from seven patients with root	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–	Proteomics	2744886

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
									canal infections.	MS/MS followed by a database search.		
Q47810	Enterococcus faecalis	Tetracycline resistance protein TetM from transposon TnFO1	x	x	endodontic infections (initial)	D005230		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q47HK2	Dechloromonas aromatica	Chaperone protein DnaK	x	x	post-treatment (NaOCl)	D004903	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q47W35	Colwellia psychrerythraea	tRNA N6-adenosine threonylcarbamoyltransferase	x	x	abscess	D004749	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q49SF0	Enterococcus faecium	Gls24	x	x	endodontic infections (initial)	D005201		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q4KFI6	Pseudomonas fluorescens	Ribosomal RNA large subunit methyltransferase K/L [Includes: 23S rRNA m2G2445 methyltransferase	x	x	abscess	D004729	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q5G3N8	Enterococcus faecalis	PcfD	x	x	endodontic infections (initial)	D005212		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q5GBH8	Enterococcus faecalis	TetT	x	x	endodontic infections (initial)	D005231		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q5KFP6	Cryptococcus	Endopeptidase, putative	x	x	initial	D00489	20 -	M/F	canals of 12 teeth with	Clinical samples were processed for	Proteomi	241431

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
	neoformans var. neoformans serotype D				(asymptomatic)	2	39		asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	cs	78
Q5L4R1	Chlamydia abortus	Putative periplasmic hydrolase	x	x	abscess	D004771	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q5L7I8	Bacteroides fragilis	Methionine--tRNA ligase	x	x	abscess	D004748	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q5LB48	Bacteroides fragilis	Putative ABC transport system, membrane protein	x	x	endodontic infections (initial)	D005158		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q5LBV7	Bacteroides fragilis	Conserved membrane protein	x	x	endodontic infections (initial)	D005157		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q5LEF4	Bacteroides fragilis	Putative outer membrane protein	x	x	endodontic infections (initial)	D005159		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q5WXX4	Legionella pneumophila	Uncharacterized protein	x	x	abscess	D004965	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever,	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole	Proteomics	24143178

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis**	Type of Study	Citation (NCBI ID)
									lymphadenopathy, and malaise.	time-of-flight.		
Q5YRY1	Nocardia farcinica	3-isopropylmalate dehydratase small subunit	x	x	initial (asymptomatic)	D004709	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q66C16	Yersinia pseudotuberculosis serotype I	Inner membrane ABC-transporter YbtQ	x	x	post-treatment (NaOCl)	D004816	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q68X10	Rickettsia typhi	Enoyl-[acyl-carrier-protein] reductase [NADH] FabI	x	x	post-treatment (CHX)	D004850	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q6ABI3	Propionibacterium acnes	Putative penicillin-binding protein	x	x	endodontic infections (initial)	D005177		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q6ACY9	Leifsonia xyli subsp. xyli	Elongation factor G	x	x	abscess; initial (asymptomatic)	D004718	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q6D738	Pectobacterium atrosepticum	Non-ribosomal peptide synthetase	x	x	abscess	D004723	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry	Proteomics	24143178

UniProtK BAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis***	Type of Study	Citation (NCBI ID)
									aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.		
Q6FCH8	Acinetobacter baylyi	Ornithine carbamoyltransferase	x	x	post-treatment (CHX)	D004740	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q6LVK2	Photobacterium profundum	ATP-dependent 6-phosphofructokinase	x	x	abscess	D004812	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q6N893	Rhodopseudomonas palustris	Probable potassium transport system protein kup 3	x	x	abscess	D004919	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q6NGP1	Corynebacterium diphtheriae	Polyribonucleotide nucleotidyltransferase	x	x	post-treatment (NaOCl)	D004741	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q6WS02	Enterococcus faecalis	Rlx-like protein	x	x	endodontic infections (initial)	D005224		M/F	Endodontic specimens were aseptically obtained from seven patients with root	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–	Proteomics	2744886

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age grou	Gender*	Methods of Sampling **	Methods of Analysis***	Type of Study	Citation (NCBI ID)
									canal infections.	MS/MS followed by a database search.		
Q73QT1	Treponema denticola	Bacterial Ig-like domain protein	x	x	endodontic infections (initial)	D005184		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q79A51	Enterococcus faecalis	Nickase	x	x	endodontic infections (initial)	D005210		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q7CI82	Yersinia pestis	Putative exported protein	x	x	post-treatment (NaOCl)	D004946	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q7MUL8	Porphyromonas gingivalis	TraG family protein	x	x	endodontic infections (initial)	D005176		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q7MWV9	Porphyromonas gingivalis	YngK protein	x	x	endodontic infections (initial)	D005174		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q7NWC3	Chromobacterium violaceum	GTPase Era	x	x	abscess	D004719	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q7USA4	Rhodopirellula baltica	Uncharacterized protein	x	x	abscess	D004839	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q7VR34	Blochmannia	Outer membrane protein OprC	x	x	abscess	D00486	20 -	M/F	canals of 12 teeth with	Clinical samples were processed for	Proteomi	241431

UniProtKB AC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
	floridanus					1	39		asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	cs	78
Q7X5P9	Anaplasma phagocytophilum	AnkA	x	x	initial (asymptomatic)	D004931	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q820V6	Enterococcus faecalis	FtsK/SpoIIIE family protein	x	x	endodontic infections (initial)	D005200		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q82ID4	Streptomyces avermitilis	Catalase	x	x	post-treatment (CHX)	D004902	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q82K95	Streptomyces avermitilis	Ribosomal protein S12 methylthiotransferase RimO	x	x	abscess	D004750	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q82YJ4	Enterococcus faecalis	Toxin ABC transporter, ATP-binding/permease protein	x	x	endodontic infections (initial)	D005232		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q82YM8	Enterococcus faecalis	Uncharacterized protein	x	x	endodontic infections (	D005220		M/F	Endodontic specimens were aseptically obtained from	Protein mixtures were subjected to tryptic in-solution digestion and	Proteomics	2744886

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
					initial)				seven patients with root canal infections.	analysed by reverse-phase nano-LC–MS/MS followed by a database search.		
Q82YN1	Enterococcus faecalis	Aggregation substance PrgB	x	x	endodontic infections (initial)	D005188		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q82ZH7	Enterococcus faecalis	Peptidase T	x	x	endodontic infections (initial)	D005214		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q82ZJ9	Enterococcus faecalis	Sortase family protein	x	x	endodontic infections (initial)	D005225		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q82ZM8	Enterococcus faecalis	Polysaccharide lyase, family 8	x	x	endodontic infections (initial)	D005218		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q82ZQ8	Enterococcus faecalis	Rhodanese family protein	x	x	endodontic infections (initial)	D005223		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q82ZX8	Enterococcus faecalis	ABC transporter, ATP-binding/permease protein	x	x	endodontic infections (initial)	D005186		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q82ZY7	Enterococcus faecalis	Potassium uptake protein	x	x	endodontic infections (initial)	D005219		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q830Q0	Enterococcus faecalis	Peptidase, M42 family	x	x	endodontic infections (initial)	D005216		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q830Y6	Enterococcus faecalis	N-acetylmuramoyl-L-alanine amidase, family 4	x	x	endodontic infections (initial)	D005209		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q831L1	Enterococcus faecalis	Teichoic acid biosynthesis protein, putative	x	x	endodontic infections (initial)	D005228		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q832B2	Enterococcus faecalis	TraG family protein	x	x	endodontic infections (initial)	D005233		M/F	Endodontic specimens were aseptically obtained from seven patients with root	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–	Proteomics	2744886

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
									canal infections.	MS/MS followed by a database search.		
Q832J2	Enterococcus faecalis	Sugar ABC transporter, sugar-binding protein, putative	x	x	endodontic infections (initial)	D005226		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q832Q0	Enterococcus faecalis	Glycosyl transferase, group 2 family protein	x	x	endodontic infections (initial)	D005202		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q832Q4	Enterococcus faecalis	Membrane protein, putative	x	x	endodontic infections (initial)	D005206		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q833M7	Enterococcus faecalis	ATP-dependent Clp protease ATP-binding subunit ClpX	x	x	endodontic infections (initial)	D005189		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q833P7	Enterococcus faecalis	Cell wall surface anchor family protein	x	x	endodontic infections (initial)	D005193		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q833W2	Enterococcus faecalis	Sulfatase domain protein	x	x	endodontic infections (initial)	D005227		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q834B4	Enterococcus faecalis	Phosphate import ATP-binding protein PstB 1	x	x	endodontic infections (initial)	D005217		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q834G2	Enterococcus faecalis	Ribonuclease Z	x	x	endodontic infections (initial)	D005208		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q835K7	Enterococcus faecalis	Drug resistance transporter, EmrB/QacA family protein	x	x	endodontic infections (initial)	D005196		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q835M5	Enterococcus faecalis	Magnesium-translocating P-type ATPase	x	x	endodontic infections (initial)	D005205		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q835S9	Enterococcus faecalis	Endolysin	x	x	endodontic infections (initial)	D005197		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
Q836M0	Enterococcus faecalis	von Willebrand factor type A domain protein	x	x	endodontic infections (initial)	D005241		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q836W3	Enterococcus faecalis	Hemolysin A	x	x	endodontic infections (initial)	D005203		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q836Z9	Enterococcus faecalis	Extracellular protein, putative	x	x	endodontic infections (initial)	D005198		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q837A1	Enterococcus faecalis	ABC transporter, ATP-binding/permease protein	x	x	endodontic infections (initial)	D005187		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q837M0	Enterococcus faecalis	PTS system, IIC component	x	x	endodontic infections (initial)	D005221		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q838B1	Enterococcus faecalis	Oligoendopeptidase F, putative	x	x	endodontic infections (initial)	D005211		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q838X9	Enterococcus faecalis	Lipoprotein, putative	x	x	endodontic infections (initial)	D005204		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q839D6	Enterococcus faecalis	Peptidase, M20/M25/M40 family	x	x	endodontic infections (initial)	D005215		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q839K7	Enterococcus faecalis	Conjugal transfer protein, putative	x	x	endodontic infections (initial)	D005194		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q88DU6	Pseudomonas putida	Carbamoyl-phosphate synthase large chain	x	x	abscess	D004716	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
Q88U41	Lactobacillus plantarum	ATP-dependent helicase/nuclease subunit A	x	x	post-treatment (CHX)	D004777	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q8D274	Wigglesworthia glossinidia brevipalpis	Inorganic pyrophosphatase	x	x	post-treatment (NaOCl)	D004851	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q8E1S1	Streptococcus agalactiae serotype V	PTS system, IIBC components	x	x	endodontic infections (initial)	D005180		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q8EN63	Oceanobacillus iheyensis	Dihydroxy-acid dehydratase	x	x	abscess	D004747	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q8FLL7	Corynebacterium efficiens	Putative virulence-associated protein	x	x	endodontic infections (initial)	D005162		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q8FS85	Corynebacterium efficiens	Elongation factor G	x	x	abscess; initial (asymptomatic)	D004718	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q8KH16	Enterococcus	Conserved hypothetical	x	x	endodontic	D00519		M/F	Endodontic specimens were	Protein mixtures were subjected to	Proteomi	274488

UniProtK BAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
	faecalis				infections (initial)	5			aseptically obtained from seven patients with root canal infections.	tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	cs	6
Q8KI44	Enterococcus faecalis	EF0053	x	x	endodontic infections (initial)	D005222		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q8KKS1	Rhizobium etli	Adenine phosphoribosyltransferase 2	x	x	post-treatment (CHX)	D004870	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q8P9G9	Xanthomonas campestris pv. campestris	Uncharacterized protein	x	x	abscess	D004973	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q8PDW3	Xanthomonas campestris pv. campestris	D-alanine--D-alanine ligase A	x	x	post-treatment (CHX)	D004763	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q8RGG3	Fusobacterium nucleatum subsp. nucleatum	Outer membrane porin F	x	x	endodontic infections (initial)	D005164		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q8RHF5	Fusobacterium nucleatum subsp. nucleatum	ABC transporter substrate-binding protein	x	x	endodontic infections (initial)	D005167		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q8RI38	Fusobacterium nucleatum subsp. nucleatum	Spermidine/putrescine transport system permease protein potB	x	x	endodontic infections (initial)	D005166		M/F	Endodontic specimens were aseptically obtained from seven patients with root	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–	Proteomics	2744886

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
									canal infections.	MS/MS followed by a database search.		
Q8RIE8	Fusobacterium nucleatum subsp. nucleatum	Oligopeptide-binding protein oppA	x	x	endodontic infections (initial)	D005165		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q8XQ83	Ralstonia solanacearum	Chemotaxis response regulator protein-glutamate methylesterase	x	x	abscess	D004774	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q8YX97	Nostoc sp.	Valine--tRNA ligase	x	x	post-treatment (NaOCl)	D004745	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q93A46	Enterococcus faecalis	D-alanine--D-alanine ligase	x	x	endodontic infections (initial)	D005236		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q97EU2	Clostridium acetobutylicum	Phosphomethylpyrimidine synthase	x	x	abscess	D004927	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q9CIL7	Lactococcus lactis subsp. lactis	Penicillin-binding protein 2B	x	x	endodontic infections (initial)	D005170		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q9K3C9	Enterococcus faecalis	PBP4 protein	x	x	endodontic infections (initial)	D005213		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
Q9PHR3	Campylobacter	Thiol:disulfide interchange protein	x	x	initial	D00492	20 -	M/F	canals of 12 teeth with	Clinical samples were processed for	Proteomi	241431

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age grou	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
	jejuni subsp. jejuni serotype O:2	DsbD			(asymptomatic)	2	39		asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	cs	78
Q9RCA7	Bacillus halodurans	tRNA modification GTPase MnmE	x	x	abscess	D004734	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
Q9RPP2	Enterococcus faecalis	Probable protease eep	x	x	endodontic infections (initial)	D005207		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
R4KGR0	Desulfotomaculum gibsoniae DSM 7213	Sarco/endoplasmic reticulum calcium-translocating P-type ATPase/golgi membrane calcium-translocating P-type ATPase	x	x	post-treatment (NaOCl)	D004820	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
T5HJG4	Bacillus licheniformis CG-B52	Uncharacterized protein	x	x	abscess	D004981	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
T5LW22	Ruminococcus sp. 5_1_39BFAA	Uncharacterized protein	x	x	initial (asymptomatic)	D004805	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and	Proteomics	24143178

UniProtKBAC	Organism	Name	Crevicular Fluid	Health	Disease name	Disease (MeSH ID)	Age group	Gender*	Methods of Sampling **	Methods of Analysis* **	Type of Study	Citation (NCBI ID)
									swelling, fever, lymphadenopathy, and malaise.	liquid chromatography-quadrupole time-of-flight.		
V5R5P6	Streptococcus agalactiae	FbsA	x	x	endodontic infections (initial)	D005181		M/F	Endodontic specimens were aseptically obtained from seven patients with root canal infections.	Protein mixtures were subjected to tryptic in-solution digestion and analysed by reverse-phase nano-LC–MS/MS followed by a database search.	Proteomics	2744886
V8M0K4	Streptococcus thermophilus TH1435	Integrase	x	x	initial (asymptomatic)	D004789	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178
W0EBA7	Desulfitobacterium metallireducens DSM 15288	Phosphoenolpyruvate carboxykinase [ATP]	x	x	initial (asymptomatic)	D004832	20 - 39	M/F	canals of 12 teeth with asymptomatic apical periodontitis and from aspiration of pus from two cases of acute apical abscess, which showed localized swelling, fever, lymphadenopathy, and malaise.	Clinical samples were processed for analysis of the exoproteome by using two complementary mass spectrometry platforms: nanoflow liquid chromatography coupled with linear ion trap quadrupole Velos Orbitrap and liquid chromatography-quadrupole time-of-flight.	Proteomics	24143178

Anexo C

Lista de proteinas excluivas da patologia endodôntica.

Codigo UniprotKB	Protein names	Organism
Q99714	3-hydroxyacyl-CoA dehydrogenase type-2 (EC 1.1.1.35) (17-beta-hydroxysteroid dehydrogenase 10) (17-beta-HSD 10) (EC 1.1.1.51) (3-hydroxy-2-methylbutyryl-CoA dehydrogenase) (EC 1.1.1.178) (3-hydroxyacyl-CoA dehydrogenase type II) (Endoplasmic reticulum-associated amyloid beta-peptide-binding protein) (Mitochondrial ribonuclease P protein 2) (Mitochondrial RNase P protein 2) (Short chain dehydrogenase/reductase family 5C member 1) (Short-chain type dehydrogenase/reductase XH98G2) (Type II HADH)	Homo sapiens (Human)
Q03393	6-pyruvoyl tetrahydrobiopterin synthase (PTP synthase) (PTPS) (EC 4.2.3.12)	Homo sapiens (Human)
Q96QF7	Acidic repeat-containing protein	Homo sapiens (Human)
F8SVK3	Cytoplasmic actin (Fragment)	Homo sapiens (Human)
Q9UJY4	ADP-ribosylation factor-binding protein GGA2 (Gamma-adaptin-related protein 2) (Golgi-localized, gamma ear-containing, ARF-binding protein 2) (VHS domain and ear domain of gamma-adaptin) (Vear)	Homo sapiens (Human)
A2A2R0	BPI fold-containing family B member 1 (Fragment)	Homo sapiens (Human)
Q693B1	BTB/POZ domain-containing protein KCTD11	Homo sapiens (Human)
Q9NYQ6	Cadherin EGF LAG seven-pass G-type receptor 1 (Cadherin family member 9) (Flamingo homolog 2) (hFmi2)	Homo sapiens (Human)
Q13557	Calcium/calmodulin-dependent protein kinase type II subunit delta (CaM kinase II subunit delta) (CaMK-II subunit delta) (EC 2.7.11.17)	Homo sapiens (Human)
B4E1B2	cDNA FLJ53691, highly similar to Serotransferrin	Homo sapiens (Human)
B4E0C4	Poly [ADP-ribose] polymerase (PARP) (EC 2.4.2.30)	Homo sapiens (Human)
A8K494	cDNA FLJ78440, highly similar to Human lactoferrin	Homo sapiens (Human)
B2RBS8	cDNA, FLJ95666, highly similar to Homo sapiens albumin (ALB), mRNA	Homo sapiens (Human)
Q8IW40	Coiled-coil domain-containing protein 103	Homo sapiens (Human)
Q8NEM8	Cytosolic carboxypeptidase 3 (EC 3.4.17.-) (ATP/GTP-binding protein-like 3)	Homo sapiens (Human)
Q9H5Q4	Dimethyladenosine transferase 2, mitochondrial (EC 2.1.1.-) (Hepatitis C virus NS5A-transactivated protein 5) (HCV NS5A-transactivated protein 5) (Mitochondrial 12S rRNA dimethylase 2) (Mitochondrial transcription factor B2) (h-mtTFB) (h-mtTFB2) (hTFB2M) (mtTFB2) (S-adenosylmethionine-6-N', N'-adenosyl(rRNA) dimethyltransferase 2)	Homo sapiens (Human)
Q8TDJ6	DmX-like protein 2 (Rabconnectin-3)	Homo sapiens (Human)
Q8WU17	E3 ubiquitin-protein ligase RNF139 (EC 6.3.2.-) (RING finger protein 139) (Translocation in renal carcinoma on chromosome 8 protein)	Homo sapiens (Human)
O60869	Endothelial differentiation-related factor 1 (EDF-1) (Multiprotein-bridging factor 1) (MBF1)	Homo sapiens (Human)
O95684	FGFR1 oncogene partner	Homo sapiens (Human)

Codigo UniprotKB	Protein names	Organism
P32314	Forkhead box protein N2 (Human T-cell leukemia virus enhancer factor)	Homo sapiens (Human)
Q9NW75	G patch domain-containing protein 2	Homo sapiens (Human)
Q9H3Q3	Galactose-3-O-sulfotransferase 2 (Gal3ST-2) (EC 2.8.2.-) (Beta-galactose-3-O-sulfotransferase 2) (Gal-beta-1, 3-GalNAc 3'-sulfotransferase 2) (Glycoprotein beta-Gal 3'-sulfotransferase 2)	Homo sapiens (Human)
A8MPY1	Gamma-aminobutyric acid receptor subunit rho-3 (GABA(A) receptor subunit rho-3) (GABA(C) receptor)	Homo sapiens (Human)
Q9NZD2	Glycolipid transfer protein (GLTP)	Homo sapiens (Human)
O00461	Golgi integral membrane protein 4 (Golgi integral membrane protein, cis) (GIMPc) (Golgi phosphoprotein 4) (Golgi-localized phosphoprotein of 130 kDa) (Golgi phosphoprotein of 130 kDa)	Homo sapiens (Human)
Q9ULV5	Heat shock factor protein 4 (HSF 4) (hHSF4) (Heat shock transcription factor 4) (HSTF 4)	Homo sapiens (Human)
Q8NE63	Homeodomain-interacting protein kinase 4 (EC 2.7.11.1)	Homo sapiens (Human)
Q14623	Indian hedgehog protein (IHH) (HHG-2) [Cleaved into: Indian hedgehog protein N-product; Indian hedgehog protein C-product]	Homo sapiens (Human)
Q8N1W1	Rho guanine nucleotide exchange factor 28 (190 kDa guanine nucleotide exchange factor) (p190-RhoGEF) (p190RhoGEF) (Rho guanine nucleotide exchange factor)	Homo sapiens (Human)
A1L179	Kinesin-like protein (Fragment)	Homo sapiens (Human)
O43300	Leucine-rich repeat transmembrane neuronal protein 2 (Leucine-rich repeat neuronal 2 protein)	Homo sapiens (Human)
Q9P2V4	Leucine-rich repeat, immunoglobulin-like domain and transmembrane domain-containing protein 1 (Leucine-rich repeat-containing protein 21) (Photoreceptor-associated LRR superfamily protein) (Retina-specific protein PAL)	Homo sapiens (Human)
O75335	Liprin-alpha-4 (Protein tyrosine phosphatase receptor type f polypeptide-interacting protein alpha-4) (PTPRF-interacting protein alpha-4)	Homo sapiens (Human)
Q86UL8	Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 2 (Atrophin-1-interacting protein 1) (AIP-1) (Atrophin-1-interacting protein A) (Membrane-associated guanylate kinase inverted 2) (MAGI-2)	Homo sapiens (Human)
Q969R2	Oxysterol-binding protein 2 (Oxysterol-binding protein-related protein 4) (ORP-4) (OSBP-related protein 4)	Homo sapiens (Human)
Q96RG2	PAS domain-containing serine/threonine-protein kinase (PAS-kinase) (PASKIN) (hPASK) (EC 2.7.11.1)	Homo sapiens (Human)
P55201	Peregrin (Bromodomain and PHD finger-containing protein 1) (Protein Br140)	Homo sapiens (Human)
P42356	Phosphatidylinositol 4-kinase alpha (PI4-kinase alpha) (PI4K-alpha) (PtdIns-4-kinase alpha) (EC 2.7.1.67)	Homo sapiens (Human)
O94827	Pleckstrin homology domain-containing family G member 5 (PH domain-containing family G member 5) (Guanine nucleotide exchange factor 720) (GEF720)	Homo sapiens (Human)
Q9UKA9	Polypyrimidine tract-binding protein 2 (Neural polypyrimidine tract-binding protein) (Neurally-enriched homolog of PTB) (PTB-like protein)	Homo sapiens (Human)
P78424	POU domain, class 6, transcription factor 2 (Retina-derived POU domain factor 1) (RPF-1)	Homo sapiens (Human)
Q6ICB4	Sesquipedalian-2 (Ses2) (27 kDa inositol polyphosphate phosphatase interacting protein B) (IPIP27B)	Homo sapiens (Human)
Q86Y26	NUT family member 1 (Nuclear protein in testis)	Homo sapiens (Human)
O15355	Protein phosphatase 1G (EC 3.1.3.16) (Protein phosphatase 1C) (Protein phosphatase 2C isoform gamma) (PP2C-gamma) (Protein phosphatase magnesium-dependent 1 gamma)	Homo sapiens (Human)

Codigo UniprotKB	Protein names	Organism
P18583	Protein SON (Bax antagonist selected in saccharomyces 1) (BASS1) (Negative regulatory element-binding protein) (NRE-binding protein) (Protein DBP-5) (SON3)	Homo sapiens (Human)
Q8WUD1	Ras-related protein Rab-2B	Homo sapiens (Human)
B7Z7W2	cDNA FLJ55558, highly similar to Regulating synaptic membrane exocytosis protein 1	Homo sapiens (Human)
Q8NE09	Regulator of G-protein signaling 22 (RGS22)	Homo sapiens (Human)
Q96R05	Retinoid-binding protein 7 (Cellular retinoic acid-binding protein 4) (CRABP4) (CRBP4) (Cellular retinoic acid-binding protein IV) (CRABP-IV)	Homo sapiens (Human)
A6NKG5	Retrotransposon-like protein 1 (Mammalian retrotransposon derived protein 1) (Paternally expressed gene 11 protein) (Retrotransposon-derived protein PEG11)	Homo sapiens (Human)
Q7L7X3	Serine/threonine-protein kinase TAO1 (EC 2.7.11.1) (Kinase from chicken homolog B) (hKFC-B) (MARK Kinase) (MARKK) (Prostate-derived sterile 20-like kinase 2) (PSK-2) (PSK2) (Prostate-derived STE20-like kinase 2) (Thousand and one amino acid protein kinase 1) (TAOK1) (hTAOK1)	Homo sapiens (Human)
Q9UBN4	Short transient receptor potential channel 4 (TrpC4) (Trp-related protein 4) (hTrp-4) (hTrp4)	Homo sapiens (Human)
Q562F6	Shugoshin-like 2 (Shugoshin-2) (Sgo2) (Tripin)	Homo sapiens (Human)
O43805	Sjoegren syndrome nuclear autoantigen 1 (Nuclear autoantigen of 14 kDa)	Homo sapiens (Human)
Q13621	Solute carrier family 12 member 1 (Bumetanide-sensitive sodium-(potassium)-chloride cotransporter 2) (Kidney-specific Na-K-Cl symporter)	Homo sapiens (Human)
Q9NPD5	Solute carrier organic anion transporter family member 1B3 (Liver-specific organic anion transporter 2) (LST-2) (Organic anion transporter 8) (Organic anion-transporting polypeptide 8) (OATP-8) (Solute carrier family 21 member 8)	Homo sapiens (Human)
Q8NA61	Spermatid-associated protein (Protein chibby homolog 2)	Homo sapiens (Human)
Q92502	StAR-related lipid transfer protein 8 (Deleted in liver cancer 3 protein) (DLC-3) (START domain-containing protein 8) (StARD8) (START-GAP3)	Homo sapiens (Human)
Q6ZVD7	Storkhead-box protein 1 (Winged-helix domain-containing protein)	Homo sapiens (Human)
Q6ZVM7	TOM1-like protein 2 (Target of Myb-like protein 2)	Homo sapiens (Human)
Q9Y4A5	Transformation/transcription domain-associated protein (350/400 kDa PCAF-associated factor) (PAF350/400) (STAF40) (Tra1 homolog)	Homo sapiens (Human)
Q9HCF6	Transient receptor potential cation channel subfamily M member 3 (Long transient receptor potential channel 3) (LTrpC-3) (LTrpC3) (Melastatin-2) (MLSN2)	Homo sapiens (Human)
Q8NDV7	Trinucleotide repeat-containing gene 6A protein (CAG repeat protein 26) (EMSY interactor protein) (GW182 autoantigen) (Protein GW1) (Glycine-tryptophan protein of 182 kDa)	Homo sapiens (Human)
P09661	U2 small nuclear ribonucleoprotein A' (U2 snRNP A')	Homo sapiens (Human)
Q14376	UDP-glucose 4-epimerase (EC 5.1.3.2) (Galactowaldenase) (UDP-N-acetylgalactosamine 4-epimerase) (UDP-GalNAc 4-epimerase) (UDP-N-acetylglucosamine 4-epimerase) (UDP-GlcNAc 4-epimerase) (EC 5.1.3.7) (UDP-galactose 4-epimerase)	Homo sapiens (Human)
Q8N4C9	Uncharacterized protein C17orf78	Homo sapiens (Human)
A3KMH1	von Willebrand factor A domain-containing protein 8	Homo sapiens (Human)
Q93050	V-type proton ATPase 116 kDa subunit a isoform 1 (V-ATPase 116 kDa isoform a1) (Clathrin-coated vesicle/synaptic vesicle proton pump 116 kDa subunit) (Vacuolar adenosine triphosphatase subunit Ac116) (Vacuolar proton pump subunit 1) (Vacuolar proton translocating ATPase 116 kDa subunit a isoform 1)	Homo sapiens (Human)
Q9H040	SprT-like domain-containing protein Spartan (DNA damage protein targeting VCP) (DVC1) (Protein with SprT-like domain at the N terminus) (Spartan)	Homo sapiens (Human)
C8C504	Beta-globin	Homo sapiens

Codigo UniprotKB	**Protein names**	**Organism**
		(Human)
B4DUI8	cDNA FLJ52761, highly similar to Actin, aortic smooth muscle	Homo sapiens (Human)
B4E1D3	cDNA FLJ53952, highly similar to Fibrinogen beta chain	Homo sapiens (Human)
E1B2D1	Hemoglobin alpha-1 globin chain variant (Fragment)	Homo sapiens (Human)
O60462	Neuropilin-2 (Vascular endothelial cell growth factor 165 receptor 2)	Homo sapiens (Human)
D3DTX7	Collagen, type I, alpha 1, isoform CRA_a	Homo sapiens (Human)
Q06278	Aldehyde oxidase (EC 1.2.3.1) (Aldehyde oxidase 1) (Azaheterocycle hydroxylase) (EC 1.17.3.-)	Homo sapiens (Human)
P16410	Cytotoxic T-lymphocyte protein 4 (Cytotoxic T-lymphocyte-associated antigen 4) (CTLA-4) (CD antigen CD152)	Homo sapiens (Human)
O95067	G2/mitotic-specific cyclin-B2	Homo sapiens (Human)
Q12905	Interleukin enhancer-binding factor 2 (Nuclear factor of activated T-cells 45 kDa)	Homo sapiens (Human)
Q9NRZ9	Lymphoid-specific helicase (EC 3.6.4.-) (Proliferation-associated SNF2-like protein) (SWI/SNF2-related matrix-associated actin-dependent regulator of chromatin subfamily A member 6)	Homo sapiens (Human)
Q96KB5	Lymphokine-activated killer T-cell-originated protein kinase (EC 2.7.12.2) (Cancer/testis antigen 84) (CT84) (MAPKK-like protein kinase) (Nori-3) (PDZ-binding kinase) (Spermatogenesis-related protein kinase) (SPK) (T-LAK cell-originated protein kinase)	Homo sapiens (Human)
Q8TF21	Ankyrin repeat domain-containing protein 24	Homo sapiens (Human)
B3KS49	cDNA FLJ35478 fis, clone SMINT2007796, highly similar to Gelsolin	Homo sapiens (Human)
B4DYU2	cDNA FLJ55996, highly similar to Conserved oligomeric Golgi complex component 8	Homo sapiens (Human)
A8K964	cDNA FLJ75071, highly similar to Homo sapiens pinin, desmosome associated protein (PNN), mRNA	Homo sapiens (Human)
Q8IVB5	LIX1-like protein	Homo sapiens (Human)
Q9HCH0	Nck-associated protein 5-like (NCKAP5-like) (Centrosomal protein of 169 kDa) (Cep169)	Homo sapiens (Human)
Q7Z517	Transgelin	Homo sapiens (Human)
Q9Y2G0	Protein EFR3 homolog B	Homo sapiens (Human)
Q8NFI4	Putative protein FAM10A5 (Suppression of tumorigenicity 13 pseudogene 5)	Homo sapiens (Human)
Q13892	Deleted.	
A2J1N9	Rheumatoid factor RF-ET12 (Fragment)	Homo sapiens (Human)
G5E940	RING finger protein 32 (Ring finger protein 32, isoform CRA_a)	Homo sapiens (Human)
Q8WUE5	Cancer/testis antigen 55 (Tumor antigen BJ-HCC-20)	Homo sapiens (Human)
B1ANS9	WD repeat-containing protein 64	Homo sapiens (Human)